



# User manual 2.13



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# Miscellaneous

## Revision History

Version number	Modification done
1	Initial version

## Notification of Serious Incident

Any serious incident in connection with the device should be notified to the manufacturer at the following email address and/or phone number:

email address: [regulatory@intrasense.fr](mailto:regulatory@intrasense.fr)

phone number: +33 467 130 134

and to the competent authority of the Member State in which the user and/or patient is established

## Request for IFU in paper format

Instructions for use are provided to user as e-documentation. Request for IFU in paper format can be done by the user by sending an email to [support@intrasense.fr](mailto:support@intrasense.fr) , and Intrasense undertake to provide it at the latest within 7 calendar days.

## Key to symbols

In this document, you will see the following symbols:



Caution, extracted from ISO 15223-1: 2021

---



Describe Technical or functional aspects of the software.

---



Tooltips or advanced functions which may help save time.

---

Throughout this manual the terms 'click' and 'clicking' without any other indication refer to a single click performed with the left button of the mouse.

## Intellectual Property

Intrasense® and Myrian®, all logos, slogans, trade names, and marks appearing in this document, whether registered or not, are the exclusive property of Intrasense, unless otherwise stated.

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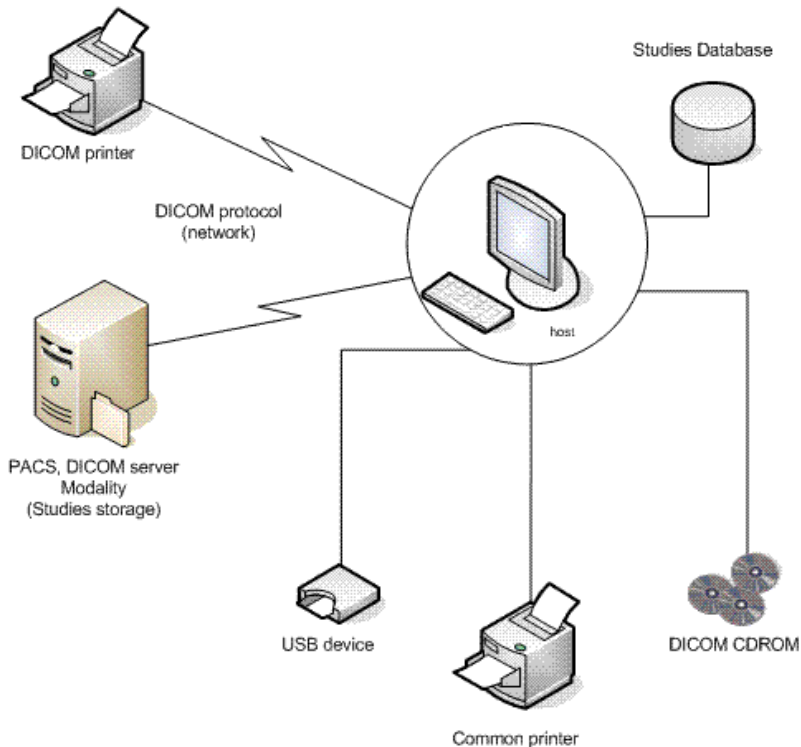


## 2 Device

Myrian® is a medical device software for processing, management, advanced visualization and analysis of multi-modality medical images.

Myrian® is designed to be run:

- on any "off the shelf" standard computer with a Microsoft Operating System, that might be purchased independently by the user
- Remotely, through a network connecting a Client Platform (standard desktop or laptop PC, Apple® Mac, etc.) to the Server Platform on which Myrian® is installed. This mode of usage of the Myrian® application is called "Remote Execution Mode".



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Basic UDI-DI : 37007197MyrianGW . The UDI is displayed in the «about» tab of Myrian.

This product uses the OFFIS DICOM Toolkit DCMTK (C) 1993-2006, OFFIS e.V. and the ECP registration technology © ECP-2008, under ECP patent license agreement.

Myrian® also includes the following open source codes:

- openssl - Copyright ©1998-2011, the OpenSSL Project. All rights reserved. This product includes software developed by the OpenSSL Project for use in the OpenSSL Toolkit (<http://www.openssl.org/>)"

Microsoft® Windows® and Microsoft® Word® are registered trademarks of Microsoft®.

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All screenshots/instructions/specifications are non contractual and subject to change without prior notice

# 3 Intended Use

## 3.1 Intended Use of Myrian® software suite

Myrian® is a medical device software for processing, management, advanced visualization and analysis of multimodality medical images. Myrian® is not intended to propose a diagnosis or a treatment. Myrian® is intended to provide information which is used to take decisions with diagnosis or therapeutic purposes, it assists decision making for radiologists and other physicians without replacing their judgment. The information provided is not intended in clinical management to trigger an immediate or near term action.

Myrian® also includes DICOM communication, media interchange (printing, CD burning, storing) and reporting features.

Myrian® can be run:

- on any "off the shelf" standard computer with a Microsoft Operating System, that might be purchased independently by the user
- remotely, through a network connecting a client Platform to the server platform on which Myrian® is installed. This mode of usage of the Myrian® application is called "Remote Execution Mode".



Certain functions described in this manual may not be accessible in your version of Myrian®

---

## 3.2 Intended Use of XM-MR Module

Myrian® XM MR is an application dedicated to the visualization and analysis of MR images. The application provides visualization, quantification and correction tools for clinical routine requiring MR images. Myrian® XM MR provides information that can be used to help to take decisions with diagnosis or therapeutic purposes.



The user of the Myrian® XM MR must be aware that the application does not diagnose lesion and does not provide therapeutic suggestions. As Myrian®, XM MR allows visualization and correction of the results computed, the user is fully responsible for the quality of data and decisions taken based on the results of the use of the tools.

---

### 3.3 Intended Use of XM-CT Module

XM CT is an application dedicated to the visualization and analysis of CT images. The application provides visualization, correction and quantification tools for clinical routine requiring CT images and automatic detection of suspected lung lesions. Myrian XM CT provides information that can be used to help to take decisions with diagnosis or therapeutic purposes.



The user of the Myrian® XM CT must be aware that the application does not diagnose lesion and does not provide therapeutic suggestions. As Myrian®, XM CT allows visualization and correction of the results computed, the user is fully responsible for the quality of data and decisions taken based on the results of the use of the tools.

---

### 3.4 Intended Use of XM-NM Module

Myrian® XM NM is an application dedicated to the visualization and analysis of PET/CT and NM/CT images. The application provides visualization, quantification and correction tools for clinical routine requiring PET/CT and NM/CT images. Myrian® XM NM provides information that can be used to help to take decisions with diagnosis or therapeutic purposes.



The user of the Myrian® XM NM must be aware that the application does not diagnose lesion and does not provide therapeutic suggestions. As Myrian®, XM NM allows visualization and correction of the results computed, the user is fully responsible for the quality of data and decisions taken based on the results of the use of the tools.

---

### 3.5 Intended users

The intended users are radiologists and radiologist technicians.

### 3.6 Intended target group

The patient population is any adult or child who has undergone a prescription medical imaging examination from a physician who is looking for any information that may help in his decision-making for diagnostic or therapeutic purpose.

### 3.7 Contraindications

There are no contraindications, as Myrian® software does not interact directly with the patient and/or the user.

# 4 Clinical Claims - Performance

## 4.1 Clinical Benefit claimed

Benefit claimed are the same for the whole device including the variants.

Device	Benefit for user	Benefit for patient	Benefit for institution
Myrian® software suite	Improve clinicians reading speed and accuracy	Improve the strategy/decision making by providing reliable patient information data Optimize care pathway by enhancing reading speed of imaging exams.	Records of measures and annotations allow us to save time on specialist decisions and to optimize patients' clinical workflows.

## 4.2 Safety claims

Myrian® software demonstrates a freedom from unacceptable clinical risks, when using the device according to the manufacturer's Instructions for Use

## 4.3 Performance Characteristics of the Device

### Myrian® Platform

Myrian® Platform is the minimum configuration of the Myrian® solution suite. It enables visualization of multimodalities images and the provision of essential analysis tools for reliable identification and analysis of regions of interest and ensures a comparative follow-up.

### Myrian® XM-MR

Myrian® XM-MR allows anatomical structures visualization of MR images. It provides advanced analysis tools to identify and analyze regions of interest, compare exams, and quantification tools to determine iron load and concentration.

### Myrian® XM-CT

Myrian® XM-CT allows anatomical structures visualization in CT images. It provides reliable visualization and analysis tools allowing to identify and analyze regions of interest and exam comparison.

### Myrian® XM-NM

Myrian®XM-NM allows visualization of functional medical images with anatomical imaging (PET/CT and NM/CT). Advanced analysis tools provide reliable identification and analysis of region of interest, and exam comparison.

# 5 Warnings

## Please read carefully before use

### 5.1 Restrictions of use



Copies of this software and/or functionalities bearing the labels “Alpha”, “Alpha-Prime”, “Beta” or “Non-MD (Not for clinical Use)” must under no circumstances ever be used for diagnostic purposes.



Caution: US Federal Law restrict this device to sale by or on the order of a trained medical professional, including surgeon, radiologist, clinician and technician.



Myrian® must not be used on portable devices such as a mobile phones or tablet computers for diagnostic purposes.



This software is a Medical Device as defined in the Medical device regulation 2017/745. Before use, please make sure that you have thoroughly read and fully understood all the safety and regulatory considerations outlined in this section.



Intrasense assumes no liability for any misuse or clinical outcome resulting from the use of the software as an aid to diagnosis. The software is made available to the User with the understanding that the software is only an aid or adjunct to processes or decisions that can be made without the use of the software.



The software is designed as a visual aid and as such it is not recommended for use in applications where the image geometry or the fused image geometry (as displayed by the software application) cannot be confirmed by other means. The software should not be used as the sole basis for surgical planning, or the preparation, execution or post-operative assessment of surgical practices.

### 5.2 User Warnings



This medical software in no way replaces the competence and judgment of a qualified medical practitioner. It should only be used by qualified and trained persons who are fully aware of the software potential and limitations in the lesion detection by scanning method.

### 5.3 Images Warnings



The User should be aware that Myrian® makes use of certain technologies that interpolate within the data provided. In cases where the pathology is near to or smaller than the resolution at which the data is acquired by the medical apparatus, the generated data may sometimes resemble healthy tissue. Occasionally, such interpolated data may equally lead to artefacts which should be identified and considered as such. The User should always refer to the image analysis performed in native mode.



The User should be aware of the relative precision and validity of any results arising from the use of Myrian® (displayed,

printed or exported). The quality of the data generated by the software is directly dependent on the original quality of the data provided and any potential manipulation by the User as well as the quality, nature and configuration of the display (or print medium) and the need to interpolate data for the purposes of display. As an example, measurement values given by Myrian® depend entirely on the calibration settings found in the DICOM image's header.



Whenever 32-bit native images are imported in Myrian®, those images are by default converted into 16-bit images which may result in the information loss in terms of image intensities.



Some DICOM image formats include a module called « Real World Value Mapping » (described in DICOM Standard part 3, supplement 103). Myrian® supports commonly used values. For security reasons, when some of those unsupported values are detected, Myrian® impedes the display of all measurements/calculations based on image intensities (i.e. "n/a" mention on measurements, parametric map computations, etc.)



The modality operator is responsible for the quality of the input data and the correctness of the patient information. Suboptimal data may induce suboptimal results.



This product has been designed to function on DICOM standard 3.0 complete data sets. There should be no missing images within the data set and the software should not be used to process interpolated data. If slices from the image data set are missing then the results are not reliable.



In your Institution, Data compression may be performed to facilitate transmission and storage. Several methods exist which may be used with no reduction in clinical diagnostic image quality, including both reversible ("lossless") and irreversible ("lossy") techniques. These methods should be used under the supervision of a qualified physician who should be responsible for choosing and periodically reviewing the types of compression used to ensure appropriate clinical image quality.



If the User opens any image which is in "lossy" format, the message 'image with lossy compression' is displayed on the corresponding image(s). The compression ratio display is available following the procedure described in the User Manual



We advise you against using DICOM images with lossy compression.



The software operator is responsible for quality control of the images. The quality of the acquisition may have an impact on the quality of the algorithm result. The radiologist must check the quality of the acquisition before interpreting the algorithm results.



Lossy compressed images and digitized film screen images must not be used for primary image interpretations.

## 5.4 ROI Warnings



Using CT scans outside the recommended parameters is not recommended and may result in inaccurate results for the identification of ROIs.



The segmentation engine performance results may be limited by the following factors:

- The quality of the image data provided as input to the segmentation engine for analysis.
- The training and experience of the clinical users in acquiring image datasets and applying post-processing software

application.

- The User's command of the functionality and application of the segmentation engine.



The User should visually check that the ROI segmentation is correct. If not correct, the User should re-segment the ROI.



Myrian® takes ROI superimposition into account. Any voxels that are shared between several ROI are counted only once.

## 5.5 Measures Warnings



As a Medical Device, Myrian® is subject to specific requirements regarding the display of measurements. In this regard, all metric units displayed in Myrian® and belonging to the Metric International System enforce the requirements of the BIPM ("Bureau International des Poids et Mesures").



When using Combined Measurements, the User must be aware that errors, inconsistencies or mistakes may arise in their definition, in particular:

- The unit of measurement may not match that used in the actual formula
- The Combined Measurement Name might not match the corresponding Description
- The Name and/or Description of the Combined Measurement may bear little or no relation to its Formula, or may be ambiguous
- Existing Formulas may contain errors, such as "operand" or "variable definition" errors
- Accidental match-ups between certain ROI and certain variables may generate Combined Measurement errors
- Combined Measurements are reconfigurable. It may therefore occur that a given factory preset may no longer be configured according to its original parameters.



Intrasense provides a number of factory Combined Measurement presets which are intended as examples, however we do not guarantee the exactitude of computed results in a clinical context. Intrasense can only warrant the exactitude of results obtained from the computation of factory preset formulas using the original factory values of variables.



Careful checking and counter-verification using other measurement methods should always be performed to validate results.



Although Myrian® software is subjected to very thorough and intensive testing by Intrasense, it is nevertheless possible that unforeseen measurement and display errors may arise during use of this software. Users should at all times be aware and warned of such an eventuality. Should the User notice any dysfunctions or faulty behaviour of the software liable to put the patient at risk, we strongly recommend that the User contacts Intrasense without delay at the following email address: [support@intrasense.fr](mailto:support@intrasense.fr)



The accuracy of the measurements displayed in Myrian® depends on the image resolution. The accuracy performance is equal to the physical voxel of the image (this information is provided in the DICOM tag).



The actions of the User may directly affect the accuracy of functions within the software environment.



It may occur that some Measurements do not match-up absolutely to anatomical measurements in the actual patient volume.





It is the sole responsibility of the User to create, modify and use any Combined Measurement in the context of diagnosis.

## 5.6 Hardware Warnings



For diagnosis on mammography images, be sure to use a certified screen.



This product should only be used with approved hardware and software. Please refer to the 'Release Notes' available in 'C:\Program Files\Intrasense\Myrian\doc' for further details.

## 5.7 Cybersecurity Warnings



For security reasons, we strongly encourage upgrading to Adobe Reader X (10) where possible to view 3D PDF files. If you upgrade to the new Adobe Reader, a separate install of Flash Player will be required by the Adobe Reader, rather than using a built-in system which was previously the case in anterior and current versions and was source of vulnerability problems.



Myrian® treats image data originating from medical Studies which may potentially contain information that identifies individual patients both in the local database and through the export of data. Even though this data encryption is disabled by default, it is the User's responsibility to prevent unauthorized access.

## 5.8 Printing



For true-size (1:1) size printing, please ensure that the DICOM Server used for printing has been properly configured for 1:1 printing to avoid any potential error.



When using 1:1 size printing functionality, please be sure to check carefully that all values which appear on the printed copy strictly match all those displayed on screen before proceeding with any critical task concerning patient security.



True-size printing may not function properly in cases when the selected the paper format does not match the actual paper size.

## 5.9 Miscellaneous



The term 'Matching' relates to the process enabling to identify and thus pair equivalent anatomical structures from two (or more) distinct series belonging to the same patient. At no time will the User access deformed anatomical or functional images.



When a Matching process between series is performed, always check the resulting synchronization validity, particularly when those series have few anatomical references such as in functional imaging (for example, diffusion series).



The image Scrapbook functionality is intended for storing images along with any Annotations to provide a qualitative overview of data. Under no circumstances should it ever be used as a primary diagnostic means.



Surfacic ROI Mode is not suitable for Diagnostic Purposes.



Clinical decisions should never be based solely and entirely upon these results. You must correlate the interpretation with the original 2D images.



LCD screens and computer projection systems may affect the display of imagery in a way which may alter perception. The display settings in Windows® should be set via the graphics card driver to the highest resolution available and the area displayed should be adjusted to preserve height/width aspect ratio (black borders may appear). Please note that such distortion of the picture quality, known as anamorphosis does not affect the accuracy of any type of measurement made or displayed in Myrian®.



The 'Set ROI' feature should only be used in 2D planes and not in the 3D Fly through. Placing a seed point on a 3D volumetric reconstruction cannot give an accurate location.



The CAD software is a detection aid, not an interpretive aid. Solely relying on CAD may lead to wrong diagnosis. Use it only after you read the images. Always read first before turning on CAD. Never change your mind about a potential finding if CAD does not mark it.



Some parts of the series may not be pre-processed by the CAD. However, the CAD is a detection aid. The absence of CAD findings does not mean the absence of potential lesions.



The CAD processing time can be up to 7 minutes. In the meantime, you can not have access to the CAD findings.

# 6 Installation guidelines

Pre-requisite before use and installation instruction

## 6.1 Hardware and software configuration



Please refer to the latest Myrian® Release Notes included in the 'Doc' folder of your installation package for detailed Configuration Specifications.



Myrian® is designed to run on a Microsoft Operating System; therefore, it is NOT compatible with Linux or MAC OS Operating Systems.



Myrian® is not supported on Windows Vista, Windows 7 & Windows 8 Operating Systems.



The minimum configuration is the minimal required for Myrian® to run according to specifications.



The system might run on computers not matching the minimal system configuration but it will not be supported by Intrasure.



Upgrading Myrian® from versions of Myrian® which are older than the 2.0 might require hardware upgrades to maintain the same level of performance.



Myrian® may run on systems with 16 or 24 bit graphics cards, however this configuration does not deliver diagnostic quality images so it is no longer supported.



Recommended resolution is 1600 x 1200/32 bits (or at least 1280 x 1024/32 bits), with the exception of certain specific modalities (MG...).

To set screen resolution parameters, Right-click on the Windows® desktop, Select 'Display settings' from the resulting context menu; in the opened window, select 'Display Resolution'; finally, modify the resolution section as required.



Myrian® provides DICOM data exchanges features in accordance with the 'Dicom Conformance Statement' available in the 'Doc' folder of the installation folder of the application.

## 6.2 Antivirus protection



The End-user should ensure that the workstation on which this software is installed is at all times adequately protected against virus/worm contamination by installing and periodically updating appropriate anti-virus software. No particular anti-virus software is recommended by Intrasure.

## 6.3 PDF 3D



Initially, opening a 3D PDF does not show 3D content. It can be enabled by simply setting the menu check-box at “Edit - Preferences – 3D and Multimedia Content – Enable 3D content”. As Adobe Reader X has a stronger security model, this change is not required if you upgrade.

Moreover, a warning yellow message bar also appears regarding viewing untrusting documents.

We also recommend you to disable Adobe Reader X automatic updates:

- Open Adobe Reader application and Choose Edit > Preferences
- In the categories on the left, click on Updater and choose ‘Do not download or install updates automatically’
- Click OK.

## 6.4 Screen Calibration



It may be necessary/mandatory to adjust the brightness and contrast settings of your monitor after installation to adapt to ambient lighting conditions. A badly adjusted screen may compromise your interpretation and analysis of medical images.

A **screen calibration tool, ‘ISCalibrator’** is integrated in this software. It is launched automatically the first time the software is run. Until the calibration has been completed, it will continue to be launched every time you run the application. You can also access **ISCalibrator** directly via the ‘Preferences/Display’ tab. It is strongly recommended to perform this calibration (please refer to Myrian® Installation Manual for further details).



Note: For mammography, please use IS Calibrator tool in MG mode.

## 6.5 Recommendations concerning your work environment

Working for prolonged periods of time on a computer can cause hazards to your health, including fatigue, impaired vision, muscular pain, poor blood circulation, strain on certain joints and general physical or mental stress.

Take a moment to consider your daily routine and establish a preventive strategy for such hazards. Modifying the position, layout or lighting of your desktop and using furniture which is more conducive to a healthy posture will help to improve your working conditions.

## 6.6 Automatic user log off after inactivity

In order to protect against unauthorized use or disclosure of individual health information in compliance with the HIPAA (Health Insurance Portability and Accountability Act, in the USA), you are automatically logged off in the following cases:

Myrian® and the Operating System remain idle for 5 minutes. In that case, a login dialog box appears asking you to re-enter your password or click “Quit” to close the application. The login cannot be changed.

When Myrian® and the Operating System remain idle for 6 minutes, the application is closed.

During the initial login when Myrian® is started, if no valid login is entered for more than 6 minutes, the application is closed.

## Chapter 7

# 7 MYRIAN PLATFORM

User Interface changes

User interface will clearly highlight Research only objects with the 'Not for clinical use' message. All workspace elements, like views and viewports, usually know which protocol they come from, so they know their status (MD or Research).

## 7.1 Protocols

In the protocol selection screen, we display a 'NON MD' icon on protocols that are not certified.

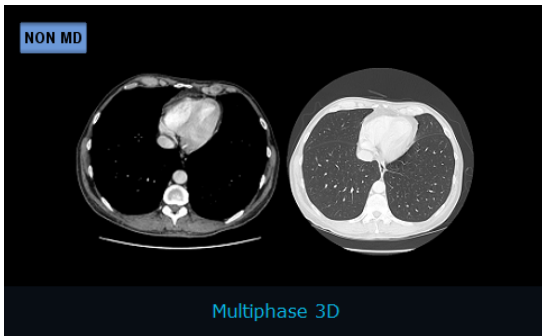


Figure 7-1 Protocol with 'NON MD' icon



If for some reason all protocols appears with the 'NON MD' icon, please contact Intrасense Support Team at [support@intrasense.fr](mailto:support@intrasense.fr) in order to check the validity of the certification zone.

## 7.2 'About' tab

In the «about» tab, you will find the legal information about the product. You will find information about contributors, non medical device applications and a regulatory tab.

## 7.3 'Regulatory' tab

In this tab, we will list all the medical devices that we have, for each certification zone (CE, FDA, etc). Each medical device is identified with a name, an UDI and a logo. A RTF file with General Terms of Use is available.

The GTU should contain the contact/address of the manufacturer (because it was removed from the "About" tab) and it is shown for the current language when available, English otherwise.

For partners distributing their own product with their own marking, they must provide an xml file. The file must be called **thirdparty.xml** and it should be available in the runtime folder. It is not part of our setup. It will be added by the partner in his own setup or in the master.

## 7.4 Title bar

In the title bar, we add a 'regulatory' icon with a tooltip. The tooltip will display the name of the medical device that is linked with the clinical application, or a line of text that says it is not a medical device. When clicking the icon, we display the about box and select the corresponding medical device.

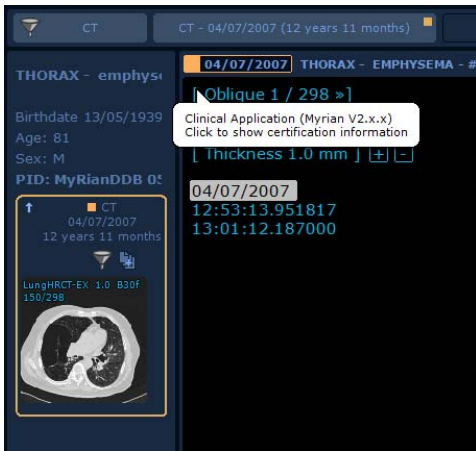


Figure 7-2 'Regulatory' annotation

For 'NON MD' views, we also display the 'NON MD' icon is centred in the view title:



Figure 7-3 'NON MD' in 'View Title' bar

## 7.5 Scrapbook/Print Composer

For all screenshots taken in a non MD view (=with 'not for clinical use' displayed on the viewports), we will include the 'not for clinical use' message inside the screenshot image (as a private DICOM field 0x1180). The scrapbook will detect that field and print the message on the screenshot, at the bottom center. We will also include the standard DICOM field (0018,9004) called 'Content Qualification' with the value 'RESEARCH'.

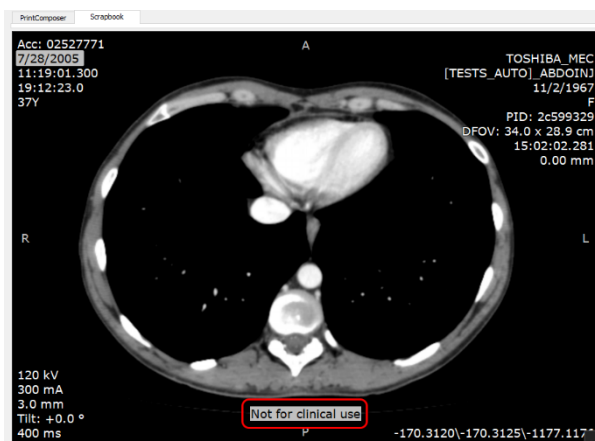


Figure 7-4 'NON MD' in 'Scrapbook/Print Composer' key image

## 7.6 Reports

When we generate a report (rtf or pdf) from a research context, we add a 'Not for clinical use' mention.

For RTF reports this will be added in the 'address' field.

For CRF reports (PDF) this will be added in the footer, next to the page number.

## 7.7 Main Windows

Main windows that are not part of a medical device will display 'Nor for clinical use' at the top of it:

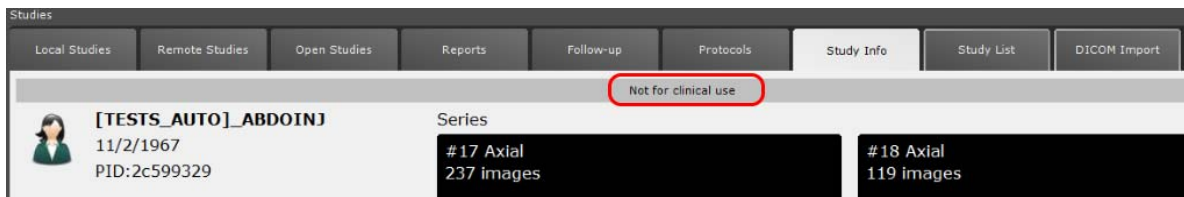


Figure 7-5 'NON MD' in main windows

## 7.8 Access to documentation

The access to the documentation is available in the «Support» tab. The «User Manual» button allows you to access the user manual, addendum, quick user guide and installation manual.

In addition, Myrian's label is displayed in the software's «about» tab

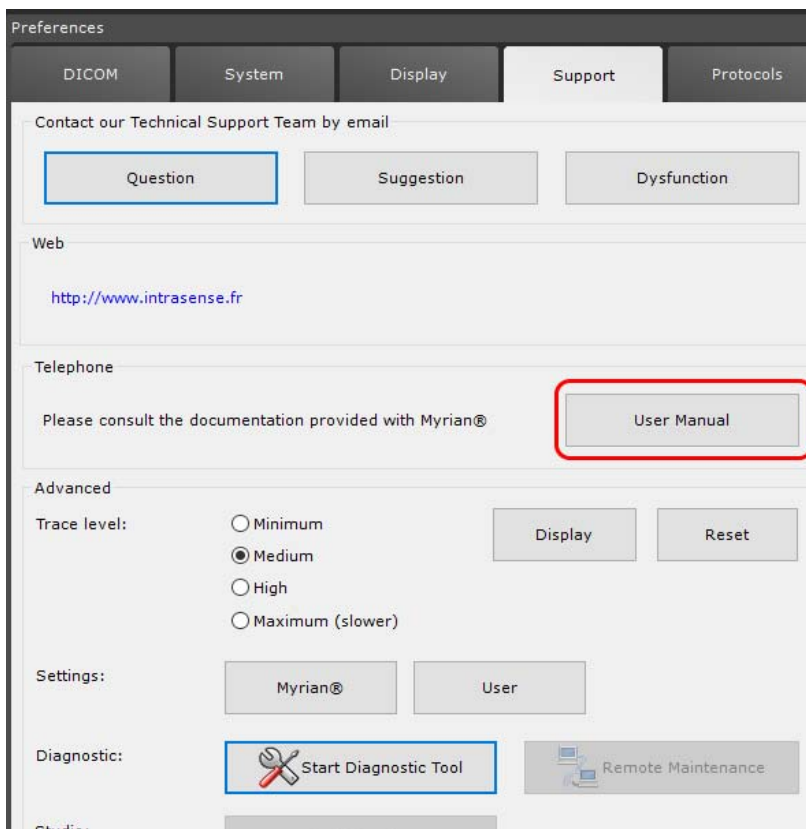


Figure 7-6 Documentation access in 'Support' tab



## Chapter 8

# 8 Start-up/Shutdown and User Management



All screens, sections and windows in Myrian® that have a cross or ✕ button in the upper right corner may be closed by clicking on it.

---

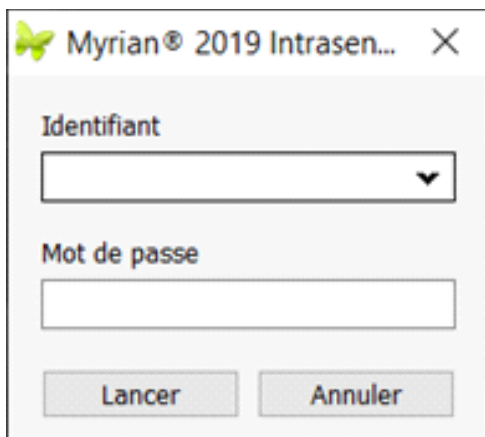
### 8.1 Opening the application and starting a session

- To **launch** the application, double-click on the Myrian® icon available from the Windows® desktop:

If the icon cannot be found:

- Open the 'Start' menu on the taskbar, at the bottom-left corner of the Microsoft® Windows® desktop,
- Open the 'Programs' folder (or 'All Programs'),
- Open the 'Intrasense' folder,
- Click on 'Myrian'.

If 'ThirdPartyLogin' parameter is setup to '1', the 'Session opening' screen appears:



In order to start Myrian® session, first register your user name as well as your unique **Login** name and **password**.

Figure 8-1 Opening a session

If your Login name does not appear in the drop-down list in the 'Opening session' screen, ask the system administrator to create a user account (see Section 8.2).



When running the application for the very first time, the screen calibration tool starts up automatically. It is highly recommended that you run the calibration utility. The software will prompt you to do this operation at each session start-up until it has been completed (see Appendix 8 for further details).

---

## 8.2 Creating a new user

All **Myrian**® users must be registered. Before you can start, please register:

- A unique user name (Login)
- Your full name
- A password

'Privileges' should be defined for each user. 'Privileges' determine access rights to various functions in Myrian®.

The following privileges are available:

Privilege type	Rights
Administrator	Can create, delete and modify other user privileges (including passwords) as well as global settings that are common to all users
Operator	Can visualize, annotate, analyze and export Studies
Observer	Can visualize Studies (including tools for analysis) but cannot modify them in any way

Table 8-1 Users' rights

The initial user Login is named 'Admin'. The user of this account may create, delete or modify any other **user account** privileges and password. Its use is reserved for system administration personnel responsible for configuring Myrian®.



When Myrian® is used for the first time, the 'Admin' account's password is set to 'Myrian®'. The system administrator is strongly advised to change this password.

---

The user has the possibility to modify the password of the account directly on the 'Session opening' window (see Figure 8-1). To enable this change, the 'Session opening' window has to be edited in order to display the modifying button. Please request assistance from an Application Engineer from Intracense to implement this.

To **add new users**:



- Double-Click on 'SvcManager' icon  on the desktop to open the **Service Manager window** (see Section 8.2.3 for detailed information on SvcManager).

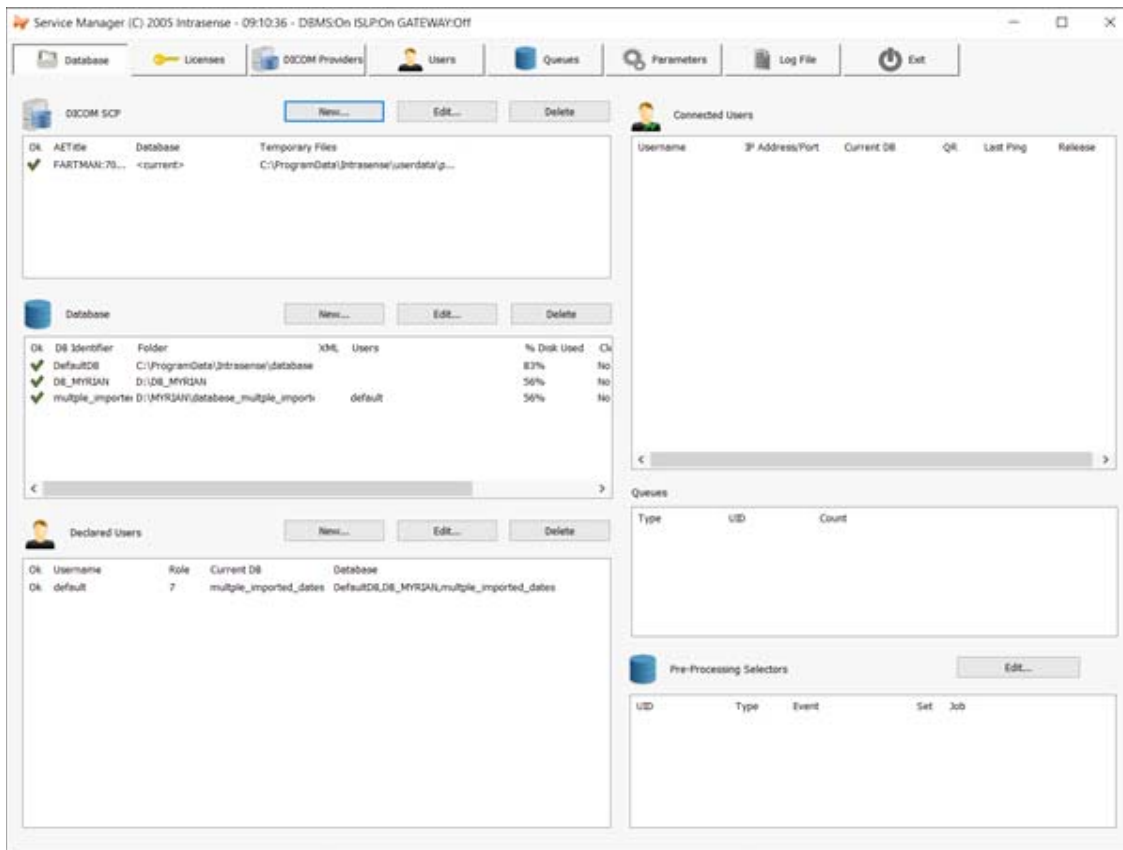


Figure 8-2 Service Manager window

- In the Declared Users section, click on 'New' and access the new user management window
- Open a session with the 'Admin' profile

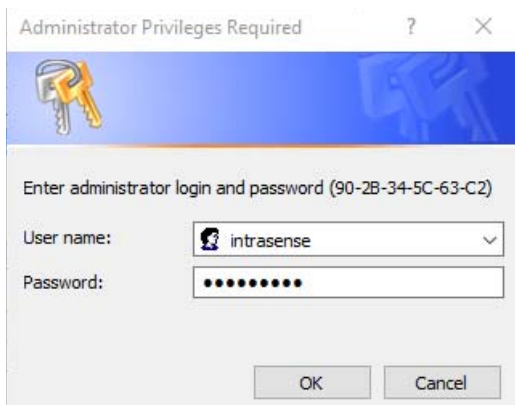


Figure 8-3 Identification window

The following 'User' window opens:

The screenshot shows a dialog box titled "User or User Group". It has a close button (X) in the top right corner. The dialog is divided into several sections:

- Login:** A text input field.
- Password:** A text input field.
- Real name:** A text input field.
- Buttons:** "Add..." and "Delete" buttons are located below the Real name field.
- License Group:** A large empty rectangular area.
- Current Database:** A text input field followed by a browse button "...".
- Authorized Databases:** A text input field followed by an "Add..." button.
- Footer:** A note stating "For the current database and the authorized database list, leave the field empty to use the default values (set with user named DEFAULT)". Below this are buttons for "Privileges...", "OK", and "Cancel".

Figure 8-4 Define User and Privileges screen

- Fill all fields with the **required login and database information**
- Define the user's **Role** clicking on the relevant button
- Confirm by clicking **OK**



Administrator rights enable total modification and/or deletion of other user accounts. Operators and Observers may change their own password.



For optimal security, passwords should include a combination of letters and digits. We also advise you to change your password regularly and keep track of it in a secure place.

## 8.3 Using Windows® user authentication to log on

On standard standalone platform, it is possible to set Windows® user authentication to identify yourself and log on to Myrian® application. In other words, when requested by the application, Myrian® will use Windows® password.

Accordingly, this allows you to use a fingerprint reader fitted on your computer to authenticate yourself instead of typing your Windows® password.

In order to activate the electronic signature of the records produced by Myrian® (that will force you to authenticate yourself by typing your Windows® password), please request assistance from an Application Engineer from Intrasense.

## 8.4 Quit session and Shut down



When you stop working, always close the session that you have opened. This will prevent someone else from using your identity.

To **close the Session:**

- Click on the main-screen button at the top-left of the screen.

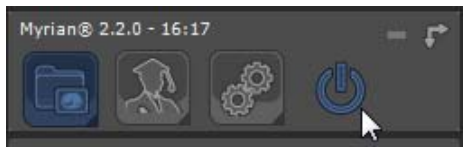


Figure 8-5 Close Session

Whenever you close a session, Myrian® saves your work as well as any preferences you may have changed. The 'Session opening' screen pops up once again (see Figure 8-1).

- To close the Myrian® application completely, click on **'Quit'**.

## Chapter 9

# 9 Study Folder: Load and Manage Studies

### Caution: Deactivated Mode/Disconnected Mode



If your application has not yet been activated, a dialog box prompts that your version of Myrian® is unauthorized. In this mode, you do not have access to all functionalities (see Appendix 9 for a comprehensive list of deactivated functions).



The installation guide (available on the application CD) includes a product activation guide. If you experience any problems with installation or activation, please contact Intrasure or an appropriate member of your establishment's IT staff.



Figure 9-1 Not Activated version pop-up screen



If your copy of Myrian® has been set-up to operate via a network and the connection is interrupted or lost, the software automatically switches to "Disconnected Mode". In this mode, the same function restrictions apply as in Deactivated Mode (see Appendix 9 for further details).

On the Main Window, the user has the possibility to show or hide the following tabs: 'Local Studies', 'Remote Studies', 'Open Studies', 'Reports', 'Follow-up', 'Protocols', 'Study Info', 'Study List', 'DICOM Import', 'Protocol Maker'. The tab displayed at the opening of Myrian can also be chosen.

By default, the Main Window contains the 'Local Studies', 'Remote Studies', 'Open Studies', 'Reports', 'Follow-up', and the 'Protocols' tab.

Please contact Intrasure's support to implement the modifications (see Section 1).

## 9.1 Local Study List

The 'Local Studies' tab lists all Studies contained in your Local Study Database.

Each Study appears in its own line, or row, which can be expanded to display all the Series it contains.

Each row contains all the DICOM fields pertaining to the Study and its Series laid out in adjustable columns.



All column widths and positions can also be modified by dragging the double arrow handles which appear when you place the mouse pointer over the boundary between two adjacent columns. Click and hold down the mouse button and 'drag' the cursor to the desired location, then release the button.



To change the position of a column, click on a column header (title) and drag the entire column to the desired position whilst holding the button down.

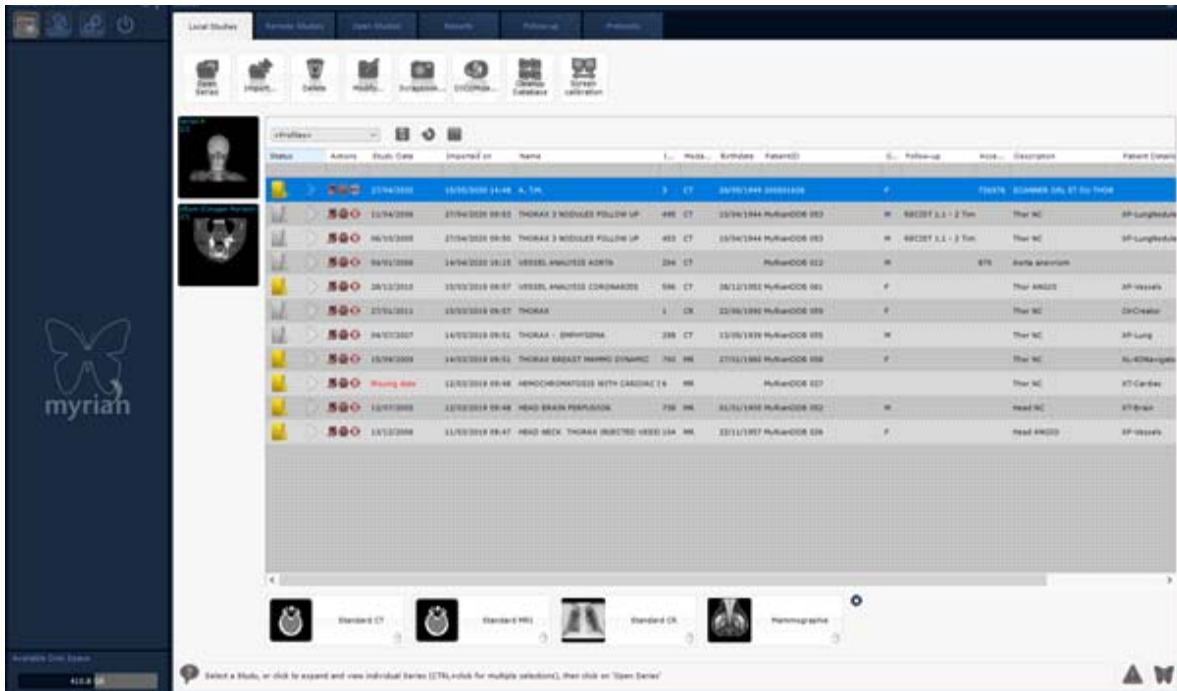


Figure 9-2 Local Study List

At the bottom-left of the main screen, you can view the available disk space of Myrian® database system.

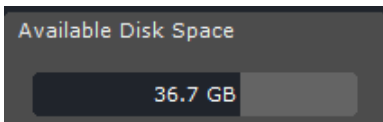


Figure 9-3 Checking the available disk space

When hovering the mouse cursor over the gauge, a tooltip appears indicating the path of the active database



Figure 9-4 Active database path

If you click on the gauge, a menu pops up enabling you to select the database to display (when several databases have been created) and also to open the User Preferences screen (see Section 8).

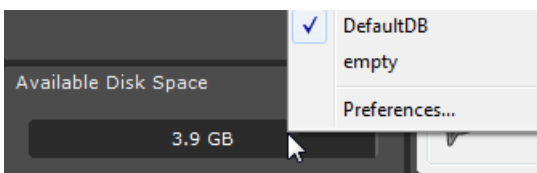


Figure 9-5 Selecting the database to display in the interface

### 9.1.1 Studies and Series

Each line represents a Study.

To view the list of Series contained in any single Study you must expand the Study line by clicking on the folder icon at left of the Study line.

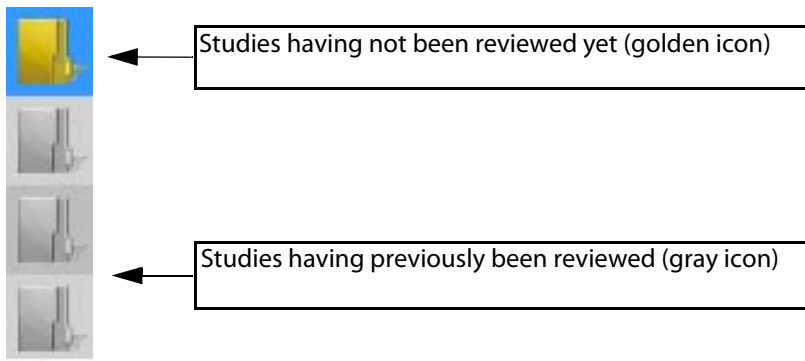


Figure 9-6 Expand Series



To help you differentiate newly imported data from existing data, the Study icon is golden if a Study has never yet been opened or gray if it has.

Study/Series/Subseries display:

- Each Series contained in the Study is displayed on its own line (see Figure 9-33),
- Information such as the number of images contained in the Series, the modality used to capture the Series, the Patient Identity, etc. is also displayed,
- If a number appears in the icon at the beginning of a Series then this number indicates the number of Subseries within the Series,
- If this number is greater than 5, an asterisk (\*) is displayed instead. These Subseries often correspond to multiple acquisitions within a given modality.

Columns contain all the information necessary to identify a Study. They include:

- Date of creation of Study,
- Patient Name,
- Number of images/slices contained in the Study/Series,
- Modality of capture,
- Patient's Date of Birth,
- Patient's Personal Identification number (PPID),
- Patient's Referring Physician.

Furthermore details such as Gender, Date of import, Study ID, Study Description, etc., are also visible. They may be accessed by scrolling right by means of the scroll bar at bottom of the Study list.

### 9.1.2 List display size

You can display the Studies/Series in the Study List as large or small icons according to your choice.

	2006/04/21	RAW_DATA_ECHO	1	US	1899/12/30	2336ba	MSK
	2006/01/05	RAW_DATA_ECHO	1	US	1899/12/30	267dbf	Adult Heart
	2005/11/21	RAW_DATA_ECHO	2	US	1899/12/30	5e5aea58	Breast
	2005/11/21	RAW_DATA_ECHO	1	US	1899/12/30	a0fabd9c	Breast

Figure 9-7 Study List (large icons)



2005/12/06	RAW_DATA_ECHO	1	US	1899/12/30	176b1c22	Adult Heart
2006/04/21	RAW_DATA_ECHO	1	US	1899/12/30	2336ba	MSK
2006/01/05	RAW_DATA_ECHO	1	US	1899/12/30	267dbf	Adult Heart
2005/11/21	RAW_DATA_ECHO	2	US	1899/12/30	5e5aea58	Breast
2005/11/21	RAW_DATA_ECHO	1	US	1899/12/30	a0fabd9c	Breast

Figure 9-8 Study List (small icons)

- To toggle the icon size large or small, check the 'Display the Study List with smaller icons' checkbox in the 'Miscellaneous' box of the Preferences>Display Tab

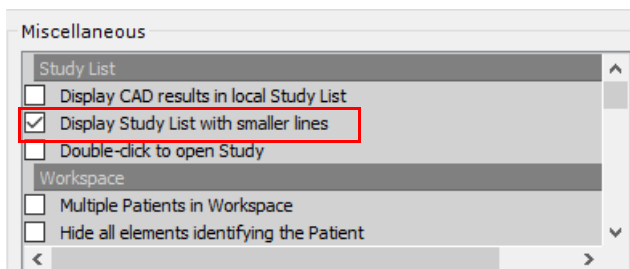


Figure 9-9 Display the Study List with smaller icons' checkbox in the 'Miscellaneous' box



You can collapse all currently open lines by holding the Control key down whilst clicking on any Study icon.

### 9.1.3 Filters

#### Overview

You can sort the Study List by Name, Status, Actions, Date, Study Type (Modality) or any other criteria.

You can also configure the order, type and size of columns as well as add new ones, etc.

All filters and column modifications can be saved as 'Profiles' for later use.

Column Configuration and Filtering Profiles are created, modified, saved and recalled via the Study List Configuration Toolbar at the top-left of the Study List.

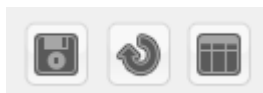


Figure 9-10 Study List Configuration Toolbar

### 9.1.4 Activate Filters

- Click on the Filter Criteria Bar directly underneath your desired Column Header,
- Type-in your condition.

Study Date	Name	Images	Modality	Birthdate	PatientID	Description
			CT			

Figure 9-11 Filter Condition bar

#### 9.1.4.1 Text filter

Depending on your search syntax for **text fields** and the fact that you can use the '\*' star mark before/between/after a 'text', the search results will be different.

Name	Images	Modality	Birthdate
onco*	--A--		
ONCO FOLLOW-UP LYMPHOMA PT + CT	348	CT/OT	03/09/1946
ONCO FOLLOW-UP LYMPHOMA PT + CT	709	CT/OT	03/09/1946
ONCO FOLLOW UP Series Selection Dashboard I 201		CT	
ONCO FOLLOW UP Selection Series Dashboard	281	CT	31/12/1946

Figure 9-12 Use of '\*' stars in Filter Conditions

When typing your request as follow:

- 'text': all target results will start by the 'text' condition (i.e. default configuration for text type filters: 'condition: begins with, see Figure 9-14)
- 'text' plus no option checked in the filter configuration dialog box: all results will be the 'text' condition only
- 'text\*': all target results will contain the 'text' condition and the 'Condition: contains' option will be automatically selected in the filter configuration box
- 'text A\* text B': all target results will start by 'text A' condition and end by 'text B' condition
- '\*text': all target results will end by the 'text' condition



According to the type of 'text' filter applied, the icon displayed in the filter field changes accordingly to illustrate your request:



: condition begins with 'text A'



: condition is 'text A' only



: condition contains 'text A'



: condition starts with 'text A' and ends with 'Text B'



: condition ends with 'Text A'

You can also use the filter drop-down menu below any column title fields by clicking on the **arrow** at right and then **<Advanced...>** to open dedicated filter configuration box.

Name	Images	Modality
XL-REGISTRATION CT/PET/CT L	0	OT
XL-REGISTRATION CT/PET/CT LA PITIE	718	CT/PT

Figure 9-13 Filter using the drop-down menu ('Name' column)

When clicking on <Advanced...>, the filter configuration dialog box related to the selected title field opens.

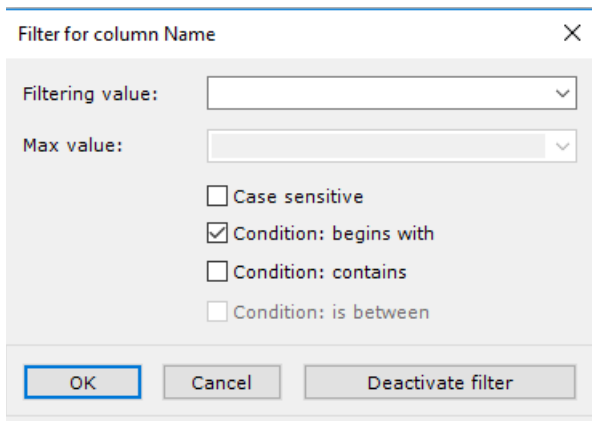


Figure 9-14 Filter configuration for the 'Name' column



By default, the 'Condition: begins with' option is preselected for all filters of 'text' type when launching Myrian®

#### 9.1.4.2 Status filter

You can filter the Study List according to the 'New' or 'Opened' status via the Status Column Filter Window which you can open by clicking on the <Advanced...> option in the Status Column Menu.

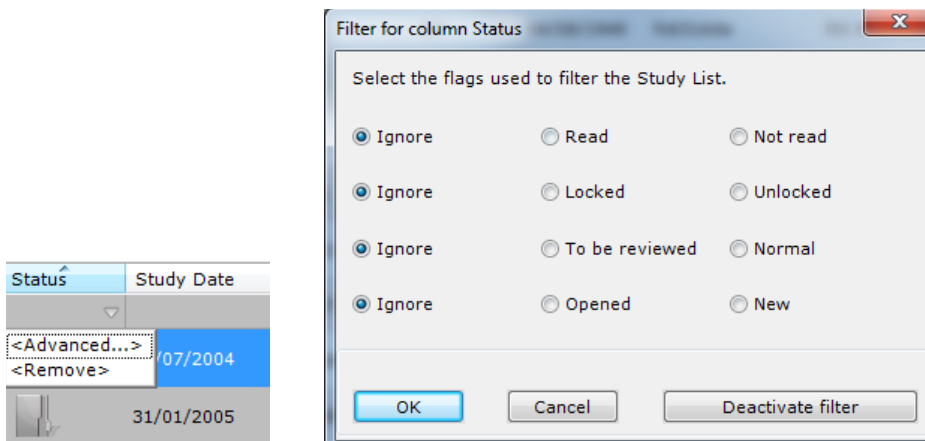
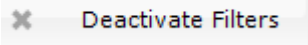


Figure 9-15 Filter Options and Column Status Menu

## 9.1.5 Deactivate Filters

- Use  to deactivate all column filters
- Or click on **<Remove>** from the column in which the filter criteria has been defined (see Figure 9-13)



This button appears at the top-right of the Study List tab only if a filter is activated.



In some cases, some information may be hidden beyond the far right-hand edge of the window. In such cases, please use the horizontal scroll bar to bring them into view.



Click on the column header to sort in alphabetical order or from large to small. Click again to sort in reverse order.

## 9.1.6 Profiles

You can save your Filter settings and Column Configuration parameters as "Profiles".



Use the "QuickProfiles" function to create quick access buttons at the top of the Study List for your favorite Study List Profiles.



You can define in your QuickProfiles which Protocols or QuickProtocols will appear in the Study List configuration, as well as column and filter settings.

- At any point when you are satisfied with your column and filtering configuration settings, click on the "Capture or

Modify current Profile" button  (floppy disc icon) to open the Current Profile modification window.

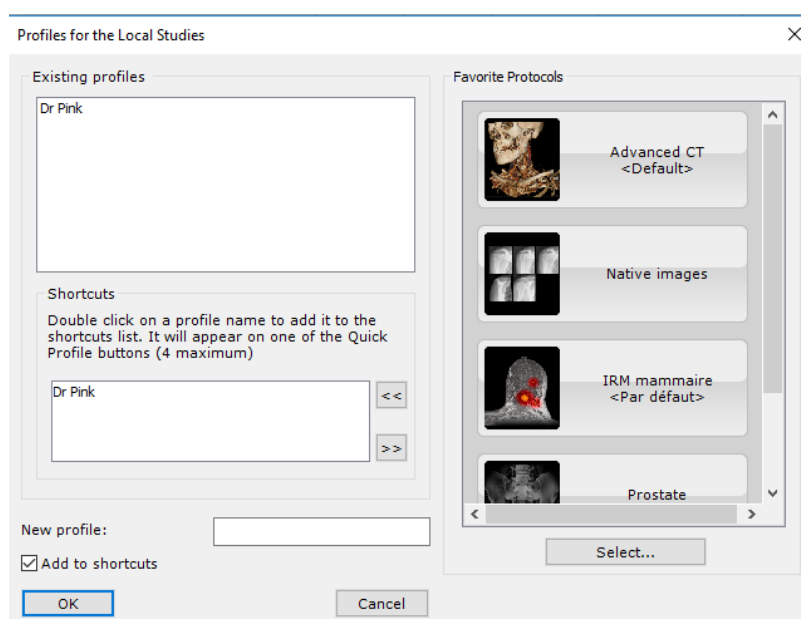


Figure 9-16 Profile Configuration

- To create a new Profile, enter a name in the "New Profile" field under the QuickProfiles list

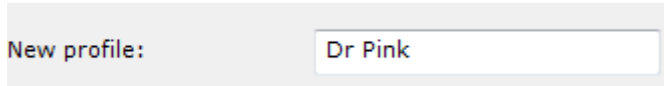



Figure 9-17 Type name for New Profile

To create a new QuickProfile:

- Double-click on a desired Profile in the "Profiles" box at top-left of the window or
- Select it and use the "Add selected Profile to QuickProfiles" button  at the right of the QuickProfiles list



Check the checkbox at the bottom-left of the Profiles window to automatically add any selected new Profile to the QuickProfiles list.

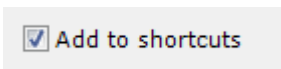


Figure 9-18 Auto-add current Profile to QuickProfiles checkbox




This will also automatically create a new QuickProfile button at the top of the Study List and activates it as the current Profile.




Figure 9-19 Profiles Bar with QuickProfiles buttons at right



To delete a QuickProfile, select it in the QuickProfiles list and use the "Remove selected QuickProfiles" button  at the right of the QuickProfiles list.

### 9.1.7 Restore Defaults



Click  to restore Default Column Configuration as set in the Column Configuration Profiles Screen and deactivate a Profile filter.

### 9.1.8 Activate Profiles

To activate an existing Profile:

- Click  and select your choice in the menu:

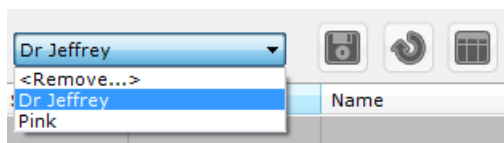
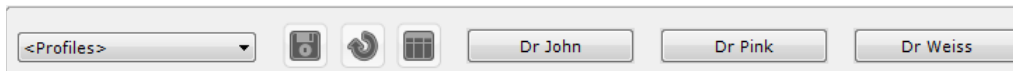


Figure 9-20 Study List Profiles



Existing profiles are directly accessible clicking on their respective button:



### 9.1.8.1 Delete profiles

To delete one or more profiles:

- Click on the Column Profiles button,
- Click on <Remove...>.

Then, in the Profiles screen:

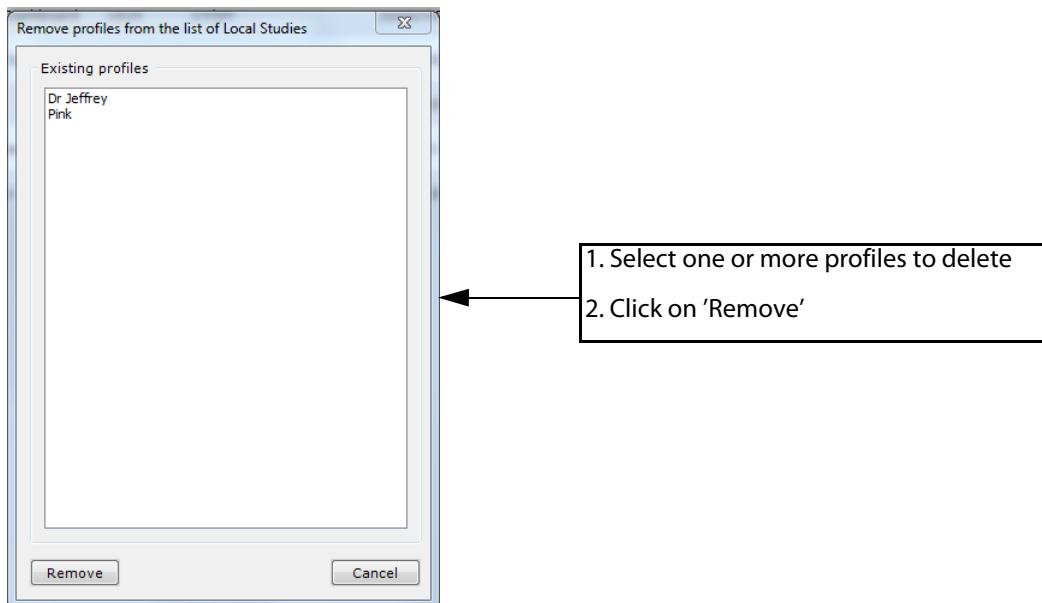



Figure 9-21 Remove Profiles



CTRL+click or SHIFT+click to make multiple selections.

### 9.1.9 Column Configuration Profiles

You can also create or modify Column Configuration Profiles by clicking on  in the Column Configuration Toolbar. This opens a column configuration screen which is laid out in 3 areas.

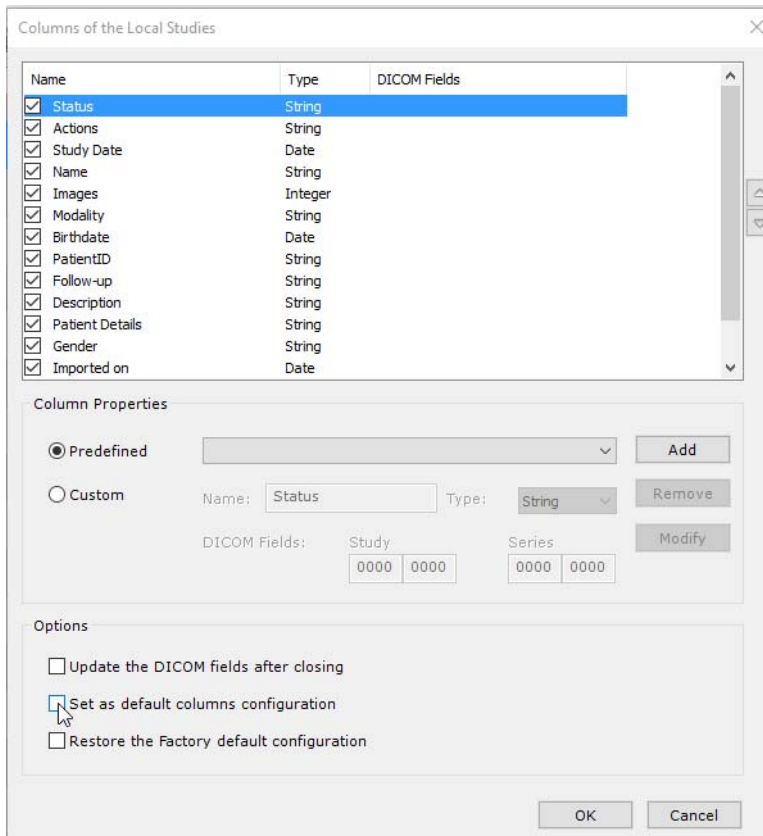


Figure 9-22 Column Configuration Screen

- To save your new column configuration profile, check the 'Set as default columns configuration' checkbox then press OK

### 9.1.9.1 Current Column list

Each Column, which bears its own name and type as well as DICOM field, can be:

- Activated or deactivated via a corresponding checkbox at left,
- Moved up or down in the list order via Up/Down arrows at left,
- Moved up or down in the list by drag and drop (maintain the mouse button down while dragging the item with the mouse).

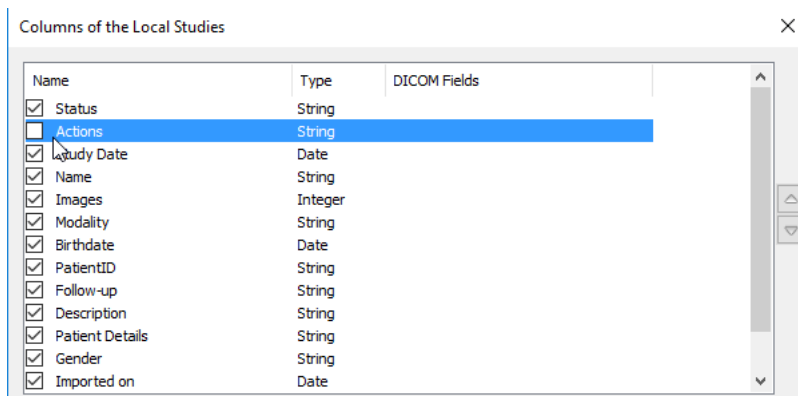


Figure 9-23 Current Columns list



The 'Status' column cannot be moved or deactivated.

### 9.1.9.2 Notes Column

Every time a New User is created, a custom column called 'Notes' is automatically added to the Study List. This column can be

used to add comments whenever you review or modify a Study.

### Add Notes Column

To add comments to the Notes Column:

- Login as the New User,



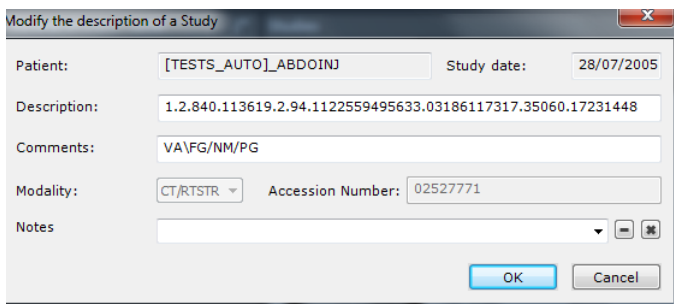
Patient Details	Gender	Imported on	Referring Physician	Accession No.	Notes
		18/01/2012 10:52		02	
	F	17/01/2012 18:20			
	M	12/12/2011 10:33			
	F	17/01/2012 18:28			
	M	13/12/2011 09:32	NEPHRO	2694	

1. Select the target Study you wish to review or modify in the Study List
2. Navigate to the 'Notes' Column using the scrollbar at the bottom of the Study List (by default the Note Column appears at the far right of the Study List)

Figure 9-24 Scroll to access Notes Column at far right of Study List

- Click on the 'Modify' Button  at the top of the Study List tab.

In the resulting window:



Modify the description of a Study

Patient: [TESTS\_AUTO\_ABDONJ] Study date: 28/07/2005

Description: 1.2.840.113619.2.94.1122559495633.03186117317.35060.17231448

Comments: VA\FG\NM\PG

Modality: CT/RTSTR Accession Number: 02527771

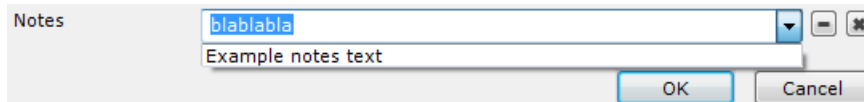
Notes

OK Cancel

3. Type your desired text in the 'Notes' field (at the bottom of the 'Modify description of a Study' window)

Figure 9-25 Modify the Notes Column

- Repeat these steps whenever you wish to add new comments to a Study by simply selecting and replacing the current text.
- All comments are available via the drop-down menu at the bottom of the window





Notes

blablabla

Example notes text

OK Cancel

Figure 9-26 Access and select new comments

- To remove any or all comments from the Notes field, simply click on the 'Remove Current Item' or 'Remove all Items' buttons   at the right of the drop-down menu.



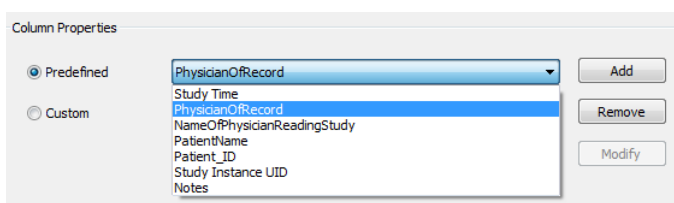
The Notes Column can be modified, deleted or moved by drag and drop just like any other column.

### 9.1.9.3 Column Properties

In this area you can add predefined or custom columns.

#### Add predefined Columns

Predefined columns are the standard DICOM columns that have not been included with the default columns



Column Properties

Predefined  Custom

PhysicianOfRecord

Study Time

PhysicianOfRecord

NameOfPhysicianReadingStudy

PatientName

Patient\_ID

Study Instance UID

Notes

Add

Remove

Modify

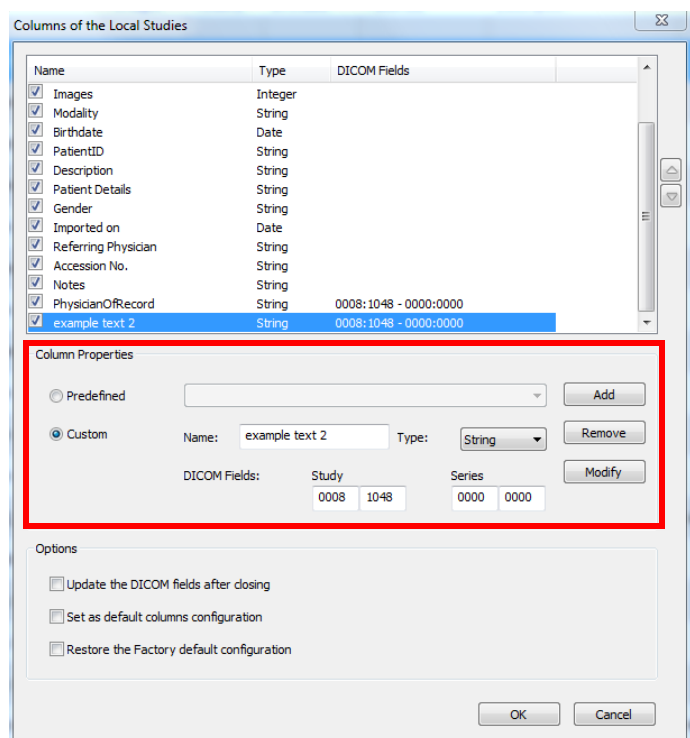
1. Activate the 'Predefined' radio button
2. Select your choice in the pull-down menu
3. Click 'Add'

Figure 9-27 Add a Predefined Column



## Add custom Columns


You can also create entirely customizable columns:

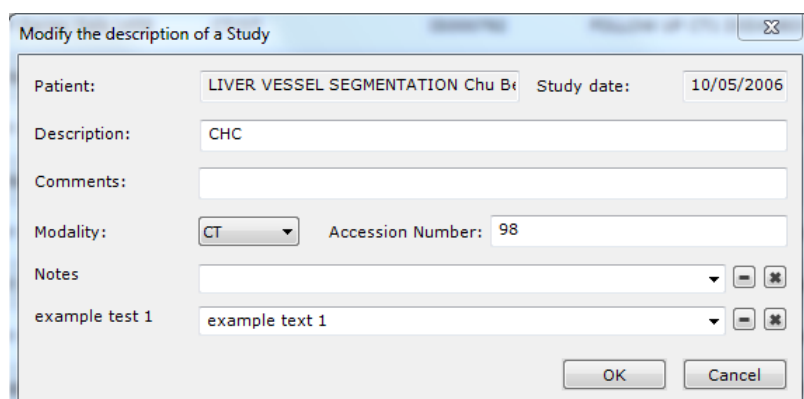


1. Select the 'Custom' radio button
2. Enter a name in the 'Name' field
3. Click OK

Figure 9-28 Create custom column

The column content can then be modified:

- Click  at the top of the Study List



1. Type-in your desired value
2. Click on the 'Remove' button at right to remove the current item.

Figure 9-29 Type-in custom column value



You can retype new values for the column as many times as you wish or access previously entered values by opening the drop-down menu using the arrow at right and selecting your desired value.

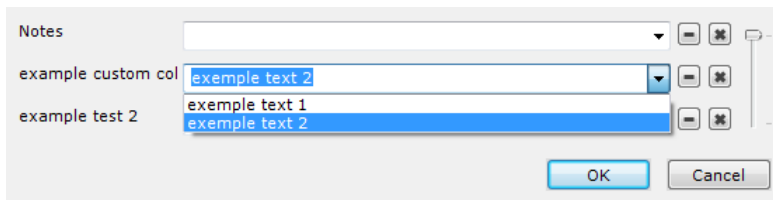


Figure 9-30 Access previous values via drop-down menu



You may need to scroll with the horizontal scroll bar at bottom to access the new column.

You can also:

- Enter a type in the 'Type' field (string, date, integer, float or unknown)
- Enter a Study/Series DICOM value, or leave this field untouched if you wish to create an open column

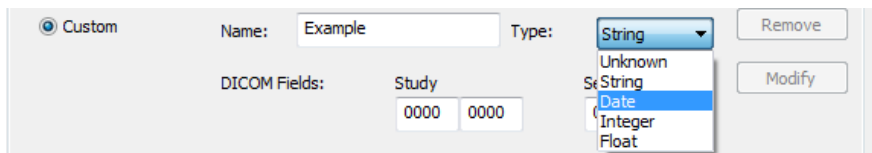


Figure 9-31 Add a custom Column

In the Column Properties Area you can also:

- Modify existing Column Fields
- Remove current columns



The default Columns cannot be removed or modified.


### 9.1.9.4 Options

In this area, 3 options can be activated via checkboxes:

- Update DICOM Fields after closing - updates the DICOM fields of the new columns on exiting the configuration screen,
- Set as Default Columns Configuration - defines your customized Column List as the Default Configuration (resets to

this when you click  in the Study List Profiles Toolbar),

- Restore the Factory Default Configuration - restores factory column parameters and overrules any custom Column

Configuration when you click  .

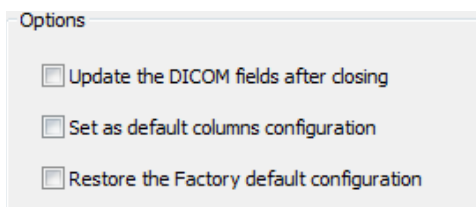


Figure 9-32 Options

## 9.2 Selecting Studies



If you have already opened the Study of one patient and then you try to open a Study of a different patient, Myrian® will, as a security measure, ask you if you wish to close the first one.

Series and Studies are opened from the 'Local Studies' screen. This can be done at different levels:

- The entire Study
- A Series (expand the list by clicking on the Study Icon)
- Subseries, marked by a number or a star, if the Series contains more than 5 Subseries

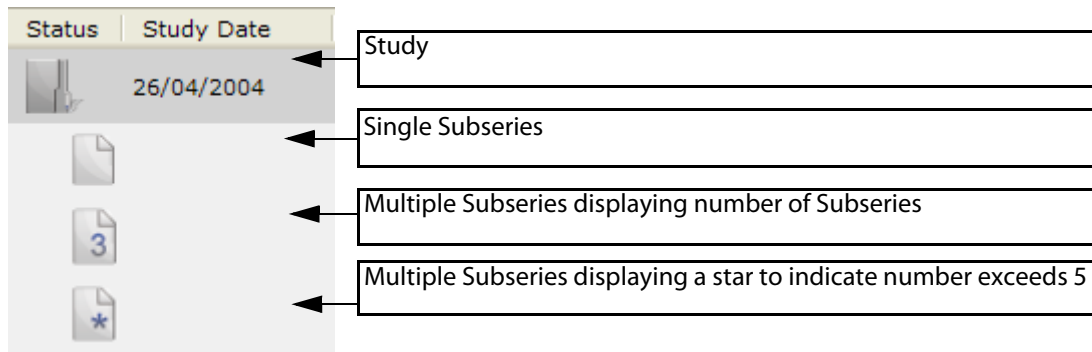


Figure 9-33 Series and Subseries

**To open the Studies, Series and/or Subseries:**

- Click on your choice
- Click the 'Open Series' button, or
- Right-click on your choice
- Click 'Open' from the context menu



For multiple choices, hold down the CTRL and/or Shift keys during mouse click (see Section 9.4).



When a Series contains more than 5 Subseries, its icon displays a star instead of a number.



You can double-click on thumbnails to open Studies directly.



It is also possible to open a single Study or Series by double-clicking on it in the list. To do this, you must first activate the 'Double-click to open a Study' option in the 'Miscellaneous' area of the 'Preferences>Display' tab.

**To open a Subseries:**

- Expand the Study
- Select Subseries,
- Right-click on your choice and
- Click 'Open' from the context menu.

To close a Series, click on the small 'X' at the top-right of the window (see Section 4.4.4).



You can close all currently open Series at once by right-clicking this 'X'.

---



When you are in the Study List tab, simply type a letter or number on the keyboard to automatically select the first study in the list with a Patient Name starting with that letter or number.

---

## 9.2.1 Loading Studies

---



In order to safeguard original Study data from accidental modification, this software automatically creates copies of Studies (stored in the Local Study database). The User works only on this identical copy of the original data.

---

Original material can be acquired from various sources including:

- PACS systems
- Any device that generates images in DICOM format
- DICOMDIR Studies located on CD's or DVD's
- Internal/External hard disk drives
- USB keys
- Any form of storage device
- Local network stored folders

The following conditions apply:

- 1 The Study should be in DICOM format
  - 2 The Study should either be accessible via the native file system (i.e. local disk, storage device or network) or accessible by a remote system that is compatible with the DICOM communications protocol and connected to Myrian® by the network (e.g. scanner, PACS, etc.)
- 



Warning on the origin of DICOM images: it is imperative that you ensure the validity and identity of the source of any DICOM images that you import. If you have any doubts about the origin or integrity of any data sources, contact an appropriate member of your establishment's personnel before proceeding.


---



Non-DICOM images in standard image format (jpeg, gif, etc.) can be transformed to DICOM format using the 'Dicomize' function (see Section 9.2.7).

---



- To view the List of Studies, click  in the Main Screens tab, top-left in the workspace.
- To close the resulting screen, click again on that same button, or click on the 'X' at the top-right of the screen.

### 9.2.1.1 Preview thumbnails

You can preview a Study or Series by clicking on it in the main list. The thumbnails appear to the left of the list, under the buttons.

When a Series or a Study containing only one Series is selected, thumbnails of the following slices will appear:

- First slice
- Last slice
- Two or three intermediate slices

In such cases, the following labels appear in white at top-right of each preview Frame:

- The image number within the Series (left digit)
- The total number of images in the Series (right digit)

If, however, the Study contains more than one Series, the thumbnails display the one image per Series/Subseries.

In such cases, the following information appears:

- The Image Number

- The Total Amount of images contained in the Series
- The Series Number

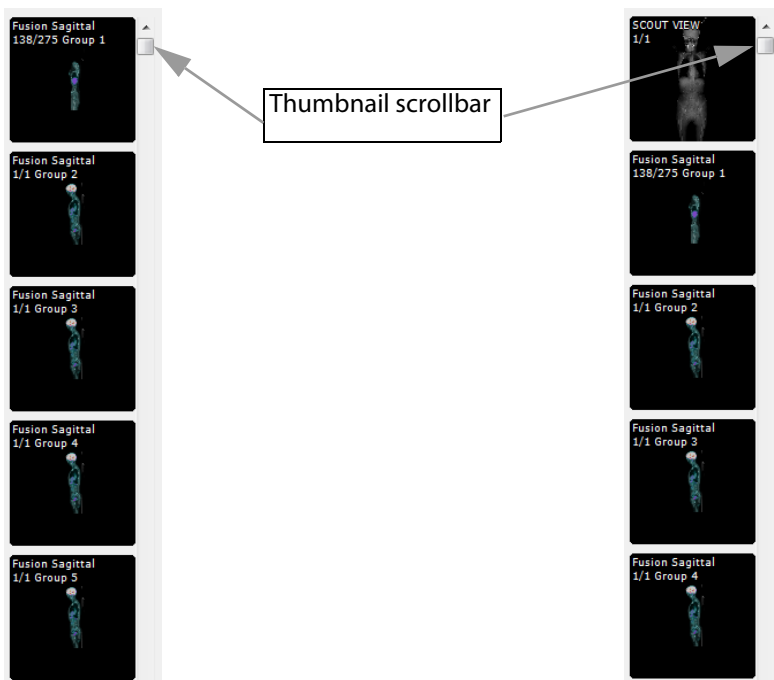


Figure 9-34 Preview thumbnails for Studies and Series




Use the scrollbar at right to scroll down and bring into view any hidden thumbnail.

### 9.2.1.2 Preview Window

- Click on a thumbnail to open the preview screen where you can scroll through the Series slices in a larger thumbnail:
  - The mouse wheel (over the images)
  - The horizontal scrollbar at bottom.

You can define a range of slices to open by scrolling selecting the first image and the last image of the range you wish to open in the following ways:

- Clicking on  to define the current thumbnail as either the first or last image of the range
- Moving the left and right cursors to the desired positions on the scrollbar
- Click on the 'Open range' button to load the range of images.

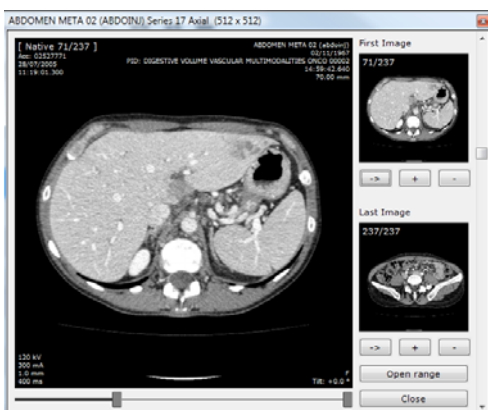


Figure 9-35 Slice range Preview and selection window



Use the '+' and '-' buttons to navigate backwards and forwards one slice at a time.

---



You can open the DICOM Dump window by right-clicking on the preview image.

---

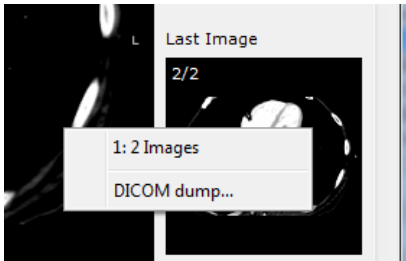


Figure 9-36 Open DICOM Dump command in Context Menu

## 9.2.2 Local Study Toolbar

In the 'Local Studies' window, a set of buttons appears above the list:

- Open Series opens the selected Study/Series of images
- Import Studies from a local disk, storage device or network (see Section 9.4)
- Delete deletes the selected Studies. Deletion may also be performed by the 'Clean database' button (see Section 9.2.6)
- Modify the description of Studies and Series
- Image Scrapbook opens the Scrapbook for the selected Study
- Dicomize adds non-DICOM images to a Study by converting images from standard image formats (JPEG, GIF, BMP, etc.) to DICOM format (see Section 9.2.7)
- Clean the database, which can be configured to remove old Studies

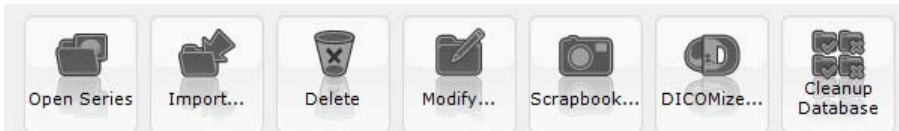


Figure 9-37 Function buttons in the Local Studies screen



Certain functions may not be accessible in your version of Myrian®

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## 9.2.3 Right-click Menus

The functions described above are also available by clicking with the right mouse button on a Study or a Series/Subseries in the list. This causes pop-up menus ('Context' or 'Right-Click' menus) to appear.

Extra functions included in the 'Study' context menu are:

- **'Read'**, to mark the Study as having been 'read' or 'not read'
- **'To be reviewed'**, to mark the Study as 'To be reviewed' (also prevents the Study from being deleted during database cleaning)
- **'Locking'**, to lock/unlock the Study. 'Locking' a Study protects it from being accidentally deleted during a 'Clean Database' command (see Section 8.3.1 for further details)
- **'Report'**, to create/consult any existing report for the highlighted patient
- **'Export Studies'**, to export the Study's Series in various formats:
  - BMP, GIF, JPEG, PNG or TIFF image formats

- AVI (Movie format)
- DICOM (.dcm) or DICOMDIR formats,
- Burn to CD as 'DICOMDIR with viewer' (see Section 5.3), which is the default Patient CD format, or as 'Patient CD with viewer'
- **'Modify'**, to edit patient/study info ('first/last name', 'Sex', 'Patient ID' and 'date of birth' fields displayed for a patient) and anonymize a study
- **'Delete'**, to delete Studies (see Section 8.3.1 for detailed information)
- **'Import'**, to import Studies/Series from a specified location (internal/external Hard Disk Drive, CD, portable storage device, USB 'flash' drive, etc.)
- **'Remote Studies'**, to perform a search of the main PACS (default setting) according to the PatientID of the selected Study and display the results in the 'Remote Studies' tab

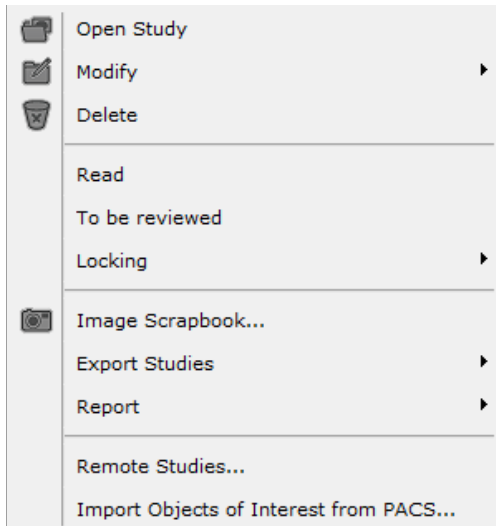


Figure 9-38 Context Menu (Right-click on a Study)



Patient Info Modification: please check thoroughly the exactitude of any modified Patient Info. The modification of any Patient data may result in inconsistencies, particularly if you are using third party software.

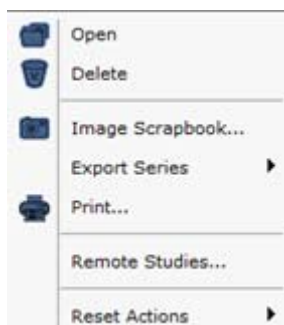


Figure 9-39 Series right-click menu



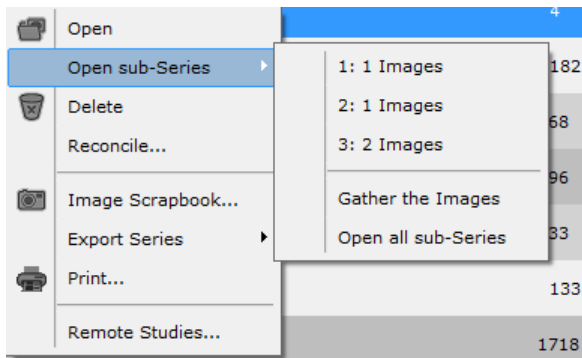


Figure 9-40 Subseries right-click menu

Extra functions available in the context menus by right-clicking on a Series or Subseries are 'Print' and 'Reconcile':

- **'Print'** sends all the images in the selected Series/Subseries to the 'Printing Layout' bay (see Section 5.1.3)
- **'Reconcile'** (Patient Identity Merge) opens a screen wherein it is possible to group together any/all Studies belonging to the same Patient. This function is useful where Studies of the same Patient originate from different establishments, have been saved using different names or spellings or in some other way differ in their identifying parameters.
- **'Gather the images'** groups Subseries into a single Series



The Reconcile operation is irreversible: be sure to check thoroughly to make sure that the Patients to be merged correspond to the same person.



Multiple sets of images such as, for instance, various phases of radio contrast medium diffusion are sometimes grouped into single sets by certain acquisition devices or protocol. This software automatically sorts such sets of images into multiple Subseries, thereby enabling comparison or individual review of any particular Subseries.



Subseries may be regrouped at any time using the 'Gather the image' function in the Subseries right-click menu.

## 9.2.4 Modifying Patient Information

### Modify




- Press  in the Local Studies Toolbar to modify:
  - The Study description,
  - Add Comments
  - Modify the Modality of Acquisition
  - Change the Accession Number of the Study

Figure 9-41 Modify Description

## Edit Patient Info

'Edit Patient Info' enables you to modify all information relative to the Patient including Name and Patient ID, Date of Birth, etc. This can be very useful to Anonymize a Study or to correct any information errors.



Click on the 'Query PACS'/'Local Database' button at right of the Patient ID box to open the list of Patients to merge your current Study with (see Section 9.4.1).

Figure 9-42 Edit Patient Info

## 9.2.5 Anonymizing studies

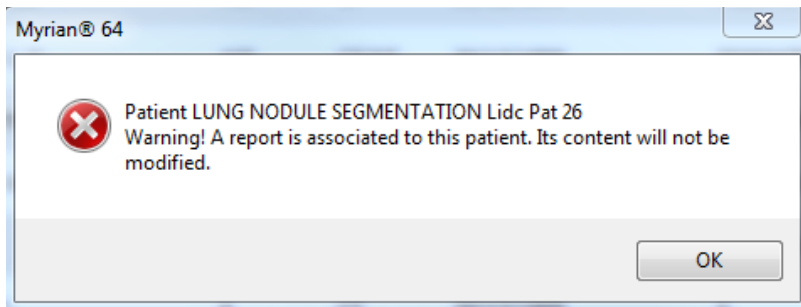
A study can be anonymized in the local database or when exporting, either in an automatic mode or according to a patient info anonymization profile (which can be useful in the context of clinical trial studies for which some data need to be preserved while some others need to be deleted).



ISAuditTrailViewer (see Appendix 10) records all changes made to the content of the DICOM tags including previous and next values in the 'Data' field used to store all 'Anonymization' information in the local database.



If you proceed to the anonymization of a patient's study to which a report is associated, bear in mind that the report content of the selected patient will not be modified. An alert message is displayed to inform you.



### 9.2.5.1 Anonymize a study in the local database

Proceed as follow:

- Select the desired study among the study list and perform a right-click to open the following submenu
- Click on 'Modify' then 'Anonymize'

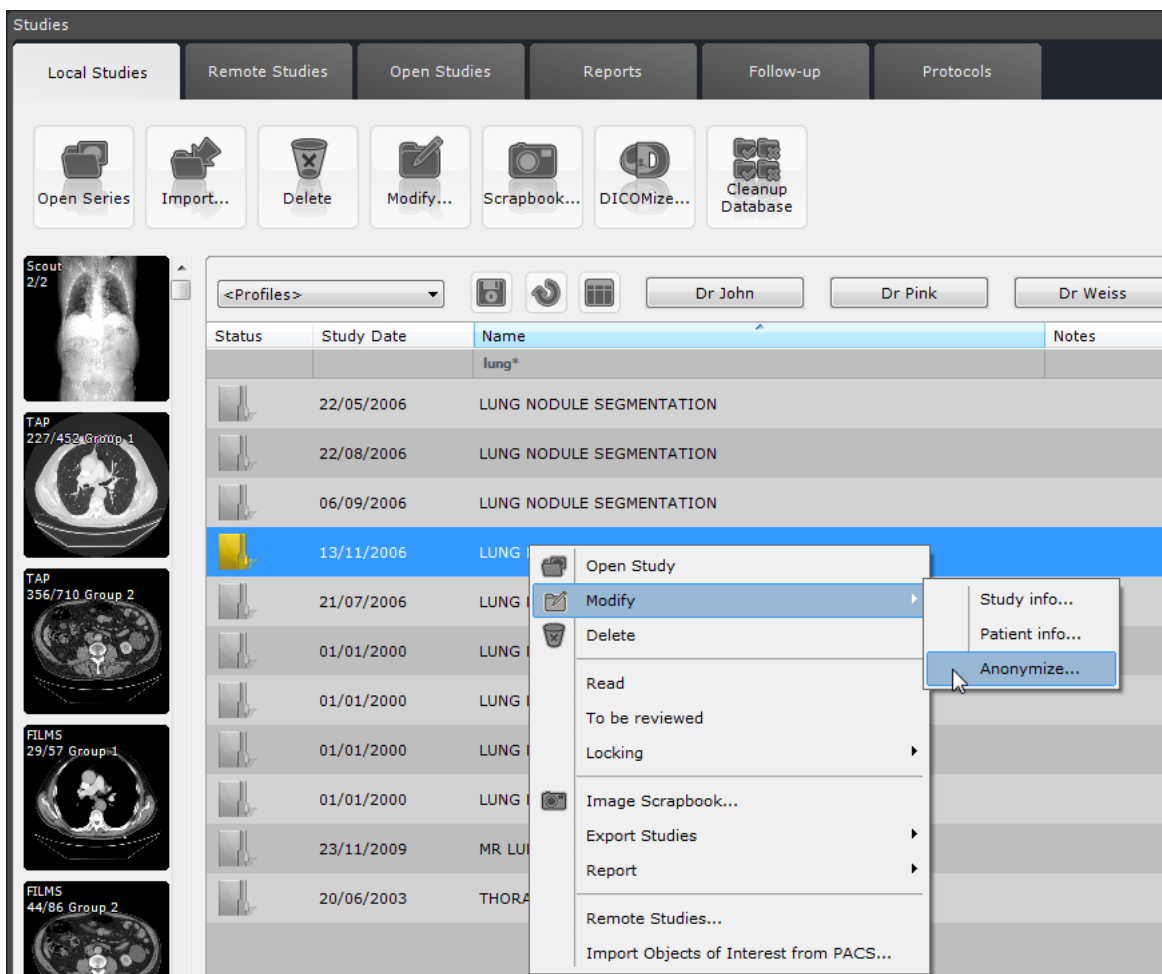
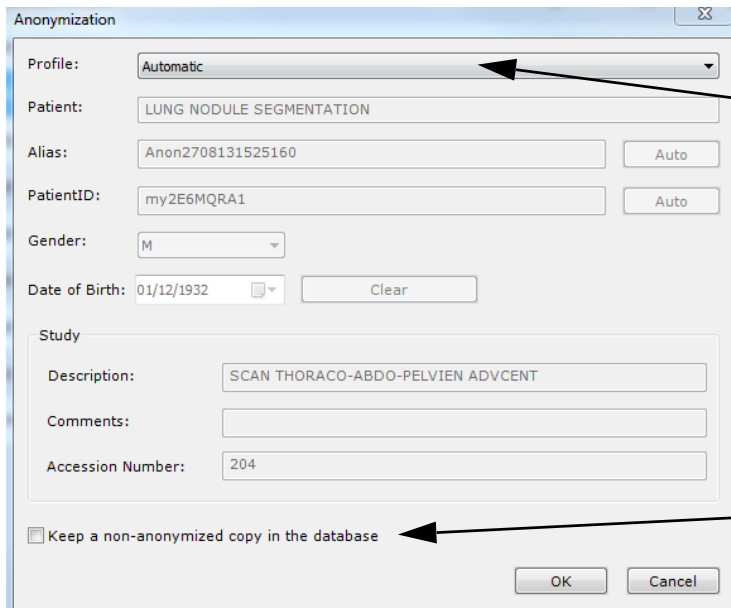


Figure 9-43 Accessing local database Anonymization window

The following 'Anonymization' window opens:



1. In the 'Profiles' combobox, select one factory anonymization profile among those two:  
 - **Automatic** (in which a predefined list of DICOM tags are erased)  
 - **Patient Info** (in which you can modify the usual patient information, i.e., name, ID, date of birth and gender, knowing that all other DICOM tag behavior is identical to the automatic profile).

2. Check the 'Keep a non anonymized copy in the database' checkbox if you wish to keep the original exam unchanged in the local database

Figure 9-44 Anonymization dialog box



If the checkbox is unchecked, anonymization of the selected study(ies) is performed directly without creating a copy.



If you choose to make a copy of the study, new UIDs are generated for all relevant DICOM tags during anonymization process (studyinstanceUID, series instance UID, SOPInstanceUID) to make sure that the copies of the study are perfectly distinct. ROIs and annotations are copied from the original series to the anonymized ones. The original study remains unchanged in the database.

It is possible to **anonymize several studies simultaneously**.

- Select all studies you wish to anonymize in your local study list
- If belonging to the **same patient**, the same patient information is used for all studies
- If belonging to **different patients**, the anonymization window only displays the automatic profile as available

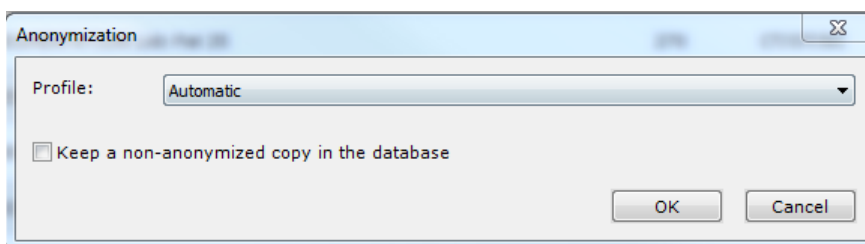
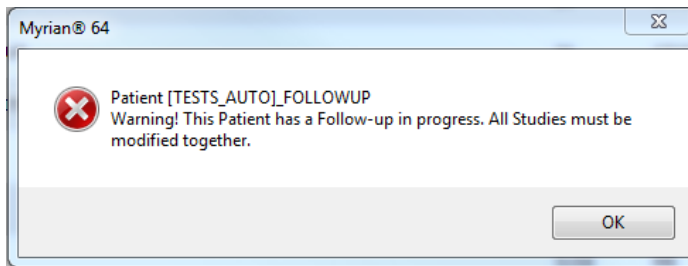


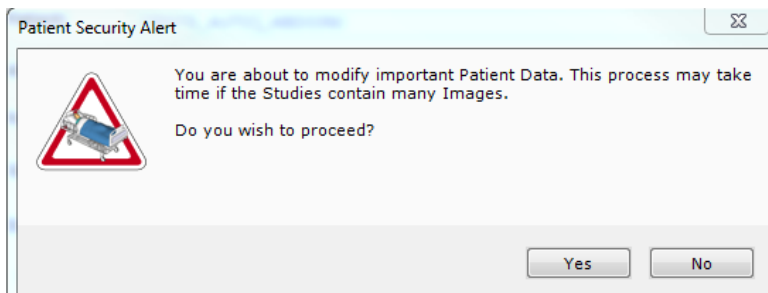
Figure 9-45 Anonymization window for several studies belonging to different patients



You cannot anonymize one single exam when this latter is part of a follow-up. In case you try to anonymize one exam that is part of a follow-up, a warning message is displayed:



If you wish to proceed anyway, all exams belonging to the patient are anonymized (using the same patient information) all the same and not only the selected one. A patient Security Alert is displayed prior to launch anonymization process requiring your final confirmation.



In reference to the case describe here-above, you can create an anonymized copy and keep the original exam unchanged in order to avoid anonymizing all the selected patient's exams.

### 9.2.5.2 Anonymize when exporting

When exporting a series to any kind of media, you can choose from the 'Export of Series' window whether or not to anonymize the selected study.

- To anonymize the series, select an Anonymization Profile from the combobox.

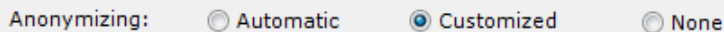


Figure 9-46 Available Factory anonymization profiles

There are two available factory profiles:

- Automatic: this profile does not require any user data input therefore the anonymization dialog box is not displayed and anonymization is automatically performed,
- Patient Info: this profile requires user data input therefore the anonymization dialog box opens when clicking 'OK' at the bottom of the 'Export of Series' window.



The patient name is displayed in shaded gray as a reminder and the Alias is saved as a user preference.

A click on the 'Auto' button in the Alias field replaces the Alias with Myrian® auto-generated value for the patient name. A click on the 'Auto' button in the PatientID field replaces the PatientID with a Myrian® auto-generated value.

The 'Anonymization' dialog box contains the following fields and controls:

- Profile:** Patient info (dropdown)
- Patient:** [TESTS\_AUTO]\_ABDOINJ (text field)
- Alias:** test export anonym (text field) with an **Auto** button.
- PatientID:** 2c599329 (text field) with an **Auto** button.
- Gender:** F (dropdown)
- Date of Birth:** 02/11/1967 (text field) with a calendar icon and a **Clear** button.
- Study:**
  - Description:** 1.2.840.113619.2.94.1122559495633.03186117317.35060.17231 (text field)
  - Comments:** VA\FG\NM\PG (text field)
  - Accession Number:** 02527771 (text field)

Buttons: **OK** and **Cancel** are located at the bottom right.

Figure 9-47 Anonymization of a study to be exported using the 'Patient Info' Profile

## 9.2.6 Delete Study/Series/Data



Make sure to delete all patient-related data saved in local on your system to prevent from any future data reuse.

### 9.2.6.1 Clear Series Data Tool

The Clear Series Data tool enables you to clear one series upon loading from all information such as:

- ROIs
  - Text annotations, Arrows, Measurements
  - Visual Masks
  - Etc.
- To launch this basic tool, first select one study in your Local Study list from which you wish to remove all data then press **SHIFT + DEL + ENTER** simultaneously.

The screenshot shows the 'Local Studies' window with a table of study entries. A confirmation dialog box titled 'Myrian® 64' is overlaid on the table, asking 'Clear series data?' with 'Yes' and 'No' buttons. An arrow points from the 'Yes' button to a text box that says 'Click Yes to confirm'.

Status	Study Date	Name	Images	Modality	Birthdate	PatientID	Description	Patient Details	Gender	Imported on	Referring Physician	Accession No.
	08/11/2006	LUNG NODULE SEGMENTATION	2	CR/OT	24/03/1948	IS000087	Lung nodule		F	12/06/2012 09:25	-	98
	09/11/2006	LUNG NODULE SEGMENTATION	1	CR	24/03/1948	IS000087	Lung nodule		F	12/06/2012 09:25	-	99
	10/11/2006	LUNG NODULE SEGMENTATION	3	CR/OT	24/03/1948	IS000087	Lung nodule		F	12/06/2012 09:25	-	97
	18/12/2003	ABDOMEN LIVER DY 82 ITEM Robert	87	CT	14/04/1964	AW2108001			M	12/06/2012 09:58		
			87	CT		#106	Album d'images Myrian® - 3f ...			12/06/2012 09:58		
	28/07/2005	[TESTS_AUTO]_ABDOINJ	600	CT/RTSTRU	02/11/1967	2c599329	1.2.840.113619.2.94.112255 VA\FG\NM\PG		F	12/06/2012 09:48		02527771
	13/04/2006	LUNG NODULE SEGMENTATION				IS000090	RX THORAX ADVCENT		M	12/06/2012 17:49		140
	14/04/2006	LUNG NODULE SEGMENTATION				IS000090	RX THORAX ADVCENT		M	12/06/2012 17:49		139
	23/05/2006	LUNG NODULE SEGMENTATION				IS000090	Sonographie essieu		M	12/06/2012 17:49		141
	20/04/2006	LUNG NODULE SEGMENTATION				IS000090	CT THORAX ADVCENT		M	12/06/2012 17:49		127
	10/07/2006	LUNG NODULE SEGMENTATION				IS000090	Unspecified CR CHEST		M	12/06/2012 17:42	UNSPECIFIED	142
	24/07/2006	LUNG NODULE SEGMENTATION	2	CR	23/08/1949	IS000090	RX THORAX ADVCENT		M	12/06/2012 17:48		126
	21/08/2006	LUNG NODULE SEGMENTATION	2	CR	23/08/1949	IS000090	RX THORAX ADVCENT		M	12/06/2012 17:41		125
	22/08/2006	LUNG NODULE SEGMENTATION	2	CT	23/08/1949	IS000090	SCAN THORAX ADVCENT		M	12/06/2012 17:38	PUOUL-J LOUIS JP	124
	04/09/2006	LUNG NODULE SEGMENTATION	143	CT	23/08/1949	IS000090	SIDPSE ABDO PELV SOUS 5		M	12/06/2012 17:38		143
	11/04/2009	LIVER SURGERY PLANNING	93	CT	30/12/1999	IS000004	ANGIO-ABD		M	24/04/2012 17:43		
	28/04/2011	EMPHYSEME	465	CT	30/08/1947	001347734	COPD		M	12/06/2012 09:45		3NSHQWWSBGTJR
			466	CT		#102				12/06/2012 09:45		3NSHQWWSBGTJR

Figure 9-48 Confirmation message for data suppression of the selected series

The series is cleared from all previous sensitive traces of data and ready to be loaded again in its original and initial state.



Studies may also be automatically removed from the Local Studies Database using the Automatic clean-up of the Database function (see Section 9.2.6.3).



Series cannot be deleted if a Study status has been set to either 'Locked' or 'To be reviewed'.



Whenever a Study is saved in the database, any ROI/Visual selection contour is saved with it. Removing a Study will also delete these additional data.

### 9.2.6.2 Clear Patient/Series/Study Data

This alternative tool can also be performed from your Local Study list but opens up a dialog box displaying the following elaborate clean-up data options:

- Clear all Data – removes completely the unwanted study/series

Referring to (according to the selection):


- Clear Series Data – enables to clear all objects related to the selected series or,
- Clear Study Data – enables to clear all objects related to the selected study or,
- Clear Patient Data – enables to clear all objects of all studies of the selected patient.

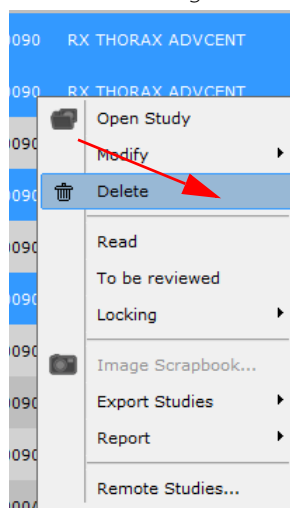
And

- Delete only ROI, Annotations and Visual Mask' - shared option by all types of selection.

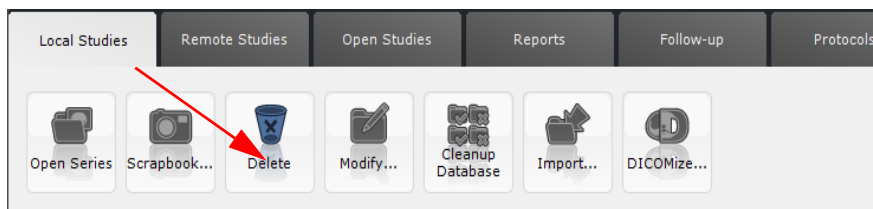


Right-clicking on the selected series/subseries/studies then selecting the 'Delete' command  from their respective

context menu or clicking on the 'Delete Selection' icon  at the top of the Local Study list tab also enables you to access the 'Delete' dialog box the same way.



OR



Or select the Study/Series and press the 'Delete' key on the keyboard



The displayed options in the 'Delete' dialog box depend on whether you have selected one or several studies/series from your Local Study list.



To perform a 'Clear Series data' on all the studies belonging to a same patient, select them in the study list (holding down the CTRL key) and click on the 'Delete' button from your keyboard.

**Method of use:**

- Select the wanted series/studies from the Study list

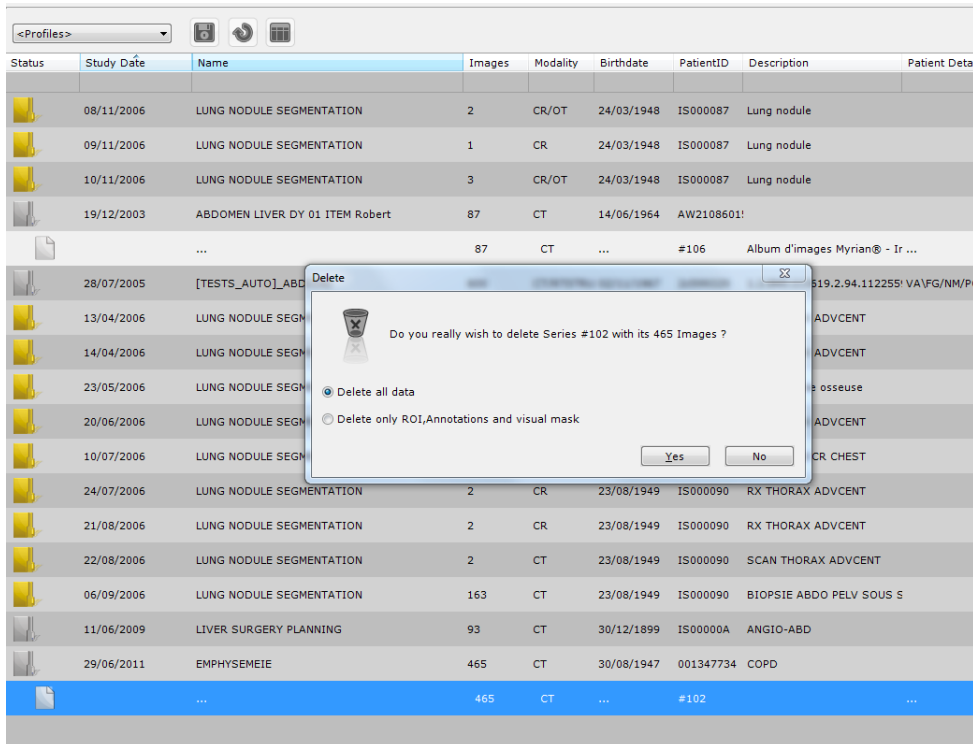


Figure 9-49 Suppression message with detailed options

- Check the radio button related to the type of data you wish to remove
- Confirm clicking 'Yes'

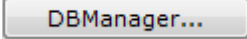
**9.2.6.3 Automatic cleanup database**



This tool is only available to users with Administrator rights.



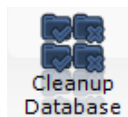
The database cleaning process is administered within DBManager (accessible from the Preferences>System tab

clicking ) and performed according to preconfigured cleanup settings. By default, automatic database cleanup is configured to delete studies older than 30 days (including studies which are 'Not Read') taking into account disk drive occupation rate.



If you wish to exclude all active Follow-up series from the database automatic cleanup, please request the assistance of an Intrasure Engineer for configuration.





However, you can still manually launch an automatic cleanup database clicking located at the bottom-left of the main screen indicates that your disk space is full.

When the process is required, the following message is displayed:

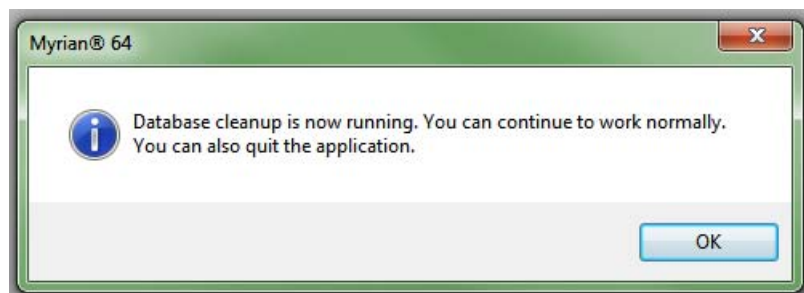


Figure 9-50 Confirmation message of the database cleanup



To prevent a Study from being deleted during a database cleaning operation, open the context menu by right-clicking on the Study in the 'Study list' Context Menu (right-click on a Study) and select the 'Lock' command from the 'Locking' menu.



Be sure that the date and time are set correctly on the computer running Myrian® as these values are used when the database cleaning function calculates the age of a given Study.



The database directory contains all your patients' data. This data is encrypted to provide maximum security and privacy. You should consider performing a regular backup of this directory to avoid any loss of data in case of a system failure or a hardware malfunction. We also recommend the use of a RAID system to increase robustness of your hardware specifications and that you check the MTBF (Mean Time Between Failure) specifications of your disks with their manufacturer in order to anticipate hardware changes.

## 9.2.7 Dicomizing add-on images

### 9.2.7.1 Overview

You can convert non-DICOM format images (JPEG, GIF, BMP, etc) to DICOM format. This creates an **SC modality** ('Secondary Capture') images which are by default added to the current Series, although it can also be added to any other Series or even stored as a new one.

### 9.2.7.2 Use

This function may be useful for storing anatomic or pathological images acquired using non-DICOM format devices (e.g. digital camera, etc.) alongside patient Studies.

### 9.2.7.3 Procedure



First gather the images you wish to convert into a single folder with an easy-to-access location.

---



All the images in the folder will be Dicomized, so be sure that the folder contains only images you wish to add to the Series.

---

To create DICOM Series:



- In the Local Study List, click on the Study to which you wish to add the new Series



- Click on the '**Dicomize**' button in the toolbar at top of the local Study list.
  - Use the '**Browse**' button to **navigate** to the folder containing the images you wish to convert to DICOM format
  - **Select** the desired folder and click **OK**
- 



If you do not wish to add the new Series to the currently selected Study, you must first deselect the Study by clicking on the Study while holding the **CTRL key** down.

---



You can use the CTRL+Spacebar keyboard shortcut to deselect all Studies/Series.

---

**Preview thumbnails** of the images contained in the selected folder are **on the right of the Dicomization screen**.

---



If the folder contains more than 3 images, use the scroll bar located under the preview area to navigate through the images.

---



Figure 9-51 Folder image scrollbar

The DICOM creation screen also contains fields for extra DICOM data such as:

- The UID (worldwide Unique DICOM Identifier)
- Description of the Study to which the Dicomized Series will be added,
- Information on the corresponding patient.

Most of the information is predetermined and therefore **cannot be modified**.

However, it is possible to add:

- A description of the Series
- Doctor and establishment names.

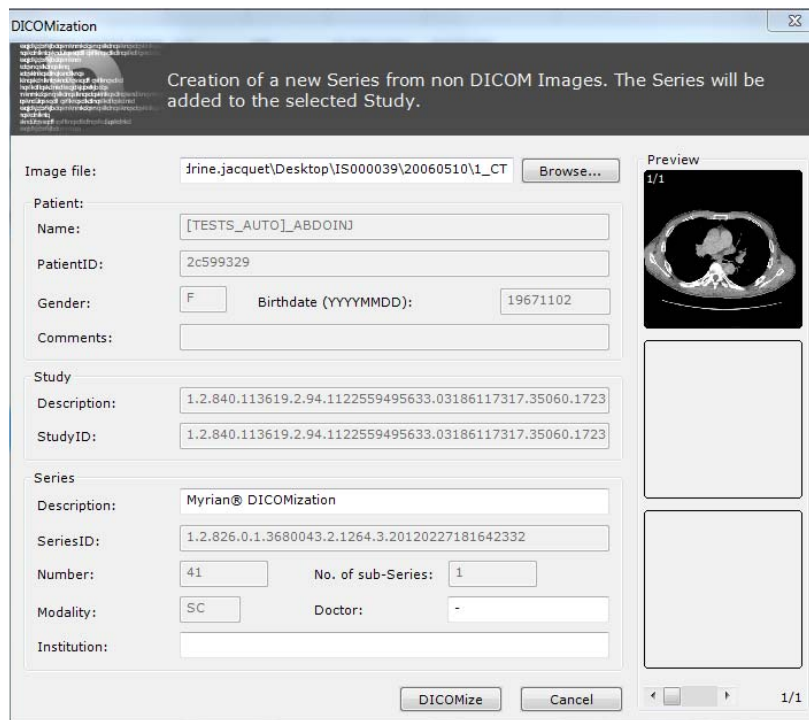


Figure 9-52 Creating DICOM Series

- Click on **'Dicomize'** at the bottom of the screen to launch the Dicomization process.

A progress bar (bottom left of the Dicomization screen) indicates the processing status and a message will inform you when it is complete.



Do not attempt to interrupt the Dicomize process once it has started.

---



DICOMized images automatically recover all DICOM information belonging to the exam in which they are imported (PatientName, PID, Accession Number, etc.)

---

## 9.3 Loading Modes

### Overview

Images are loaded via Display Protocols either in Native Image format or, if available, in 3D.

This option activates a function which enables you to open Series directly from the Workspace.

Protocols predefine specific display/toolbar settings and layouts in the software. A collection of basic general-purpose protocols are available in Myrian®. Alternatively, they can be user-created/modified "on-the-fly" in the main Workspace during Series Review.

### 9.3.1 QuickProtocols

QuickProtocols are user-defined Protocols which you can set up to appear at the bottom of the Study List for quick access.

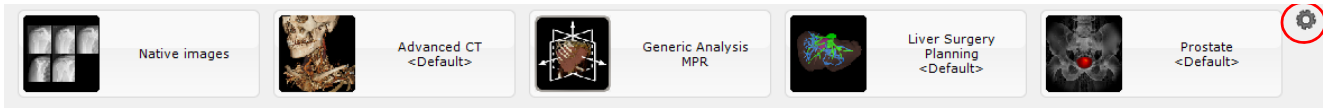



Figure 9-53 QuickProtocols

Configuration process:

- Click on  at the bottom-right of the Study List
- In the QuickProtocols Configuration Window, select a Protocol in the QuickProtocols Box at left and modify its properties via the fields at right. You can specify or modify:
  - The "Protocol", to define what type of Display Protocol you wish to use
  - The "Application Protocol" and/or the associated Protocol step when available, to define what specific Tools and Toolbars, etc. will be available
  - Which "Viewport Layouts" will appear in the given Protocol
  - The Name of the QuickProtocol (you can rename any Protocol freely)
- You can also associate the double-click to a given protocol associated to the requested modality(ies).

In that case, double-clicking on the desired series will automatically open it using the assigned protocol.

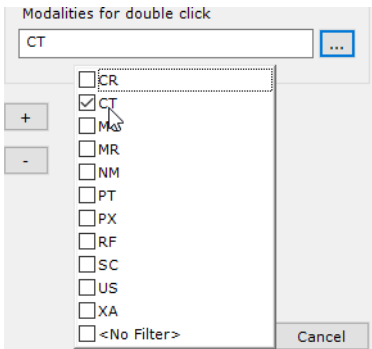


Figure 9-54 Allocating the double-click to a protocol associated to a modality

When a double-click has been allocated to a given protocol, the related protocol thumbnail displays the following mouse

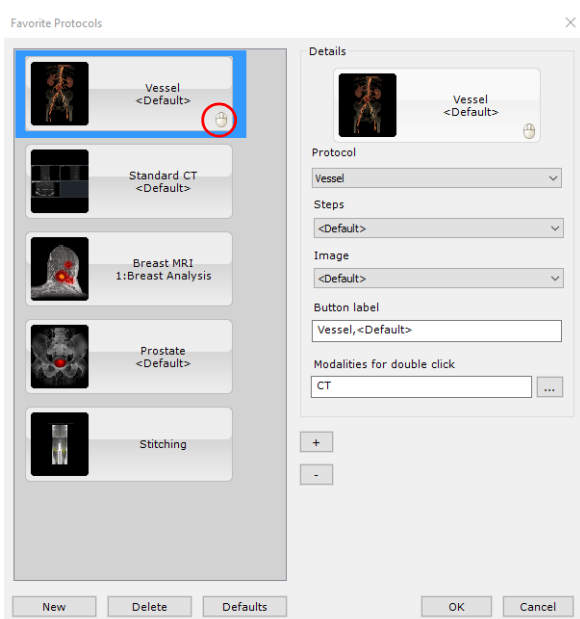




Figure 9-55 QuickProtocols Configuration Screen



You can select any QuickProtocol and modify it freely.

---



Use  /  to move Quickprotocols up/Down and modify the order they appear in.

---



Click  under the QuickProtocols list to create a New QuickProtocol.


---



By default, all new QuickProtocols are set to "Native Images". Once selected, they can be modified in the ways described above.

---

To remove a QuickProtocol:

- Select it
  - Click  to the right of the 'Create New QuickProtocol' button
- 



Click  to restore Factory Settings for QuickProtocols.

---



Some Series cannot open as a volume. Reasons for this include:

- Unknown image format
  - Series contains multiple and various image format (size, orientation, etc.)
  - Incompatible Multiframe format (e.g. "US", "OT", MR, etc.)
- 



In order to be able to reformat Multiframe NM Series, copies of the original Series are generated during the import process in a form which can be reconstructed in MPR.

---



Such copies are automatically given a new SeriesID to differentiate them.

---



The software automatically stores the original Multiframe NM Datasets. The original NM Multiframe Series are used whenever the Series are exported again from the Study List.

---



When a Series is opened in Native Mode, the word 'Native' appears in the top-left corner.

---



3D ROIs are not accessible in 'Native Image Mode'.

---

### 9.3.2 Combined protocol menu from the Workspace

When series are loaded in the Workspace whatever the protocol used, right-clicking on the title bar of any displayed view or performing a drag & drop from one series to another enables to display a combined protocol menu.

However, the protocol list displayed in the combined protocol menu depend on the modalities of the open series. Therefore, **only compatible protocols** are suggested:

- In case of a right-click on a view title bar, the modalities taken into account are those of all the series opened in single views in the workspace.



Figure 9-56 Example: Display of the compatible protocol list when right-clicking on the title bar of CT series view opened in Native mode

- In case of a drag & drop, the modalities taken into account are those of the series from the two involved views.

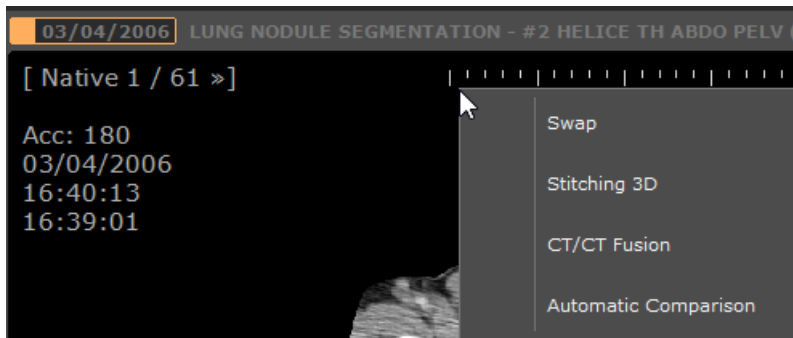


Figure 9-57 Example: Displayed compatible protocol list when drag & dropping a CT series opened in Native mode on another one.




Right-clicking on a view title bar displays the following options: "Open a copy" + as well as the default compatible protocols. In the same way, drag & dropping a view on another displays the following options: "Swap" + default compatible protocols.

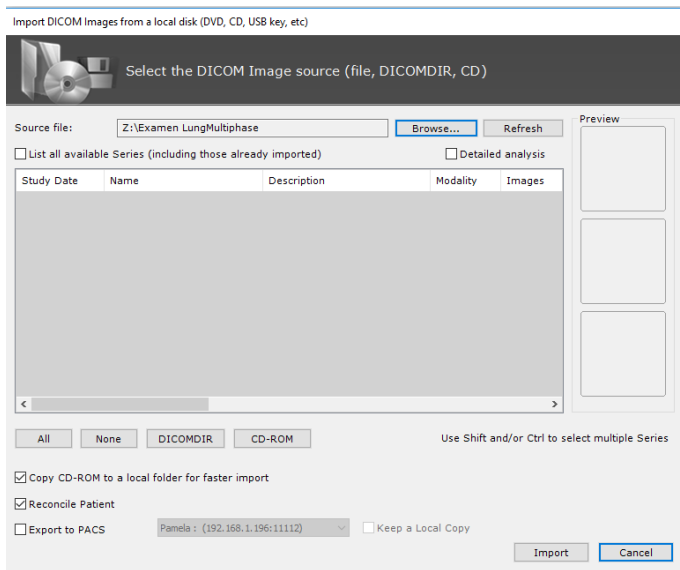


The combined protocol default menu is Stitching, Fusion and Multiphase protocol (when relevant).

## 9.4 Importing from a local drive or network location



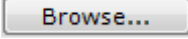
By clicking on  at the top of the 'Study list' window or in the context menu described above, a DICOM Series importer window appears.



Specify the location of the DICOM images to be imported by clicking on the 'Browse...' button and selecting the appropriate folder on the drive, device or network in the resulting folder selection window.

Figure 9-58 Importing DICOM Series from a local drive or network location



If you browse for a new location clicking , Myrian® first looks for a DICOMDIR file and reads it if it exists: this process is really time-saving. If none, the application starts scanning the disk.

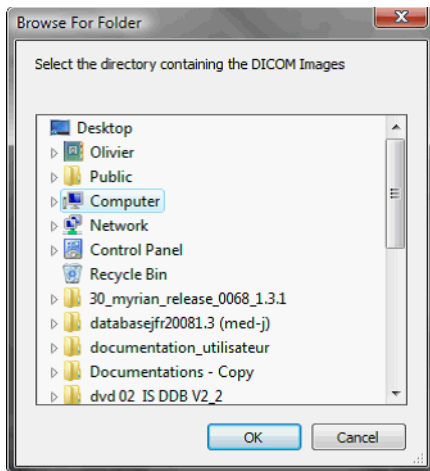
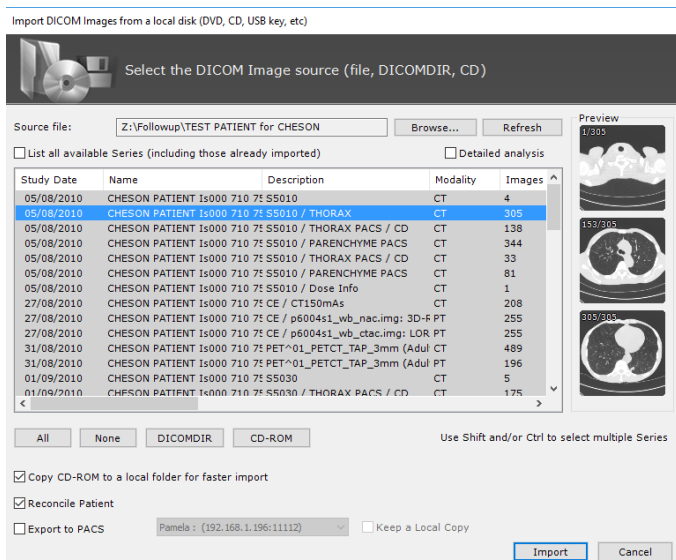


Figure 9-59 Choosing the import folder

Once you confirm your choice of folder by clicking OK, all DICOM format Studies or Series in that folder and any of its sub-folders will be presented in the importer window.

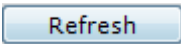
A progress bar indicates the state of the search.



1. Select any Series in the list to display preview thumbnails.
2. Click on any of the thumbnails to preview and navigate through the entire Study before loading it.

Figure 9-60 List of all Series found under the import folder

If new Studies are added to the chosen import directory whilst using the importer, you will need to click the 'Refresh' button to have new Study data taken into account. By doing so, any new Studies will automatically be added to the current list.



If you click **Refresh**, the same process takes place: Myrian® first looks for a DICOMDIR file and reads it if it exists (time-saving process). If none, the application starts scanning the disk.

The 'DICOMDIR' button in the Import window (see Figure 9-58) locates this index.



A file named 'DICOMDIR' is an index which describes Studies that are present on a hard disk or remote/removable media.

The 'CD-ROM' button located at the bottom of the window will search for and display all DICOMDIR files on a CD-ROM. Note that Myrian® recognizes DICOM files on a CD-ROM automatically.

- Check the 'Detailed Analysis' box to force the search engine to browse all media and devices for DICOM files.



Selecting the 'Detailed Analysis' checkbox may slow down the browsing process considerably.

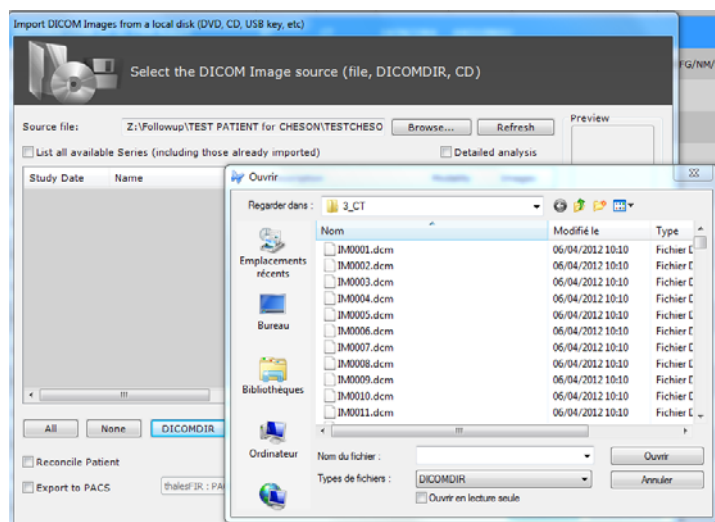


Figure 9-61 Opening a DICOMDIR file





If you cannot find the location of any Studies that you have saved, contact an appropriate member of your establishment's computing staff.

---

Once you have obtained the list of Studies in the import window (see Figure 9-58), select those you wish to import in one of the following ways. Either:

- Click on a single Study to select it, or
- Select the entire list of Studies with the 'All' button and deselect the whole list with the 'None' button.

To select several Series:

- Click on the desired Studies whilst holding down the CTRL key. This will add/remove Series from the current selection, or
- Click on the Series with the Shift key held down. This will select all the Series between this one and the last one clicked upon. Deselect a range in the same way.

Example:

If you wish to select all but two Series:

- Click the 'All' button, then
  - Click once on each of the undesired Series with the CTRL key held down,.
- 



You can use the CTRL key and the Shift key in conjunction to add or remove ranges of Series.

---

Once you are satisfied with the selection,

- Click on 'Import' to start importing them.

A DICOM importing queue window which monitors the progression of the import then appears (see Figure 9-74 and see Section 9.6).

---



You may close the import queue window and carry on working in Myrian®, without disrupting the import in progress by clicking on the Myrian® icon at bottom-right of the application. This action displays/hides the import queue window. The butterfly icon is animated while import is in progress.

---



It is inherent to DICOM image transfer protocol that an import might abort without further notification before image transfer is complete.

---

Once importing is complete, the new Studies or Series automatically become available in the list of local Studies.

### 9.4.1 Reconcile and Modify Patient Info from PACS

When the 'Reconcile Patient' checkbox at the bottom-left of the Import window is activated, the Patient Reconciliation window opens automatically as soon as you click the 'Import' button.

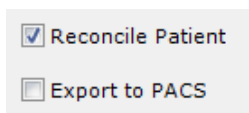


Figure 9-62 Reconcile Patient and Export to PACS Checkboxes

---



Activate the 'Export to PACS' checkbox to launch an automatic Export to PACS process of the selected Studies.

---

- Activate the 'Use Patient Data from Imported Series' radio button to override Patient Reconciliation.

The Patient Information from the Imported Series alone will be used.

- Otherwise activate the 'Reconciliation from the PACS' option: you can perform a search based on either the Name, the Date of Birth or the PID or even a multi-criteria to reduce patient occurrences.

Similarity	Name	Birthdate	PatientID	Gen...
100	VESSEL SEGMENTATION TSA St Colombe/lyon	12/04/1939	IS000120	F
80	VESSEL SEGMENTATION TSA Gui De Chauliac	04/08/1944	IS000113	F
80	VESSEL SEGMENTATION TSA Gui De Chauliac	09/05/1923	IS000134	F
80	VESSEL SEGMENTATION TSA Rennes	27/02/1933	IS000131	F
80	VESSEL SEGMENTATION TSA Maroc	15/12/1959	IS000107	F

Figure 9-63 Patient Reconciliation from PACS screen

- Click  to launch Reconciliation.

An alert message indicating that you are about to overwrite the patient information of the study being imported by the patient information of the study selected on the PACS, automatically pops up requiring your confirmation.



Activate the 'Reconciliation from PACS' radio button to automatically launch a query for all Studies stored on the PACS bearing the same Patient Name.

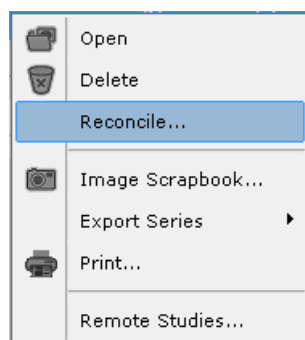


The Reconcile Patient feature is not available for Follow-ups.



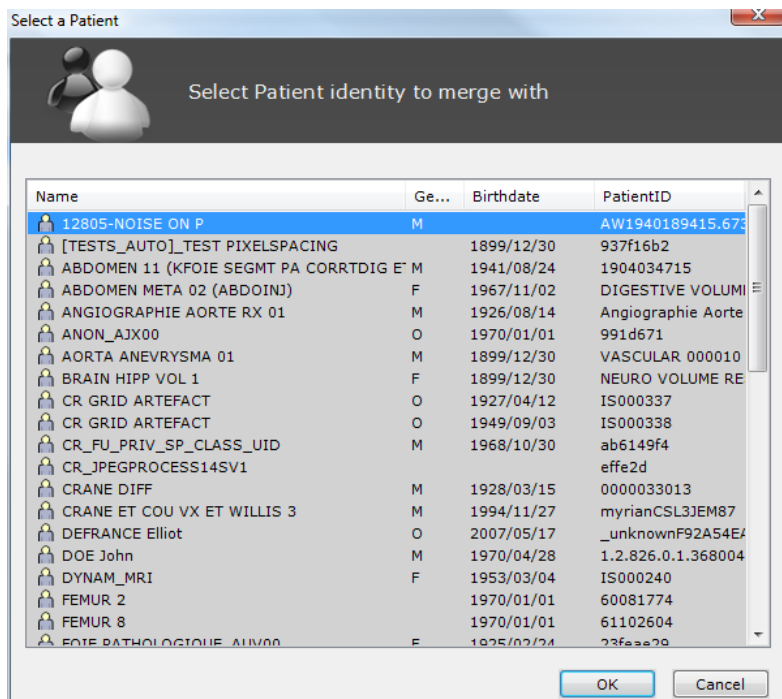
The Reconcile Patient feature changes Patient Info of Series only.

## 9.4.2 Semi-automatic Reconciliation from PACS



1. Right-click on a series and select 'Reconcile...' from the contextual menu

Figure 9-64 Select 'Reconcile...' from series submenu



2. Select the most appropriate Patient in the List and Myrian® updates the Patient Data.

Figure 9-65 Patient Reconciliation Screen

The following DICOM Fields are modified during Patient Reconciliation:

- Patient Name,
- Patient Gender,
- PatientID,
- Patient Birth Date,
- Patient Age



All Studies and related DICOM files of a Patient are modified.



If several Studies have the same initial Patient Identifier, they are automatically changed.



This functionality is accessible via the Study Context Menu in the Local Study List.



A message appears to warn you that you are modifying important Study Data and that the modifications will apply to all images in the study.

## 9.5 Import and Export of Myrian® Objects of Interest (OOI)

### 9.5.1 Overview

The following types of Objects can be imported and/or exported manually to and from a PACS or Other DICOM Entity:

- Scrapbook and PrintComposer Images
- Annotations (Text, Arrows, Quantification Shapes)
- ROI, POI, ROI Sets, etc.
- Visual Selections



Objects of Interest are automatically stored in DICOM files in the Local Database.



You must have Operator Privileges at least to Import or Export OOI



The Database must be in a write-enabled mode

### 9.5.2 Export Myrian® Objects

To export Myrian® Objects:

- Open the Local Study List
- Right-click on the Study of your choice containing the Objects to export
- Select "Export Studies" from the context menu
- Click on "Objects of Interest" in the resulting submenu

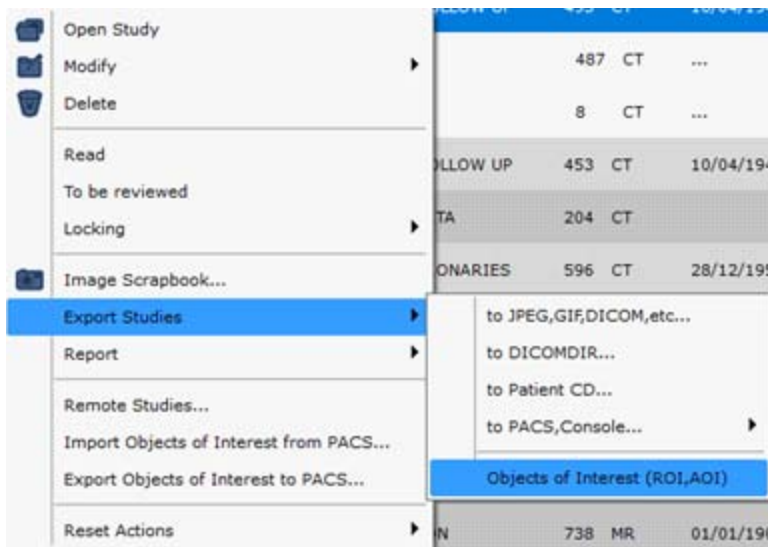


Figure 9-66 Export Objects of Interest option in the Study List Context Menu

The Export Window opens in which you can select your target Destination Media in the Media drop-down menu.

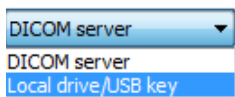


Figure 9-67 Destination Media menu

You may also modify your Destination PACS in the "PACS" drop-down menu.

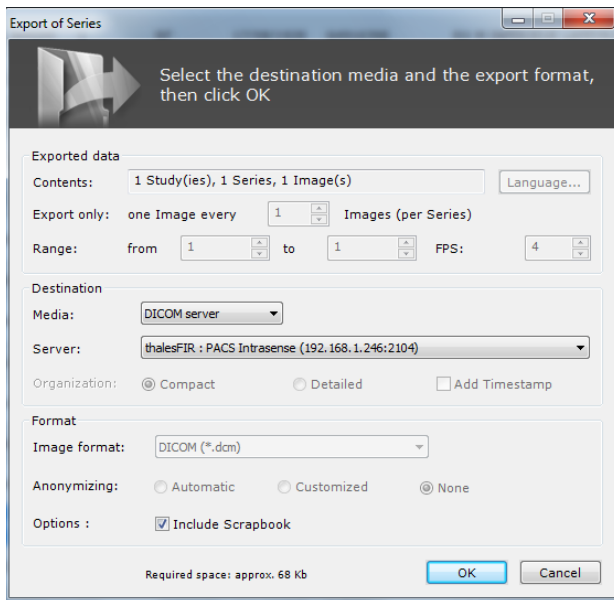


Figure 9-68 Export Window



Default destination is your Main PACS.



Objects are exported in the background. Export progress can be tracked in the DICOM Job Queue Window, at bottom-right of the application window.



Activate the 'Include Scrapbook' checkbox to automatically export all the Images in the Scrapbook Module.

### 9.5.3 Import/restore Objects of Interest

If a Study containing Objects of Interest is already available in the Local Database, it will appear in the Study List.

- Right-click on the corresponding Series and select "Extract to Database".



If the Dataset is not yet in the Local Database, you must import it first like any other DICOM Series then use the "Extract to database" Context Menu option.

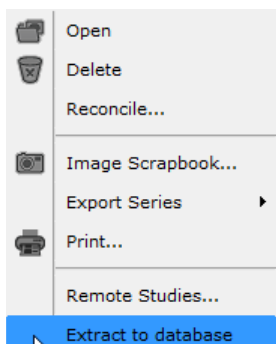


Figure 9-69 Restoring Myrian® Objects to the corresponding Study

- Use the "Import objects of interest from PACS" command to combine the following operations automatically:
  - Query the Main PACS for available Datasets
  - Check if there is any Dataset that is more recent than the one in the Local Database
  - Import the most recent Dataset with a Query/Retrieve action
  - Extract the Dataset to the local database

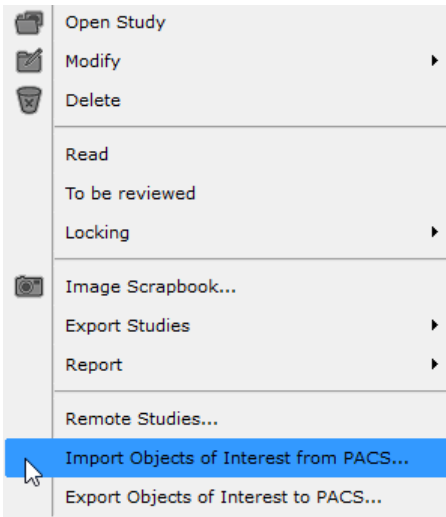


Figure 9-70 Import Myrian® Objects from a PACS



If several Datasets are available, the most recent will be downloaded.



By default, the Main PACS is used to retrieve Datasets. If no Main PACS has been consigned, the first available PACS is used.



All Private Myrian® Objects are encapsulated within Private DICOM fields of Secondary Capture Images.

## 9.6 Remote Studies

Lists of Studies located on remote DICOM servers (PACS, Modality, Archive, etc.) can also be imported via the Remote Studies tab.

Status	Study Date	Name	Images	Modality	Birthdate	PatientID	Description	Patient I
01/08/2008	ANON0108081348160	4	US	04/11/1932	00000S1365			
18/03/2009	???	1	CT	07/11/1974	000820981	n++a+p		
03/12/2007	ANON0412071252495	2	CR	04/12/1953	07337104	MEMBRE SUPERIEUR		
14/04/2008	TEST-IMAGES	118	SC	28/04/1970	1.2.826.0.1.368004			
17/09/2008	LIVER VESSEL SEGMENTATION Kumamoto	610	CT	03/04/1961	IS000000	LIVER contrast-enhanced CT		
02/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	271	CT	01/01/2000	IS000001	Healthy Liver		
03/03/2008	LIVER VESSEL SEGMENTATION Kumamoto	655	CT/OT	23/03/1979	IS000002	Liver Gallbladder and Pancre		
29/12/2007	LIVER VESSEL SEGMENTATION Kumamoto	640	CT	31/01/1957	IS000003	Liver Gallbladder and Pancre		
13/11/2008	LIVER VESSEL SEGMENTATION Kumamoto	490	CT	22/03/1967	IS000004	Liver Gallbladder and Pancre		
25/04/2008	LIVER VESSEL SEGMENTATION Kumamoto	351	CT	16/05/1967	IS000005	Liver Gallbladder and Pancre		
23/01/2008	LIVER VESSEL SEGMENTATION Kumamoto	546	CT/OT	21/04/1972	IS000006	Liver Gallbladder and Pancre		
04/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	532	CT	01/01/2000	IS000008	Healthy liver		
04/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	1258	CT	01/01/2000	IS000009	Healthy liver		
18/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	2783	CT	01/01/2000	IS000010	Healthy liver		
04/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	575	CT	01/01/2000	IS000011	Healthy liver		
17/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	2263	CT	01/01/2000	IS000012	Healthy liver		
17/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	1123	CT/OT	01/01/2000	IS000013	Healthy liver		
17/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	1030	CT	01/01/2000	IS000014	Healthy liver		
17/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	1140	CT	01/01/2000	IS000015	Healthy liver		
03/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	242	CT	01/01/2000	IS000016	Healthy liver		
02/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	281	CT	01/01/2000	IS000017	Healthy liver		
16/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	1831	CT	01/01/2000	IS000018	Healthy liver		
22/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	1145	CT	01/01/2000	IS000019	Healthy liver		
04/05/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	1348	CT	01/01/2000	IS000020	Healthy liver		
25/01/2008	LIVER VESSEL SEGMENTATION Chu St Eloi	1167	CT	01/01/2000	IS000021	Healthy liver		
26/02/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	500	CT	01/01/2000	IS000022	Healthy liver		
26/02/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	1045	CT	01/01/2000	IS000023	Healthy liver		
26/02/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	495	CT	01/01/2000	IS000024	Healthy liver		
27/02/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	1309	CT	01/01/2000	IS000025	Healthy liver		
27/02/2009	LIVER VESSEL SEGMENTATION Chu St Eloi	838	CT	01/01/2000	IS000026	Healthy liver		

Figure 9-71 Remote Study screen

### Configuration



Myrian® should be configured to connect to a remote server by a competent member of the personnel following the guidelines presented in Section 8.1 (see the 'DICOM' tab in 'Preferences'). If you have difficulty connecting to a remote server, please contact your establishment's network or system administrator.

Most of the parameters for the remote Study communication depend on the DICOM network settings, which are usually set by Myrian® installation personnel.

The IP address and TCP/IP port values for the retrieval of Series should be the parameters you would normally provide for any DICOM system that provides Series to Myrian®.

#### 9.6.1 Filter



To save time you can use filters which work similarly to the Local Study List filters described above in Section 9.1.3



You can also create column Configuration Profiles in the same way as the Local Study List Tab (see Section 9.1.8).

Status	Study Date	Name	Images	Modality	Birthdate	PatientID	Description	Patient Details	Gender	StudyID
	07/02/2008	LIVER COLORECTAL META SEI 424		CT	24/03/1938	IS000110	Liver metastasis from colorec		M	1.2.840.11
	23/01/2008	LIVER VESSEL SEGMENTATIO 541		CT	21/04/1972	IS000006	Liver Gallbladder and Pancre		F	1.2.392.20
	25/04/2008	LIVER VESSEL SEGMENTATIO 351		CT	16/05/1967	IS000005	Liver Gallbladder and Pancre		F	1.2.392.20

Figure 9-72 Request filter

You may equally filter the Studies by PPID.

### Searching for Studies

- Define a DICOM server and filter (see Section 9.1.4 for detailed information about filter configuration)
- Click on the 'Search' button at the bottom of the filter section to send the request to the server.

The screenshot shows the 'Studies' interface with several tabs: Local Studies, Remote Studies, Open Studies, Reports, Follow-up, and Protocols. The 'Remote Studies' tab is active. In the top right, the 'Modalities' filter is highlighted with a red box, showing radio buttons for 'Any' and 'All', with 'All' selected. Below this, a dropdown menu for the 'Modality' column is also highlighted in red, showing a list of modalities with checkboxes: CR, CT (checked), MG, MR, NM, PT (checked), PX, RF, SC, US, OT, XA, and '<Advanced...>'. There is also a '<Remove>' option at the bottom of the dropdown.

Figure 9-73 Multiple Modalities Search Filter Options

Whenever you add a modality to the 'Modality' column filter field in the Remote Studies tab, the 'Any'/'All' Modalities filter options appear at the far right hand-side of the search parameters bar at the top of the window.

- If you select 'Any' in the Modalities Filter Options, your query will retrieve all Studies containing at least one Series of at least one of the selected Modalities,
- If you select 'All' in the Modalities Filter Options, all Studies containing at least one Series of each of the selected modalities will be retrieved.



The 'Any'/'All' Modalities option is used for multiple modality query/retrieve operations when you are searching for specific Studies such as dynamic CT/PT Fusion Studies.



Once the 'Search' button activated, it switches to a 'Cancel' button thus allowing you to cancel at any time and for



any reasons, the search for studies in progress.

Matching Studies are displayed as soon as they are found.

If the Study or Studies that you are searching for appear in the list, you may select them for transfer. This will terminate the current search.

Once the search is over, you may further filter the list of Studies found by changing the filter criteria.

## Importing

To retrieve Studies:

- Select the corresponding entries in the search list (using the CTRL and/or Shift keys if necessary),
- Click on 'Import' to transfer the Studies to the local Myrian® database. The DICOM import queue screen will then appear.

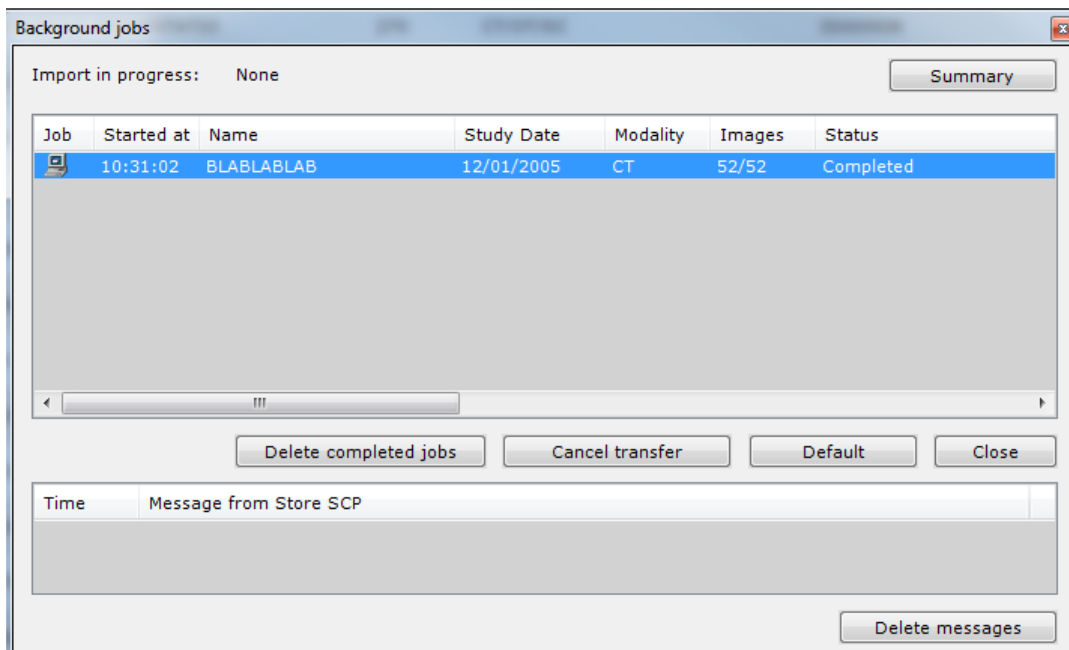


Figure 9-74 DICOM import queue



The transfer of images may take several minutes, depending on the total size of the Series that are being retrieved.



You can carry on using Myrian® whilst import is in progress. The DICOM import queue screen monitors the status of the import. It automatically appears at the start of the import and it can be closed without disrupting the current task. Click on the 'Status' button in the 'Remote Studies' window or click on Myrian® icon at the bottom-right of the application. This icon is animated during the import.



You may choose to view only the progress by clicking on 'Summary' or to see more information and functions by clicking on 'Details' at the top-right of the window.

You may abort the import task by selecting any one of the Studies being imported and clicking on 'Cancel'. If you cancel the transfer, any images already received will be discarded.

When the 'Import status' is 'Complete', the Series automatically becomes available for loading and being worked upon in the list of local Studies.

Transfers that are completed may be removed from the import queue list by clicking 'Remove completed'.



When you import remote Series, Myrian® ensures there is sufficient space on the host machine to receive them. If this is not the case, you should clean the database (see Section 9.2.6.3) or remove any unnecessary files via Windows®.



Even if Myrian® can import, archive in its local database and export to supported media any type of DICOM file, the software may not handle image processing of certain unrecognized file formats.



Studies with different Patient Names, Dates of Birth or Genders may at times bear the same PatientID. You can check for such conflicts during the import by activating the 'Verify conflicts on PatientID' option in the list of Preferences>Display>Miscellaneous options

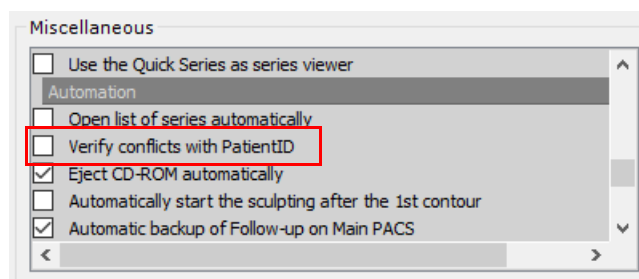


Figure 9-75 Verify conflicts on PatientID option in the Miscellaneous Options

## 9.7 Open Studies

The 'Open Studies' tab displays all the currently open Studies.

From this screen, you may close a Study, bring a Study to the foreground and/or open a copy of a Study (for example, to view one Study using 2 or more different settings such as Windowing, etc.).

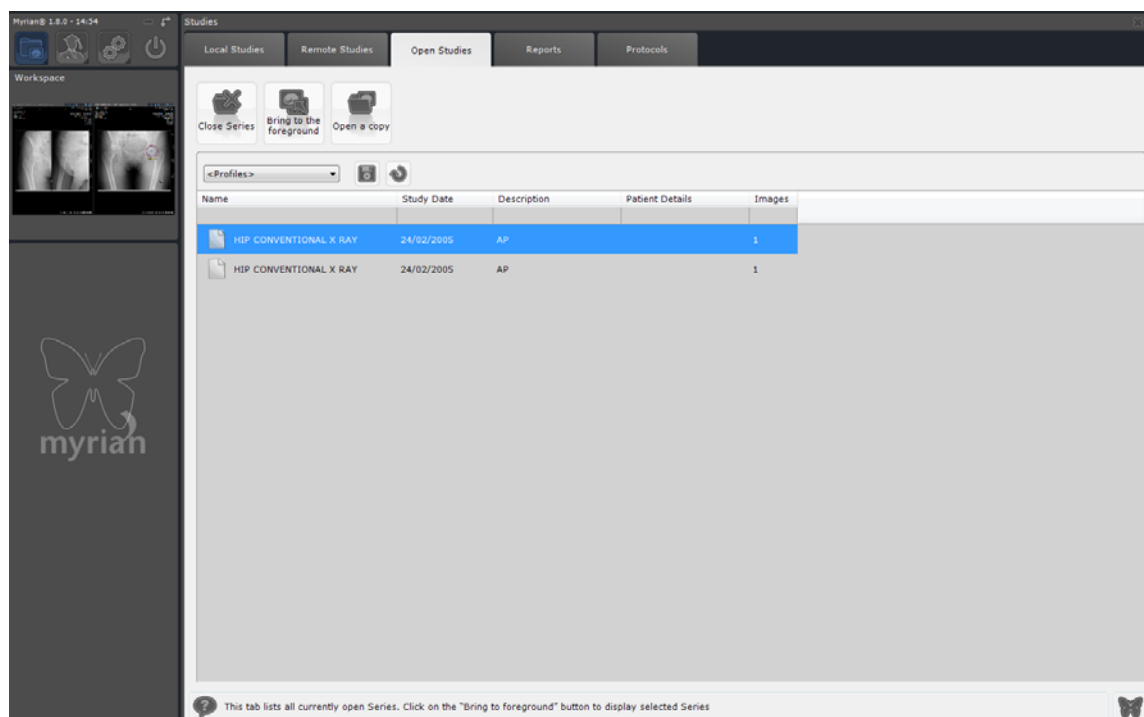


Figure 9-76 A list of all Studies currently open in Myrian®



You can also use filters and create column Configuration Profiles in the same way as the Local Study List Tab (see Section 9.1.3 and see Section 9.1.8).

### 9.7.1 Interactive Side-panel

Once a Series is open in the main Workspace, the side-panel displays a shortcut thumbnail of any work going on in the Workspace. You can click on this thumbnail to return to the main viewing area.

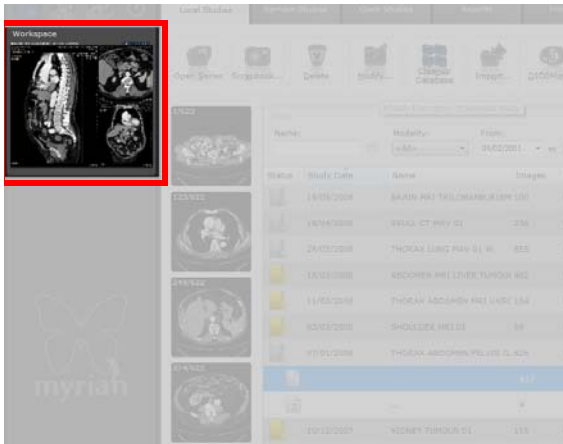


Figure 9-77 Shortcut thumbnail in the Side-panel (Study List tab)



As long as a Series is open, the Workspace thumbnail is present at all times in the Side-Panel of any of the main button screens (Study List, Remote/Open Studies, Protocols, Preferences, etc.)

## Chapter 10

# 10 Viewing Image Series in the Main Workspace

## 10.1 Overview

Once loaded, Studies open in the **Main Workspace**. The Workspace is laid out in **three zones**:

- 1. The **'Image zone'** (see Section 10.2) displays the images for the currently open Series. **All the images** of the current Series are grouped together in this area, which bears the Series' identification at the top of the frame. Depending on the **visualization mode** (grid, MPR), other frames may be displayed within this frame. The disposition of the frames depends on the page layout selected for the Series (2x2 grid, horizontal sequence, vertical sequence, etc.).
- 2. The **Toolchest** (see Section 4.1) is made up of sets of function buttons to edit, measure, annotate etc. It can be 'snapped' to sit vertically on the left or horizontally at the top of the screen and is divided in three areas:
  - The **Main Screen buttons** (see Section 4.2) top-left and groups of contextual buttons.
  - The **Toolbars**
  - The **Mouse-button** assignment area (see Section 4.9)
- 3. **Information/help panel** (see Section 10.6)
  - The **Help Bar** displays a brief description of functions currently being used. The Wizards, an interactive guided assistance module, can be launched from here (see Section 10.6.1).
  - The **Scrapbook Bar** displays thumbnails of the Series currently being visualized (see Section 10.7)
  - The **Mouse-over information bar** (see Section 10.8) provides technical information on the **specific area in an image** that is **under the cursor** (e.g. the Hounsfield value of a pixel in an image that has come from a medical scanner)
  - The **Warning Bar** (see Section 3.9) provides a summary of different kind of information/error messages
  - The **Workspace saved states** enable to retrieve and restore a workspace as saved at a given time.
  - The **Cancel Task** button (see Section 7.15.12)
- Click on the **Background Task** button to display/hide the 'Background Jobs' window.
  - The icon is animated during **import/export** and **print** operations.



You can hide all toolbars as well as the bottom information panel if you wish to toggle the image display to full screen mode: press CTRL + I. To restore the overall layout mode back to normal, simply press CTRL + I again.

---



To visualize the images without display of all button panels, press Ctrl+i (lowercase or uppercase) over a viewport. To deactivate the option, press Ctrl+i again or Escape.

---



Double-click on any toolbar category name to minimize or maximize its display.

---

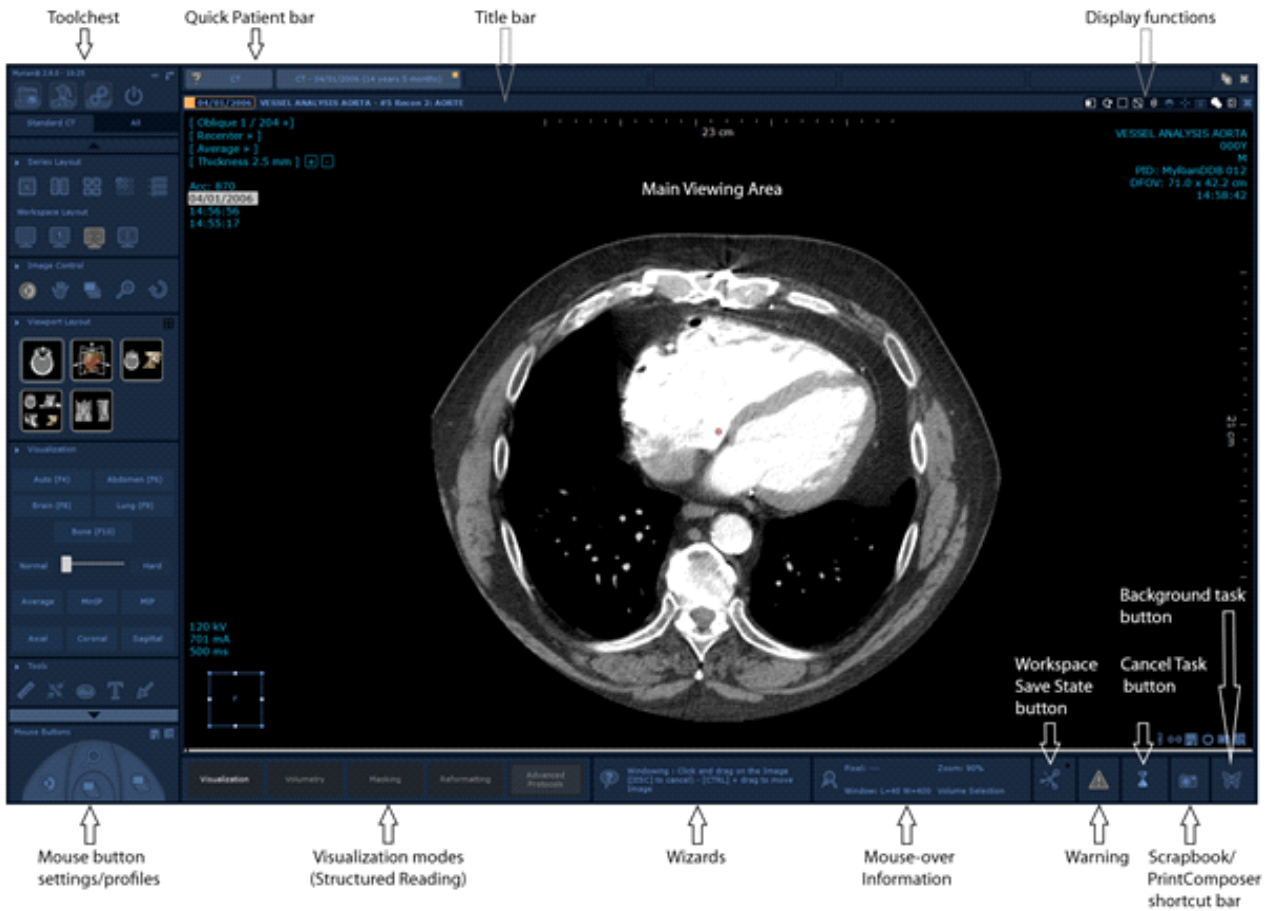


Figure 10-1 Main Workspace areas



To show or hide the information panel at the bottom of the workspace, go to the Visualization contextual menu and activate/deactivate the Information Panel option.

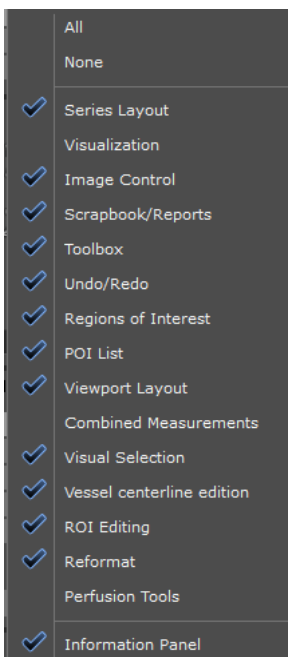


Figure 10-2 Information panel display

## 10.2 Image area

The Image area, which takes up the largest part of the workspace, displays the images of the Series being currently viewed, as well as information relative to these images. It contains the views and Viewports and can be spread-out over several monitors. Various display settings can be adjusted using the Display Function Tools at the top-right of the Image Area (see Section 4.4.3).

You can visualize and manipulate the images in the Viewports in single or multiple frames according to the **visualization mode**.

When several Series are loaded at the same time, they are displayed in the image area according to the **Series Layout settings** (see Section 4.3 for more information on **visualization modes** and **page layouts**).

### Introduction

The software displays images in **Native Mode** or in **MPR Mode (Multiplanar reconstruction)** (see Section 6.1).

- **Native Mode** displays the **original, unaltered 'stack' of image slices** in a user-definable 2D grid layout.
- **MPR Mode** displays a **homogeneous reconstruction** of the slices. Images are displayed in **either 2D frames or in 3D frames**.



By default, the software does not allow you to open Series belonging to more than one Patient(\*) with the same Workspace.

---

If you attempt to open Series of more than one Patient from the Study List, the following warning message appears:

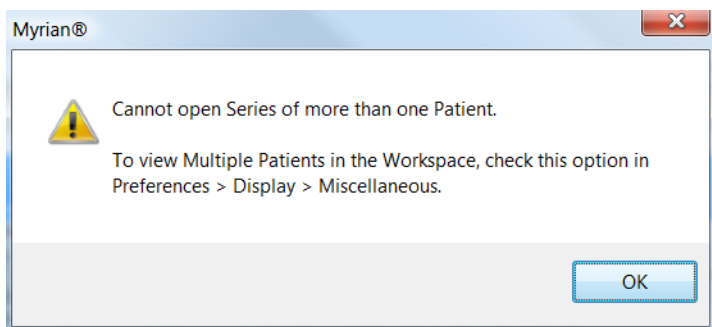


Figure 10-3 Cannot open Multiple Patient Series error message

If you open a Study whilst a Study of another Patient is already open, the Study which is currently open is automatically closed.

If, however, you do wish for any reason to open multiple Patient Studies at the same time, you must click on the checkbox to activate the 'Multiple Patients in Workspace' option in the Miscellaneous list of the Preferences>Display tab.

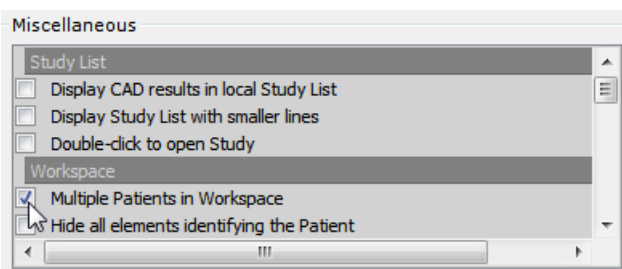


Figure 10-4 Multiple Patients in Workspace Option in Preferences>Miscellaneous



You will still be prompted by a warning message when you attempt to open Series of more than one Patient.

- Click on 'No' in the warning window to proceed with opening multiple Patient Series.

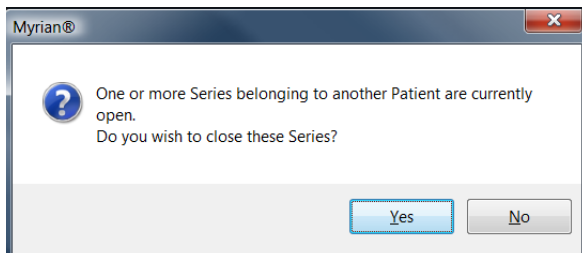


Figure 10-5 'Multiple Patients in Workspace' warning

## 10.3 Viewing Series

### 10.3.1 Native Mode

When Series are loaded in **Native Mode**, the DICOM images are displayed in their initial **state** (thickness, orientation, number of slices, etc.), **as they were captured**.

They contain all the **original DICOM information**:

- **The Individual image** (time and date of capture, image number and position, etc.)
- **The Series** (Patient Name, Gender, etc.).

In Native Mode, view panes:

- Are **two-dimensional**
- Display the title '**Native**' in the Orientation Menu (at top-left of the frame).

### Functionality and behavior






The following tools are available for Native Mode View Frames:

- Basic **image display adjustment controls** (Grayscale Windowing, Zoom, Magnifying lens, etc.)
- **Annotation tools** (Distance measurements, Text and Arrow-Pointer Annotations).

### 10.3.2 Native Image Format using compression

When Series are loaded with JPG images that underwent compression, a message is displayed to your attention indicating that the image is in a "lossy" format.

You may wish the compression ratio to be visible on the view in order to have an accurate knowledge of how much the quality of the image is affected.

- To access the image compression value, follow those steps:
- At the upper-right corner of the view, click-right on the DICOM icon  to open the following settings panel.
- In the 'Image fields' category, scroll down the DICOM Field list until reaching 'LossyImageCompression Ratio' field corresponding to the 0028,2112 ID.
- Once selected (the cell color changes in blue upon selection), customize the information display on the view:
  - at the upper left 
  - at the upper right 
  - at the bottom left 
  - at the bottom right 

You can previsualize the DICOM information on the view either in terms of 'Field Names' or 'Contents'.

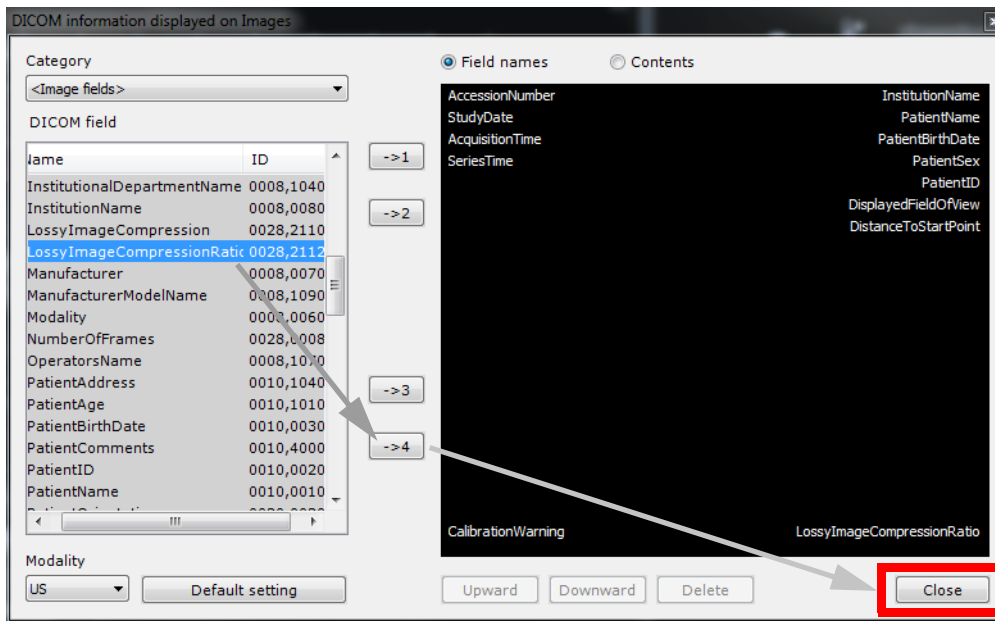


Figure 10-6 DICOM 'Lossy' Image compression ratio' field and DICOM information display customization

- Click on 'Close'.

Compression ratio result appears on the image.



Figure 10-7 Visualization of compression ratio on the 'lossy' image

### 10.3.3 Navigate in Native Mode

When you are viewing studies in **Native Mode** (including MR studies), keyboard cursor arrows can help you navigate through the images/series:

- Up Arrow Key - Go to the previous image of the series
- Down Arrow Key - Go to the next image of the series





You can also use the mouse wheel to navigate from one image to the other.

---

- Left Arrow Key - Go to the previous page of the series belonging to the patient exam
- Right Arrow Key - Go to the next page of series belonging to the patient exam

### 10.3.4 Multi-view display

If your Multimonitor option is activated (see Section 8.3.7), all images of the study are displayed all together in a workspace divided into 2 parts:

- The left view includes all the images of all series of the whole study that are stacked with one another and, in which you can navigate in a continuous loop
  - The right view displays again all the images but this time, one next to another as a grid. When clicking on one given image, those behave like preview thumbnails and the clicked image is automatically displayed in the stack in the view at left.
- 



It is possible to display up to 34 images separately

---

This visualization mode is specifically designed for images of CR modality.



Figure 10-8 Standard CR protocol in Multimonitor mode

If the Multimonitor option is not activated, select the 'Stack & Grid' mode in the protocol

#### 10.3.4.1 Procedure

- Open CR series

All images are displayed in grid mode (one view per image) in the workspace.

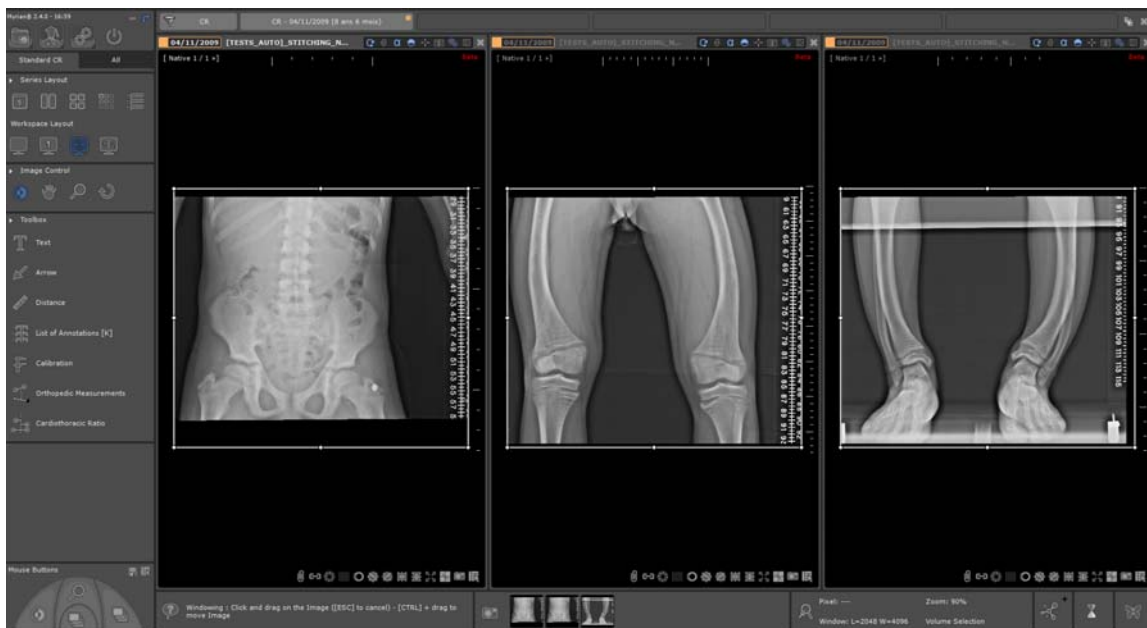


Figure 10-9 Standard CR protocol: Images displayed in auto-Grid mode

All useful tools are available from the Toolchest.

## 10.4 Active viewport

Each view includes an **active viewport** which by default is the first viewport located at its left. The active viewport which is represented by a **white frame**, is a viewport to which predefined actions (for example, windowing, orientation, etc.) are set to apply to this selected viewport only instead of applying to all viewports of the selected highlighted view. Therefore, only the active viewport of the active view (in case there are several) will receive the action.

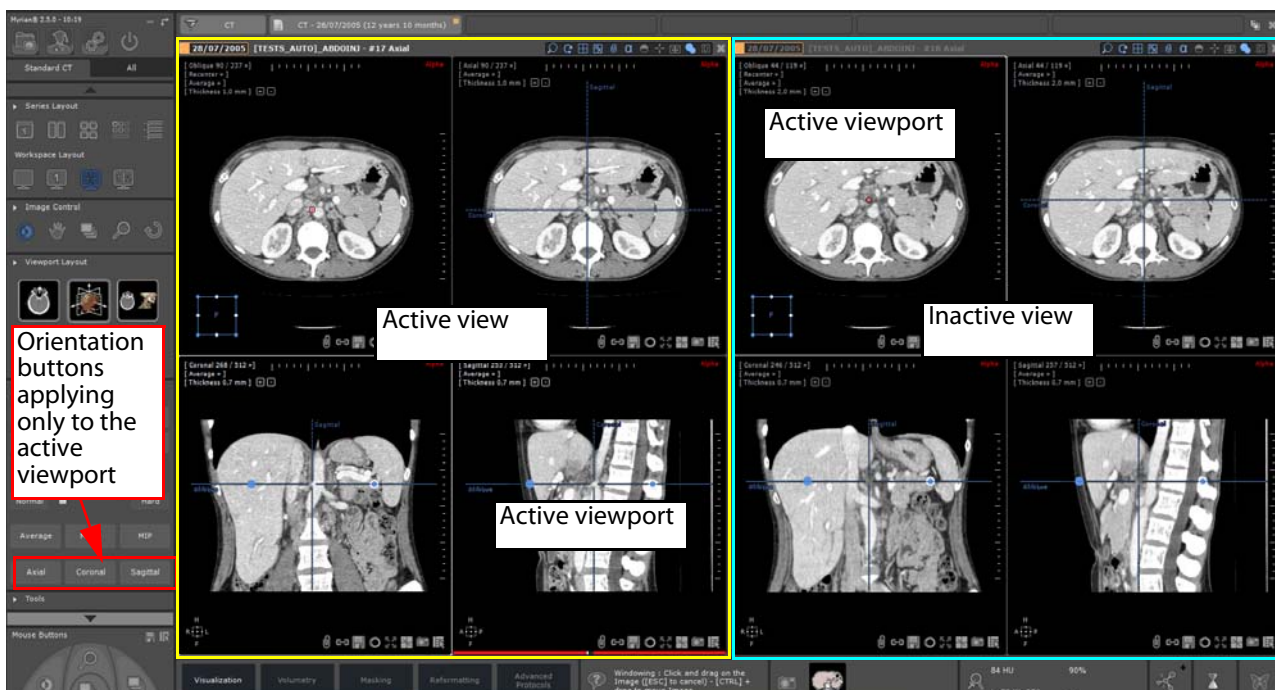


Figure 10-10 Visualization of the active viewport of the active view in the Standard CT protocol

- Click on the viewport of your choice to switch the active viewport.



The 'active viewport' notion as well as the related actions that can be performed is a configurable protocol parameter

which applies for some predefined protocols only, specifically for multiphase one.

---













The active viewport applies to any type of viewports including 3D viewports.

---

## 10.5 Viewport Buttons

A set of buttons at the bottom-right hand side of 2D Viewports give access to various functionalities:

-  /  Show/Hide annotations
-  Activated/Deactivated anatomical center synchronization
-  Grid Filtering, to remove Grid artifacts (see Section 10.5.4)
-  New Series creation, to create a new Series based on the image settings of the active Viewport
-  Shutters (see Section 10.5.2)
-  Edge Enhancement, to harden or soften the edges of the active image (see Section 10.5.5)
-  Image Full-screen/restore
-  Capture Menu (see Section 5.1.1)
-  Context Menu which gives access to all functions in the software



These tools may or may not appear depending on the modality or settings.

---

### 10.5.1 Create New Series

#### 10.5.1.1 Overview

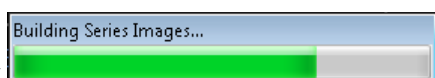
The New Series function  enables the creation of new Series in the orientation of the active Viewport.

#### 10.5.1.2 Method of use

- Whenever you wish, click on  at the bottom-right of your target Viewport.



Figure 10-11 Create New Series in Oblique Mode



A progress bar appears and as soon as processing has terminated, the New Series opens alongside any open Series. The new series is also listed in the Study List within the target Study.

The New Series will be in the exact orientation of the export and will be configured with the same Rendering Mode and Slice Thickness parameters as it was captured with.



The newly created local series are DICOM images to which is automatically allocated « SeriesInstanceUID » and « SeriesNumber » DICOM fields with unique values so as to be easily identified whenever the new series is exported onto the PACS (as a result of its unique identifier).



The « SeriesNumber » DICOM field is a configurable setting. Go to the [PRINTING] section of the \_intrasense.txt file and insert the following command:

```
EXPORTSCRAPBOOKMODE=1
```

```
SERIESNUMBERBASE = 500 [(for example) knowing that default value is 100]
```

This base number increments each time a new series is created (unique ID number): 501, 502, etc. according to the above example.

## 10.5.2 Shutters

### 10.5.2.1 Overview

Display Shutters are overlays which enable you to hide or “black out” unwanted parts of CR-like images (CR, DR, XA, RF...), such as unexposed parts of an X-ray which appear very bright and may affect the visibility of relevant parts of the image.



There are 2 types of Shutters:

- **DICOM Shutters** are circular or rectangular masks which are generated by the radiographer at the time of the acquisition of the images. DICOM Shutters can be switched on or off whenever they are present in an image but cannot be moved or modified.
- **User Shutters** are rectangular masks which are automatically generated by the software around X-ray images that do not already contain any DICOM Shutters. You can change the size or position of User Shutters freely by click and drag.





Similarly, any DICOM Overlay added to the X-Ray at the time of capture will be included on the image and visible in Myrian®.

### 10.5.2.2 Method of use

When you load X-ray images into the Workspace, the Shutters will by default be active. The Shutters can be deactivated/ reactivated by clicking on the Shutters icons  /  at the bottom-right of the Viewport.

---

 If the Shutters icon is in the 'closed' position , this indicates that Shutters are present in the image and that some parts of the image are hidden.

---

When the images contain User Shutters, a white frame appears around the images.

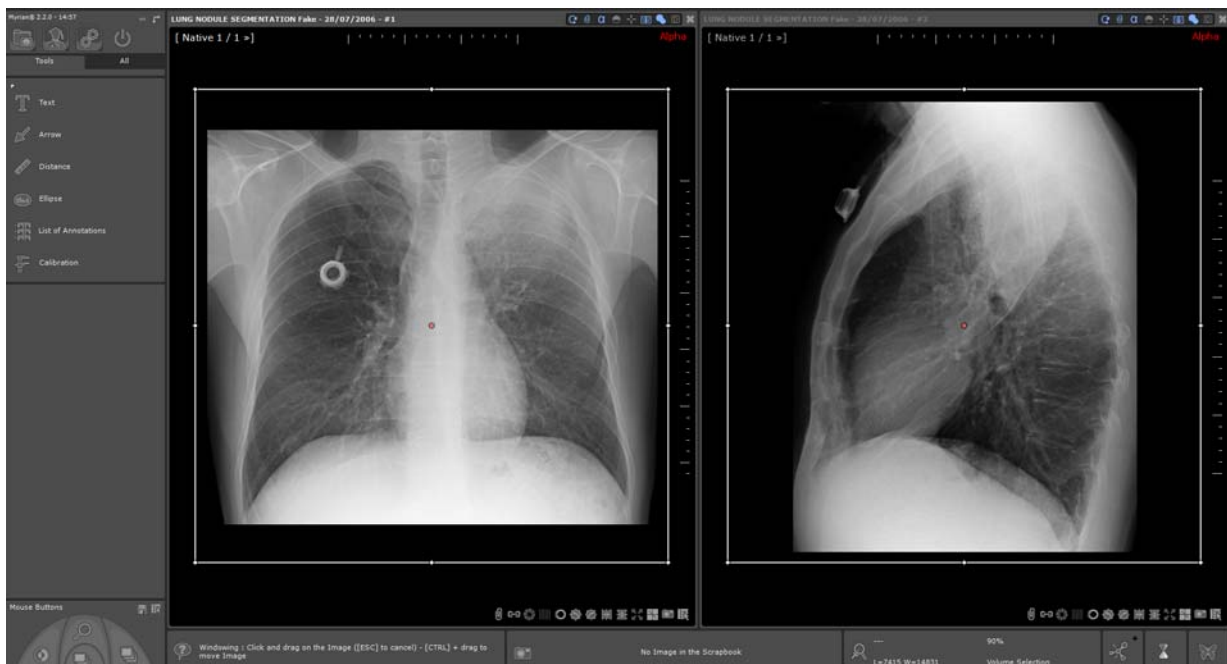
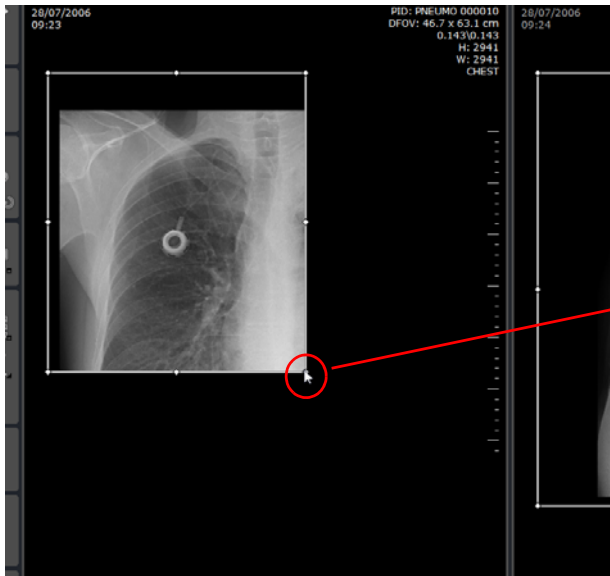


Figure 10-12 User Shutters



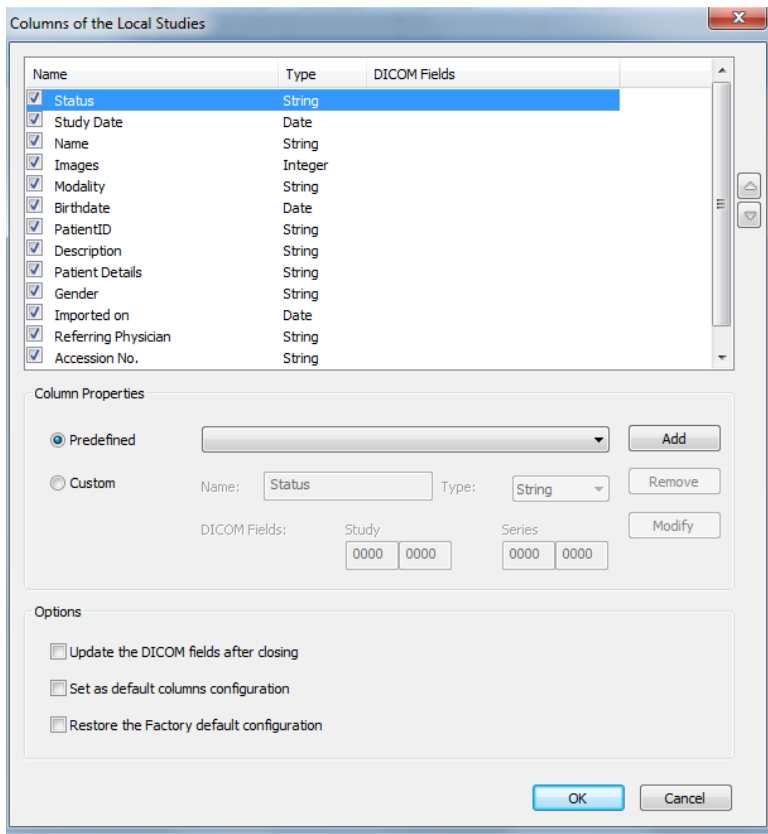
Click and drag the borders or corners of the shutters to resize or move the frame accordingly.

Figure 10-13 Adjust User Shutters

You can create a custom Column in the Study List to automatically display all Studies which contain DICOM Shutters:

- Click on  above the Local Study List

In the Configuration Window:



1. Click on 'Custom'
2. Edit the Name field for your Custom Column
3. Type-in a corresponding value in the DICOM fields box(es)

Figure 10-14 Column configuration window

The new Column will then appear every time you access the Local Study List.

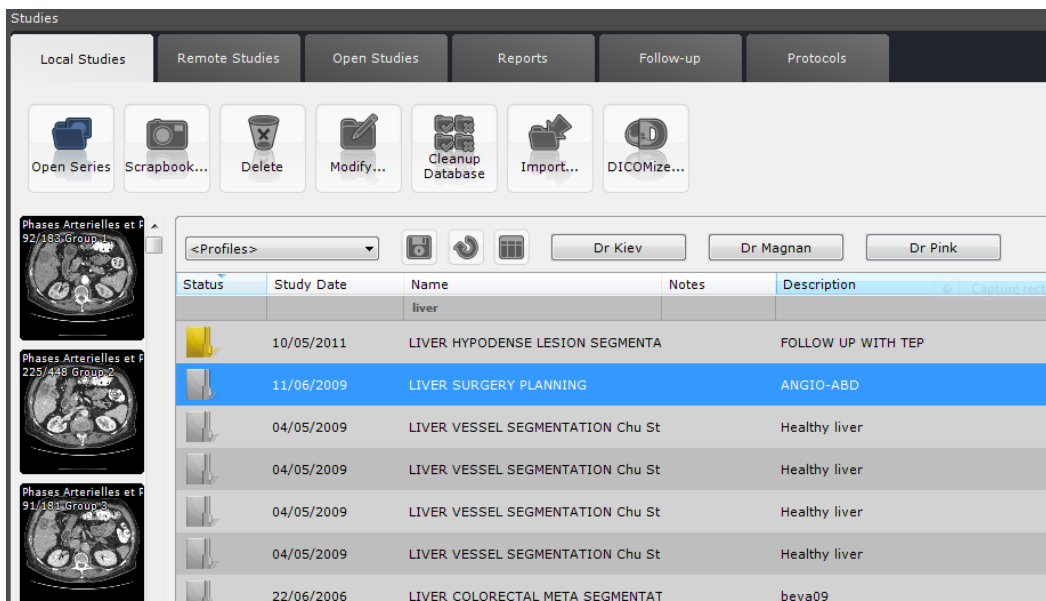


Figure 10-15 Custom Shutters Column in the Study List

### 10.5.3 Flip/Rotate

All 2D images can be flipped (horizontally/vertically) or rotated 90° to the right/left using the Flip/Rotate buttons



which appear at the bottom-right of CR, DR, DX, RF and XA images.

**For all other modalities**, please use the Flip/Rotate menu which appears when you click on the orientation square at

bottom-right of each frame.

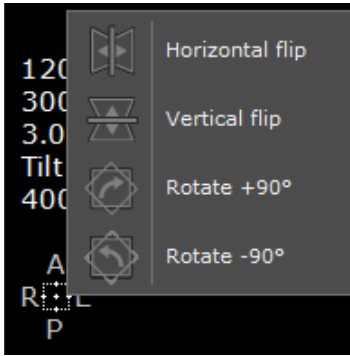


Figure 10-16 Flip/Rotate menu

### 10.5.4 Grid Filtering


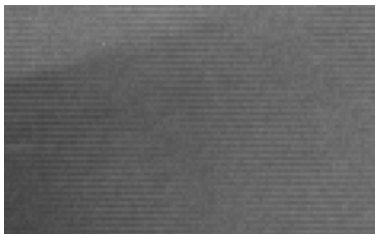
This function  enables you to remove artifact caused by Anti-Scattering X-ray grids used on DX, CR, DR, DX, RF and XA Modalities.



Figure 10-17 Anti-scattering Grid Artifacts on CR image

To use the Grid Filter:



Zoom highly into the image to visualize the direction of the noise caused by the Grid (Vertical or Horizontal)

Figure 10-18 Horizontal Grid 'noise' on zoomed-in X-ray



Figure 10-19 Filtered image

Click on the 'Grid Filtering' button  at the bottom-right of the Viewport to switch the Filtering on or off



Grid Filtering modifies the appearance of the original image and therefore can potentially hide important parts of the



Image or alter your perception.

---



The filtering setting is persistent. The filtered images will therefore remain filtered from session to session until it is removed.


---

#### 10.5.4.1 Remove Grid Filtering

You can remove the Grid Filtering to view the original, unaltered image by clicking on the Grid Filtering button and selecting 'None' from the resulting Grid Filtering Menu.

#### 10.5.5 Edge Enhancement

To sharpen the definition of any image:

- Click on  at the bottom-right of the corresponding Viewport and choose the desired image sharpness filter setting from the Edge enhancement Menu.

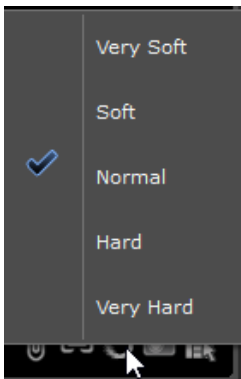


Figure 10-20 Edge Enhancement Menu

---



When this option is activated in Native mode, the image filter applies to **all the images of the series**, except for those from 2D modalities (CR, DX, RF, XA...).


---

## 10.6 Wizards and Context-sensitive help

The context-sensitive help panel is at bottom left of the image zone. It constantly displays simplified information about the tool or zone being currently used. This information panel is particularly useful for learning supplementary key and mouse combinations to access various visualization and editing controls (see Appendix 3). You can minimize this panel by clicking on it with the right mouse button.

### 10.6.1 Wizards and Guides

"Clinical guides and Wizards" are an interactive set of tools that provide step-by-step guidances on where to find and how to use various features in Myrian®. They are operated as follows:

- Click once on  in the Context help tab to open the 'Clinical Guides and Wizards' screen

Click here to start wizard interactive functions

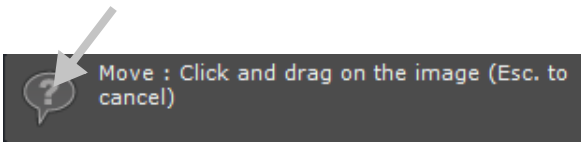


Figure 10-21 Context help tab

- Select a Guide of your choice from the list on the left (you may also enter a keyword in the 'Filter' box)
- Click 'Start' to launch the Wizard (or double-click on its name in the list)

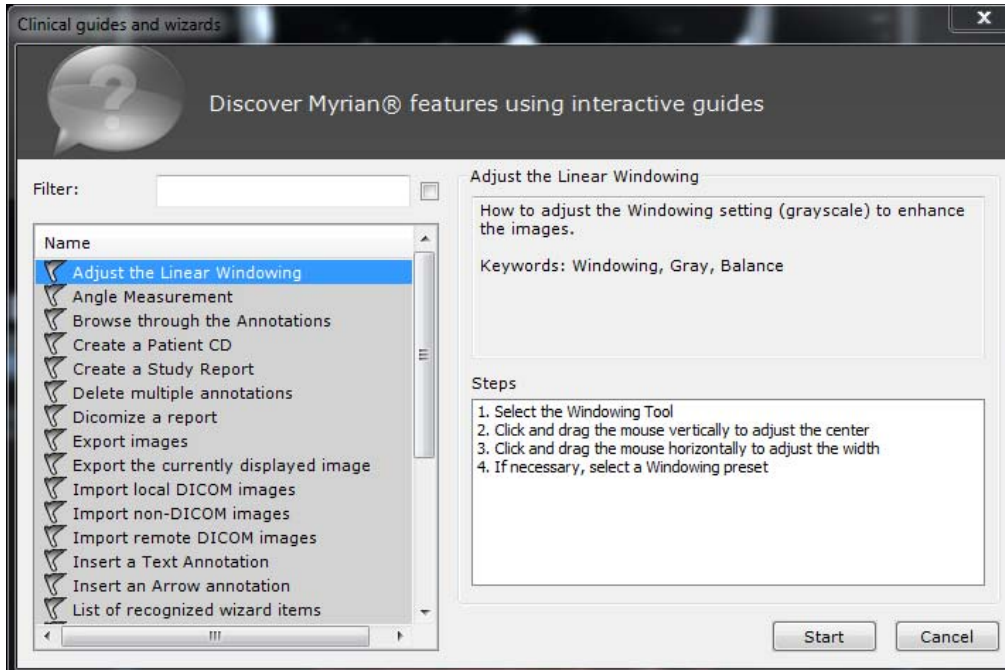


Figure 10-22 Clinical guides and wizards screen

The right-click menu on the list of Clinical Guides makes it possible to:

- **Print** the Tutorial
- **View** the Tutorial
- **Refresh the List** of Tutorials

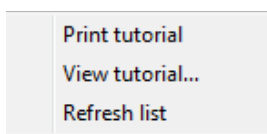


Figure 10-23 Right-click menu (list of Guides)

When a wizard is launched, an 'Always on top' floating panel appears displaying all the steps required to carry out the action.

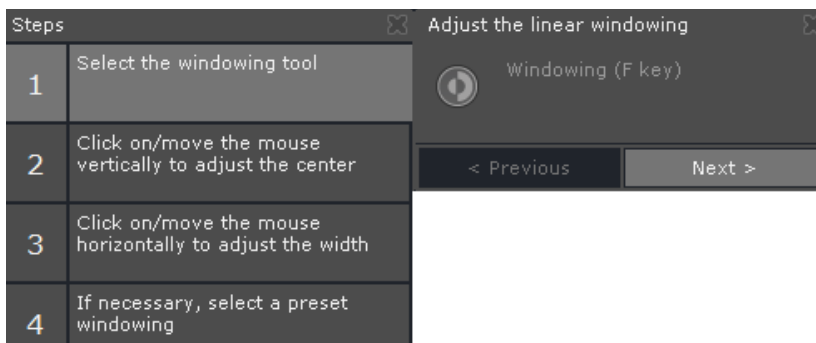


Figure 10-24 Wizard floating panel


The first step is highlighted and the command key required to carry out the **current step** automatically begins to blink.

It continues to blink until the user has carried out the step.

The Wizard displays the next command and the next tool then begins to blink until it has been carried out or the Wizard has been closed.

The Wizard is closed by clicking on  at top right on the right panel.



By default, this is a double-panel describing at left each operational step and at right a summary of the tool and of its functions (the two panels can be minimized to a single panel taping  on the left panel, and restored using the white Arrow at bottom left in the 'steps' area of the minimized screen).



In cases when a command key required by any step is located on a floating toolbar, the toolbar automatically appears and the key starts to blink. Both the floating toolbar and the blinking command key disappear as soon as the step has been completed.



A small icon  appears to the left of the upper-right 'Quit' cross when there are other Wizards that deal with similar subjects. Click on this icon to open a window displaying the list of these Wizards.

## 10.7 Scrapbook thumbnails

This panel shows thumbnails of the various Scrapbook images that you have chosen for the current Series or Study.

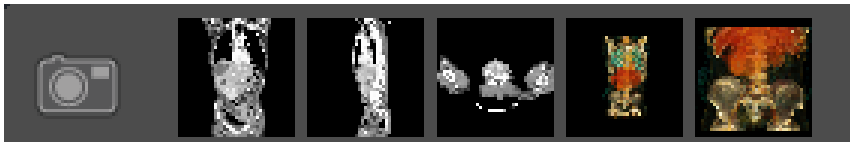




Figure 10-25 Scrapbook thumbnails

- Click **with the left mouse button** on  to open/close the Scrapbook.
- Click **with the right mouse button** on  to minimize/restore the panel by hiding/displaying the thumbnails.



If the Scrapbook is set to display images in a 1x1 grid layout, clicking on a thumbnail opens the Scrapbook directly on the thumbnail clicked upon.

## 10.8 Mouse-Over information

At the bottom-center of the workspace is the **Mouse-Over tab**. This tab displays **zoom level** and **grayscale ('Window') value** information for the current view being passed over by the cursor. It also provides **constant updates** on the **specific point that the mouse cursor is passing over**.

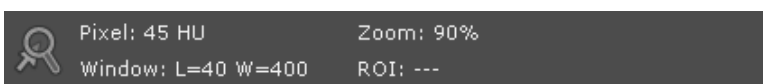




Figure 10-26 Mouse-Over tab

Information displayed in the tab:

- The **value of the pixel** hovered over by the mouse-pointer (if the mouse is in an image area)\*.
- The **Windowing settings** of the current view being passed over by the mouse (center point and width of the grayscale)\*.
- The **zoom level**, in %.
- If the optional ROI and visual selection modules are installed with your application, the **name and color of the region of interest** (ROI) hovered over is also indicated

\* (Values given in HU if the images are (CT) scanner modality-originated and as signal intensity for other modalities)

Additional features:

- Click with the **left mouse button** on  at the left to toggle the display of this tab and display the **slice thickness** and **coordinates** of the point hovered over. Click again to restore display to standard information.
- Click with the **right mouse button** on  to minimize/restore the Mouse-Over tab.



You may also display density of the pixel under the pointer by pressing the 'Alt' key while moving the mouse.

---

---

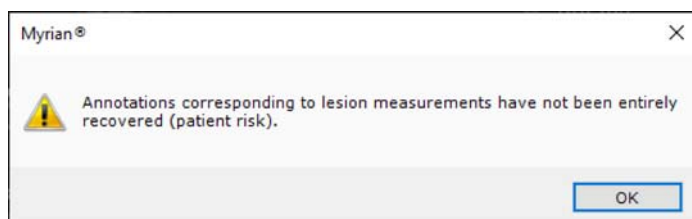
## 10.9 Warning Box

Warning messages are displayed in a dedicated warning box from the workspace. This information bar will be visible from main windows and from workspace.

- A click on the warning icon allows to display/hide the Warning box
- The warning icon flashes when a warning message is received by the warning box
- The addition of new messages is indicated by an animation.
- The icon's colour is representative of the highest level of message displayed in the toolbox (black for information messages, orange for warnings, or red for regulatory messages).

Myrian messages in three categories:

- **Information messages:** an information message is displayed in blue at the bottom right of the screen
- **Warning messages WITHOUT patient risk:** warning message without patient risk does not block the user. This message is displayed in orange at the bottom right of the screen
- **Warning messages WITH patient risk:** warning message with patient risk blocks the user. We need to be sure that the user has seen the message. This message is displayed in a blocking message box

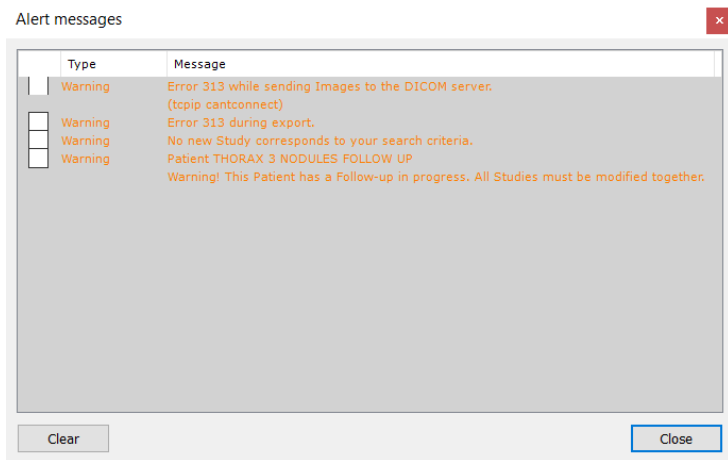


All displayed messages are listed in the toolbox, composed of three columns:

- The first column is a checkbox that is associated to each message to allow the user to acknowledge the messages.
- T

- The second column is the message type; two different types of message can be displayed: information and warnings.
- The third column is the message itself.

Information messages are displayed in black and Warning messages are displayed in orange.



3-27 Warning bar window

This toolbox is kept during an entire user session. The content of this window can be cleared manually by clicking on 'Clear' button. It also be cleared when the application is closed and relaunched.

## Chapter 11

# 11 Toolchest

## 11.1 The Toolchest

All tools and functionalities appear in the Toolchest. They are divided into two areas:

- The Main Screen buttons situated at the top-left,
- The Display Function buttons which appear at the top-right of the Workspace. They are grouped by function



Some protocols (Native Images, Advanced CT, Standard CT, PET/CT Fusion, NM/CT Fusion, Standard MRI, etc.) provide you with a structured reading mode (see Section 6.1.3) in which only relevant tools are displayed, as well as the legacy protocol interface accessible from the 'All' tab' in the Toolchest.

---



Some tools are hidden by default in various Protocols. To bring all your activated tools back into view, right-click on the Toolchest and select 'All' from the context menu.

---



An easy way to find out the purpose of any button is to read its 'tooltip'. To do this, place the mouse over the button. After a short while, a small tooltip callout will appear containing a short description of the button's function. Move the mouse away and the tooltip will disappear. Tooltips are available for most of the information fields found in the various screens, as well as alphabetic and numeric entry areas, lists and checkboxes.

---



Tooltips often contain shortcut keys whereby various commands may be operated directly from the keyboard.

---



At all times, the context help provides a succinct user guide for the function you are currently using.

---

## 11.1.1 Toolchest

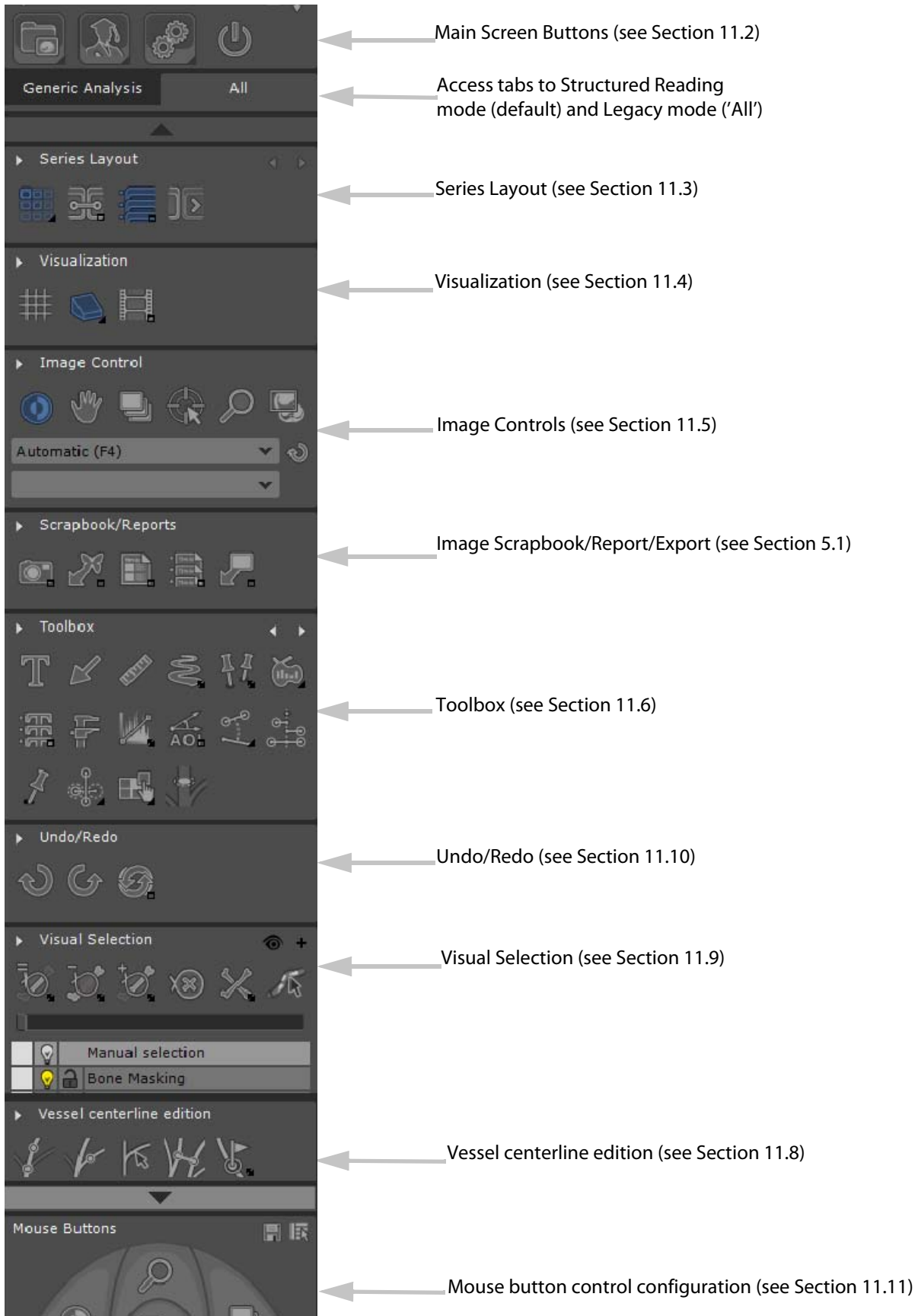


Figure 11-1 Legacy toolchest (vertical layout)

The Toolchest function keys are grouped by category:

- Series Layout,

- Visualization,
- Image Control,
- Scrapbook/Reports,
- Toolbox,
- etc.

All toolbars are detailed in the sections below.

Some icons bear additional distinguishing marks:

- Certain buttons simply attribute a set of functions to the mouse buttons. Their icons bear no distinguishing feature.
- Certain buttons toggle between an activated or deactivated state (e.g. 'hide/show' or 'preserve/overwrite'). This type of button has a small check mark at its bottom-right corner.
- Certain buttons open other screens which can be closed either by clicking again on the same button or by clicking on the cross ('X') at the top-right corner of the window. Such buttons have a small window icon at their bottom-right corner.
- Certain buttons affect a tool's behavior and/or display modes. They have a small triangular Arrow at the bottom-right corner. Click on these Arrows to reveal floating menus displaying various choices. Certain tools (e.g. Regions of Interest tools, if installed) may also be opened by double-clicking on their button to provide a set of choices.

### 11.1.2 Customizing the Toolchest

The Toolchest display can be customized in various ways.

#### Horizontal/Vertical layout


You can toggle the Toolchest from vertical to horizontal by clicking  to the right of the Main Screen buttons.



Figure 11-2 Toolchest (horizontal layout)

- When the Toolchest is in vertical position, each Toolbar can be rolled-up/rolled-out by double-clicking on its title.
- When the Toolchest is in horizontal position (at top of the screen), some sections need to be rolled-out by clicking on the small Arrow beside the category title.

#### Hide/Display Toolbars

- To hide or display any Toolbar, right-click on any part of the Toolchest and use the individual checkboxes in the context menu that appears.



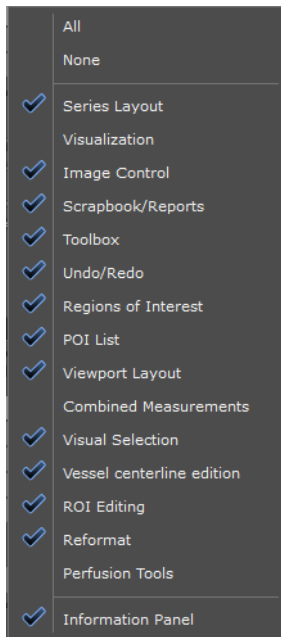


Figure 11-3 Toolbar context menu



If the screen resolution of your computer is set to less than 1600 x1200, some parts of the Toolchest may be beyond the visible area of the screen (below or to the right, depending on the Toolchest layout). Use the Scroll Arrows that automatically appear in such cases, or the mouse wheel to bring the hidden parts of the Toolchest into view.

## Use of the mouse and keyboard

Functions in Myrian® are activated/deactivated via a combination of keyboard and mouse actions.

Certain guidelines apply:




Mouse/keyboard action	Effect
Left, middle or right mouse click	Operates all icon functions (mouse-over tooltips pop-up to describe icon functions) Any left-click mouse action initiated may be aborted by clicking with any of the other two buttons (i.e. middle or right) or by pressing the 'Escape' key
Keyboard shortcut	Certain functions may also be activated through keyboard shortcuts. Shortcut keys are described in mouse-over tooltips as well as in Appendix 3
Holding down the CTRL key	Temporarily associates the three mouse buttons to a 'translation' of the image. The original function of a mouse button is restored when the CTRL key is released
CTRL+Z CTRL+A	Undo  restores a previous state by undoing the last action Redo  to redo an action which has been canceled by the 'Undo' function The 'History' button  opens the Undo/Redo Commands History window which lists all the current session's actions which have been done or undone.
CTRL+I	Toggle Full screen display
ESC (top left of the keyboard)	Any keyboard action can be aborted by pressing the 'Escape' key before the release of the mouse-button

Table 11-1 General rules for Myrian® keyboard and mouse usage



When the mouse is over an image area, the cursor takes the shape of the functionality associated with the left mouse button.

---



Tooltips, context-sensitive help menus and interactive Wizard guides are available at all times for assistance.

---



All Myrian® commands are also accessible through the Context menu at bottom-right of all image views as well as by using the menu key (to the right of the spacebar on recent keyboards).


---

## 11.2 Main Screen toolbar

It enables access to the main screens which are explained hereafter.



Figure 11-4 Main screen buttons

- Press  to close the current Myrian® session.





Button	Function
	Toggles display between List of Studies (local Myrian® database) and the currently open Study (in main Workspace)
	Current Quiz (optional add-on)
	Shows user preferences and global options
	Closes the current session

Table 11-2 Main screen buttons

### 11.2.1 Study List

- Click on the 'Study List' icon  to open the Study List screen (see Section 2.3.1).

This screen enables access to:

- The list of locally stored Studies,
- The Remote Studies tab,
- The Opened Studies tab,
- The Reports tab,
- The Follow-Up tab and
- The Protocol tab.



Click on that same icon again to return to the currently open Study.

---

## 11.3 Series page layout

When you load series, whether the workspace is empty or not, Myrian® automatically switches to AutoGrid in order for you to visualize all loaded studies. The grid is pre-dimensioned according to the number of series to load.

You can load up to 64 views in a non-multiphase protocol.

When trying to open more than 64 series, the following message is displayed.

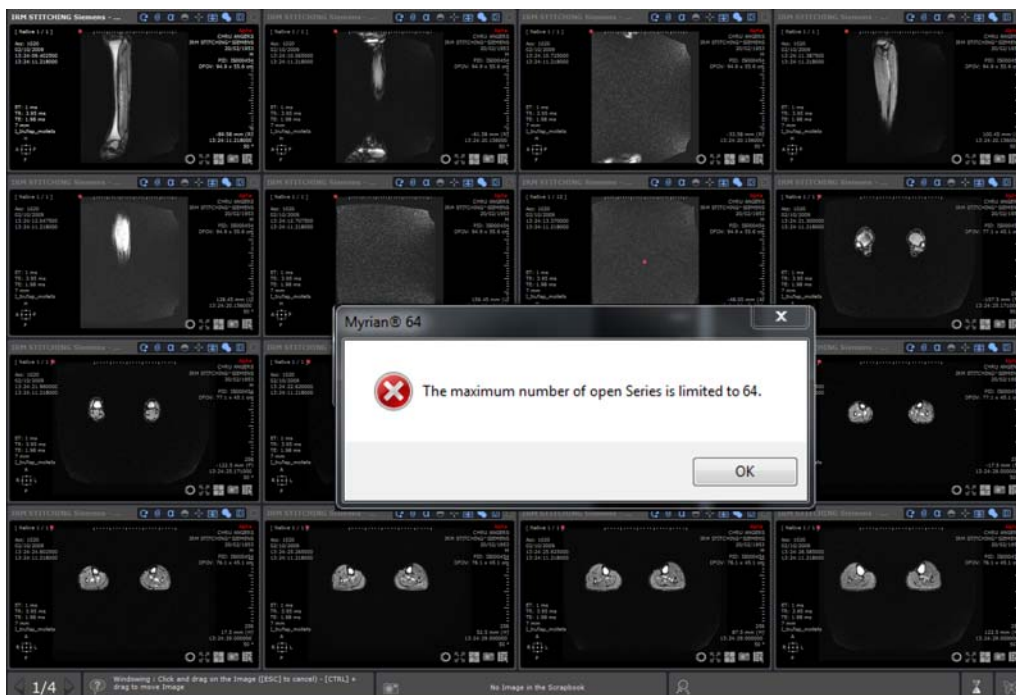


Figure 11-5 Alert message when opening more than 64 series in Native mode

Additionally, the series layout automatically switches from auto-grid mode to a fixed 4x4 grid (up to 16 series displayed at a time). To visualize hidden series, a page menu is automatically created.

- To switch pages, use the page bar located in the information bar at the left-bottom side of the workspace

The page bar indicates the number of total pages and the index of the current page enabling you to display previous/next page clicking on one of the two dedicated buttons. You can also switch between pages via the page navigation menu which can be displayed clicking on the page number.

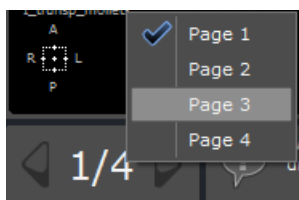
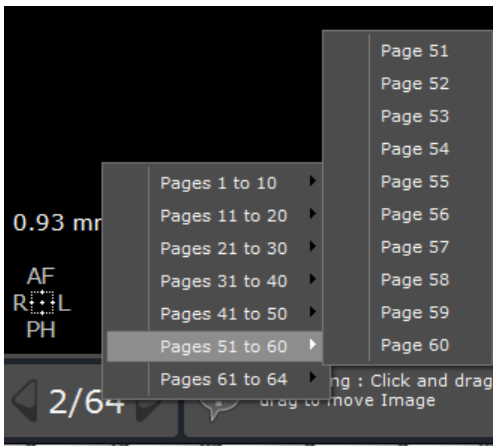


Figure 11-6 Page bar

You can also go back to autogrid to visualize a maximum of 64 views.



According to the number of open series and the selected series layout, the number of pages in the page bar is automatically updated. If there are more than 40 pages, or if the menu is too high to fit on the monitor, the menu is divided into submenus displaying a maximum of 10 pages each.



You can also use the mouse wheel to cycle through pages: first click on the page bar to activate the mouse wheel.



In a double monitor configuration, the page bar always changes pages on the monitor with the active view. If both monitors have the same layout and grid size, pages are changed on both monitors simultaneously.

Besides, when more than one Series is open at the same time, you may also choose from a variety of layouts using the far left key in the 'Series Layout' tab.

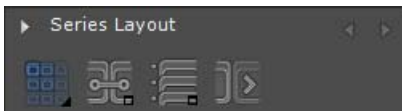




Figure 11-7 Series layout toolbar

This key, identified by the lower-left corner '▲' arrow, opens the menu of layout choices described in the table below.

- To access the menu and the available series layouts, click on "Auto-grid" icon .



When Myrian® is used for the first time, this key defaults on . Thereafter, the icon represents the last layout used.










Button	Function
	All Series are automatically laid out side-by-side (up to 16 Series may be displayed at a time)
	All Series are laid out on top of one another (up to 16 Series may be displayed a time)
	Full Screen layout: a single Series takes up the entire image zone (default load-up layout)
	2 Series laid out side-by-side
	4 Series in a 2 by 2 grid layout
	9 Series in a 3 by 3 grid layout
	16 Series in a 4 by 4 grid layout
	Auto-grid: selects an optimal layout for all Series (up to 16 Series may be displayed a time)
	One or more Series laid out across 2 screens

Table 11-3 Series layout function buttons



This menu is also accessible by right-clicking on the title bar. Via this right-click menu, it is possible to open a copy of the current Series.



You may switch to a full screen view of a Series by double-clicking on its title bar.



To rearrange multiple Series layouts, drag-and-drop individual Series by clicking on the title bar and holding down whilst dragging. Drop on another Series to switch Series places. Series are surrounded by a red contour-line during drag.

The 'Display the Previous/Next Page' buttons display the next/previous Series in the order in which they were loaded.








Button	Function
	Display the Previous Page
	Display the Next Page
	Series Layout
	Adjust the Series synchronization settings
	Display the list of series/studies for the current Patient
	Open Next Study

Table 11-4 Series Layout toolbar

## 11.3.1 Series Synchronization

### 11.3.1.1 Overview

Synchronized Series Navigation enables slice-by-slice synchronized comparison of images in Viewports of the same plane of orientation. The Series Synchronization settings are available via the 'Series Sync' button  in the Series Layout Toolbar (see Figure 11-7) or pressing the 'L' keyboard shortcut.

Locked navigation enables side-by-side viewing of the same anatomical zones.

### 11.3.1.2 Options

By default, all Series in the same plane of orientation are synchronized at load-up. You may also choose to synchronize either:

- 'None', to deactivate synchronization altogether,
- 'All', to synchronize all Series which are open in the Workspace (for example, the same Patient with different PIDs),
- 'All Series of the same Patient', to synchronize all Series of the same patient which are open in the Workspace,
- 'All Series of the same Group', to synchronize Series which are grouped together, as defined in the Grouping area below.

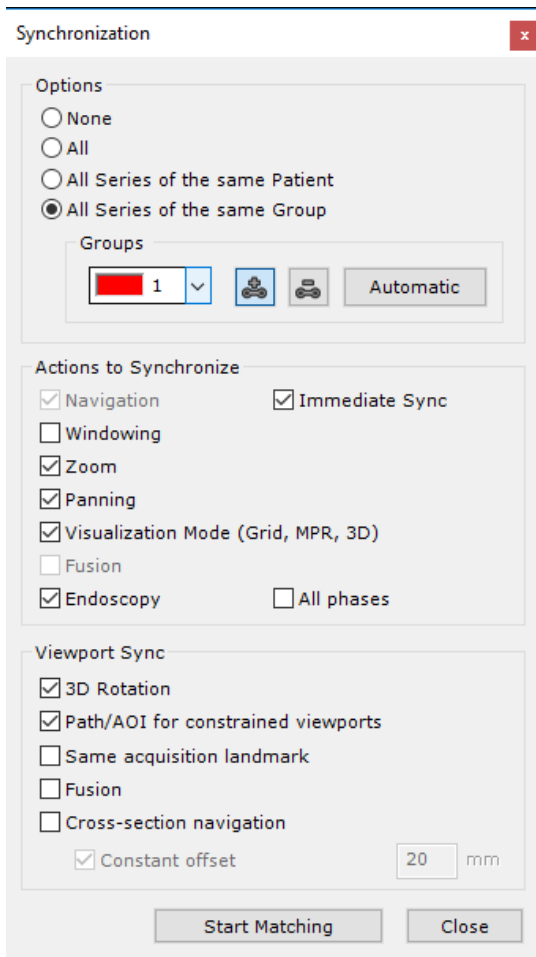


Figure 11-8 Series synchronization screen



When the 'Same acquisition landmark' checkbox is checked, only the series having the same Frame Of Reference UID will be synchronized.

### 11.3.1.3 Groups

This option enables you to create groups of synchronized Series. This can be useful when viewing a large number of Series if you wish to synchronize only certain Series, leaving others un-synchronized.

Groups can be created manually or automatically, each Series can be added to or removed from any Group. Each Group bears a distinctive selectable number and associated color.

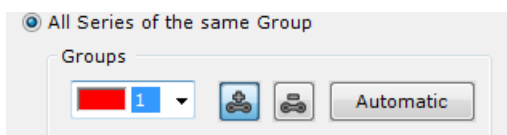


Figure 11-9 Series Grouping Area

By default, the current synchronization group is displayed.



### 11.3.1.4 Operations to Synchronize

You can compare Studies/Series by synchronizing actions such as:

- Navigation
- Windowing (grayscale settings)
- Zoom
- Panning
- Visualization (Viewport layout settings)
- Fusion (enables to sync the fusion mode (overlay/blending) from all fusion viewports between views)
- Endoscopy



You can choose to apply Navigation and Windowing settings either 'immediate' or 'delayed' (after mouse-button is released) via the 'Immediate Sync' checkbox (center-left of the Screen).

### 11.3.1.5 Create Group



Navigation synchronization is automatic for Series originating from the same Study where there have been no significant changes of the patient's position between various captures. Otherwise, synchronization between corresponding slices must be activated manually.

To compare Groups of Series:

- Open all the Series you wish to synchronize
- Click  in the Series Layout Toolbar
- Click on the 'Add to Group' button 
- Click on the image of one of the Series you wish to synchronize to highlight all the Series that can be synchronized with this Series



The titlebars of all the Series that can potentially be synchronized together are automatically highlighted.

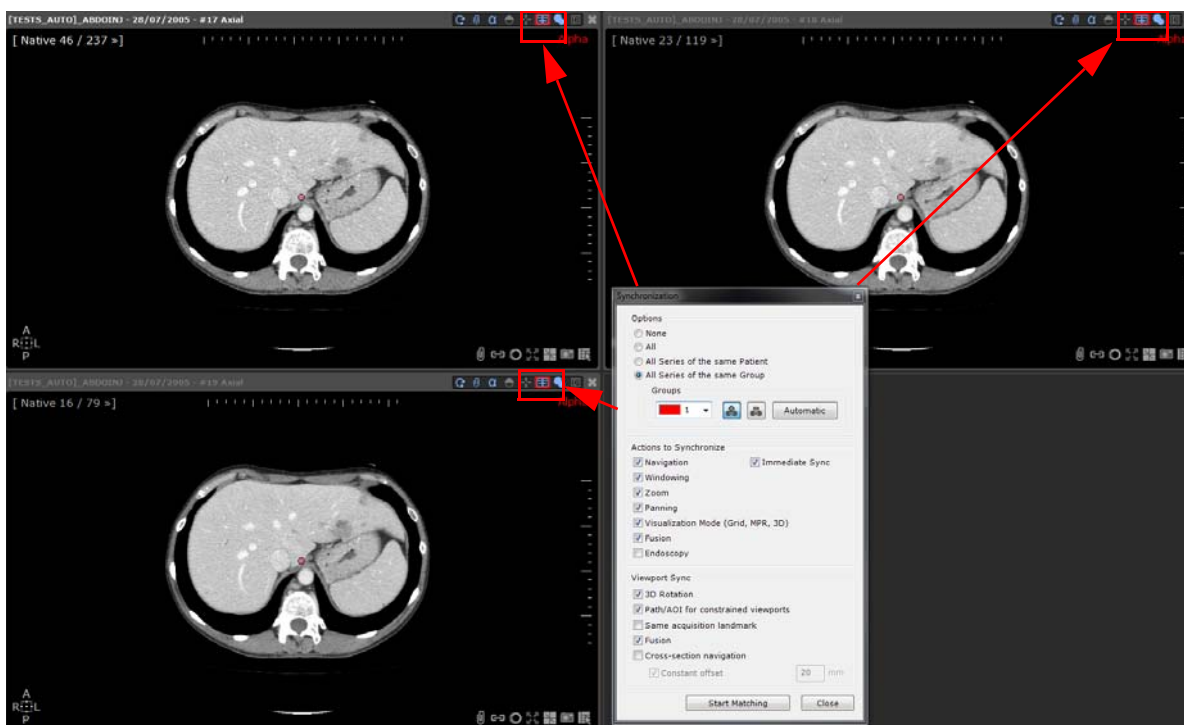



Figure 11-10 Goupable Series titlebar highlighting

- Click directly on the images of each Series you wish to add to the current Group
- If you wish, you can repeat this procedure to create multiple synchronized groups



The 'Sync button'  at the top-right of each grouped Series will be surrounded by the color corresponding to its Group.





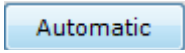
When the display is optimized for black and white monitors in the Preferences>Display>Miscellaneous options, the corresponding Group number is displayed to the left of the 'Sync' button 



Figure 11-11 Layout Options (upper-right of Main Workspace) showing the Group Color surrounding the Sync button preceded by its corresponding number

### 11.3.1.6 Create Groups automatically

You can also create Synchronization Groups automatically in the following way:

- Click  in the Series Layout Toolbar
- Select 'All Series of the same Group' in the Series Synchronization Window
- Click on  at center-right of the Window.

An automatically-generated grouping of the Series will then be proposed which you can accept, modify or decline as you wish.

### 11.3.1.7 Modify Group Number/Color

You can modify the default currently selected Group in the following way:

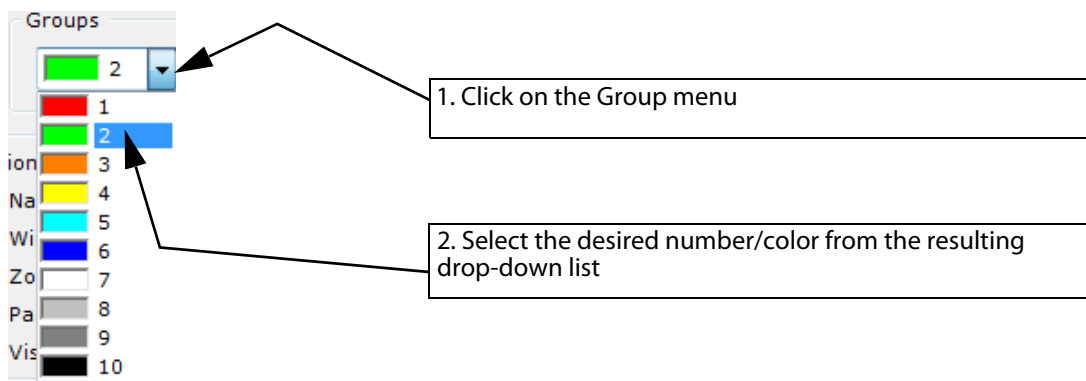





Figure 11-12 Group Colors and Numbers

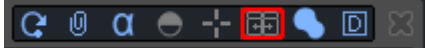
### 11.3.1.8 Remove Series from Group

- Open the Series Synchronization Window
- Select the Group from which you want to remove any or all series in the drop-down menu then click on the "Remove Series" button 
- Click directly on the Images of the Series you wish to desynchronize from the Current Group

### 11.3.1.9 Desynchronize


- Click  to open the Series Synchronization window
- Select 'None' to deactivate synchronization altogether

You can desynchronize the Series directly by simply clicking on  located in the Layout Options at the top right-hand side of each view.



- To resynchronize the Series, click  again

### 11.3.1.10 Synchronization Modes

The 'Sync' button  gives you access to several synchronization modes.

- Click on it to display the following contextual menu with the three following options:

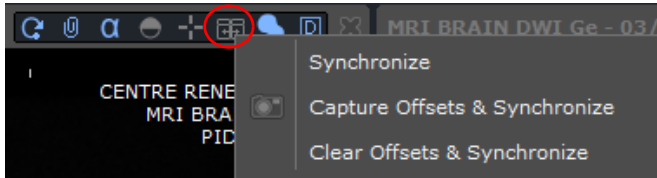



Figure 11-13 Synchronization mode contextual menu


- **Synchronize:** Reactivate synchronization between views (as initially configured)
- **Capture Offsets & Synchronize:** Maintain all offsets between views and reactivate Synchronization (in the case you have navigated through one of the image slices and that they are no longer aligned but you still wish to synchronize those series keeping those offsets constant)
- **Clear Offsets & Synchronize:** Reset all previously captured offsets between views and turn on again Synchronization

### 11.3.1.11 Shortcuts

You can use the following shortcuts to open the series Synchronization Window:

- Right-click on  in the Layout Options at the top-right of the Views
- Press the 'L' keyboard Key




When you use the 'L' shortcut, the Series Synchronization Window opens and automatically proposes the first available Group and also activates the 'Add to Group' button .



The 'L' key keyboard shortcut automatically increments the Group (Number and Color).

### 11.3.1.12 Manual alignment of Series

To realign slices manually in 'Native mode' only:

- Unselect  (upper-right over the workspace)
- In the first Series, locate a prominent anatomic reference such as a vertebrae or a vascular bifurcation
- Navigate through the images of the other Series to the same anatomic reference point

- Click again  to reactivate synchronization selecting the option of your choice in the contextual menu.

The example below shows two Series from two Studies which were made six months apart and which are synchronized

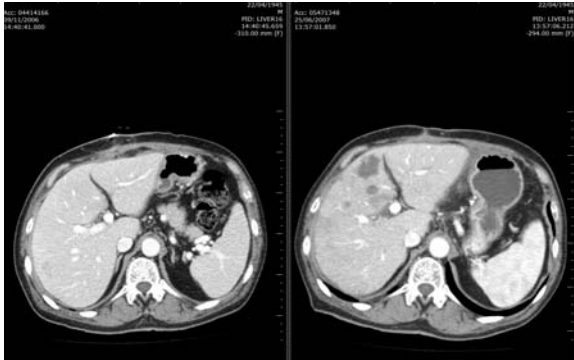


Figure 11-14 Example of a synchronized Study comparison



In MPR Mode, make sure that each plane of view has been realigned before resynchronizing the Series.

---



Synchronized "Reference Lines" may also be displayed across different planes of view to locate zones accurately (see Section 6.1.3).

---

## 11.3.2 Fusion

### 11.3.2.1 Overview

The "Fusion" option enables pairs of Series to be superimposed and blended, for instance to monitor the progress of pathology. You can use Fusion with the following pairs of modalities:

- CT/CT
- MR/MR
- PET/CT
- NM/CT

These are **multiphase-based** protocols.

---



If you have activated the multiple "Patients in Workspace" option in Preferences>Display>Miscellaneous, whenever Series from different Patients are opened simultaneously a warning message is displayed.

---



Scrapbook contents are not saved upon exiting the Fusion View.

---

### 11.3.2.2 Launch Fusion Protocols

If you have the XL-Fusion option activated, you can launch Fusion Mode directly via the Fusion Protocols located in the "CT Standard CT, PT, NM" Protocol Family.

The XL-Fusion option gives you access to the following Fusion protocols:

- PET/CT Fusion

- NM/CT Fusion



The PET/CT Fusion protocol supports the double monitor configuration.

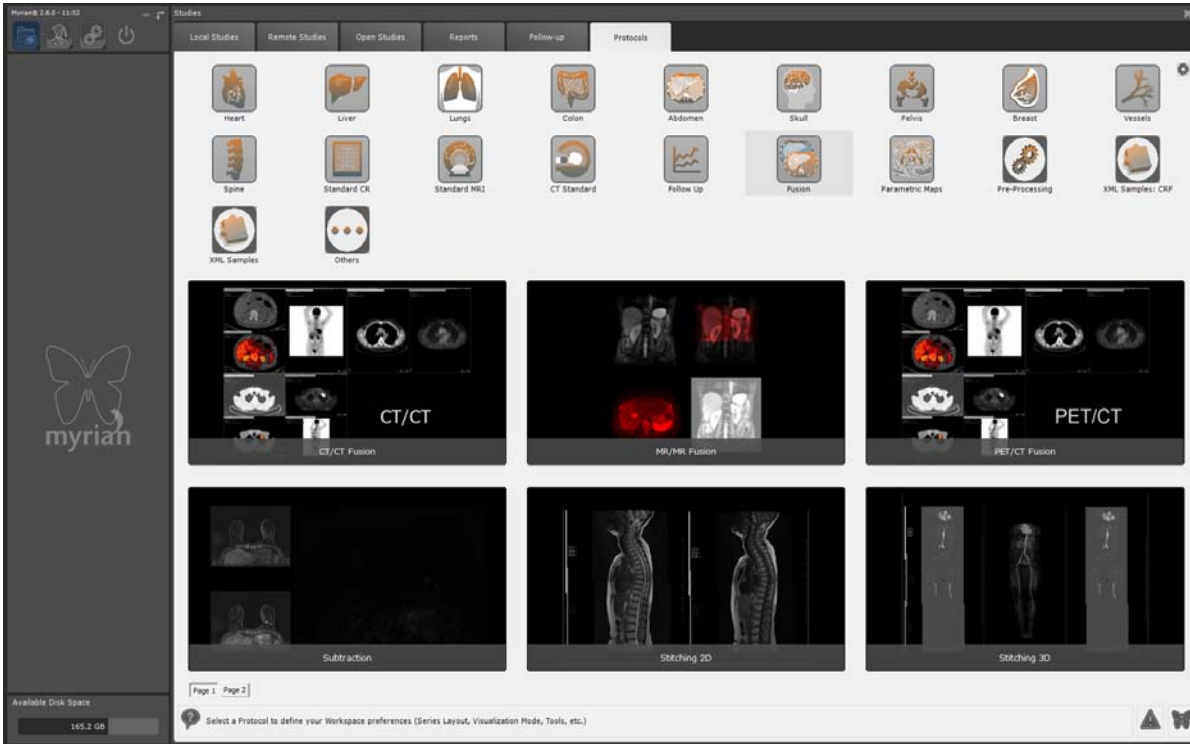



Figure 11-15 Fusion Protocols family



Click on the 'Page 2' button  located at the bottom-left of the protocol screen to access the next protocol page from the 'CT Standard' protocol family. You can also use the mouse wheel to scroll through protocol pages.

### Loading series:

- Select the series in the Study list you wish to open with the required fusion protocol

The category selector window is opened enabling you to modify by drag & drop the automatic preselection:

- Anatomical series,
- Functional series,

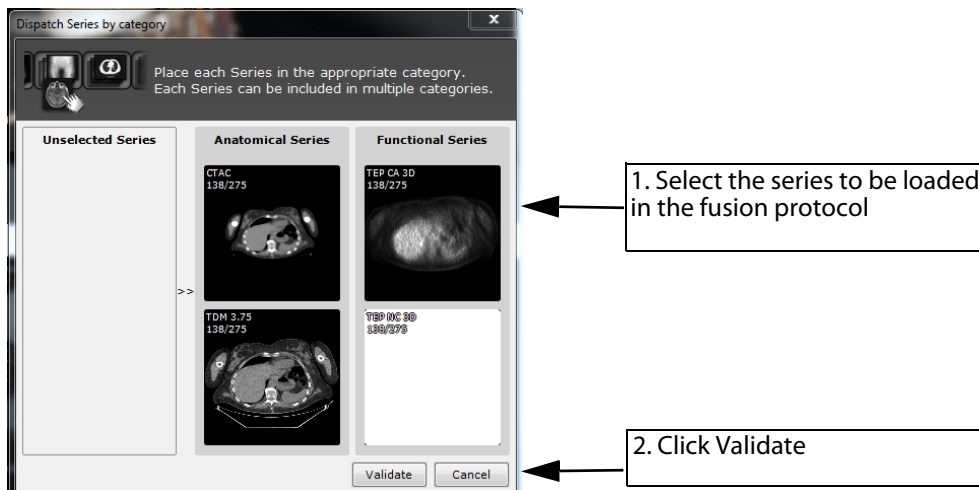


Figure 11-16 Fusion series selector for PET/CT protocol



Only one series accordingly from the 'Series Localizer' and the 'Anatomical series for fusion' categories can be selected



A <categoryset> is applied on the selection to dispatch series in the corresponding categories. Although protocols using Fusion viewports do not allow the selection of more than one phase in the 'anatomical series for Fusion' category, this limitation which is also set in the <categoryset> can be configured.



Several series can be selected in anatomical and functional categories.

### 11.3.2.3 Activate Fusion mode

To access all other fusion protocols (CT/CT, MR/MR, generic), you can perform a drag & drop in the workspace of a view above an other.

In that case, only two series can be selected: the first one is automatically selected in the anatomical and fusion categories while the second one is automatically selected in the functional and localizer categories.



The Functional series is **always** the series that is dragged and dropped on the other series

- Open the desired Series
- Click on the titlebar of one of the Series to be fused
- Drag and drop it onto the other Series to be fused
- Select "Fusion" from the Drag Series menu

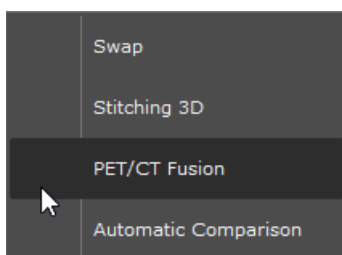
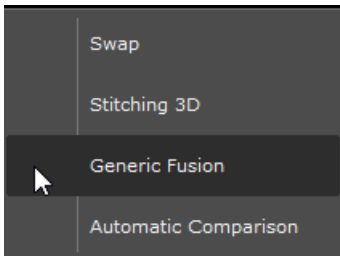


Figure 11-17 Drag and Drop Series Menu



By default, when you drag and drop Series of Modalities for which no specific Protocol exists, the 'Generic Fusion' Protocol is used.



---

### 11.3.2.4 Fusion view



According to the selected fusion protocol, the workspace displays its own specific viewport layout (see Figure 11-25).

---

#### Description

At the opening the PET/CT protocol, the Fusion View contains 2 viewports:

- The **Anatomical Series Viewport** (with each series corresponding to a phase) at left which contains a grayscale Slider (the Slider is hidden by default and only appears when you hover over the left side of the Viewport with the mouse).
- The **Fusion Viewport** at right which contains a docked Fusion slider on the left side of the Viewport and an auto-hide Color Lookup Table (CLUT) Slider at the bottom of the Viewport.



The docking status for both toolbars (CLUT and/or Fusion) is a configurable protocol parameter.



The sliders which are by default set to "auto-hide" can be "pinned" to the side of the Viewports, thereby switching their visibility to continuous, by clicking on the pin symbol at the bottom of the sliders. (on)/ (off).

---

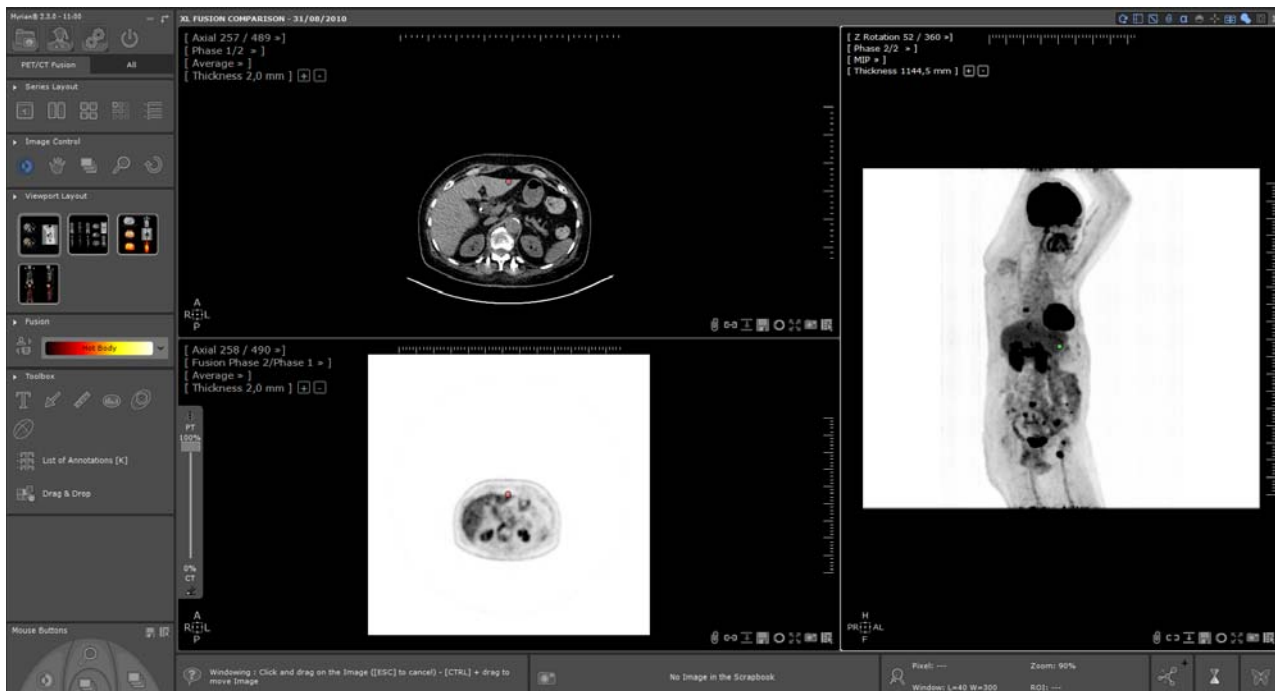


Figure 11-18 Loading series in the PET/CT fusion protocol

### 11.3.2.5 Multimodality view

In a multimodality view, the Fusion viewport allows you to select which functional (e.g. PET) series should be fused with the anatomical (e.g. CT) Series altogether through the phase menu:



Figure 11-19 Phase selection menu: a) functional series b) anatomical series

The first Phase menu item group shows the 'Functional' phases while the second Phase menu item group shows the 'Anatomical' phases.

- Select a phase for each group (the current phase from each group is checked when opening the menu)



If a <shortname> element is specified for each Category, this shortname will be used instead of the 'Phase' term.



### 11.3.2.6Z Rotation

For PET/CT Fusion, the default Factory Protocol also includes a 'Z Rotation' Viewport at far right.

- Drag the mouse in 'Navigation' Mode on the image (using the mouse wheel) to rotate the Volume about the Patient 'Z' (Head>Foot) Axis.



Figure 11-20 'Z Rotation' Viewport displaying Windowing Slider at left ('in Pinned' Mode) and the 'Fast Scroll' Slider at right




Adjusting windowing in the Z rotation viewport has no impact on any other viewports.

---



By default, the Z Rotation viewport launches in Invert Black and White Inversion Mode.

- Click  at the top of the Windowing Slider which appears when you mouse-over the left side of the Viewport to swap modes.

---



Patient orientation letters are displayed at the bottom-left of the Z rotation viewport and are designated by the following capital letters: L (left), R (right), A (anterior), P (posterior), H (head), F (foot)  
Clicking on the orientation square opens the Flip/Rotate menu (see Section 3.4.3).

---



In a multiphase view workspace where navigation synchronization is activated, rotation is synced in all displayed Z rotation viewports.

---

### 11.3.2.7 Series Fusion adjustment

At launching, the overlay opacity in the Fusion viewport is by default set at 100%: only the functional image is displayed, the CT image cannot be visualized at all.

Additionally, the overlay series is initially displayed in inverted Black & White (i.e. the CLUT is deactivated) and the fusion mode is automatically set to Blending mode.

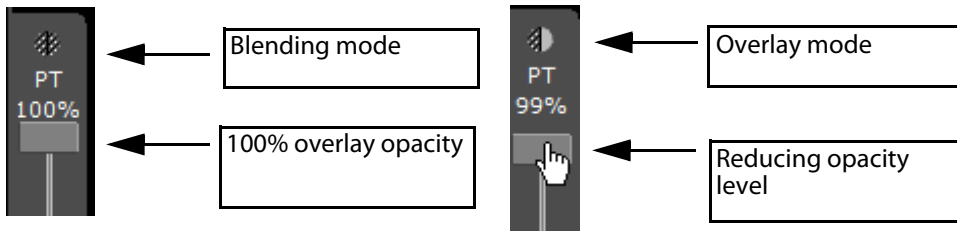


Figure 11-21 Adjust series fusion

You can choose from 2 Modes of Fusion:

- **Overlay Mode** - all parts of the image in Functional Series that are black are transparent and all colored parts are considered as hotspots. The slider gradually overlays the hotspots 100% opaque over the image in the Anatomical Series.
- **Blending Mode** - the slider affects the transparency level of both Series: at one end of the slider, the Anatomical Series is 100% opaque and at the other, the Functional Series is 100% opaque. At the center, both Series 50% visible.

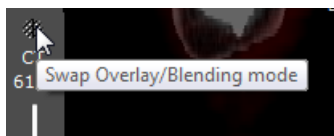


Figure 11-22 Select 'Overlay' or 'Blending' Mode

- Use the Fusion slider located on the left side of the Fusion Viewport to adjust the mixing levels between the CT and PET Series.

When you move down the transparency slider (under 100%), the Blending mode automatically switches to Overlay mode, the CLUT is activated (the Black & White reverse mode is deactivated) and the Anatomical series appears.

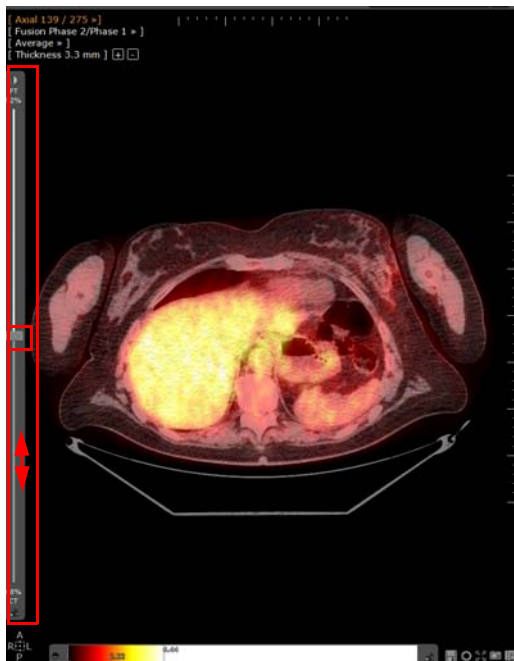


Figure 11-23 Set the mixing PET/CT level in the Fusion Viewport

### 11.3.2.8 Viewport layouts

The Viewport Layout Toolbar at left of the Image Zone displays a range of various different possible layouts and orientations for the Series as thumbnails.



Figure 11-24 Viewport Layout Toolbar in the PET/CT protocol



The Series to be fused can be of different orientation.

According to the modalities and the related fusion protocol, specific viewport layouts and orientations are available.



Figure 11-25 Available viewport layouts in the MR/MR protocol



Each viewport corresponds to a category (e.g. anatomical viewport, functional viewport, fusion viewport, Z rotation...).

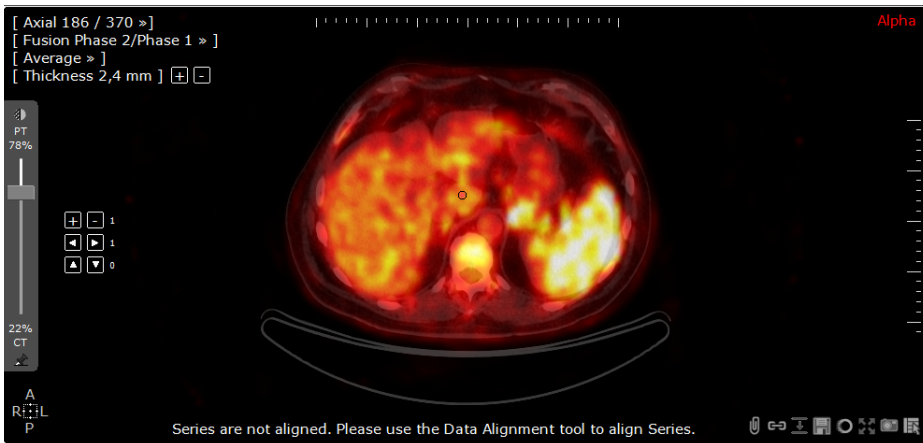
### 11.3.2.9 Series Alignment



The User should always make sure that fused series are properly aligned.




In some cases, based on DICOM information, Myrian® automatically detects that series have not been acquired using the same standards and that those are not correctly superimposed. In that case, a warning message appears at the bottom of the fusion viewport to inform you.



In order to prompt you to perform the data alignment correction, the Alignment pad is automatically displayed in the viewport.



- Use the Alignment Pad (i.e. if applicable, initially activating  in the Fusion Toolbox, see Figure 11-27) to align the Series manually Up/Down, Forward/Backward or Left/Right.

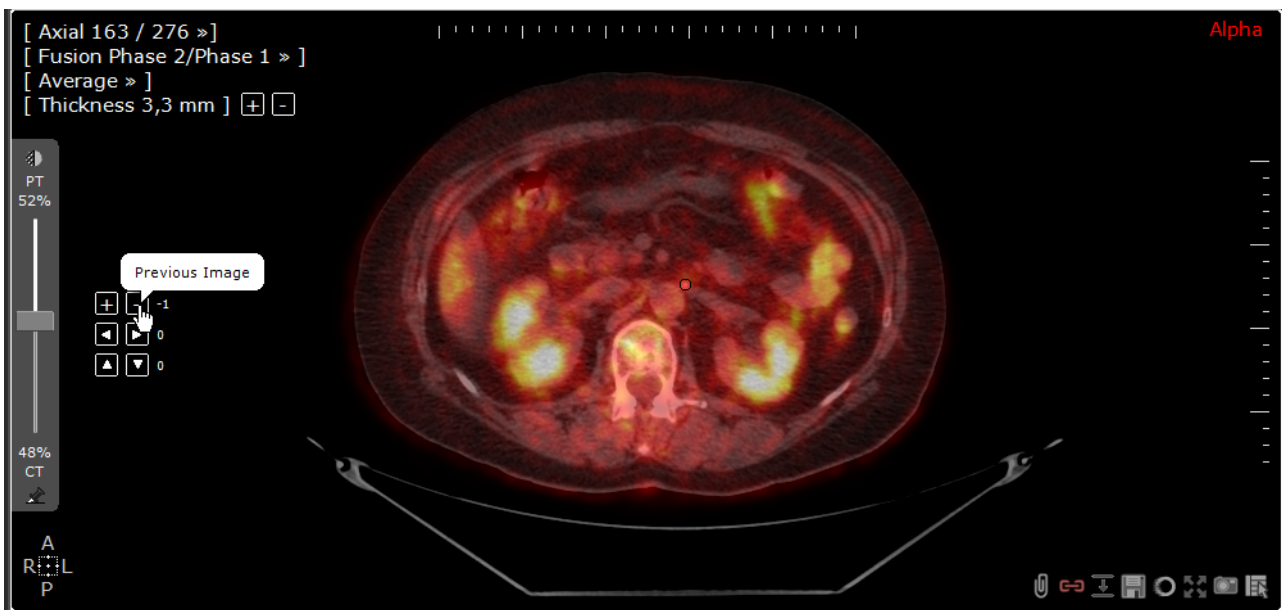



Figure 11-26 Alignment Pad in the Fusion Viewport

- Once you are satisfied with the Series Alignment, click  in the Fusion Toolbar at left of the Workspace to deactivate the Alignment tool.



Figure 11-27 Fusion Toolbar



Series manual realignment can also be performed using the 'Capture Offset & Synchronize' feature  (see Section 6.8.5 for detailed information)

### 11.3.2.10 Color Look-up Table (CLUT)

- Once you have aligned your Series, set the color range of your overlaid Series (the 'Functional' Series):



1. Select the most adapted CLUT preset in the CLUT drop-down menu in the Fusion Toolbar

Figure 11-28 CLUT drop-down menu



2. Use the CLUT slider which appears when you mouse-over the left side of the Functional Series Viewports to adjust the CLUT settings as desired

Figure 11-29 CLUT Slider

The CLUT slider is used in the same way as the normal Viewport Windowing Slider.



Drag the mouse vertically and horizontally to adjust the CLUT windowing as desired in Anatomical Series.



Hold the ALT key and drag the mouse vertically and horizontally to adjust the CLUT windowing as desired in Functional Series.

In the illustrated example below, the view CLUT preset selected in the Fusion toolbar applies to all viewports in which the CLUT is activated. It is the view common CLUT.

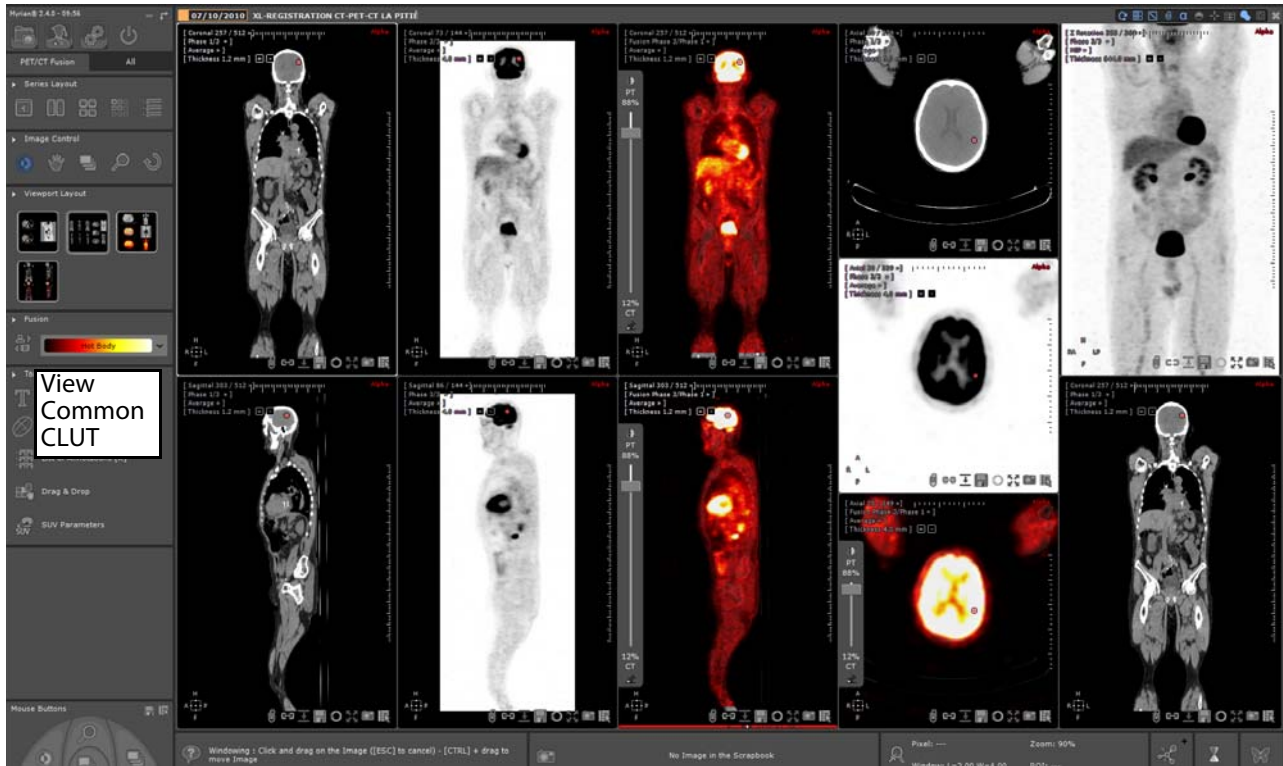


Figure 11-30 Fusion view between a CT Series and a PT (PET) Series with the Fusion Viewport at center and Z Rotation Viewport at far right

You can also choose to apply a specific CLUT to each displayed series. In fact, each viewport can either use the view common CLUT, or have its own separate CLUT.

- To access the viewport CLUT menu, perform a right-click on the selected viewport CLUT, then click on "Select CLUT":



By default, the 'Use common CLUT' is activated.

- Select the CLUT of your choice in the CLUT drop-down menu

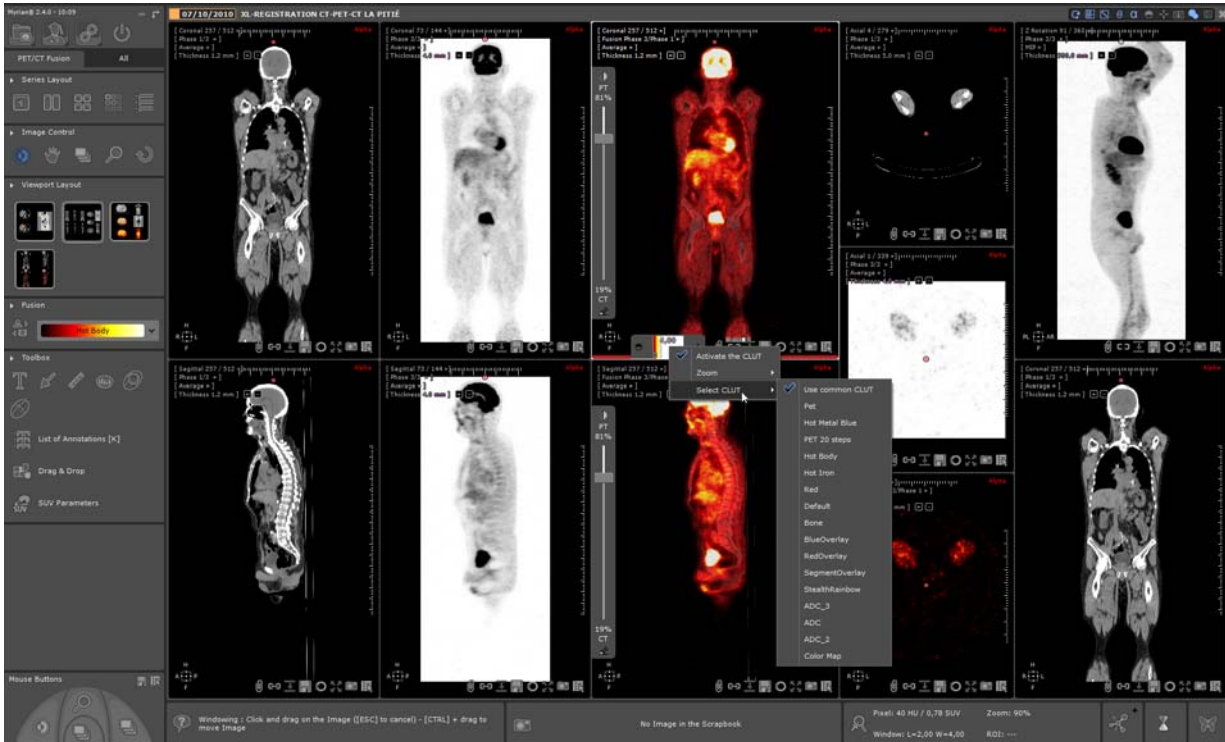


Figure 11-31 Set a specific CLUT to a Fusion viewport

The selected CLUT is immediately applied to the desired viewport.  
You can apply a specific CLUT to any/all viewport(s).



The viewport CLUT is not be synchronized with the view common CLUT: if you modify the view CLUT from the Fusion toolbar, it will not be applicable to viewports with specific CLUT.

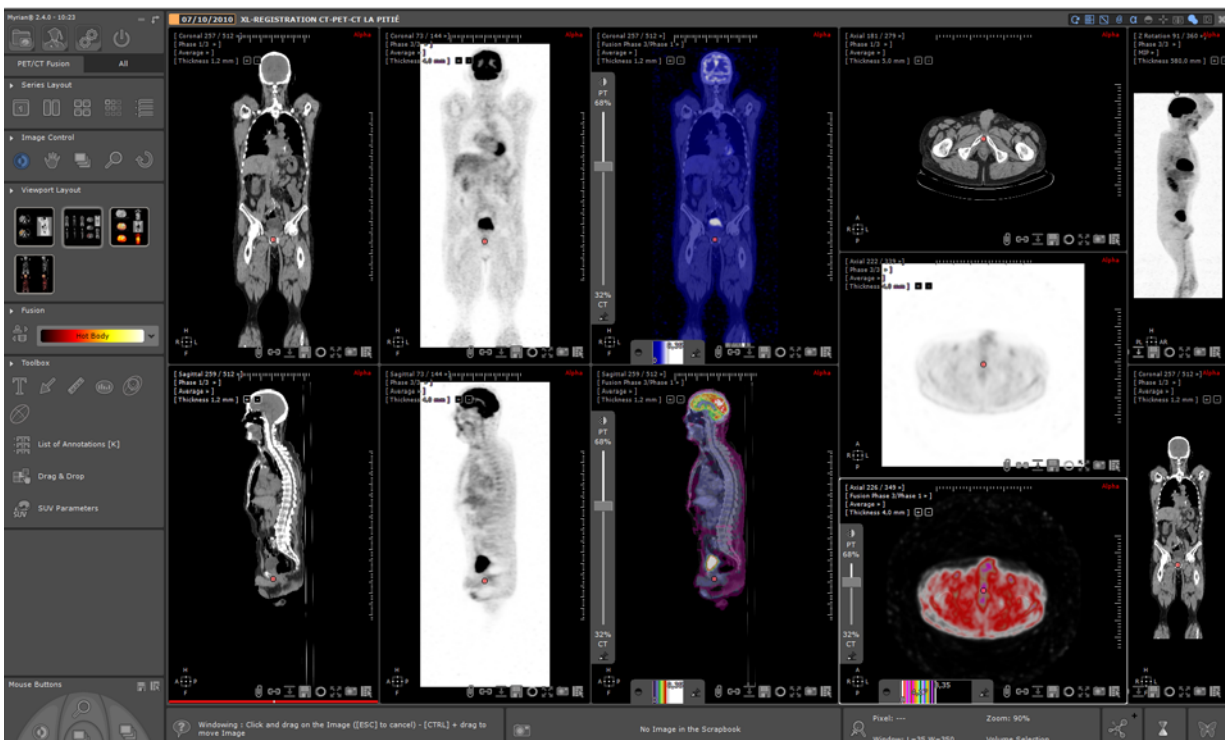


Figure 11-32 Applying specific CLUT to selected viewports

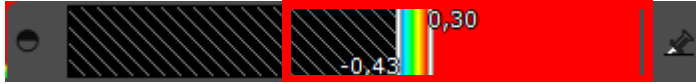




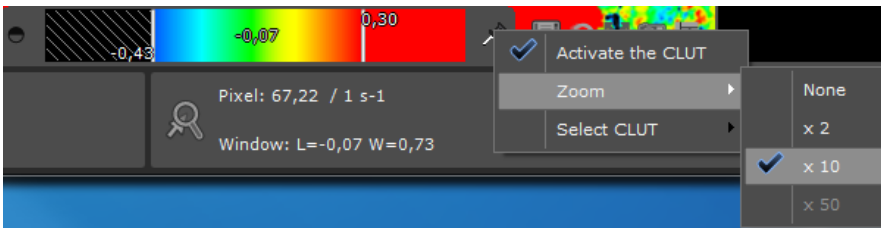
CLUT parameterizing is not preserved when changing layouts.



CLUT zoom (set to None by default) which enables to optimize the CLUT precision among is a configurable setting



CLUT zoom set to 0



CLUT zoom set to x10

### 11.3.2.11 Standard Uptake Value (SUV)

SUV which stands for Standard Uptake Value is a standardized unit used in PET imaging acquired after a radioactive material attached to a form of glucose is injected in the patient.

This radioactive material (FDG [18F] fluoro-2-deoxyglucose is the most common tracer) accumulates in organs and lesions having a very active metabolism (i.e. that consume a lot of glucose like brain, heart, tumor or any infectious lesions).

The PET modality is used to calculates how much radioactivity is accumulated in the body and where.



The exams are a set of around 350 axial slices (always) of low resolution, the pixel size is around 6 mm. The value of the pixel gives the radioactive activity of the patient body so the higher the accumulated dose, the higher the signal.



When selecting a Study to load in order to perform a SUV Calculation, you must be careful to select attenuation compensated and decay corrected PET Series with a valid acquisition start time according to the following prerequisites.

- Attenuation compensation: DICOM Corrected Image tag (0x0028, 0x0051) is set to "ATTN" and "DECY";
- Decay correction: DICOM Decay Correction tag (0x0054, 0x1102) is set to "START".
- the DICOM Pixel Value Units tag (0x0054, 0x1001) that is supported by Myrian®. Compatible DICOM Pixel Value Units are as follow
- Counts per second (only for Philips modalities)
- Becquerels/milliliter



If prerequisites are not fulfilled, the SUV calculation cannot be performed.

When a PET study is loaded that can be converted to SUV, this is automatically done.

The signal for PET Series is normalized using the **Patient Weight SUV Normalization formula (default method)** and SUV calculation performed according to the QIBA guidelines which required parameters are:

- Patient Weight (in Kg)
- Injected Dose (MBq)
- Decay Time



- Half-Life

A SUV Parameters window automatically appears at the Series load-up stage if any corresponding values are missing. From this dialog box, you can also edit any predefined values as well as the default transformation method used for SUV calculation.

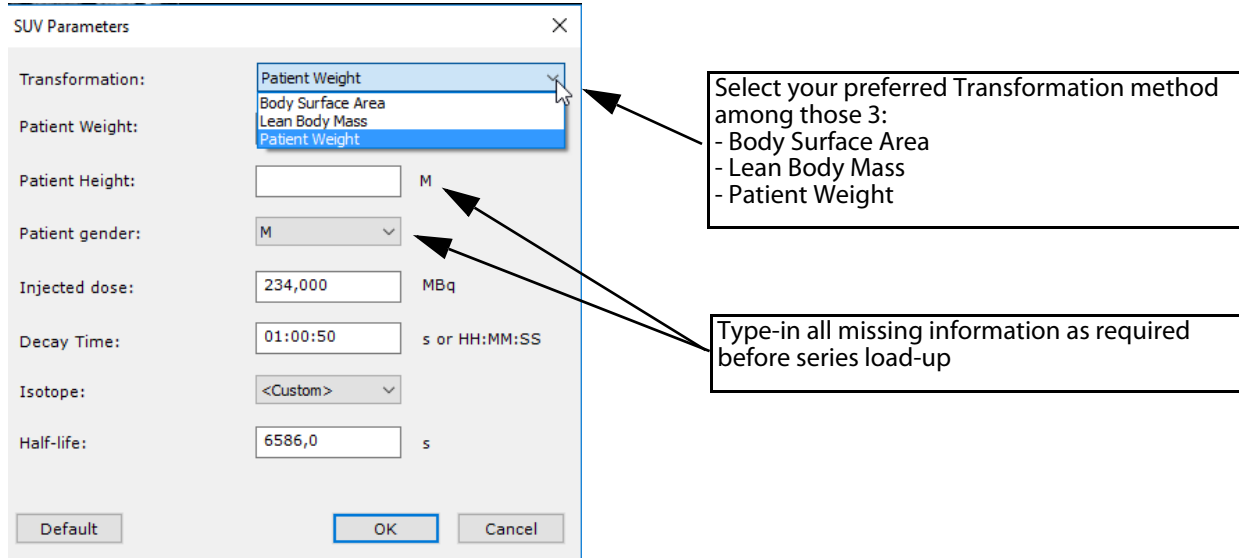



Figure 11-33 SUV Parameters window



The SUV Parameters window which you can also access by clicking on  in the Toolbox Toolbar, enables you to manually enter or edit the Standardized Uptake parameter values for PET Series.

According to the selected method, some values (patient gender, height or weight) are required. If missing or not completed, the **SUV calculation cannot be performed**.



The 'Default' button sets back all values to those detected in the DICOM series

To check that the SUV calculation has been properly performed as requested, you can display the SUV information proceeding as follow:

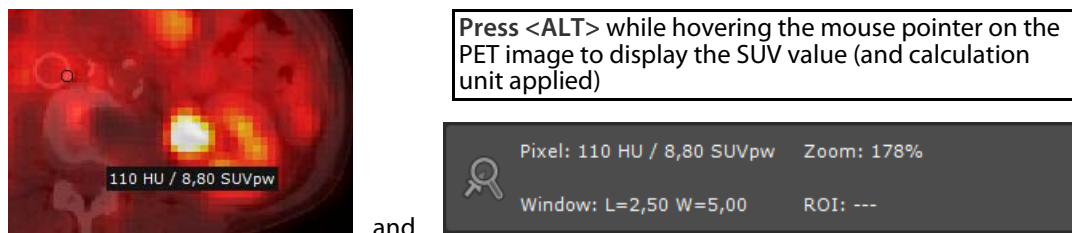


Figure 11-34 Intensity measurement information for PET Series after SUV calculation based on Weight Transformation method.

According to the applied transformation method, the relevant SUV calculation unit is also displayed on the image when pressing <ALT> that is to say:

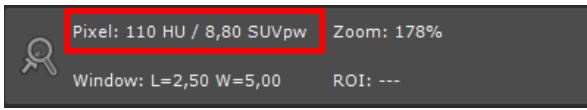
- Patient Weight: SUVpw
- Lean Body Mass: SUVlbm
- Body Surface Area: SUVbsa



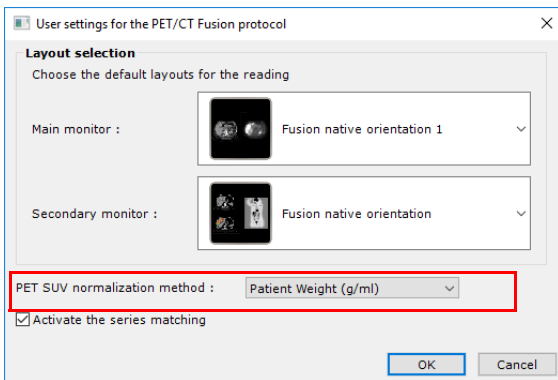
In CT viewports, only HU value is displayed while in PET viewports, both HU and SUV are displayed.



Any data modified in the SUV Parameters Window will affect the overall SUV results, displayed in the Mouse-over information bar at bottom-right of the Main Workspace.



The default PET SUV normalization method can be configured (among certain other settings) through the 'User settings for the protocol PET/CT Fusion' screen that can be accessed right-clicking on the protocol thumbnail (see Section 8.5.8)



Select the default normalization method (using the drop down list) to apply upon launching the PET/CT Fusion protocol

### 11.3.2.123D Fusion Rendering Modes

A 3D Rendering can be applied to fused Series of CT/PT or CT/NM modalities.

Fusion Rendering is accessed in the Rendering Menu of 3D Whole Volume or VOI Fusion Viewports.

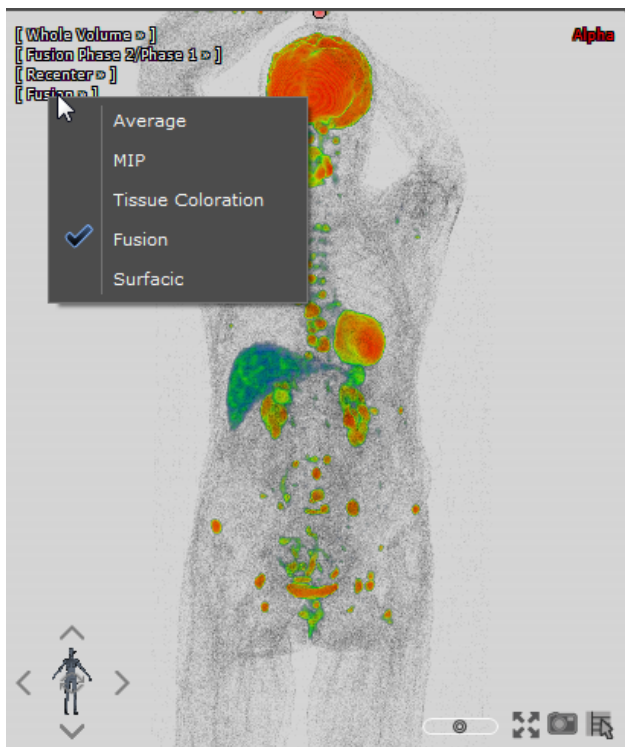


Figure 11-35 3D Fusion in Whole Volume Mode

In the illustration below, Fused Anatomical and Functional Series are displayed in Whole Volume Fusion Rendering Mode.

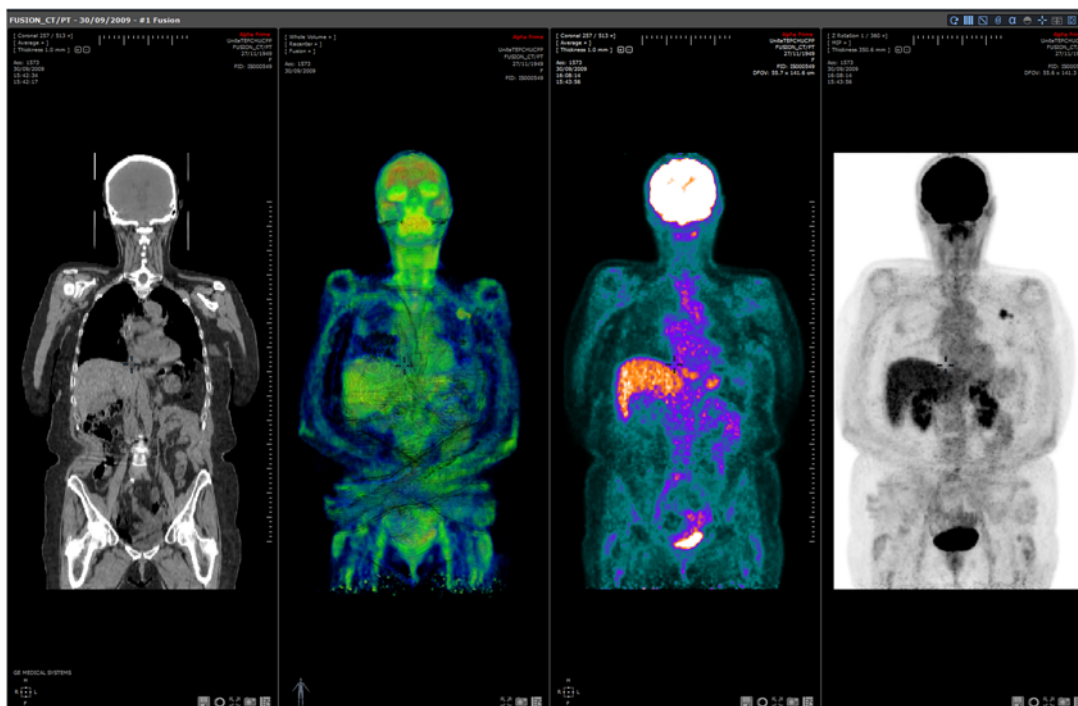


Figure 11-36 Fusion Viewport with 3D Fused Rendering Mode

Anatomical and Functional Series each have their own dedicated 3D Rendering Palettes which are applied automatically

when loading the 3D Viewport:


- The "Silhouette" Palette for Anatomical Datasets (CT-Scanner)
- The "Functional Overlay" Palette for Functional Datasets (PT or NM modalities).



These palettes are also available in the Tissue Coloration menu of the 3D Viewports of the corresponding modalities.

---



Windowing  can be used on Anatomical Series directly.

---



Press the "ALT" key with the Windowing tool for Functional Series.

---



Double-click on any point in the 3D Fused Volume to recenter the Anatomical Center on the point of maximum intensity in the Functional Series.

---

### 11.3.2.13 Save Fused Series

You can save your entire Fusion work as a new Series by clicking on the 'Create New Series' button  at bottom right of the Fusion Viewport.

A progress bar will appear to chart the progress of the Series creation process.

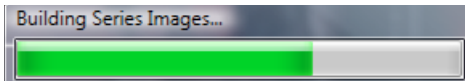


Figure 11-37 Series creation progress bar

Once you have created your New Fused Series, it will open alongside your open Series and be added to the corresponding Study as a 'Secondary Capture' (SC) modality Series.

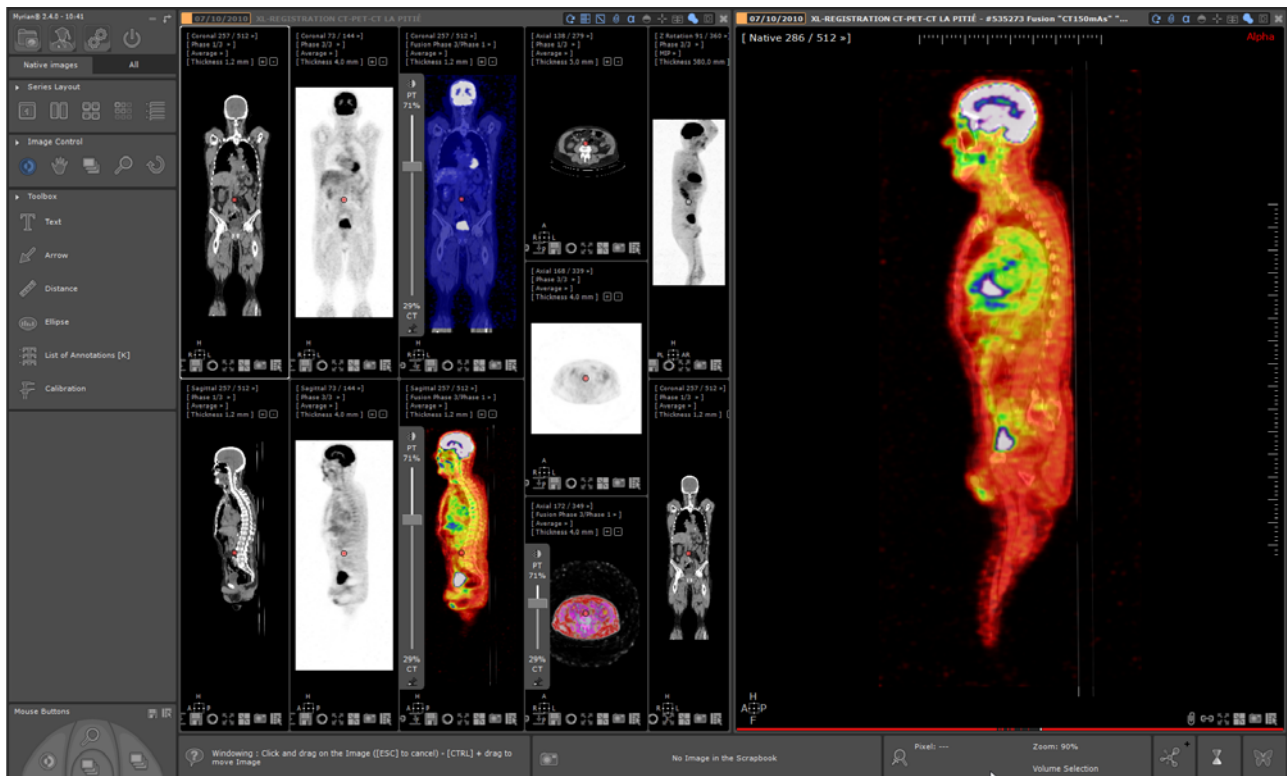


Figure 11-38 New Series View

### 11.3.2.14 Fusion views in Multimonitor configuration

The PET/CT protocol supports dual monitors and provide you with specifically adapted viewport layouts.

On a dual monitor configuration (see Section 8.3.7), Myrian® opens 2 views, one on each monitor:

- On the left monitor, Layout 7 displays CT axial, PET axial, inverted B/W PET/CT fusion Axial and PET Z rotation
- On the right monitor, Layout 8 displays CT coronal, CT sagittal, PET/CT fusion coronal, PET/CT fusion sagittal

Windowing synchronization on dual monitor configuration:

When two views of the same exam are opened with the same protocol, the windowing applied to one series category (i.e. one viewport) is replicated to all viewports displaying that same series category whatever view they belong to.



If all views are not opened with the same protocol, any windowing adjustments performed are applied per category-related viewport allowing for the fact that the views probably display different category viewports.

PET/CT or NM/CT fusion synchronization in multiview mode:

In a multiview workspace (a matching process is automatically performed), the **fusion blending/overlay mode** as well as the **PET/CT mixing level** are synchronized by default so that the same settings are replicated from one fusion view to another.

Fusion synchronization automatically applies as soon as you adjust the mixing levels between the CT and PET Series moving the Fusion slider or switch Fusion mode in one fusion viewport (see Section 11.3.2.7).

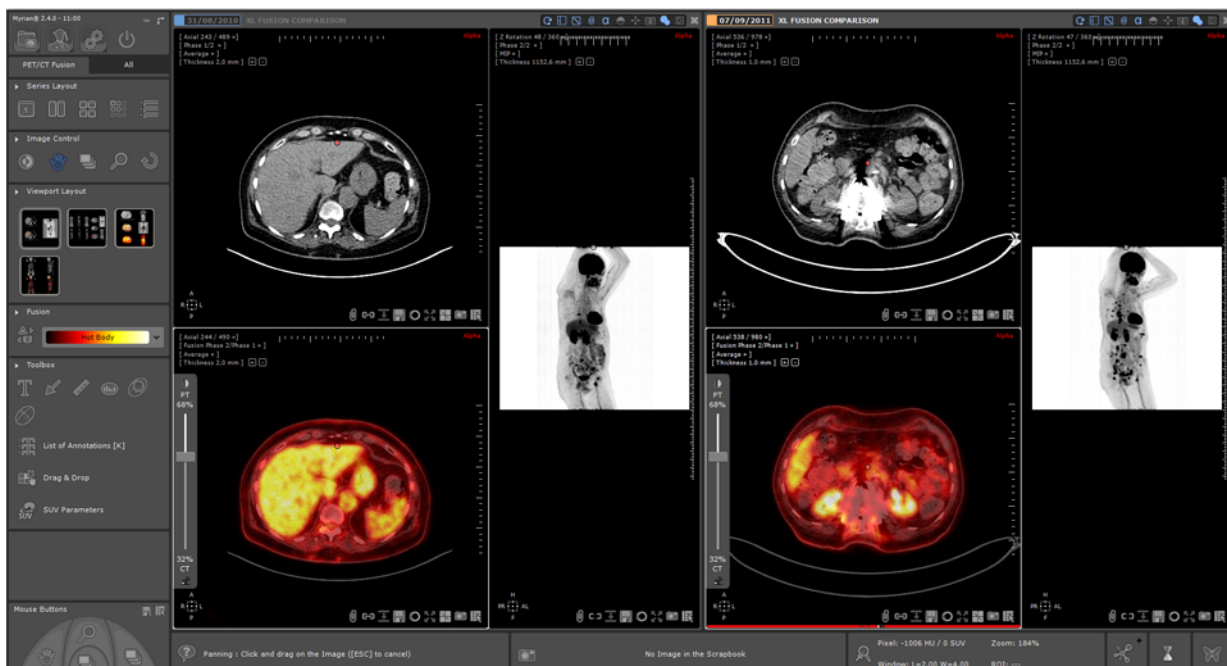



Figure 11-39 Synced fusion views (same Fusion mode and PET/CT percentage) in a multiview workspace

All fusion views are synchronized.

- If you wish to edit those default settings, right-click on the  icon located at the right of the title bar of any view to open the Synchronization window (or press the L keyboard shortcut):

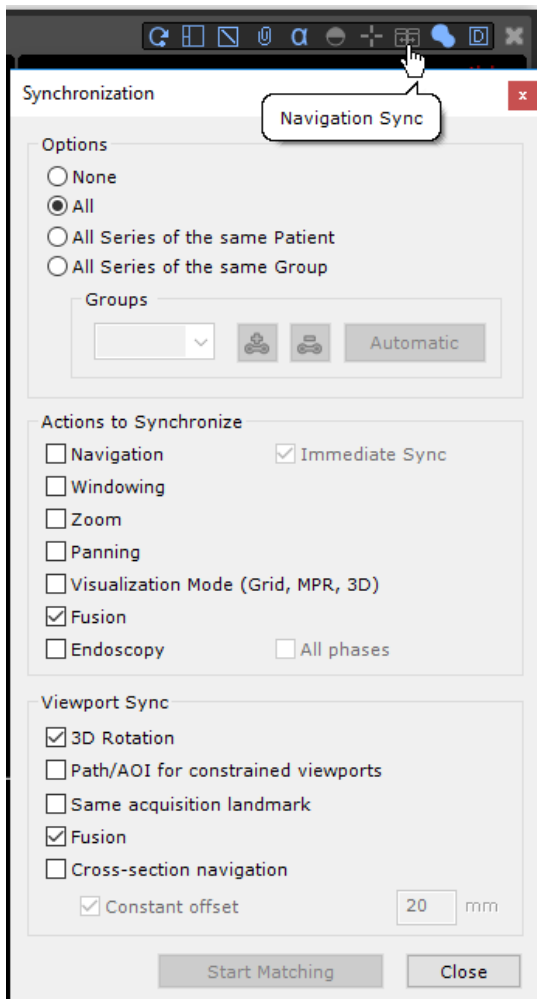


Figure 11-40 Editing default fusion synchronization settings

If required:

- Uncheck the 'Fusion' checkbox in the 'Action to Synchronize' section (PET/CT levels are desynced between fusion viewports)
- Uncheck the 'Fusion' checkbox in the 'Viewport Sync' section (the overlay blending mode is desynced between fusion viewports)
- Click on 'Close' to validate


Modifications automatically apply.



### 11.3.2.15 Manual resynchronization of two multiphase views containing fusion viewport(s)


If you have two multiphase views opened in your workspace, whether those views have been opened with the same multiphase view protocol or not, you may not be entirely satisfied with the view synchronization navigation (which is automatically performed based on DICOM information).

Should this be the case, you can manually reset it:



If the Matching  is activated, make sure to deactivate the process in both views.

- Click once on  at the top-right corner of a view to deactivate the current synchronization performed between the views
- Search for an identical anatomical point navigating in each view (using ) and move the anatomical center over this point in each view

- Press again  and select 'Capture Offsets & Synchronize' from the Synchronization contextual menu. Accordingly, views are now correctly synchronized based on the anatomical center position.
- 



Once multiphase volumes are synchronized with 'Capture Offsets & Synchronize', the reset of the data alignment



in a fusion viewport is incorrect and induces a gap between the layers of the fusion viewport. To solve this problem, you can:

- Undo the Reset or
  - Manually realign the layers of the fusion viewport(s) or
  - Do a 'Clear Offsets & Synchronize' which will reset the fusion viewport(s), followed by a 'Capture Offsets & Synchronize' to resynchronize both views or,
  - Close all views and open the faulty view again with a Clear series data.
- 




When synchronizing two views selecting the 'Clear Offsets & Synchronize' mode, any manual change to the data alignment in the fusion viewport(s) is lost.


---

### 11.3.3 'QuickPatient': loads other series or studies of the current patient

#### 11.3.3.1 Opening the QuickPatient in the workspace



The QuickPatient window  is a preview window enabling you to access and open any or all Series or Studies belonging to the current Patient directly from the Workspace without having to return to the Study List. Those can be of different modalities and will be loaded in the workspace using an appropriate default protocol (see Section 11.3.3.3).

- With your series already open in the Workspace, click on  in the Series Layout toolbar (or press the '**S**' keyboard shortcut) to open the **QuickPatient window** and access the complete list of Series/Studies recognized as belonging to the current Patient (same Name, DOB, PID, gender, etc.) available from the Study list.
- 



If you wish to have a permanent access to the QuickPatient, check the 'Open list of series automatically' option in the Preferences>Display>Miscellaneous menu.

Whenever you open a series from one patient, the QuickPatient window listing all series belonging to that same patient is automatically displayed in the Workspace.

---

By default, the QuickPatient **opens docked horizontally at the top** of the workspace although it can be set **at the bottom or vertically on the left or right side of the workspace**, as preferred.

- Click in the intermediate area highlighted in yellow as illustrated hereafter to select the QuickPatient window.
- While pressing down the mouse left button, start dragging and moving the mouse cursor until reaching the wanted location.

A phantom of the new position is visible depending on the cursor position.



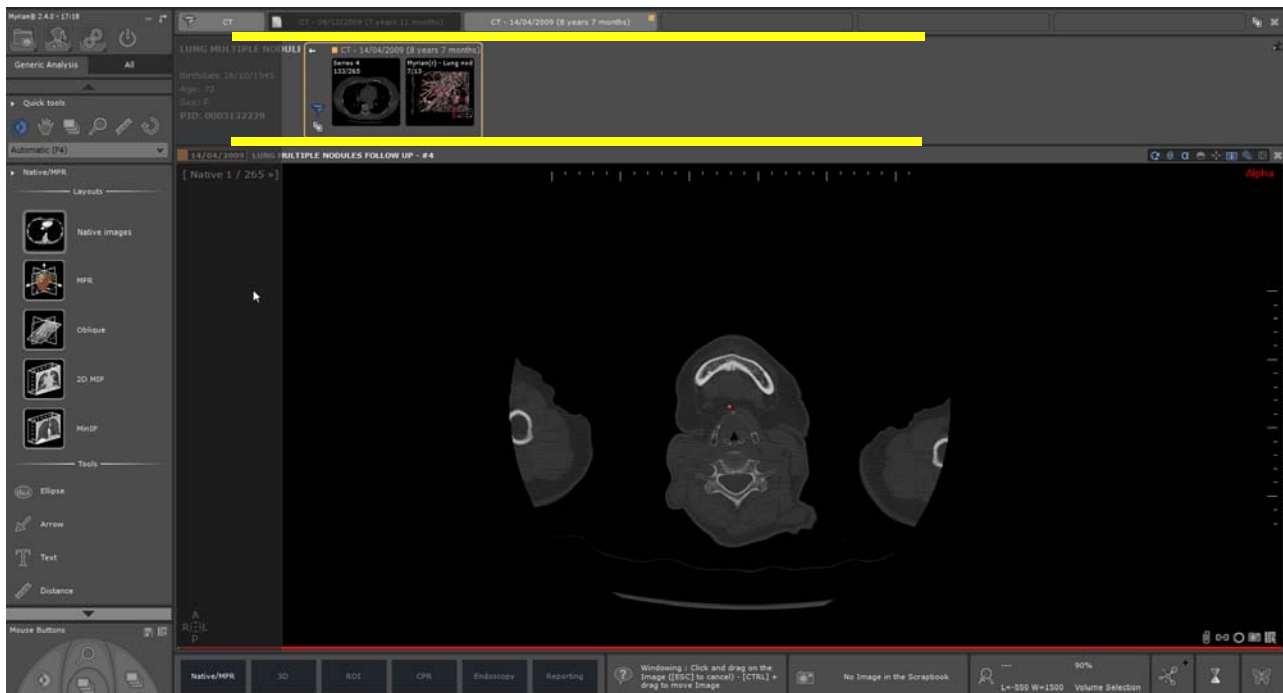


Figure 11-41 QuickPatient phantom display

- Drop it

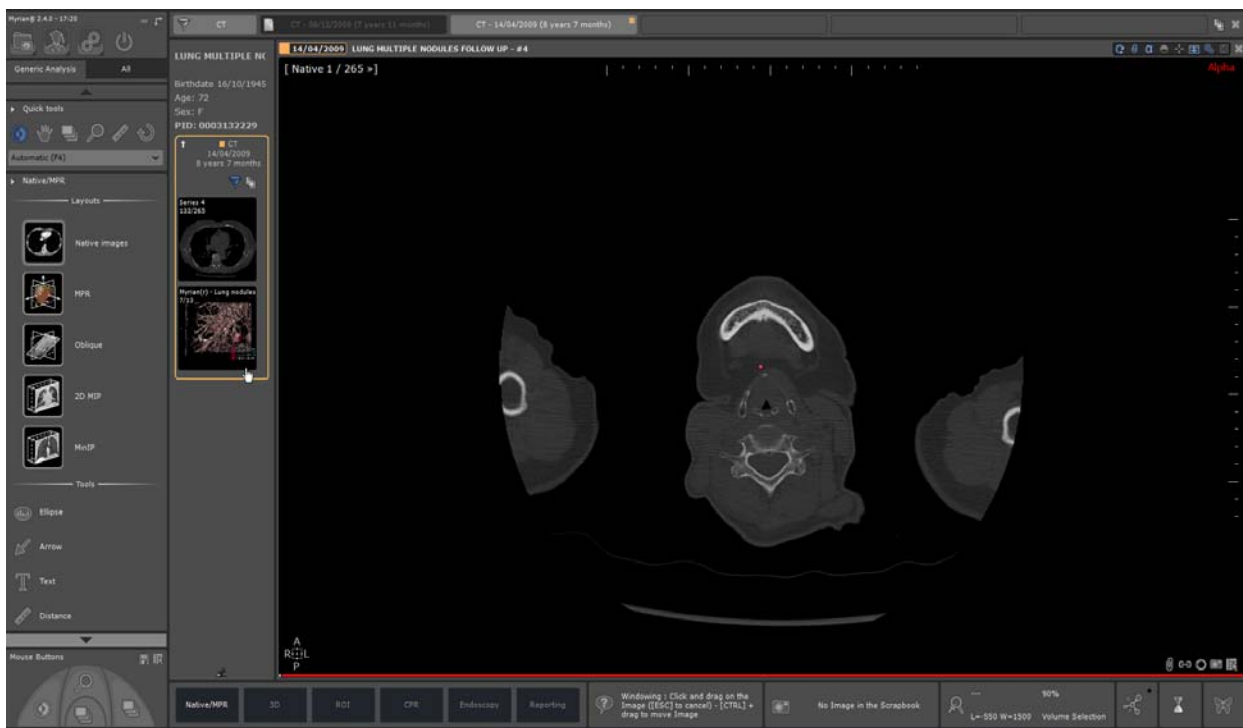


Figure 11-42 QuickPatient vertical display

The QuickPatient can also be used as a floating dialog box. When undocking the QuickPatient window clicking on the pin button, it switches to a floating resizable dialog box as illustrated hereunder:

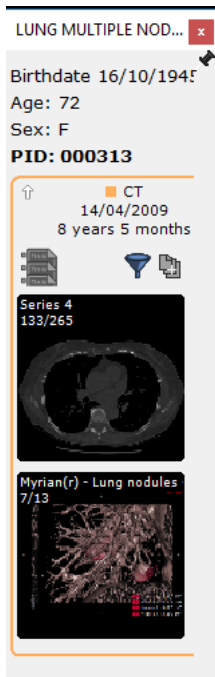


Figure 11-43 QuickPatient floating dialog box

- Click on the pin button again in the undocked dialog box to dock it back in its previous position.

According to your needs, you can then either move the QuickPatient dialog box in the workspace or switch from one docking position to another.

- To hide or show the QuickPatient window according to your convenience, click on



The QuickPatient window can also be displayed as a treeview. Please request the assistance of an application engineer of Intrasure for configuration.

### 11.3.3.2 QuickPatient window

The QuickPatient window is defined according to the three following hierarchical levels:

- Folder
- Study
- Series (or sub-series)

All available study folders for the current patient are displayed on a chronological Timeline (**from the most recent on the left to the oldest on the right**) and the series/subseries within the available **folders as thumbnails** (default display mode). The Timeline displays one tab for every existing folder.

From the QuickPatient window, you have access to:

- The **Patient data**:
  - Study name
  - Patient birth date
  - Age
  - Gender
  - Patient Identity number (PID)
- The **Timeline** composed of all study folders belonging to the current patient and corresponding to the selected or default modality

The folder which the series open in the workspace belongs to, is **highlighted in a default color** in the Timeline and its content displayed by default.

The most recent study is highlighted in orange, the second most recent is blue, the third yellow, the fourth violet and the fifth

turquoise.



The visualization of the Timeline is associated to the QuickPatient. Since they come together, they are always both visible or hidden.



The study and date to which belong the loaded series from the Study list are **outlined in its default color**.

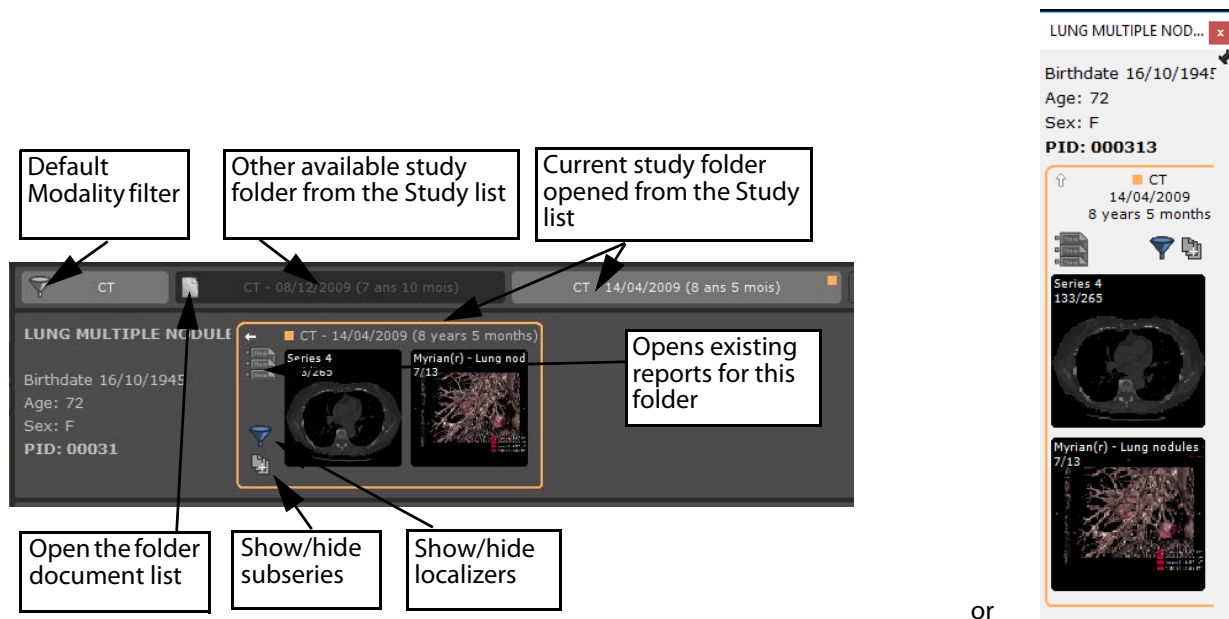


Figure 11-44 QuickPatient features

One click on the 'Show/hide localizers' button or the 'Show/hide subseries' button enables to select the detail level in the preview window switching from the Mode On to the Mode Off:

- Exclusion selector: Mode On (default) and Mode Off
- Subseries display: Mode On and Mode Off (default)

When existing reports have been identified, the icon shows the number of available reports



Tooltips are available simply hovering the mouse pointer over any icon of the QuickPatient window.



Clicking on opens the Patient report window from which you can select a report and open it in your default word processor.

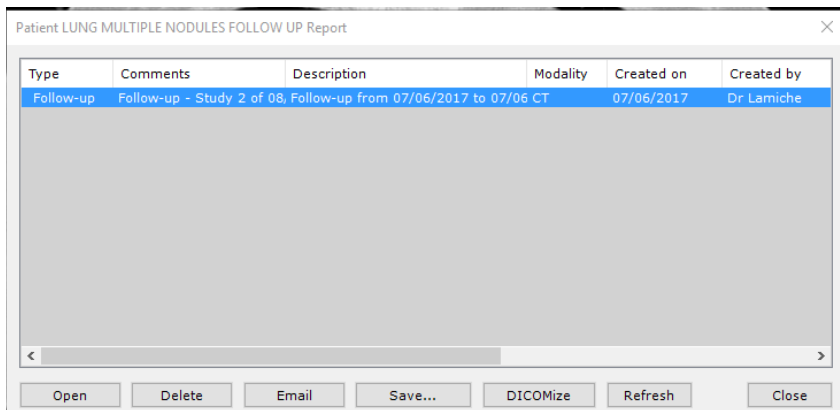



Figure 11-45 Opening the Patient report window from the QuickPatient screen

Clicking on the little white arrow  located in the top-left corner of the folder enables to **expand or minimize the folder** as illustrated hereafter.

In 'Folded' mode, the folder displays the following information:

- Modality(ies) of the series included in the folder
- Folder date
- Folder age
- Number of studies belonging to this folder

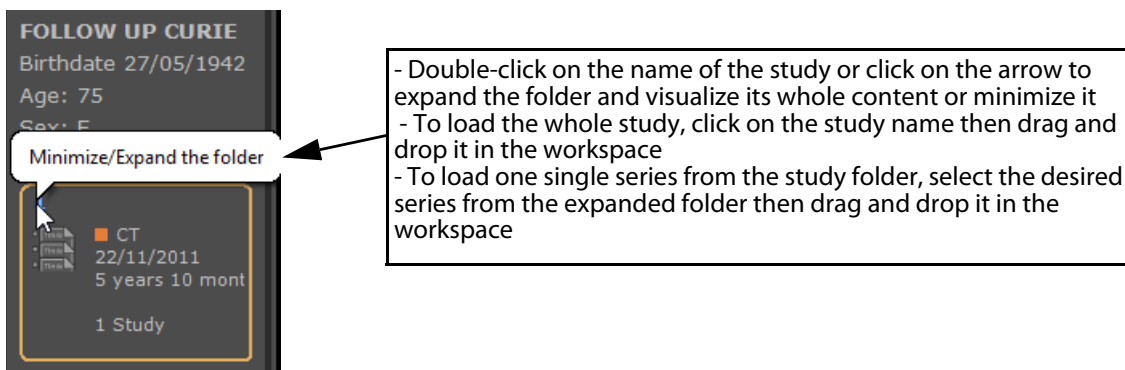


Figure 11-46 QuickPatient folded folder

The **little white circle** shows the current folder (i.e. the one opened from the study list). By default, the contents of the other study folders available from the study list are hidden:

- To visualize its contents, click on the relevant 'Folder' button as hereafter:

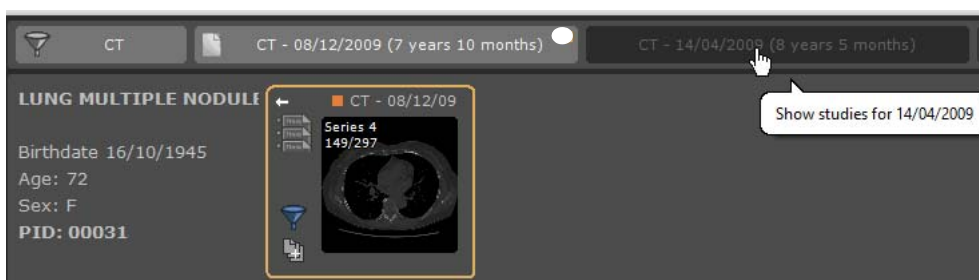



Figure 11-47 Selecting another folder from the QuickPatient Timeline

Clicking again will mask the contents of the selected folder.

Each 'Folder' tab in the Timeline is a toggle display button enabling you to hide and/or display its contents as wanted.



A 'Close' button  on the far right corner of the Timeline bar allows closing all the views simultaneously in the workspace.



By default, you cannot select more than 10 folders in the Timeline.



The rules when a new folder is selected are the following:

- If the maximum count is not reached, the folder is selected
- If the maximum count is reached, the folder is selected, but another folder is unselected.



The rules to unselect a folder are the following:

- If the current folder is selected, the other one is unselected
- If the current folder is not selected, the older one is unselected.

A scrollbar appears when all folders cannot be fully displayed in the Timeline enabling you to visualize the whole folder list.

In the same way, if the focus is on the folder content and the size of the folder window doesn't allow to display all thumbnails, you can scroll the window content using the mouse wheel or using the slider that appears when the mouse cursor is hovered at the bottom of the preview window.

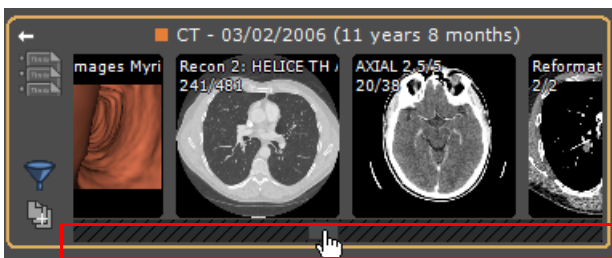
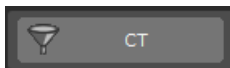


Figure 11-48 Using the scrollbar in the QuickPatient window



The 'Modality' button allows filtering study folders by modality.

Other 'Folder' tabs correspond to the folders that satisfy to the modality filter.

By default, the automatic filtering is applied: only the modalities corresponding to the open study are used.

You can then modify or remove the filter to modify the list of the displayed folders.



Figure 11-49 QuickPatient modality filter

When clicking on this button, the usual modality list opens:

- If no modality is selected, all studies are displayed.
- Otherwise, only the ones corresponding to the selected modalities are kept.

Each time the modality filter is modified, the content of the QuickPatient is refreshed to display only the folders containing studies belonging to the relevant modality(ies).



When a filter is active, the corresponding modalities are displayed on the 'Filter' button.

---



The specific <Radiology X-Ray> option selects the following modalities: CR+DX+RF.

---

### 11.3.3.3 Loading series/studies from the current patient into the workspace

According to the modalities of the series that are dragged and dropped in the workspace, the series are loaded using the following predefined protocols:

- CT series > Standard CT protocol
  - MRI series > Standard MRI protocol
  - CR, DX or RF series > Standard CR protocol
  - NM, PET or all other modalities > Native protocol
  - CT and PET series included > CT/PET Fusion protocol (see Section 11.3.3.3.2)
  - CT and NM series included > NM/CT Fusion protocol (see Section 11.3.3.3.2)
- 



**Click once** on a thumbnail to open the preview screen or **click and hold** to drag and drop it in the workspace.

---



Use the **right-mouse click** to open a series directly **alongside** the currently open Series

---



Distance measurements and quantification shape annotations performed on dropped series are preserved upon closing the series.

---

#### 11.3.3.3.1 Drag and dropping one single series

When dragging **one single series**, you can drop it in the workspace as follow:

- **Above a single view:** the series is loaded in a single view at the view location using a standard protocol and the target view is first closed.
  - Drag and drop the desired Series belonging to the study folder of your choice directly from the QuickPatient window onto the desired spot of the image zone of the Workspace to open the selected series
  - Repeat the same operation to load another series from the study

By dragging thumbnails of the Series near to or over the edges of an open Series window, a shaded zone containing arrow markers appears indicating the way in which the Workspace will be divided when dropping the thumbnail. For example:

Dropping here,

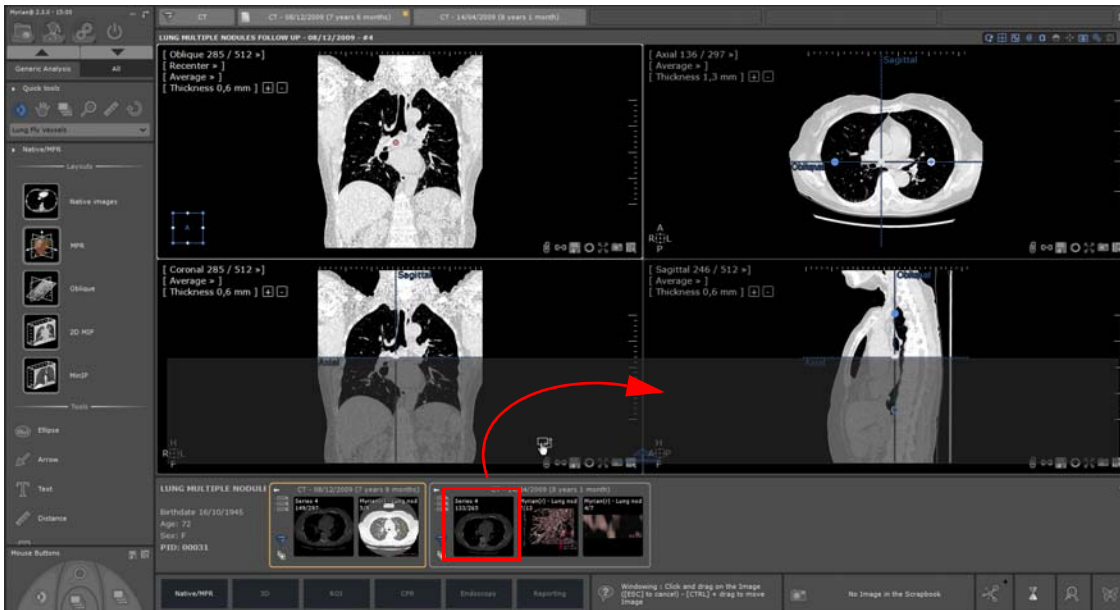


Figure 11-50 QuickPatient: Drag and dropping one single series from the study folder in the bottom part of the workspace

Results in the following:

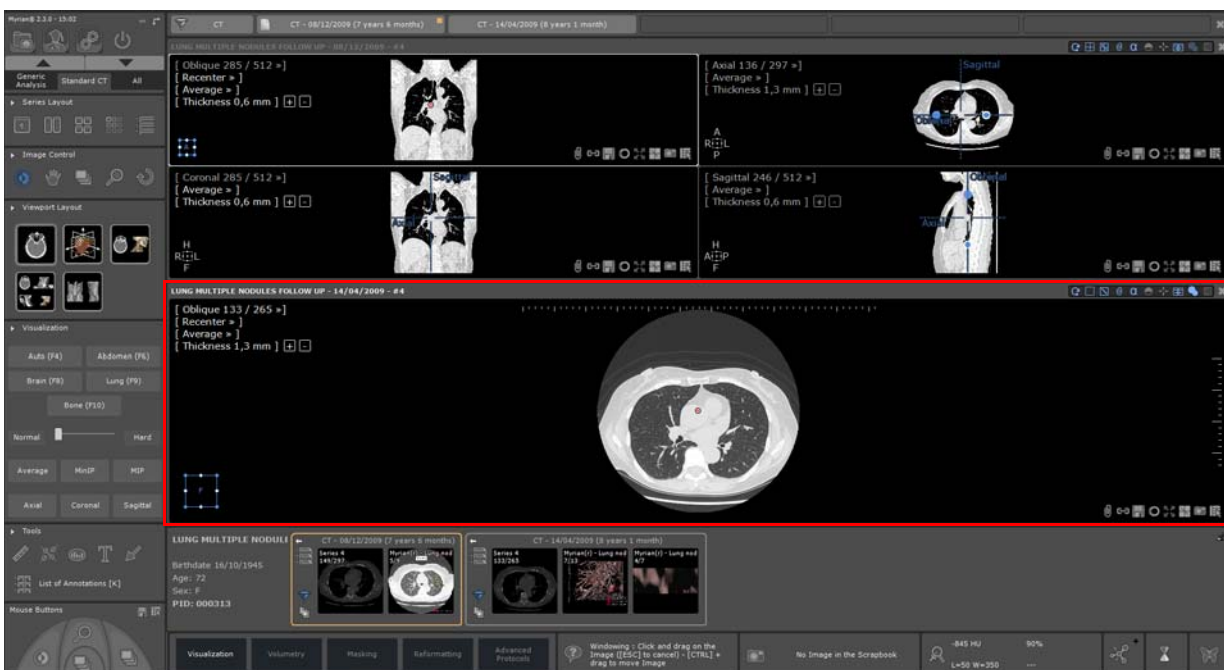


Figure 11-51 QuickPatient: visualization of the added series in the workspace in the newly created view (at the bottom)



While dropping here,

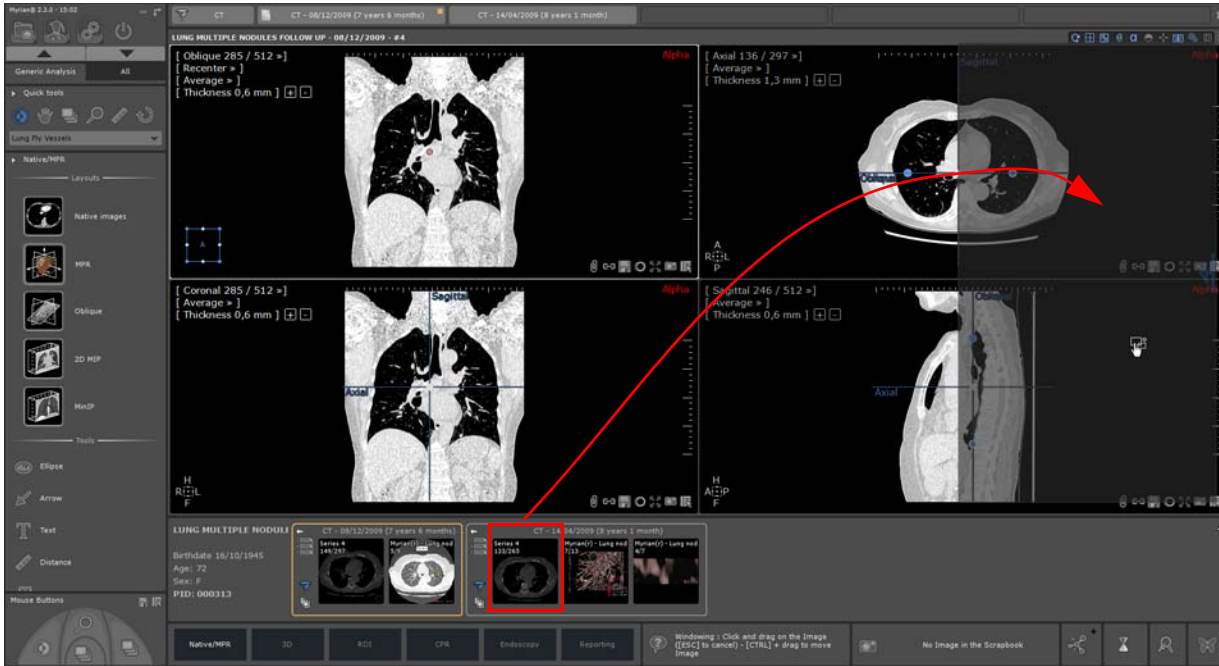


Figure 11-52 QuickPatient: Drag and dropping one single series from the study folder in the right part of the workspace

Results in the following:

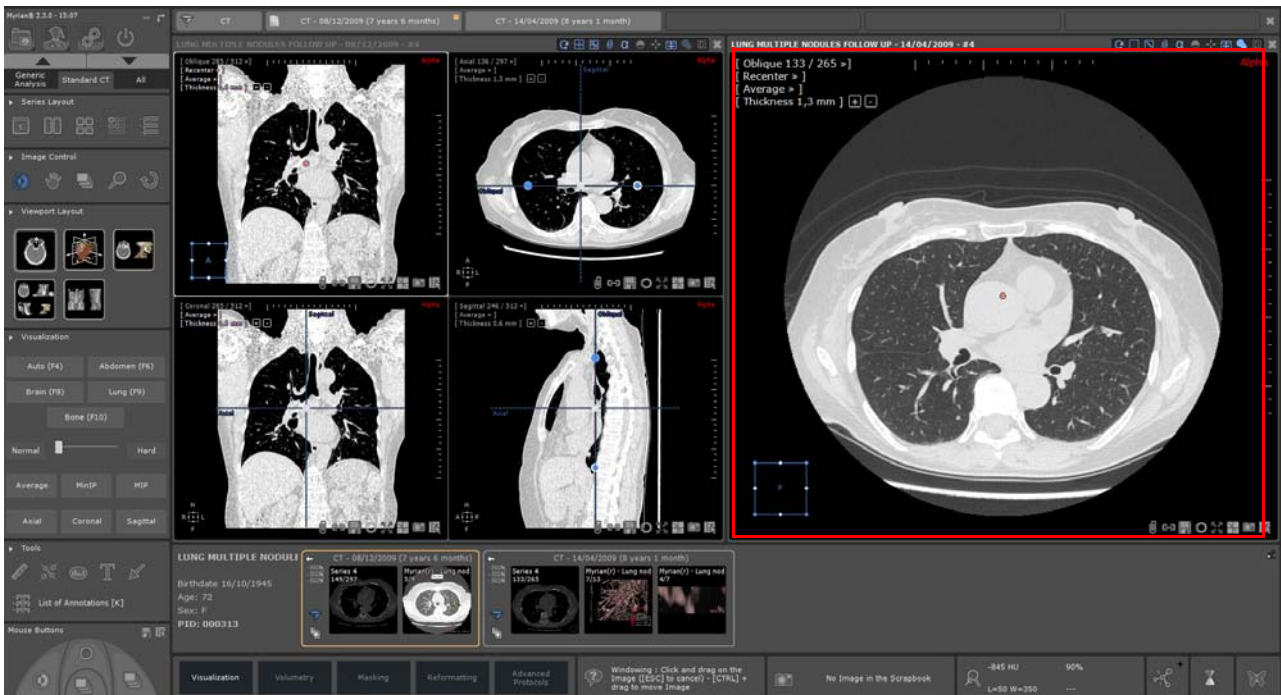


Figure 11-53 Visualization of the added series in the workspace in the newly created view (at right)

- **Above a free location:** the series is loaded in a single view at this location using a standard protocol corresponding to its modality.



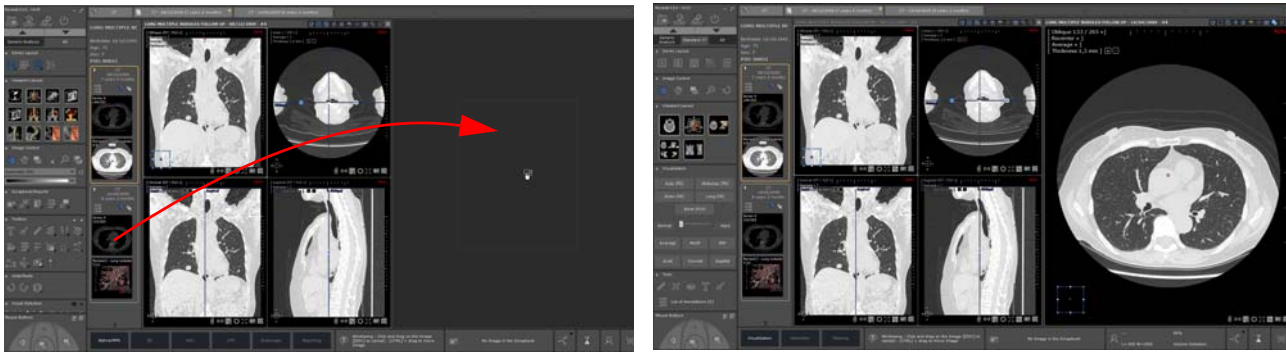


Figure 11-54 Drag and dropping one single series in a free location



If the series is dropped while **pressing down the <Ctrl> key**, the target series is not closed. The view is added in the workspace at the first free location. A free location can be added if needed, regarding the current view layout mode.

- **Above a multiphase view from a protocol without series category selector** (XP-Liver protocol for example): the series is added inside the view when compatible. Otherwise, the dropped series is loaded in a separate view in Native mode.

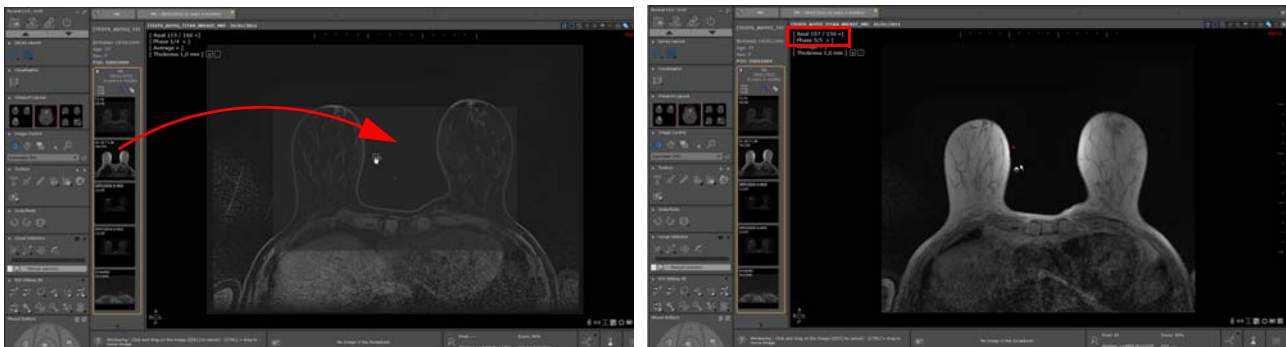


Figure 11-55 Drag and dropping one single series in a multiphase view

The added series is automatically displayed in the workspace as a **regular phase** initially loaded in the view and registered in the 'Phase' menu as the last phase of the view (phase 5/5 as illustrated here-above). The dropped series in the viewport is loaded in native orientation, native thickness and average mode.

Any phase can be selected using the 'Phase' menu in any viewport.

As the number of dropped series increases, the phase number displayed in the menu increases accordingly.

Like any other regular series loaded in a multiphase view, the same synchronization rules applies to the dropped series meaning that navigation, panning, zooming and windowing are synchronized between series.

When switching series layout, the dropped series remains displayed as a regular initially loaded series. The series drag & drop is **permanent** until closing the series.



When drag & dropping an already opened one:

- If the series is loaded on an empty view, the series is opened a second time.
- If the series is added on top of an open one, the phase corresponding to the dropped series replaces the previous one.

- **Above a multiphase view from a protocol including a series category selector but NO new volume computation** (as it is the case for any Fusion protocols or some protocols from the Female Pelvis family):
  - If the dropped series is an already open series, the viewport is automatically refreshed to display the dropped series only, hence replacing the previously loaded series.
  - If the dropped series has not been opened yet in the workspace, the dropped series is then referred to as 'Other 1' in the Phase menu of the selected viewport, hence replacing the previously loaded series
- **Above a multiphase view from a protocol including a series category selector and new volume computation** (like for the Prostate or Breast protocols):



The **dropped series/subseries** (which can be a **computed volume also** such as a subtraction series or an ADC map) should be **MPR-compatible** to be added in the view. If not, the dropped series is opened in a different view in Native mode.

When dropping an already opened series:

- If the series is dropped to an empty view, the series is opened a second time.
- If the series is dropped on top of an open one, the dropped series replaces the previous one.

On the contrary, when the dragged and dropped series has not been **opened before in the workspace**, the viewport is automatically refreshed to display the dropped series only, referred to as 'Others (1, etc.)' in the viewport menu and hence replacing the previously displayed series in the viewport.

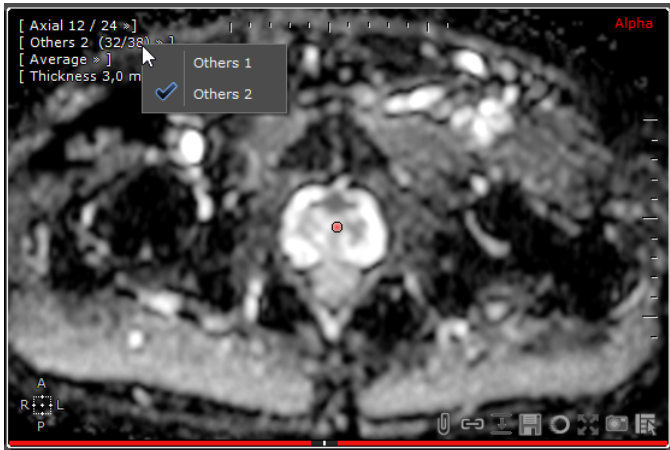


Figure 11-56 Dropped series replacing all previously loaded series in the selected viewport

In either case, the visualization of those dropped series is **temporary**: upon switching viewport layouts, the dropped series is no longer visible.

- To view it/them again, **redo the drop** from the QuickPatient window

If measurements were initially performed on the dropped series, they will be restored when dropped again.

### 11.3.3.3.2 Drag and dropping multiple series



Dragging and dropping **multiple series or subseries simultaneously using the CTRL shortcut key is not supported** by the QuickPatient feature.

When dropping a study that includes several series (i.e. a folder), a **single view is opened for each series using the standard default protocol** corresponding to each series modality.

If the study is dropped above a view, the target view is first closed, except if the <Ctrl> key is pressed down.

- Pass the mouse cursor over the folder name which highlights in orange then drag and drop it into the workspace.

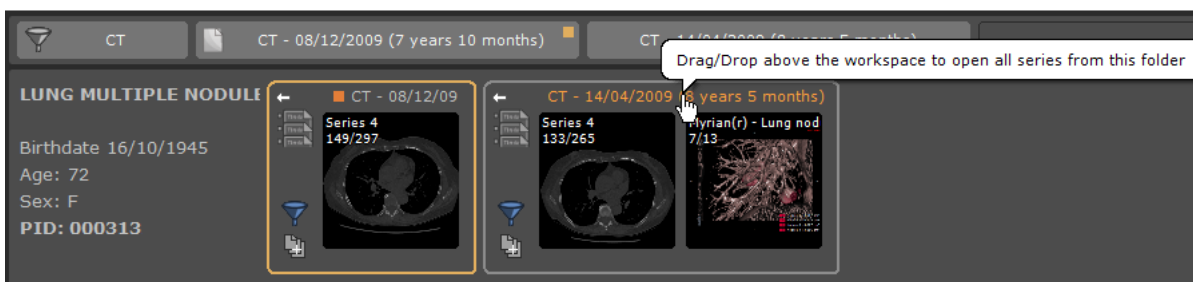


Figure 11-57 Drag and dropping a whole study folder from the QuickPatient Timeline

- Drag it into the workspace over the existing view



Figure 11-58 Phantom position of the new location of the selected folder will be before dropping it

- and drop it



To each study folder/date is allocated a default color to help you distinguish series from one another folder.



Figure 11-59 Visualization of the selected folder content dropped in the workspace

Otherwise, all the series are added on a free location, creating one or more if needed.

### 11.3.3.4 Patient case with multiple identities

When launching the QuickPatient while a study belonging to a patient with an identity conflict is open in the workspace, a warning icon appears instantly next to the patient name in the patient data area.

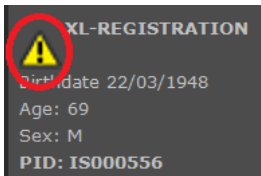


Figure 11-60 Patient Identity conflict alert

A Patient Security Alert window pops up indicating the various identities found for the given patient.

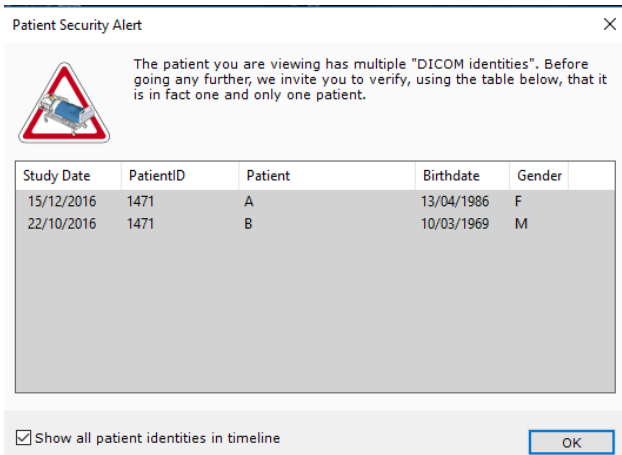


Figure 11-61 Patient Security Alert window

The study list displays the list of all the studies found for the corresponding patient ID including the patient details (name, gender, birth date) for each one.

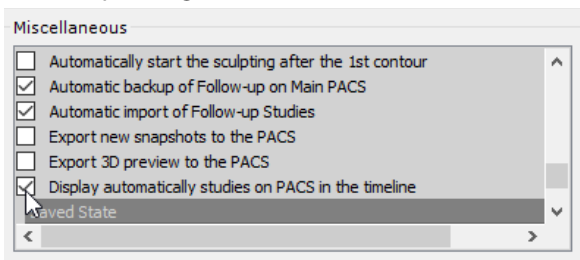
The 'Show all patient identities' checkbox allows to display or not the whole study list in the Timeline of all patient identities and Quick Patient window. If not checked, only the studies with patient details identical to the opened study will be displayed.

### 11.3.3.5 Viewing and importing remote series using the QuickPatient

The Timeline and the QuickPatient can also display studies and series that are not in the local Study list but on a PACS, as if performing a search in the Remote Studies screen.



Populating the Timeline with PACS studies is enabled by default in the Preference>Display>Miscellaneous menu.



If you don't want to have those available remote studies displayed in the Timeline, you need to disable this option.

In the Timeline, studies that are **not yet in the local Study list** appear with a **hatched background**. When clicking on the title bar of such a study in the Timeline, the QuickPatient shows the corresponding series.

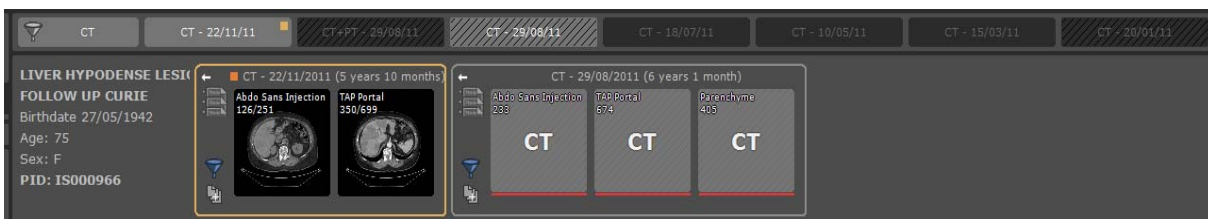
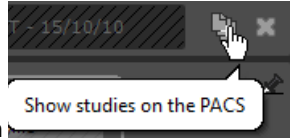


Figure 11-62 Remote series available from the PACS for a given patient



The remote series thumbnails are a simple gray hatched background with only the modality displayed over it since those series are not local yet and so, image of the series cannot be displayed as real thumbnail.

By default, only studies that are **less than 12 month old** are displayed. If you want to change that setting, you can do so using the "Show studies on the PACS" menu in the Timeline.



You can display this menu by clicking the button **Show studies on the PACS** next to the "Close" button, on the right of the Timeline.

From this menu, you can also select the PACS and the study age for those to import.

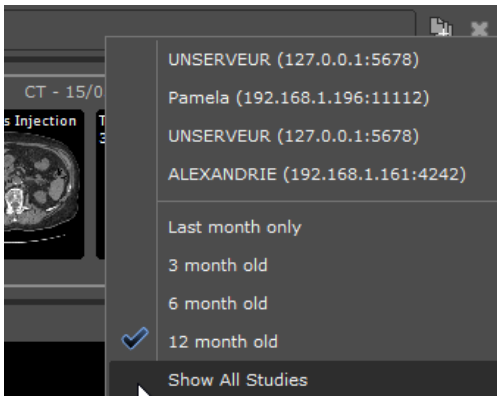


Figure 11-63 'Show studies on the PACS' menu

This menu can also be used to do a manual search on any of the available PACS.



Only the Main PACS (if defined) is queried or the first PACS in the list (if any PACS is defined).

**Drag and dropping any one of those remote series inside the workspace launches the whole study downloading** from the PACS.

During the series download, you can visualize the import progress directly inside the QuickPatient window for each study:

- A red progress bar for remote series which are not yet in the local study list
- Or a green progress bar for imported series.

Once the series is downloaded in the workspace, the real thumbnail of the series can be visualized.



Figure 11-64 Study download progress bars in the QuickPatient window



You can also visualize the series download using the background jobs dialog . from which you can cancel any



pending transfer.

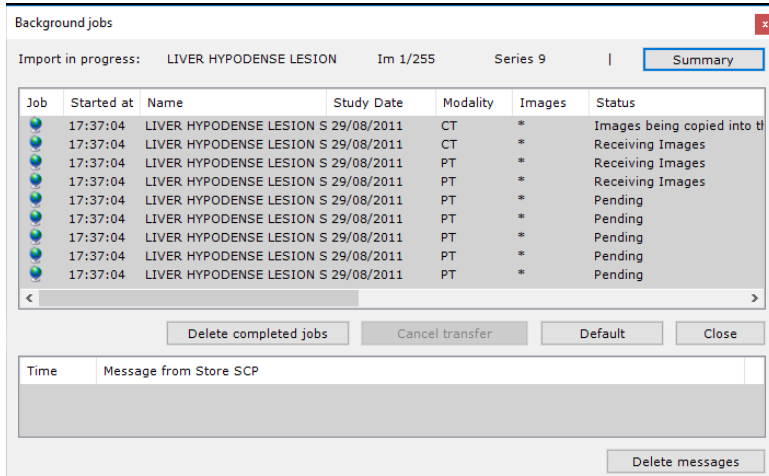


Figure 11-65 Visualizing study import from the QuickPatient in the background job dialog

In the case where series from different studies are dropped in the workspace, a default color is allocated to each study folder in order to better distinguish the dropped series from one another. In the same way, the study date of the view title bar is framed accordingly.

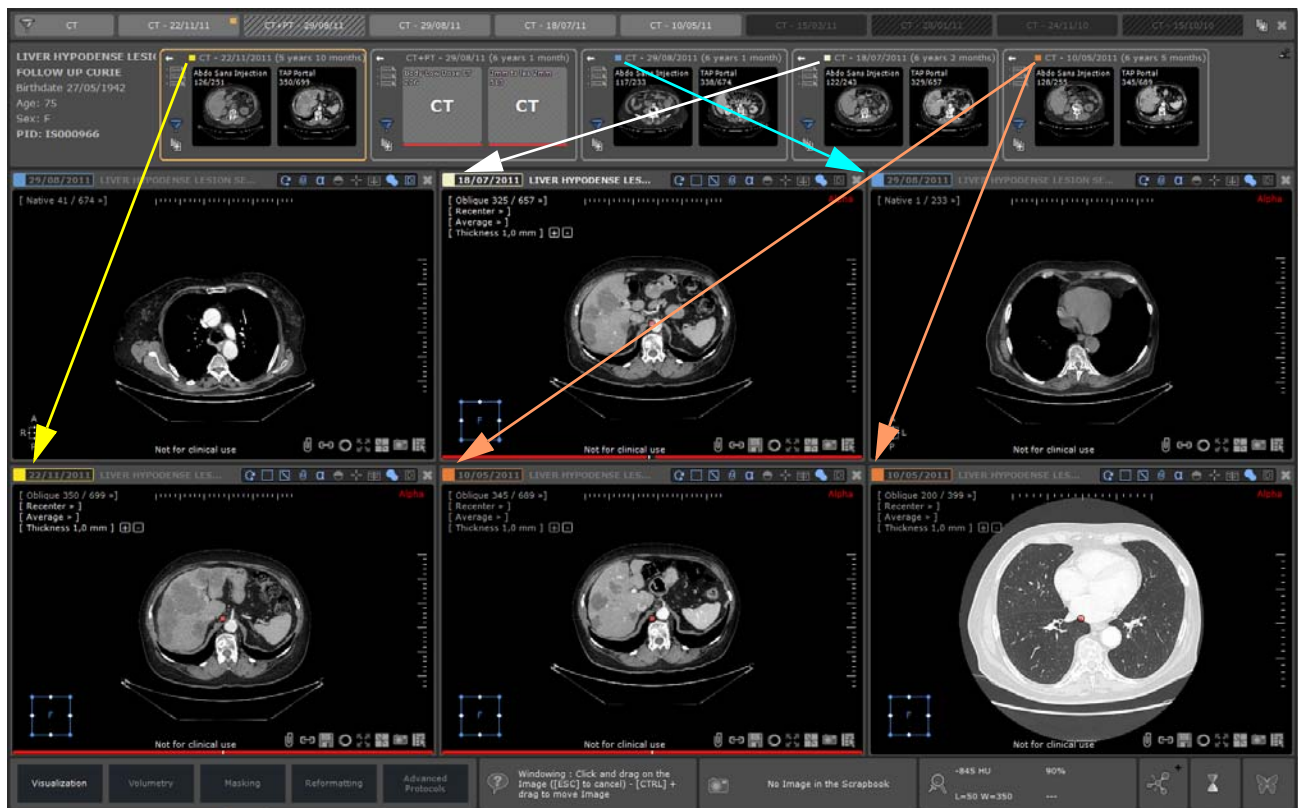
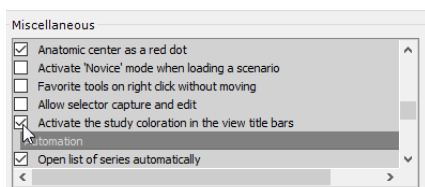


Figure 11-66 Visualization of the color-framed view title bar of each series displayed according to the folder they belong to




The coloration of the study date in the view title bar can be disabled from the Preferences>Display>Miscellaneous menu




---

### 11.3.4 Opening Studies from the Workspace

The "Open Next Study" button  enables you to load and review your entire Local Study List, Study by Study, directly in the Workspace without having to return to the Study List.



---

 This mode takes into account any active filtering (Name, Modality, Gender, etc.) you have applied to the List (i.e. if you have filtered your Study List to display only "CR"-type images created on a specific date, the function will load only those types of Studies).



The feature closes all open Series and open the next Study in the Study List directly from the 'Series Layout'

Toolbar in the Workspace by clicking 

- Click  to access the Local Study list
- Open a Study/Series using the desired Protocol
- When you find yourself in the Main Workspace, click  to launch the next Study in your Local Study List automatically closing the current Series

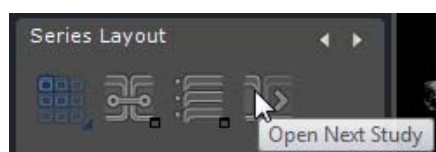




Figure 11-67 Open Next Study in the Series Layout toolbar


---

 The Study List is reviewed taking into account any active filtering or sorting.

---

 If a Study is opened via a QuickProtocol, the next Study will be opened with the same Protocol.

---

 If a Study is opened via a Protocol selected by the user in the Protocols tab, when the next Study is opened, the Protocol selection screen will be opened again.

---



This function to close all currently open Studies and open the next Study listed in the Study List in one click without needing to return to the Study List.

---

If the currently open Study is the last Study in the Study List, you get an alert message informing you that you've reached the end of the study list.

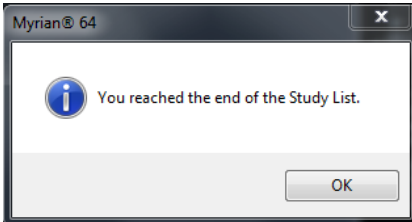


Figure 11-68 You reached the end of the Study list' message

## 11.4 Visualization Toolbar

---




For security reasons, if a Study or Series is still open, Myrian® requires user confirmation before opening another Study or Series belonging to a different patient.

---

To open Studies and/or Series (see Section 2.3.1 for further details on opening Studies):



- Click on  to open the Local Study List screen
- Locate the Study/Series/Subseries of your choice
- Use the CTRL or Shift keyboard keys to select more than one Study
- Click 'Open Series' to load the Series in the main workspace

Visualization settings are selected and modified in the Visualization Tab (at left of the main workspace)

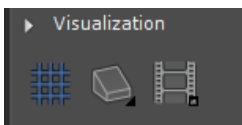


Figure 11-69 Visualization tab

### 11.4.1 Image visualization mode

Available modes are:

- 'Grid' mode (up to 10x10)
- 'MPR' mode volume reconstruction in any plane:
  - 'Canonical' planes ('Axial', 'Coronal' and 'Sagittal' planes)
  - 'Oblique MPR' mode plane for which the orientation is user-definable
- 'Tissue Coloring' 3D rendering mode
- '3D Volume' mode 3D rendering of the complete Study volume. Add-on Tissue Coloration filters can also be applied



'Cinema' mode automatic scrolling through the image slices




Buttons	Function
	Grid mode: images are displayed in the form of a grid of N by M images in axial view (see Figure 11-70). When the grid mode is selected, a set of grid size choices appears (1x1 ~ 10x10)
	MPR Reconstruction modes: MPR + Oblique 3D (Volume/Endoscopy)
	Cinema mode: allows you to animate the images in the Study

Table 11-5 Visualization mode buttons



In grid mode, the images are visualized in native format (often Axial plane orientation).

### 11.4.2 Grid display mode

Same Series images are viewed in a single frame. Their layout within the frame depends on the visualization mode selected. The grid function (also accessed by pressing the 'G' key of the keyboard) activates the grid layout display of up to 10x10 images per image zone. When this function is selected, a grid appears. You must then:

- Select the desired number of images by clicking and moving the mouse without releasing the button.
- Left-click on the desired grid-format (highlighted)

Frames (images) can be resized:

- Place the cursor over the horizontal or vertical border between two images
- Click and drag without releasing the mouse-button to increase/decrease the frame size at will.
- Release the mouse-button



Keyboard shortcut: click on the 'I' key of the keyboard to toggle between Grid mode and Full Screen view of the (current) image under the cursor. This function is also available in the context menu (bottom-right of the image or available via the assignment of mouse buttons).



You can use the icon at the bottom-right of each frame to toggle the Full Screen mode on/off.

A 3x4 Grid mode display example of is shown below:

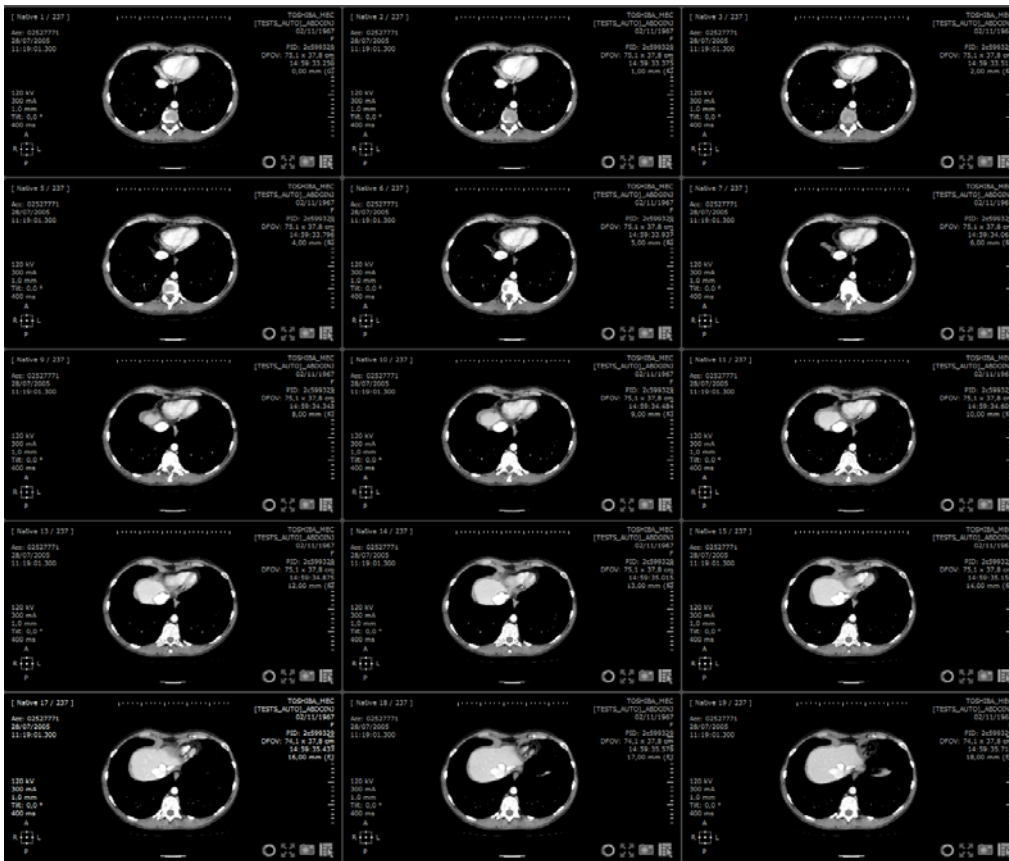



Figure 11-70 Grid mode (4x3)

The Movie mode  lets you cycle through the images at a constant speed.

- To activate this mode, click on the corresponding icon or with the 'C' keyboard shortcut key.

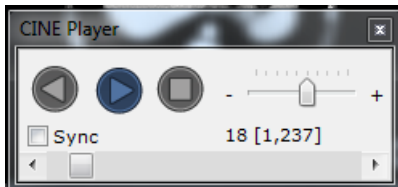





Figure 11-71 Cinema mode controls

The Movie navigation control bar has the following functions:

- Reverse Play button  (cycles through the slices in reverse order)
- Forward Play button  (increments the slices)
- Stop button  (stops the cycling)
- Play speed '+/-' slider (at right)
- Slice location 'jump to' slider (at bottom)
- 'Sync' checkbox to synchronize the slice animation between same-patient Series in 'Native mode' (requires 'Navigation' to be synchronized in the Series synchronization screen(see Section 11.3.1))

## 11.4.3 Information displayed in the Viewports

### 11.4.3.1 Image information display

Each frame contains the following information (on the image itself):









- A counter, top-left, continuously indicates the current image number over the total number of images in the corresponding axis
- Ruler gradations, in centimeters, are provided above and to the side of the image
- A direction reference with orientation indicators (L=left, R=right, A=anterior, P=posterior, H=head, F=foot) is given at the bottom-left
- DICOM data (see Section 11.4.4)
- Reference lines for the MPR mode (axial, sagittal and coronal axes). Their colors are based on the "Color scheme" settings in the Preferences>Display tab.
- Any existing Annotations that have been created
- The 'Show/Hide annotations' icon 
- The 'Activate/deactivate anatomical center synchronization' icon 
- The toggle Full-screen  icon (bottom-right)
- The 'Edge enhancement' icon  at bottom-right to sharpen the definition of any image
- The 'Add image to Scrapbook' icon  at bottom-right to add the view to the Scrapbook
- The context menu direct access icon  at far bottom-right of each frame



Figure 11-72 Image frame displaying overlaid information

Furthermore, if more than one Series is open from the same patient, the cross-reference marker lines icon  appears at the bottom right.

If the corresponding Myrian® modules are installed on your workstation then the following will also be displayed:

- The 'Add to current Quiz' icon  (if a Quiz is currently open)
- The volumes of the Regions of Interest (ROI) that you have edited (see Section 7.16). They are provided at the top-left of the view. if no ROI is defined then the indication 'No volume defined' appears.



The Patient Name, Study date and Study description appear top-left in the title bar of the main workspace frame.

### 11.4.3.2 Information Display Command Keys

At the top-right of the main workspace is a set of buttons to adjust the display of the images. The following table describes these buttons:



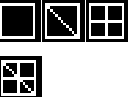







Button	Function
	Switches ROI freehand drawing mode (continuous mode, point by point or assisted mode (see Section 7.15.4 for further details)
	Adds the current view to the PrintComposer
	Displays/hides reference lines (MPR mode)
	Displays/hides Annotations
	Toggles 'Invert Colors' Mode on/off
	Recenter on Anatomical Center
	Activates/deactivates Series altitude synchronization (see Section 11.3.1)
	Toggles ROI Coloring on/off (3 modes available)
	Left-click: displays/hides DICOM overlay information (image size, slice thickness, position in mm, etc.). Right-click: opens the 'DICOM information displayed on images' choice screen (see Section 11.4.4)
	Closes the Series. Right-click to close all currently open Series

Table 11-6 Displayed information buttons

The functions of the first six buttons are described in more detail in their related chapters.

### 11.4.3.3 The superimposed menu

In the MPR/Oblique modes or 3D, a set of commands is available on each frame at the top-left.

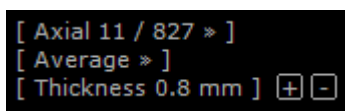


Figure 11-73 MPR frames' Orientation Menu

These commands enable to change the following:

- Choice of plane of view/mode
  - Coronal/Sagittal/Axial,
  - Oblique and
  - 3D Volume
- Render mode,
  - Average
  - MIP
  - MinIP
- Slice thickness (mm).

To adjust the Choice of plane/mode and Render mode, click on a command and select your choice from the sub-menu.

To adjust the slice thickness:

- Click on 'Thickness' and enter the value directly, or

- Click on the '+/-' icons to increase/decrease the thickness at will.



Hold the 'CTRL' button down and press the '+/-' keyboard number pad keys to toggle the Maximum/Minimum slice thickness.



When the '3D Volume mode' is selected, supplementary choices that are specific to 3D rendering modes appear in the command submenus (see Section 6.7 for further details).

### 11.4.4 DICOM information fields

By default, a certain amount of DICOM information is provided on the native axial image, regardless of modality/device. These are:

Name of DICOM field	DICOM ID	Description
Institution Name	(0008,0080)	Establishment where the Study's images were acquired
Patient's Name	(0010,0010)	Name and surname of the patient
Patient's Date of Birth	(0010,0030)	The date of birth of the patient
Patient's Sex	(0010,0040)	The patient's gender
Patient ID	(0010,0020)	The unique patient identifier as attributed by the establishment
Accession Number	(0008,0050)	The identification number of the Series
Study Date	(0008,0020)	Date of the Study's acquisition
Acquisition Time	(0008,0032)	Time at which the Study was acquired
Series Time	(0008,0031)	Time at which the Series was acquired

Table 11-7 List of generic DICOM fields available for all modalities

Appendix 6 provides a list of all DICOM fields for the principal modalities.

The following image gives an example of the DICOM information display, superimposed onto a view:

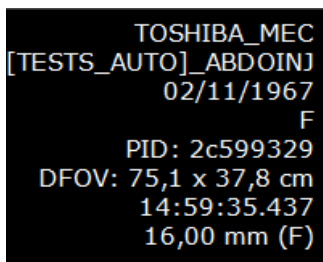



Figure 11-74 Example of a DICOM information display



Press D key shortcut to toggle DICOM information display on/off.

#### 11.4.4.1 DICOM Dump

You can access the entire DICOM contents of a Native Image via the 'DICOM Dump' function in the context menu  at bottom-right of the Native viewport.

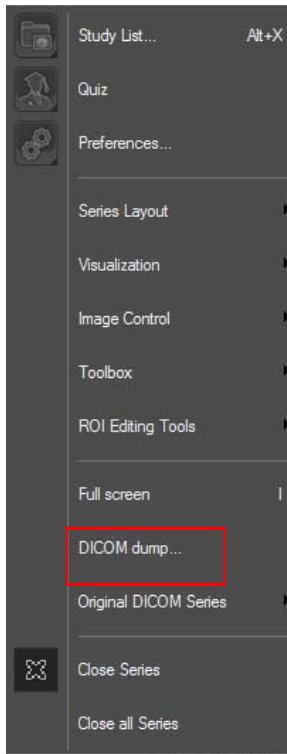
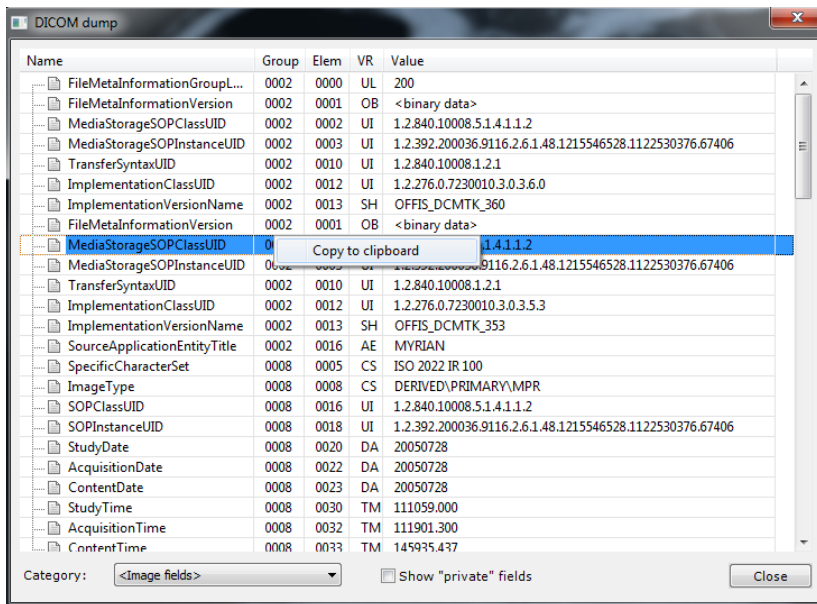


Figure 11-75 Open 'DICOM Dump' Screen via the Context Menu in Native Mode



Each field displays:  
 - A unique Group/Element identifier  
 - A Value Representation (type)  
 - A Name  
 - A Field Value for active image (except for binary data such as pixel values)

Figure 11-76 DICOM Dump screen



The 'Name' column is laid out as an expandable/collapsible 'tree' view so you can view or hide relevant elements of information.




You can copy the values of any element you wish to by right-clicking on it and selecting 'Copy to Clipboard'. The element can then be pasted into any word processing application installed on your PC.



A checkbox at bottom center of the screen toggles the display of Private fields on or off.

### 11.4.4.2 Display/hide DICOM overlay fields

- Locate  (top-right above the main workspace, see Section 11.4.3.2).
- Left-click on it to toggle display/hide DICOM overlay fields.
- Right-click on it to display the 'DICOM information displayed on images' screen (see below).

This screen is also available via Preferences>Display>DICOM Overlay button (see Section 8.4).

- Use this screen to choose which DICOM fields to display/hide.

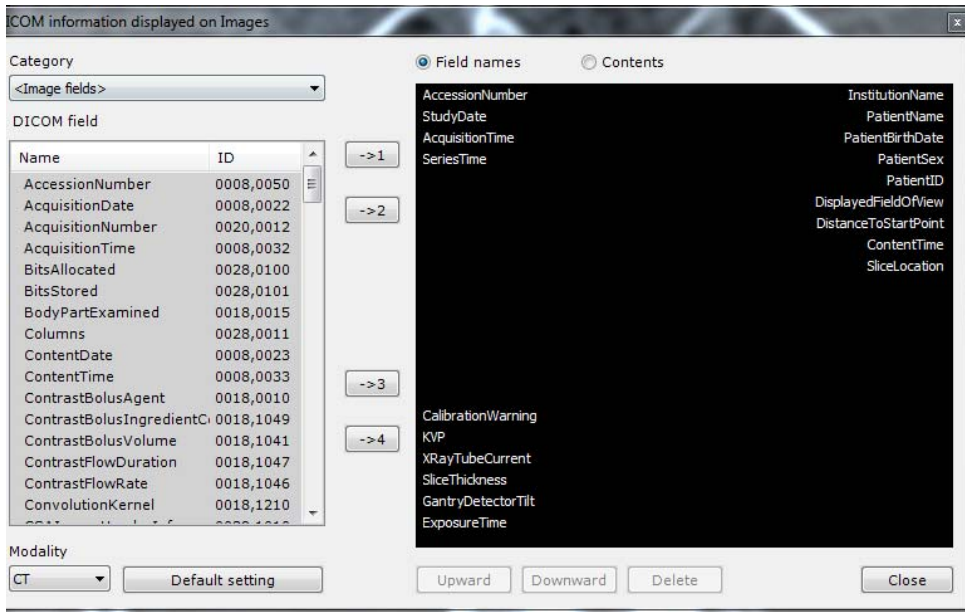


Figure 11-77 DICOM information displayed on image screen

In this window:

- Select a modality at the bottom-left,
- Select the desired DICOM fields from the 'DICOM fields' list.

The 'Category' list lets you filter the DICOM field list by theme.

To add a field to the image:

- Select desired field in the list,
- Click, as desired, one of the four buttons labeled '1', '2', '3' and '4'. These correspond respectively to top-left, top-right, bottom-left and bottom-right

The field is then displayed in the preview area.

A number of supplementary functions for adjusting the order in which information appears are below the preview area.

- Click on one of the fields on the image, then:
  - Click 'Upward/Downward' keys to move a field label to desired position.
  - Click 'Delete' to remove a field from display
  - Click on 'Default setting' button, underneath list of fields to revert to the default display
- Click on the small 'X' cross (top-right) or 'Close' button to exit.

Overlay info display is immediately updated for current and future sessions.

---



Use the Field names or Contents option buttons at top to configure display according to generic titles or Visualizing actual content of a currently open Series.

---



Keyboard shortcut: click 'D' to toggle DICOM overlay display on/off.

---



## 11.5 Image Control

The Image control tab settings enable viewing adjustment of various display aspects.



Figure 11-78 Image Control Toolbar

Image adjustment	
Button	Function
	Windowing
	Zoom in/out
	Pan the image sideward
	Navigate through the images in the Series
	Move the anatomical center to a new position clicking on the 2D/3D image
	Open the Magnifying lens
	Restore Default Grayscale Windowing settings

Table 11-8 Image controls functions



These controls do not change the image data in any way



Use the Spacebar to cycle from one primary tool to another (see Section 11.11.7) and change mouse-button assignments. Repeated use of the spacebar cycles through the following primary tools: Windowing, Zooming, Pan and Navigation.

- Hold the Shift button down to cycle in reverse order.

## 11.5.1 Windowing

### Overview

Standard monitors display around 256 shades of gray, of which the human eye can distinguish less than a hundred. The DICOM range of values, on the other hand, is far greater.

Default values for the center and width of the grayscale range or "Window" are attributed at the time of reconstruction. The values for each pixel must then be converted into grayscale values.

This conversion involves two important parameters:

- The Windowing width: every pixel with an original value below the minimal value is converted to black and every pixel with an original value above maximal value is converted to white.
- The Windowing center: the central pixel value of the range.



Before making Windowing adjustments, it is strongly recommended to perform a calibration of the monitor, if this hasn't already been done. A screen calibration tool is provided for this purpose with Myrian® (See Appendix 9 for more information).

---



Windowing is a filter which modifies the original image and therefore can potentially hide important parts of the Image or alter your perception.

---



By default, any Windowing changes are applied synchronously to all planes of view in the same Intensity Rendering Mode (Average, MIP or MinIP).

---



Hold the 'Shift' key down whilst adjusting Windowing settings bypass synchronization and apply different settings to views of same orientation (e.g. simultaneously view and compare both the Mediastinum and the Parenchyma of a Coronal lung view).

---



Windowing is not synchronized between views with different rendering settings.

---

Grayscale values for CT scanned images are expressed in Hounsfield units.

In all other cases (RGB images for example), these values correspond to light intensity.

---





Windowing values are permanently displayed in the mouse-over tab at the bottom-left of the main workspace (unless the latter has been switched to display thickness and position).



---

#### 11.5.1.1 Method of Use

To adjust Windowing Manually:

- Click on the 'Windowing' button  in the Image Control Toolbar, or the 'F' keyboard shortcut
- Click and hold the Mouse-button on the image
- Drag the mouse horizontally to adjust the Windowing Width
- Move the mouse vertically to adjust the Windowing Level
- Release the button to validate your settings, or press the ESC key on the keyboard to abort.

The small  button at left of the Windowing Presets Menu in the 'Image controls' tab restores default Windowing settings.

 The  button in the image commands top-right of the main workspace inverts the black and white values of the pixels, thereby displaying a 'negative' of the image (default settings for some modalities).

### 11.5.1.2 Windowing Slider

When you hover over the left side of 2D Viewports with known intensity values, a Windowing Slider appears.

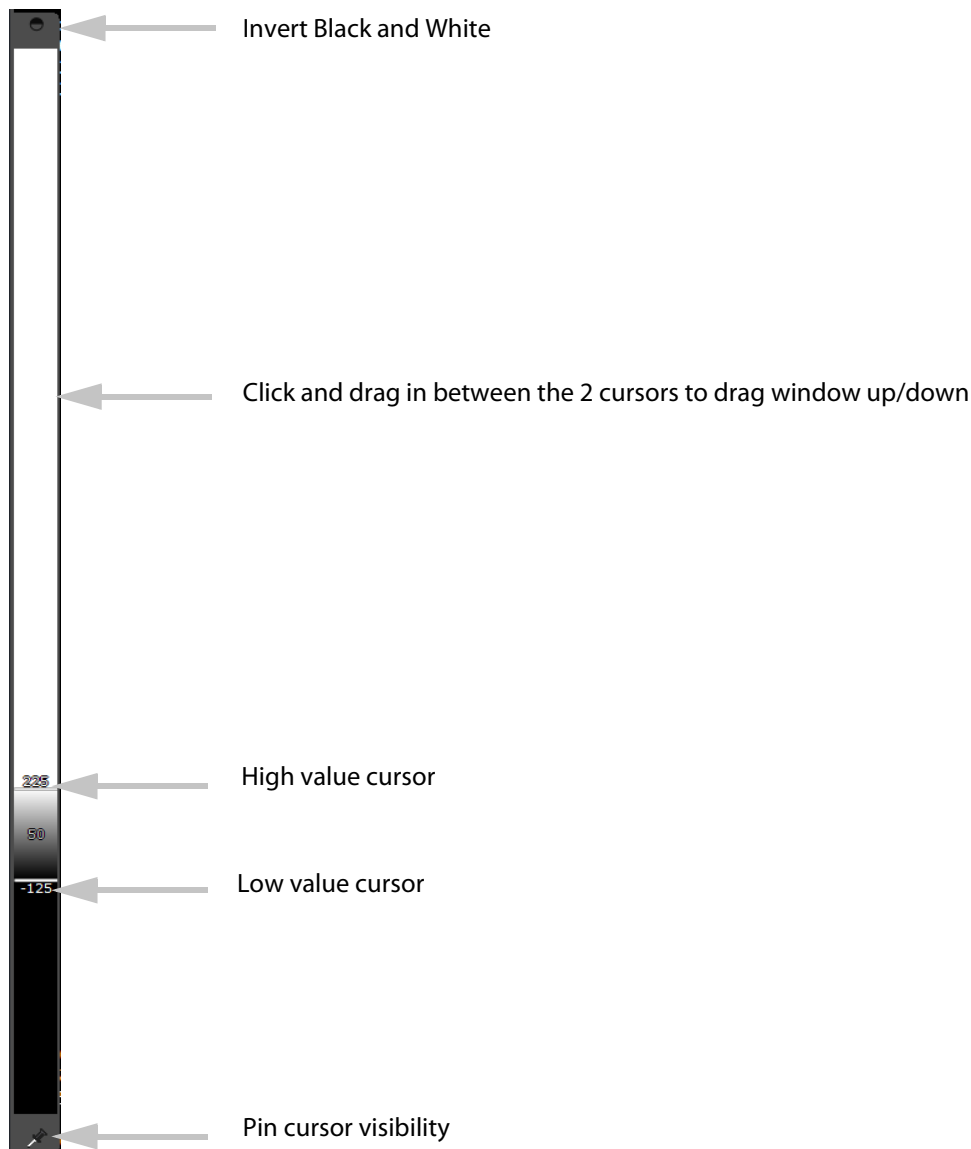


Figure 11-79 Windowing Slider

The Slider enables you to set:

- The width, or range of your Windowing via the cursors at top and bottom
- The Windowing value by click and drag in between the cursors which moves the Window up/down
- The Invert Black and White button at top to invert all grayscale values of the image
- The Pin Cursor to the Viewport to force continued visibility regardless of mouse movement

### 11.5.1.3 Windowing Preset Customization

#### Overview

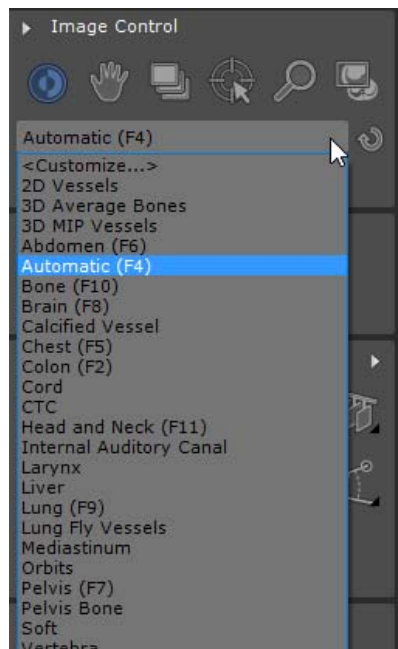
You can tailor existing Windowing Presets to own needs or create entirely new ones "from scratch" by entering each

parameter yourself. Furthermore, you can also configure the lists of Presets which will appear in the Windowing Menu for each Modality.

## Method of Use

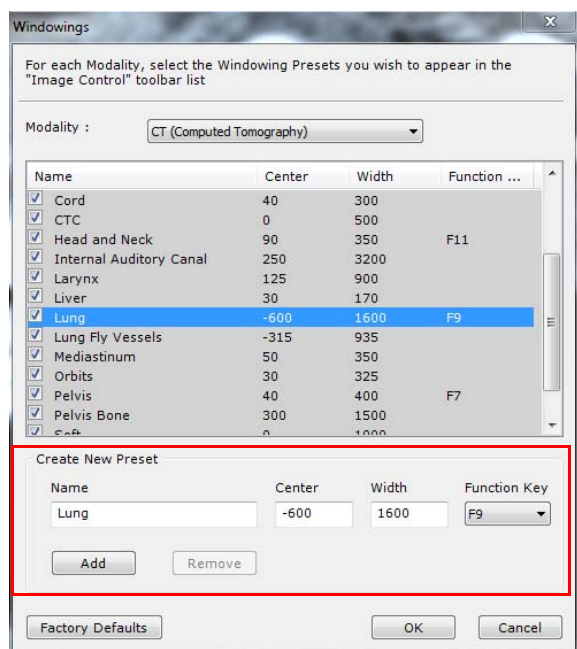
To modify an existing Preset or create a new one:

- Open the Windowing drop-down menu in the Image Control Toolbar:



1. Select <Customize...> in the resulting drop-down menu

Figure 11-80 Windowing Presets drop-down Menu

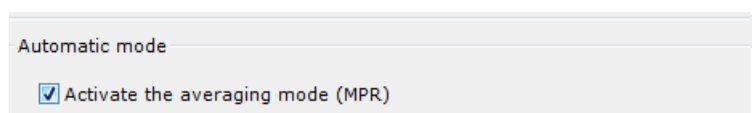


2. Select a Windowing Preset in the list and/or:
3. Type a new or modified name in the 'Name' field under the Current Presets list
4. Enter the desired parameters in the Windowing 'Center' and 'Width' customization fields and, if you wish, a shortcut Function ("F") key at right
5. Click the 'Add' button underneath the Name field to add your new Windowing Preset to the list then press OK

Figure 11-81 Windowing Presets Customization Screen

## Apply an averaging windowing to automatic mode for Multiplanar Reconstruction

For series with a large variation of windowing values across the slices in Native mode, this option enables to customize the <Automatic> mode by averaging the windowing for MPR viewports only.



Check the 'Activate the averaging mode (MPR)' option



The averaging windowing is computed from the native slice values as follow:

- the center value is the average of all native slice center values
- the range value is the average of all native slice range values

## Customize Windowing Presets Menu for each/any Modality

To customize the list of Windowing Presets that appear for each Modality:

Name	Center	Width	Function ...
<input checked="" type="checkbox"/> Head and Neck	90	350	F11
<input checked="" type="checkbox"/> Internal Auditory Canal	250	3200	
<input checked="" type="checkbox"/> Larynx	125	900	
<input checked="" type="checkbox"/> Liver	30	170	
<input checked="" type="checkbox"/> Lung	-600	1600	F9
<input checked="" type="checkbox"/> Lung Fly Vessels	-315	935	
<input checked="" type="checkbox"/> Mediastinum	50	350	
<input checked="" type="checkbox"/> Orbits	30	325	
<input checked="" type="checkbox"/> Pelvis	40	400	F7
<input checked="" type="checkbox"/> Pelvis Bone	300	1500	
<input checked="" type="checkbox"/> Soft	0	1000	
<input checked="" type="checkbox"/> Vertebra	120	750	

Figure 11-83 Customize list of Windowing Presets

## Delete a User Windowing Preset

To delete a User-defined Windowing Preset, either:

- Highlight the desired User Preset in the Windowing Presets list
- Click 'Remove' at bottom center of the Customization Window, or
- Click 'Factory Defaults' to delete all User-defined Presets at once and restore the Windowing Presets to their original state



You can also hold the CTRL key while you click on Presets to make multiple selections.

### 11.5.1.4 Windowing in the Standard CT protocol

In the Standard CT protocol, the user has the possibility to choose the windowing buttons to display in the 'Visualization' tab (see Figure 11-84) within the toolbar of the workspace. By default, the windowing buttons displayed are 'Auto', 'Abdomen', 'Brain', 'Lung' and 'Bone'.

In order to add or hide some windowing buttons, the user has to open the 'User preferences' related to this protocol and select the windowing button needed. This step is described in the Section 15.6.8.

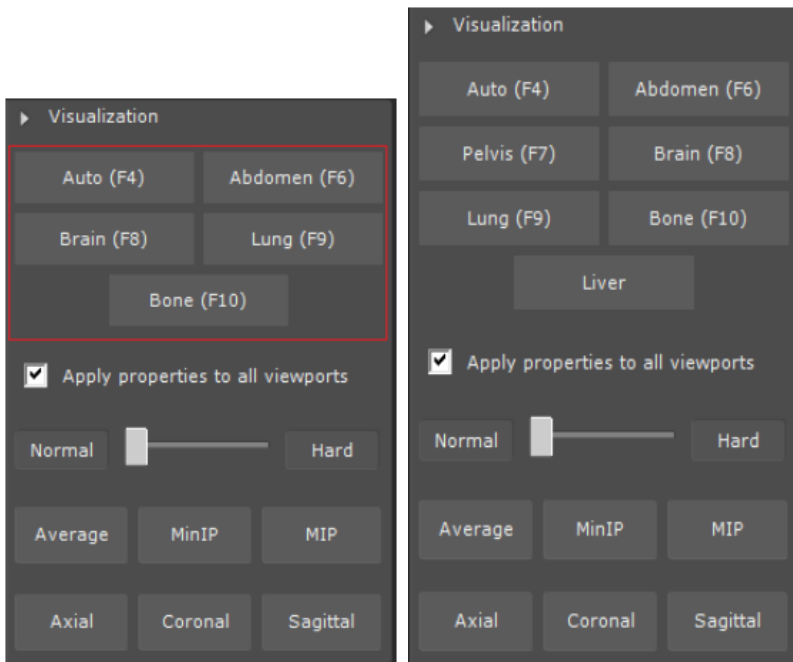




Figure 11-84 'Visualization' tab - The five default windowing buttons on the left and these five buttons plus two added by the user on the right

## 11.5.2 Panning

The 'Panning' function  moves an image horizontally and vertically within its frame. This function is available as a standard Primary Tool function assigned to a mouse button or simply by holding down the CTRL key at any time, regardless of the currently selected function.

To use it:

- Click  (or hold down the CTRL keyboard key)
- Click on the image without releasing the mouse button/CTRL key
- Move the mouse
- Release the mouse to confirm the changes or press ESC to cancel

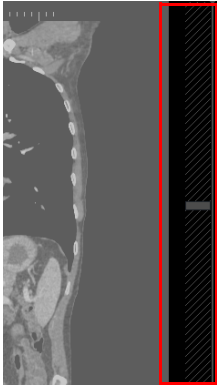
## 11.5.3 Navigation through the images



While navigating in the active series, a red progress bar located at the bottom of the viewport appears to visually indicate real-time the images that have been/not been displayed yet (in red). When skipping slices, the following message pops up to notify you: 'Slices might have been skipped while scrolling' as illustrated hereunder:



Use any of the following methods to navigate through the image slices:




1. Click  with any of the three mouse buttons. This assigns the command to the chosen mouse-button
2. Using this same mouse button, click on a view in the Study and hold the mouse-button down
3. Drag the mouse horizontally (left/right) or vertically (up/down) to navigate through the slices of active frame
4. For fast navigation, use the auto-hiding Viewport Navigation Slider which appears when you move the mouse cursor near the right side of any 2D frame.

Figure 11-85 Viewport Navigation Slider



When the 'Image per image navigation' mode (see 'Miscellaneous' in Section 8.4) is activated, if the mouse moves beyond the top or bottom edge of the viewport, navigation continues until either the mouse is moved in the opposite direction or you reach the end of the stack of slices.



Navigation through slices does not apply to 3D Volume.


Image Navigation Tools
Mouse wheel if the 'navigation' function is assigned to it
Click on  then click-and-drag the mouse on the Study without releasing the mouse button (works with all three buttons).
Drag out of the frame at the top or bottom to activate auto navigation
Viewport auto-hide Navigation Slider

Table 11-9 How to navigate through images


### 11.5.4 Zooming



- **Zoom** to **increase** and **decrease** the size of the current image.

The Zoom function zooms into or out of the point clicked upon or directly under the Mouse Cursor.

It is used as follows:

- 1 **Click on**  or press **Shift+'Z'** key on the keyboard
- 2 **Click on a point in the image** without releasing the mouse button
- 3 **Move the mouse** (horizontally for a rapid zoom, vertical for a slower zoom)
- 4 **Release the button** to confirm changes or press **ESC** to abort.



It is also possible to use the Mouse wheel to zoom in and out on a target zone.



To reset the zoom level to normal and restore instantly the image to its default size, click on the **Z Keyboard**

## shortcut.



Myrian® automatically applies a Smoothing filter to the original image to improve the image quality regardless of the zoom setting.

### 11.5.5 Magnifying lens



The 'Magnifying lens' function is a magnifying window that increases the size of the part of the image that lies beneath it.

It is used as follows:

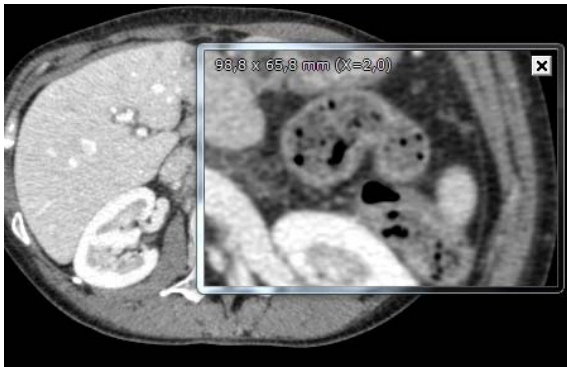


Figure 11-86 Magnifying lens over the axial plane of view



1. Click
2. Click on the Magnifying lens window, hold down and drag it over the desired part of the image.
3. Roll the mouse wheel to zoom the Magnifying window in/out.
4. The Magnifying window may be resized by dragging its edges.
5. The current zoom level and the size (in millimeters) of the zone displayed by the window are shown at all times in the top-right corner of the window.

## 11.6 Toolbox toolbar

The 'Toolbox' toolbar to the left of the main workspace may contain the following annotation and measurement tools according to your activated modules:

- Insert Text
- Insert Pointer
- Add length measurement (distance annotation)
- Create Path
- Create Generic POI
- Measurement tools (lines, shapes, complex shapes)
- Annotation List
- Pixel Calibration tool
- Contrast Curve tool
- Matching toolbar
- Complex AOI (requires activation of AOI tools)
- Cardiothoracic Ratio tool (see Section 7.14)
- ADC tool (see Section 7.13)
- DragDrop tool (see Section 5.3.5)
- Add a diameter measurement (3D)






Figure 11-87 Toolbox

### 11.6.1 Annotations and length measurements

The Image Annotation and Length Measurement tools add:

- Text zones onto an image,
- Pointers (Arrows indicating precise points),
- Length Measurements between two specific points,



Those annotations are also available clicking on the AOI button 



Text, Pointer and Measurement annotations are saved automatically when closing a session or Series.





Annotations	
Button	Function
	Creates a Text Annotation
	Draws an Arrow to indicate a point of interest
	Makes a Length Measurement.
	Opens the 'List of Annotations' screen

Table 11-10 Annotation buttons

To use these functions:

- Click on the desired function button, or
- Assign the function to one of the mouse buttons (see Section 11.11).

Since the pointer and length Annotations are Secondary Tools (see Section 11.11.1), depending on the 'Primary/ Secondary tool' checkbox settings in the 'Preferences> Display> Miscellaneous' tab, you may have to click again on the tool button or reselect the mouse assignment for each new Annotation.

To move any Annotation:

- Click on the Annotation you wish to move
- Hold the mouse button down
- Move the mouse to the desired position

To edit any Annotation:

- Make a double left-click on the Annotation you wish to edit

By making a double right-click on the Annotation, the following contextual menu pops up from which you can choose to:

- Hide the annotation
- Remove the annotation
- Change its color
- Increase and/or Decrease text size

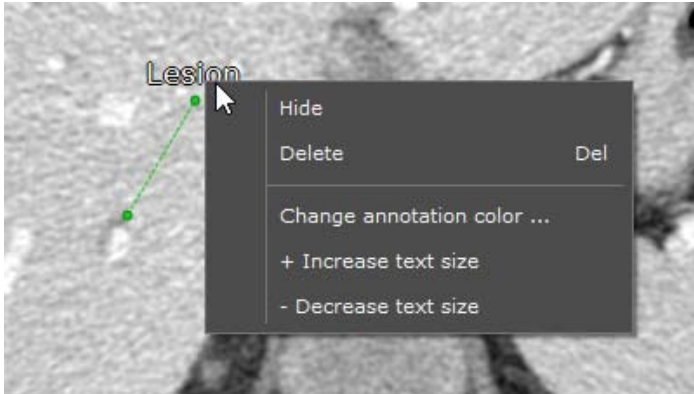



Figure 11-88 Annotation contextual menu

Annotations can be hidden/displayed by clicking on the  icon in the Display Function Toolbar at top-right above the main workspace.

- To display/hide annotations on one given viewport, click on  located in the concerned viewport (the annotation display is activated by default on all viewports)



Press the K key shortcut to toggle the annotation list display on/off

To delete any Annotation:


- Left-click on the Annotation you wish to delete
- Press the Delete button on the keyboard,

Or

- Right-click on the Annotation
- Select 'Delete' from the context menu

## 11.6.2 Text annotation

To create a Text Annotation:

- Click on the  icon in the Toolbox (or select 'Text' in the mouse button menu)

The 'Predefined text' window will appear bottom-right of the screen with a list of predefined text labels.

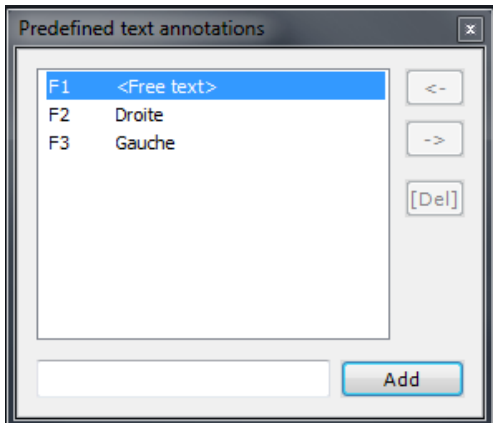


Figure 11-89 Predefined Text Annotations

- Select the desired text
- Click the 'Add' button (bottom-right)
- Click a spot in the image where you wish the Annotation to appear

To add your own text:

- Type-in the desired text in text field (left of 'Add' button)
- Click the 'Add' button.
- Click a spot in the image where you wish the Annotation to appear

To change the list order:

- Use the '->' or '<-' Arrow buttons above-right.

To select a Text label in the list:

- Click on it, or
- Use the corresponding F1 to F10 function keys (top of keyboard)

To delete Annotations from the list:

- Select the desired Annotation
- Click the 'Del' key at right

Each list of Text Annotations is automatically saved from session to session and is dependent on the user profile.

If you select the 'Free text' entry in the list, you may type freely onto the image.

- To do this, click on the image at the desired location and a small window will appear where you may type in your Annotation.

A dash line appears with a text label associated.

- Click on the dash line extremities to relocate either the dash line or the label
- Double-click on the 'Text Label' and type-in the desired text in the text field

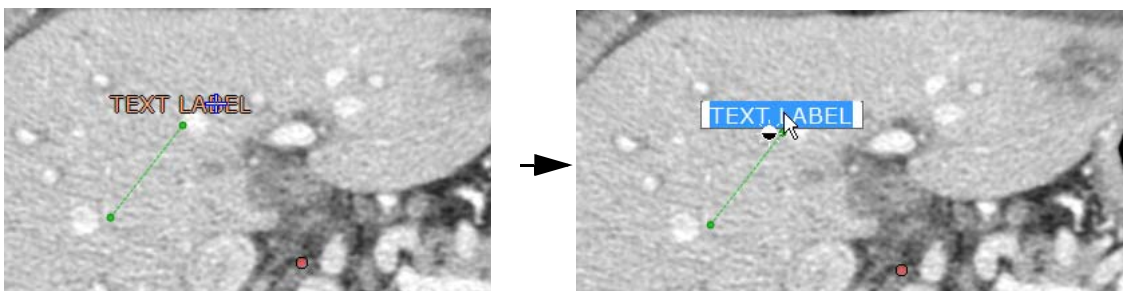


Figure 11-90 Creating a text label

- Click a point on the image outside the label text to validate the text entry

The label is created.

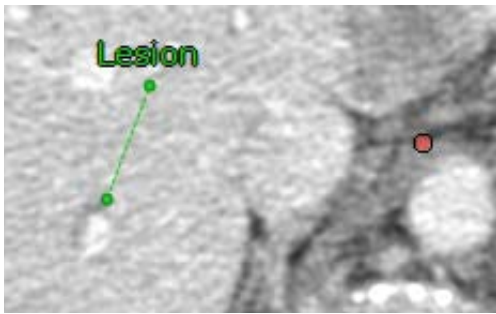




Figure 11-91 Text annotation

- To move an Annotation, place the pointer over it (which changes to ) then press and hold down the mouse button while moving the mouse.
- To edit an Annotation that has already been placed, right-click on it to open the annotation edition menu (see Figure 11-88)

### 11.6.3 Pointer/Arrow annotation

To add a pointer:

- Click on the  button (or select 'Arrow' in the mouse button menu)
- Click on the image without releasing the mouse-button
- Move the mouse to the desired position.

To move a pointer Annotation:

- Click on the Annotation
- Hold the mouse-button down
- Move the mouse to drag the Annotation to the desired new position.

To change the size and direction of an Arrow pointer:

- Move the mouse pointer to one of the Arrow extremities (the cursor becomes a cross)
- Click and move the point with the mouse-button held down.

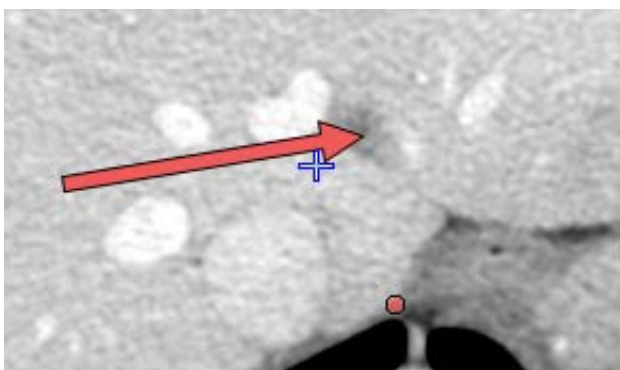


Figure 11-92 Pointer Annotation

You can add a text label at the end of the arrow.

## 11.6.4 Length measurement

- To add a length measurement, click on the  button (or select 'Distance' in the mouse button menu)
- Draw a segment and adjust the length using the segment extremities

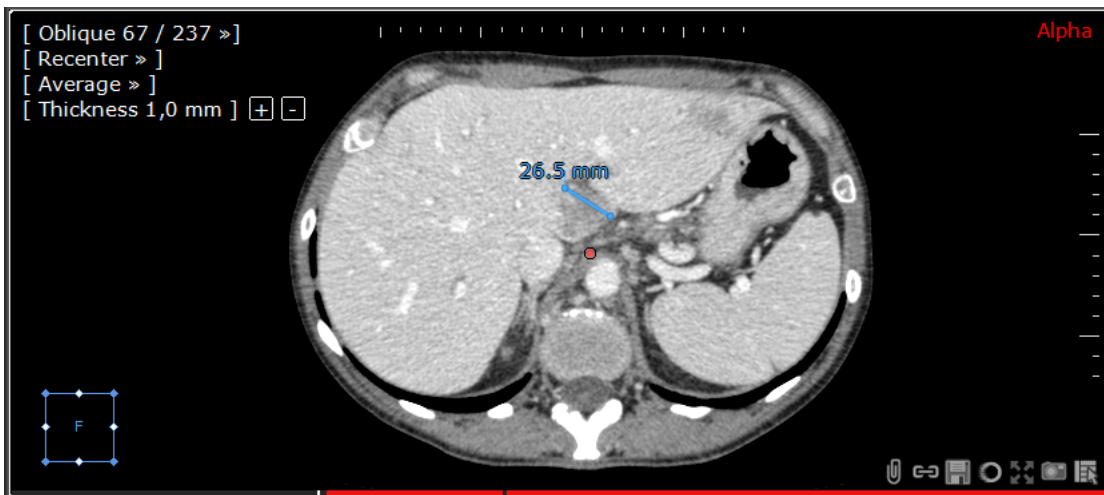


Figure 11-93 Length measurement

The length measurement tool supports mm,  $\mu\text{m}$  and pixel units and can be used on MIP and MinIP images.

It displays 2D distance as well as 3D distances. When the displayed distance is a 3D distance, it is automatically specified in the measurement label.

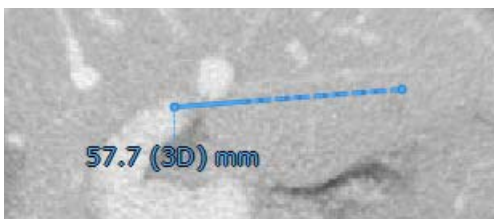


Figure 11-94 3D length measurement



The unit is automatically chosen by the AOI as follow:

- mm: Any measurements greater than 1mm
- $\mu\text{m}$ : Any measurements lower than 1mm
- Pixels: Any uncalibrated or not natively calibrated images.

To move measurement Annotations:

- Click and hold the mouse button (color of the measurement annotation changes to orange) to select the annotation

- Move the mouse to the desired new position.

Length measurement Annotations have a small label which shows the distance between the two endpoints. This label is positioned automatically, either in the middle of the line representing the measured distance or at one of the endpoints if the line is too short to display the distance label at its middle.

To move any label's position manually:

- Click on the desired Annotation (color of Annotation label changes to orange) and move the label to the desired position.

To edit the length value measured:

- Make a double left-click on the label, this will highlighted in blue the part that will be edited
- Write the new value and press 'enter', the blue line length will be automatically updated

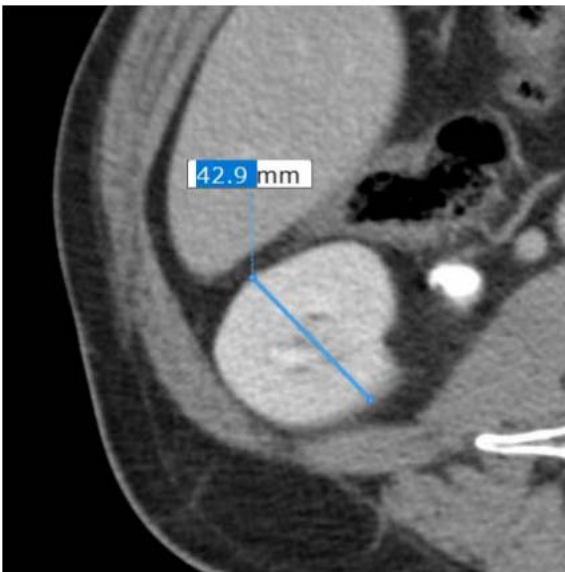


Figure 11-95 Editing of the length measurement



Press the H key shortcut to automatically have the distance annotation tool selected and ready for use

## 11.6.5 Annotation list



The icon brings up the 'Annotations and measurements list' window for the current Series/Subseries.

To locate an Annotation:

- **Highlight** an Annotation in the list and click on the '**Find**' button (bottom-left of list screen)

The slice containing the Annotation will automatically be brought to the forefront and displayed.

- To **navigate** through the list of Annotations, click on an Annotation or use the '**Next**' button.
- To toggle display of any Annotation, check/uncheck the checkbox at left of every Annotation listed.
- To **delete** an Annotation, highlight desired Annotation and click on the '**Delete**' button.
- To exit the list screen, use the 'X' cross (top-right) or click on 'Close' (bottom-right).

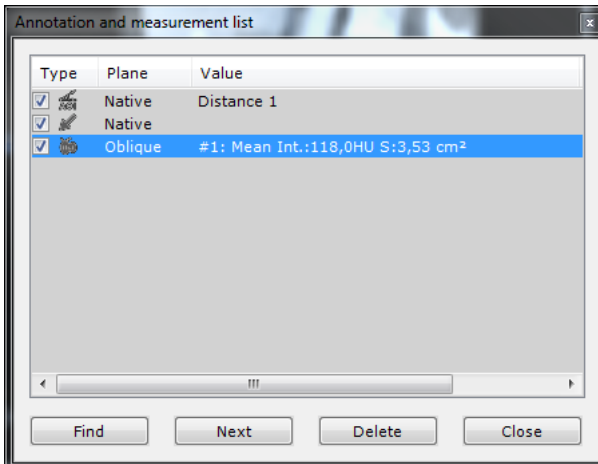


Figure 11-96 Annotation list



The undo/redo (or CTRL+Z) function is applicable to the actions found in the Annotation list window.



Up/Down cursor arrows on the keyboard can also be used to navigate between annotations in the list.

### 11.6.6 Measurement window

The free-shape measurements window gives access to a list of measurements (Volume, Slice-by-slice area, Standard deviation, Mean density, Intensity sum, etc.) as well as the Density Histogram for the contoured zone.

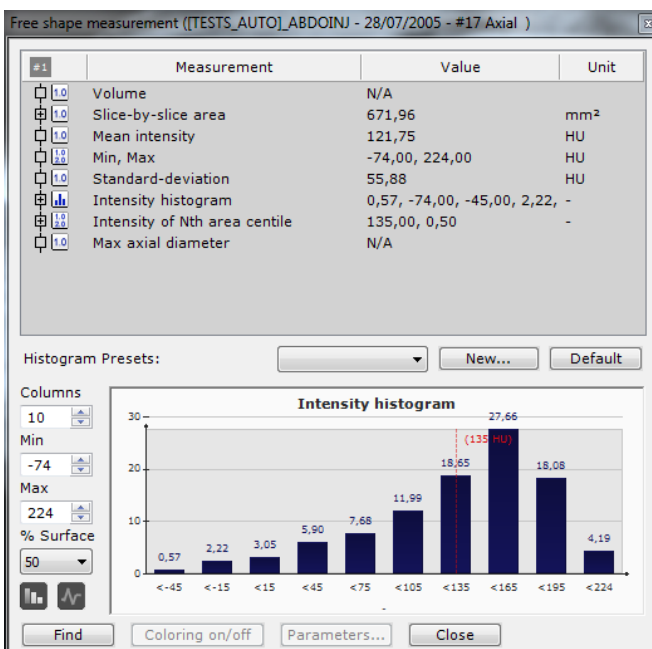


Figure 11-97 Free shape Measurement window

The drop-down menu at center of the Histogram screen displays the Preset List.

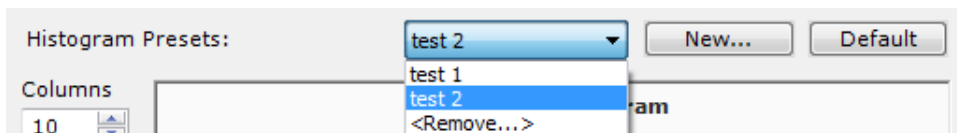
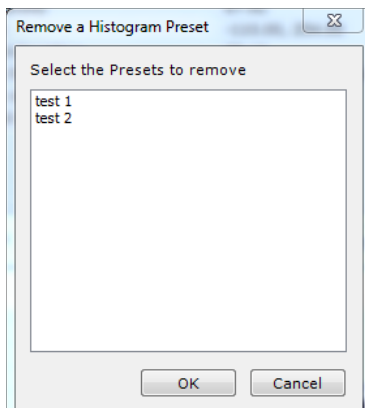


Figure 11-98 Histogram Preset List

To delete Presets:



1. Click on the "Remove" option in the Preset List

2. Select your choice of Presets from the list in the resulting Remove Histogram Preset window

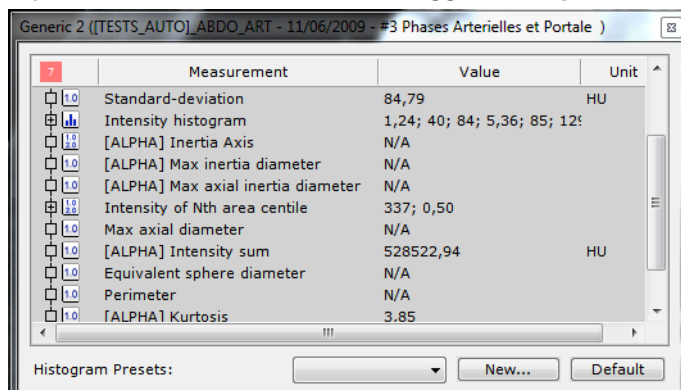
Figure 11-99 Remove Histogram Presets window



Use the CTRL/SHIFT + mouse click to make multiple selections.



The voxel intensity sum calculation which is also available both in the 'ROI measurements' and the 'ROI combined measurements' windows is part of the experimental measurements hidden by default. To change this setting, go to 'Preferences' > 'Display' > 'Miscellaneous' and check the 'Display experimental measurements' checkbox. All experimental measures will then be tagged as '[Alpha]' in the Advanced Measurement window.



You can customize display parameters (number of columns as well as the minimum and maximum density HU count) via the fields at left of the Density Histogram area or via the right-click menu on the Histogram itself.



Click **Defaults** to restore all default Histogram settings (10 columns, Min and Max ROI intensity values, 50% volume).

Three 'Copy' options are available via the right-click menu:

- **Copy to Clipboard**, enables 'Paste' function of the list of current contour's measurements to other applications (MSWord, MExcel, etc.)



- **Copy to Scrapbook**, copies the Measurement window to the Image Scrapbook
  - **Copy to Print Layout**, copies the Measurement window to the PrintComposer bay, ready for print-out
- Plus the access to the **Histogram Parameters** dialog box

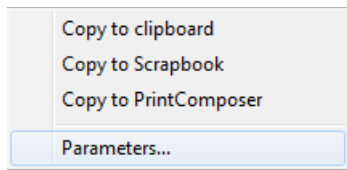

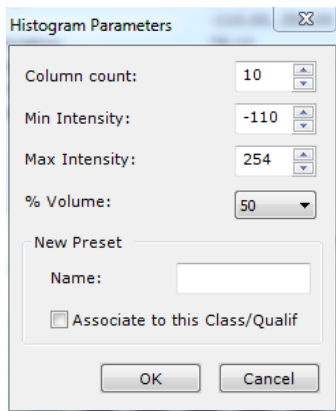


Figure 11-100 Histogram right-click menu

### 11.6.6.1 Configuration Presets

Your settings can be saved as new presets by clicking  in the "Histogram Presets" area at center of the Histogram (see Figure 11-97).



1. Modify the settings in the Histogram Parameters dialog box as desired to create your new Presets
2. Rename it
3. Click OK

Figure 11-101 New Preset Parameters window



Activate the "Associate to this Class/Qualif" checkbox to associate the current Preset with Histograms of the same type of ROI.



A newer instance of an existing name replaces the existing preset.

## 11.6.7 Path Tool

### 11.6.7.1 Overview

A 'Path' is a set of lines linking points together. Points are 3D coordinates which are not necessarily located in the same plane as one another. A Path may split off into any number of separate lines from any given point, however no part of any Path may ever loop or contain a loop.

You can create several different Paths and later join them together, combining them into a single Path. At any time, you can also define any Path point as the Point of Origin.



Figure 11-102 Valid Paths

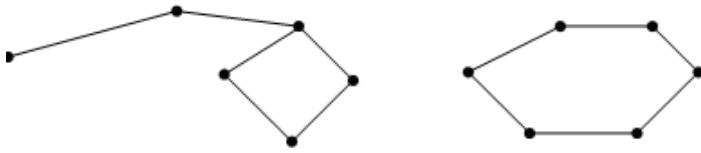


Figure 11-103 Invalid Path




For any given line, a point may be either the starting point or the ending point, but never both.

### 11.6.7.2 Usage

A Path has 3 basic functions:

- 1 To guide the 'Virtual Camera' along the pertinent route during Virtual Endoscopy
- 2 To calculate distance measurements of vessels or any tubular tissue/structure more accurately.
- 3 When used as a single segment, a Path may also be used to calculate the straight-line distance between 2

Points in a 3D Volume (unlike the Distance Measurement tool , Points on the Path tool are not necessarily located on the same plane as each other)

### 11.6.7.3 Procedure

To create a Path:









- Press the 'Path creation' tool  in the Toolbox to open the Path Creation Floating toolbar




Figure 11-104 Path Creation Floating Toolbox

- Select the Create New Path tool  (if not automatically activated)
- Using the Mouse-Pointer, click on a desired image to add a Point (which automatically activates the 'Add Point' tool )
- Repeat the process to add as many Points as required
- If necessary, redraw a part of the path , remove a selected Point pressing , or a selected Path pressing 
- A Path or Point may also be renamed pressing  (default names are Path 1, Path 2, etc.)
- A path can also be extruded to a selected ROI 

### 11.6.7.4 Freehand Path editing

If, for any reason, you wish to modify any part of a Path, you can trace any section again by hand.

To do this:

- Click on the Path point before the section you wish to modify
- Press and hold the ALT key (or click on the 'Redraw a part of the path' button  available in the Path floating toolbar).

- Trace the new Path line by hand until a desired Path Point linking the first selected point to another point from the initial centerline
- Wait until a red circle appears to release the mouse on the desired Path Point

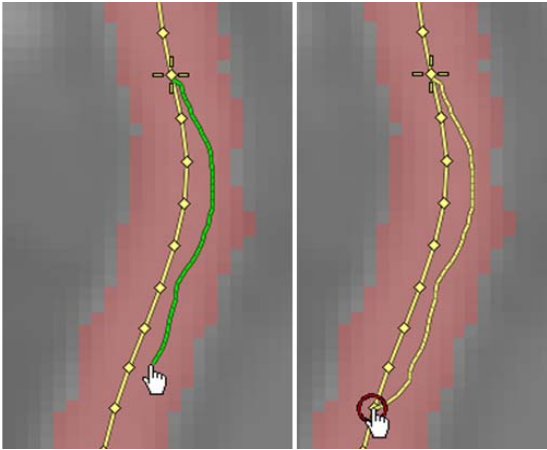



Figure 11-105 Modify Path by hand

### 11.6.7.5 Connecting Paths

You can append a Path to another and combine them into one:

- Click on the 'Create a New Path' Tool 
- Click on the End point of the first Path you wish to connect
- Press and hold the SHIFT key
- Click on the Start point of the Path you wish to append to it
- When asked to confirm whether you wish to combine the 2 Paths together, click 'Yes'.

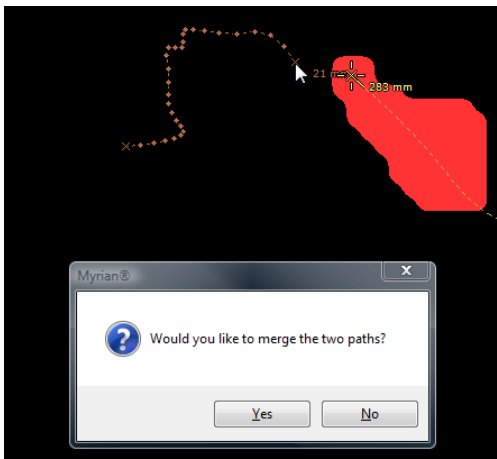


Figure 11-106 Connect 2 Paths together

The result is a single Path which starts at the Origin of the First Path and which ends at the Endpoint of the second Path (the total length is then displayed by this new Endpoint).

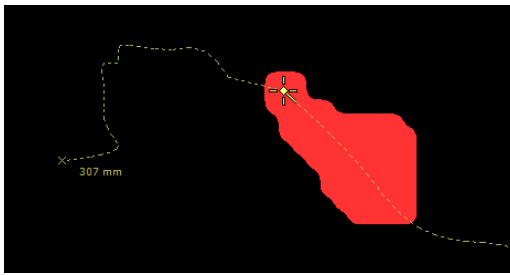


Figure 11-107 Resulting Combined Path

### 11.6.7.6 Context Menu

Right-clicking on a Path or a Path Point opens a dedicated menu (see Figure 11-171) enabling you to:

- Delete a point along a Path
- Delete a Path
- Add Name to/Rename a Path or Point
- Label Submenu (see Figure 11-171):
  - Add Name...
  - Automatic label
  - Remove this label
  - Remove all labels from here
  - Remove all labels
  - Explore the whole branch
  - Explore the selected zone
- Tools Submenu:
  - Smooth the Path, i.e. make the Path Line less 'jagged'
  - Reduce the Smoothing of the Path
  - Set a Path Point as New Origin of the Path
  - Truncate the Path
- Add a new Point after a selected Point
- Constrain the Viewport navigation to the Path
- Curvilinear Plane reformatting (CPR) along the Path
- Switch to Cross Section.

### 11.6.7.7 Set New Path Origin

If you wish, you can then redefine any of the Path points as the 'New Origin' of the Path:

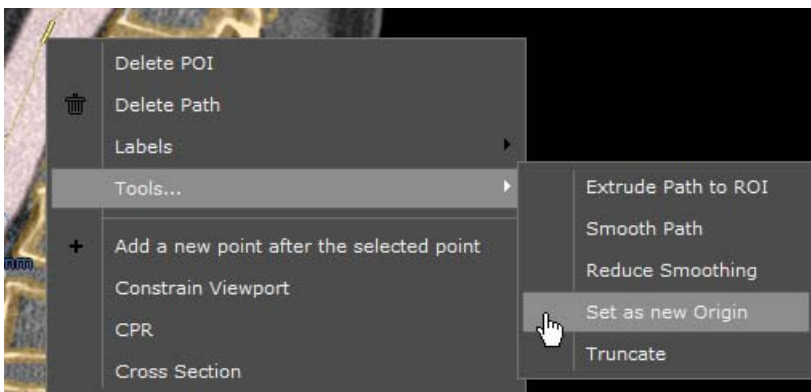


Figure 11-108 Set a Point as New Origin of a Path

1. Right-click on the desired Path point

2. Select 'Set as New Origin' from the resulting context menu



If a new Path Point is added while the Path Origin is selected, the newly created Path Point becomes the new Path Origin.

### 11.6.7.8 Truncate Path

You can truncate a Path via the Path Context Menu Tools:

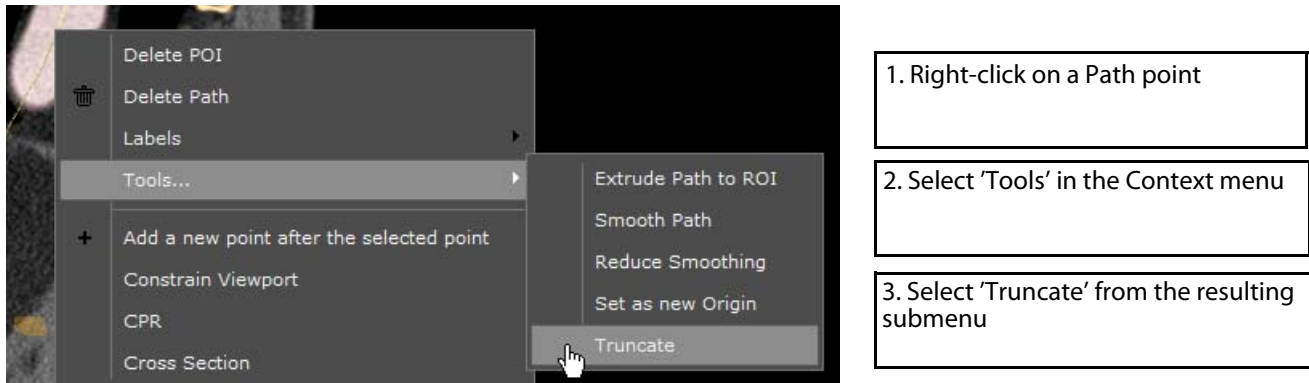


Figure 11-109 'Truncate' option in the Path Point Tools submenu

### 11.6.7.9 Extrude path

The “Extrude” option in the Path context Menu Tools allows you to extrude a ROI along a selected Path. The current selected ROI is used, and a circle having the size (in pixels) of the currently selected brush thickness is extruded.

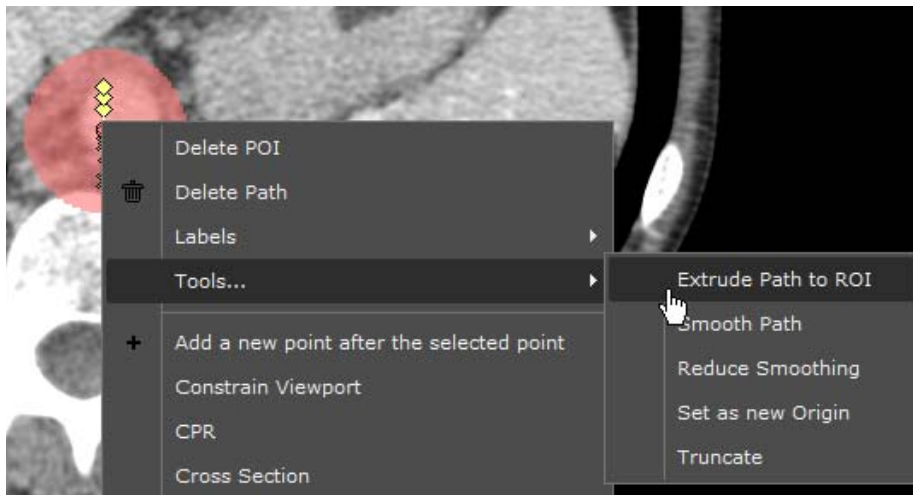


Figure 11-110 'Extrude path to ROI' option in the Path Point Tools submenu



A dedicated button is also available for this function in the Path Edition Floating Toolbar .

### 11.6.7.10 Delete Path

- To delete a Path, simply select 'Delete Path' from the Path or Path Point Context Menu.



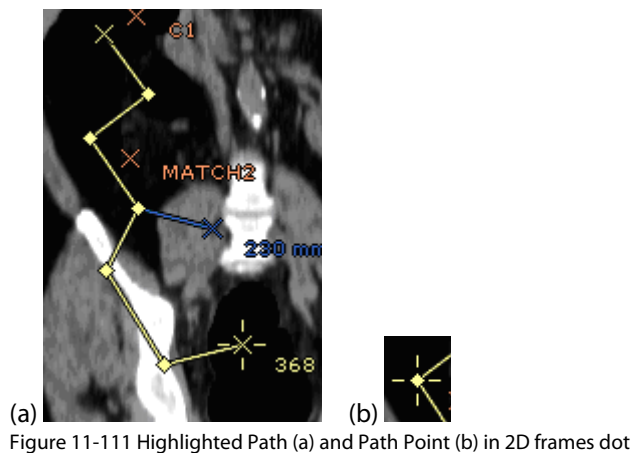
If a ROI to which is associated a Path is deleted, then the associated Path is deleted too.

### 11.6.7.11 Display

The Start and End points of a Path are represented by 'x'-cross symbols. All intermediate Path Points are represented as small diamond-shaped points.

The Length Measurement of a Path, calculated from its Start Point, is displayed beside the End Point of the Path or Path Branch.

A Path is highlighted when it is selected. Similarly, when a Path Point is selected, it is both highlighted and surrounded by a large '+' cross mark as with the Anatomical Center.



Use the 'Home'/'End' keys of your keyboard to go to the Start/End of the active Path or the Left/Right cursor keys to move to the Previous/Next Point.



Both Paths and POI are also listed in the Annotations List.




Neither Paths nor Path Points can be selected in 3D frames; however a Path can be clicked upon to re-position the Virtual Camera.



By default, Paths and POI annotations that are generated by Segmentation engines may or may not be 'Visible' depending on the settings of the engine concerned. These settings may however be modified by ticking or in-ticking the corresponding checkboxes in the Annotations List accordingly. These settings are persistent.

## 11.6.8 POI Toolbar



The POI creation tool  may include several types of POI according to the specific modules that have been activated (XP-Colon, XP-Liver, etc). In standard mode, only the 'Generic'-type POI is available.

### 11.6.8.1 Overview

'POI', or 'Points of Interest' are dot-markers that can be placed by hand or automatically to demarcate a spot requiring more specific attention such as potential polyps, nodules, etc.



POI can be created in any Canonical MPR View or Endoscopic View.

### 11.6.8.2 Add POI/Modify POI List

There are 2 methods of creating POI:

- By a single mouse click directly on a single spot in an image to create a Point of Interest (POI).
- By dragging the mouse over an specific area inside an image to create a POI with an associated Diameter Measurement.



During the creation process, available Assistance Engines may be triggered depending on the elements defined in the following paragraphs.

### POI Creation mode property

- Each POI has two properties which define its creation mode.

Creation Mode (mutually exclusive)	Explanation
CLICK	The POI can be created only with one click (actual mode for Lung for instance)
CLICK_OR_DRAG	The POI can be created with a click or with a diameter (actual mode for the liver POI)

Table 11-11 Available POI Creation modes (mutually exclusive)

### POI Segmentation mode property

Segmentation mode (can be combined or not set)	Explanation
SEG_ON_CLICK	The segmentation engine is run if the POI is created with a click
SEG_ON_DRAG	The segmentation engine is run if the POI is created with a drag
NONE	No associated segmentation

Table 11-12 Available POI Creation modes (can be combined or not set)



The drag mode creation has been added in the endoscopy viewport for POI colon.

To create a POI List:

- Select the '+' symbol in the POI List tab and choose either 'Generic', 'Colon', 'Liver' or 'Lung' POI (among those available) from the resulting menu.



Figure 11-112 Create POI menu

This creates an empty POI List.

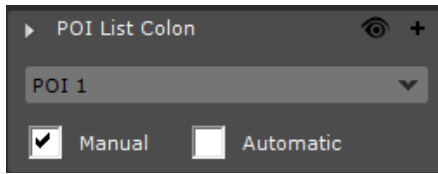




Figure 11-113 POI list



To create a POI:

- Select the desired list of POI in the POI List drop-down menu
- Click on the 'POI' Tool  in the Toolbox and select the 'Add POI' Tool  in the floating toolbar for POI Lists.

It opens a floating toolbar which gives the option to add a manual POI to a POI List and/or rename a POI List.

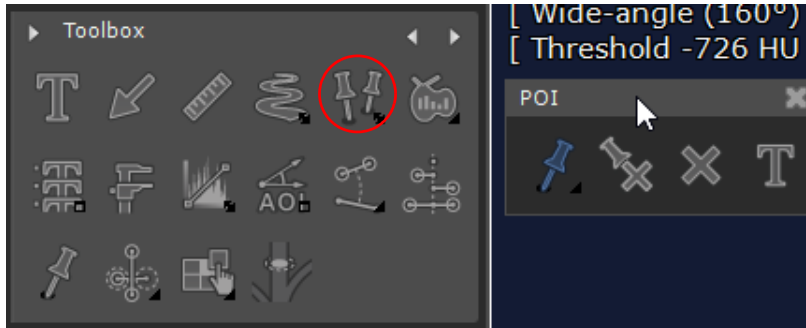



Figure 11-114 Toolbox showing 'Add POI' button and POI Floating Toolbar

- Click on the location in the viewport where you would like to place the POI.

This action automatically creates a POI List and adds a POI in this POI List

- Once the POI is placed, select the Diameter Measurement Tool  (automatically assigned to the Left Mouse button)
- Click on the outermost limit of one side of the Greatest Diameter (Click on the outermost limit of the other side of the Greatest Diameter to define the Diameter of your Finding.

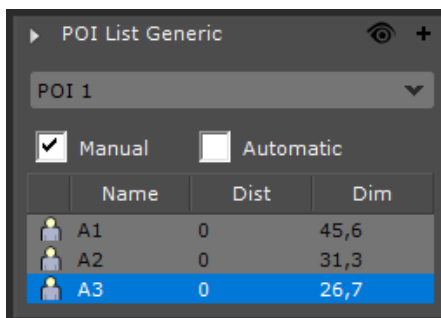


Figure 11-115 POI list drop-down menu

- To display all measurements related to one given POI, select the relevant POI in the list.

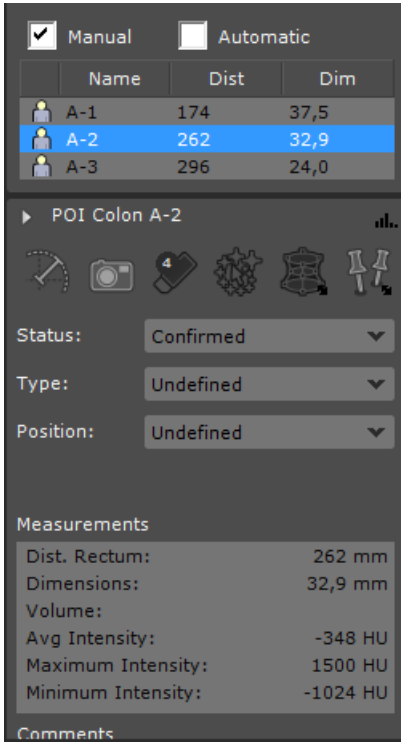



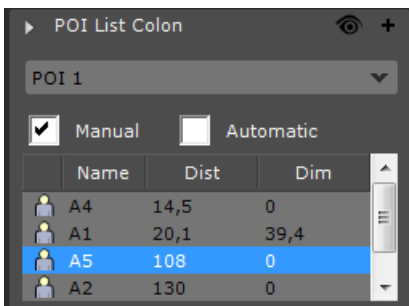
Figure 11-116 POI toolbar displaying selected POI Measurements



Once you have finished creating your POI, the Diameter Measurement Tool  remains active so you can either edit the existing POI or create new ones directly.




If the number of created POI exceeds the number of POI defined in the POI display settings (see Section 11.6.8.4.1), a slider appears to go up and down the list and visualize all created POI within that list.



Open/Close the Floating Toolbar for POI lists. If you have not yet created a POI List, selecting the 'Add POI' Tool

opens the 'Create POI List' menu as soon as you click on any image.



Whenever a manual 'Colon' POI is created using the 'Add POI' Tool , if a semi-automatic 'Polyp' segmentation engine is available, an attached ROI is automatically created. The Segmentation process to calculate the

ROI begins automatically as soon as the POI is placed.



The attached ROI is automatically listed in the POI Toolbar bearing the same name/number as the POI it is attached to.



POI Lists are also listed in the Annotations List  accessible in the Toolbox (see Figure 11-120).



The “Distance Along Path” measure is stemmed from the Position of the POI regarding the nearest Path while the “Dimension” is stemmed from:

- the Attached ROI largest diameter if only an Attached ROI exists.
- the manual dedicated “Largest Diameter” tool if it has been used, in all other cases.



By default, ‘Colon’ POI are ordered in the POI List according to distance to Rectum.

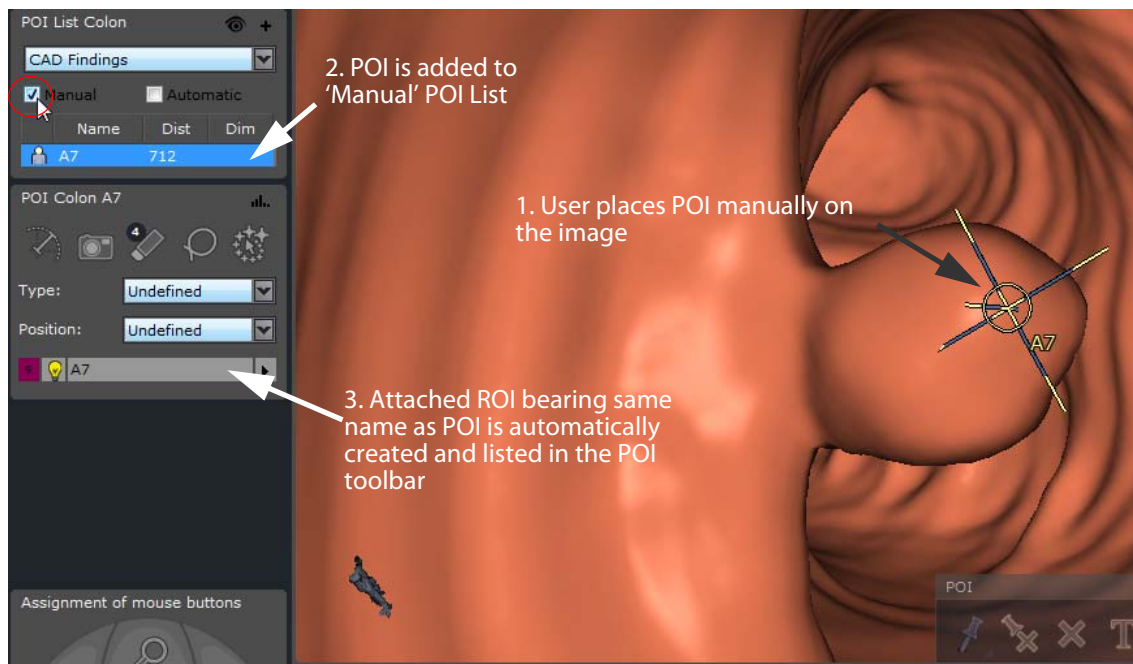


Figure 11-117 Add Manual POI



It may be necessary to scroll down the Toolchest or to collapse one of the visible toolbars by double-clicking on its title to access the POI List and POI tabs.



Use the up/down cursors of the keyboard to navigate from one POI to another.



Use the checkbox in the Annotation List window to display/hide the selected POI List.

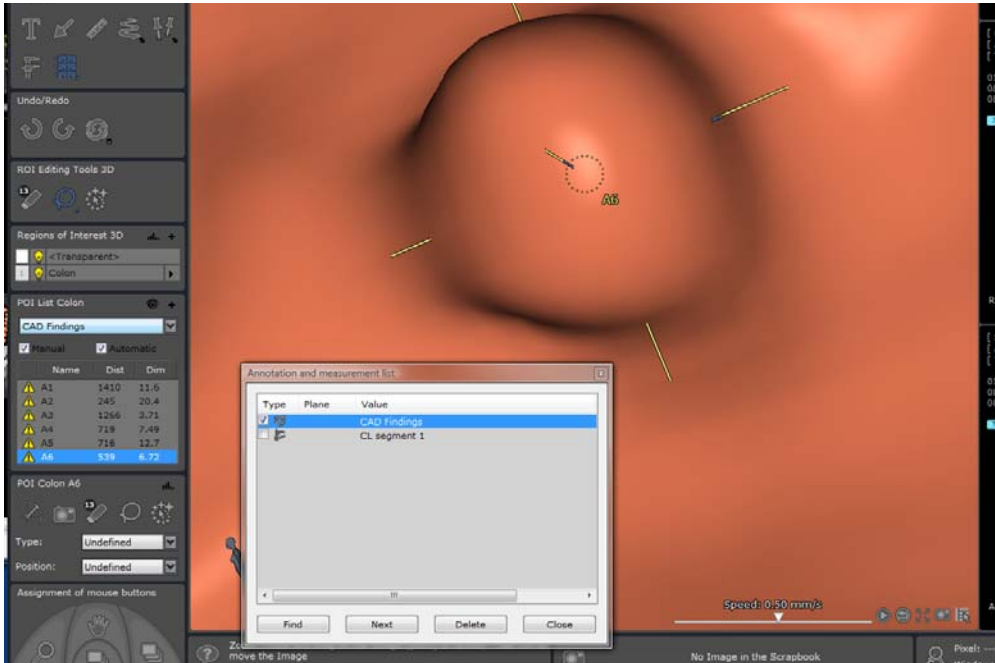




Figure 11-118 Colon POI referenced in both the POI List and in the Annotations List

### 11.6.8.3 Delete POI

To delete POI, do either one of the following:

- Select a **manually added POI** in **any** frame/viewport and press 'Del' keyboard key
- Right-click on a POI in the **Manual POI List** at left of the Workspace and click on 'Delete POI' in the subsequent Right-click menu.
- Select the 'Delete selected POI'  or 'Delete selected POI List' button  in the POI Floating Toolbox

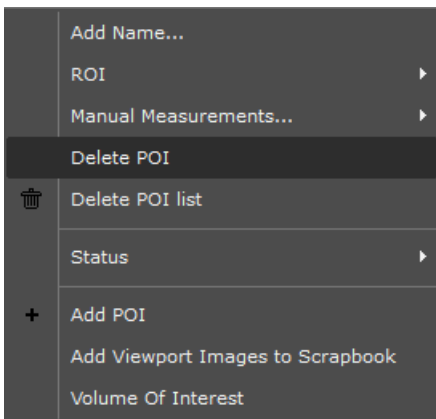


Figure 11-119 'Delete POI' in the Right-click menu



Automatic POI cannot be deleted.

### 11.6.8.4 Display (Automatic and Manual POI)

#### 11.6.8.4.1 POI Display Settings

- Click on the 'Eye' button  at top-right of the POI List.

This feature gives the option to display or hide all the POIs or the POIs on a current slice and their associated information

When activated, all POI are listed in the 'POI List' Toolbar as well as in the Annotations List .

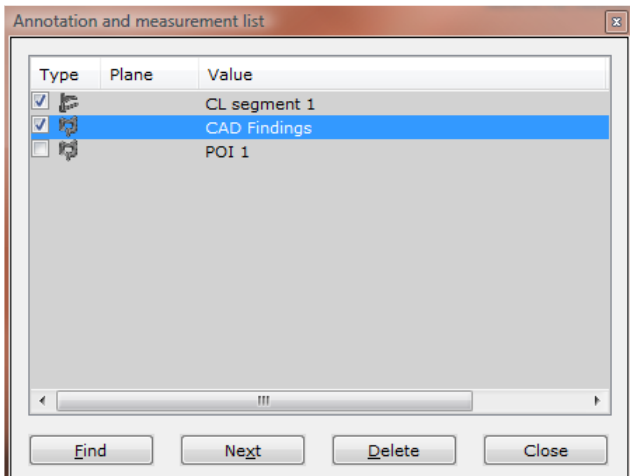


Figure 11-120 Annotations List



The Annotations List checkbox settings are persistent, i.e. their state is saved at the closing of a session.

To be displayed in the Workspace:

- Their corresponding checkbox(es) must be ticked in the Annotations List
- Their corresponding (Manual/Automatic) checkbox(es) must be ticked

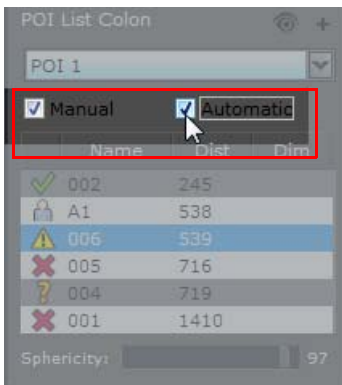



Figure 11-121 POI List display checkboxes

- Click on the  icon at top-right of the POI List Toolbar to select one of the following options:
  - Display all POI
  - Display only the POI on the current slice
  - Show the Measurements of the selected POI (opens a submenu to activate a choice of Measurements)
  - Display all ROI
  - Parameters (opens a dialog box enabling to define the number of POI maximum count to display in the POI list)

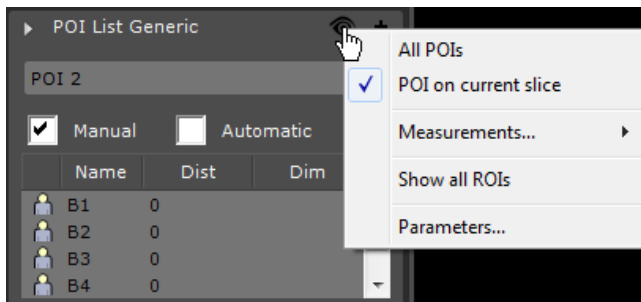


Figure 11-122 POI Display Context Menu

#### 11.6.8.4.2 POI List Checkboxes

'Manual' checkbox:

- Checked: All manually created POI will be listed and displayed
- Unchecked: Manually created POI will neither be listed nor displayed

'Automatic' checkbox:

- Checked: All Automatic POI will be displayed
- Unchecked: No Automatic POI will neither be listed nor displayed



POI Display Modes are automatically saved to the User Captured Protocols.

#### 11.6.8.5 POI representation and behavior

##### 11.6.8.5.1 Canonical MPR (2D) frames

POI are represented by circles (around 20mm in diameter) which are yellow when the POI and containing list are selected and orange when not selected. In all viewports, the POI circles become **smaller** when navigating away from them, and **larger** when navigating towards them. Depending on your theme settings in the Preferences>Display tab, in the Endoscopy frame, POI are colored as follows:

- Yellow when a POI (and its containing list) is selected,
- Orange when not selected

##### 11.6.8.5.2 Endoscopy Frame

As well as the circle locator, 3D Crosshairs also mark the exact position of POI in the Endoscopy Viewport. The ends of the 3D Crosshairs are colored white to differentiate this locator from the 3D Anatomical Center which is colored blue.



The crosshairs may be partially or completely hidden from view by any object, tissue or anatomical structure obstructing the view-path between Endoscope and POI.

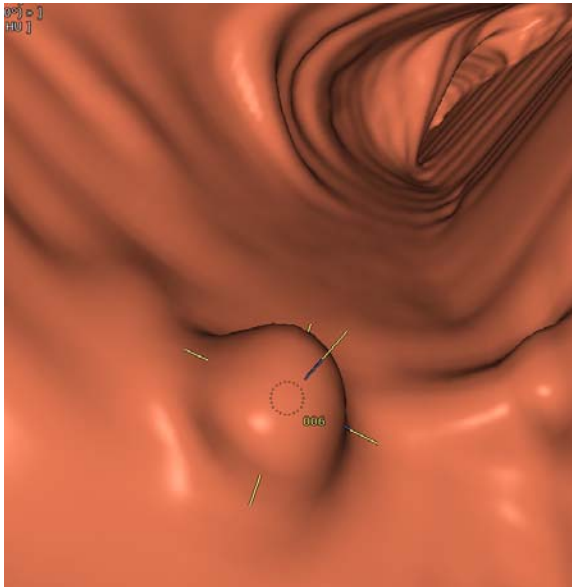




Figure 11-123 3D POI displaying both circle and 3D Crosshair locators

### 11.6.8.5.3 Navigation behavior

A POI circle becomes **smaller** when it is **behind** the current slice and the circle becomes **larger** when the POI is **in front of** the current slice.



Rotate around a POI by clicking on it with the hand cursor  which appears when you mouse-over the POI and holding the mouse-button down while moving the mouse. Press ESC or click on another mouse-button to abort, or

Undo (CTRL+Z)  to restore the previous position.



You can also rotate around the Anatomical Center in Endoscopy Mode by holding the ALT key down while clicking on it and dragging the mouse around.

### 11.6.8.5.4 Visible/Masked POI

POI are considered either 'Visible' or 'Masked'. Lines representing them are accordingly:

- Solid, when the POI is 'Visible' or
- Dotted when the POI is 'Masked'



Figure 11-124 Point of Interest symbol on image ('Visible' status)



Figure 11-125 Point of Interest symbol on image ('Masked' status)

A POI is considered 'Visible' when:

- The distance between the 'Camera' and the POI is **less than 8 cm**

- The line of sight between the 'Camera' and POI is clear of any tissue or structure  
Otherwise, the POI is considered as 'Masked' and represented by a dotted line.



It may occur that POI be represented as 'Masked' (dotted line) even when it appears that no obstruction exists between the 'Camera' and the POI. This may happen when, for example, the center of the POI is situated slightly within the tissue wall.



POI Markers start to become visible to the Endoscope from a distance of 8 cm.



For reasons of clarity, POI that are located beyond 8 cm from the Endoscope are not displayed.

### 11.6.8.6 Selected POI tab

The POI tab displays details concerning the currently selected POI and associated ROI, including its type ('Generic' or 'Colon') in the heading.

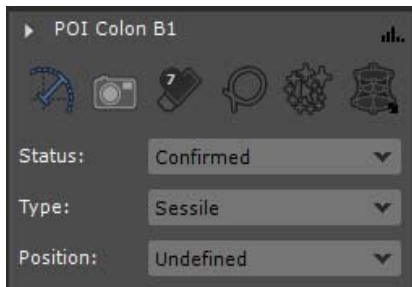


Figure 11-126 POI Tab (displaying 'Colon'-type POI)

The following functions are available here:

- Measure the largest diameter. This measure takes precedence over the associated ROI diameter (if any)
- Take a snapshot of each frame linking each image to the active POI
- Select the attached ROI and activate the Eraser (click on the white numeral at top-left to modify the size of Eraser stroke)
- Select the attached ROI and activate the Lasso to create a filled shape
- Select the attached ROI and launch the semi-automatic segmentation process
- Opens the POI toolbar to create/delete POI or POI list



The 'Type' and 'Position' fields enable to associate more precise position and category definitions to a 'Confirmed' POI. The 'Status' field enables you to manually edit the automatically allocated status of a given POI (from 'Confirmed' to 'Queried', and vice et versa)





### 11.6.8.6.1 Overview

POI (Points of Interest) Manager lists both the manual and automatic POI for a specific Study/Series. It also provides all tools and options to manipulate both manual and automatic POI.

The POI Manager displays the following information:

### 11.6.8.6.2 POI Information

Among the elements of information attached to POI are the following:

- Icons indicating a Status:
  - : Manual POI ('Confirmed' status)
  - : Automatic POI ('Candidate' status)
- Name: each POI has a name and unique number (in the order it was created)
- Dist: a number indicating the distance of the ROI in centimeters from the Rectum corresponding to the start of the Centerline




The 'Distance from Rectum' calculation is an approximation and it is intended as a reference to locate ROIs in the colon during CTC examinations. The Distance from Rectum measurement must NOT be used as a guide for OC examination.

- 
- Dim: an automatically generated number indicating the largest diameter, in millimeters, of an Automatic POI Finding or User Identified ROI

Each POI will display the following information:

- Largest diameter
- Volume
- Average HU
- Minimum HU
- Maximum HU



POI Segmentation Coloring can be toggled to display solid color, outline or none via the 3-position toggle-switch at top-right of the Main Workspace 



To navigate through POI annotations in the POI List you can click on each POI. All views will update to display the selected POI.



When two Series which include POI are open simultaneously, the POI List is switches to 2 columns each one displaying the POI of one Series.


---

## 11.6.9 Area and Intensity Measurements

### 11.6.9.1 Overview

A set of 2-dimensional Quantification Shapes is at your disposal with which you can draw **2D shapes** to perform **various types of pixel measurements**.

Quantification shapes can also be converted to **Regions of Interest (ROIs)**.

The **Quantification Tool** button,  by default, displays the **last used** Area Calculation Shape (Free form, Ellipse or Rectangle).

- Click on the button to open the menu below and choose appropriate tool among the following shapes available:

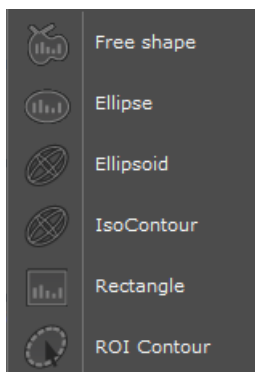


Figure 11-127 Quantification shape menu








All Quantification shapes are persistent: they are saved from one session to another.





2D quantification shapes do not support intensity measurement on thick slices. In that case, the returned value will be set as N/A.



Example of use: the Ellipse tool is often used to perform cranial diameter measurements in ultrasound (US) Studies.

Measurement tools	
Shape	Function
	Draw a <b>Freehand</b> shape
	Draw a <b>Rectangular</b> shape
	Draw a round or <b>Elliptic</b> shape
	Draw an <b>Ellipsoid</b> (3D)
	Draw a 3D <b>IsoContour</b> ellipsoid (on PET exam only)

	Draw a 3D <b>SUV Threshold</b> ellipsoid (on PET exam only)
	ROI Contour: automatically traces the <b>contour of a ROI</b>

### 11.6.9.2 Method of use

To draw a shape:

- **Click on the desired view** in the Image Zone
- **Hold down** the mouse-button
- **Drag the mouse as required to draw shape contour**
- **Release** the mouse-button

On mouse-release, the **following measurements are immediately displayed** at bottom-right of the relevant image view:

- **Two linear diameter measurements** (not applicable for the Freehand tool)
- **Surface measurement**
- **Mean intensity**

Once the shape has been drawn, it is possible to:

- **Modify it by using the handles,**
- **Move it** by drag-and-drop (the cursor becomes a cross when passing over a shape)
- **Copy it** using the 'CTRL+C' keyboard keys
- **Paste it** elsewhere (in any frame) using the 'CTRL+V' keyboard keys
- **Delete it** by using the keyboard **delete** key



In some cases, a copied contour/shape may be larger (in number of pixels) than the image in which it is pasted. In such cases, the pasted shape may slightly vary from the copied shape.




To reshape homogeneously the drawing of an Ellipse into a perfect circle, hold down the CTRL key while dragging one of the four handles using the mouse (holding down the mouse click on the handle of your choice), release the mouse first then the CTRL key.



To reshape the drawing of a rectangle homogeneously, hold down the CTRL key while dragging any side handles only (corner handles act in a free way).



You can activate the '2D assisted contour' tool  to automatically adjust a freehand contour around the outlined target zone (see Section 7.7.4).



To reshape the drawing of a freehand shape/contour, press ALT using the mouse left button like for the Path annotation: the correction of the contour only applies to the edited portion of the contour.



Figure 11-128 Example of manual modification of a cross-section contour using the 'Alt' key and the left mouse button



Hold down the CTRL key to select/deselect more than one contour. Double-click on a shape/contour to select/deselect all the measurement contours contained in the plane of view.

---



Density measurement values of quantification shapes in MPR mode do not take into account slice thickening.

---



The Ellipse can be used in sonography to measure the cranial diameters.

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The ROI contour feature can be used in Vessel studies where the ROI is a carotid and the plane in which the contour is calculated is a Cross-Section, perpendicular to the path.

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The ROI contour and ISoContour features are accessible in Oblique MPR.

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### 11.6.9.3 Copy/Paste a quantification shape

Once you have created a measure in one series, you have the possibility to duplicate it in a different viewport of the same image or in another image of the same series as many times as you wish.

First copy the annotation to the clipboard:

- Select the annotation and press CTRL+C or right-click on the annotation and select 'Copy to Clipboard' from the context menu.

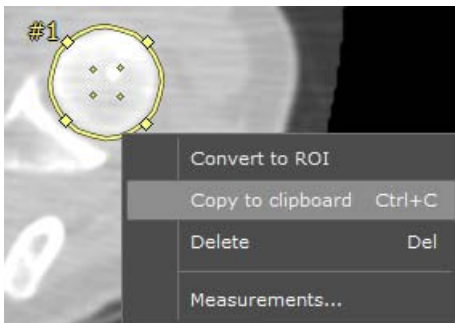


Figure 11-129 Quantification shape right-click menu

Paste the annotation from the clipboard:

- Select the destination viewport/image from the same Series
- Put the mouse over the destination viewport and/or navigate to the destination image
- Press CTRL+V
- Use the drag & drop method to move the copied quantification shape to the relevant spot.

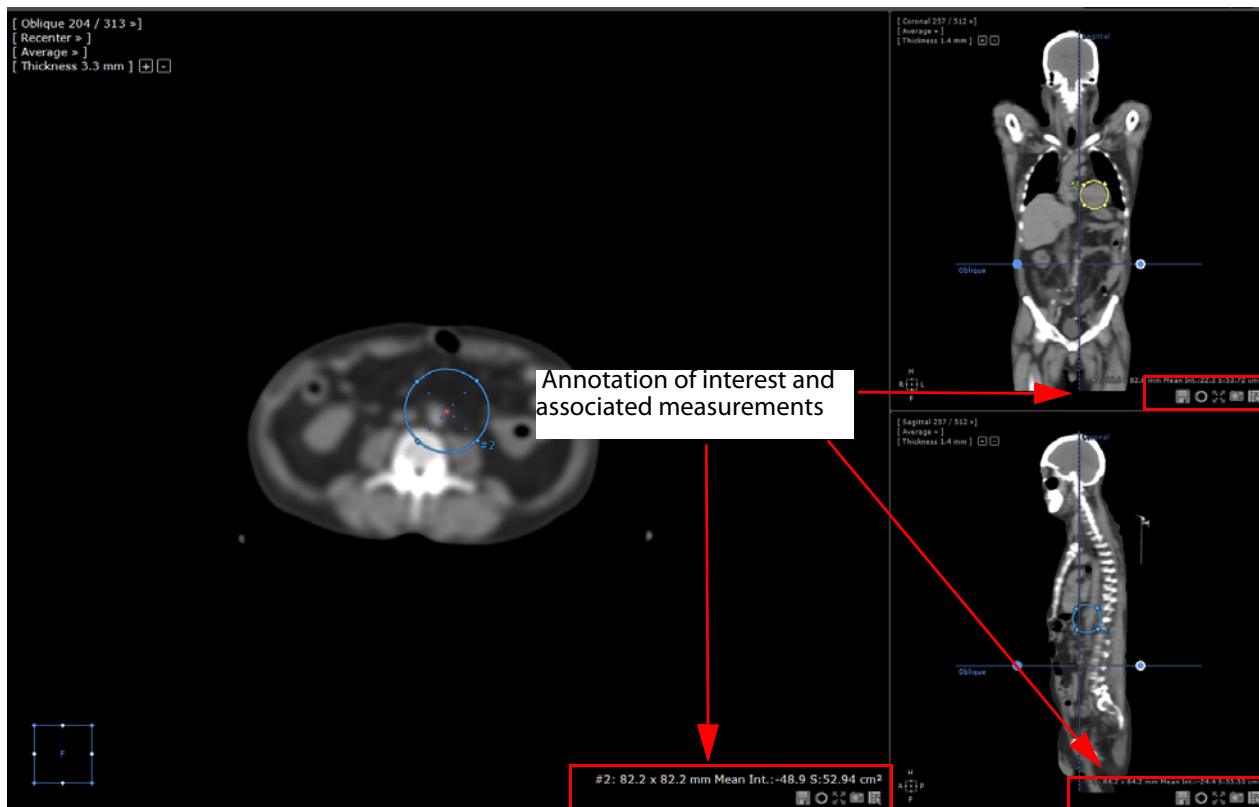


Figure 11-130 Copy/Paste of quantification shapes and display of their respective measurements

- To access the detailed 'free shape measurement' window related to each quantification shape, select one and click on 'Measurements...' from the right-click context menu.

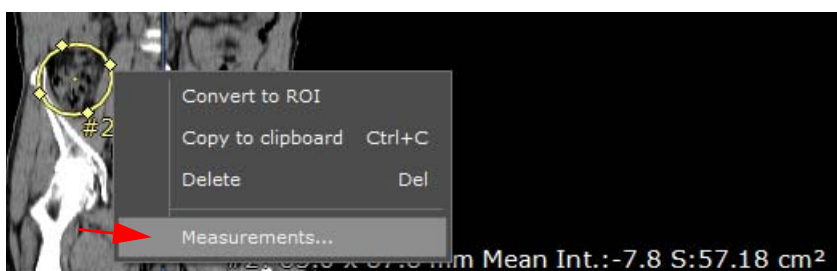


Figure 11-131 Opening quantification shape measurement window



Pasting to a different series is possible although the cloned quantification shape will be dropped in the center of the current image in the viewport right under the mouse cursor.

#### 11.6.9.4 Ellipsoid (3D)

The center of the ellipsoid  is, according to its thickness, in either one of the following rendering modes:

- Average: at the center of the thick slice
- MIP: at the point of maximum intensity of the ellipsoid center
- MinIP: at the point of minimum intensity of the ellipsoid center




When a 2D slice is thickened, the center of the Ellipsoid becomes the reference point.

To set the slice thickness:

- Click / to increment/decrement the value
- Click on the word 'Thickness' (top-left in the viewport menu)
  - Enter a value in the resulting box using the number keys of the keyboard or by using the '+' / '-' keys (keyboard's number pad) to increase or decrease the value

### 11.6.9.5 SUV Threshold IsoContour measurement tool

This ellipsoid-based measurement tool  enables to calculate the metabolic volume of a lesion. It generates a 3D ellipsoid in which a segmentation is launched, which selects all the voxels whose intensity are equal or higher than a threshold value and that are convex with the highest intensity.

**Default threshold** is set to **4 SUV** but this value can be adjusted.



The usage of this quantification shape is limited to **attenuation-corrected PET study with SUV normalization only**.




In the Image Control Toolbar, switch from 'Automatic' to 'PET' windowing preset to improve lesion visualization.



We recommend you to deactivate the Smoothing selecting 'None' in the Preferences > Display tab to make voxels clearly visible.



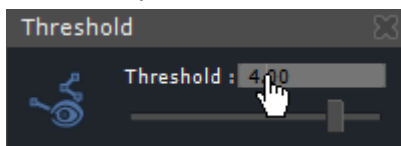
Preliminarily, you need to enter the selected study-related SUV parameters clicking on the  icon (see Section 4.3.2.12 for detailed information) in the Toolbox.

- Select  in the Quantification Tool menu  and click on the area in the **axial view** to draw the shape on the area to be measured.

A Threshold floating toolbar appears once starting to draw the ellipsoid.



To adjust the Threshold, click on the default value and enter your own or move the slider.



You can also adjust the ellipsoid size and shape as required; displayed measurements are automatically updated.

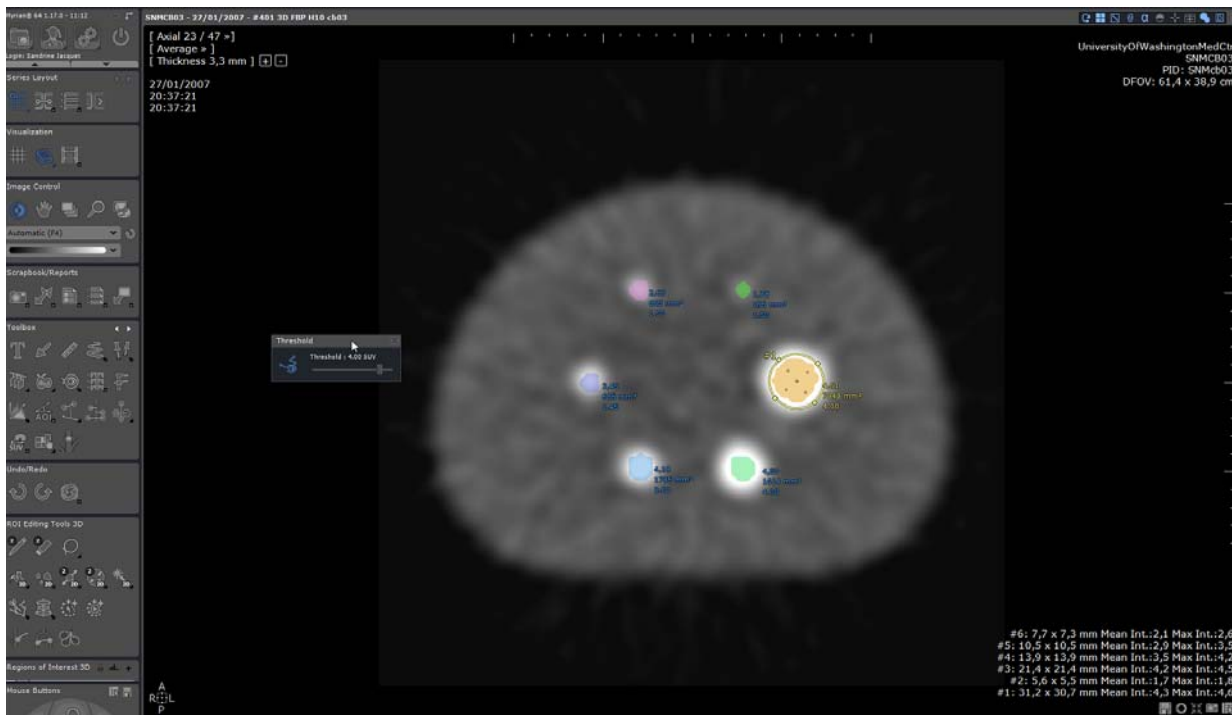


Figure 11-132 Using SUV threshold measurement tool on a PET study



The ellipsoid disappears when not selected in order to have a good visibility over the lesions. To make it visible again, just click on its attached measurements in the viewport.


Displayed measurements attached to the ellipsoid are:

- ROI maximum intensity
- ROI volume (mm<sup>3</sup>)

### 11.6.9.6 IsoContour measurement tool



It is highly recommended to center the Isocontour on the hotspot.

The 3D IsoContour measurement tool  is a combination of the ellipsoid tool with an intensity “threshold” based segmentation.

- Select  in the Quantification Tool menu  and click on the area to draw the shape on the area to be measured



The technical behavior of the IsoContour measurement tool is the following: the 3D ROI is computed so as to find the maximum intensity value in the ellipsoid and select all connected voxels, starting with the maximum one, with intensity equal or greater than x% of the maximum intensity so the region may or may not be greater than the ellipsoid.



A click on a PET/CT view automatically activates the IsoContour measurement tool.

The 3D region used for measurement appears as a yellow contoured ellipsoid, visible on each viewport according to



their plane orientation.

Displayed measurements are:

- Minimum intensity / Maximum intensity / Mean intensity / Standard deviation
- Region volume
- Threshold used
- Voxel count
- Adjust the ellipsoid (localization and dimension) on the view and/or the intensity threshold % value using the slider in the dedicated IsoContour panel which appears in the viewport.
- Adjust the ellipsoid and/or the % value using the slider in the dedicated IsoContour panel which appears in the viewport.

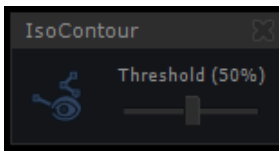


Figure 11-133 Threshold settings floating menu



Any data modification generates the automatic recomputation of the region as well as measurements.

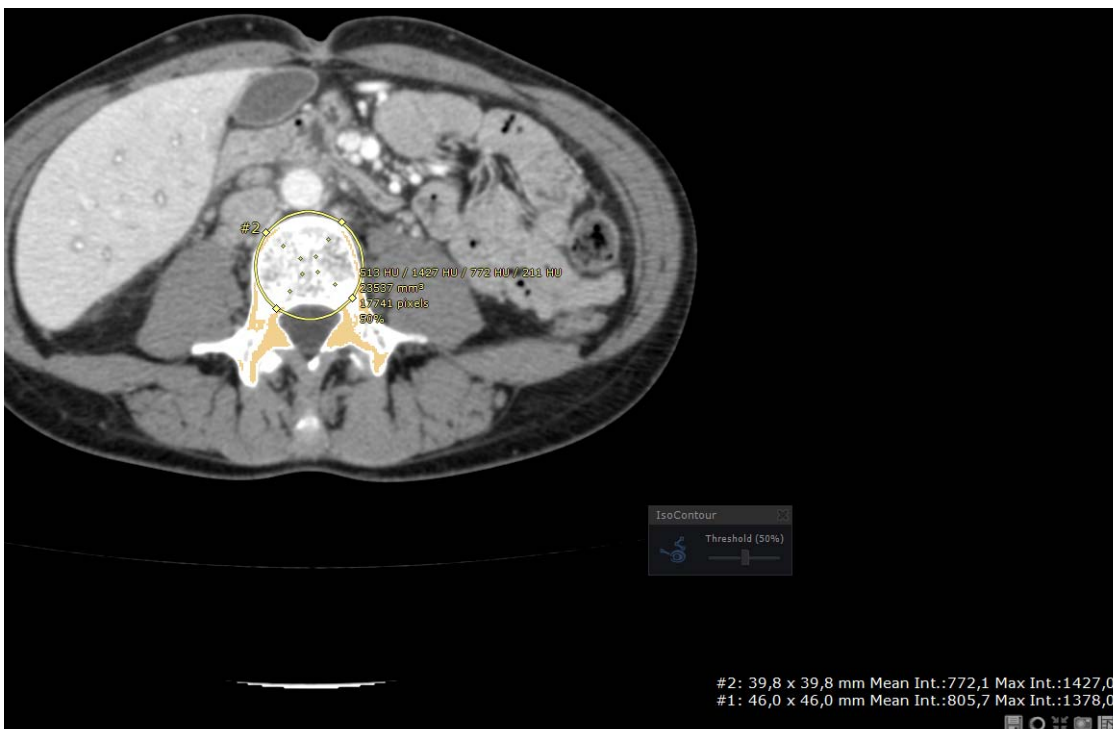


Figure 11-134 IsoContour measurement tool



The default threshold value is set to 50%. However, this is a configurable setting. Please contact an Intracense engineer for assistance.



When not selected, the ellipsoid may disappear from the view enabling a better visibility on lesions. Just click on the measurements in the viewport to make it visible again.



The icon in the floating menu enables you to Show/Hide the ellipsoid according to your needs.

---

### 11.6.9.7 Context menus

The context menu is opened by clicking with the right mouse button on a shape.

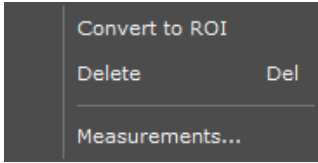


Figure 11-135 Quantification shape right-click menu

As well as **Copy**, **Delete** and **Select** functions a number of actions are available via this menu:

Quantification shape context menu	
Command	Function
<b>Convert to ROI</b>	Converts selected shape to a ROI (requires the ROI Creation add-on)
<b>Duplicate</b>	Duplicates the selected shape in the currently active view pane
<b>Copy to Clipboard</b>	Copies the selected shape(s) to the Clipboard for 'Pasting' in any view pane
<b>Delete</b>	Deletes the selected shape(s)
<b>Select all</b>	Selects all shapes in the currently active view pane
<b>Measurements</b>	Opens the Advanced Measurements screen which lists all measurements including the density histogram for the current shape

Table 11-14 Right-click menu

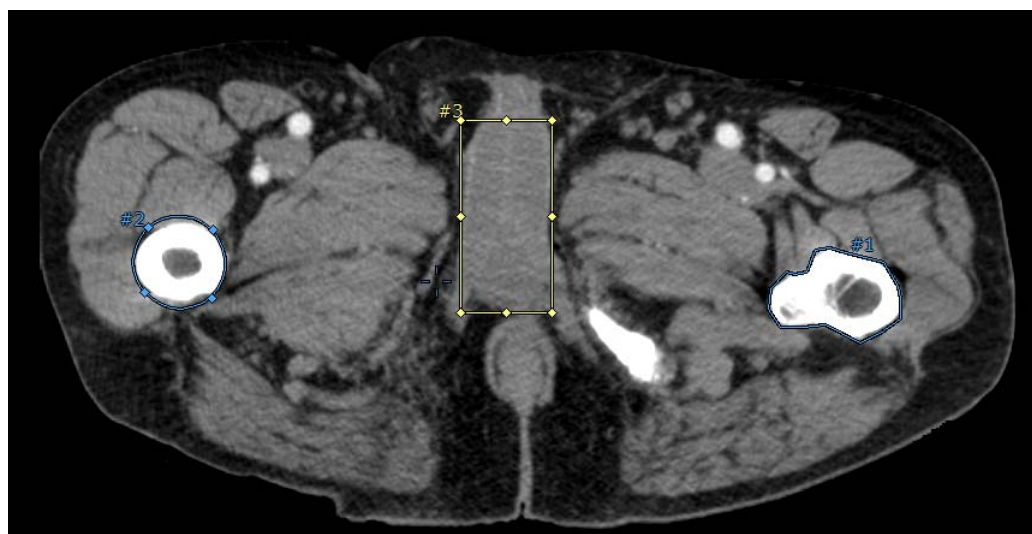



Figure 11-136 Example of the three basic measurement shapes

## 11.6.10 Contrast Curve

### 11.6.10.1 Overview

The Contrast Curve tool  enables the analysis of the contrast uptake dynamics of Multiphase Contrast-Enhanced MRI Series. The kinetics of contrast uptake is used to characterize lesions. You plot time/temporal order - intensity using circular, rectangular and freehand shapes to outline target anatomical areas.

### 11.6.10.2 Method of Use

- Open a Multiphase Dynamic Contrast-Enhanced MRI Study in Native Mode.

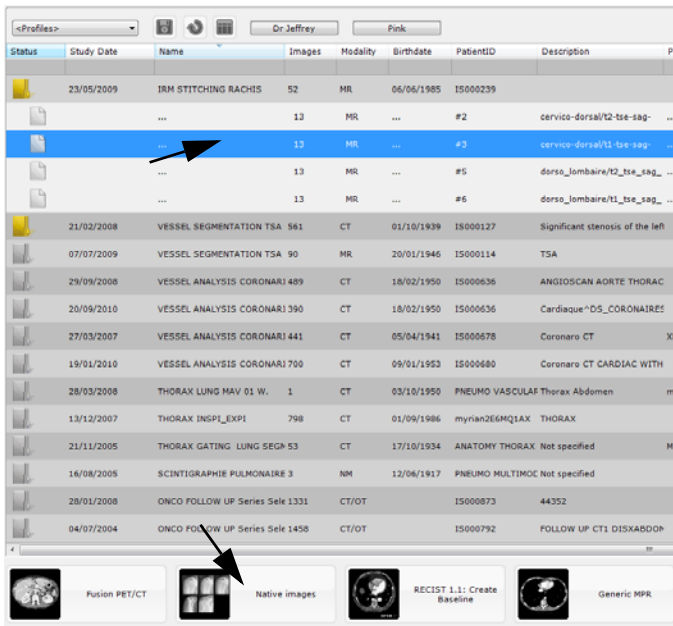


Figure 11-137 Open Dynamic Series in 'Native Mode'



- Click on the Contrast Curve tool  in the Toolbox (opens the Contrast Curve Floating Toolbar).
- Make sure that Synchronized Navigation is activated in the Series Synchronization Screen  (see Section 11.3.1)
- Select desired tool (i.e. free shape or ellipse) to trace an outline around target zone(s).



Figure 11-138 Select outline tool

- Trace outlines around the target ROI (e.g. a tumor and an area of healthy tissue).



The position, shape and size of each ROI is replicated in all Phases.


- Modify the shape or position of each target as desired.



When editing a target and modifying the ROI shape and/or position, all modifications are automatically propagated to all the phases.

However, in some situations (when the patient has been moving during the acquisition for instance) you might want to modify the ROI on a single phase: in that case, press the **SHIFT** key before editing the ROI in the slice of your choice.



If selecting the free shape, you can activate the '2D assisted contour' tool  to automatically adjust the freehand contour around the outlined target zone (see Section 7.16.4).



The Contrast Curve target outlining tools are used in the same way as the standard area quantification tools (see

Section 7.9 for further details).



To move one target ROI in a single preferred phase only, hold the SHIFT key down while you drag it.



Right-click on the targets to rename them.



When the target shape or size is modified in a slice, the contrast curve is automatically updated real-time.



Targets cannot be moved from one slice to another.

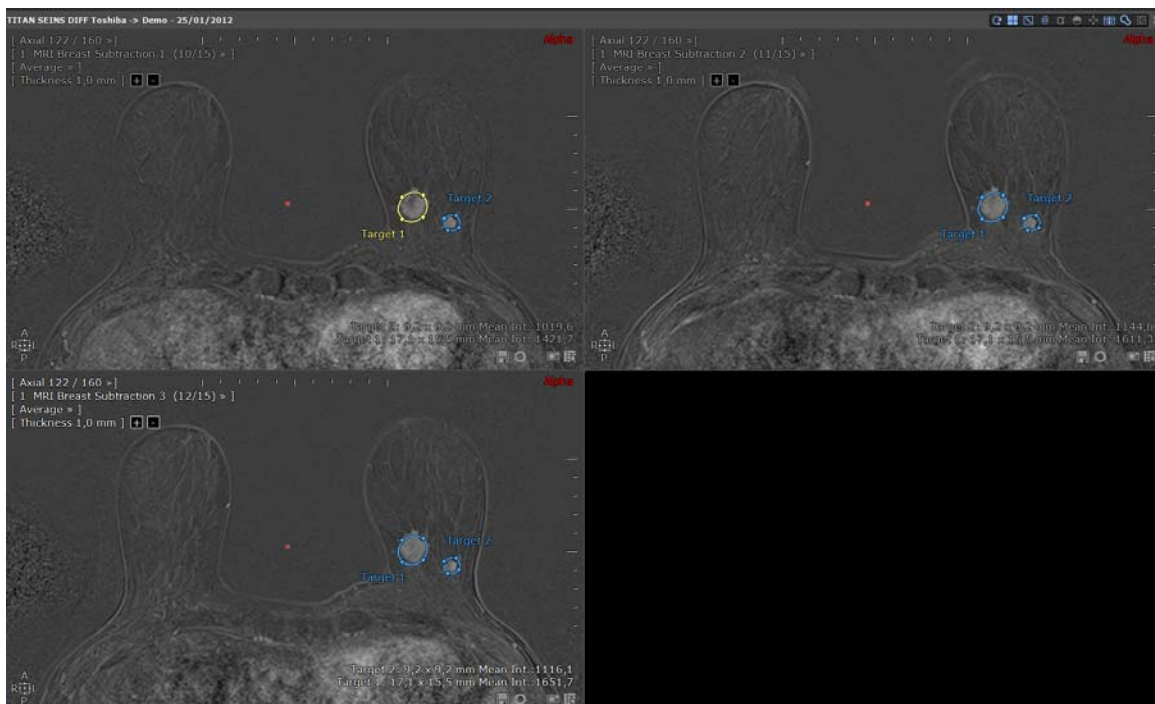



Figure 11-139 Trace Outlines around target regions

- Click  in the Floating Toolbar to display the Contrast Curve(s).

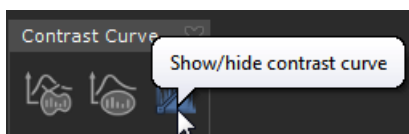


Figure 11-140 Display Contrast Curve

### 11.6.10.3 Target annotation contextual menu

- Right-click on a selected target lesion to open the contextual menu from which you can:
  - **Delete the selected target** on all views
  - **Delete all targets** on all views
  - **Rename the selected targets** on all views: this option allows you to identify several 'Reference' targets

(from 1 to n) from other 'Targets' (from 1 to n)

Via this contextual menu, you can also **Convert the target to ROI**, **Copy it to clipboard** or access the **Advanced Measurements** window.

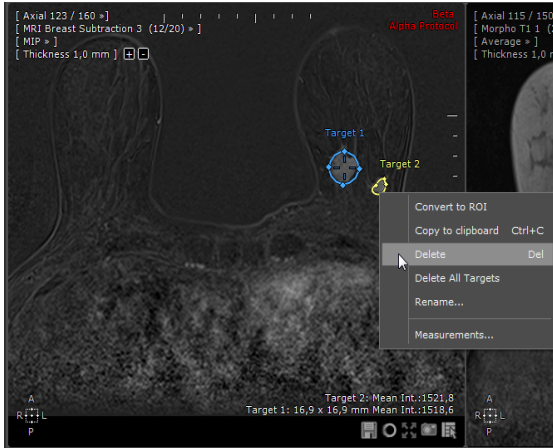


Figure 11-141 Target Lesion contextual menu

### 11.6.10.4 Contrast Uptake Curve

The creation of all targets results in the computation of a contrast curve associated to each target and represented as a Time/Temporal order - Intensity graph depending on the 'Time' value read from the acquisition times of the dynamic MRI series (see Section 11.6.10.5 for detailed about **acquisition time correction** enabling to generate a 'Time-Intensity' curve in certain cases).



It is your sole responsibility to ensure the compliance of the generated curve based on the following criteria:

- The intensity values match those displayed on the images
- The series are correctly sorted.
- All selected series have been taken into account in the contrast curve computation.

Consequently, you should make sure that the parameters enabling to generate the contrast curve are correctly configured according to the explanations described hereunder:

### Contrast curve configuration

The contrast curve is a Time/Temporal order (x-axis) - Intensity (y-axis) graph in which the units displayed on each axis depend on the selected display mode and the acquisition modality.

At the top of the Contrast Curve window (see Figure 11-142) is displayed the contrast curve toolbar from which you can set various parameters:

- The 'Measurements' pull-down menu lets you choose whether to plot the '95 area centile' (by default), 'Maximum', 'Minimum', 'Mean' (Average) or 'Standard Deviation' values of Intensity



Figure 11-142 'Measurements' menu



The 95<sup>th</sup> centile is a statistical measure indicating the value below which 95% of the values are below and the 5% remaining of those values are above.

- The Combo box allows you to set the contrast curve display mode either in Normalized mode (by default) or in Absolute Values.

### Normalized display mode

The displayed values on the y-axis correspond to the percentage of the intensity average value of the target lesion.



The percentage is calculated according to the following formula:

Percentage=abs [(Sn - S0)/S0x100], where Sn is the intensity average value of the lesion ROI at time point n (phase n) and S0 the intensity average value of the lesion ROI at time point 0 (phase 0).



For **MR series only**, an additional point '0' is displayed on the curve associated to a percentage of 0%.

The x-axis is expressed either in Time unit (in minute or second) provided the dedicated DICOM AcquisitionTime tag (0008,0032) can be read or if not, as a unitless index.



For most of the manufacturers, the DICOM tag used to display the time unit is the AcquisitionTime unlike Toshiba which uses the TemporalPositionIdentifier DICOM tag.

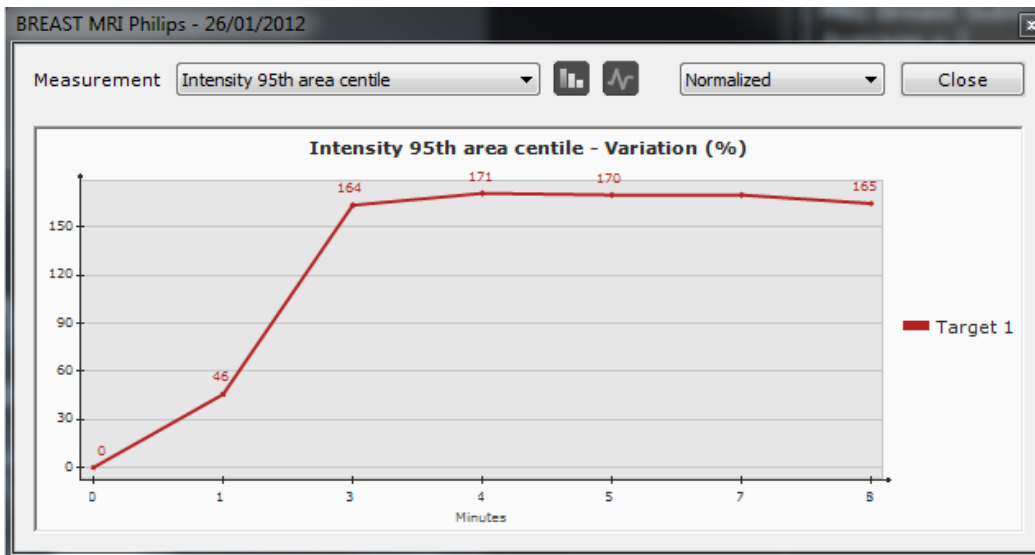


Figure 11-143 Contrast Curve set on Normalized mode (Time expressed in minute on the x-axis)

If the acquisition time values cannot be read, Myrian® displays a warning message to inform you.

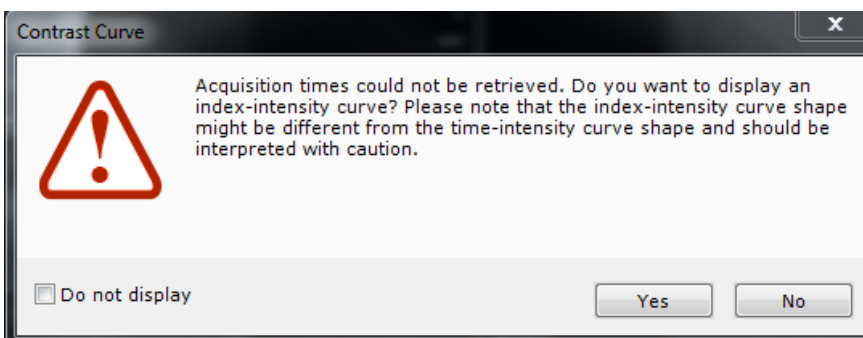


Figure 11-144 Warning message indicating that acquisition times enabling to generate a time - intensity contrast curve could not be read

- Click Yes to display, all the same, an index-intensity contrast uptake curve

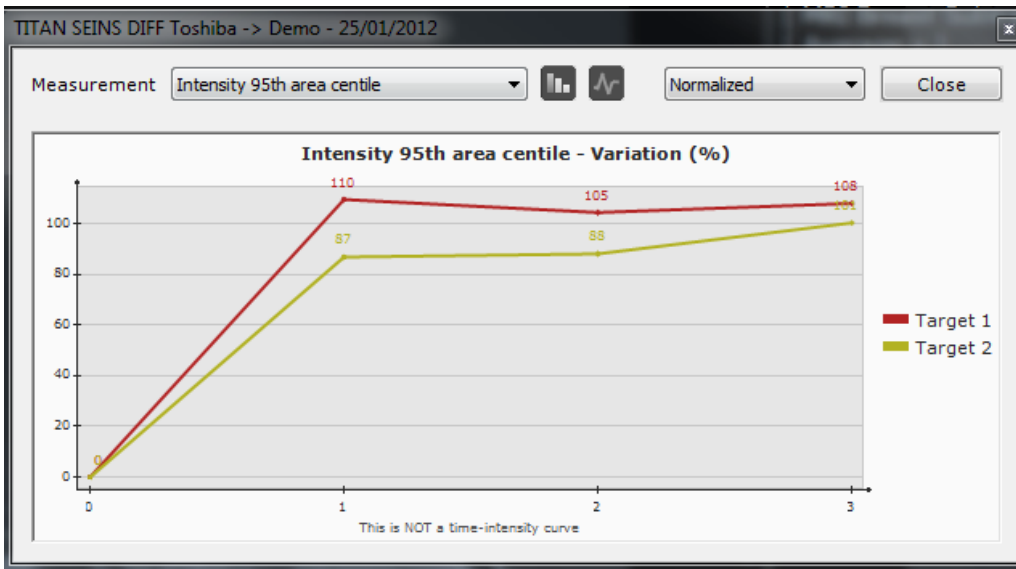


Figure 11-145 Contrast Curve set on Normalized mode (Index on the x-axis)

In that case, an appropriate warning is displayed under the chart.

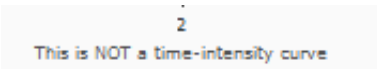


Figure 11-146 Contrast uptake curve displaying a unitless index on the x-axis

#### Absolute value display mode

The y-axis represents the intensity values while the x-axis sorts the Series in a timely or temporal order manner, depending on the following cases:

- AcquisitionTime DICOM fields of all involved Series are distinct: the x-axis of the contrast curve is expressed in Time unit (minute or second)

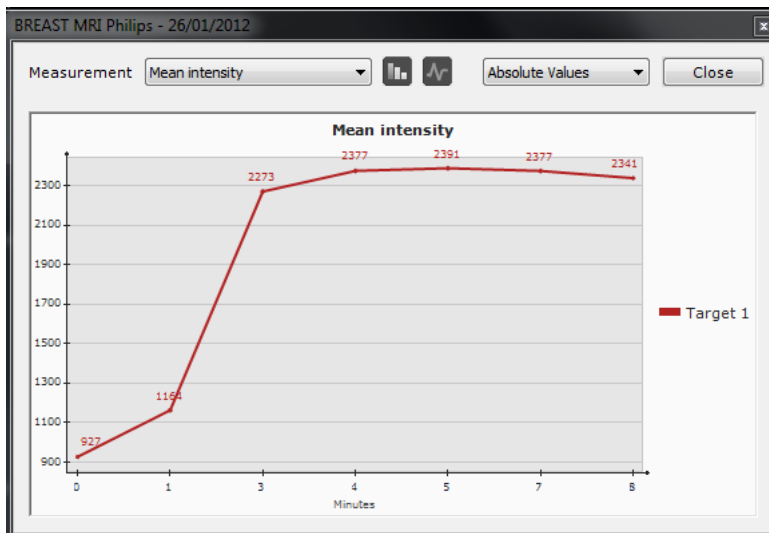


Figure 11-147 Time (Minute) - Intensity graph

- AcquisitionTime DICOM fields of all involved Series are identical: the x-axis of the contrast curve is a temporal order index based on the TemporalPositionIndex or TemporalPositionIdentifier DICOM fields (note that the x-axis is labelled "TemporalID" in this case). An appropriate warning is displayed under the chart (⚠)



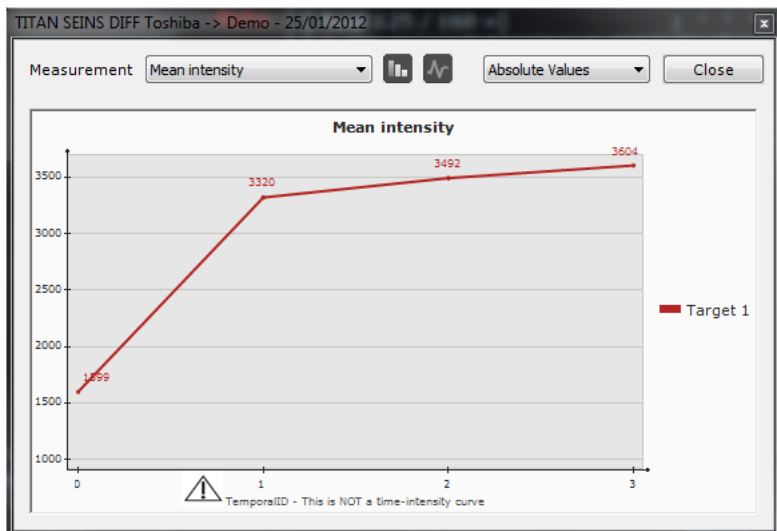


Figure 11-148 Contrast uptake curve (x-axis displaying a temporal order index)

- Involved Series are a mix of the above-mentioned ones: Series are sorted according to AcquisitionTime, TemporalPositionIndex and/or TemporalPositionIdentifier DICOM fields. In this case, the x-axis is a unitless index.

An appropriate warning is displayed under the chart (⚠)




Figure 11-149 Contrast uptake curve displaying a unitless index on the x-axis

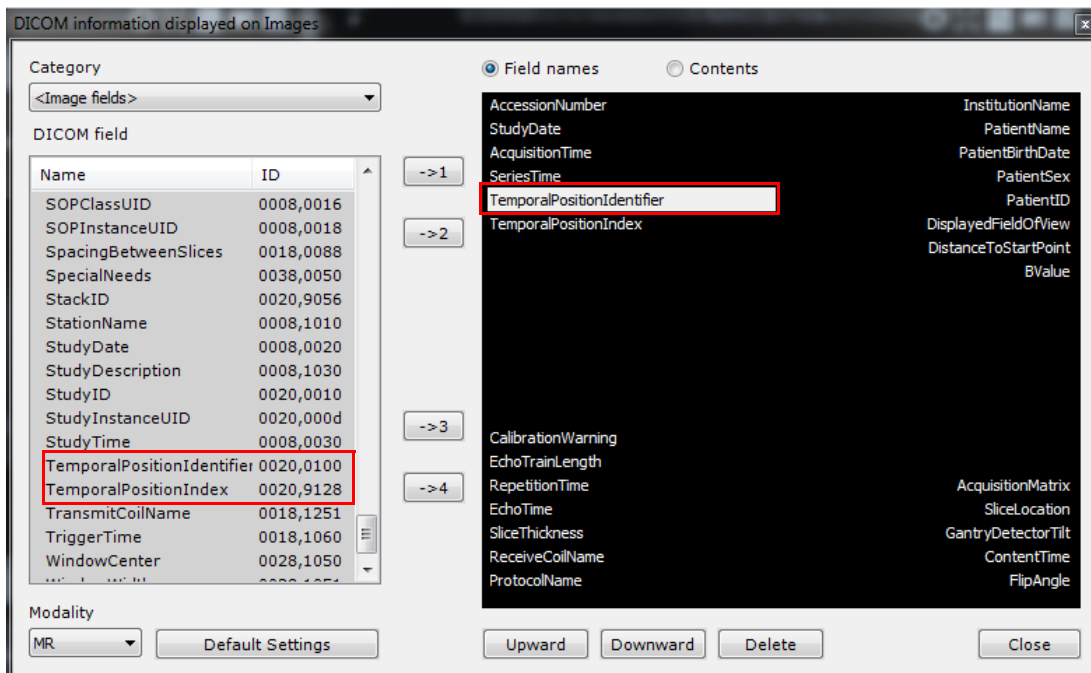


You should be aware that the x-axis type will have an impact on the shape of the curve.



To retrieve the series DICOM AcquisitionTime and/or temporal information:

- Open the series in Native Mode,
- Right-click on DICOM icon  located at the upper-right corner of a view to open the DICOM Information panel,
- Scroll down the DICOM field list until reaching the TemporalPositionIndex (0020,9128) if present, or a mix of TemporalPositionIdentifier (0020,0100) and the EchoNumbers (0018,0086),
- Select one of those fields and customize the information display on the view,



- Close the DICOM information window.

## Graph Types

You can display either 'Curves'  or Histogram 'Bars' 

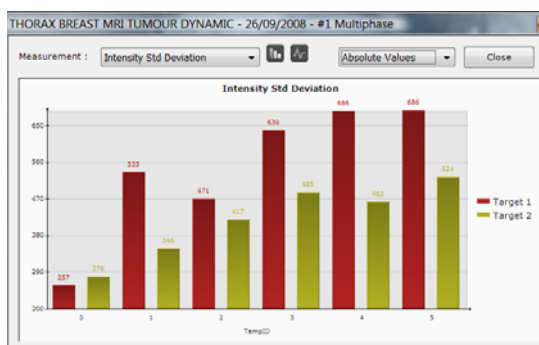
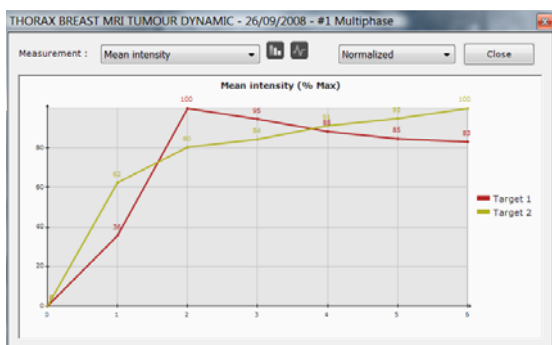


Figure 11-150 Contrast Curve Screen 1)'Curve' view 2)'Bar Chart' view


### 11.6.10.5 Acquisition time correction

According to the manufacturer, it may happen that the correct acquisition times of dynamic MRI series cannot be read in DICOM tag AcquisitionTime (0008,0032).



This is particularly true with regard to Toshiba for which all the phases are regrouped in the same series. In that case, Myrian® divides the series into subseries (one for each phase) but all the subseries have the same AcquisitionTime. Therefore, Myrian® has to use other temporal information to order the subseries and display a contrast curve which is then not a "Time -Intensity" curve as the unit displayed in the x-axis is "temporalID".

An acquisition time correction mechanism based on several methods and enabling to make up for this typical case,

automatically launches as soon as you click on the 'Hide/Show Contrast curve' button 

If one of those methods works, an Acquisition Time checking dialog box pops up asking you to confirm that the new acquisition time values obtained are correct before using them to generate a Time - Intensity curve:

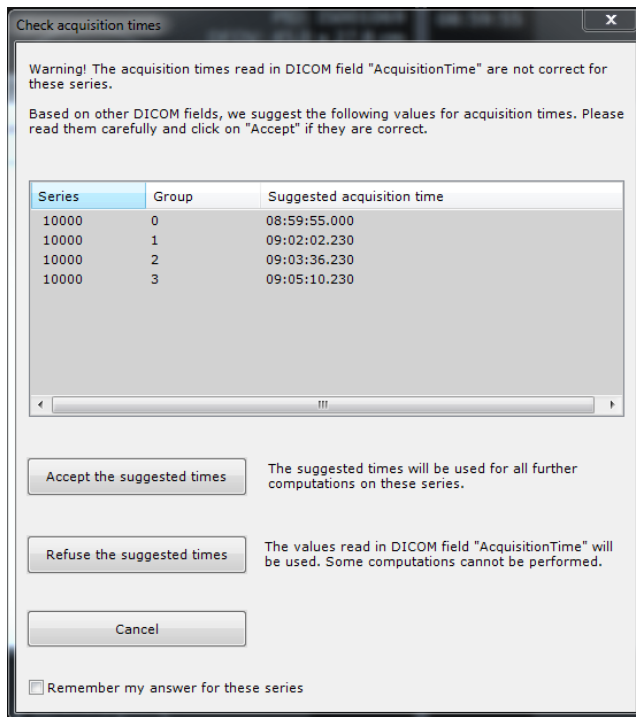


Figure 11-151 Acquisition time checking window



The "user check" popup window only applies if:

- The input phases belong to distinct series \*or\* the input phases are all the subseries of a given series
- Inside a phase, all the slices have the same acquisition time.

You have three options:

- **Accept** the suggested times: The new acquisition times are taken into account to automatically display a Time-Intensity curve.
- **Refuse** the suggested times
- **Cancel**

If you click "Cancel" or "Refuse", those new acquisition times cannot be used and the contrast curve displays a temporalID x-axis once the following warning message has been validated (see Figure 11-144).



Accepting suggested times applies to all the images of the series.



Checking the "Remember my answer" checkbox allows you to store your answer (Accept or Refuse) in Myrian® database for the current series and the popup Acquisition Time checking window will not be displayed for these series again.

## 11.6.11 Matching tool

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Requires the activation of the XL-Matching Option (advanced module for elastic registration inter- and intra-series).

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The Matching\* process enables to identify and thus pair equivalent anatomical structures from two (or more) distinct series belonging to the same patient. Those volumes can have same or different dimensions but nevertheless shall represent the same body area. At no time will you access deformed anatomical or functional images.

\* Based on the Registration advanced technology developed by the Ecole Centrale Paris (ECP), France.

---

Matching is automatically performed to synchronize series using dedicated protocols (such as in the Liver Surgery Planning Protocol).

You can however launch Matching manually by clicking on the 'Matching' button  in the Toolbox.

A Matching floating toolbar pops up prompting you to activate Matching clicking on the 'Start Matching computation'


button 



Figure 11-152 Matching process in progress (indicated by a yellow light bulb)

---



When the Matching Process is complete, both the Matching Toolbar button and the 'Start' icon in the Matching Floating Toolbar exhibit green checkmarks  showing that the Matching Process has been performed and is active.



You can also edit Matching parameters clicking  in the Matching floating toolbar.

---



Modifying Matching parameters is to be performed by advanced users only.

---

The Matching Parameters window opens:

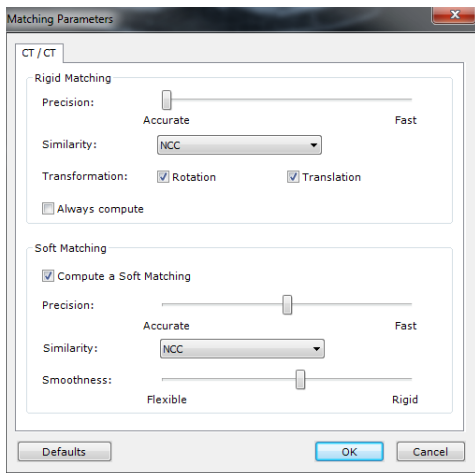



Figure 11-153 Matching Parameters window

 The acronyms for similarity methods used for parameterizing Matching stand for:

NCC: Normalized-Cross-Correlation  
 NMI: Normalized Mutual Information  
 SAD: Sum of Absolute Differences  
 SSD: Sum of Squared Differences


If there is a noted difference between the Phases due to a rapid evolution of pathology or a sudden change in the patient's position for instance, set the 'Soft' or 'Non-Rigid' Matching parameter as desired and launch Matching again

manually by clicking  in the Matching floating menu.



Figure 11-154 Matching floating menu

### 11.6.12 Iron Load calculation

The 'Measure Iron Concentration' tool  enables you to quantify the Liver Iron Concentration (LIC). The calculation is based on the analysis of the average density of Target regions.

The accuracy of this technique has been validated by Pr Gandon and al. [1, 2].


[1] Guyader D; Gandon Y; Robert JY; Heautot JF; Jouanolle H; Jacquelinet C; Messner M; Deugnier Y; Brissot P. [Magnetic resonance imaging and assessment of liver iron content in genetic hemochromatosis. J Hepatol 1992 Jul;15\(3\):304-8.](#)

[2] Gandon Y; Guyader D; Heautot JF; Reda MI; Yaouanq J; Buhe T; Brissot P; Carsin M; Deugnier Y. [Hemochromatosis: diagnosis and quantification of liver iron with gradient-echo MR imaging. Radiology 1994 Nov;193\(2\):533-8.](#)

The Iron Concentration tool is intended to be used only with images acquired on 1.5T and 1.0T MR scanner. Consequently, exams obtained on other image acquisition devices are not supported.

However, Myrian® can detect the type of exams via DICOM data, so that when the DICOM tag is another value, no calculation is provided.

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 FOR US MARKET, please note that the Iron Concentration tool has only been cleared to be used with images acquired on 1.5T MR scanner.

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### 11.6.12.1 Open Study using the Native Mode Protocol

Proceed as follows:

- Open the desired Study in the Study List in Native Mode Protocol

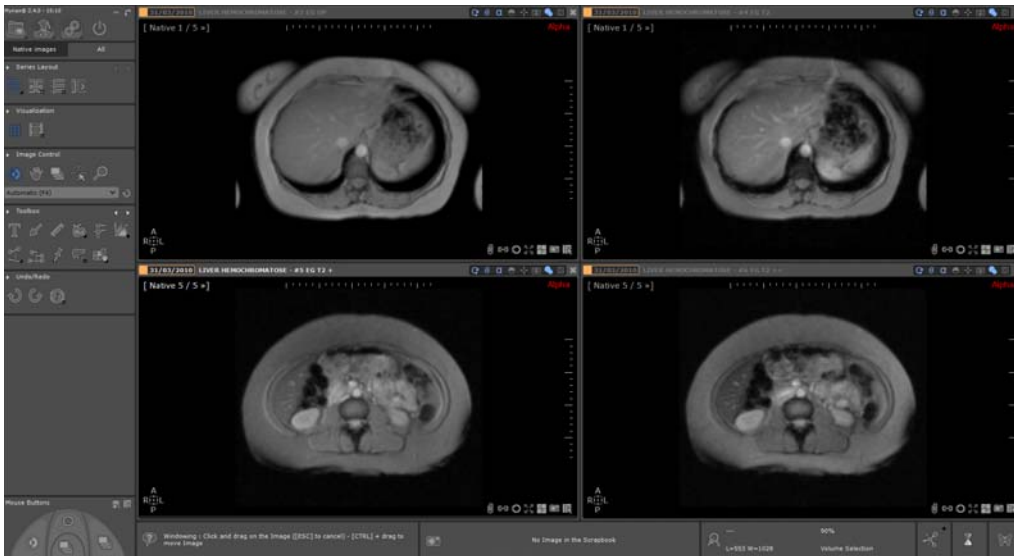


Figure 11-155 Open Series in Native Mode

- Click on the 'Measure Iron Concentration' button  in the Toolbox



The 'Measure Iron Concentration' button is only active with compatible Series.

The page displays a line for each sequence that can be used according to the magnetization strength of the study.

	Liver1	Liver2	Liver3	Muscle1	Muscle2	LIC
T1	--	--	--	--	--	
DP 120/20/4	121	149	137	429	461	280.00
T2 120/20/9	24	33	25	408	444	170.00
T2+ 120/20/14	19	22	12	335	357	130.00
T2++ 120/20/19	23	16	12	291	316	95.00

LIC: > 280  $\mu\text{mol/g}$  (N < 36  $\mu\text{mol/g}$ )

Series Used: DP

Figure 11-156 Iron Load Concentration window



The Name of the active Series is always displayed in the title bar.



All sequences for which a valid Series has been found are enabled, others are disabled.




In order to be able to use two Series for the same evaluation, both Series must have been acquired in the same plane of orientation.

### 11.6.12.2 Create Targets

To calculate the LIC, each Series must contain five Targets.

To create the Targets:

- Click on the 'Target Creation' button  to activate the tool.



The Target tool is automatically assigned to the left mouse button by default.

- Navigate to the relevant slice in one of the selected Viewports of your choice
- Click on the image to place the Targets.

Targets are automatically created in the following predefined order:

- Liver1, Liver2, Liver3, Muscle1, and Muscle2



For each Series, all Targets must be created in the same slice.



Each Target can be modified individually (moved or resized using the handles) in its corresponding Viewport (to compensate for potential Patient movements for instance).



Modifications carried out on Targets in one image are not reflected on the corresponding Targets in any other image.



The Target creation tool is automatically deactivated once all five Targets have been created.

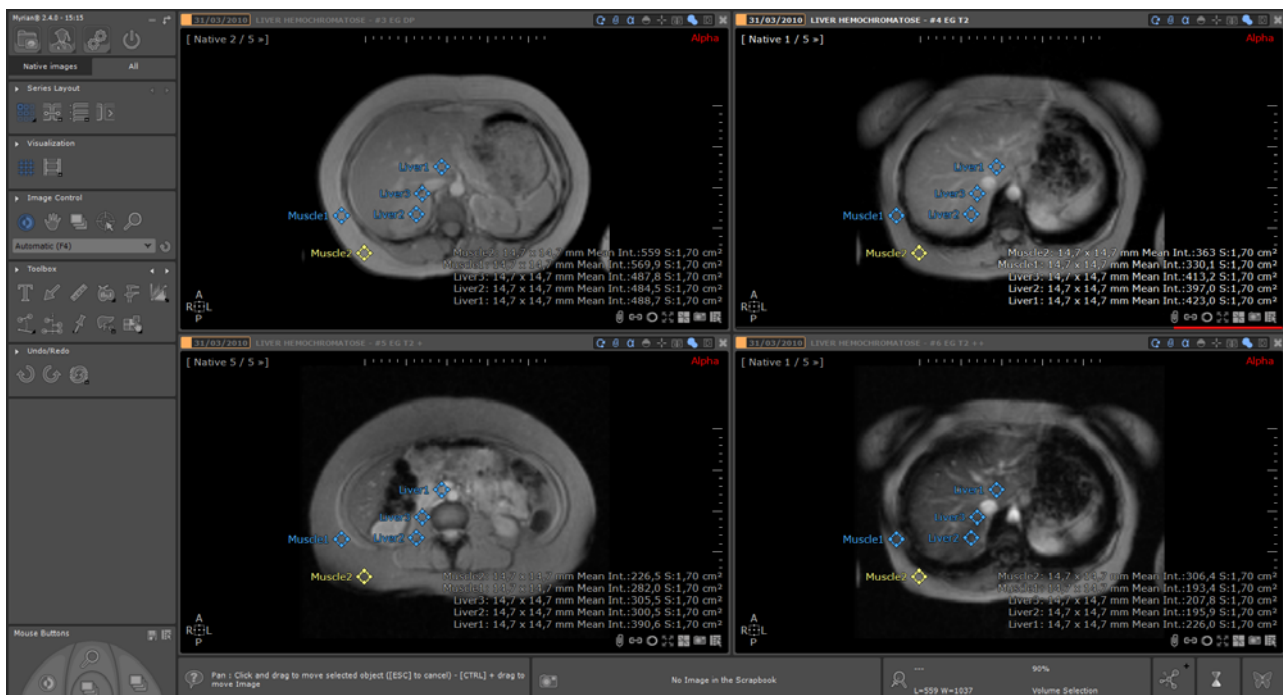



Figure 11-157 Place Target ROI in relevant Series

### 11.6.12.3 Delete Targets

Target ROI can be deleted by using the 'Target removing' tool  or via the context menu of each Target.



Targets cannot be deleted individually. The Target Removal function deletes all Targets at once systematically.

### 11.6.12.4 Iron Load Calculation

The average density of each Target is refreshed in the corresponding area of the Iron Load Concentration Window every time it is created or modified.



The LIC of a Sequence is calculated as soon as the five Targets have been created.



LIC are displayed in the last columns of the corresponding lines for each Sequence.



The Iron Load feature determines in real time with each new LIC result which is the most appropriate sequence to use to evaluate the overall LIC.

The selected Series and the corresponding results are displayed at the bottom of the LIC table:

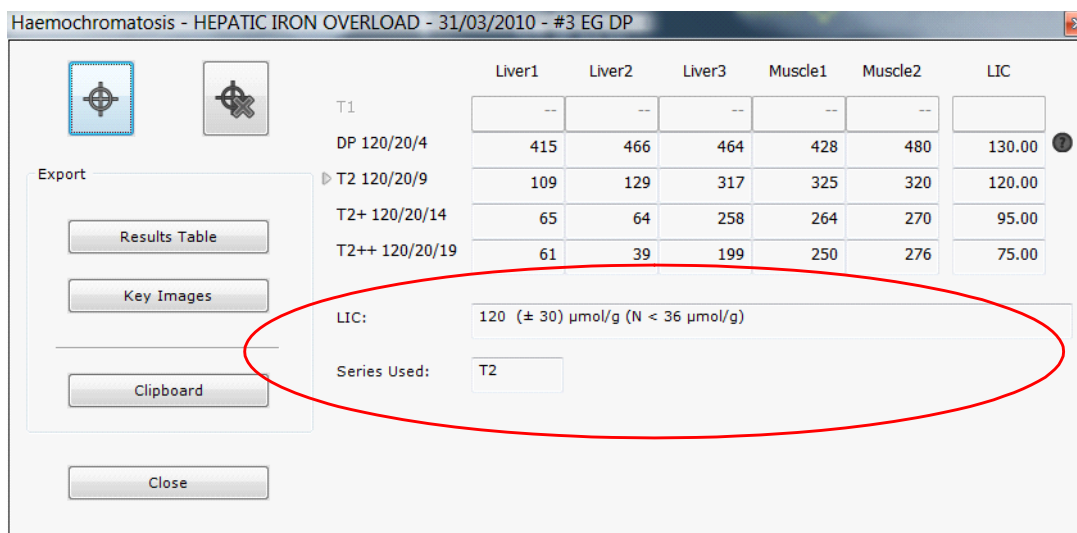


Figure 11-158 Result of the Iron Load analysis



If the LIC value is deemed below or above a certain value, a question mark appears beside the LIC value.





When you mouse-over this 'question mark' icon, a warning message appears to with information about the LIC value concerned.



Series acquired using parameters which are not compatible with LIC Acquisition Protocols can be evaluated, however a warning message is displayed to warn that echo time, flip angle and/or repetition time cannot be assessed satisfactorily.



If one of the Series is acquired without a "Body Antenna" (DICOM TAG TransmitCoilName 0x0018:0x1251) and if there is a difference of more than 50% between the lowest and the highest mean intensity value among the Liver ROI, a warning message appears to alert on the fact.

### 11.6.12.5 Export Results

All results can be exported from the Iron Concentration Window:

- To the Scrapbook as a Key Bitmap Image and by clicking on the "... to Scrapbook",

Name HEPATIC IRON OVERLOAD  
PatientID IS000654  
Study Date 31/03/2010

	Liver1	Liver2	Liver3	Muscle1	Muscle2	LIC	
T1	--	--	--	--	--		
DP 120/20/4	415	466	464	428	480	130	Low sensitivity
T2 120/20/9	109	129	317	325	320	120	
T2+ 120/20/14	65	64	258	264	270	95	
T2++ 120/20/19	61	39	199	250	276	75	

Figure 11-159 Key Image Export (BMP)



The Results Table is sent to the Scrapbook along with captures of all Viewports containing Targets.



The Table is also captured to the Clipboard as a bitmap image.

- To the Clipboard in a tabulated editable text format by clicking to the "... to the Clipboard" button.

### 11.6.13 Pixel calibration tool


Depending on the acquisition modality (e.g. the radiographic device and the digitizer), certain Studies may contain no dimensional information to establish measurements of distance. Such cases will require the use of the image pixel calibration tool.



The image pixel calibration tool enables a user-defined dimension (in mm) to be allotted to a pixel in cases where this value is absent, as it is the case for 'SC'-type (Secondary Capture) DICOM images, etc.

Once calibration has been performed, accurate measurements can be applied with such tools as the Length Measuring tool, etc.

To use the image pixel calibration tool:

- Click  or assign it to a mouse button. The mouse cursor will then change, indicating that you may draw a line on the image
- Locate an appropriate area to calibrate as a "Standard Measure" (it is recommended to calibrate over at least 200mm, see below)
- Click on a point in an image to place a starting point and drag the mouse holding down the left mouse button to draw your Calibration Line,
- Release the mouse button at the endpoint of your Calibration Line

The Calibration Distance Value screen will then appear.

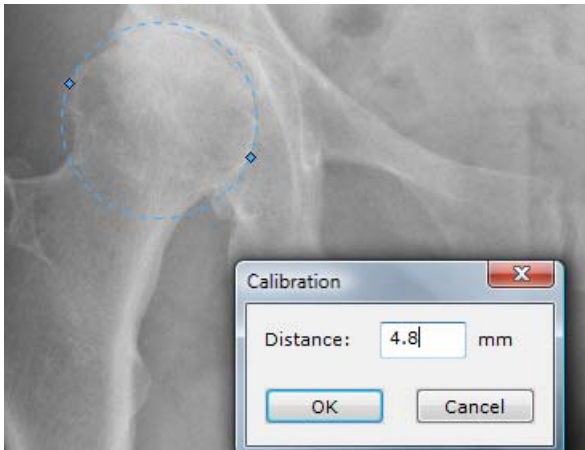


Figure 11-160 Pixel calibration example

- Enter a value in the "Distance" field
- Click OK



Calibration performed in this way can be canceled at any time by repeating the process and entering a value of '0'mm in the Calibration Screen.

---



For maximum accuracy, you should calibrate as near as possible to the center of image and over a distance of at least 200mm. Please read carefully Appendix 7 "About geometric distortion: known issues with CR and RF modalities".

---



The Calibration step must be completed for measurements to be reliable.

---

## 11.7 Reformatting & New series creation toolbar

---



Reformatting planes only apply in MPR mode (i.e. the reformatting tools cannot be used in a Native viewport) for series showing a coherent volume.

---



The 'Reformatting' and 'Create New series' toolbars are available from the Toolchest when clicking on the

'Reformatting' task bar in the **Standard and Advanced CT protocols** only.






---

### 11.7.1 Overview

The 'Create New Series' tool enables the **creation of new DICOM Series from existing Series**, using user-defined reformatting rakes.

The Series can then be saved, exported to the current Study or printed as a **native Series** or in **RGB format**.

The 'Create New Series' toolbox include 5 different **rakes** or reformatting planes:

- The **Linear Rake**  creates new Series of parallel images.
- The **Curve Rake**  creates new Series by reconstructing images perpendicular to a freehand line.
- The **Radial Rake**  creates a new Series of images rotated about the center of a circle.
- The **Spine MPR Rake**  creates new Series of parallel images but between two vertebrae.
- The **CPR Rake**  creates new series by reconstructing images perpendicular to a CPR

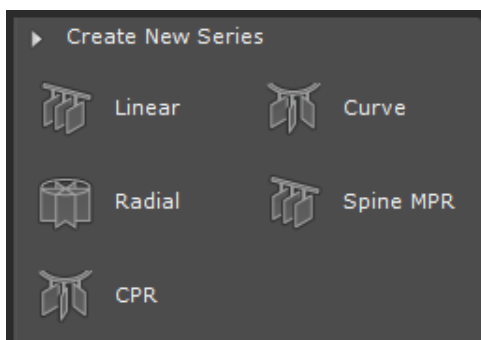


Figure 11-161 Multiplanar Reformatting (MPR) Series Creation tools

### 11.7.2 Procedure

To use the Linear and Radial Rakes:



- Click on the spot you wish to designate as the center-point of the new Series in the appropriate frame **without releasing the mouse-button** and start drawing from the first slice,
- Drag to the desired end-point of new Series without releasing the mouse-button (to the last slice),
- Release to define the initial size or diameter.




The reformatting planes related to the Radial and Linear rakes are deployed around the clicked center of interest.


---

To use the Curve Rake:

The way to use the Curve Rake depends on whether the general freehand drawing mode is set to continuous line  or Point by Point . This setting can be modified using the corresponding Display Command Button in the toolbar at the top right corner of the Workspace (see Section 11.4.3.2).

- Click and drag to draw a continuous  freehand line
- Release to define the initial size or diameter

Or:

- Click and drag to draw a segment of your Point by Point  freehand line
- Release to define the endpoint of each segment
- Press "Escape" to define the initial line




Freehand lines drawn with the Curve Rake are smoothed.

To use the Spine MPR Rake:

- Click one point between the Spine vertebrae to create the rake. Once the rake is placed, you can manipulate it just as the Linear Rake and also create multiple stacks of images, the only difference is that a predefined vertebra label shall be assigned to each stack upon validation.

To use the CPR Rake:

- Click and drag to draw a path of your Point by Point  freehand line

The Reformatting Rake appears in 2 Planes of View. The position, orientation, spacing and size of Rake can be modified by hand. The preview window (see Section 11.7.3) allows you to visualize real-time the reformatted images.

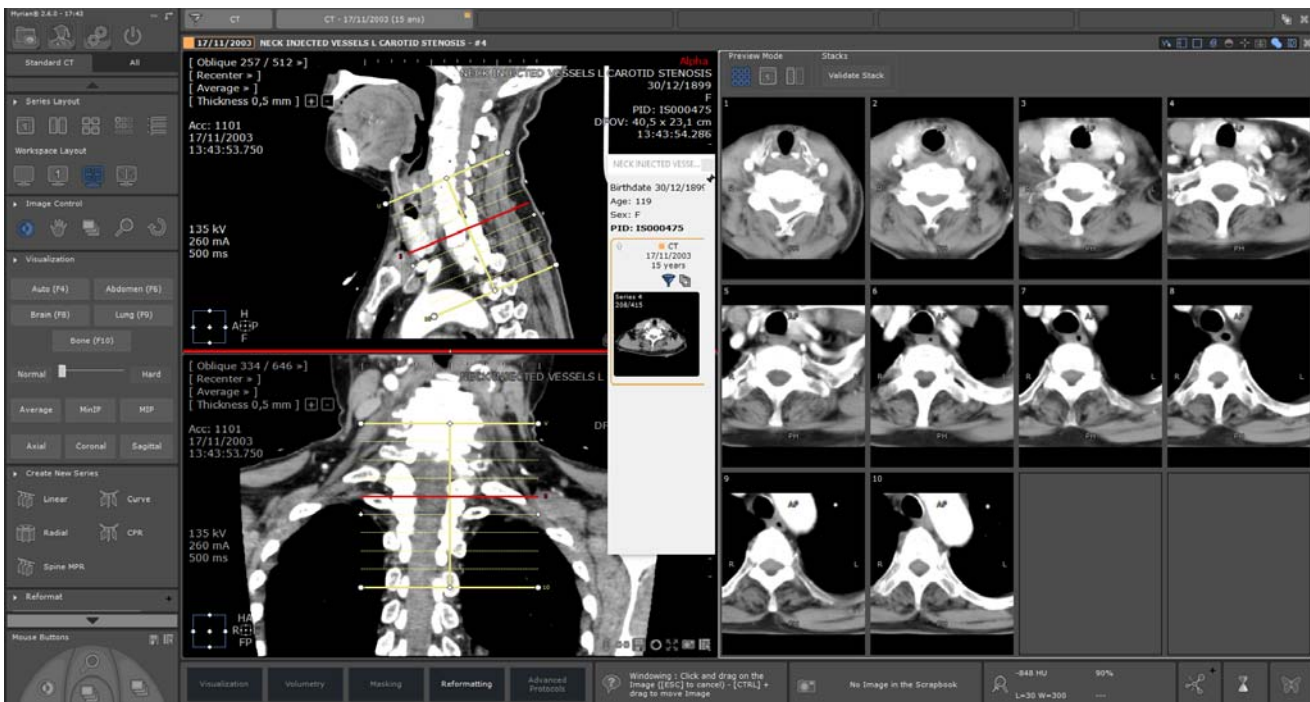


Figure 11-162 Creation of new Series using the Linear reformatting plane

The reformatting Rake can be manually **moved, rotated or resized** in either of the frames (length, width, etc) using the appropriate rake handles (round or square) by pointing, clicking, dragging & dropping the mouse.

You can also customize dimensions, image count and spacing typing in your own parameters directly in the relevant fields related to the 'default selection':

- Image count: the number of images you want to generate
- Spacing: the spacing between two generated images (in millimeters)
- Length: the length of the Rake (in millimeters)

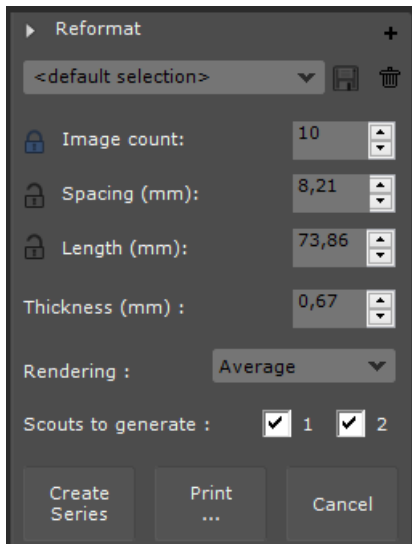



Figure 11-163 Customization of the Reformatting values

Clicking  enables to set permanently one of those three parameters (image count set to 10 by default) during reformatting plane manipulations. You can set the parameter of your choice at any time.




As one parameter is set permanently, modifying the dimensions of a reformatting Rake automatically modifies the other parameters accordingly.



After each change, the preview is automatically updated to reflect the new rake dimension and position.



You can abort the process at any time by clicking on the "Cancel" button.

Also, clicking on the  icon opens the 'Advanced settings' dialog box enabling you to define the following values and settings for the **Generated Images**:

- Size of the generated images
- Image Resolution
- Pixel Dimension
- Format (Native for a DICOM Series, RGB for a stack of RGB screen captures)

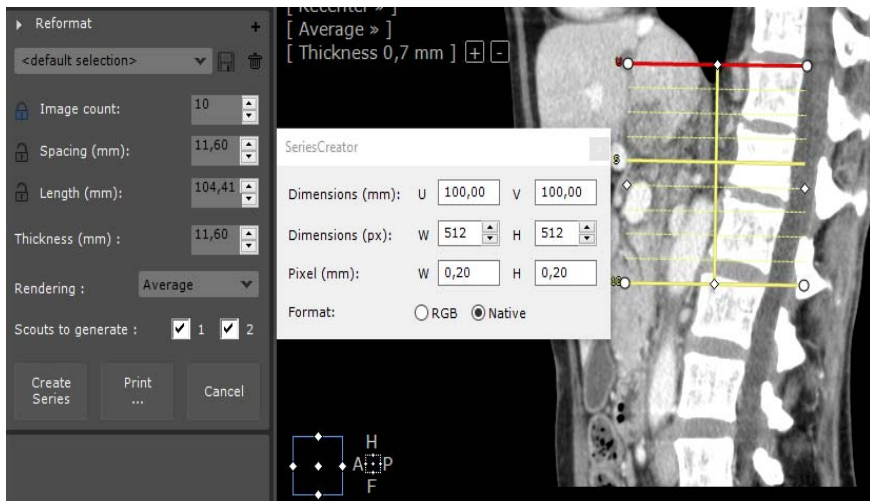
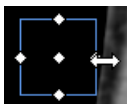


Figure 11-164 Reformatting advanced settings related to the generated images



You can also resize the generated images manually dragging the mouse over any white handles located on the



blue square. The preview images update accordingly in real-time.

Before validating, you should also confirm or modify:

- The **Image Thickness**
- The **Rendering** (Average, MIP, MinIP)
- **Scouts** (both selected by default) to generate choosing the number of scouts (1: top plane control viewport and 2: bottom plane control viewport) via checkboxes: you can opt for none, one of them or all of them.
- Click on the **“Create Series”** button to validate the settings and generate the new Series.

User-defined reformatting plane settings can be saved for subsequent Series Creation by renaming and saving the

newly-created rake profile  (by default, <default selection>).

The new Series will be **added to the current Study**.



The so-called ‘scout view’ images come along as subseries in RGB format, associated to the created series in order to indicate the reformatting plane location.



Click on the ‘Print...’ button to print the preview images without needing to actually create the Series. This function sends all the preview images to the PrintComposer. A message pops up to ask you whether or not you wish to empty the current content of the PrintComposer.

### 11.7.3 Visualize the generated images in the Preview window

Upon placing one reformatting plane on any of the plane of view, a preview window pops up in the right-part of the workspace displaying the generated images or the current stack of slices. The preview window reflects in real-time any changes performed on the rake.

This preview windows allows you to get a close-up of the results of your reformatting before creating a new series.



All standard Image Control Tools (Panning, Windowing, Zoom, Navigation and Magnifying Glass) can be used on the preview images though zooming actually changes the size of the rake.

### 11.7.3.1 Previsualization modes

By default, the generated images are displayed in the Preview area as **thumbnails**. You can click any preview thumbnail to get a full size view of the image.

You can also opt for **full size** or **column** preview mode clicking on the corresponding icon above the Preview Area.



Figure 11-165 Available preview modes for the generated image visualization

In Preview Mode, while mouse is over the image (Thumbnails, Full size or Column), it highlights in red the corresponding slice on the rake.

### 11.7.3.2 Single and Multiple stack display and validation



Multiple stack creation is supported by the Linear rake and the Spine MPR rake only.

Each stack can have its own settings although it is recommended to keep them consistent from stack to stack and simply change the position and orientations of stacks.

The stack toolbar allows you to manage and validate stacks:

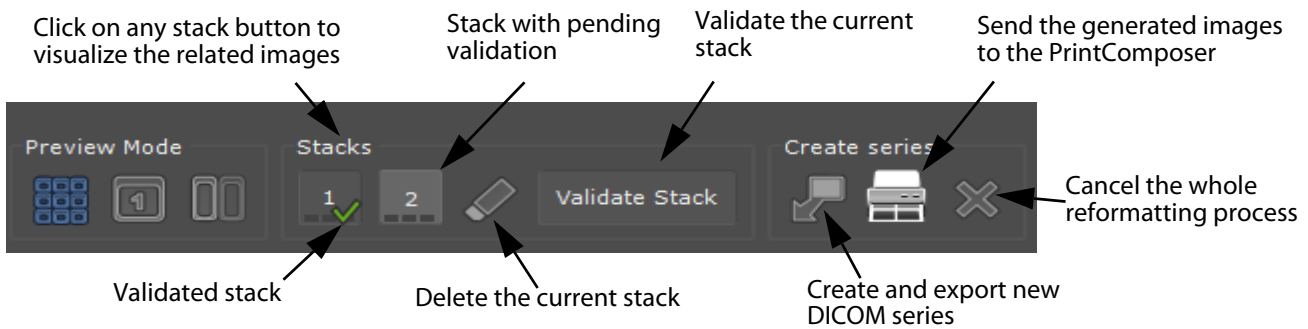



Figure 11-166 Stack toolbar

When a stack has images defined, small dark rectangles are displayed on the stack button concerned.

Upon stack validation, a green checkmark  is displayed on the relevant stack button and a new stack is automatically generated in the stack toolbar. In the end, all stacks are merged into one DICOM series upon new series creation.



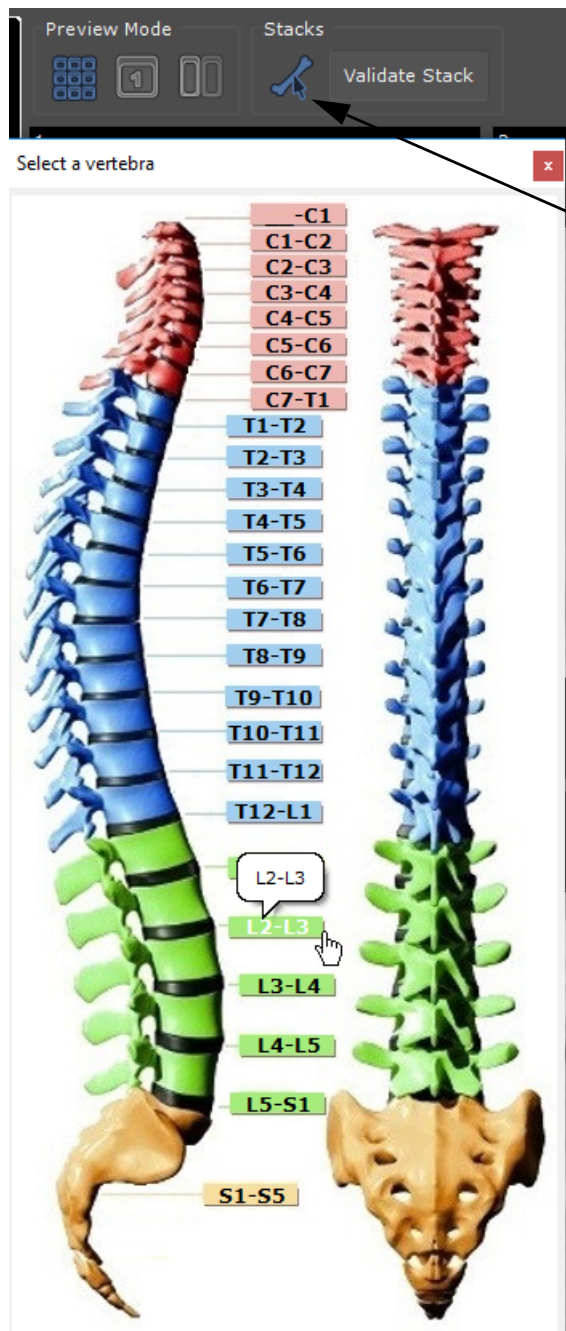
The preview window only displays the slices of the selected stack. When unselecting all stacks, the preview window displays all slices of all stacks.




With reference to the Spine MPR rake, each stack has to be validated and the vertebrae identified using a label.



If a stack is not validated, it will not be included in the final DICOM series.

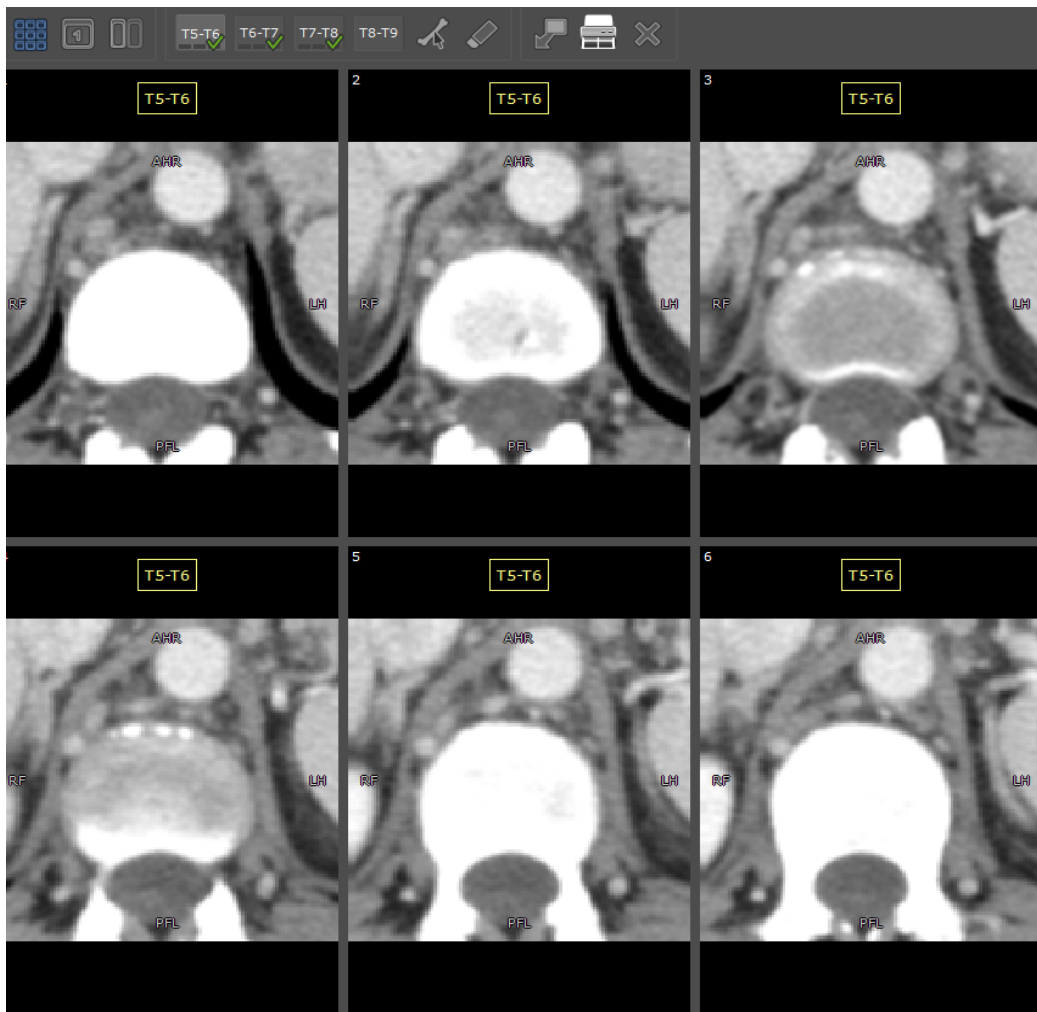


Click on the 'Select label for current stack'

- icon  to display the vertebrae diagram:
- Click on the vertebrae corresponding to the rake positioning to select the relevant label

Only the first stack needs to be given a label as other labels are figured out automatically by assuming that each consecutive stack corresponds to the consecutive vertebrae. The label is automatically displayed above each preview thumbnail.





### 11.7.4 Launch series creation or printing

The images generated by the Reformatting planes can either be turned into a new series related to the current study or directly sent to the PrintComposer. In that case, no new series is created.

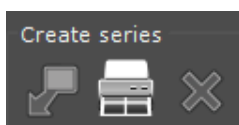




Figure 11-167 Printing/Exporting the generated images as a series

In case of multiple stacks, they are all merged in one series including the scouts created for each stack (one or two according your choice). All scouts are generated upon placing the reformatting rake and appear at the beginning of the created series.

- When clicking  , the PrintComposer module automatically opens displaying the validated images as well as the scout images for immediate editing, arranging and printing (see Section 5.2.6)
- When clicking  , the newly created DICOM series is automatically displayed in the workspace in the Native Image Protocol.

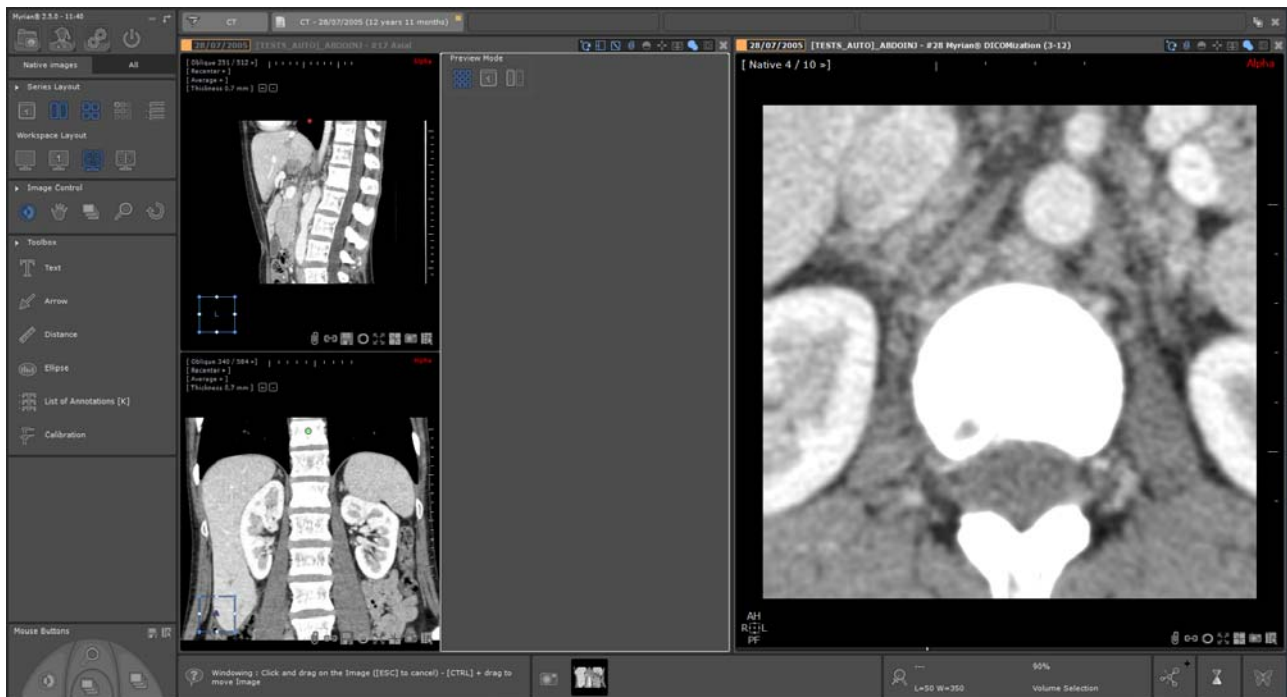



Figure 11-168 Visualization of the new DICOM series created from the reformatting plane tool in the Native protocol

- When clicking  , the whole reformatting process is aborted.



For stacks with label, the title is burned on the scout images and included in each image (scout and slices) as a DICOM field (0070,0080).

## 11.8 Vessel Centerline Edition toolbar

### 11.8.1 Overview

The 'Vessel centerline edition' toolbox provides a comprehensive range of tools allowing you to **interactively create and/or edit** missing vascular branches and trees. This toolbox is particularly dedicated to the XP-Vessel module.

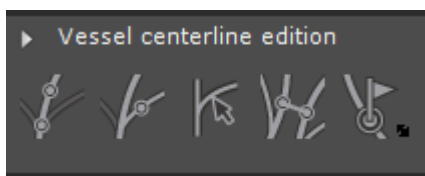









Figure 11-169 Vessel centerline edition toolbox

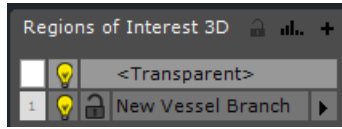
It includes the following tools:

- 'Create a new vascular tree' button  (without any connection to the existing one)
- 'Connect a vessel to an existing vascular tree' button 
- 'Detect a vessel progressively' button 

- 'Fuse two vascular trees' button 
- 'Vessel labeling' button  which opens a vessel labeling floating toolbox.



If no Vessel ROI has been initially created and you are using one of those tools,  or , a new ROI is



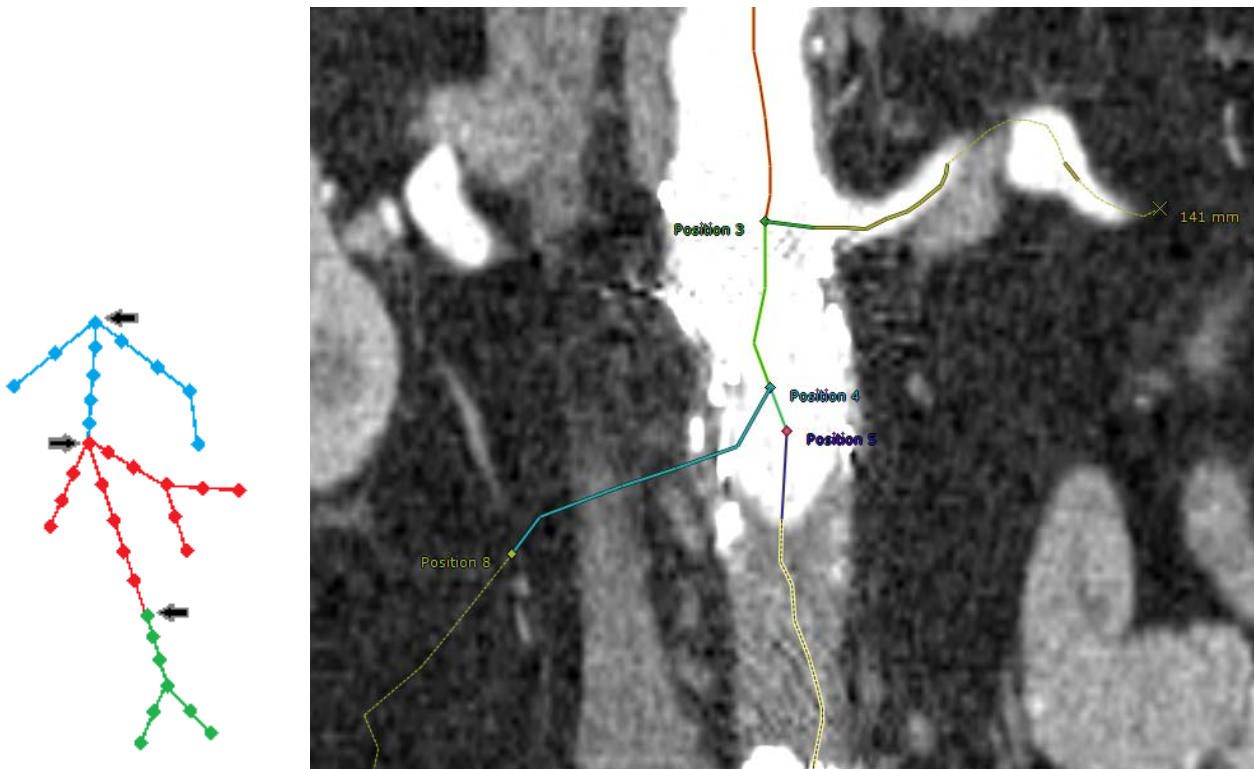
automatically added in the ROI list whereas if a vessel ROI is preexisting, this latter is automatically updated.

### 11.8.2 Path labeling

The Path labeling allows you to name desired branches of a path either on **2D or 3D viewports**.



A specific color is assigned to each labeled segment allowing you to visualize the different parts of the path.



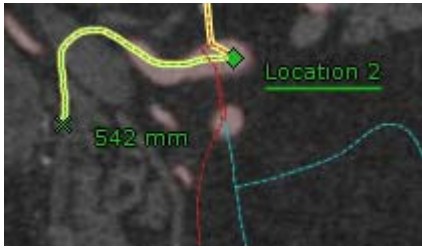
All points belonging to a given label are displayed with the allocated label color. The label name is always displayed next to the first labeled point.



The label name display is a configurable setting.



Once labeled, the active path is highlighted in yellow.









- To open the dedicated toolbar, click on  in the 'Vessel Centerline edition' toolbox.



Figure 11-170 Vessel/Path labeling toolbar

The vessel labeling floating toolbar includes the following tools:

- 'Enable/Disable the label creation' button 
- 'Remove the label linked to the selected point' button 
- 'Remove all labels from selected point' button 
- 'Remove all labels' button 
- 'Enable/Disable the label mode for vessel exploration' button 
- 'Change the label description of the selected point' button 

All features described here-above are also accessible through the path contextual menu.

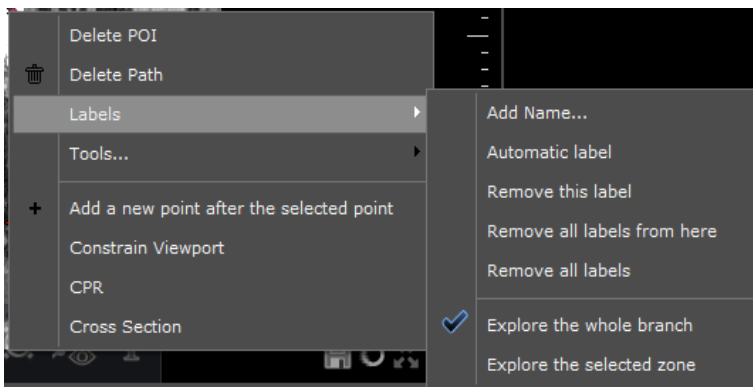


Figure 11-171 Label contextual menu

### 11.8.2.1 Create labels

- In the dedicated toolbar, click  to activate the **Creation mode**.



The tool is enabled when the icon is colored blue.



This feature is also accessible from the path labeling contextual menu selecting 'Automatic label'.

- In the 2D or 3D viewport, click on a path point from which you want to place a label proceeding in a top down approach.



The mouse cursor changes to a flag icon as long as you are moving the mouse pointer over a path point.

Upon clicking, a colored label (i.e, default name is 'Location') including an index is automatically allocated to the selected point. When a label is attached to a point, all subsequent points in the path, in all branches, are named with the same label starting from this point.

For each branch, the labeling stops on the last point, or when a new label starting point is found.

At creation time, the point property window is automatically open to let you modify the label name and/or color.

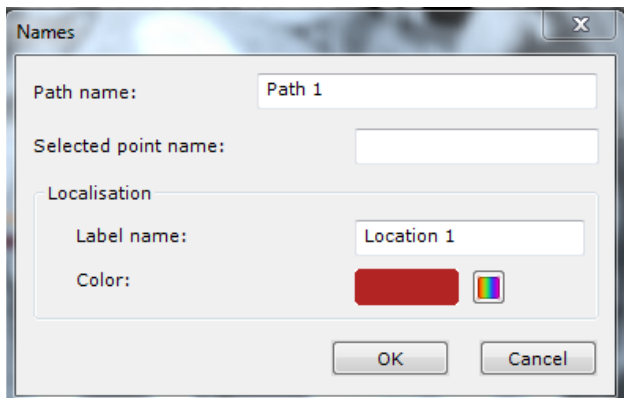


Figure 11-172 label properties



This dialog box can be accessed at any time simply clicking



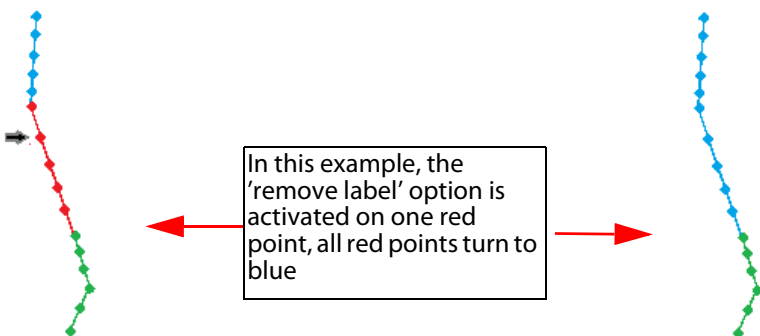
from the label or the path floating toolbar.

### 11.8.2.2 Remove the label corresponding to the selected point




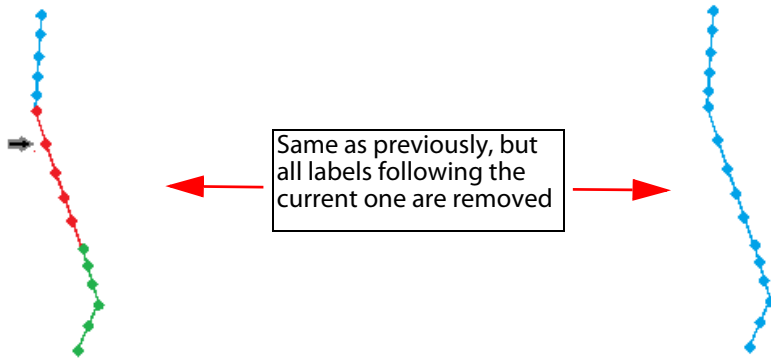
- Click to remove the label corresponding to the current point.

All corresponding points will be given the label of the previous point (or won't be labeled if the previous point is not) as illustrated hereafter:




### 11.8.2.3 Remove all labels starting from the selected point


- Click  to remove all labels starting from the selected point.



### 11.8.2.4 Remove all labels from the path

- Click  to remove all labels from all points for the selected path.

### 11.8.2.5 Change the label description of the selected point

- Click  to edit the label description of the active path (see Figure 11-172) such as its color, its name.

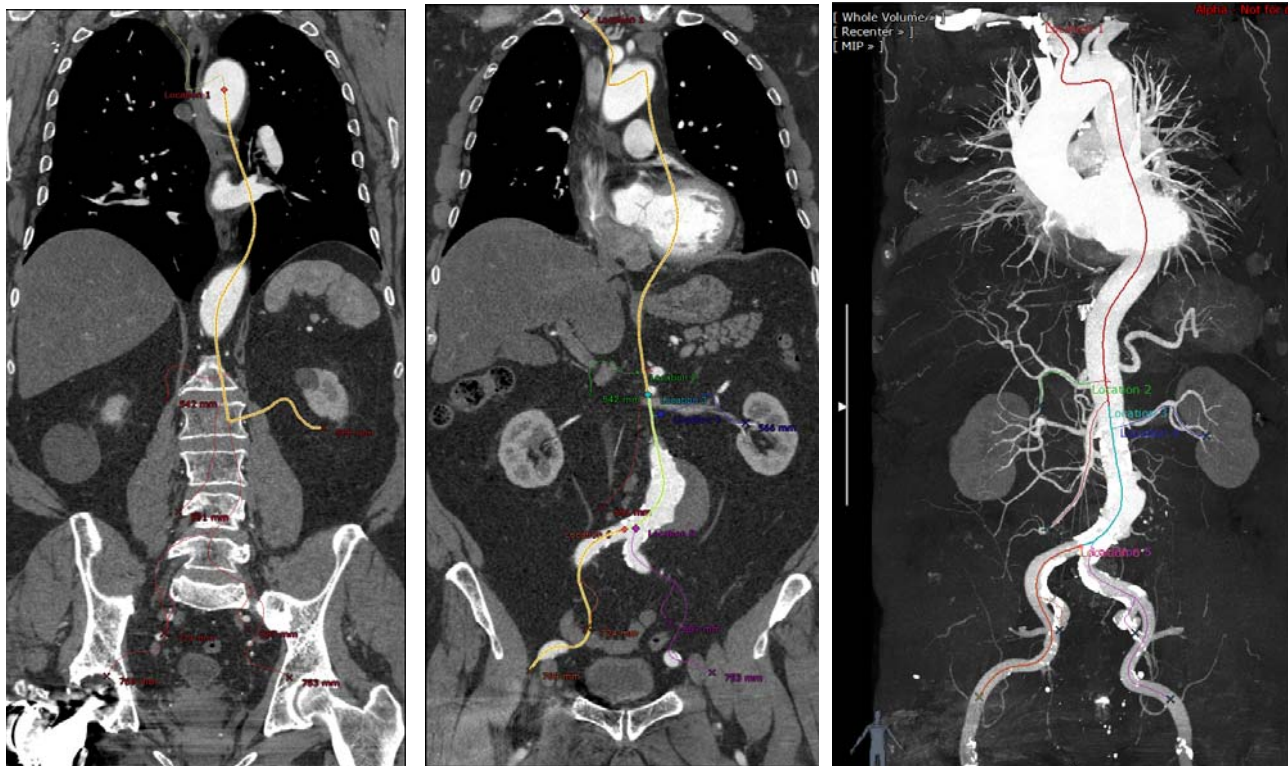



Figure 11-173 Example of labeled path creation with visualization in a 3D MIP view




To select the labeled branches (or not) of your choice without creating new labels, deactivate the Creation mode

clicking again on  .



### 11.8.2.6 Switch label visualization mode

When several labels have been created (or at least one label not created on the origin point) on the active branch,

clicking the **ON/OFF** button  enables you to change the exploration mode in the beforehand open **CPR viewports**:

- Button **OFF to explore the whole branch**: all points of the active branch are visible in the CPR viewport
- Button **ON to explore the selected labeled branch**: only the part corresponding to the label of the selected point (i.e. the active label) is visible in the CPR viewport.



When this mode is selected, the display of any open CPR viewport is updated with the active label and the selected point corresponding to the selected path.

---

## 11.9 Visual Selection toolbar



The Visual Selection masking only appears in 3D Viewports.

---



Contouring can either be performed in 2D or 3D viewports (including in oblique mode).

---



It is important to note that the Visual Selection is a non destructive tool that is being used to mask or make visible existing volume parts of the current exam.

---

### 11.9.1 Overview

The **Visual Selection** tool enables you to **modify** the display of a 3D image by **excluding** or **including** any part of the 2D/3D image creating user-defined **Volume selection** via contours

It is particularly useful for advanced study analysis (i.e. vessel systems) by selectively masking some anatomical structures (i.e. bone tissues), highlighting some of them or isolating them from the rest of the structures.

---



The Visual Selection tool is available in 3D Whole Volume, and MIP rendering modes.

---



The Visual Selection tool is not available in Native mode.

---

### 11.9.2 Presentation and usage

The Visual Selection toolbar is directly accessible from the Toolchest.

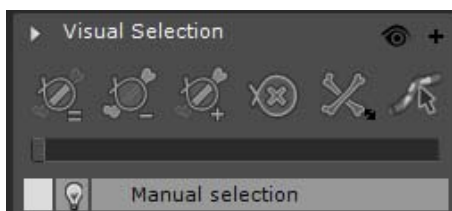


Figure 11-174 Visual Selection toolbar

---



Some Tools are hidden by default in various Protocols. If not visible, right-click on the Toolchest and select 'Visual Selection' from the context menu.

---








#### 11.9.2.1 Visual Selection toolbar

The visual Selection toolbar comprises the following function buttons:

- **Three visual selection sculpting modes:**

- 'Sculpt the Visual Selection (Preserve mode)' : this mode enables to create a volume preselection from the complete 3D image,



- 'Sculpt the Visual Selection (Include mode)' : all contoured parts are kept and added to the preselected Visual Selection,
- 'Sculpt the Visual Selection (Exclude mode)' : all contoured parts are suppressed from the preselected Visual Selection,
- A 'Clear Visual Selection' button  enables you delete all previously defined contours and restore the whole volume,
- A 'Bone masking correction' button ,
- A 'Calcification correction' button ,
- An 'Add a New Masking ROI' button ,
- A 'Series display mode' button .

### 11.9.2.2 Masking ROI

Masking ROIs enable you to hide specific structures that may impair the full visualization of the vessels.



You should always check the quality of the resulting bone masking based on native images and MIP rendering.

There are four available:

- One default generic « Manual selection » which relates to the whole volume,
- A Table mask segmentation engine dedicated to automatically hiding the table,
- A Bone mask segmentation engine dedicated to automatically hiding all bone structures.
- A Peri-cardiac bone mask segmentation engine
- A Vessel calcification mask segmentation engine dedicated to automatically hiding calcifications on vessels



The extraction of the calcifications which are defined as structures close to the vessel lumen with significantly higher intensities, is based on the initial segmentation of any vessel structure. Prior to create a calcification mask, you need to create a vessel ROI (please refer to the XP-Vessel User Manual for detailed information).

- To create any of those masking ROIs, click on the «+» button in the Visual Selection toolbar that opens the dedicated segmentation engine submenu.

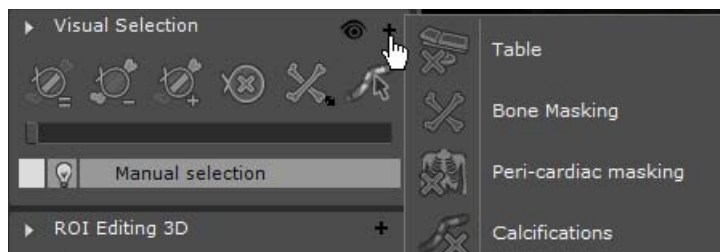


Figure 11-175 Masking ROIs

This menu prompts you to specify the removal engine appropriate to your CT series (see Section 11.9.3 for detailed procedure).

Once selected, these Masking ROI are automatically added to the masking ROI list and segmentation launches.

### 11.9.2.3 Editing a Masking ROI

Once you have contoured a structure in the image and according to the selected mode and the current masking ROI, the editing mode changes as described hereafter:

When used with the **generic <Manual Selection> selected**, if you activate:

- '=' button: All that is outside the contours is removed from the volume selection and added to the <Manual selection>
- '-' button: All that is inside the contours is removed from the volume selection and added to the <Manual selection>
- '+' button: All that is inside the contours is removed from the <Manual selection> and added to the volume selection
- When used with the **Bone Masking/Table or any other Masking ROI selected**, if you activate:
  - '=' button: All that is outside the contours is removed from the selected masking ROI and added to the volume selection
  - '-' button: All that is inside the contours is removed from the selected masking ROI and added to the volume selection
  - '+' button: All that is inside the contours is removed from the volume selection and added to the selected masking ROI

#### Method of use:

- Select the relevant sculpting mode

The extrusion floating toolbar (see Section 7.7.5) automatically appears. The extrusion tool can either be used on 2D or 3D viewports.

- Draw the contour and launch extrusion from the Extrusion floating toolbar



When defining a visual selection in 3D viewports, **only one single contour** is required while in 2D viewports, several contours can be defined.



To launch extrusion from the 1st contour, check the 'Automatically start the sculpting after the first contour' option available from the Miscellaneous box, Preferences>Display tab. Once activated, the extrusion floating toolbar becomes obsolete and is no longer displayed as the extrusion starts right after the first contour is defined.

The current sculpting mode is always visible in the extrusion toolbar.



Figure 11-176 Extrusion toolbar 1) in 'Preserve' mode (=) 2) 'Exclude' mode (-) 3) 'Include' mode (+)







When one extrusion mode is activated, the generic « Manual selection » is automatically preselected. To edit any other masking ROI (i.e. Table or Bone Masking), reselect the relevant one instead of the generic « Manual selection » before launching the extrusion process.



ROI edition tools can also be used for masking ROI edition.

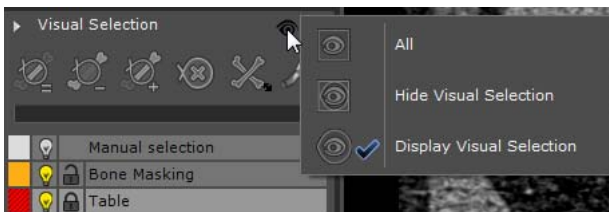
### 11.9.2.4 Volume display mode

The 'Series Display Mode'  button provides the following visualization modes:

-  Displays the **complete 3D Image**
-  Hides the **Visual Selection only**
-  Displays the **Visual Selection only**



The Series Display Mode menu can be opened from the Visual Selection toolbar, clicking on the dedicated icon



The last used Display Mode setting remains current until another is selected.

When a series contains a Visual Selection, a dedicated icon  appears at the bottom-right of the 3D viewport.

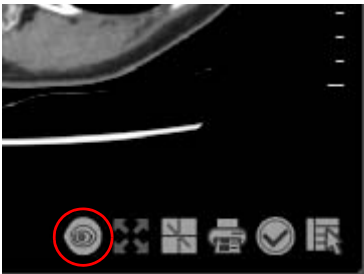




Figure 11-177 Active Visual Selection icon in MIP mode

### 11.9.2.5 Bone masking correction toolbar



The Bone Masking correction toolbar applies to **CT studies only**.

The floating Bone Masking Correction toolbar  enables you to **manually correct**, in 2D/3D mode, the bone masking previously performed and thereby adjust the visual selection when the bone masking is incorrect or erroneous: indeed, it may happen that the bone mask includes regions that should not be included (i.e. vessels) and alternatively, that some bone regions remain visible.

When clicking  in the Visual Selection toolbar, the floating bone masking correction toolbar opens:

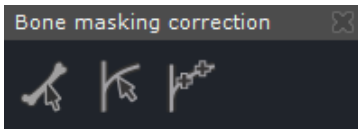








Figure 11-178 Bone masking correction floating toolbar

This toolbar includes three dedicated tools enabling to either remove from the visual selection the bones that were not detected by the automatic segmentation engine, or to remove from the bone mask any vessels erroneously added to it (see Section 11.9.5 for use procedure):

- A manual bone masking correction button 
- A one-click vessel correction button 
- A two-click vessel correction button 

### 11.9.3 Creating a Mask

Clicking on the 'Add a New Masking ROI' button  enables to generate Masks to **automatically hide or display** all

bone structures (Bone Masking ) or the examination table (Table ) from the current Series in **one click**.


All those structures that should not be visible are then removed from the original volume and added to a dedicated mask via the launching of the corresponding segmentation engine.

#### 11.9.3.1 Procedure



Table and Bone Masking segmentation engines only apply to CT Studies. They are not activated for any other modality.

Table Masking:

- Click  located at top-right of the Visual Selection toolbar

- To activate the Table Masking, click 



Figure 11-179 Visual selection before table masking

The segmentation **automatically** launches. A ROI list is automatically created displaying the Table masking ROI.

While the recognition process is underway, a progress bar appears in the active ROI entry(s) in the list of masking ROIs.

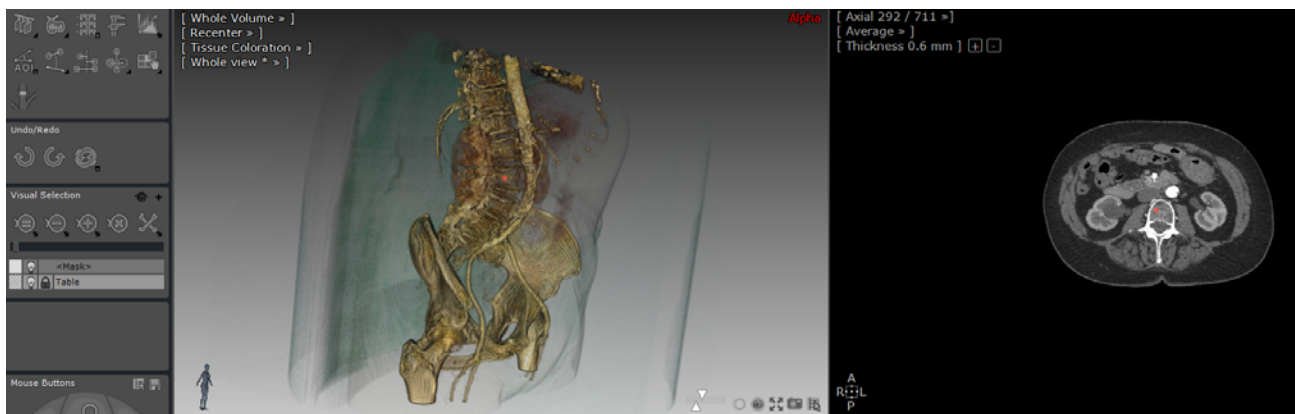



Figure 11-180 Visual selection after table masking

### Bone Masking:

- Click **+** located at top-right of the Visual Selection toolbar



- To activate the Bone Masking, click 

The segmentation **automatically** launches. The masking ROI list is automatically updated with the Bone Masking ROI.

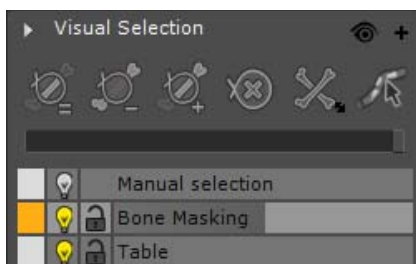


Figure 11-181 Bone Masking ROI progress bar

The 3D viewport is automatically updated.

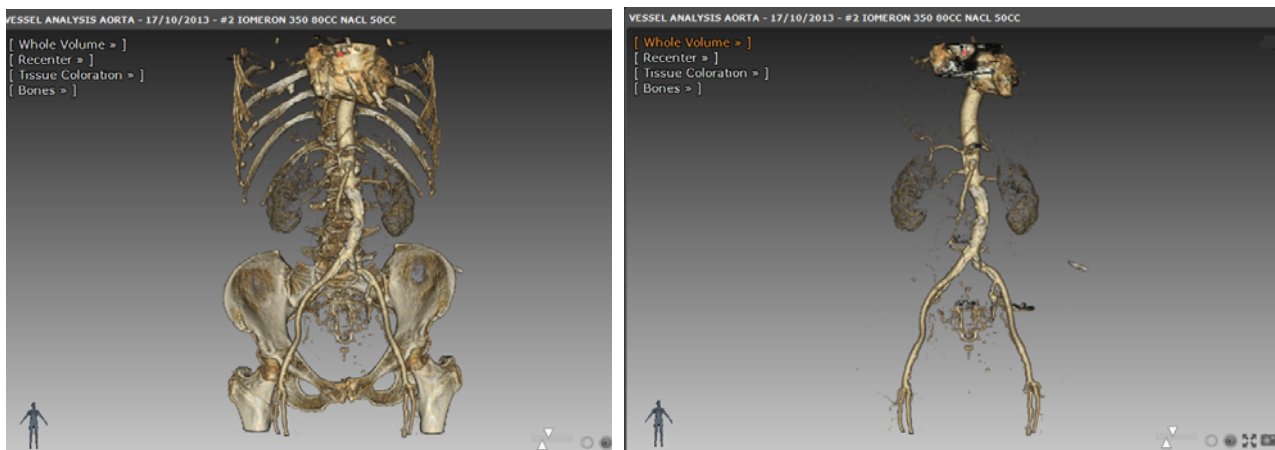


Figure 11-182 Bone masking: before and after extrusion in the 3D Whole Volume view

### Vessel calcification masking:



The extraction of the calcifications is based on the initial segmentation of any vessel structure.

- Click **+** located at top-right of the Visual Selection toolbar



- To activate the Calcification Masking, click 

The segmentation **automatically** launches. The masking ROI list is automatically updated with the Calcification ROI.

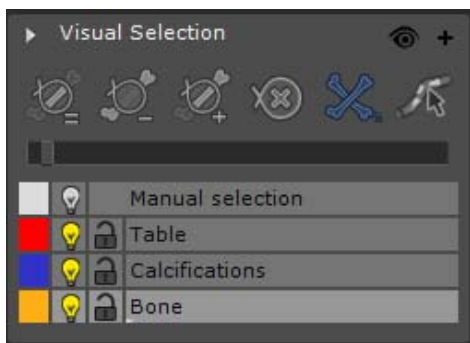


Figure 11-183 Calcification masking ROI segmented

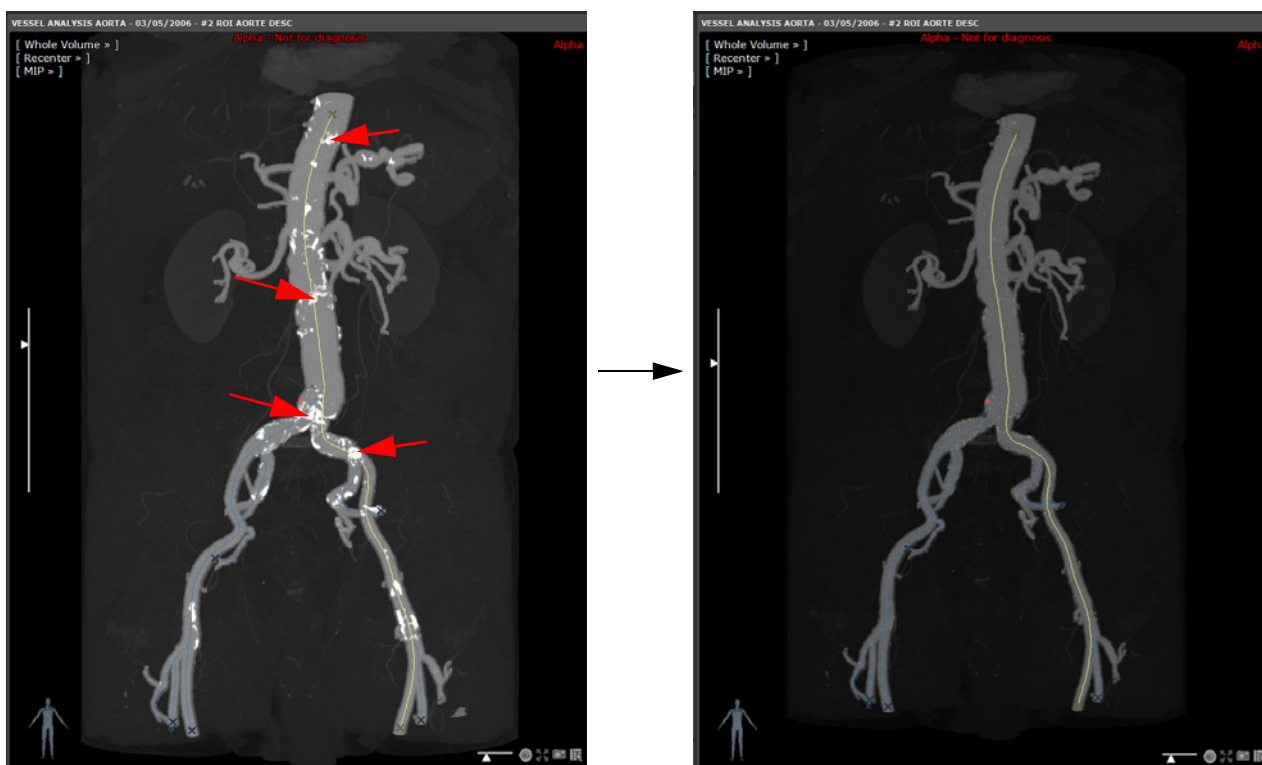



Figure 11-184 Before and after calcification masking

Calcifications are automatically masked.

However, there may be some left. In that case, you can still proceed to a manual correction:

- Zoom-in and in the Visual Selection toolbar, press 
- Simply click on the remaining calcifications on the 3D image to mask as many deposits as possible

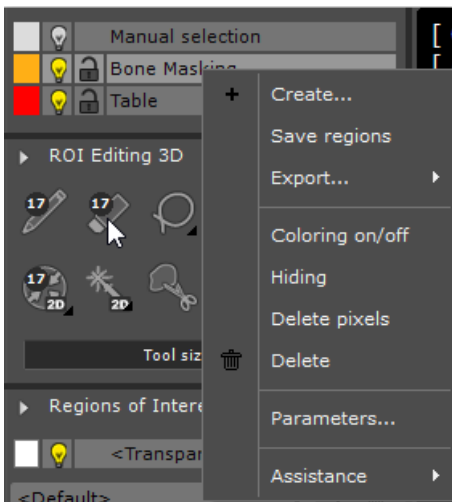


Masking ROIs can be edited using the Visual Selection toolbar as well as using ROI Editing tools.



Masking ROI display can be adjusted just as regular ROIs simply right-clicking on the corresponding entry in the ROI masking list.





Just as for regular ROIs, the colored square displays the default ROI color (in 2D viewports only) while the light bulb enables to show/hide the ROI voxels (in 2D viewports) and the padlock allows the modification of the ROI lock status.

Each of these masking ROIs can be visualized individually in 2D or 3D viewports.

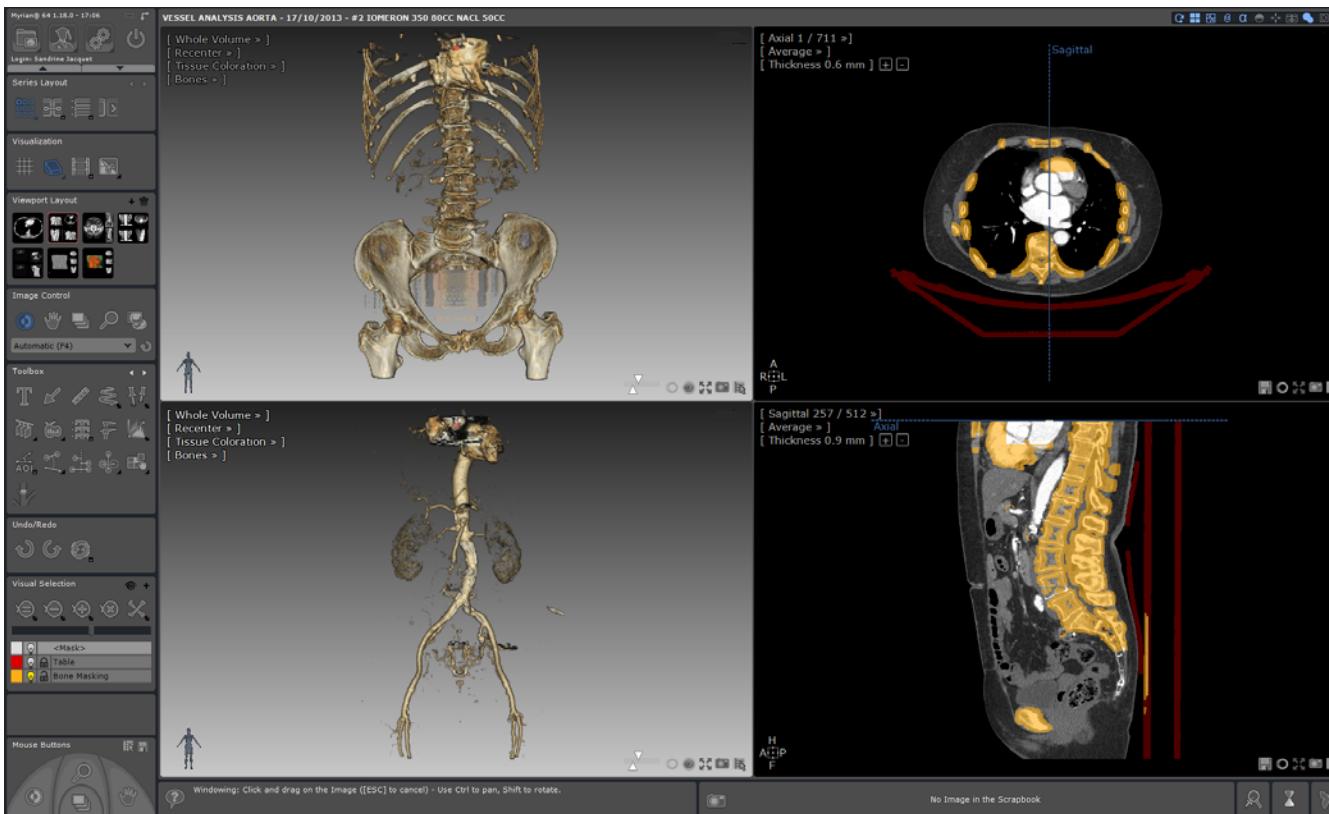


Figure 11-185 Masking ROIs displayed on 2D/3D viewports

### 11.9.3.2 Masking ROI display mode

Visual selection is displayed in 3D viewports only.

You can, in each viewport, independently select:

- The current volume (always displayed in 2D viewports)
- Any of the existing masking ROIs.

For example, you can choose to display:

- A 2D viewport with the volume including the Bone masking ROI
- A 3D viewport with the volume alone
- A 3D viewport displaying the bone masking ROI only



By default, all viewports show the current volume only. The display mode may be changed in each viewport.

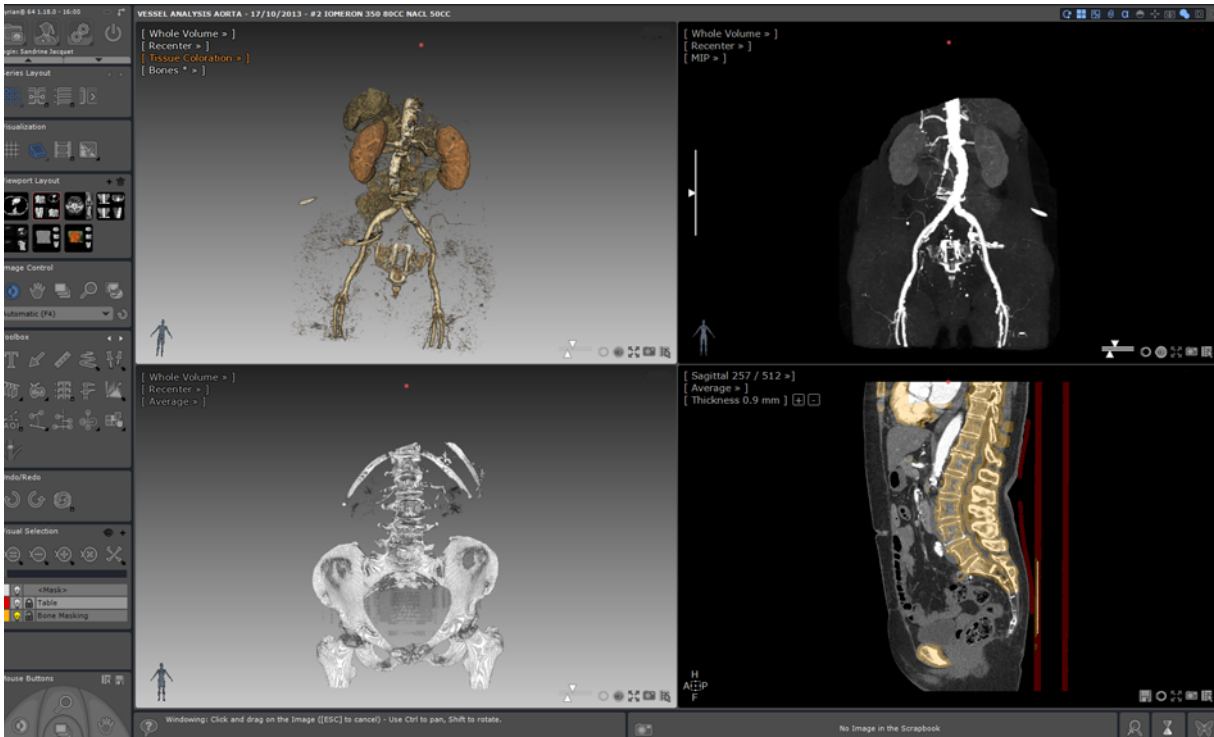


Figure 11-186 Visual selection/Bone Masking/MIP (3D viewports) and Bone and Table masking ROIs in the 2D viewport

### In a 2D viewport

Obviously, the volume is always displayed in all 2D viewports.

Masking ROIs can be visualized like any other 'regular' ROIs (see Figure 11-186).

You can activate the coloration of each masking ROI clicking on its respective colored square in the masking ROI list.

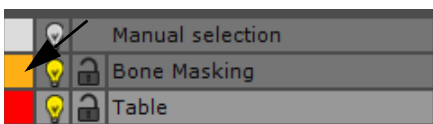


Figure 11-187 Activating masking ROI coloration

As for any other ROIs:

- Left-click on the colored square to toggle the coloration status of the ROI
- Right-click on the colored square to open the Color level slider and move the slider to the desired color level



Figure 11-188 ROI color opacity slider

- Left-click on the bulb to toggle the ROI visibility.
- Right-click on the bulb to open the visibility level slider and move the slider to the desired visibility level



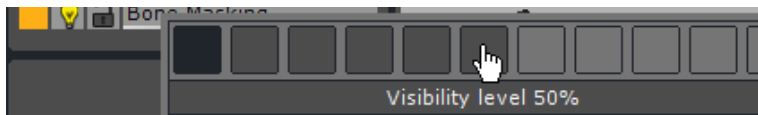


Figure 11-189 ROI transparency slider




When the ROI opacity level is changed, all 2D viewports are updated to reflect those changes.

### In a 3D viewport

In 3D viewports, you can choose to:

- Show/hide the volume
- Show/hide each masking ROI
- Change the visualization mode of the visual selection.
- Modify the transparency level of the masking ROIs

By default, all viewports only show the current volume.

You can change the Visual Selection display mode clicking  at the bottom-right of the 3D viewport. This dedicated viewport button opens the following visual selection visualization mode menu:

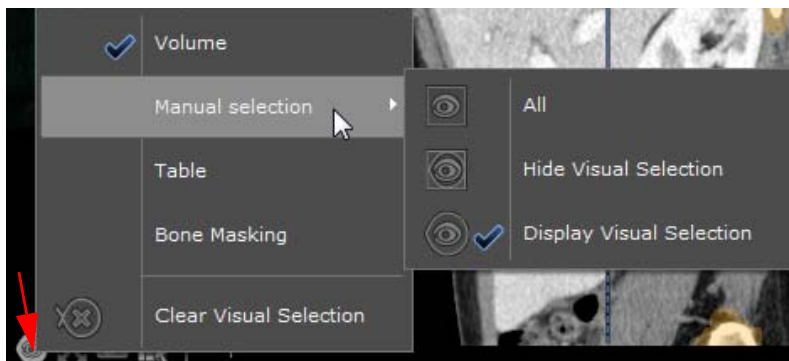


Figure 11-190 Mask visualization mode menu



Press the V key as a shortcut to toggle between Hide/Display Visual Selection only mode.



Only available masking ROIs appear in the menu. If no masking ROI is created, only the Mask menu as illustrated here-above is displayed. If, on the other hand, a Table and/or a Bone masking ROI are created, they will be displayed in the visualization menu as a result.

- **Volume:** Show/hide the current volume.



This option is shown only if one masking ROI at least has been created.

- **Table, Bone masking:** Show/hide individually each masking ROI

Each item in the menu can be checked/unchecked. Upon opening, the menu always reflects the current viewport configuration.

- **Manual Selection:** Open the specific visual mask submenu.

Each item allows selecting the visualization mode of the visual selection.



Mask visibility/transparency, which relates to 3D viewports only, cannot be changed individually for each 3D viewport. The visualization mode is updated in all 3D viewports simultaneously.

- To modify the balance of visibility/transparency of the currently selected Masking ROI on a 3D viewport, use the Transparency Slider above the masking ROI list in the Visual Selection toolbar.

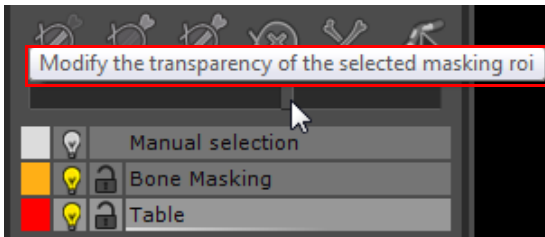


Figure 11-191 Mask Transparency slider (Bone Masking ROI selected)



Bone masking transparency is independent of ROI coloring.



By default, Masking ROIs are created with a visibility set to 100%. To decrease visibility level on 3D viewport, move the slider from right to left.

#### 11.9.4 Use case scenario: example of visual selection and bone masking


- Load appropriate series in Generic MPR 3D mode (in Whole Volume or MIP rendering),



In the Image Control toolbox, use the windowing tool and/or select the appropriate Windowing presets for an optimal visualization of the preferred structure.




Note that the Visual Selection is initialized with the whole volume.

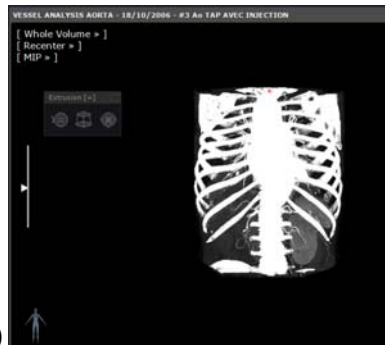
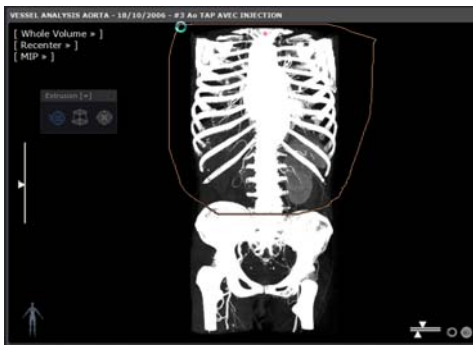
- **Predefine** a Volume preselection pressing the 'Preserve as Visual Selection' button  in the Visual Selection Toolbar,
- **Create one extrusion contour** in the relevant 2D (oblique plane of view included)/3D viewport to define the part of the image **you wish to isolate**.





The Extrusion floating toolbar automatically appears displaying the selected current mode.

- Press the 'Launch Extrusion' button  (when the contour is defined in the 2D viewport only).

As soon as the mouse button is released, the 3D viewport is updated accordingly.



1) 2) Figure 11-192 Drawing a contour in the 3D viewport to chisel out a zone of interest before launching extrusion (Preserve mode).

- **Activate** the required sculpting mode clicking on the relevant button,  or  to improve your Visual Selection if needed,
- Launch the bone and/or table masking if required,

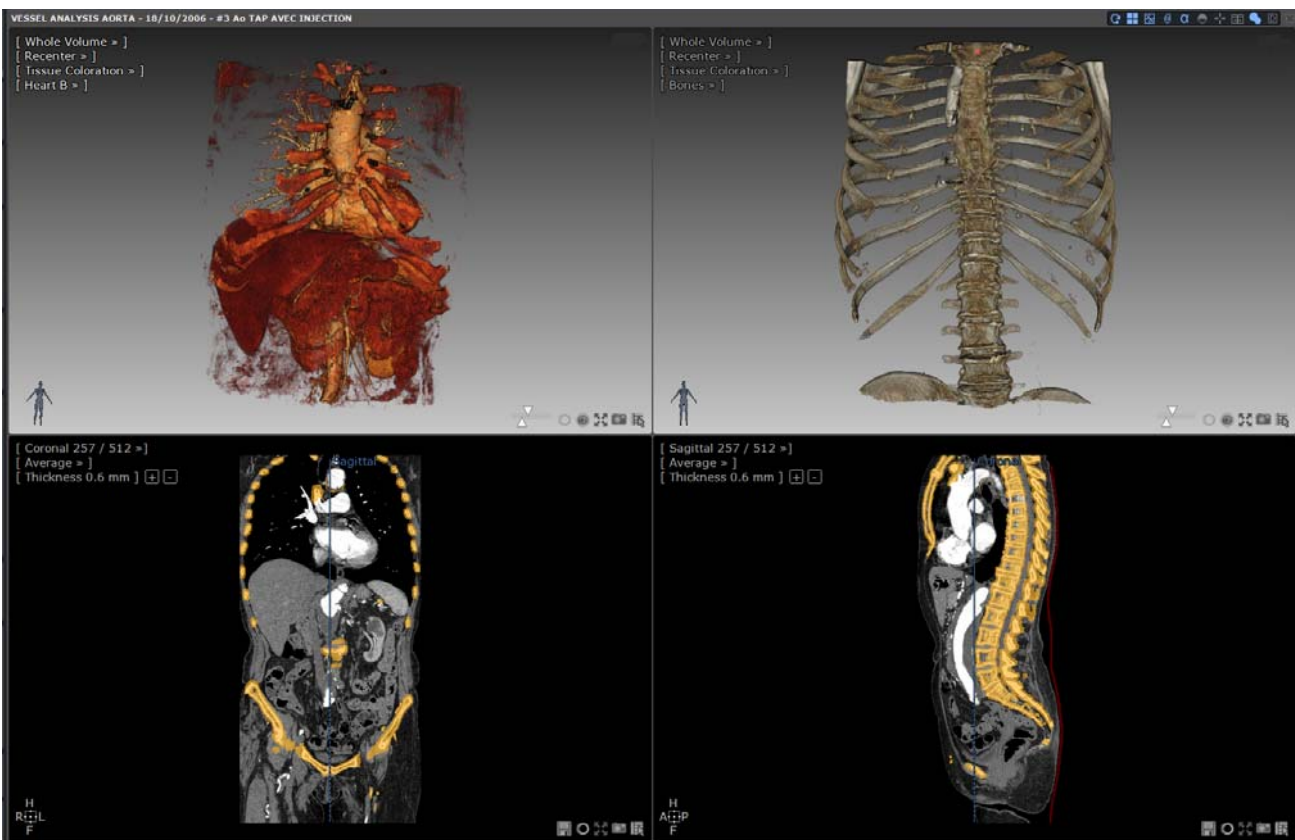




Figure 11-193 Visual selection of the heart and bone masking in respective 3D viewports



At anytime, you may delete all contours previously defined by clicking the 'Clear Visual Selection' button .



You can use the Undo/Redo tab to restore visual selection actions (up to four)

- Click on the 'Visual Selection' status icon  to access the following menu enabling you to switch from one Visual Selection display mode to another.

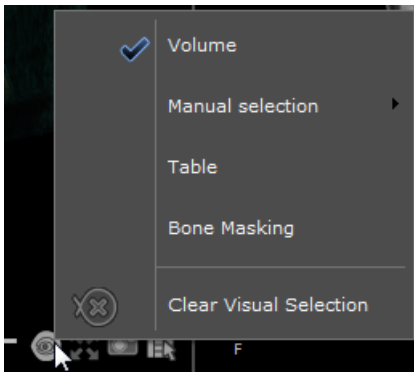


Figure 11-194 Available Visual Selection display modes

- Assess the rendering before manually proceed to possible corrections (see next section)



All Visual Selection contours are automatically saved when a session is closed and reappear when a session is reopened.




Masks might hide some important parts in a Study. Be sure to check the Visual Selection status icon at the bottom-right corner of any view before making a diagnosis.

### 11.9.5 Interactive Bone/Vessel masking adjustment in 2D/3D



This functionality (described in Section 11.9.2.5) enables you to manually adjust automatic bone masking **previously performed** when incomplete or erroneous.

This tool can be used either in **2D or 3D viewports**.

- Click  to open the Bone masking correction floating toolbar (see Figure 11-178) and access to all the corrective tools available.

#### 11.9.5.1 Using the Manual Bone Masking tool



This tool allows you to add/remove bone fragments to/from the Bone Mask. Depending on your action, it can either work as a **one-click** or as a **progressive** tool.


Bone fragment which has not been included in the Bone Mask and that is therefore visible in the visual selection



Figure 11-195 3D Visual Selection display with bone fragment remaining after automatic bone masking.

### One-click correction

To add to the Bone Mask:

- Identify bone fragments remaining on the 3D viewport (Whole Volume or MIP mode)
- Select the manual bone masking tool 
- Click and release the mouse button on the remaining bone fragment on either the 2D or 3D viewports

The bone correction engine launches automatically and hides the bone fragment from the Visual Selection and add it to the Bone Masking if it exists or to the selected Masking ROI otherwise. All viewports are immediately updated accordingly.

To remove from the Bone mask:

- Change Mask display mode to display Bone Mask only.
- Click on a connex bone masking region to remove it from the bone masking.

The clicked bone fragment is removed from the Bone Masking and automatically added to the Visual Selection.

- Switch to the visible view (masked bones) and assess the rendering.
- Repeat the same process until achieving the intended masking result.

### Progressive correction

As for the one-click bone correction tool, the bone progressive correction can either be used to add to or to remove from the Bone Mask.

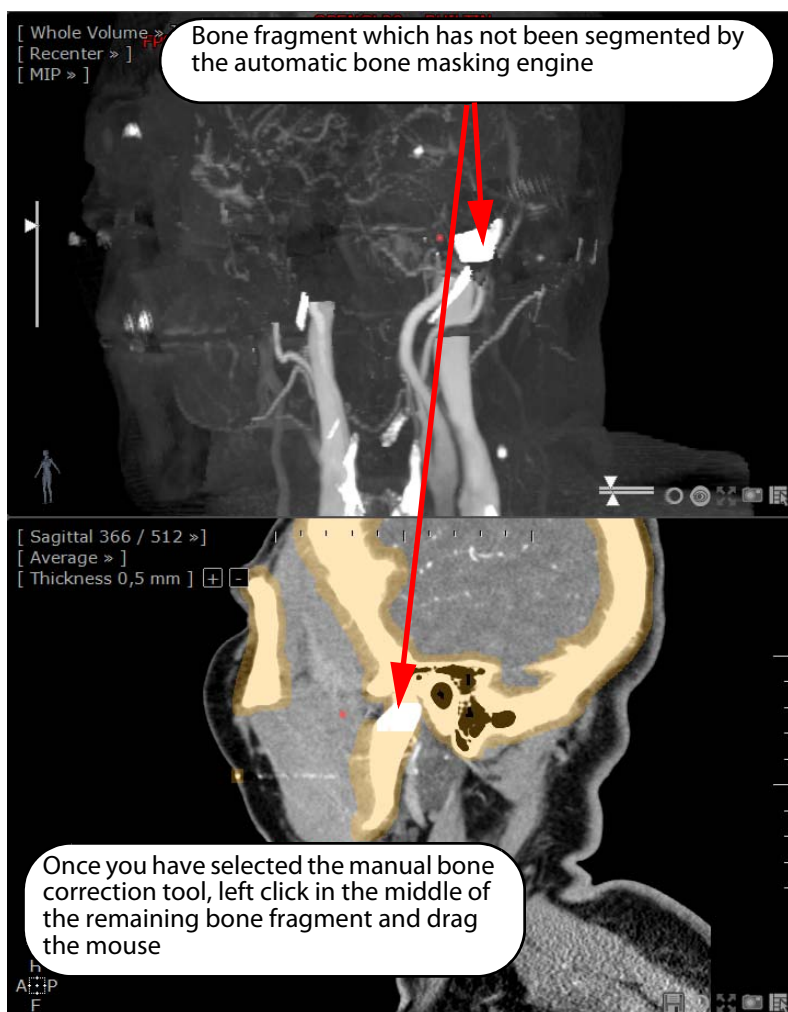


Figure 11-196 Removing a remaining bone fragment from the visual selection (MIP view): the 3D viewport shows the Visual Selection only while the 2D viewport shows the colored bone ROI.

- Press the left mouse button at the initial point of the remaining bone fragment and keep it down while dragging the mouse on the required region.

You can **drag the mouse forward and backward** to adjust accurately the region to select.



The mouse drag on the region is highlighted in blue with ROI growing/shrinking visual feedback on all viewports.



The bone correction engine launches in an incremental way (blue display on the 3D view), showing the result of the segmentation for each step. The display is refreshed continuously to visualize the current result in real-time:

- In 2D viewports, impacted voxels are shown with the ROI color when adding voxels to the mask, or lose their ROI color when removing voxels from the mask.
- In 3D viewports, impacted voxels are displayed in blue to show the region growing, whatever the action (adding or removing voxels).

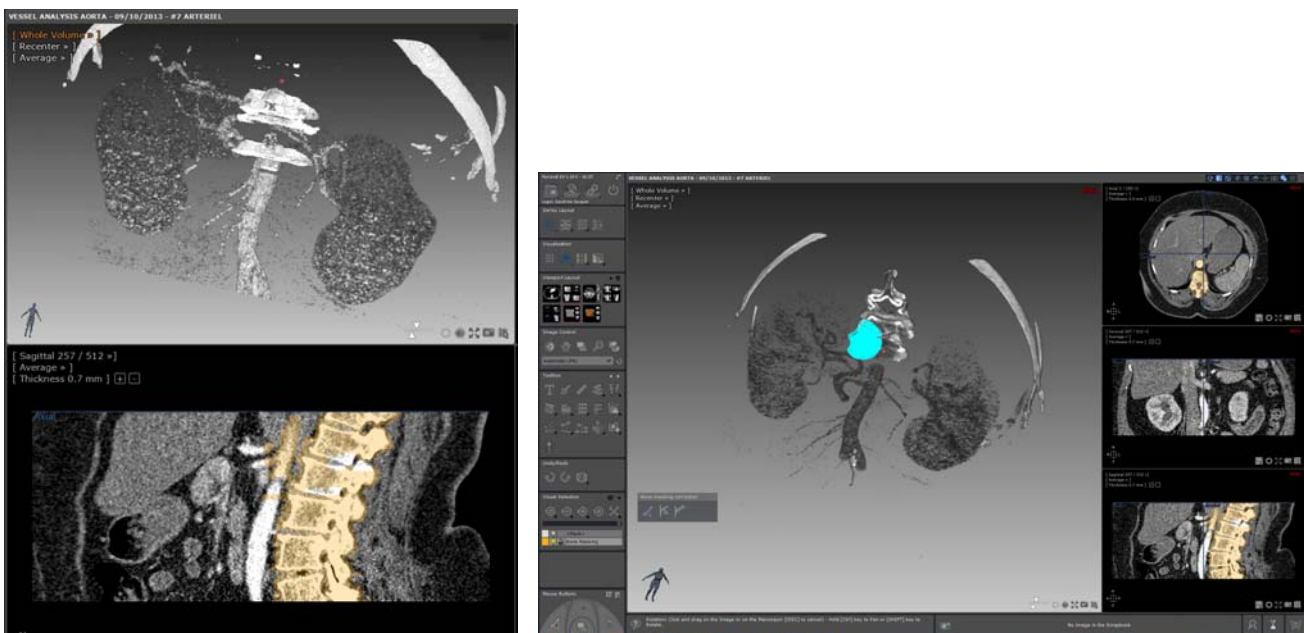


Figure 11-197 Correction of the bone masking using the bone progressive correction tool (the clicked region represented in blue is to be added to the Bone mask)

- Once the left mouse button is released, the currently displayed region is added to or removed from the current masking ROI.

The 3D and 2D viewport (only if the coloration of the Bone Masking ROI is activated) display is refreshed accordingly.



If you press the <Escape> key before releasing the mouse button, the segmentation is canceled.





Whatever way the tool is implemented, if the clicked bone fragment belongs to a Masking ROI, the segmentation result is removed from this ROI. On the other hand, if the clicked bone fragment belongs to the Visual Selection, the segmentation result is added to the Bone ROI if it exists, or to the selected Masking ROI otherwise.

### 11.9.5.2 Using the One-Click/Progressive Vessel tool

In case the selected bone masking includes regions that should not (i.e. vessels), you can still perform a **manual correction** clicking either in the **3D** or the **2D**.




This tool  enables to remove pieces of a vessel from a target mask.


 The target mask is set to the Bone mask if it exists, otherwise to the user selected mask.

As for the bone segmentation tool, depending on your action, the segmentation launches locally (via a single click) or in a progressive way (via click-and-drag).

However, the result is always removed from the Bone Mask whatever the starting point.

### 11.9.5.3 Using the Two-Click Vessel tool

 A step-by-step wizard guides you through the process.

This semi-automatic vessel correction tool  enables the reconstruction of a vessel using seed points from either the bone mask or the visual selection.

- Select the Vessel correction (multi-click) tool

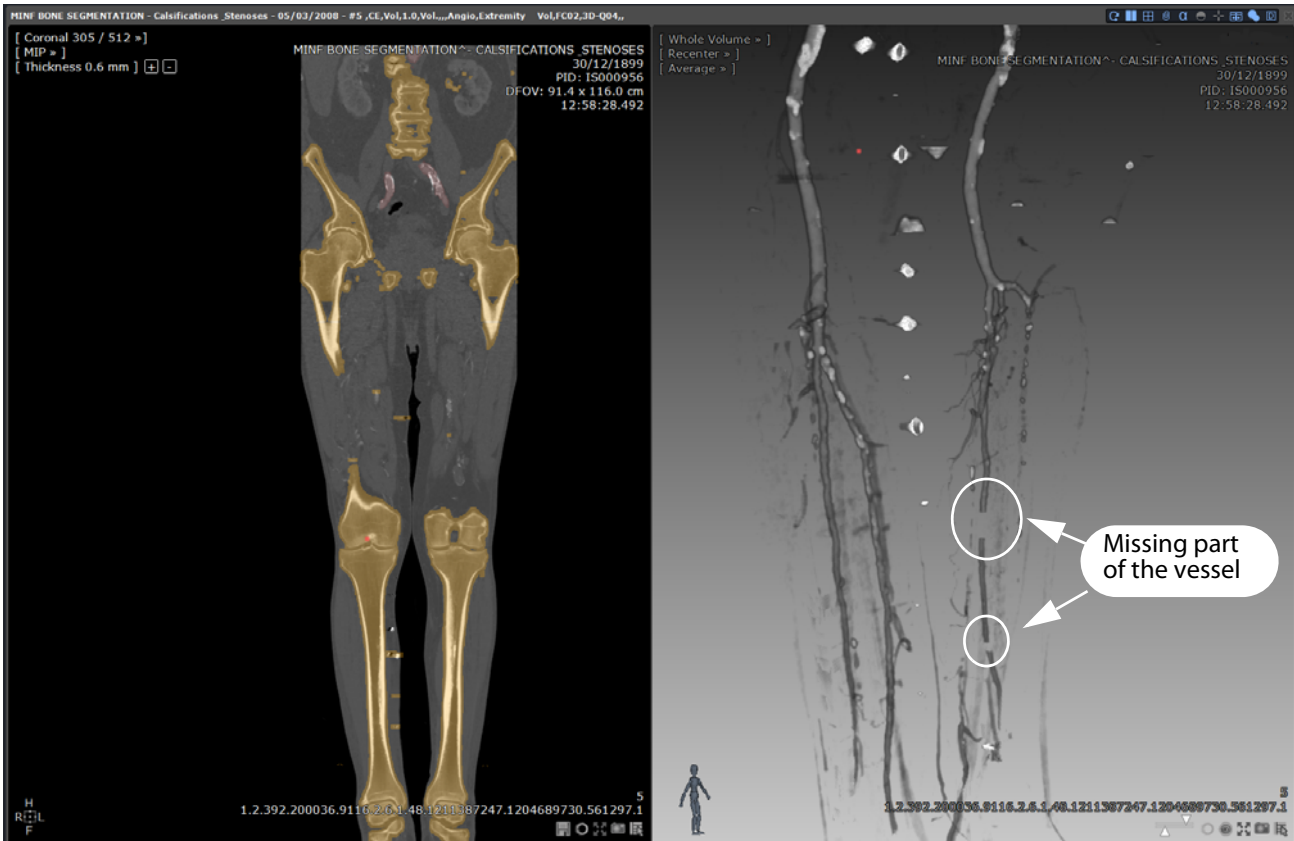


Figure 11-198 Missing part of a lower limb vessel identified on the 3D Whole Volume view

- Locate and click two seed points (either on 2D or 3D viewport) on each extremity of the missing vessel

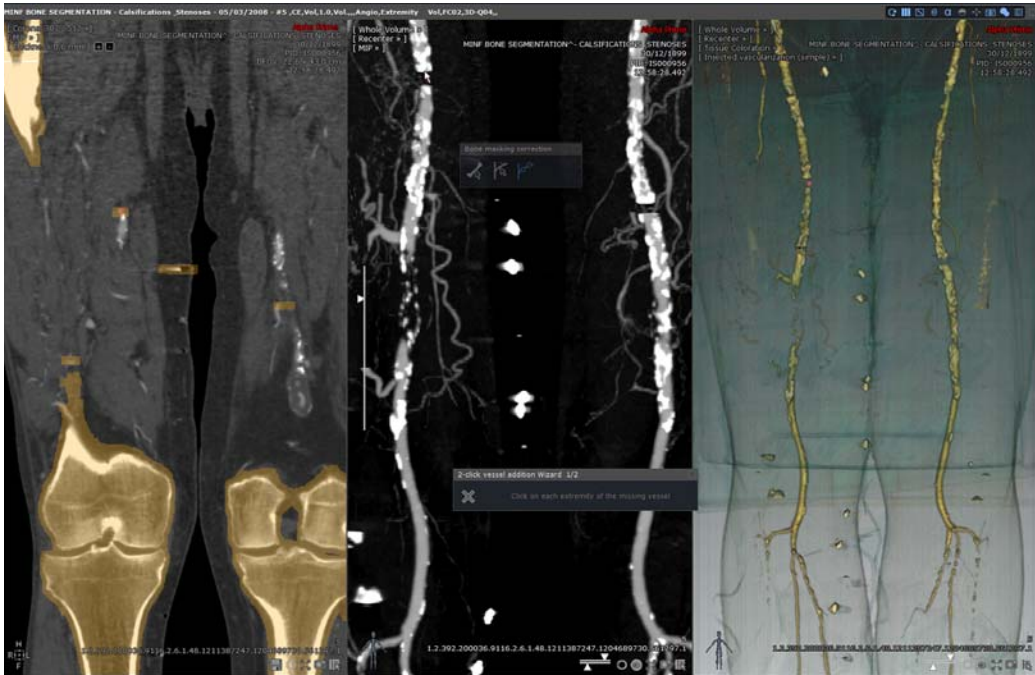


Figure 11-199 Correcting the erroneous segmentation of the bone mask by restoring the missing part of the vessel

The missing part of the vessel is automatically reconstructed between the two seed points. The corresponding region is removed from the Bone Mask if it exists (or from the current mask) and added to the Visual Selection.

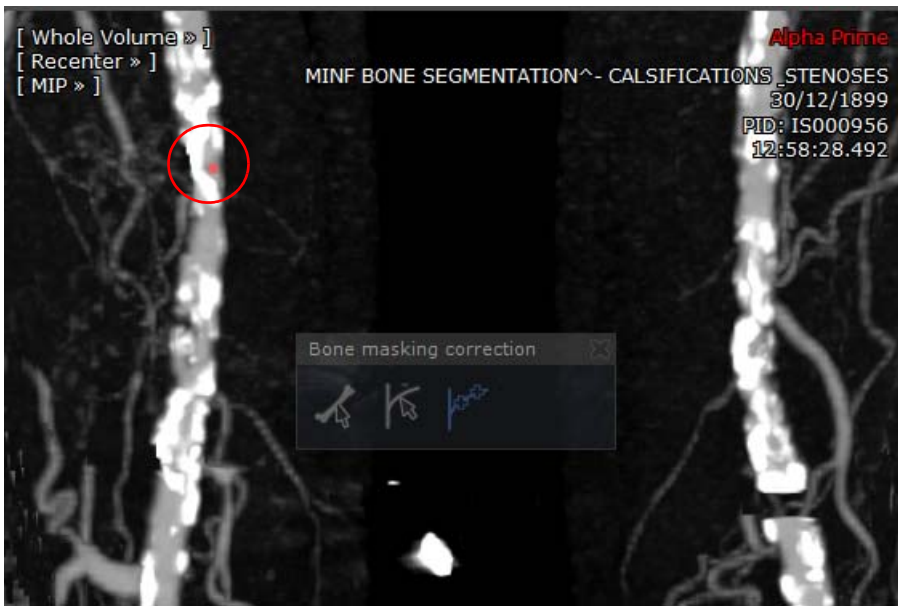


Figure 11-200 Visualization of the corrected segmentation of the vessel in 3D viewports



In 2D viewports, the two seed points can be located on different slices.

## 11.10 Undo/Redo bar

The Undo/Redo bar enables you to cancel or restore any action you have carried out. A commands history button



enables you to see the list of actions carried out in the course of the current session.




Figure 11-201 Undo/Redo bar

## 11.11 Mouse-button function settings and profiles

### 11.11.1 Primary and Secondary Tools

The Primary Tools are the Image Controls:


- Windowing 
- Translation 
- Zooming 
- Navigation 

The Secondary Tools cover all the remaining functions, such as making Annotations and Measurements.

#### Behavior

Both Primary and Secondary Tools remain assigned to a mouse button until another tool is assigned to this same button. By default, Secondary Tool mouse button assignments revert to the last assigned Image Control Function when the 'ESC' ('Escape') key is pressed.

You can configure the Secondary Tool Mouse button assignment function to revert to the last assigned Image Control automatically after the first release of the mouse-button:

-  Select the 'Preferences' tab
- Select the 'Display' tab
- Locate the 'Miscellaneous' area at bottom of the tab
- Check the 'Auto-revert to Image Controls' checkbox



You can cycle from one Primary Tool to another by pressing the Spacebar of your keyboard in this order: Windowing, Zoom, Pan, Navigation (reverse order: SHIFT+ Spacebar).

---

### 11.11.2 Factory mouse profiles

By default, the applied mouse button profile is the default configuration.

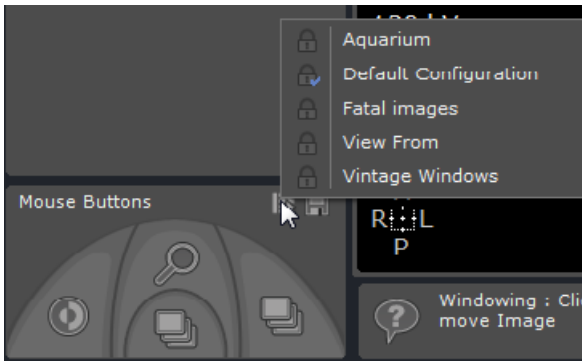



Figure 11-202 Available factory mouse profiles

- If you wish to switch from the mouse default configuration to another mouse factory profile, click on the  icon and select a mouse button profile among those listed.

### 11.11.3 Modifying a factory mouse profile

You can modify any factory mouse profile as you wish.

- Assign any tool to any of the mouse-buttons by simply clicking with the desired mouse-button on the tool you wish to assign it to, or
- Click with the corresponding mouse button on the Mouse illustration at the bottom of the Toolchest to select (with the left mouse button) your choice from a tool contextual menu.

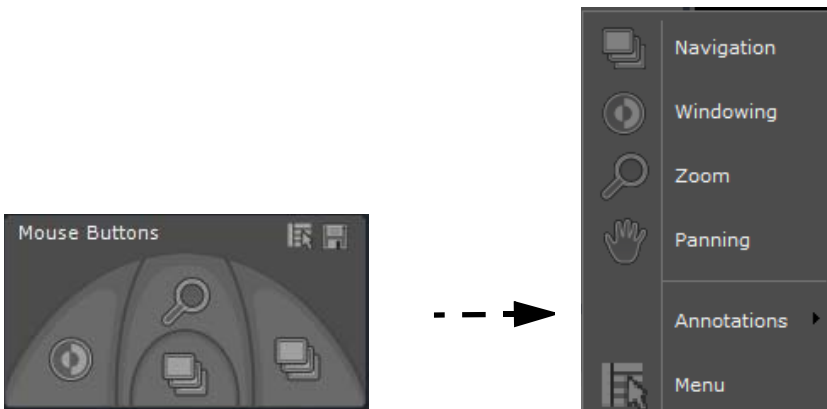

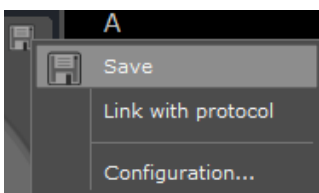


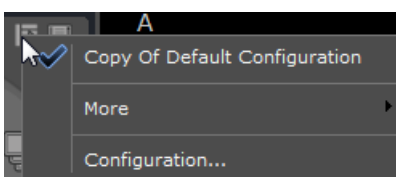
Figure 11-203 Modifying mouse profile

- To save it, click on the disk icon  then select 'Save' from the resulting contextual menu.



This customized profile becomes the default configuration profile and is automatically:

- Updated with the new added tools when opening a view in the workspace
- Named 'Copy of (factory name)'

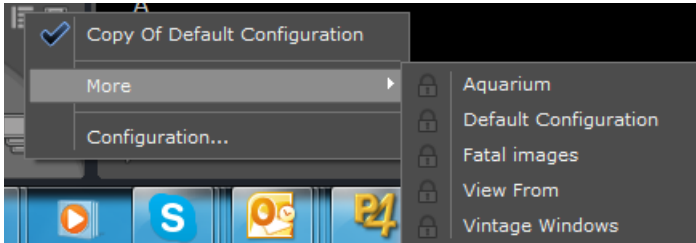




You can rename this 'Copy of (factory name)' profile via the 'Configuration...' button.



To switch from the customized mouse profile to one of the existing factory mouse profiles, click on 'More' to display the mouse profile list.



### 11.11.4 Creation and edition of a mouse button profile

- Click on 'Configuration...' from the mouse profile contextual menu to open the Mouse Profile Editor.

The following configuration window opens:

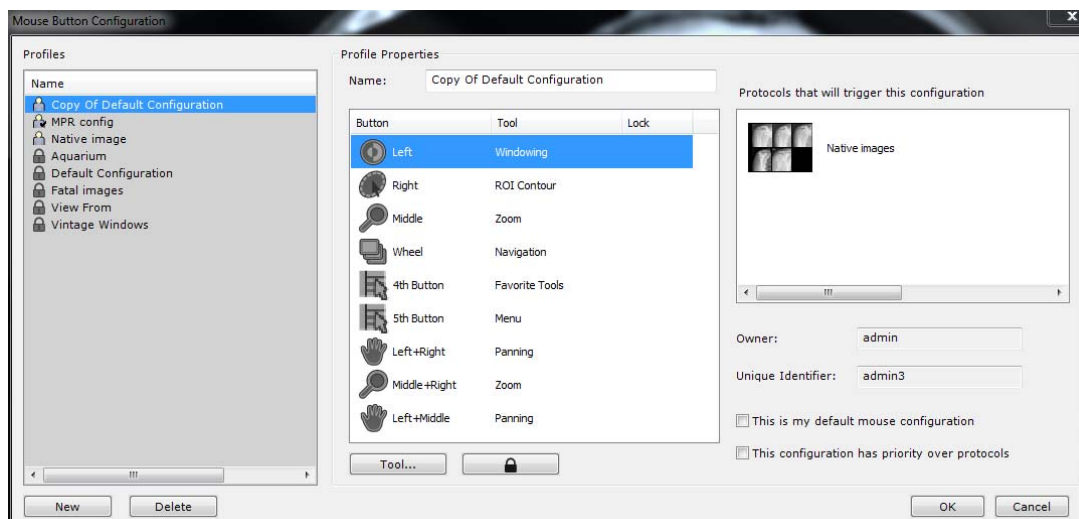
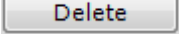




Figure 11-204 Mouse button configuration window



Factory mouse profiles (represented by the padlock icon ) **cannot be edited nor deleted.**

Only user-defined mouse profiles can be removed clicking .



A user-defined mouse profile can be identified by its user icon  (in the above illustration, it is displayed beside the Copy of Default Configuration profile) instead a padlock. Additionally, a checkmark  is displayed over the user icon whenever it is the current default configuration.

- Click 
- Rename this new mouse profile in the Name field

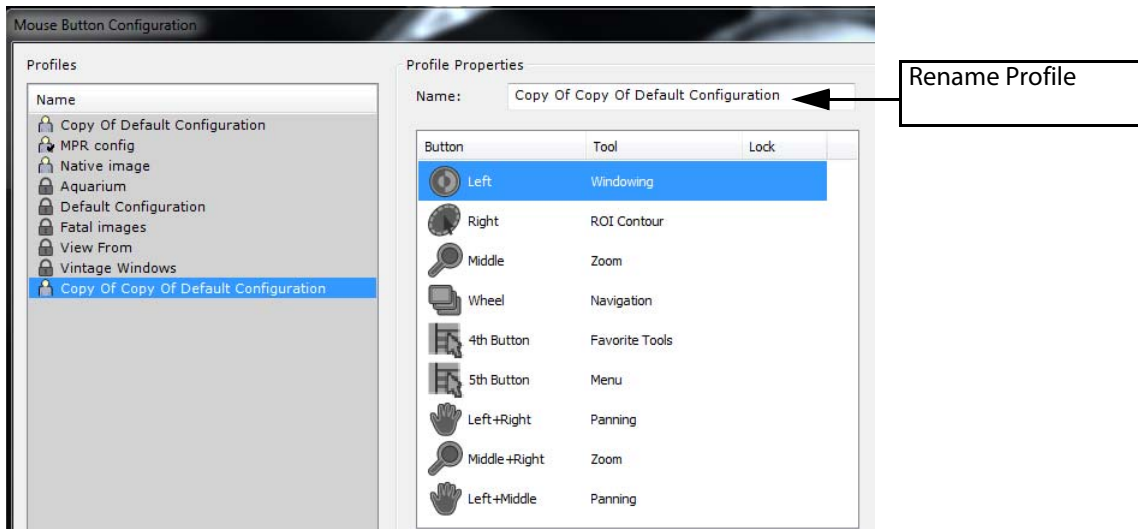


Figure 11-205 Create New Mouse profile

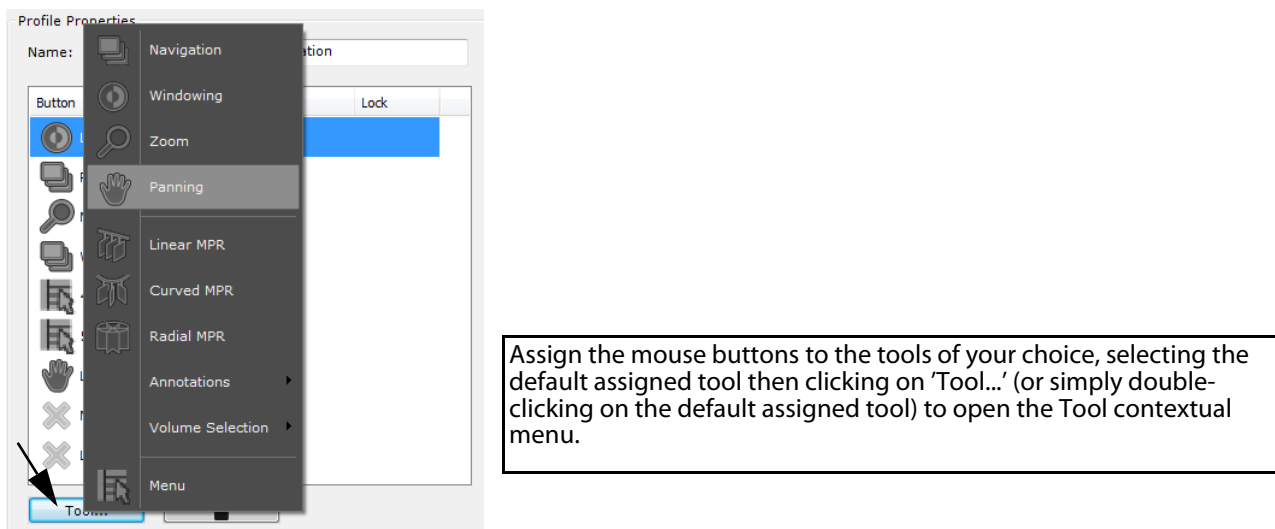
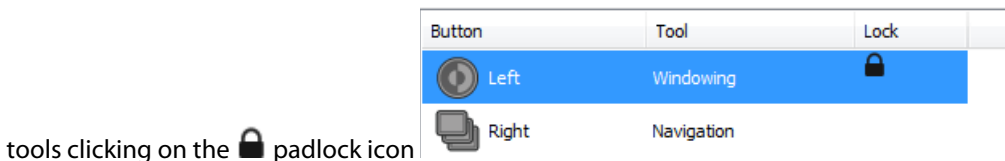


Figure 11-206 Assign specific functions to your mouse profile



To prevent any modification of the button assignment in a given mouse button profile, you can lock any of those



tools clicking on the padlock icon

- Define the following profile properties:

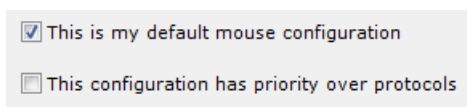


Figure 11-207 Mouse profile properties

- Press OK to validate and close the mouse configuration window.




New tools can still be assigned to a given mouse profile at any time (but won't be saved unless clicking on the Save button ).

Right-clicking on the 'Select a mouse profile' button  will reset the tools on each button to the ones saved in the profile.

---


### 11.11.5 Associate any mouse profile to the current protocol

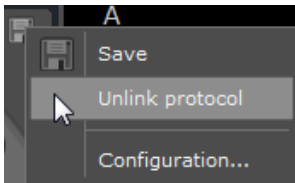
- Click on 'Link with protocol' from the disk icon  contextual menu
- 



Each time a series will be opened with this protocol, the associated mouse button profile will be the default configuration.

---

- To cancel this preselection, click again  and select 'Unlink protocol' from the contextual menu.



If a factory profile is linked to a protocol, a copy of it is automatically created and becomes the default profile.

---

The Mouse button assignment tab is at bottom of the Toolchest (or top-right when the Toolchest is set to horizontal mode).

The four icons represent the current function assigned to each mouse button.



Figure 11-208 Mouse button assignment tabs (vertical and horizontal modes)

In vertical mode (representation of a mouse), the left and right icons respectively indicate the purpose of the left and right mouse buttons. The lower middle icon represents the function assigned to the mouse wheel and the upper middle icon, the function assigned to the middle button (in most cases, clicking with the mouse wheel itself).

In horizontal mode, each function is labeled with its corresponding button

You may customize the mouse and wheel button assignment in two ways:

- 1 Click on a command button using the left, middle or right mouse button that you would like to assign to that function.
  - 2 Click on the icon of the mouse button of your choice in the assignment tab and choose the tool you wish to assign to it from a context menu.
- 



The mouse wheel may only be assigned to navigational or zooming functions through the context menu.

---

### 11.11.6 Mouse button double-click

Irrespective of previous mouse button settings, double-clicking with the mouse button on a viewport displayed on the main Workspace enables you to perform the following actions:

- Double-clicking with the **right-mouse button** enables to locate the anatomical center under the mouse cursor.

- Double-clicking with the **left-mouse button** enables to reframe the viewport in **full screen mode**



Double-clicking again on the enlarged viewport will restore the workspace layout.

### 11.11.7 QuickTools



This feature requires a 5-button Mouse.

The QuickTools feature enables you to configure sets of favorite Tools. You can customize your own palettes which you can then call up at any time during a Series review on a floating Toolbox.

When a Series is open in the Main Workspace, press the '**Q**' **shortcut key** to open the QuickTools Toolbox.

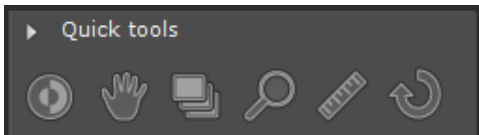




Figure 11-209 QuickTools floating toolbox



If you have used any tools before calling up the QuickTools Toolbox, a 'Recent' palette displays the 3 most recently used tools.



Use the "Forward"  and "Back"  arrows at the top of the QuickTools Toolbox to cycle through the various existing palettes.



By default, there are 3 available QuickTools Palettes: 1 Image Control and 2 Measurement palettes.

- Click on the 'Create New Palette button '+' at the top-right of the Palette to open the Palette Configuration Window

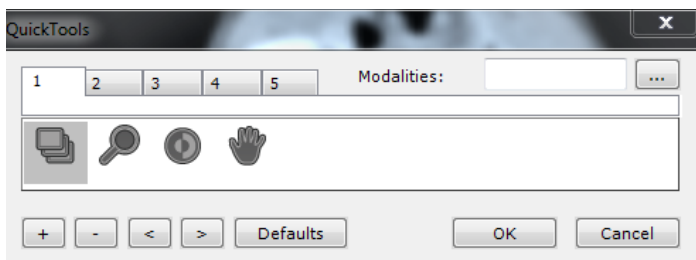


Figure 11-210 QuickTools Palette Editor

The QuickTools Palette Editor enables you to create up to 5 different palettes, each of which is represented by a separate tab.



Tabs are numbered 1 to 5.






- Click on the 'Add Tool' button  at the bottom-left of the Editor to open the Mouse Tool Context Menu and choose items from this menu



Figure 11-211 Tools context Menu

- Remove elements from the Palettes using the 'Remove Selected Tool' button  beside the Add Tool button,
- Rearrange the order of the tools by using the 'Move Left/Right' buttons   to the right of the Add/Remove buttons

You can define a list of modalities for which each set is designed:

- Click on the Browse button  at right of the 'Modalities' field (at the top-right of the QuickTools Editor)
- Select desired modality (ies)

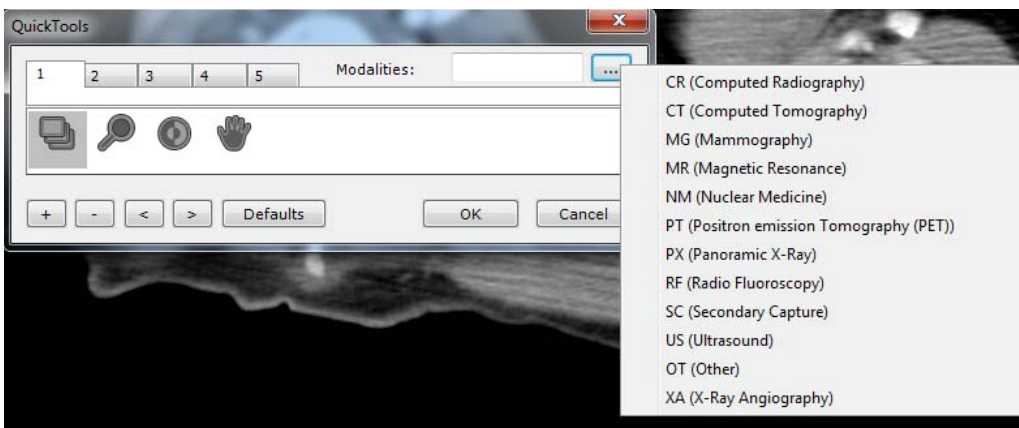


Figure 11-212 Select applicable modalities for current palette



The modalities can be further edited directly in the 'Modalities' field.

---



If any modalities have been defined when the QuickTools palette opens it will default to the set that matches the modality in the active viewport.

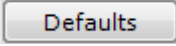
---



You can use the mouse wheel to cycle through the sets.

---




Click  to restore factory settings.

---

## 11.12 Save your workspace

### 11.12.1 Overview



The 'Workspace saved states' feature  at the bottom-right of the information panel enables you to record the state of your workspace **at a given time for any given study**.

---



This feature is available for any protocol (including in Structured Reading mode) with the exception of Follow-Up views. Therefore, if one of the view is a follow-up, the icon will be masked.


---



In the case of protocols in which volumes can be calculated (via a Volume Processor referred to as VOP), the Save State feature is disabled except when computations are unchecked and/or already precomputed volumes are loaded. The Prostate protocol which includes parametric map computation is the perfect illustration of this case.

---



The feature is disabled when the icon  is displayed without the **+** symbol next to it.

---

The backup includes all the following elements:

- Loaded series in the workspace,
- 



There might be more than one series belonging to more than one exam open in the workspace.

---

- Workspace layout and series location in the workspace, including multiple pages and multi-monitor,
- Application protocols being used for each view,
- Active view,
- Viewport layouts of each open view, (same as the feature used to Capture a Layout Protocol),
- Rendering, orientation and panning of each viewport,

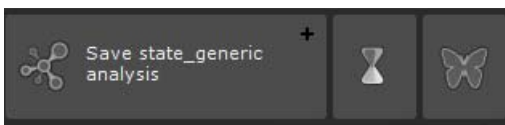


- Anatomical center synchronization between the open series,
- Activated synchronization options,
- Global panel settings (panel on top, left, toolbars visible or not, etc.),
- Visible toolbars and tools for each view,
- Selected 2D and 3D ROI, as well as selected ROI set,
- Selected/displayed annotation (if any),
- Status of the scenario in progress (if any),
- Any additional data stored by add-ons (custom viewports, CRF),
- Content of the categories being used (even modified upon initial loading),
- ROI, annotations, masks (zoning),
- Position of the anatomical center.

When reopening a saved state, all these data are automatically restored in the workspace.




If a saved state is currently loaded in the Workspace, its allocated name is displayed in the information panel



### 11.12.2 Method of use

To create a Workspace saved state:

- Click on **+** next to  so as to capture the workspace state at the convenient time for you.

The following dialog box opens:

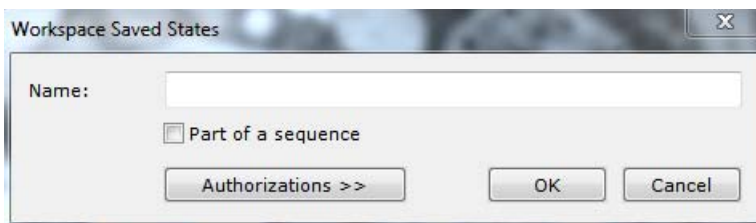


Figure 11-213 Saving a Workspace state

- Name it



When no name is specified, a default name is allocated.

- Define if this saved state will be part of a sequence by checking the 'Part of a sequence' checkbox



When creating saved states as steps of a later review, you may wish to order them in a sequence so that any potential reviewer can load them in the correct order automatically. Myrian® will parse the existing saved state list and figure out the sequence index of the new saved state. Then, when loading a study, if Myrian® is configured to load saved states automatically, the first saved state in the sequence will be loaded (instead of the most recent one). You can then navigate from one saved state to the other.

- Click on 'Authorization>>' and check the relevant Public/Private privileges to control access for Loading/Deleting a given Saved state.

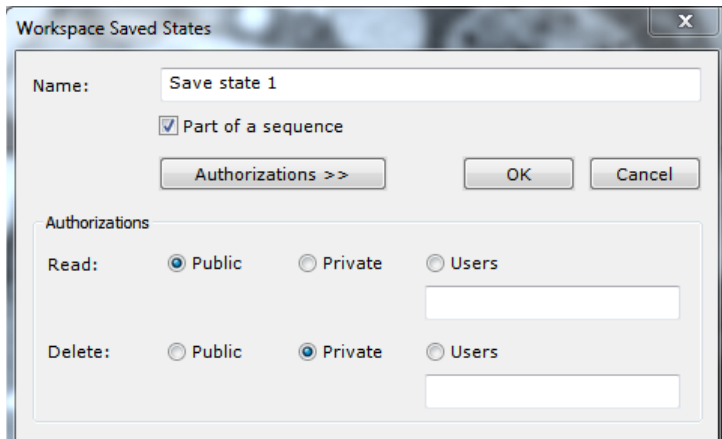



Figure 11-214 Define Workspace saved state user authorizations

- Click OK to validate

### 11.12.3 Reopening a saved state

A saved state appears as a regular series **within the study** for which it was created in the Local Study list. To distinguish it from any other series, a specific status icon  is displayed.

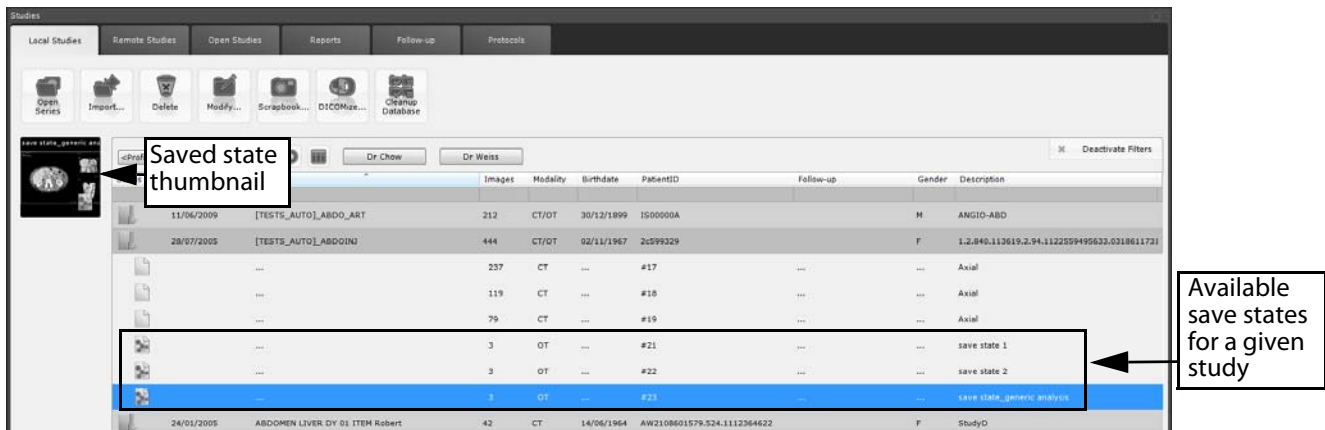




Figure 11-215 Select a saved state to load from a given study


- Double-click on the selected saved state to load it in the Workspace

 If you load one series from a study for which saved states have been created, the following icon  is displayed in the information panel to let you know that there are existing saved states for the selected study.

- Click on the Saved state toolbar to access the 'Saved state selection screen' (see Section 11.12.4).

The selected saved state is loaded in the workspace in the state it was saved previously.

### 11.12.4 Selecting a saved state from the Workspace

 If a saved state is currently loaded inside the workspace, its name is displayed on the toolbar. Otherwise, there is only the main icon and the **+** icon used to create a new saved state with the content of the workspace.

Clicking on the **saved state toolbar** opens the '**Saved state selection**' screen.

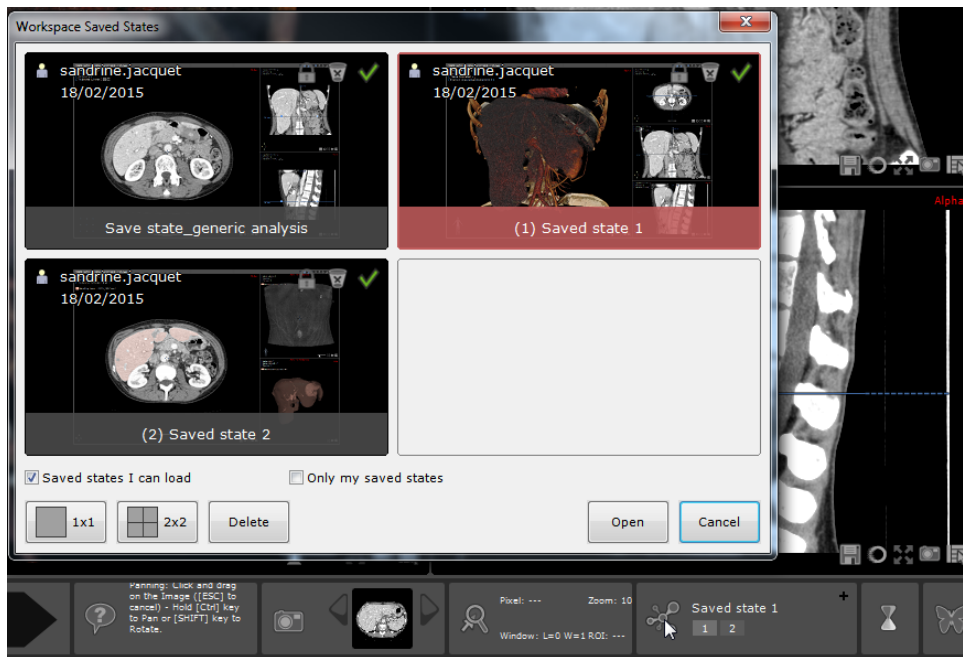


Figure 11-216 Opening the 'Saved state selection' screen



The selection screen is resizable as needed knowing that its newly-defined display is memorized in the user settings.

From this screen, you can:

- Visualize all available saved states created for one given study.
- Select a saved state and open it double-clicking on its thumbnail
- Select one or more save states and delete them

You can also opt for a 1x1 state or a 2x2 state visualization by clicking on dedicated button:

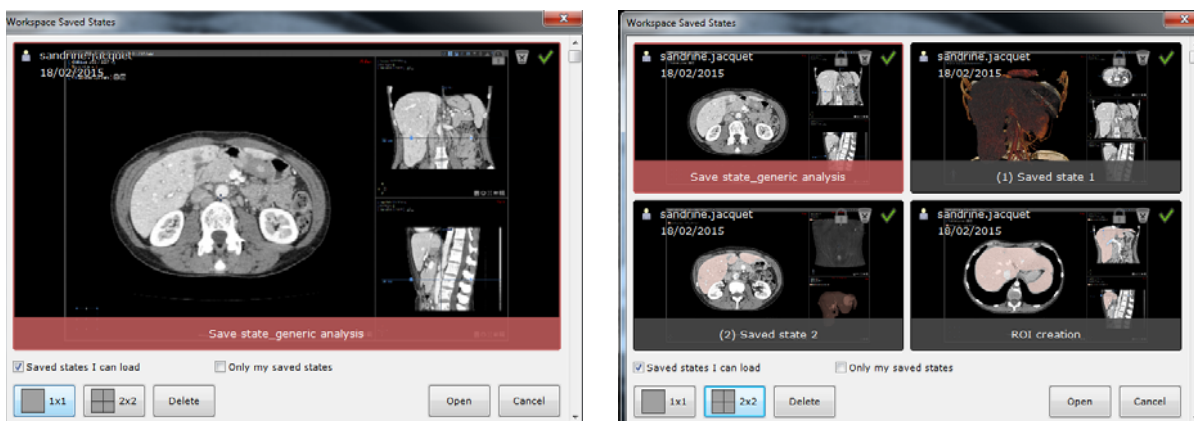
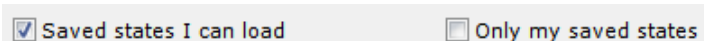




Figure 11-217 Saved state thumbnail layout

Also, you can choose to display in the 'Saved state selection' screen only the saved states for which you have the reading rights or only those you have created checking the corresponding checkbox:

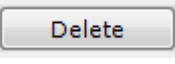


For each saved state is displayed:

- A thumbnail on which is displayed the state name, the owner's name, the creation date and the rights:
- A green check mark  if you are allowed to load it and a red cross  if not.

- A gray bin  if you are allowed to delete it, a gray bin with a red cross  if not.

To delete a saved state:

- Select the relevant state then click 

An alert message pops up for confirmation.

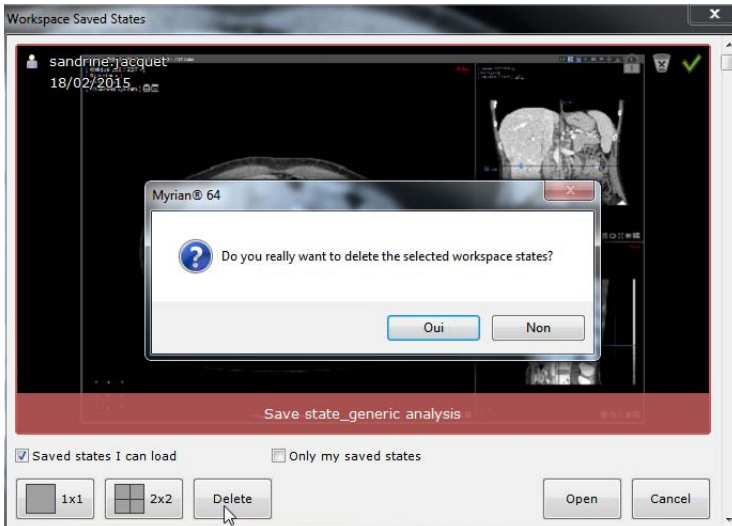



Figure 11-218 Delete a saved state

Finally, passing the mouse over the  icon enables you to visualize the authorizations for a given saved state.

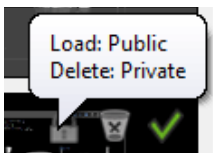


Figure 11-219 Saved state status

### 11.12.5 Options

- Go to the Preferences>Display>Miscellaneous options to activate the following settings:
  - 'Open saved states automatically' **whatever the study loading mode** (using either 'Open series' button, double-click or QuickProtocol: If saved states exist in the selected study to be opened, the first saved state of any existing sequence of a saved state is automatically loaded, and if not applicable, the most recent one is automatically open,
  - 'Create a state when closing a study': every time the workspace is closed, a new saved state is created with a default name, unless the workspace was opened to load another saved state,
  - 'Export saved states to the PACS'.

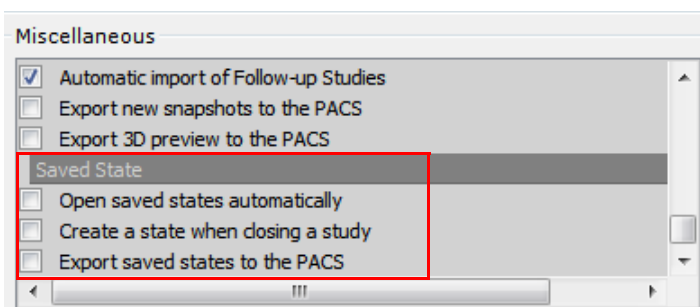


Figure 11-220 Saved state options

## Chapter 12

# 12 Scrapbook, PrintComposer, Report

### Overview

Images, Reports and Workspace parameters can be captured, stored, edited, printed and exported to/from the following modules in Myrian®:

- **Scrapbook/PrintComposer**
- **Reports** and
- **Captures** copied to other applications via the clipboard.

Images can be **printed** and **exported** in various formats.

The **Image Scrapbook/Reports tab** (in the Toolchest at the left of the main workspace) enables management of Reports and Exports as well as the Image Scrapbook for the current Series.

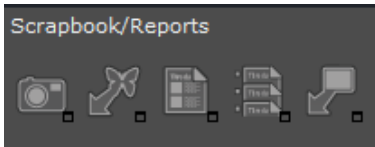


Figure 12-1 Scrapbook, Reports and Export Toolbar






Image Scrapbook and Reports tab	
Button	Function
	Opens the <b>Image Scrapbook</b>
	Export selected images to the Operating room
	<b>Creates a report</b>
	Displays the <b>list of reports for the current Study</b>
	<b>Exports the current Series</b>

Table 12-1 Scrapbook, export and report buttons

**Key images** that have been placed in the **Scrapbook** are automatically **saved from one session to another**. Each Study/Series has its own Scrapbook which reappears in the identical state it was in at the last close of session.



Only images placed in the Scrapbook can be exported to the Operating room.

**Images** are placed in the **PrintComposer** for immediate editing, arranging and printing. PrintComposer images are also saved for future sessions. You can copy/duplicate images from the Scrapbook to the PrintComposer and vice-versa.

Both the Scrapbook and the PrintComposer share a number of features:

- **User-defined Page Layout** management
- **Customizable image display adjustment** (grayscale Windowing, zoom, Pan, customizable DICOM overlay)

properties/information)

- **Management of Annotation display**
- **Single function** Windows®/DICOM **printing of all the images** in the Layout bay or Scrapbook
- **Export of images** in various formats to other media/locations



Images can easily be transferred/duplicated from one tab to the other.

---



Export to Patient CD: when creating a Patient CD, both Scrapbook and PrintComposer content is automatically copied onto the CD.

---


At the bottom-center of the main workspace under the image zone, the 'Scrapbook' panel displays the contents of the Scrapbook as a set of thumbnails



Figure 12-2 Scrapbook thumbnail bar

---



The Scrapbook is also accessible via the 'Scrapbook' preview toolbar on the bottom-center of the main workspace, or tapping the  icon in the 'Local Study' tab or even via the right-click menus in the Study List itself.

---



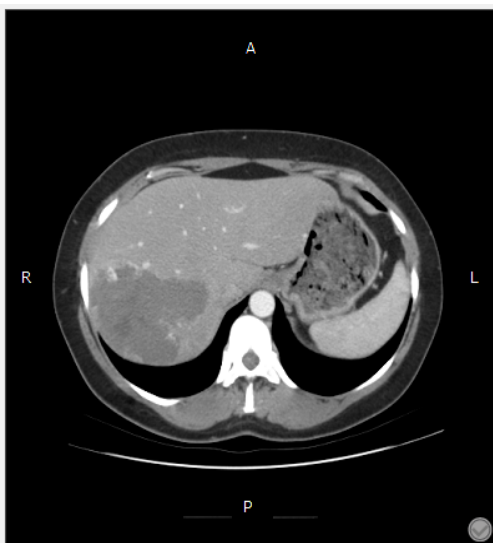
When images containing ROI volumes are captured, the latter are displayed at the bottom-right of the snapshots.

---



All orthogonal MPR images in the Scrapbook/PrintComposer bear capitals clearly marking the orientation of the patient. Orientation marks on the exported/printed or displayed images are in block capitals and appear to the left/right or above/below the images.

---



### Orientation marks:

In the Axial plane:

- A = Anterior
- P = Posterior
- R = Right
- L = Left

In the Coronal Plane:

- R = Right
- L = Left


In the Sagittal Plane:

- A = Anterior
- P = Posterior

Figure 12-3 Axial view displaying orientation marks in block capitals

## 12.1 Scrapbook and PrintComposer

### 12.1.1 Capture Menu

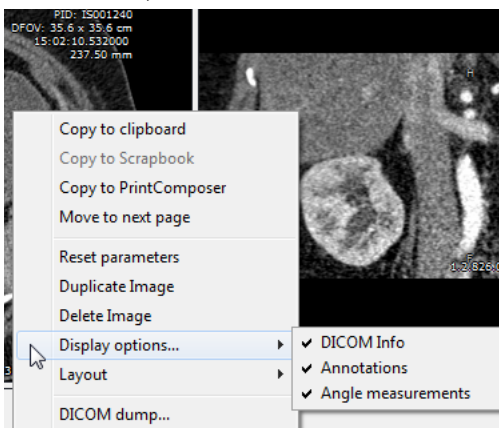
- Click  at the bottom-right of any viewport to open the Capture Menu.

The following functions are available for either Scrapbook or PrintComposer:

- **Selected Image:** Captures the active Viewport Image.
- **All images in View:** Captures all Viewport images currently displayed in the Workspace as separate images.
- **Combined Images:** Captures all Viewport images currently displayed in the Workspace combined into a single image.
- **All visible images for the Current Study:** All the viewports belonging to the active Study will be captured. If a view contains several viewports each viewport will be sent individually (not as a combined image).
- **Whole Study:** Every image contained in the whole Study to which the active Series belongs will be sent to the Scrapbook/PrintComposer in Native Mode.
- **Screen Capture:** Captures the entire Image Zone in RGB to the Scrapbook/PrintComposer and to the Windows® Clipboard.



Images in Grayscale are captured in their native format and cannot be further edited once placed in any of the modules. Only Text, Arrow and Measurement Segment annotations and DICOM information display can be managed.



If the Modality of acquisition is natively in RGB (US, SC, etc.), all ROIs, Annotations and Annotations of Interest are automatically included in captures to the Scrapbook/PrintComposer although their display cannot be further edited.



If the Album/PrintComposer contains any images at the time of 'Whole Study' capture, a prompt screen will appear to ask you whether or not you wish to empty it.



If the PrintComposer contains more than 32 images, you will be prompted that the process might take some time.

Additionally, the Capture Menu gives you the possibility to save the current image to a location of your choice or to copy it to the Clipboard in order to be able to paste it directly into another compatible application.

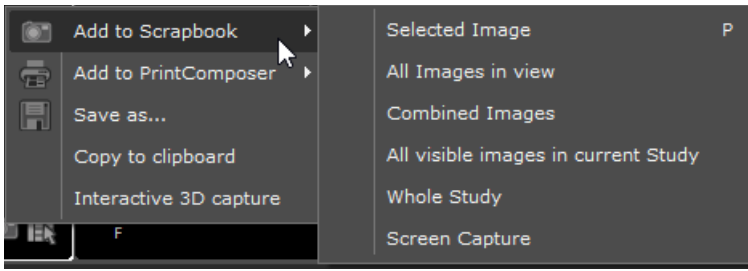


Figure 12-4 Scrapbook Capture Menu

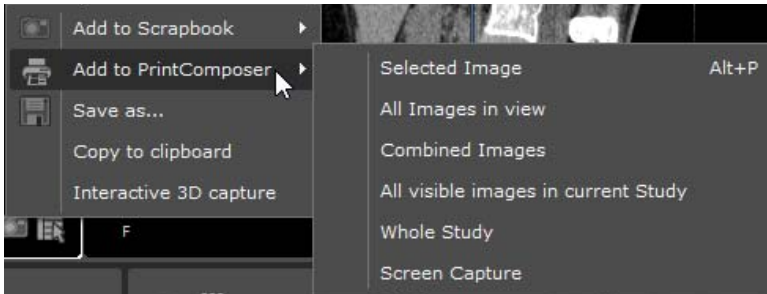


Figure 12-5 PrintComposer Capture Menu




In cases where a Series contains over 32 images, a prompt window will appear requesting user confirmation before printing.



All screen captures are subject to auto-cropping to automatically eliminate superfluous black border areas.

## 12.1.2 Capture Image: Scrapbook

To capture images:

- Click  **at bottom-right of the viewports** (see Section 12.2)
- Select the desired type of capture from the resulting Capture Menu (see Figure 12-4), or



Press the **P key** as a shortcut to capture the active image to the Scrapbook. Depending on whether the image includes annotations of Interest such as Paths or ROI, it will be captured respectively in RGB mode, and if not, in Native mode.



To capture images with Annotations of Interest such as ROI or Paths (in RGB mode), press the CTRL key whilst clicking the desired item in the Scrapbook menu or press the **CTRL+P keyboard shortcut on the active image**.



Hold the "CTRL+SHIFT" keys to force Native Mode capture (without Annotations of Interest such as ROI or Paths) whilst clicking the desired item in the Scrapbook menu or press the **CTRL+SHIFT+P keyboard shortcut on the active image**.



Captures made using the 'CTRL+capture' function are also automatically copied to the Windows® clipboard and available for pasting in any image-supporting software.








Grayscale adjustment is not available for Color image captures (RGB mode).

---

### 12.1.3 Capture Image: PrintComposer

There are various ways of adding images to the Printing Layout:

- **“On-the-fly”**: click on the printer icon  in the Capture Menu at bottom-right of the image pane or use the ALT+P keyboard shortcut (see above section)
- **Click on the ‘Print’ key** in the **Scrapbook/PrintComposer tabs**
- **Click on the ‘Print’ key** in the **‘SeriesCreator’ window**
- **Select ‘Print’** in the **‘Series/Subseries’ right-click menu** in the ‘Local Studies’ screen (see Section 2.3.2)
- **Click**  in the Display Function Toolbar top-right of the main workspace (automatically sends all active images to the PrintComposer)
- **Select ‘Print’ function** from the **‘Original DICOM Series’** sub-menu (pressing  at bottom right of every pane). This function sends all the images of the original Series to the PrintComposer tab.



Press the **ALT+P shortcut** to capture the image in active frame to the PrintComposer. Depending on whether the image contains Annotations of Interest such as Paths or ROIs, the captured image will be processed in RGB or if not, in grayscale (Native mode).

---



Hold the "ALT+CTRL" keys whilst clicking the desired item in the PrintComposer menu to force RGB capture or press the **ALT+CTRL+P keyboard shortcut on the active image**.

---



Hold the "ALT+SHIFT" keys whilst clicking the desired item in the PrintComposer menu to force Native Mode capture (even if the image displays ROIs or Annotations such as Path) or press **the ALT+SHIFT+P keyboard shortcut on the active image**.

---

### 12.1.4 Save As/Copy to Clipboard

It is also possible to save an image or to copy the image to the Clipboard for subsequent use in image-supporting software. The “Save as” enables customized embedding of a certain amount of extra information, such as:

- DICOM info
- ROI Volumes
- Black & White inversion
- Annotations

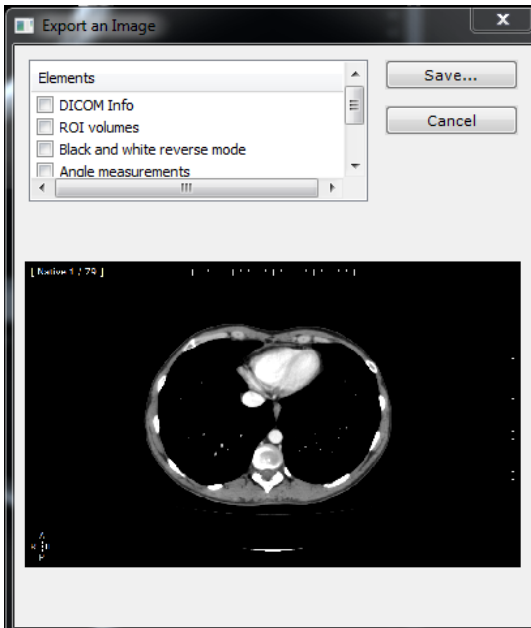


Figure 12-6 'Save as' option in Capture menu

## 12.1.5 Generate and export an interactive 3D capture



Interactive 3D capture option is available for 3D viewport in **Whole Volume** or **Surfacic ROI** mode only.

- Open any MPR compatible series in the Advanced CT protocol and switch to the 'Tissue Coloration 3D' layout

### 12.1.5.1 Capturing a 3D volume

- At the bottom-right of the 3D viewport, click on , then select 'Interactive 3D capture' from the menu

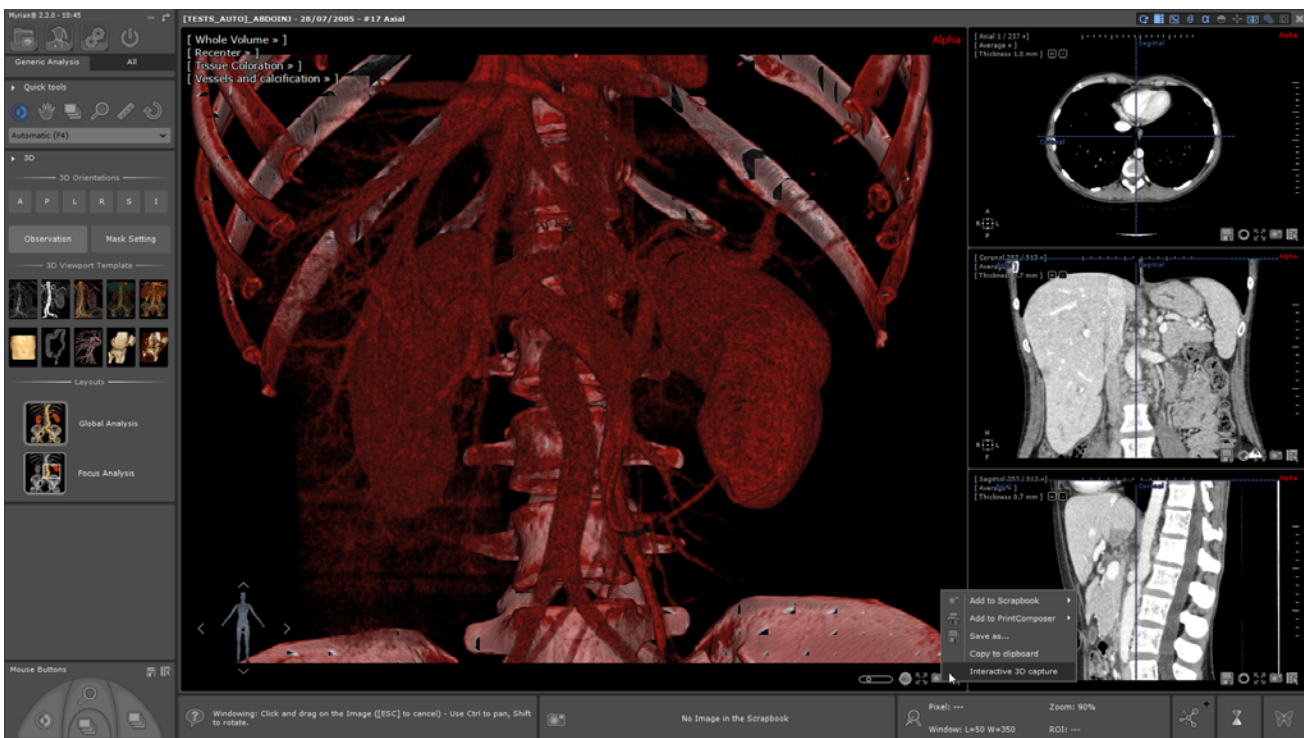


Figure 12-7 Capturing a Preview 3D volume



To navigate, rotate the 3D view by dragging the mouse over the Mannequin.

---



To launch the 3D capture, you can also use the CTRL + 3 keyboard shortcut.

---

Upon initialization, the Preview 3D capture process starts capturing a Preview 3D volume based on the current viewport and the computed result is automatically displayed in a dedicated screen once complete.

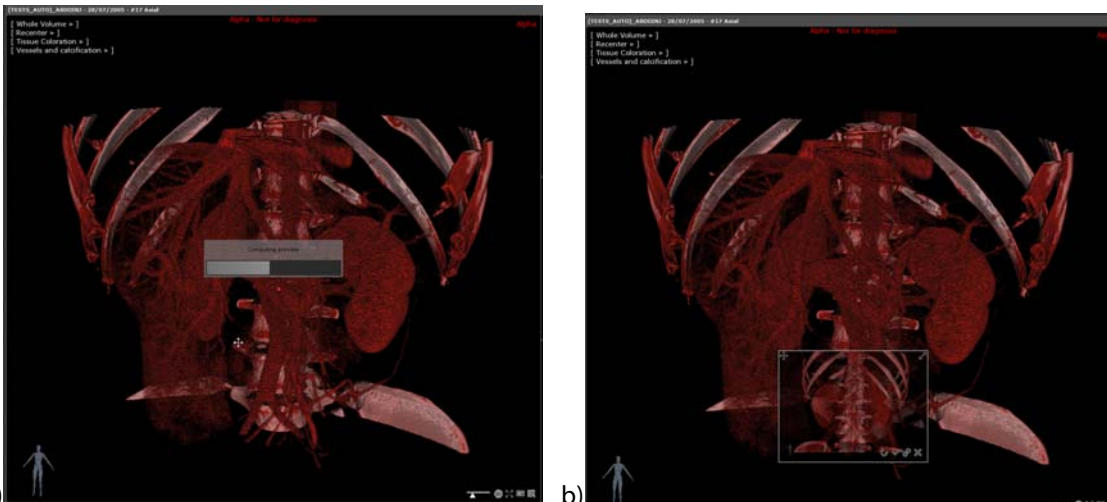


Figure 12-8 a) Capture of the Preview 3D volume in progress      b) Visualization of the Preview 3D volume

- Left-click and drag to navigate within the preview.

If you are not satisfied with the result, you can change 3D viewport parameters (i.e., zooming, panning, coloration preset...)

and regenerate the preview clicking on the 'Refresh' button



Current palette, windowing and zooming are captured.

---

### 12.1.5.2 3D preview screen description

From the 3D preview screen, clicking on the dedicated icons, you can:

- Move the 3D preview screen within the 3D viewport
- Resize the 3D preview screen
- Navigate in the 3D preview
- Refresh the 3D preview when changes have been made in the 3D viewport
- Proceed to Automatic validation of the 3D preview
- Proceed to Manual validation of the 3D preview
- Close the screen to cancel the preview

Move the 3D preview screen



Resize the 3D preview screen

Orientation mannequin





-  Refresh
-  Automatic validation
-  Manual validation
-  Close

Figure 12-9 3D preview screen





Note that **no modification** (i.e. windowing, zooming, panning) can be performed in a **3D preview screen**.



When the mouse pointer is on the 3D viewport, the preview background becomes transparent.

### 12.1.5.3 Validating 3D preview export

There are two available modes:

- Automatic validation 
- Manual validation 

Manual validation:

Upon clicking on  , the following dialog box opens in which you can define several parameters as described hereafter:

Capture description

Rendering parameters

Width	Height	Rotations	Tilts
512	512	10	8

Export destination

Directory (PNG files)

PACS (DICOM format)

PACSDB\_OFFICIAL
PACSDB\_OFFICIAL(192.168.1.224;25556)

Local database (DICOM format)

Export
Close

Enter a capture description for the newly created Preview 3D volume

Modify if required default rendering parameters:  
- Image width & height  
- Number of rotations on x and y axis

Select Export destination:  
- Directory: browse for folder  
- PACS (DICOM format): browse in the drop-down list and select the remote PACS  
- Local study database (DICOM format)

Figure 12-10 3D preview manual validation screen



A minimum of 4 Rotations and 4 Tilts are required.

- Enter/Modify all required information then select the Export destination type among the following:
  - Directory: exported files are in .PNG format



If no directory is chosen, a default path is proposed to you.


- Local Database
- PACS: Export is done in the local study database and to the remote PACS of your choice



In order to import flyover series via the PACS, your PACS system should be configured to support Raw Data series.

- Click **'Export'** to validate or **'Close'** to cancel

#### Automatic validation:

Automatic validation  can be performed using previously setup parameters without opening the validation window.

- Simply click the validation button to generate and export those 3D flyover series



Several 3D flyover series can be created from Myrian® for a same series. In that case, a timestamp will enable to distinguish them from one another.

Upon validation, the export process starts first followed by the import in the local database as requested earlier in the 'Manual validation' window.

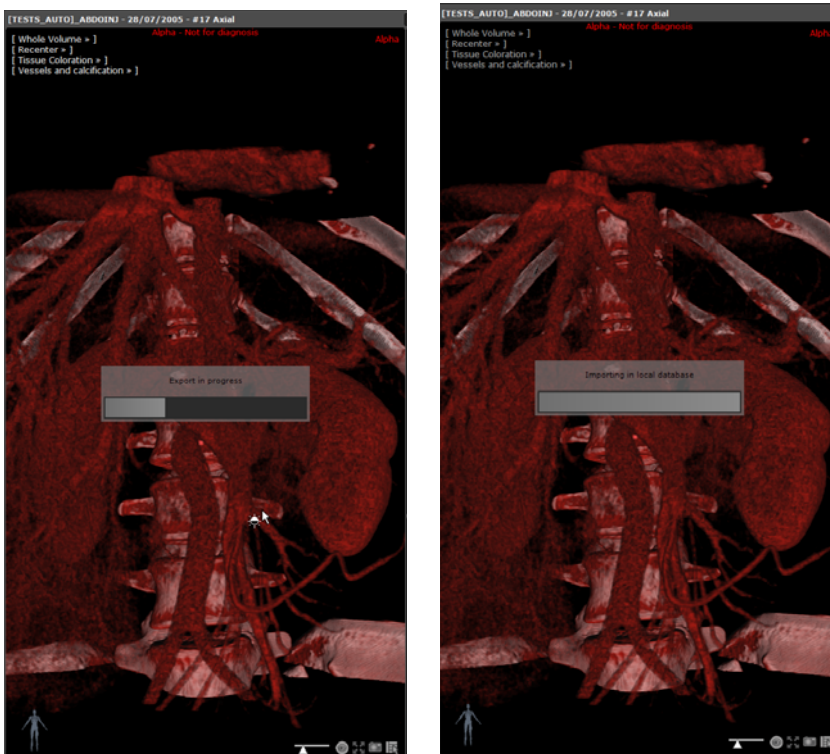


Figure 12-11 3D volume capture export to the Local database



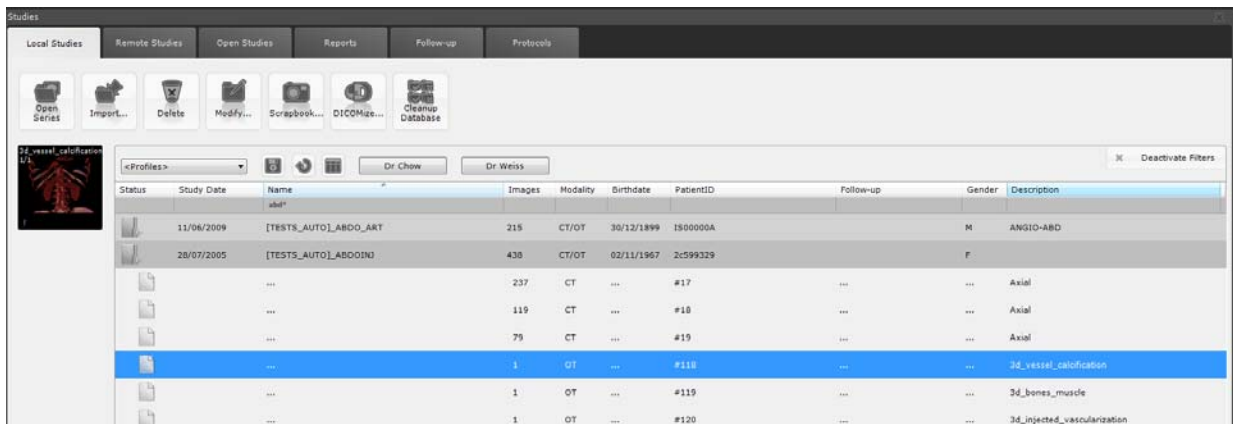


Figure 12-12 Imported 3D flyover series in the Local Study list

### 12.1.5.4 Visualizing computed 3D preview

Once export complete, the newly-created flyover series is automatically available for visualization in the workspace, in a dedicated viewport called 'Interactive 3D capture' viewport.

- Click and drag on the 3D image to navigate

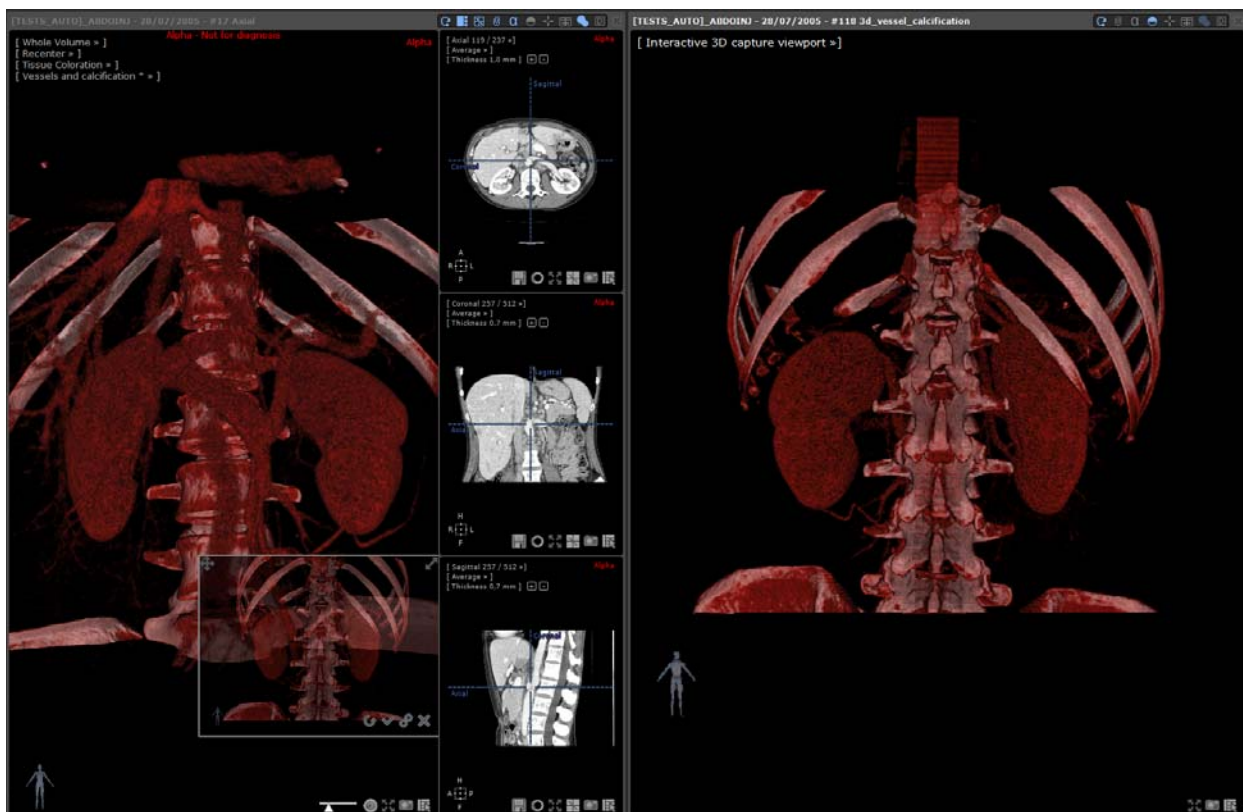


Figure 12-13 Automatic opening of the 3D capture in a dedicated viewport

The computed preview 3D volume is added to the viewport menu

- Click on the viewport menu to open it to display its Unique Instance Identifier

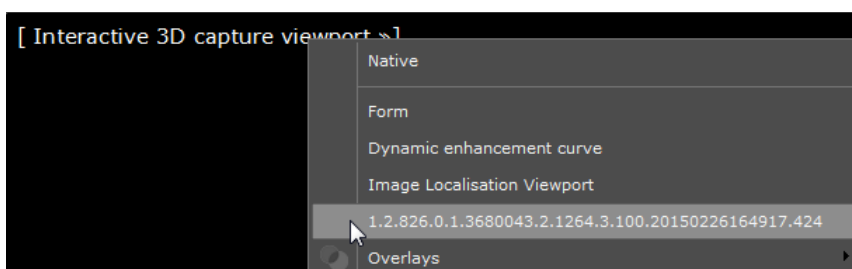


Figure 12-14 Interactive 3D capture viewport menu



Series are listed using their SeriesInstanceUID.

When several preview 3D volumes are created, each one is displayed in an individual 'Interactive 3D capture' viewport.

### 12.1.5.5 Reopening 3D flyover series using dedicated protocol

- Open the relevant **patient exam** with the dedicated '3D Preview' protocol to visualize those computed 3D flyover series.




Figure 12-15 Preview 3D protocol

## 12.2 Scrapbook and PrintComposer tabs: available tools

Both the Scrapbook and the PrintComposer modules provide a whole set of tools enabling you to select your print layout and export options.



- Click  (from the dedicated toolbox at right side in the Workspace or on the icon located in the Scrapbook thumbnail bar) to access the Scrapbook and PrintComposer modules.

The following screen containing **Scrapbook and PrintComposer tabs** appears:

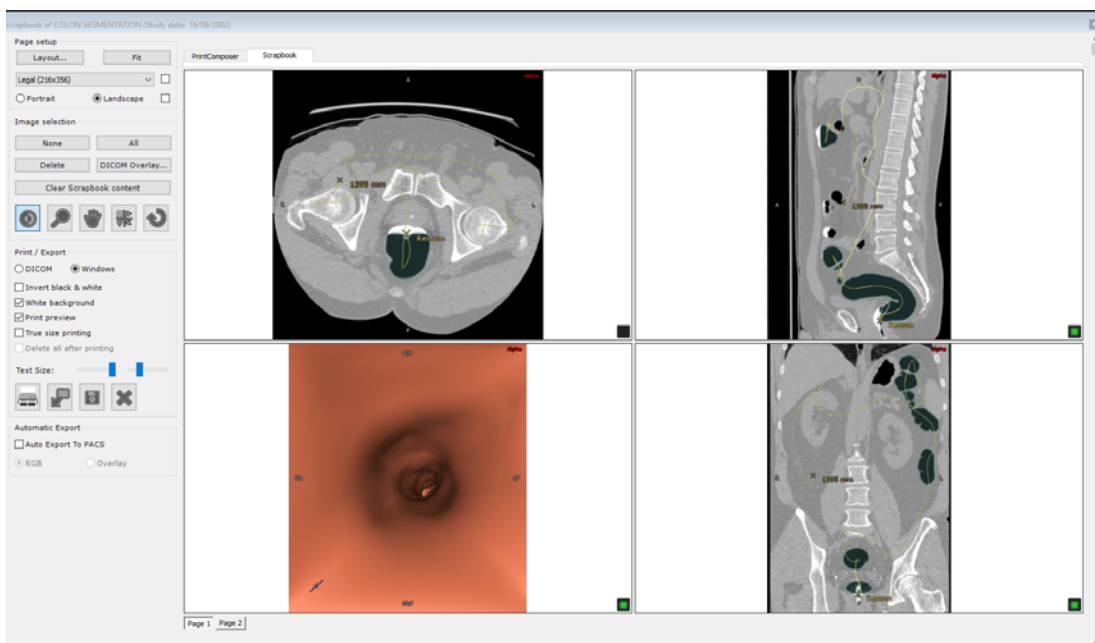


Figure 12-16 Scrapbook/PrintComposer Module

The Scrapbook contains **all the images** that have been selected for a given Study, even if they belong to **different Series within that Study**.



For safety reasons, a Scrapbook is associated with one and only one Study (although it may contain images coming from different Series within that Study). Myrian® prohibits images from different Studies to be placed in the same Scrapbook.

---



The Scrapbook/PrintComposer window can be freely resized by dragging the double-arrow handles which appear when you hover the mouse over the edges.

---



This window can also be moved freely by the user to any location on one of the available screens.

---

## Common tools

Identical Page Layout, Adjustment, Printing and Exporting tools are available for both the Scrapbook and Printing Composer modules.

---



When the number of pages exceeds 1 page, navigation buttons appear at the bottom-left to change the page.

---



You may also use the mouse-wheel to navigate through the layout pages.

---

### 12.2.1 Multiple image selection in the Scrapbook

You can select or deselect each image added to the Scrapbook or PrintComposer.

- To select an image, click anywhere on the image.

The square icon at the bottom right of the image turns from black to green.

- To deselect an image, click anywhere on the selected image.

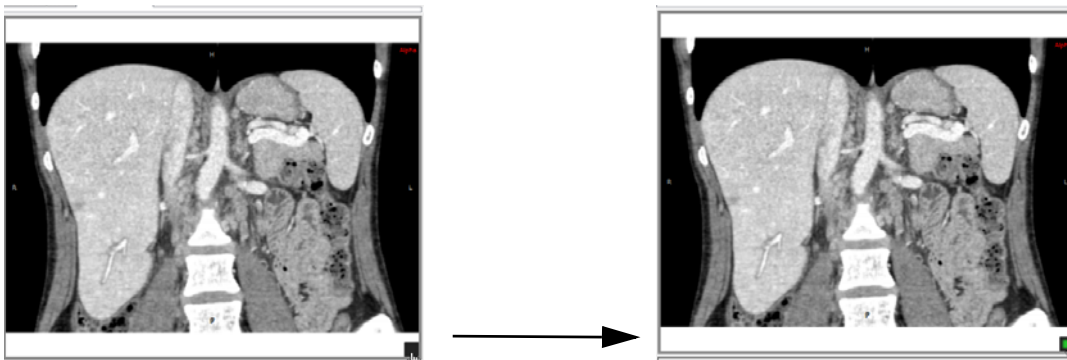
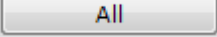


Figure 12-17 Selecting images for the Scrapbook clicking on the square icon

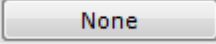
---



You can select all images at once by clicking  in the 'Image Selection' area of the Scrapbook/PrintComposer tabs.

---



To deselect all images at once, click  at left in the 'Image Selection' area.

---



To select a range of images:

- Click on the first image you wish to select (the image becomes active and is outlined with a gray border), then
- Press the 'SHIFT' key and click on the last image you wish to select
- Follow the same process to deselect a range of images.



The Scrapbook and PrintComposer display the print output aspect ratio, i.e. the shape of the film or paper preview windows represent the aspect ratio of the selected output media such as, for example, A4 paper or 36 x 43cm film, as well as the page layout which can be either portrait and landscape.



The Scrapbook and PrintComposer film or paper layout aspect ratio (number of images, size of the images, form factor of each image, etc.) represents on the screen what will appear on the printed hard copy.

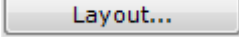


Any annotations displayed in the Scrapbook or PrintComposer, including the font size for DICOM annotations as well as user annotations (measures, text, arrows, etc.) are also represented as they will be printed out on film or paper

## 12.2.2 Page setup

Depending on your choice, image captures are placed in the Album/Scrapbook module and arranged in a grid.

### 12.2.2.1 Selecting a predefined layout

In both the Scrapbook and PrintComposer tabs, you can select your print layout clicking  at left of the Page Setup field.

A Layout editor window opens enabling you to select your preferred layout among predefined ones (either Standard grid or Asymmetric) or to create a customized one.

**Different print layouts** can be selected **for each page and one layout** can be selected **as the default layout for one or all pages** (See Figure 12-19)

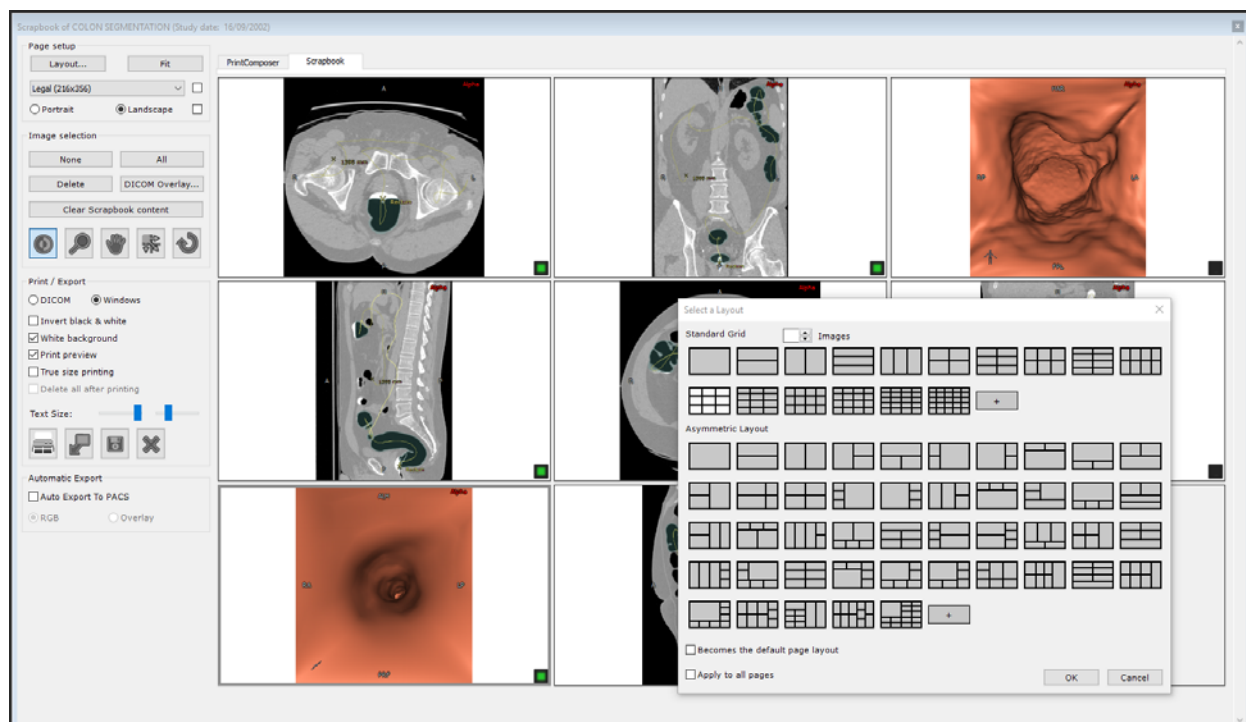


Figure 12-18 Opening the Layout editor window



Layouts are ordered by image count.

---



Asymmetric layouts are supported both for Windows® and DICOM printing.

---

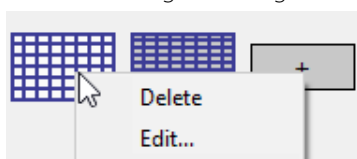


Predefined layouts can combine factory layouts and user-defined layouts. They can be distinguished by their color (**black gridlines** for factory layouts against **blue gridlines** for user-defined ones).

---



When right-clicking on the newly defined layout, the following menu pops up:



A predefined layout can only be edited.

---

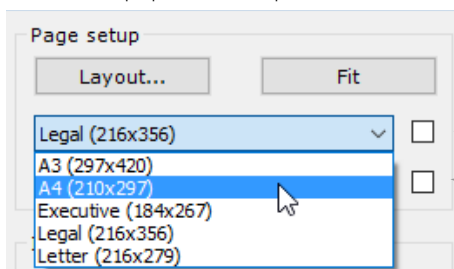


If you wish to remove some predefined layouts from the Layout editor window (i.e. those you never use) for an easier access to your preferred ones, please request the assistance of an application engineer of Intrasense.

---



The paper size drop down menu enables you to select the page format of your choice.



Check the following checkbox to make the selected paper size become the default paper size

Check the following checkbox to make the selected paper orientation become the default orientation size

A **Landscape/Portrait** option is also available for you to select preferred paper orientation. Predefined layouts will then match the selected orientation.

---



The 'Fit' button on the right of the menu field automatically selects the most economical grid layout for printing in terms of paper.

---



The thumbnail layout at right automatically adjusts to display the layout of the selected media and selected paper or film size.

---

In the top part of the dialog box, an image spin button allows you to filter those layouts according to the image count.

---

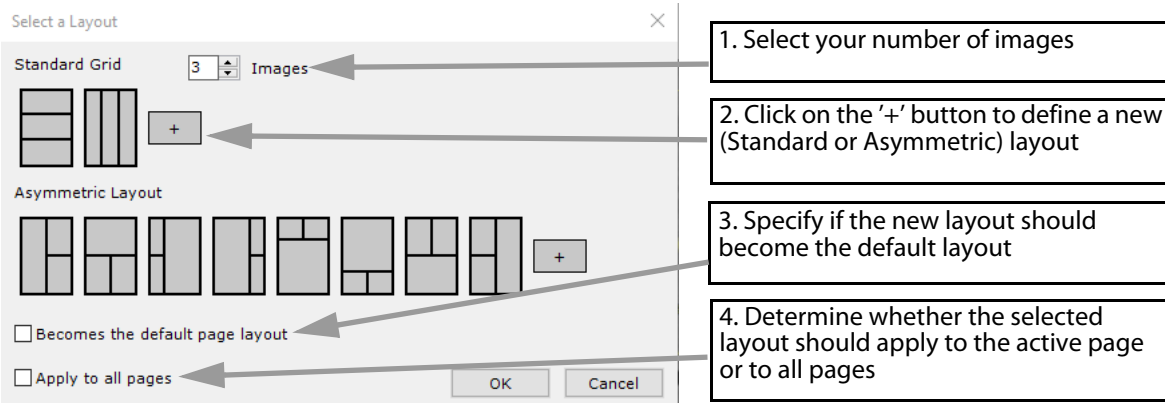


Figure 12-19 Selecting a print layout

- To choose a given layout, select the preferred layout icon then click on the OK button, or double-click on the corresponding layout icon.
- To apply this layout to all the pages of the Scrapbook, check the 'Apply to all pages' checkbox



By default, whether you have checked the 'Apply to all pages' checkbox or not, the last choice is preserved whatever the study you open

- To create and add a new layout, click on the "+" button in the corresponding grid layout section.

### 12.2.2.2 Creating new Layouts

Clicking on the "+" button in the **standard grid layout section** opens the following grid selector.

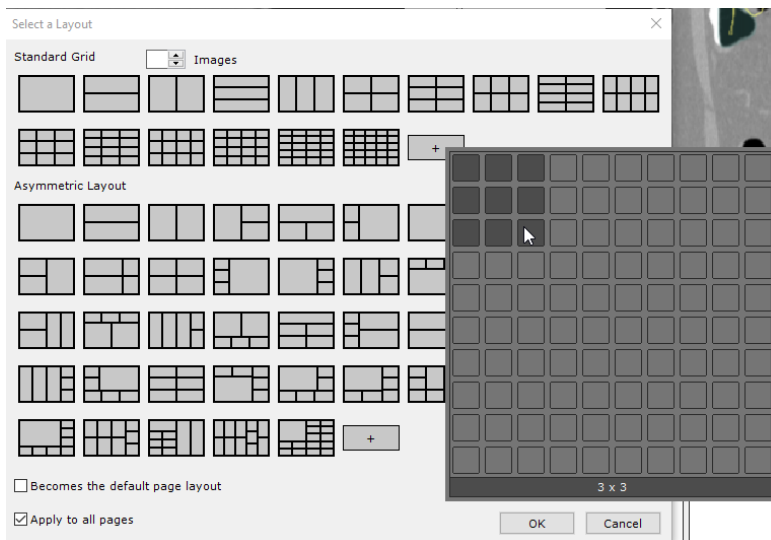


Figure 12-20 Creating a new page print layout

New layouts are displayed in blue color.



Figure 12-21 Visualization of the newly defined layout

When clicking OK, the following message is displayed:

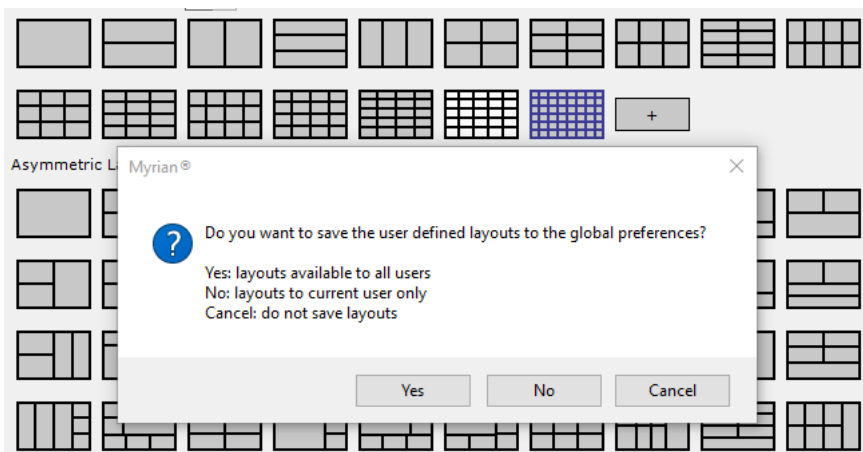


Figure 12-22 Saving the newly defined layout

- Click on the relevant button.

The newly defined layout is definitively added to the preexisting (standard or asymmetric) layout list and preserved upon closing Myrian® and whatever study is open.



If you select a grid that already exists, the existing layout is selected. No new layout is created.

Clicking the “+” button in the **asymmetric layout section** will open the layout editor. The layout editor is initialized with the currently selected layout in the layout selection dialog box. When no layout is selected, a 1x1 grid is displayed.

This Layout Editor box displays layout icons using the page orientation selected in the Scrapbook window (portrait or landscape).

Clicking on one selected cell belonging to the currently selected layout opens the following contextual menu from which you can:

- Resize any cell
- Cut an existing cell in one or more columns
- Cut an existing cell in one or more rows
- Rotate the layout
- Flip the layout horizontally or vertically

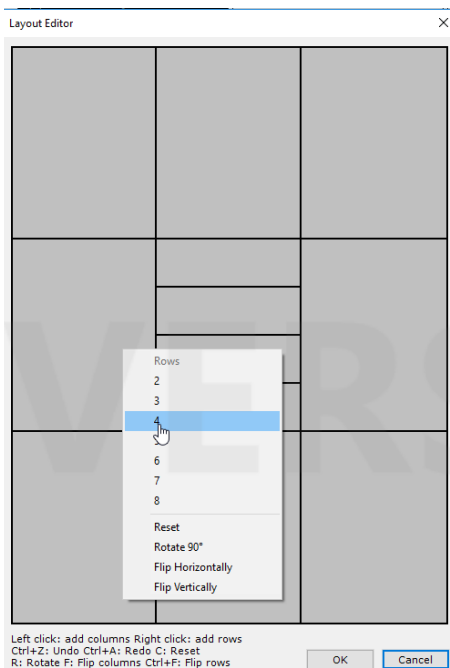


Figure 12-23 Layout editor window

All these features can be activated using left and right mouse buttons or keyboard shortcuts.



Every action is undoable and redoable using respectively Ctrl+Z and Ctrl+A.



If you create a layout that already exists, the existing layout is automatically selected. No new layout is created.

### 12.2.2.3 Image contextual menu

An image context-sensitive menu is available right-clicking on an image or on an empty cell/page. This menu enables you to perform several actions including quick access to a layout contextual menu.

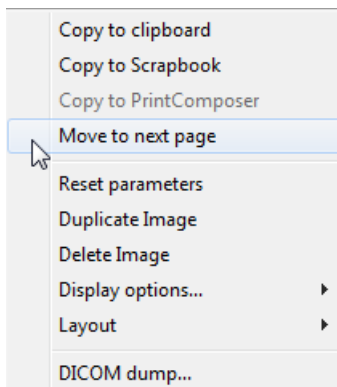


Figure 12-24 Image contextual menu

:

Function	Action
Copy to Clipboard	<b>Copies current image</b> to the clipboard in <b>RGB format</b>
Copy to Scrapbook/PrintComposer	<b>Copies current image</b> to Scrapbook/PrintComposer module
Move to next page	<b>Moves the current image</b> to the next page
Reset parameters	Resets all display adjustment values to default values
Duplicate image	<b>Duplicates current image</b> in the <b>same tab</b> , enabling multiple print-outs of the same image with different settings
Delete image	<b>Deletes</b> selected image
Display Options	<b>Toggles on/off</b> display of various elements, such as overlaid DICOM info, Annotations, Distance measurements, etc.
Layout	Enables to edit the active page layout (see hereafter for description)
DICOM dump	Displays the list of DICOM fields for the selected image

Table 12-2 PrintComposer/Scrapbook contextual menu

You can, among others, move images across pages either to previous page (only if you are not on the first page) or to next page.



If you are on the last page and move an image to the next page, a new page is created using the same layout as the current page.

If you are on the last page and move an image to the previous page then, if the last page becomes empty, it is deleted.

Using the « layout » menu, you can add columns or rows to the layout of the current page.

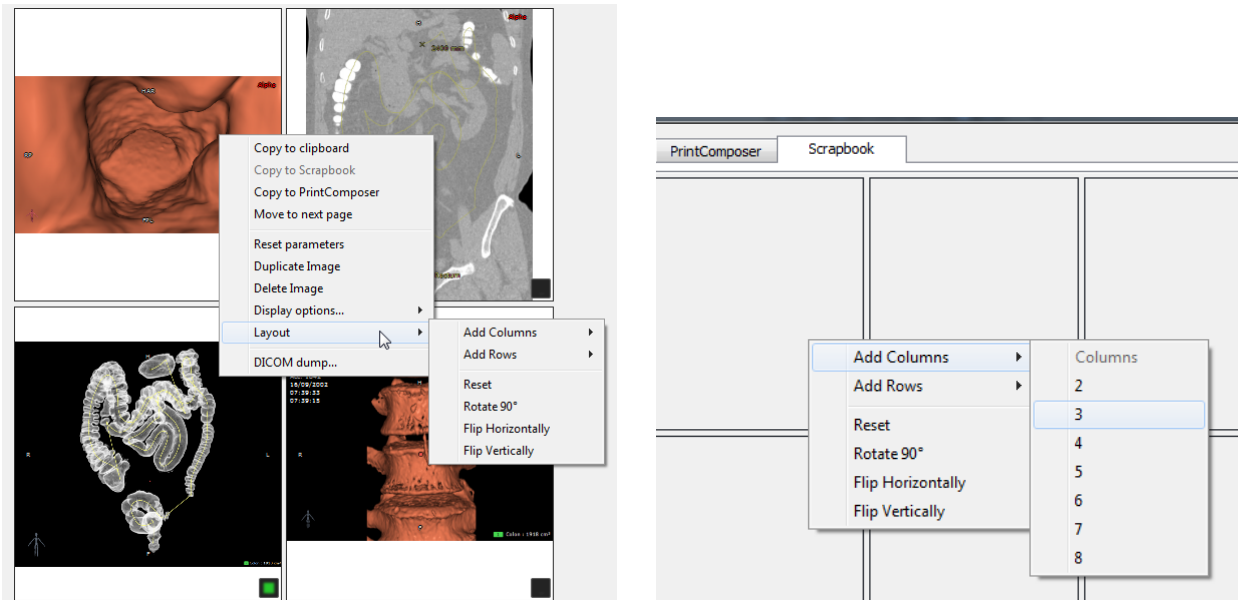


Figure 12-25 Modify the layout of the current page

You can also rotate the layout, flip it vertically or horizontally, or reset it to a 1x1 grid. Only the current page is affected.



To resize any cell directly on the page, simply place your mouse cursor in-between two cells or at the crossing of multiple cells and start dragging.

### 12.2.3 Image selection toolbox

You can **select** and/or alter various settings for **any or all images** in the Scrapbook and PrintComposer tabs using the **Image Selection toolbox**.

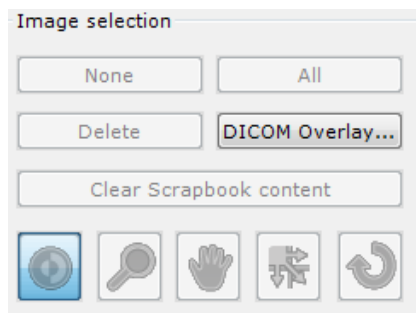


Figure 12-26 Image selection toolbox

Image Selection Toolbox functions are described below:





Pad	Function
None	Deselects all images in current tab
All	Selects all images in current tab
Delete	Deletes all selected images in current tab
Clear Summary/Print Layout	Deletes all the images in the current tab
DICOM & Overlay	Displays the 'DICOM information displayed on images' customizing screen
	Grayscale Windowing
	Zoom
	Image Pan
	Rearranges the order of the images in the grid (default selected tool at module load-up)
Reset Parameters	The Reset Parameters button resets all tool settings to default (grayscale, zoom, pan)

Table 12-3 Image selection toolbox functions

The three following tools enable to modify the image settings: Windowing, Zoom and Image pan.

**Adjustment tools** are applied to any **selected image** or to the **'active' image** (even if no image is selected).

### 12.2.4 Print/Export Area

The Print/Export area contains various tools that are described below.

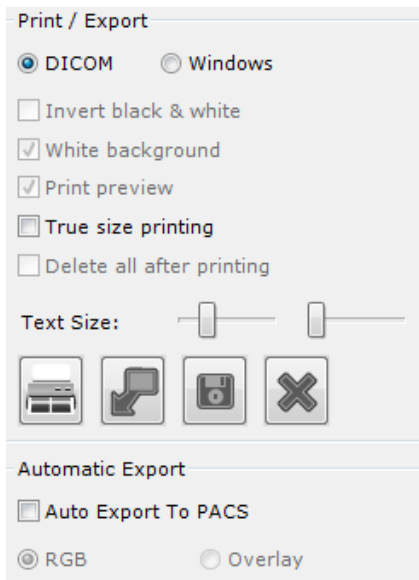


Figure 12-27 Print/Export area






Option button/Pads	Function
DICOM/Windows®	To select the <b>type of printer</b> . Note: DICOM printing (see Section 12.2.6) is only available if you have the “DICOMPrint” add-on installed
Invert black & white	<b>Inverts colors</b> in the selected images (available for <b>Windows® printers only</b> )
White Background	Converts the parts of the background which surround the images to white, to save on ink when printing. By default, this option is activated but you can uncheck the box to deactivate it
Print preview	Displays the <b>print preview screen</b> before printing (available for <b>Windows® printers only</b> )
True size printing	<b>Prints images in true native size format</b>
Delete all after printing	Clears automatically the PrintComposer after printing (once completed)
Print 	<b>Launches</b> the ‘Print’ command screen. <b>All images</b> contained in the current tab <b>are printed</b>
Export 	The ‘Export’ command <b>exports all the images in the folder</b> in DICOM format to <b>any desired device/media in DICOM format</b> . The Print Options do not affect export.
Create a new Series 	Creates a new Series from the image content of the Scrapbook/PrintComposer with unique automatically generated SeriesInstanceUID and « SeriesNumber » DICOM fields (see Section 3.4.1.2 for detailed information)
Close 	<b>Exits</b> the Scrapbook/PrintComposer module



Table 12-4 Print/Export functions



You can modify the size of the font of all the annotations/overlaid DICOM information on the image by adjusting each

respective "Text size" slider  at bottom-left of the Scrapbook/PrintComposer window. Hover the mouse pointer over the cursor to display tooltips.

## 12.2.5 Customize printout titles

By default, when launching an image printing, the page header indicates the following information:

- Name of the application
- Patient name
- Study date



Activate the preview option if using a Windows® printer.

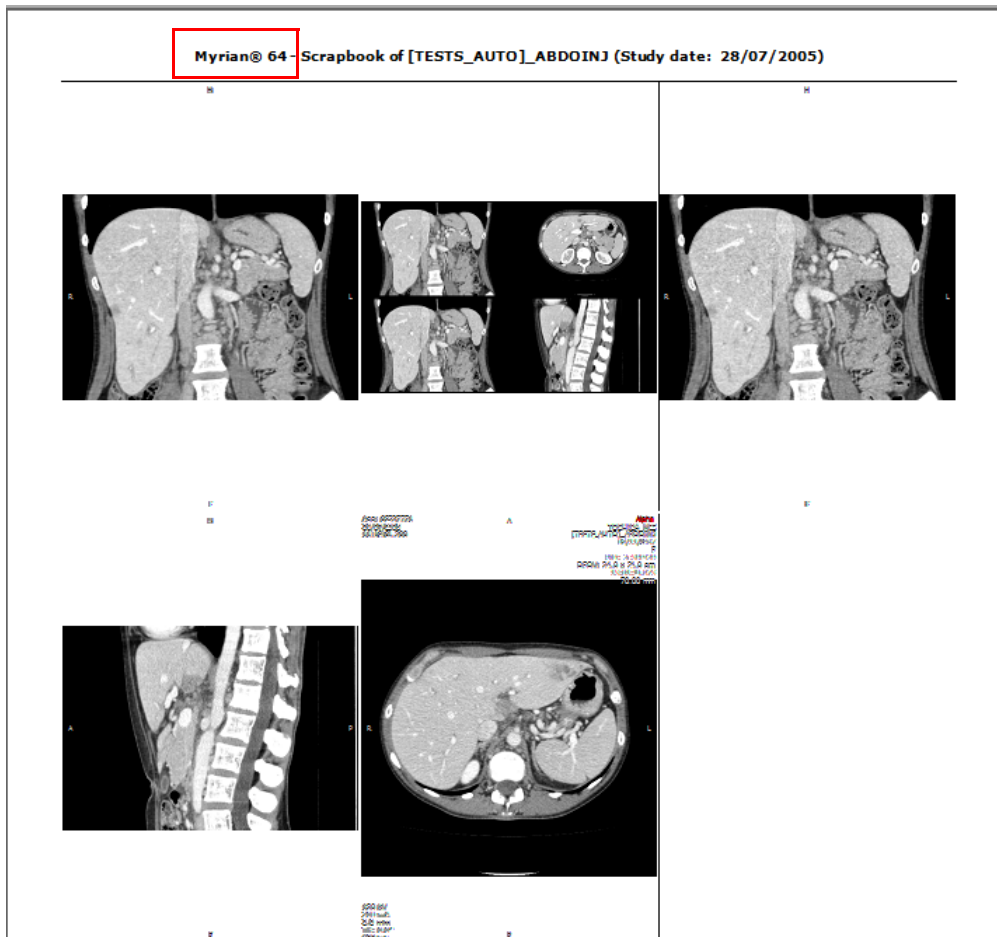


Figure 12-28 Image preview screen before printing

If you wish to customize the printout title by replacing the name of the application with the information of your choice, please request the assistance of an application engineer of Intrasure.

## 12.2.6 DICOM print

### 12.2.6.1 Overview

DICOMPrint enables export to a DICOM Printer directly from the Myrian® Scrapbook and PrintComposer modules. You can access the command from several locations in the software, including:

- The Series context menu in the Study List (launches the PrintComposer)

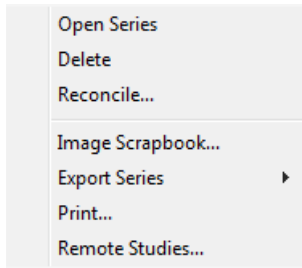


Figure 12-29 Series context menu (Study List)

- The SeriesCreator screen, if you have activated the module (launches the PrintComposer)

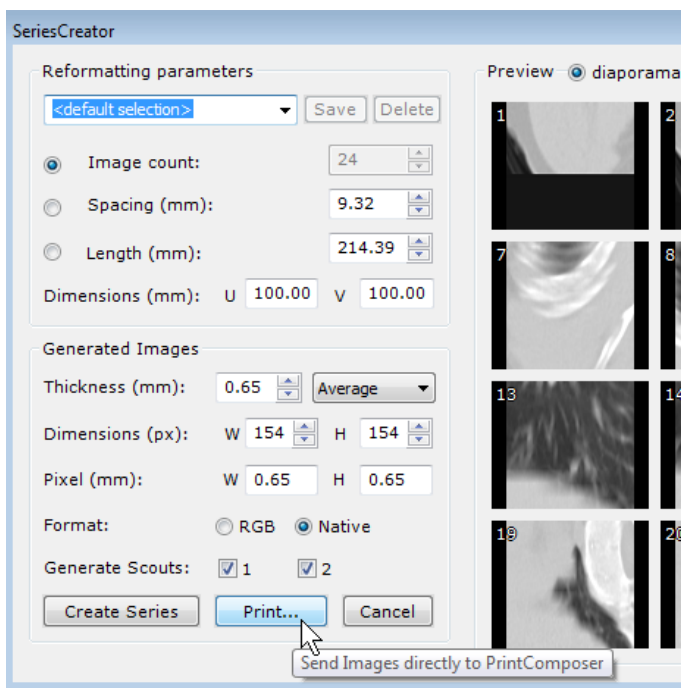


Figure 12-30 Print button in SeriesCreator screen

Finally,

- The 'Print' command in the Scrapbook and PrintComposer modules

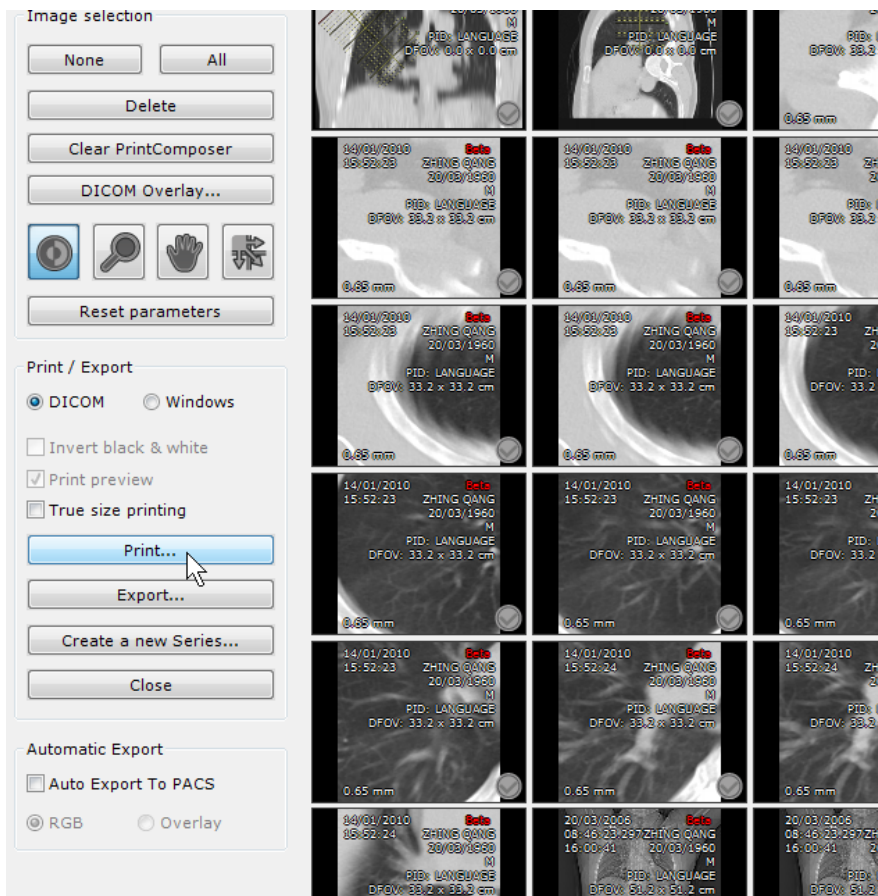


Figure 12-31 Print button in the Scrapbook/PrintComposer

### 12.2.6.2 Method of use

- Click on the 'Print' button in the Scrapbook or PrintComposer
- Adjust the settings as required in the DICOM Printing Parameters screen

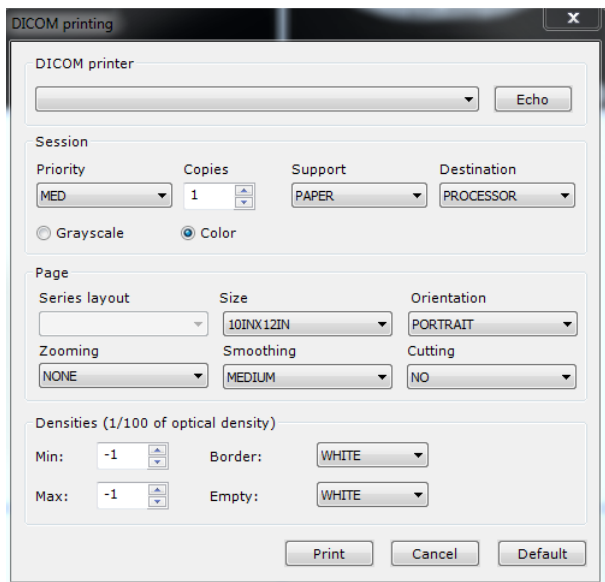


Figure 12-32 DICOM Printing Parameters

- Click **Print**



Click 'Cancel' to abort the procedure

---



Click 'Default' button to re-initialize all settings in the DICOM Printing screen

---

### 12.2.6.3 True size printing

In order to perform a DICOM print in true size, as recommended by DICOM standards, Myrian® calculates the number of pixels in the width of the image and uses the pixel spacing value to define precisely the real size of the image.

---



Number of pixels multiplied by pixel spacing value equals the true size of the width of the image

---

Once the real size of the image is defined by Myrian®, depending on the film or paper format, a reconstructed image is generated to match perfectly with the chosen format.

- For example, if you print an image in A4 (210x297) the value sent by Myrian® in requestedimagesize will be always 210 in portrait and 297 in landscape. The reconstructed image is designed to represent the real size of original image in 210 mm of width:
  - RequestedImageSize(0x2020, 0x0030): 210
  - RequestedDecimateCropBehavior(0x2020, 0x0040): CROP

Some printers cannot use the full surface of paper and apply minimum margins (most of the time, it applies with standard Windows® printers as DICOM printers are designed to print the full surface of the paper or film). Even in this case, the printer should not resize the image because the value CROP is sent by Myrian® in the RequestedDecimateCropBehavior DICOM field (in the print request). The printer should preserve the image true size and decimate the parts of image which overpass the margin limits.

---



It is strongly recommended to test your printer beforehand:

- From Myrian® workspace, draw an arrow with two length measurements (100 mm for example) in the image, then print it with the option true size activated. Then check that the length of the segments in the print result matches exactly with the measurements displayed in Myrian®.
-

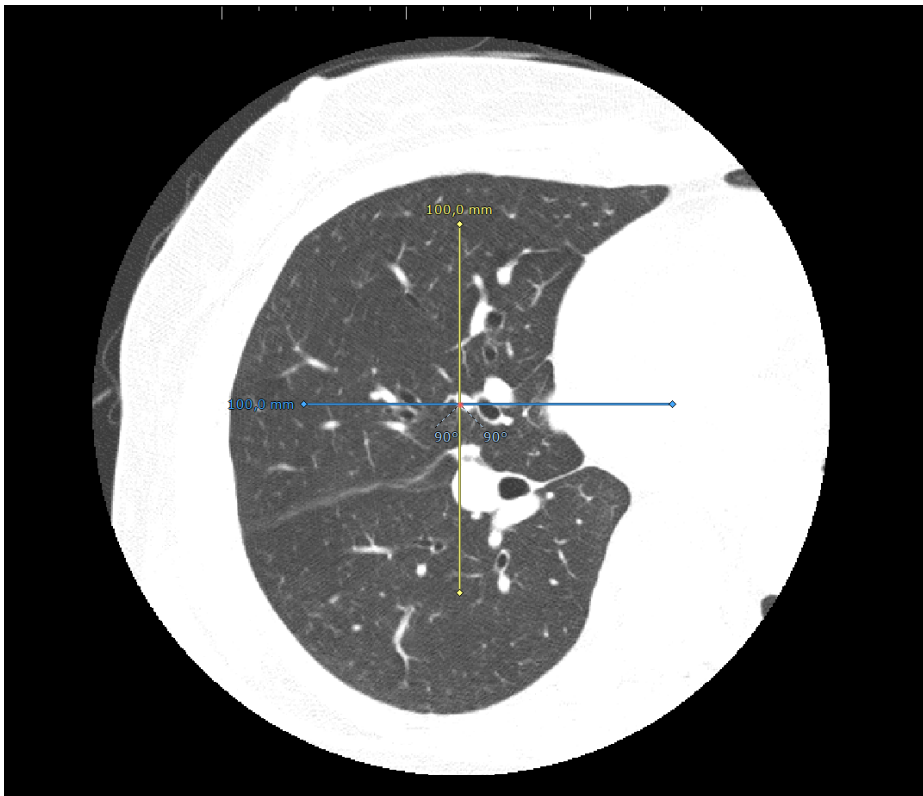



Figure 12-33 DICOM printing test

If the results do not match between measurement values displayed on screen and on print result, the reasons can be:

- The printer do not understand the parameter CROP in the print request (RequestedDecimateCropBehavior DICOM field). Maybe the printer need to receive the value DECIMATE instead of CROP.
  - 1 Close Myrian®
  - 2 Edit the preferences file \_intrasense.txt located in C:\ProgramData\Intrasense\settings
  - 3 In the section [DICOM] create the following line PRINTDICOMDECIMATECROPBEHAVIOUR=2 (1=CROP / 2=DECIMATE)
  - 4 Save the file modification and restart Myrian®
  - 5 Reissue the test to ensure that the length of the segment in the print result matches exactly with the measurement displayed in Myrian®
  - 6 Optionally you can check in the log isdicom located in C:\ProgramData\Intrasense\log that the value CROP has been replaced by the value DECIMATE in the last print job. (Information available on log trace level maximum).
- The printer resizes the image and applies minimum margins in the print results:
  - 1 First you need to measure the height and width of minimum margins applied by the printer by printing an image that covers the maximum surface of paper and overpass the margins limits:



- Click on DICOM Printer button  to open DICOM printing parameter window
- Then set the Border and Empty parameters to Black Color
- Click on the 'Print' button

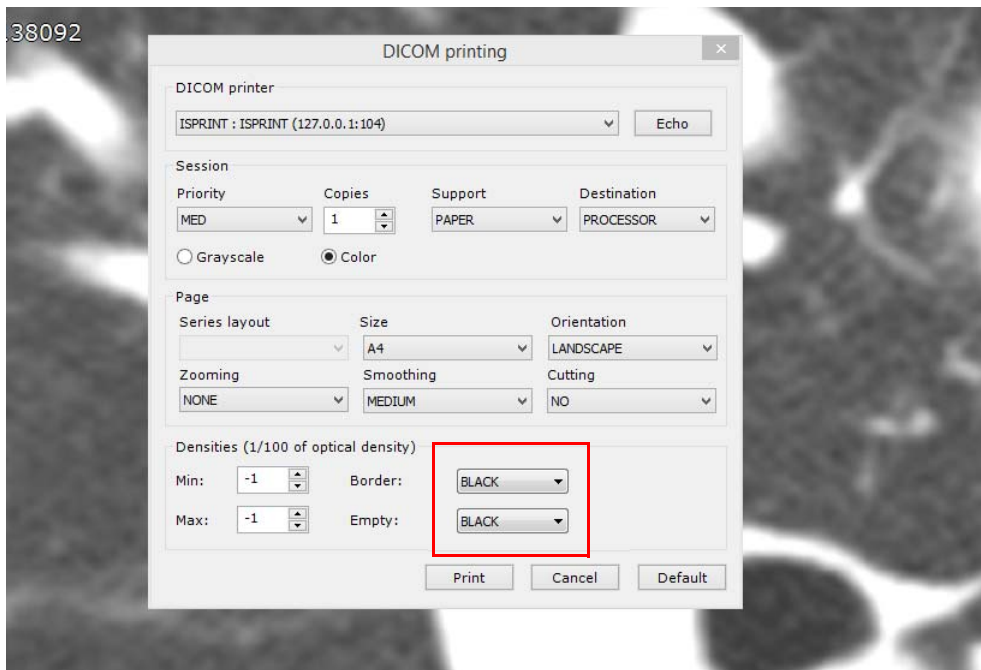


Figure 12-34 Setting DICOM Print

- Then measure manually the margins (surface not printed)

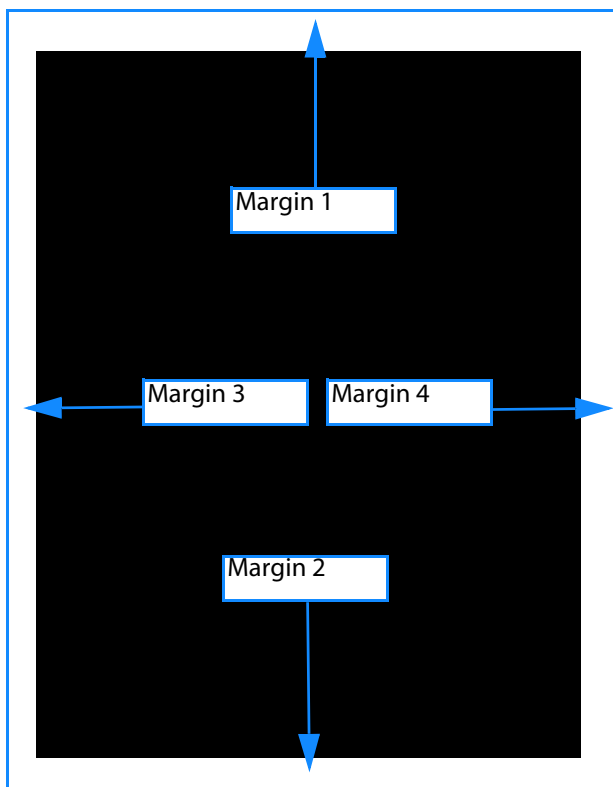


Figure 12-35 Margin representation

- Sum the values in mm of margin 1 and margin 2
- Sum the values in mm of margin 3 and margin 4

Then proceed as follow:

- 1 Close Myrian®
- 2 Edit the preferences file \_intrasense.txt located in C:\ProgramData\Intrasense\settings
- 3 Add a section with the name of the AET declared in Myrian® corresponding to your printer
- 4 Enter the following lines under this section

- WYSIWYGCOLUMNMARGIN=0
  - WYSIWYGPAGEMARGINHEIGHT=<value in mm result of the sum of margin1 and margin2>
  - WYSIWYGPAGEMARGINWIDTH=<value in mm result of the sum of margin3 and margin4>
  - WYSIWYGROWMARGIN=0
- 5 Save file modifications
  - 6 Start Myrian® and issue a new test to check that the length of the segments in the print result matches exactly with the measurements displayed in Myrian®



For example, (ISPRINT is the DICOM AET of the printer declared in Myrian®):

[ISPRINT]

WYSIWYGCOLUMNMARGIN=0

WYSIWYGPAGEMARGINHEIGHT=14

WYSIWYGPAGEMARGINWIDTH=12

WYSIWYGROWMARGIN=0

14 being the sum of margin 1 and margin 2 measurements

12 being the sum of margin 3 and margin 4 measurements.

## 12.3 Exporting and printing images

### 12.3.1 Exporting from the Scrapbook

You may **export Scrapbook images to a folder** or device of your choice (local hard drive, USB key, network location, Patient CD, etc.).

#### Procedure:

- Click **'Export'** button (bottom-left). The 'Export of Scrapbook images window shown below will open
- Choose a **Destination Media** type (local drive, USB key, CD-ROM, etc.) and location ('File' – browse as necessary)
- Choose desired image **Format** from the available formats: most standard image formats (JPEG, GIF, BMP, PNG, etc.) as well as **DICOM, DICOMDIR** and **Patient CD** are supported
- Select a desired **level of anonymization**
- Click **OK**

After validation, the standard file browsing window opens:

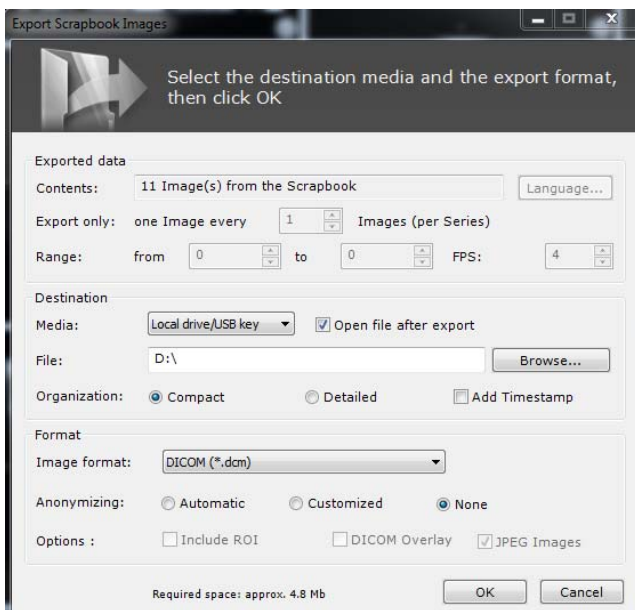


Figure 12-36 Exporting images from the Scrapbook

### 12.3.2 Auto Export

It is possible to configure Myrian® to **automatically export all the images contained in a Study's Scrapbook** whenever the Study is closed.

- To do this, simply check the **'Auto Export to PACS'** checkbox located at the bottom-left side of the Scrapbook/PrintComposer module.

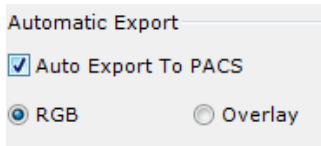


Figure 12-37 Auto Export checkbox

The function generates a DICOM Series copy of the entire content of the Study's Scrapbook which it exports to your system's Main PACS.



If no 'Main PACS' is declared on your system, the Auto Export tool exports to the first available PACS listed in the Preferences>DICOM tab.



At any subsequent opening or closing of the Study, only those images which have been added to the Scrapbook since the last Automatic Export will be exported.

---

### 12.3.3 Patient CD

You can create Patient CD/DVDs which automatically include the free Myrian® Robot viewer. Two formats are available for the export to CD function:

- Patient CD with Viewer
- DICOMDIR with Viewer

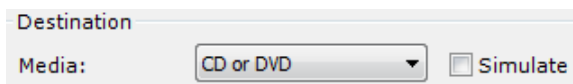


Figure 12-38 Export to CD or DVD

**DICOMDIR with Viewer**, the default format, is compliant with IHE recommendations. It exports neither ROI, nor annotations, simply the images in DICOM format. Although the basic Viewer is included in the CD package, the images can be viewed on any standard viewer.

**Patient CD with Viewer** format **is not IHE compliant** however **all annotations** which are contained in the Series at the time of export **are exported** in this format. A warning message appears when this format is selected to remind users that the format is not IHE compatible.



Choosing DICOM as the export format also enables Dicomization of a 3D view contained in the Scrapbook.



The CD/DVD writing process is a background task. The Export screen disappears as soon as the Export command is launched.

---





Click on the Myrian® icon at the bottom-right of the screen to view the progress status of Patient CD writing process.

---



In some cases, it may not be possible to burn Patient CD/DVD directly onto external discs. In such cases, you must first export the Patient CD to another location on the hard drive then use the CD-burning software of your choice to write the CD.

---



The Myrian® CD Viewer tool only operates when launched from a CD.

---



When a Patient CD is launched, the Local Studies screen automatically opens fully deployed, displaying all Studies and contained Series and Subseries.

---

**Patient information (PPID) is exported with, or stamped onto** the exported image when exported in DICOM format. A checkbox in the 'Options' menu at the bottom of the screen toggles on/off display of DICOM overlays on images in standard image formats (jpg, bmp, png, tiff, etc.).

If you are exporting images for use in an area where confidentiality is not guaranteed, it is possible to hide all identifying information going to 'Preferences' > 'Display' > 'Miscellaneous' and then checking the **'Hide all elements identifying the patient'** checkbox.

#### 12.3.3.1 Generate JPEG Image folder

By default when Patient CDs are created, a folder containing JPEG format copies of all the exported images is generated alongside the other folders.

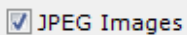


Figure 12-39 Generate JPEG Images option

This enables you to view the images on your Patient CD even on systems that do not support a DICOM Viewer.

---



You can deactivate this option, thereby gaining some space on the CD, by unchecking the 'JPEG Images' box at bottom-right of the Export Window.

---

### 12.3.4 Exporting from the local Study list or the context menu

It is also possible to export images directly from **the local Study list**.

Procedure:

- Right-click on a single/multiple selection of Studies/Series
- Select the **'Export'** command
- **Choose the destination type** from the **sub-menu**
- In the ensuing 'Export' window, **choose:**
  - **Destination,**
  - **Spacing** of the export (e.g. every other image, every third image, etc.)
  - **Anonymization** level (see Section 2.3.5 for detailed information)
- Click **OK**

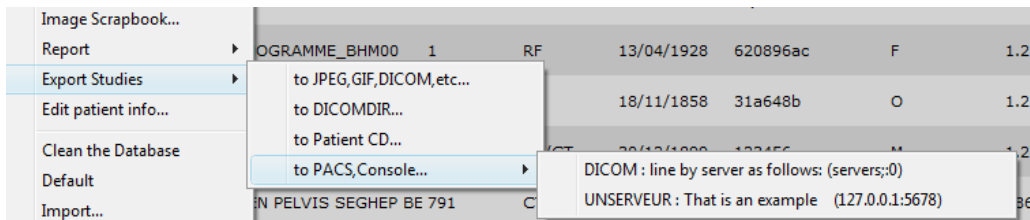


Figure 12-40 Exporting to PACS from the local Study list



If more than one PACS system is configured a sub-menu appears to choose.

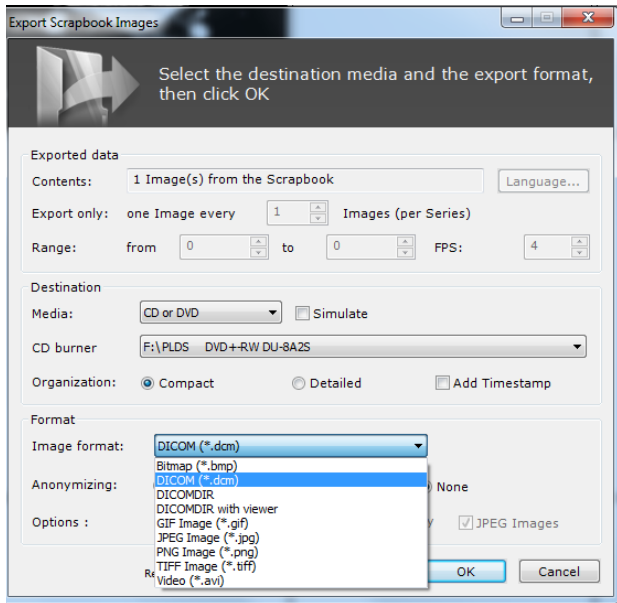


Figure 12-41 Exporting Studies or Series from list of Studies (displaying 'Export to Video' format)



Exporting to video format (.avi) is available using the drop-down menu in the Export windows or using the 'Export' function in the Scrapbook/PrintComposer tabs.




Video compression CODEC selection is automatic. Compressed video quality and size may vary depending on available CODECs.



It is also possible to export a Series using the  key in the Scrapbook/Reports tab at left of main workspace.

### 12.3.5 Export to a third-party application

If you are running simultaneously Myrian® as well as a third-party application supporting image files (Word, Paint, Outlook, Explorer, etc.), you may wish to drop images in that application. This action can be performed by **Drag & Drop**.

- In your workspace, click on the  icon in the Toolbox

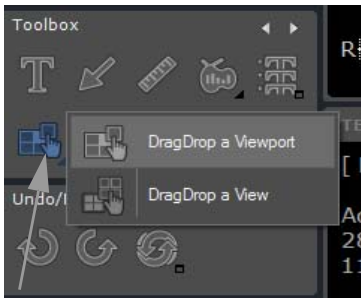


Figure 12-42 'DragDrop' contextual menu

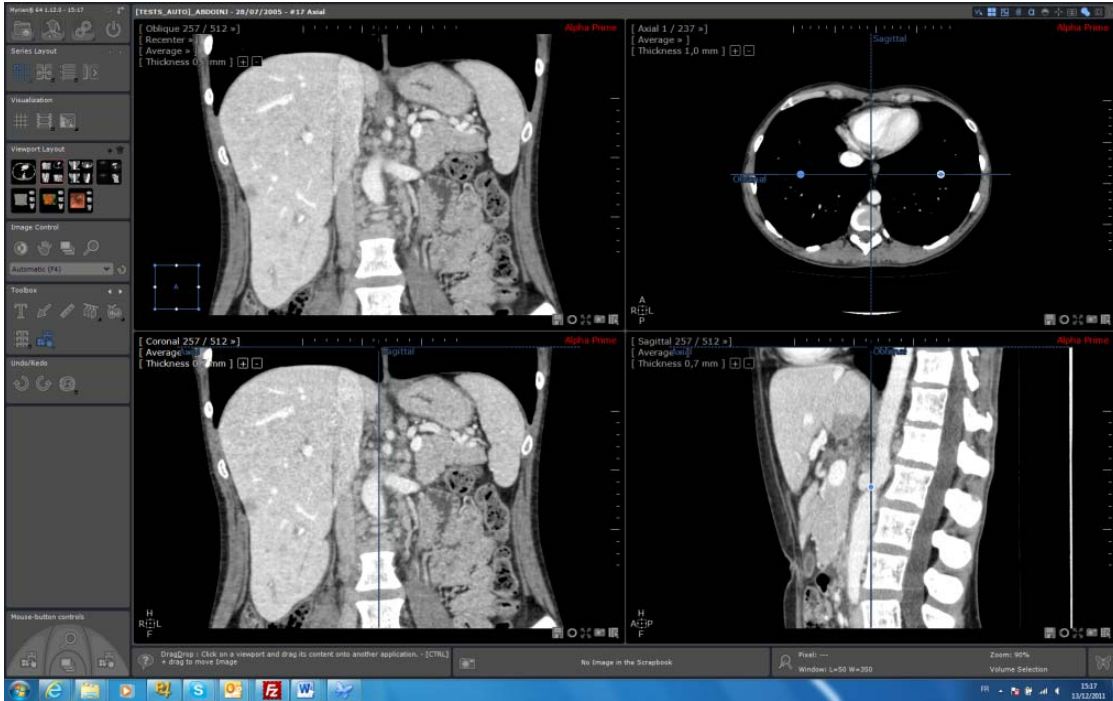


Figure 12-43 Drag & Drop a view content

You have two options available to click on:



- You can choose to **drag & drop one viewport** only (either 2D or 3D).

Or

- You can choose to **drag & drop the full view content**. In this case, the image is equivalent to the one generated with the Capture View tool (all viewports combined in one big image).

Whenever selected, use the **drag & drop functionality** as follow:


- Click on any viewport and start dragging toward the desired application, keeping the left mouse button down.

During the drag, if the mouse flies over an application supporting image file dropping, the standard cursor is displayed  otherwise, the cursor indicates that no drop is available .

- Release the left mouse button when the mouse is over the target application



All files created during drags & drops are stored in the **\Users\Username\Documents\Intrasense\Capture**. An exception is when dropping an image in the Windows® Explorer. In this case, the image is copied in the destination folder and removed from the source folder. If the user wants to keep a copy (in fact the original image) in the Capture folder, he can keep

the **<CTRL> key** down during the drag. The cursor shows a copy operation will occur .

The filename is generated automatically as follows:

- Drop a viewport: Filename = patientName-se number-se desc-orientation-elevation-yyymmdd-hhmmss.jpg (no

elevation for 3D viewport)

- Drop a view: Filename = patientName-se number-se desc-yymmdd-hhmmss.jpg



The default file format is JPEG (.jpg). To change your user preference settings, go to **c:\programdata\intrasense\settings** and insert in the userfile **<username>.txt** the following section:  
- Enter **[DRAGDROP]** followed by **DRAGDROPIMAGEFORMAT=idx** specifying your preferred idx format identifier (for example, DRAGDROPIMAGEFORMAT=2).

---

For your information, please note the following **idx correspondence**:

0	Bitmap file (.bmp)
1	JPEG file (.jpg)
2	GIF file (.gif)
3	TIFF file (.tif)
4	PNG file (.png)

Table 12-5 Idx correspondence files

Another setting allows you **to drop directly the image bitmap without generating a file** whenever possible:

- Type in **DRAGDROPALLOWBITMAP=1** (default is 0)

In that case, the target application can choose between file or bitmap format.

For instance, if you drag & drop an image in Outlook, the image will be dropped by default as an attached document while if you proceed as mentioned above, the image will be directly included in the mail content.



This option should be used only if necessary to perform a drop in an application which does not support file dropping. Otherwise, many applications would use the bitmap format by default as target destination (even if they can accept files).

---

### 12.3.6 Export to DICOM RT



**MPR ROIs can be exported only if the reconstructed volume have the same number of slice and same intensity as the native volume.** Otherwise, a message will pop up indicating that the volume is not supported.

---

You can export any visible ROI (either from MPR or Native images) to DICOM RT format by right-clicking on the desired ROI in the ROI List and selecting "Export to DICOM RT format" from the resulting context menu.

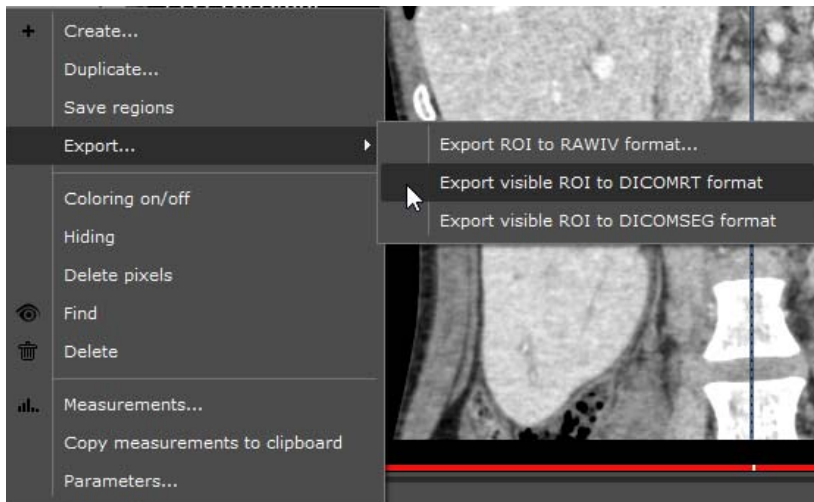


Figure 12-44 'ROI Export' in ROI contextual menu




The "Visibility Level" of the ROI you wish to export must be set to any number greater than '0' to be able to be exported. This is achieved by right-clicking on the light bulb icon  at left of the listed ROI and selecting the desired visibility level from the resulting slider.



Figure 12-45 ROI Visibility slider



This function automatically generates a new Series in DICOM RT format which will be added to the corresponding Study and visible in the Local Study List.



The new Series can be exported to a PACS, external drive, etc. using the right-click menu on the corresponding Series.

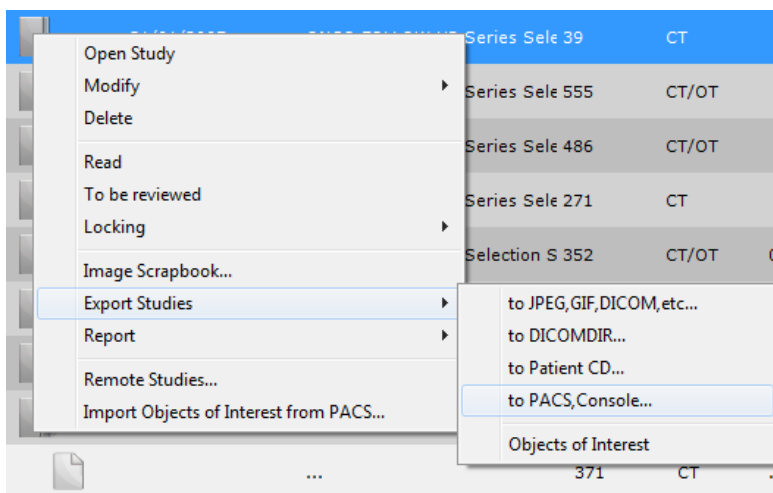


Figure 12-46 Export Series to PACS

### 12.3.7 Export to DICOM SEG format

In the same way, ROIs can be exported to DICOM SEG format\* (See Figure 12-44).

Those DICOM Segmentation series are automatically added to the corresponding Study and visible in the Local Study List.

\*Please refer to DICOM PS 3.3 C.8.20 Segmentation at the following address:

<http://dicom.nema.org/medical/dicom/current/output/pdf/part03.pdf>



Provided a Main PACS has been defined in the application, those new series in DICOM SEG format are automatically pushed to the PACS upon creation and conversely can be imported in the Study List.

---

### 12.3.8 3D Mesh Export

You have the possibility to proceed to a mesh export of a Surfacic ROI to an **.OBJ format\*** enabling you, for example, to do a 3D printing.

\*Please refer to [http://en.wikipedia.org/wiki/Wavefront\\_.obj\\_file](http://en.wikipedia.org/wiki/Wavefront_.obj_file)



The OBJ. format is supported by a large number of 3D printers.

---

Provided ROIcreator option is activated, you can save all meshes visible in the Surfacic ROI Viewport in .OBJ format proceeding as follow:

- Create a ROI in the selected study
- Switch to the **Surfacic Visualization mode**
- Press the **'E' key** on your keyboard whenever the mouse cursor is over the Surfacic ROI Viewport

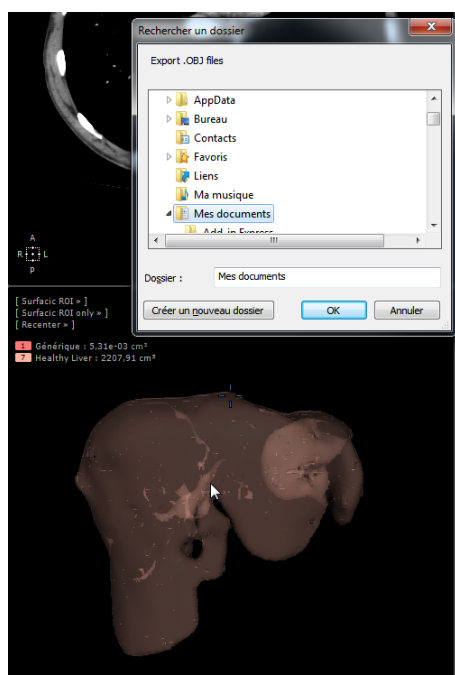


Figure 12-47 Saving Surfacic ROI meshes as an obj. file for 3D printing

The .obj format is automatically created and ready to be saved.



Upon pressing the 'E' key, when several ROIs are visible in the Surfacic ROI viewport, an OBJ. file per ROI is automatically created.

---

## 12.3.9 Selecting the organization and name of the exported folder

When exporting to any format except DICOM server, DICOMDIR, DICOMDIR with viewer or CD Patient, you can choose to select the folder organization: **Compact** or **Detailed**. You can also **Add Timestamp**.

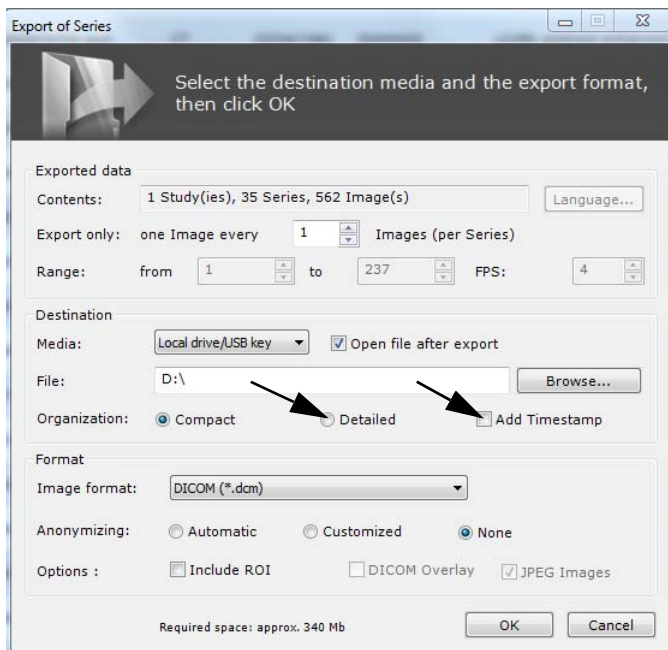


Figure 12-48 Organization in Export of Series

- In Export Series, once you have selected your destination media, choose the **Organization** preferred to allocate to the folder:
  - If you select **Compact**, your folder will be structured as follow: Patient Id/Study date/series number – modality.
  - If you select **Detailed**, your folder will be structured as follow: Patient Name - Patient ID / Modality – Study Date – Desc / Studies Number.

You can either choose to add exportation date in the export folder name by ticking the box **Add Timestamp**.



Please note that flying over **Compact**, **Detailed** and **Add Timestamp** items will automatically display the information related to each item.

## 12.4 Creating a Report

### 12.4.1 Overview

From Myrian®, you can **create, edit, archive** and **access share patient-specific** Reports and information. You can create a report from the Study List and also from the Main Workspace.




All reports relative to a patient are archived 'per patient' in a sub-folder named "reports" which is located in each patient's '\* (PPID)\*.pa1' directory in the local database.

## 12.4.2 Create Report

From the **Study List**:



- Click  (top-left main screen buttons) to open the main Study List
- **Right-click** on the desired Study
- Select '**Report**' in the menu
- Click on **Create**

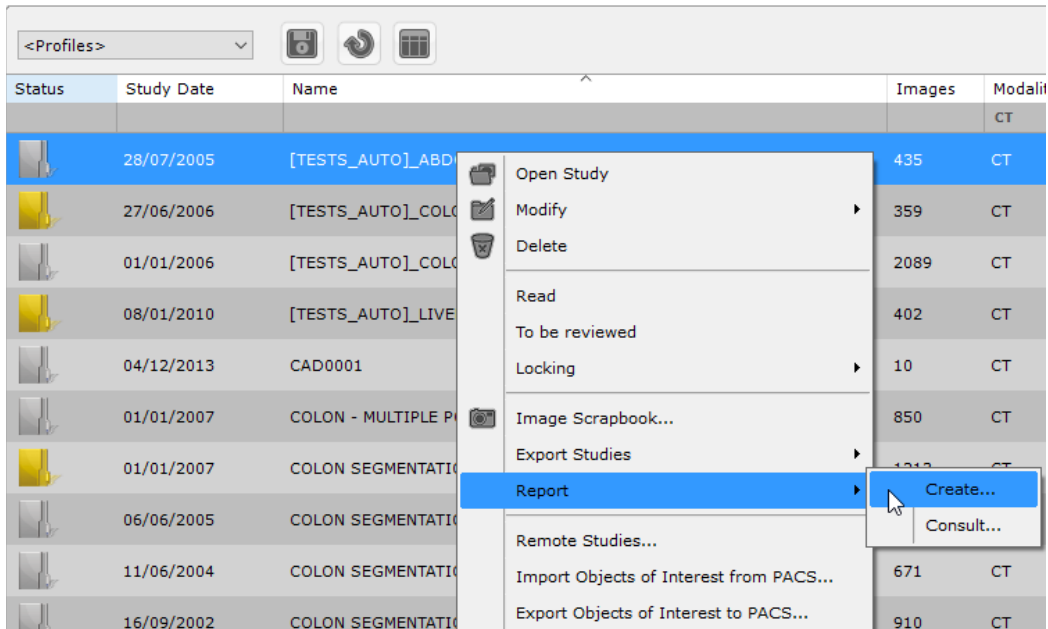



Figure 12-49 Report menu (context menu in the Main Study List)

If the Study is open, you can create a Report from **the main workspace** by clicking on the '**Create Report**' button  in the Scrapbook/Reports tab at left of the workspace.

### Report creation screen

In the following screen, the 'Report Creation' screen, do as follows:

- Type-in the **Patient name, comment/title, Doctor name and clinical/hospital name** (and address if you wish)
- Select a report template in the 'Model' drop-down list
- Select the image layout of your choice via the 1, 2 or 3 column layout buttons
- Check or uncheck the following checkboxes:
  - Edit Report, to carry on modifying the Report after it has been generated in your word processor
  - Optimize Report size for printing
  - Make the Report compatible with the Microsoft Wordpad text editor and DICOM exports
- **Click on 'Images'** to view the content of the Scrapbook and select/deselect images to be included in the report
- **Click on 'Create Report'**

The report will open in your default word processor (an example is shown in see Figure 12-52)



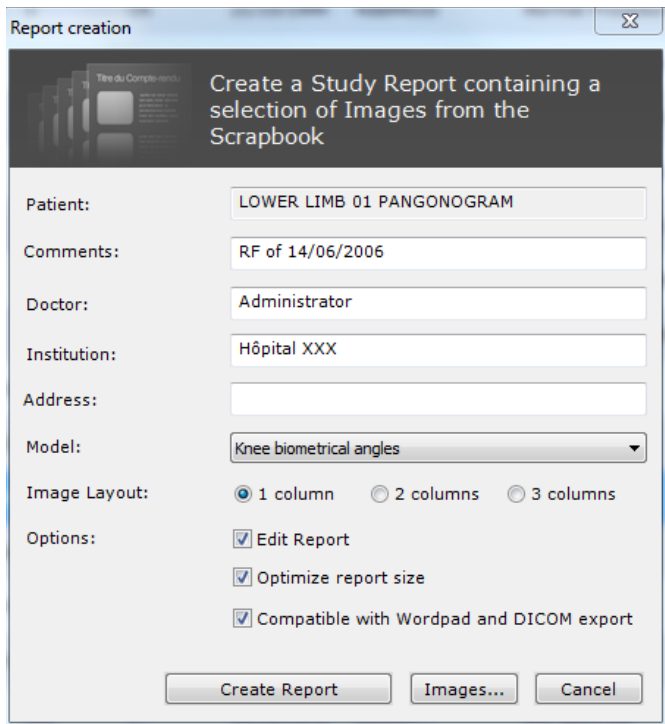


Figure 12-50 Creating a report



Reports can only be opened or modified if your workstation has a text editor installed.



If the report does not open or appear the way you expect, contact a member of your establishment's IT staff to verify that your word processor supports 'Rich Text Format' files (.rtf extension).



Use the Step-by-step wizard to create or Dicomize a Report by clicking



at bottom-left of the screen and selecting appropriate tutorial from the Wizard list.

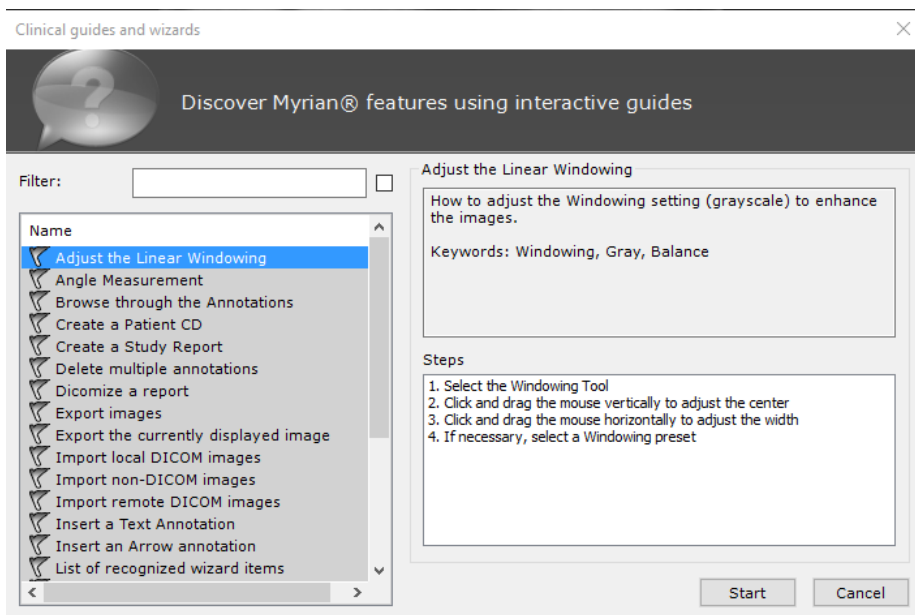


Figure 12-51 Wizard tutorial list

### 12.4.2.1 Edit Report (.rtf)

The Report header displays the **name** of the institution and a small grid containing vital **identification data** (Patient ID/ name/gender/date of birth as well as the date of Study and report creation).

The following sections may also be edited as required:

- **Procedure:** modality (IRM, CT, etc.), whether Study was injected or not, the anatomic zone of interest, notable incidents, etc.
- **Techniques:** the radiological technique that was used and any technical elements (incidences, settings, periods). These technical elements can be further edited in cases where non-standard protocols were employed, when a Study has involved complications, or where the interpretation of the images requires a good understanding of the technique
- **Measures:** this field can include a summary of measurements made by the Myrian® operator, such as values of volumes calculated in the Study's ROIs. Length and Text Annotations must be edited by the user
- **Comments:** this field can include a reminder of the clinical indications and the problems encountered, a semiotic description, a differential diagnosis or a Study/conclusion perhaps with a suggestion of a complementary Study or Studies

Scrapbook Images included in the report appear in the following pages.

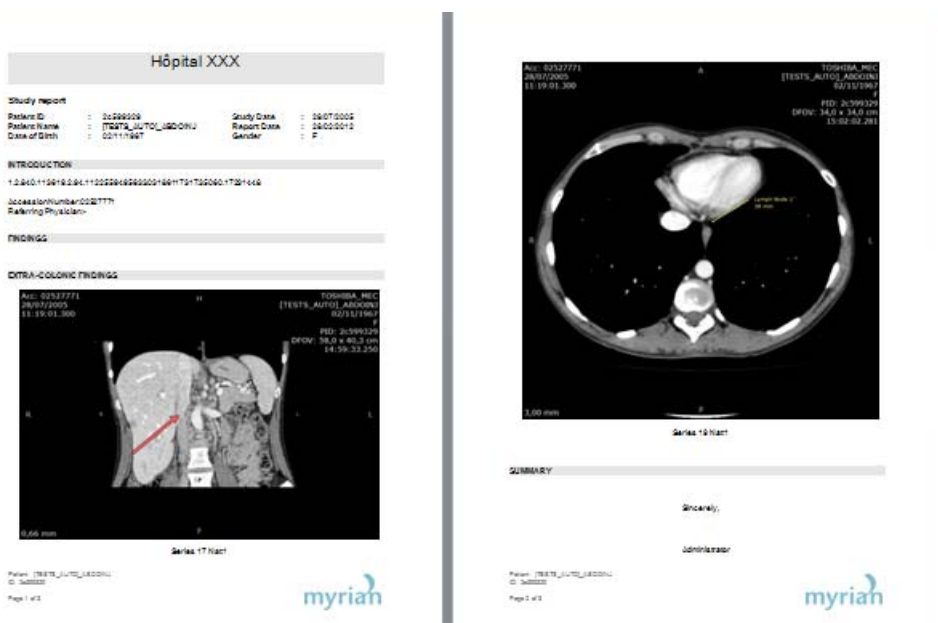


Figure 12-52 Example of a report



In order to facilitate the reading and printing of any .rtf report in regular DICOM viewer (as well as in Myrian®), the report is generated in a format close to the A4 size: scale is adjusted so the image fits the page and page break is made according to free space available to prevent image or text from being cut off at the bottom of a page meaning that the generated page can be taller or smaller than theoretical height.

The contents in RTF format is encapsulated within the DICOM file and can be extracted via **“Export Series...” > “Extract Report”** item from the Series contextual menu (to your word processor).

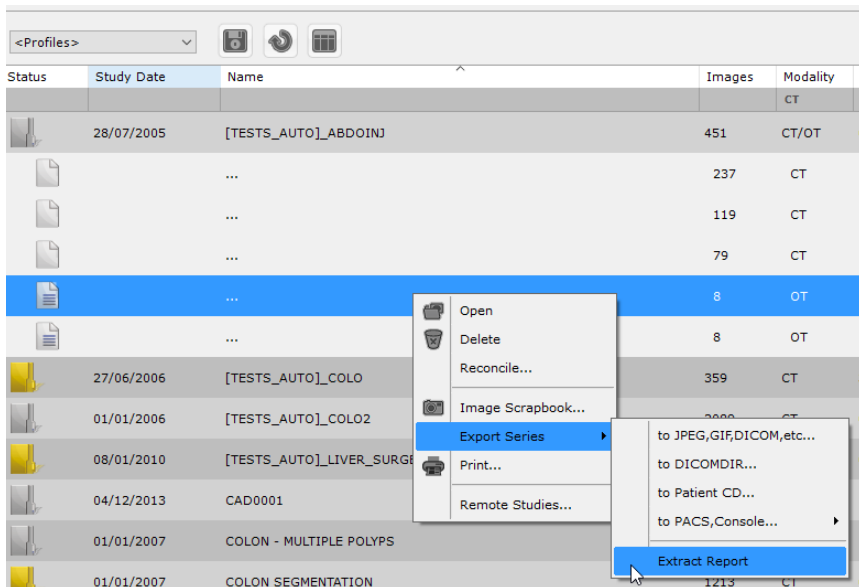



Figure 12-53 Extract a report

### 12.4.3 Consulting one patient's reports

- Select **'Consult'** , to access all reports that have been created for the current patient.
- **Click** on the desired report listed in the 'Reports' screen to select

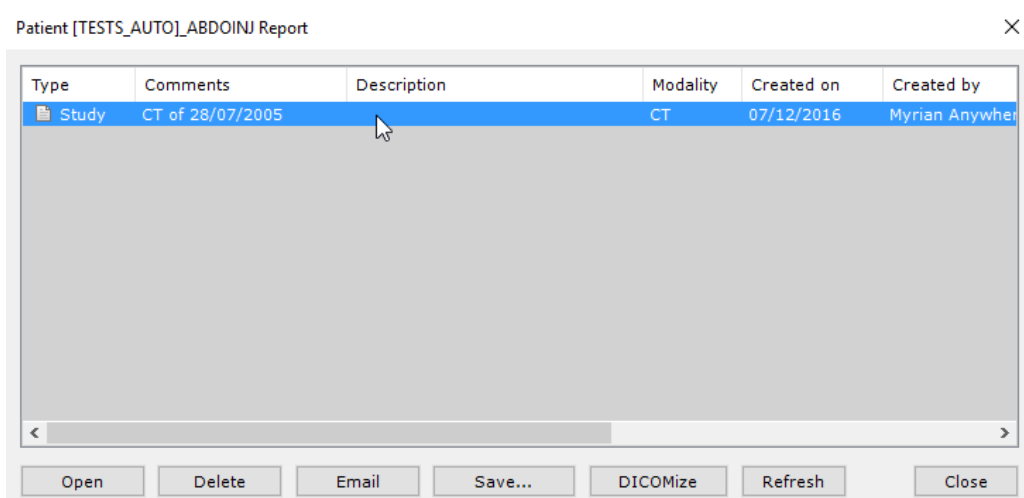


Figure 12-54 Available Reports screen (patient-specific)

A set of buttons at bottom enable various functions for the selected report(s):

- **Open** to edit report(s)
- **Delete** to erase report(s)
- **Email** to share report(s)
- **Save** to choose a location to save report(s) to local disk drive, USB key, etc.
- Click **Refresh** to force update of the list after editing a report (this is automatically done when the window is closed).



Use CTRL/Shift + mouse-click to select more than one report.



To save time, you can use filters which work similarly to the Local Study List filters described above in Section Section

2.1.1.



You can also create column Configuration Profiles in the same way as the Local Study List Tab (see Section 2.1.6).

You can also access the Report List for all Studies contained in the Local database via the **'Reports'** tab, which is part of the



Study List folder.

The tab displays a comprehensive list of reports relevant to patients in the local database.

The list features expandable rows:

- 1st level: the Patient
- 2nd level (expandable by clicking on the '+' sign at left): the Report(s)

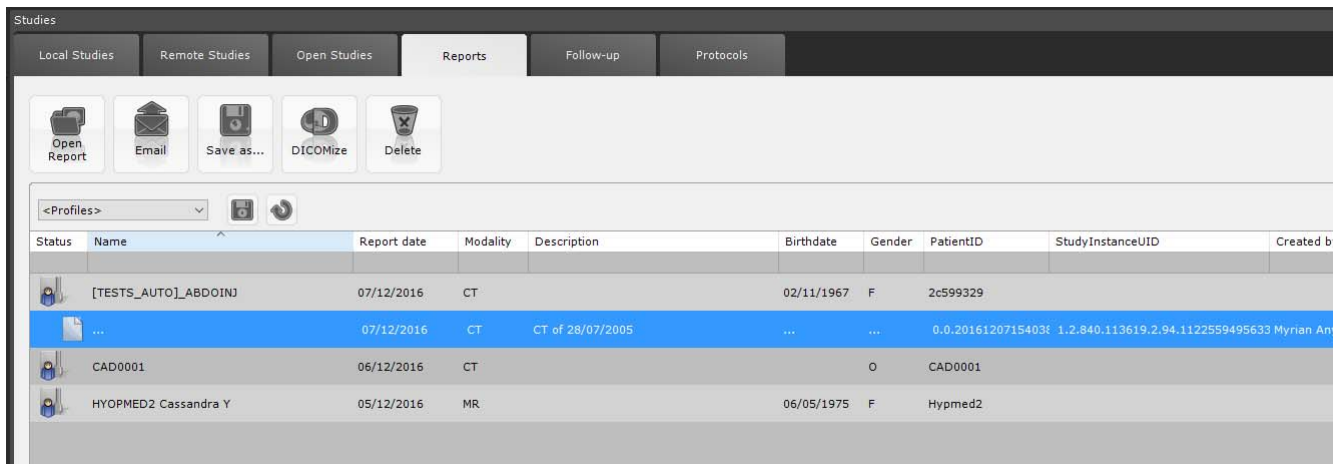


Figure 12-55 Reports tab

A set of function buttons at top of the 'Reports' tab includes:

- **'Open report'**, to open the report
- **'Email'**, to send the report by email
- **'Save as'**, to save the report in a location of your choice
- **'Dicomize'**, Dicomize a Report and add it to the Study (as an extra Series) in an image format (DICOM)
- **'Delete'**, to delete the report

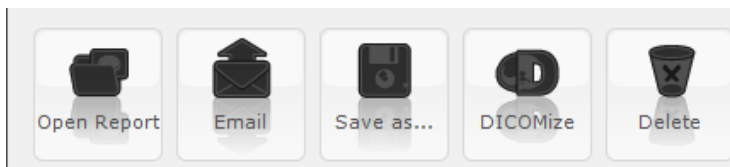


Figure 12-56 'Reports' tab function buttons

# 13 Advanced Visualization Modes

## 13.1 MPR Navigation

### 13.1.1 Overview

MPR Navigation enables Multiplanar Reconstruction of image Series in the orthogonal planes of view (Axial, Sagittal and Coronal alignments). MPR mode makes it possible to navigate freely throughout a volume in 2D, facilitating the evaluation and interpretation of anatomical and pathological structures.



MPR Reformatting process requires a homogenization of slice thickness and of slice numbers which may, in some cases, augment/diminish the original number and thickness of slices.



Depending on the type of source modality or volume information available, some Studies cannot be viewed in MPR mode

### 13.1.2 Launch procedure

#### 13.1.2.1 Launching MPR Mode from Native Images

If a CT Series that is opened with the Native Images protocol qualifies for MPR reconstruction, you can switch to MPR Mode viewing from the Workspace:

- Click  in the Visualization Toolbar.



Press the 'M' key to activate current MPR setting.

The default page layout will then switch to the MPR Oblique Mode Viewport layout displaying:

- 1 Coronal View
- 1 Sagittal View
- 1 Axial View
- 1 Oblique View



Figure 13-1 Example of oblique MPR view

You can change the orientation of any Viewport to display any other plane of orientation via the 'Views' Menu at top-left of any image frame.

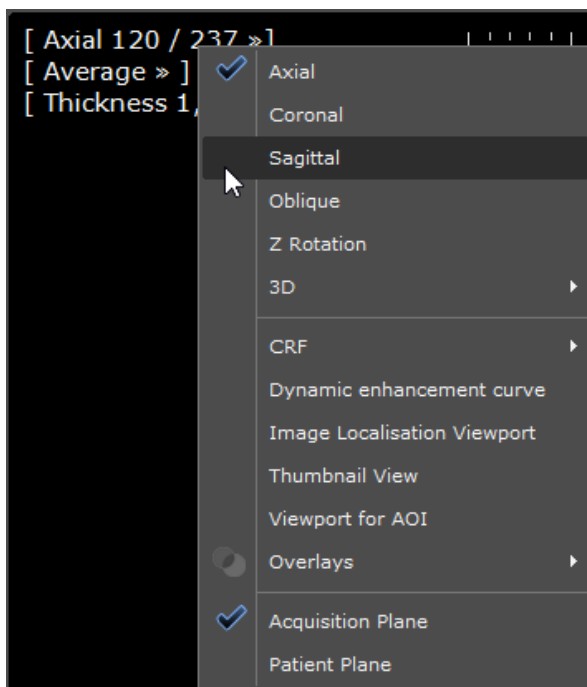


Figure 13-2 View Menu



Each frame can be manually or automatically resized and set to display any MPR Mode or plane of view

### 13.1.2.2 Navigate in MPR mode

Keyboard cursor arrows can help you navigate through the images/series:

- Up Arrow Key – Navigate to the previous slice of the series in the viewport
- Down Arrow Key – Navigate to the next slice of the series in the viewport



You can also use the mouse wheel to navigate from one slice to the other

- Left Arrow Key – Go to the previous page of the series belonging to the patient exam
- Right Arrow Key – Go to the next page of the series belonging to the patient exam



The functionality enabling the navigation from one page to another is useful only if the series layout is not displaying all views (for example, Grid 1x1 with more than one view).



Depending on the context in the workspace, the **Left/Right Arrow keys** are also used **to move from one AOI to another** provided one AOI is selected and visible where the navigation occurs. If present, those features have priority over page navigation.



The selection status of an AOI can be toggled clicking on it using the <Ctrl> key

### 13.1.2.3 Toggling frame display mode

You can toggle between views in any frame at any time by:

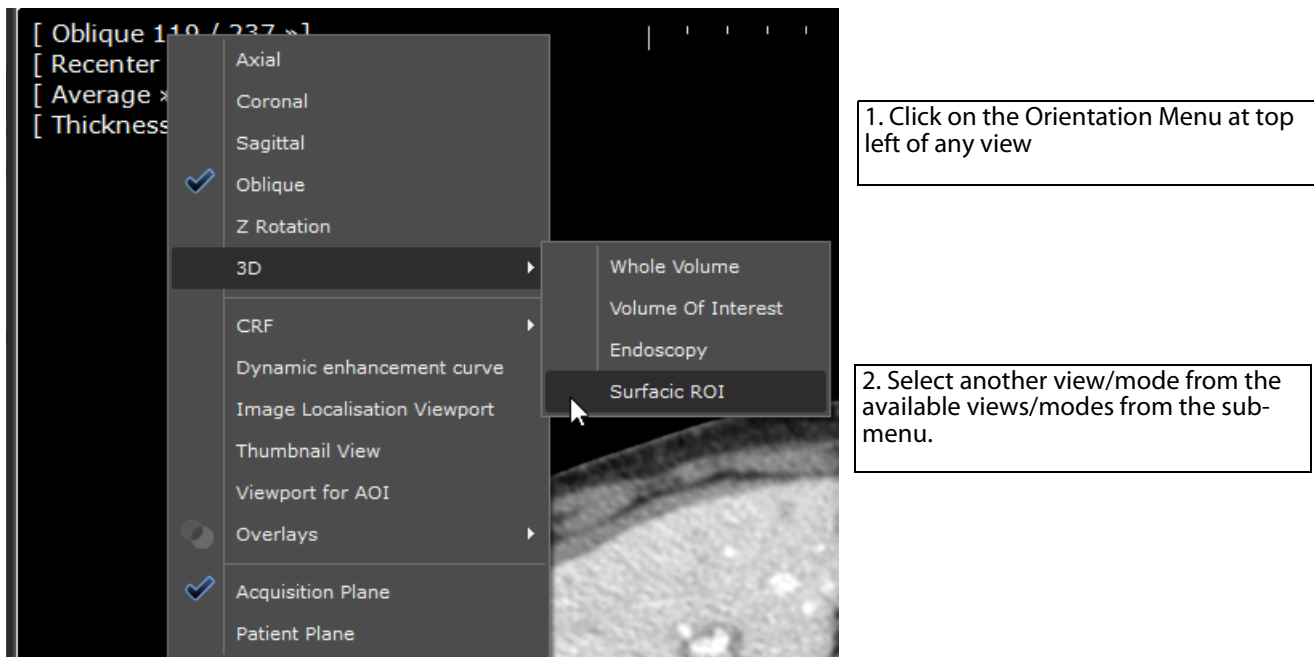


Figure 13-3 Right-click pane of view/mode options (top-left Orientation Menu in any frame)

### 13.1.2.4 MPR Layouts

You can open as many frames as you wish and modify their size freely by dragging the borders of each frame. A basic MPR layout preset menu is available via the 'Image Layout' command key, at the top-right of the Main Workspace.



Figure 13-4 Display Function Toolbar (upper-right of Main Workspace) showing the Page Layout button

For example a 3+1 MPR layout can be used to highlight one particular view by displaying it in a larger frame than the other three.

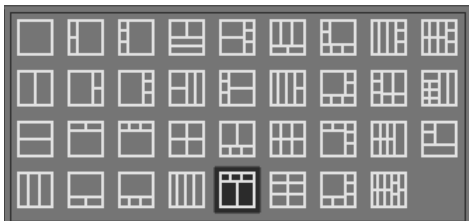


Figure 13-5 Image Layout menu



Cycle through the MPR layouts using the 'ALT+M' keyboard keys.



When changing the Page Layout, the settings from each viewport are maintained from one layout to another.



When changing to a greater number of viewports than the current layout, all extra viewports are automatically initialized in 'Axial' Mode.




Figure 13-6 MPR Layout - right-side 3+1

To resize any of the four frames manually:



Figure 13-7 Example of manual frame resizing

1. Click on horizontal or vertical intersection between frames (the mouse pointer changes to a multiple Arrow )
2. Hold the mouse button down
3. Drag the mouse as desired
4. Release the mouse button once adjustment complete

These settings enable a larger, more comfortable view of any desired panel



### 13.1.3 Launch 3D MPR protocol in Structured Reading mode

The Structured Reading mode provides you with only the relevant tools and layouts for you to proceed to the generic reading and analysis of the selected study. This user-friendly interface with clear options enables to simplify your workflow.

- Select a MPR reconstruction compatible series in the Study list
- Open the selected series with the Advanced CT protocol (dedicated to the 3D Generic Analysis) from the 'CT Standard' family

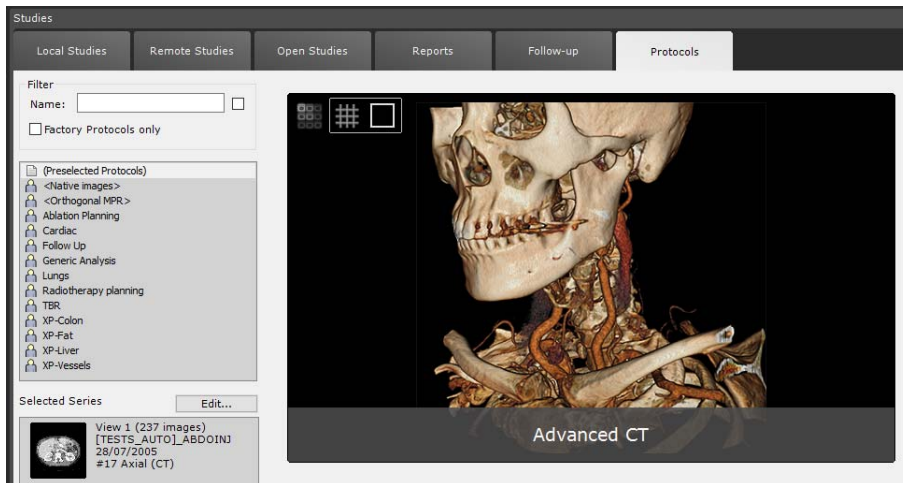
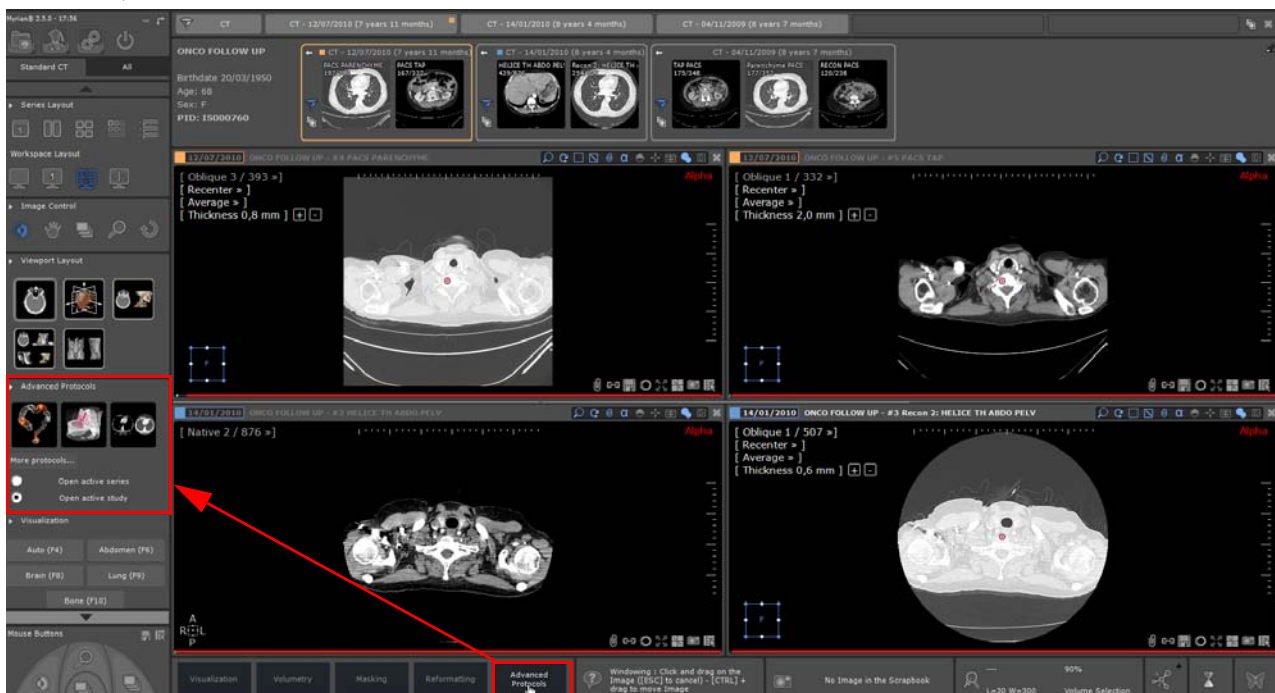


Figure 13-8 Opening the selected series for MPR reconstruction in Structured Reading mode



A Standard CT protocol providing access to standard functionalities only, i.e. image visualization, ROI creation, Reformatting and Bone masking, is also available from the 'CT Standard' family (a Standard MRI protocol is also available from the 'Standard MRI' family). The Standard CT protocol specifically allows:

- Possible automatic loading of the previous study (if applicable) when a whole study is open from the study list, according to the modality(ies) of the initially loaded series (see Section 8.5.8 for user settings configuration applying to Standard-type protocols only).
- Direct launching from the workspace, of your active series/study in the **advanced protocol that best matches your needs** (depending on your activated options) clicking on the 'Advanced Protocols' button displayed in the task scenario bar. Also, depending on whether you wish to open only the active series or the whole active study, the list of the suggested protocols will be adapted.



By default, upon launching the Advanced CT protocol, the series opens in Native view in a dedicated workspace.

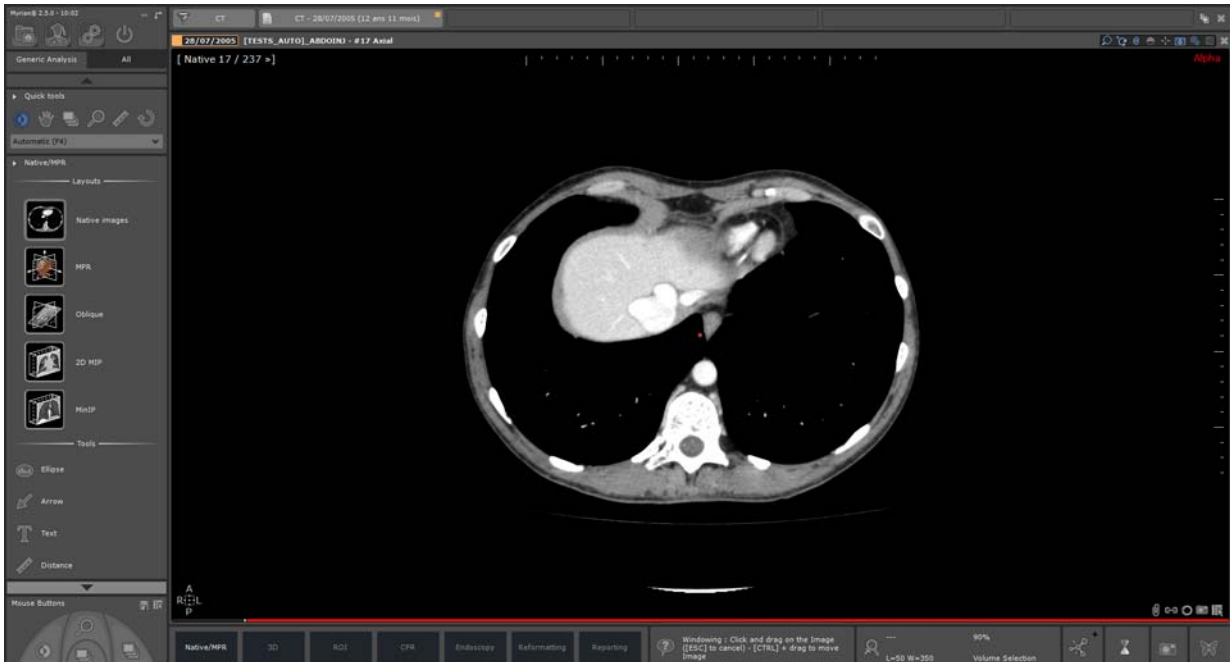


Figure 13-9 Native mode visualization of the loaded series

Several layouts and tools are available in the Toolchest for you to proceed to the 2D analysis of the images.

From that screen, and according to your needs, you can switch from the task scenario toolbar at the bottom of the workspace to the following modes:

- Native/MPR visualization
- 3D visualization
- ROI creation
- CPR creation and exploration
- Endoscopy
- Reformatting
- Reporting

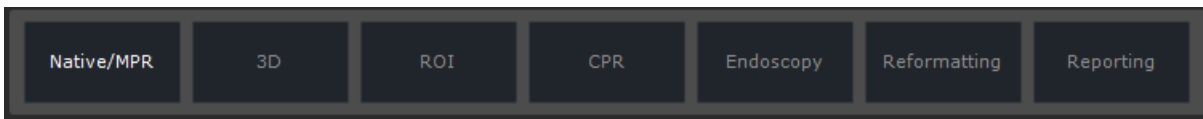


Figure 13-10 Available analysis modes



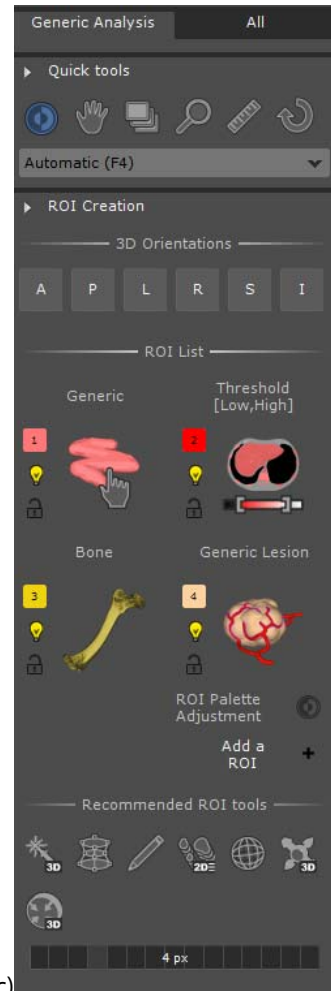
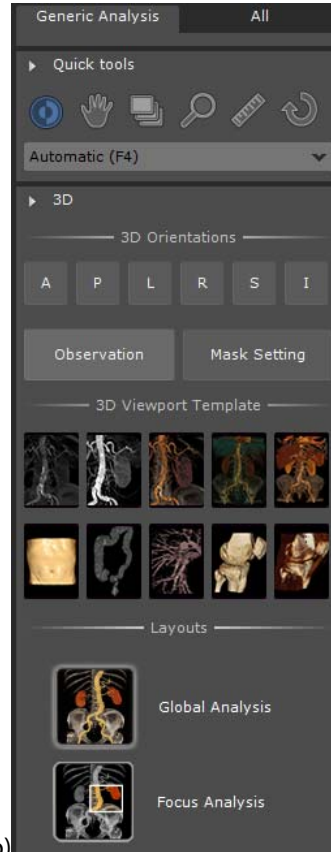
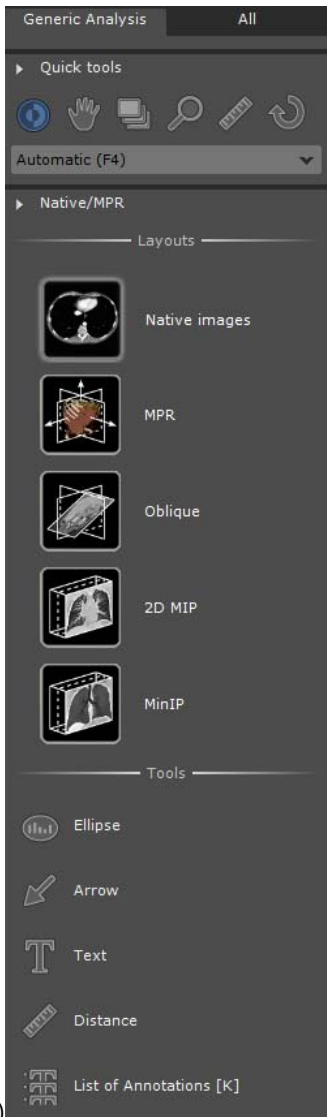
In any protocol including a structured reading mode, you can switch from one task/step to another using the following keyboard shortcuts:

- <Ctrl>+<PageUp>: previous step
- <Ctrl>+<Pagedown>: next step
- <Ctrl>+<Home>: first step
- <Ctrl>+<End>: last step



The selected analysis mode is highlighted.

For each mode, a set of appropriate tools and viewport layouts is provided.



a) Native/MPR image visualization toolchest b) 3D Visualization toolchest c) ROI creation toolchest



The 'ROI Palette Adjustment' mode enables to access automatically to the 'Apply per ROI' mode (see Section 7.15.27) to enhance specific tissue.



To adjust a ROI palette, select a ROI and adjust its own windowing level  using the left mouse button on a 3D viewport.



To go back to the ROI creation mode when the ROI palette adjustment has been activated, simply click on 'ROI creation'

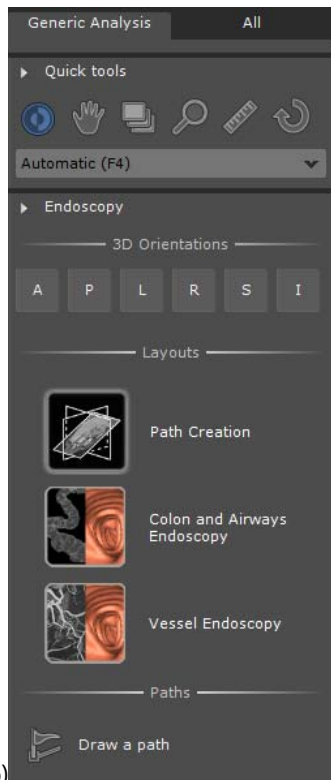
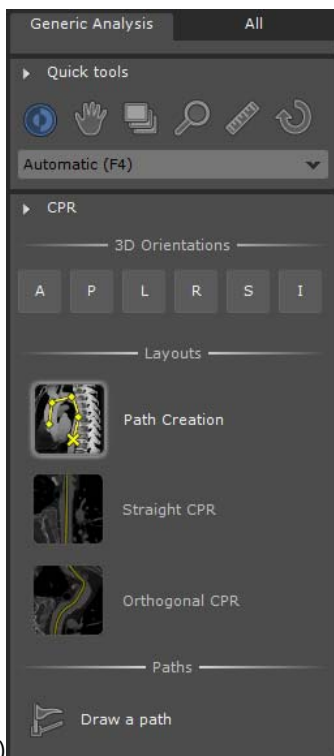
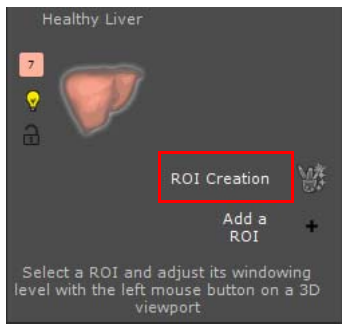


Figure 13-12 a) CPR creation toolchest b) Endoscopy mode toolchest

According to the selected layout, the toolchest adapts itself and displays the relevant tools.



By default, 'CPR' layouts **are disabled until a Path has been created** using for example, the 'Draw a path' tool.



Tooltips are available simply hovering the mouse pointer over **any icon in the Toolchest**.



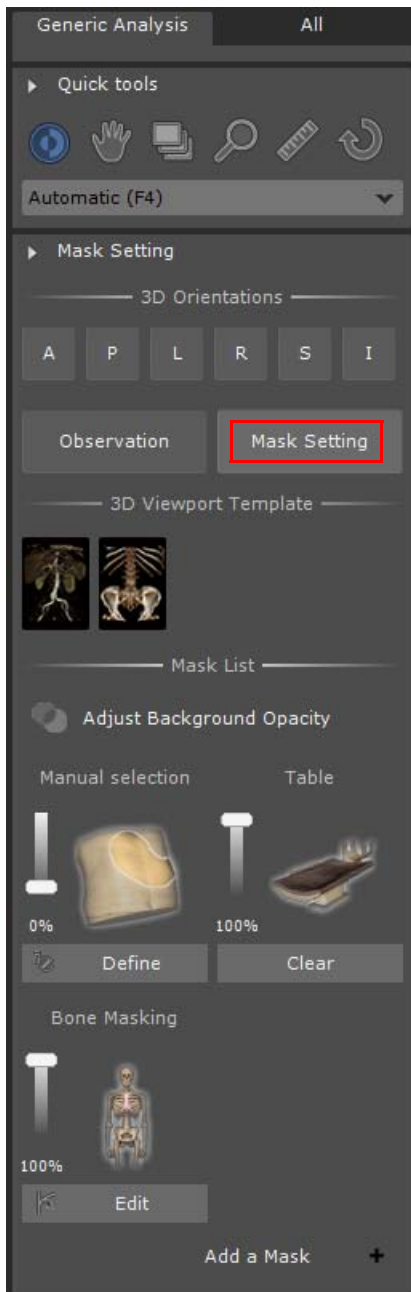
The '3D reading' step is composed of two optional modes

Observation

Mask Setting

. By default, the

'Observation' mode is activated. Click on 'Mask Setting' to display the following toolchest:



Windowing preset drop-down list

Patient orientation:  
 - A: Anterior  
 - P: Posterior  
 - L: Left  
 - R: Right  
 - S: Superior  
 - I: Inferior

To adjust Background opacity, click on the icon and from the slider, define the visibility level

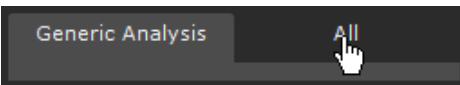
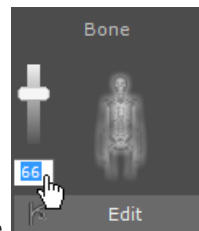
Table and Bone Masks are automatically created upon loading the series:  
 - Move slider up/down to adjust the

Click on '+' to create a new mask

- Click on the mask icon to Display/Hide the selected mask on the 3D (if existing) and assess its quality
- Click on the 'Edit' button to access dedicated Edition tools associated to the selected mask



Click on the transparency percentage to enter your own preferred value



At any time, you can click on the 'All' tab to access the standard protocol interface. You can freely move back and forth between those two modes.

All functionalities available in the Structured Reading mode work exactly the same way as in the Standard interface. Please refer to the relevant sections of this manual for details about any of those.

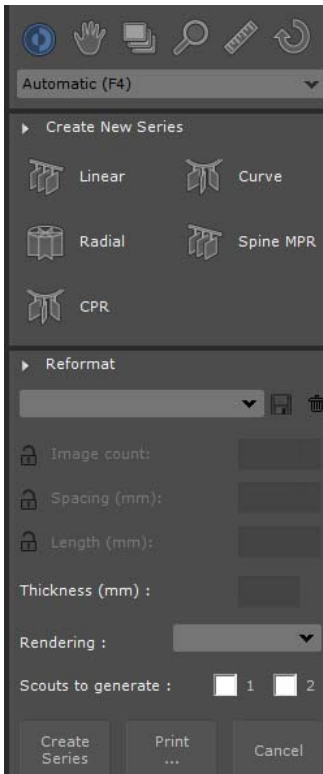
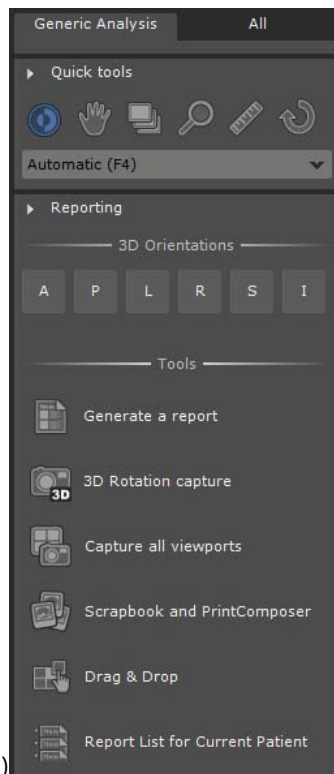


Figure 13-13 c) Reformatting toolchest



d) Reporting toolchest

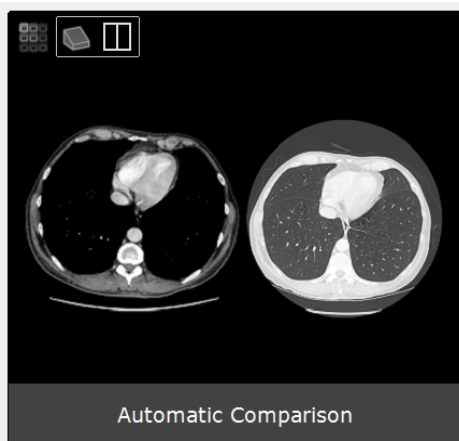


Please refer to Section 4.7 for detailed information about Reformatting and Creating New Series.

### 13.1.4 Launching automatic series comparison using drag & drop



A dedicated Automatic Comparison protocol is also available from the CT/MR Standard Family



When a series is opened in the workspace whatever the protocol that is used (for example, Standard CT, Advanced CT or any other protocols), you can drag & drop other series acquired at different time points from the QuickPatient list. Once in the workspace, you can load them from Drag Series menu accessible on the titlebar of any series in the **'Automatic comparison' protocol**.

**This protocol allows you to perform a comparative analysis in MPR mode of multiple series.**

Those loaded series are automatically aligned using the rigid or non rigid matching depending on the user settings of the protocol.

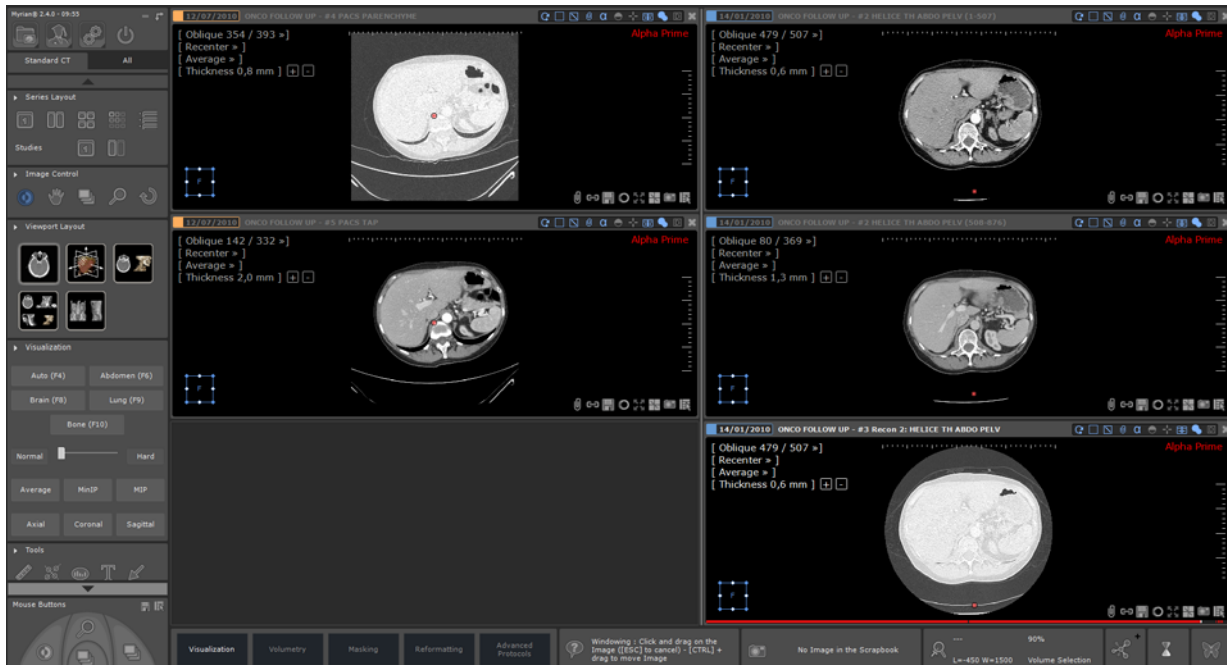


### 13.1.4.1 Method of use:

- Open one/several series or the whole study in the Standard CT protocol and proceed to the series analysis



When loading a whole study in the Standard CT protocol, by default the previous study (if applicable) is simultaneously loaded in the workspace. A default color code is allocated to each study to help you distinguish series belonging to each study/time point.



When loading a single series in the Standard CT protocol, open the QuickPatient window pressing the 'S' shortcut to access the QuickPatient list, then drag & drop into the workspace the desired series from another time point to visualize it simultaneously in the workspace



Figure 13-14 Display of the QuickPatient window in the workspace

- Click on the titlebar of one of the desired Series then drag and drop it on the titlebar of the other series to compare with
- From the drag series menu that pops up, select 'Automatic Comparison'

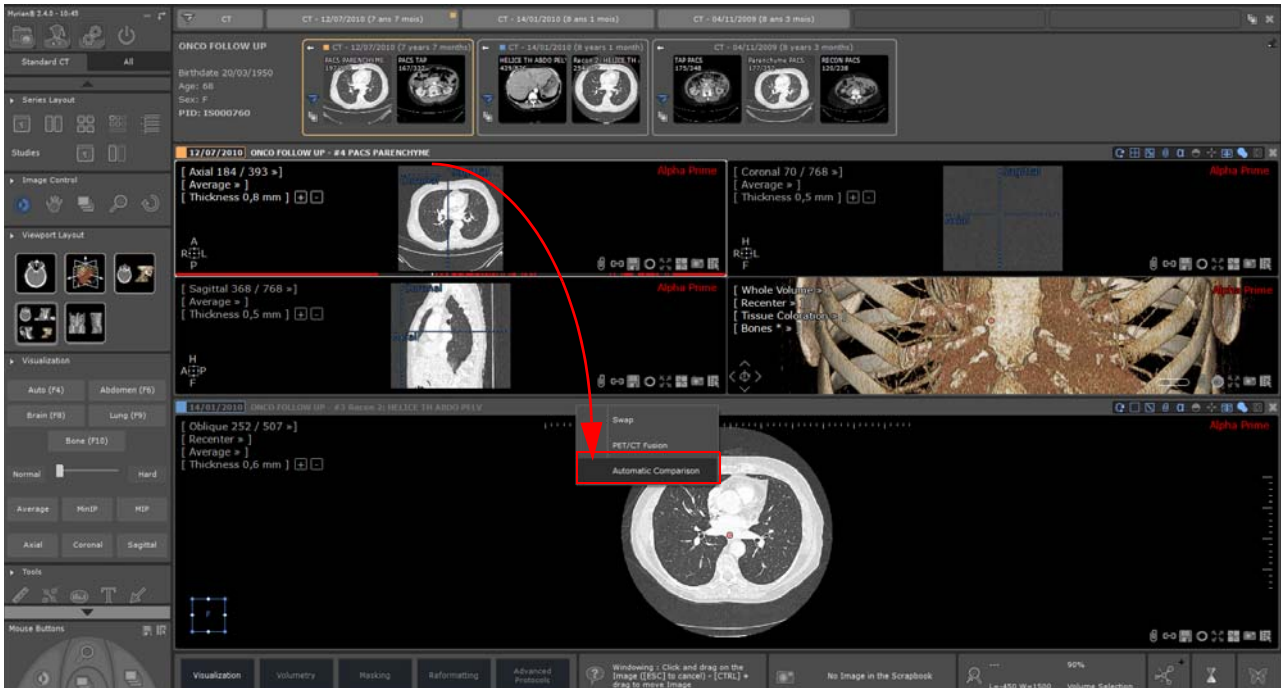


Figure 13-15 Automatic opening of the desired series in the 'Automatic Comparison' protocol using drag & drop

The selected series are automatically opened in the Automatic Comparison protocol and default matching is automatically performed to synchronize series navigation. Synchronized Series Navigation enables slice-by-slice synchronized comparison of images in Viewports of the same plane of orientation.



Figure 13-16 Visualization of the selected series side by side in the Automatic Comparison protocol


The Automatic Comparison protocol includes two different viewport layouts enabling you accordingly to visualize 2 or 3 series in comparison mode.

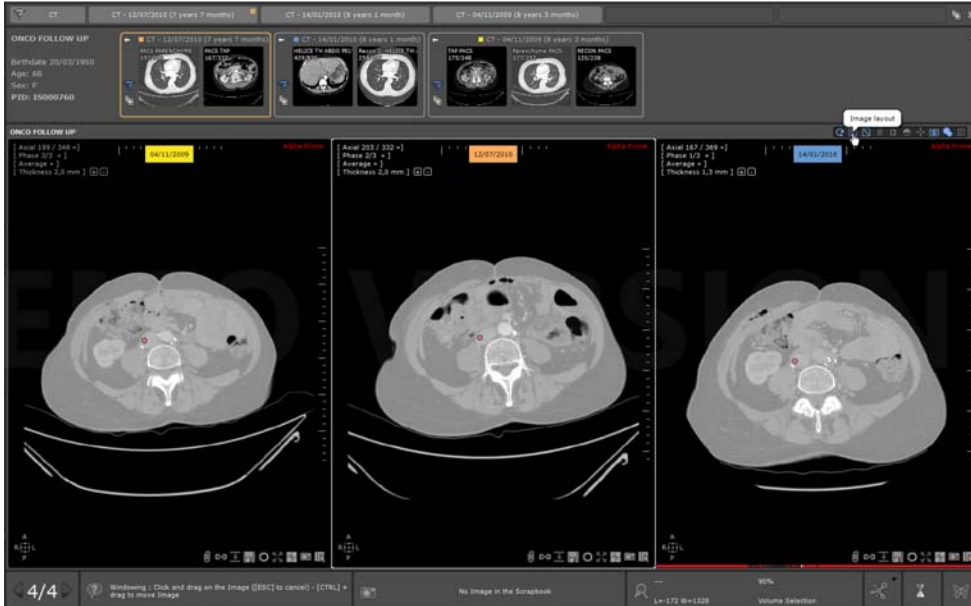




Figure 13-17 Available comparison-dedicated viewport layouts



Use the image layout  located in the view titlebar to adjust the display if you have more than 3 images to visualize



### 13.1.4.2 Visualization modes

In the Toolchest, a set of series visualization modes is available:

- Windowing presets (Auto, Abdomen, etc.)
- Edge enhancement (adjusting the slider from Normal to Hard)
- Rendering mode (Average, Minip or MIP)
- Plane of orientation (Axial, Coronal or Sagittal)
- Click the dedicated buttons to activate the desired visualization modes

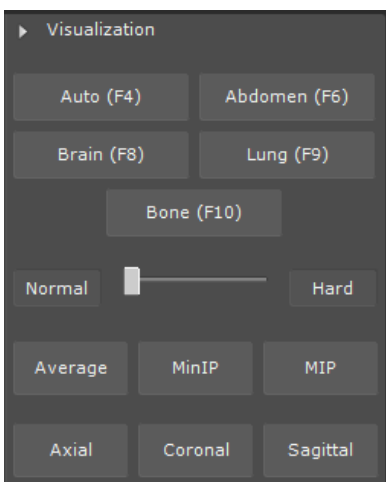


Figure 13-18 Visualization modes

Any visualization actions performed apply simultaneously to all series displayed in the workspace.

Besides the standard image control tools (navigate, zoom, translate, windowing) and the standard annotation and

measurement tools, the tools bar includes:

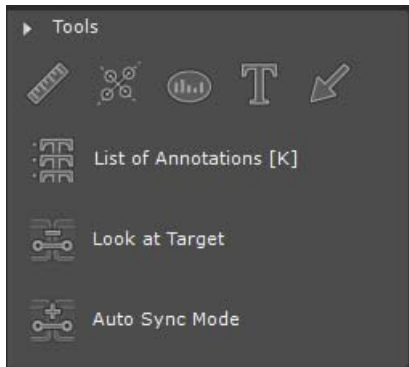




Figure 13-19 Tools bar

- The 'Look at Target' tool  enabling to move the anatomical center over the region of interest while desynchronizing series navigation

When activating the '**Look at Target**' tool, **series navigation** is automatically **desynchronized** between viewports.

The mouse cursor displays a gray cross  representing the anatomical center.

- Click a point of interest on the image to locate and better observe this point of interest in the other viewport automatically.

The other viewport automatically refreshes to locate the target as a gray dot representing the anatomical center.

- To **resynchronize series navigation**, click on the '**Auto Sync Mode**' tool 

When several series have been opened, a page navigation menu (see Section 4.3) is displayed at the bottom of the workspace enabling you to go back and forth between open series in the associated protocols.

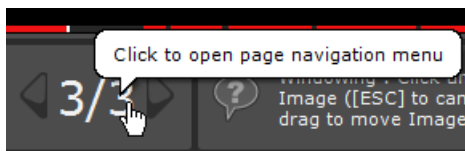


Figure 13-20 Page navigation menu

### 13.1.5 Reference Lines (Crosshairs)

Each view contains reference lines which indicate the exact position of the other MPR planes of view.

You may move these lines in order to adjust the view of the corresponding frame.

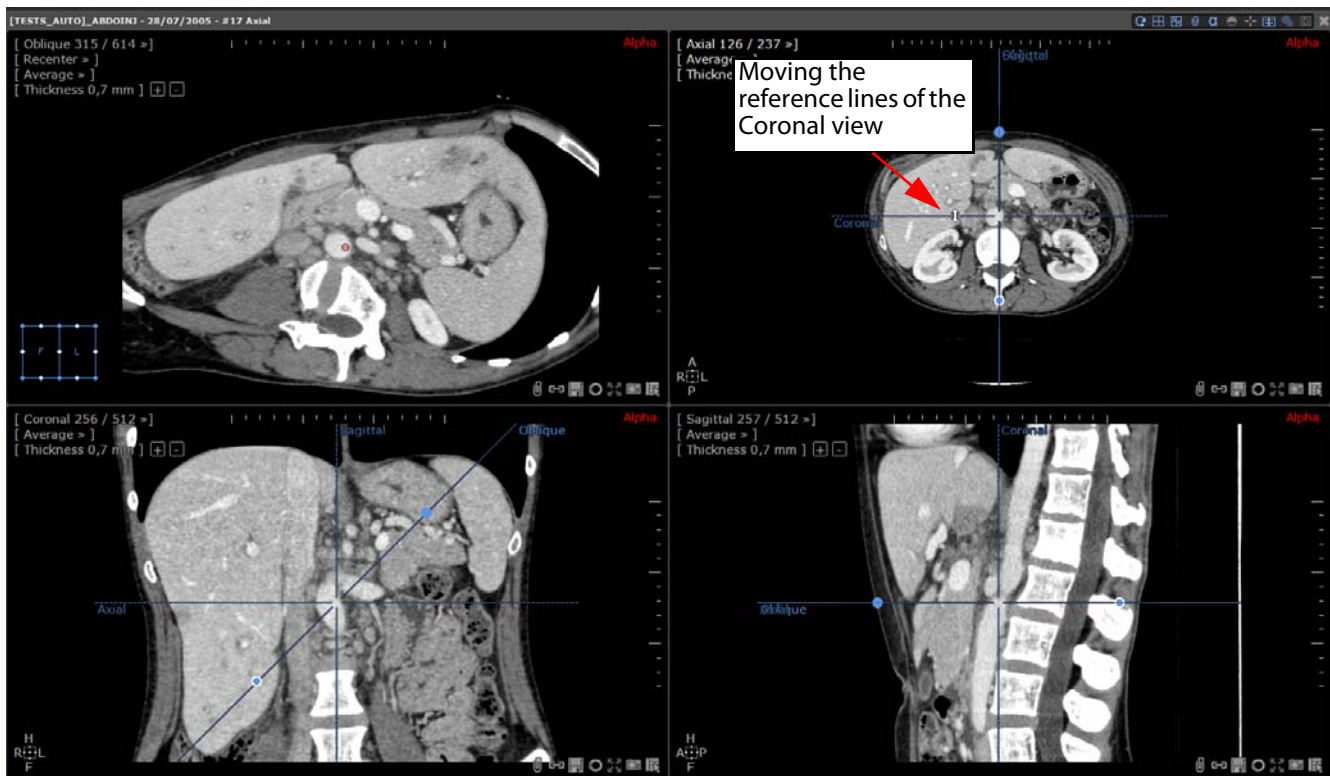


Figure 13-21 Updating a view according to the adjustment Reference Lines in other views

Reference lines may be shown or hidden by clicking on the Crosshairs Cycle button found at the top-right of the image.





Figure 13-22 Reference line cycle

Display modes, from left to right:

- Oblique plane reference line displayed alone
- All reference lines are displayed
- The Canonical Planes (Axial, Sagittal and Coronal) are displayed
- No reference line displayed.

### 13.1.6 Cross-Series Synchronization

Other than the MPR Reference lines mentioned above, it is possible to display and manipulate synchronized reference lines between MPR Mode Series and/or volumetric Native Mode Series via the 'Cross-Series in the following way:

- Open desired Series
- Locate 'Activate/deactivate cross-Series reference lines' button  (bottom-right in each frame)
- Click on  to activate the frame's axis reference line across all other frames/Series (automatically overrides any other cross-reference line).

The active frame's cross-reference line appears in red in other frames, other reference markers are drawn in light blue.

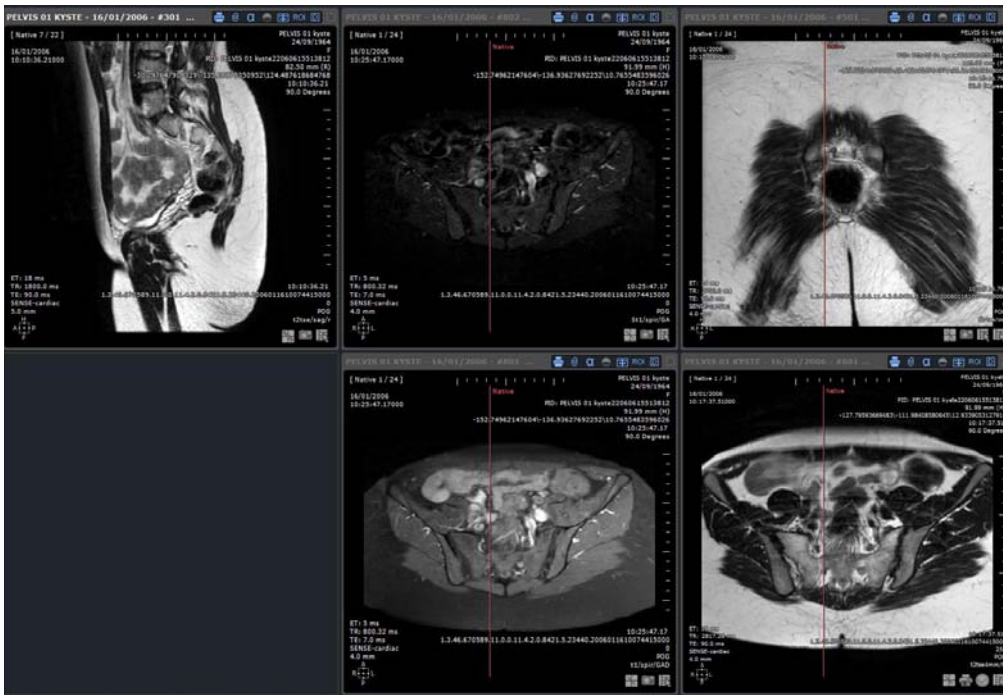


Figure 13-23 Example of Cross-Series Reference lines



Cross-Series Reference lines are only available for Series of the same patient



Use the 'Shift' key to ignore the Reference lines and click on an underlying point



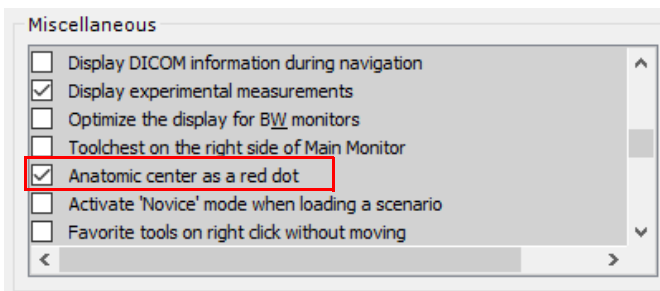
Several Series of the Same Patient which have the same Acquisition landmark can be synchronized together in Native Mode or even between MPR and Native Mode. The Anatomical Center is then visible in both Series and refreshes during navigation.

### 13.1.7 Anatomical Center

The **Anatomical Center** appears as a **red dot** in each MPR view. It is a synchronized 3D **reference** Point of Interest.



By default, the Anatomical Center is displayed as a red dot. However, you can opt for a red cross: simply deactivate the 'Anatomical center as a red dot' option in the 'Miscellaneous' box of the User Preferences>Display tab



You can move the Anatomical Center red dot by dragging it on an image. All images which are synchronized with the Anatomical Center will be refreshed accordingly.

This allows you to **easily locate** an anatomical structure of interest in each plane of view **simultaneously**.

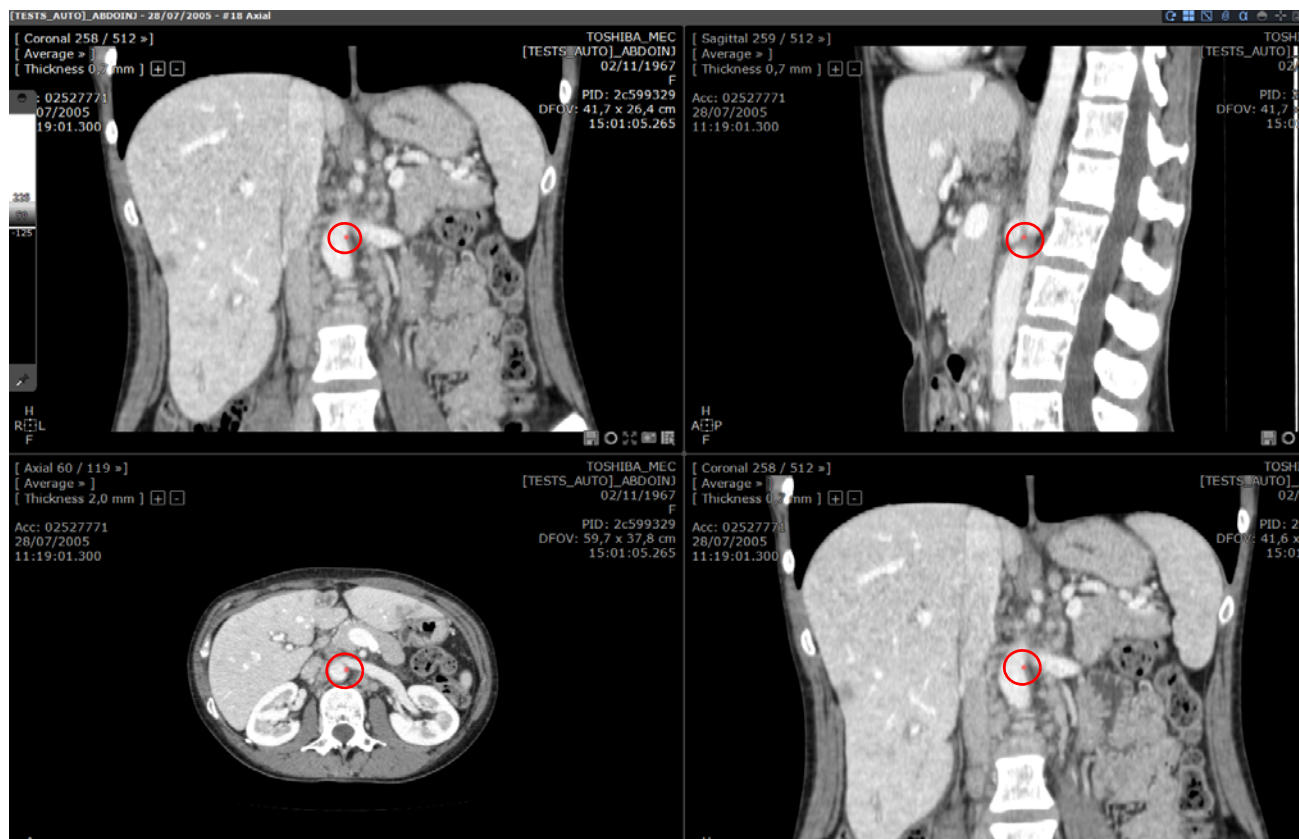


Figure 13-24 Example of the Anatomical Center (red dot)

If you navigate through a plane of view, the Anatomical Center will follow the direction of the navigation and move accordingly.

There can only be one Anatomical Center in a Series, and all images are synchronized around it by default.

### 13.1.7.1 Deactivating synchronization

It is possible to deactivate the synchronization of a plane of view with the Anatomical Center:



1. Right-click on the red dot
2. Select the 'Sync Off' option from the menu.

Figure 13-25 Desynchronization of the Anatomical Center (axial plane of view)

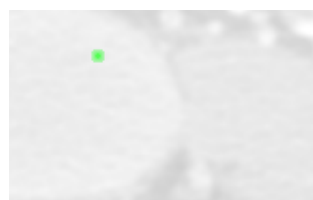


Figure 13-26 Synchro-off in the axial plane of view



The red dot in the desynchronized plane of view becomes a **green dot**. This visible marker displayed on the Viewport is only a projection of the actual Anatomical Center.



The Sync On/Off option is also available at the bottom-right of any viewport, clicking on the  button (that switches to  once synchronization deactivated).

---



If the anatomical center is displayed as a red cross , it becomes a green cross  when the Synchro is deactivated.

---



When the Anatomical center is desynchronized in a plane of view whilst another frame is set to MPR Oblique Mode a blue-colored cross appears in addition to the green cross (or green dot). The blue-colored cross displays the axis around which the Oblique Reference Line revolves (please refer to Section 13.3 for further details about MPR Oblique Mode)

---



Press the 'SHIFT' key to 'ignore' the Anatomical center and click on a point underneath


---



For reasons of clarity, when the Anatomical center is close to or above an Oblique Handle, the handle disappears and only the Anatomical center is displayed

---



Use the  'center Viewports on Anatomical center' button in the Display Command Options at top right of the Workspace to toggle on/off automatic re-centering of zoomed-in MPR Viewports. When activated, this function centers all MPR viewports on the Anatomical center (with the exception of views which are zoomed-out, constrained to a Path, or in CPR Mode)

---

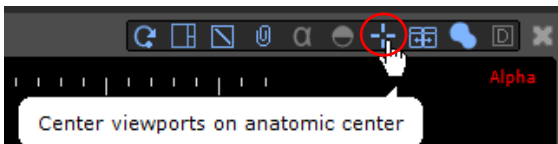


Figure 13-27 Center Viewports on Anatomical center in the Display Command Options Toolbar

### 13.1.7.2 Synchro-off in oblique plane of view

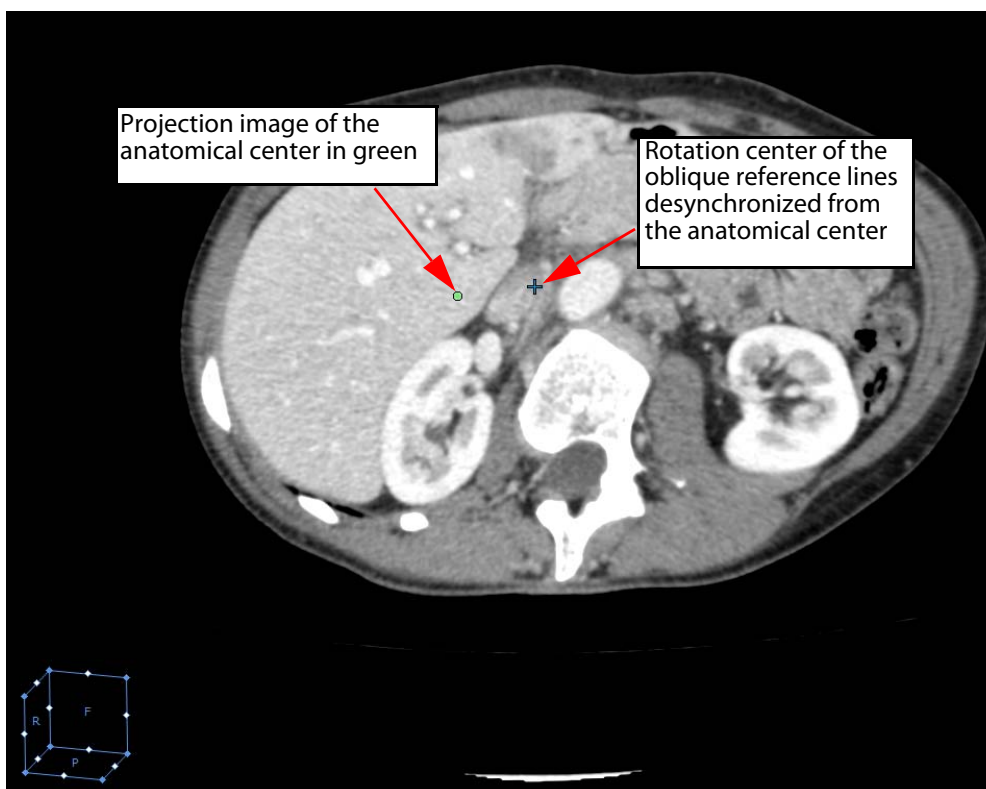
When the Anatomical center is desynchronized in a plane of view whilst another frame is set to MPR Oblique Mode, a green-colored cross appears in addition to the red dot.

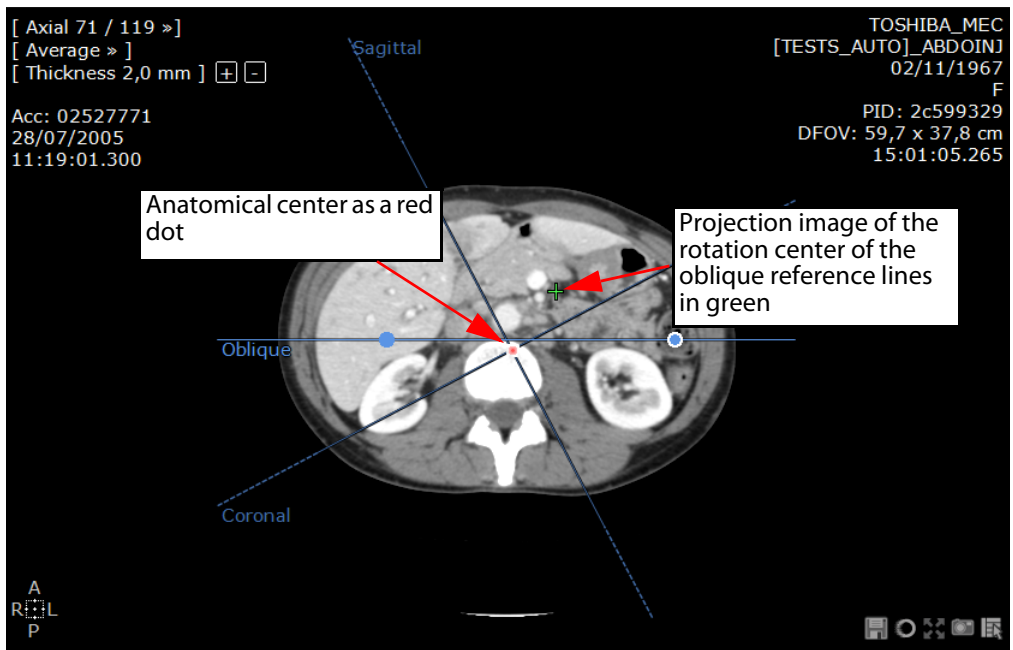




Figure 13-28 Example of Synchro-off

The green-colored cross displays the axis around which the Oblique Reference Line revolves (see Section 13.1.7 for further details about MPR Oblique Mode)





## 13.2 Thick Slice Navigation

### 13.2.1 Overview

in MPR Mode, you can adjust the Slice thickness of the Study volume. It can be used to remove image "noise"



Slices are thickened symmetrically, both in front of and behind the current slice

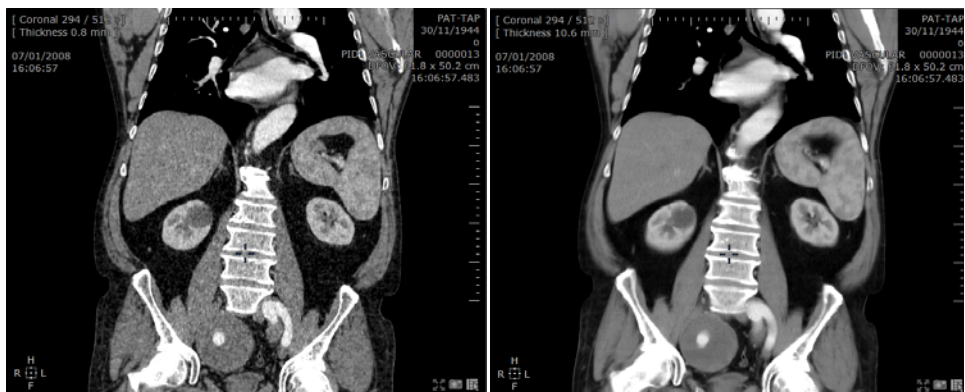


Figure 13-29 Example of use of Thick Navigation

### 13.2.2 Method of use

The Slice thickness is displayed in the menu at the top left of every frame. This menu enables free manual slice thickness adjustment.

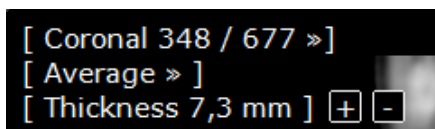
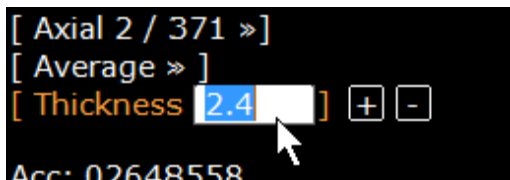


Figure 13-30 Orientation Menu in a Canonical MPR frame

To modify the slice thickness:

- Click on **'Thickness'**

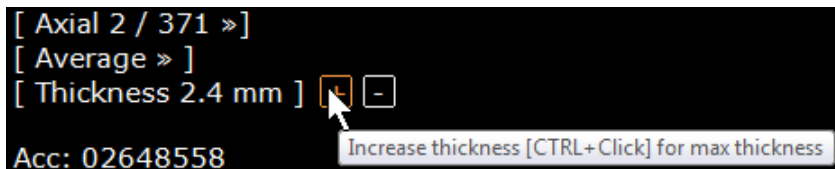




Enter a free slice thickness **one decimal value** directly (millimeters or micro)

Figure 13-31 Setting the slice thickness

or,



Press **+** **-** to increase/decrease the thickness of the slice by 1mm/1µm per click

Figure 13-32 Increasing the Slice thickness incrementally

Whenever the thickness is inferior to 0.01 mm (type in your value), the micrometric dimensionality is automatically activated (for example, 0.09 mm and below, becomes 90µm and below).

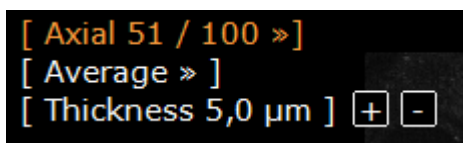
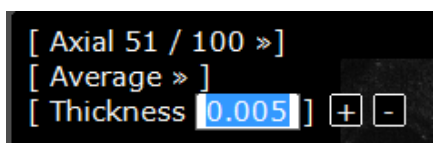


Figure 13-33 Micrometric value activation



Hold the CTRL key while you click on the +/- buttons to set the thickness to maximum/minimum available value



If reference lines are displayed when slices have been thickened, two dashed lines appear before and after the line representing the current slice. The dashed lines represent the boundaries of the thick slice.

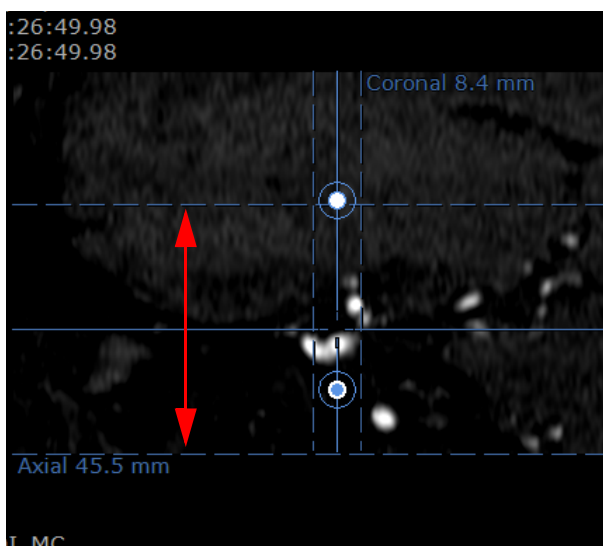


Figure 13-34 Thick Slice Reference lines



2D quantification shapes (see Section 7.9.2) do not support intensity measurement on thick slice


## 13.3 Oblique Navigation

### 13.3.1 Overview

ObliqueNavigator enables you to navigate randomly through a reconstructed volume and visualize it in any plane of orientation.

### 13.3.2 Method of Use

To activate MPR Oblique Mode:

- Select MPR Mode  from the Visualization tab
- Select 'Oblique' view from the Orientation Menu (at the top-left of the frame)

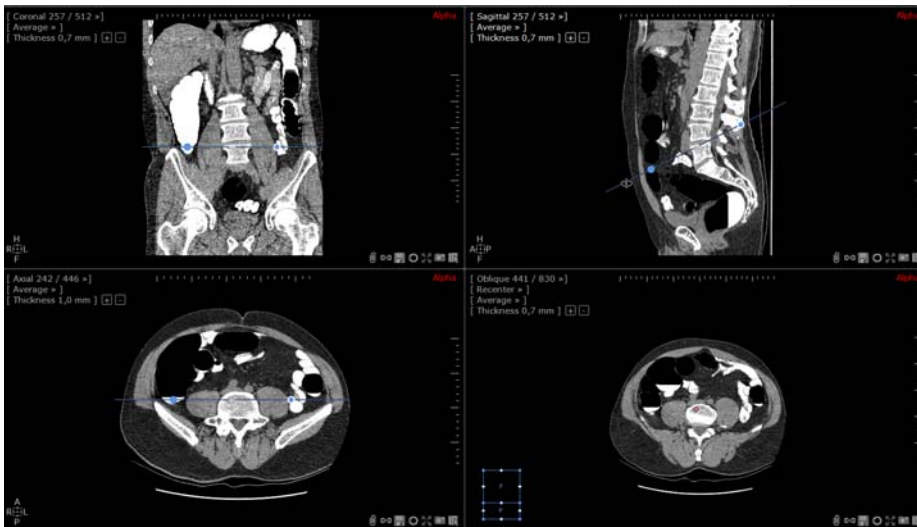
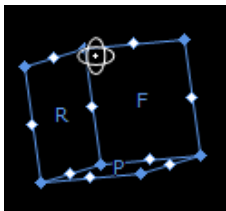


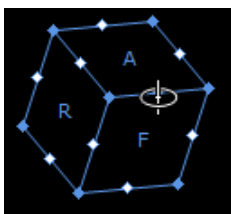
Figure 13-35 Example of MPR + Oblique

To adjust the plane of orientation using the Orientation Cube:



Click on a corner point and drag the mouse to rotate the image volume randomly about the Anatomical center

Figure 13-36 Corner point rotation



Click on an intermediate point and drag the mouse to rotate the image in a constrained way about an axis parallel to the line on which the intermediate point lies

Figure 13-37 Intermediate point rotation



Click on the letter at the center of a face to rotate the image about the center of the image

Figure 13-38 Letter rotation



Each face of the Orientation Cube contains an indication of that face's orientation (L=left, R=right, A=anterior, P=posterior, H=head, F=foot).

---



Press the 'ALT' key to automatically place the Anatomical center under the Mouse Pointer in the Oblique Viewport.

---



Hold the 'ALT' key while you drag the Mouse over the Image to swivel around the Anatomical center.

---

### 13.3.3 Single-oblique and Double-oblique

You can also use the Oblique Reference Line handles to modify the Oblique Plane of View

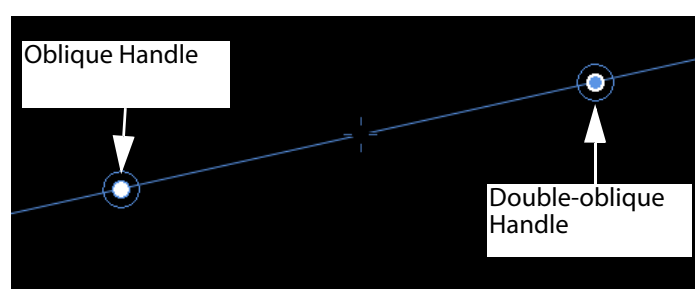


Figure 13-39 Oblique Reference Line



When the Double-oblique Handle (blue) is used to rotate the Oblique View, it maintains previous modifications to the Oblique View.

---



When the Single-oblique Handle (white) is adjusted in any viewport, it instantly resets the Oblique View and Reference Lines in all viewports, canceling any previous Oblique modifications.

---

### 13.3.4 Coordinate System selection for improved volume visualization

This function enables you to set the MPR either to the patient canonical planes or to the acquisition canonical planes when the Native image orientation is significantly "tilted". The coordinate system can also be rotated manually to any arbitrary orientation.

Specifying your own coordinate system is a good option to get the best reconstruction plane to use for diagnosis, saving time and memory, and avoiding the creation of an infinite number of slices.

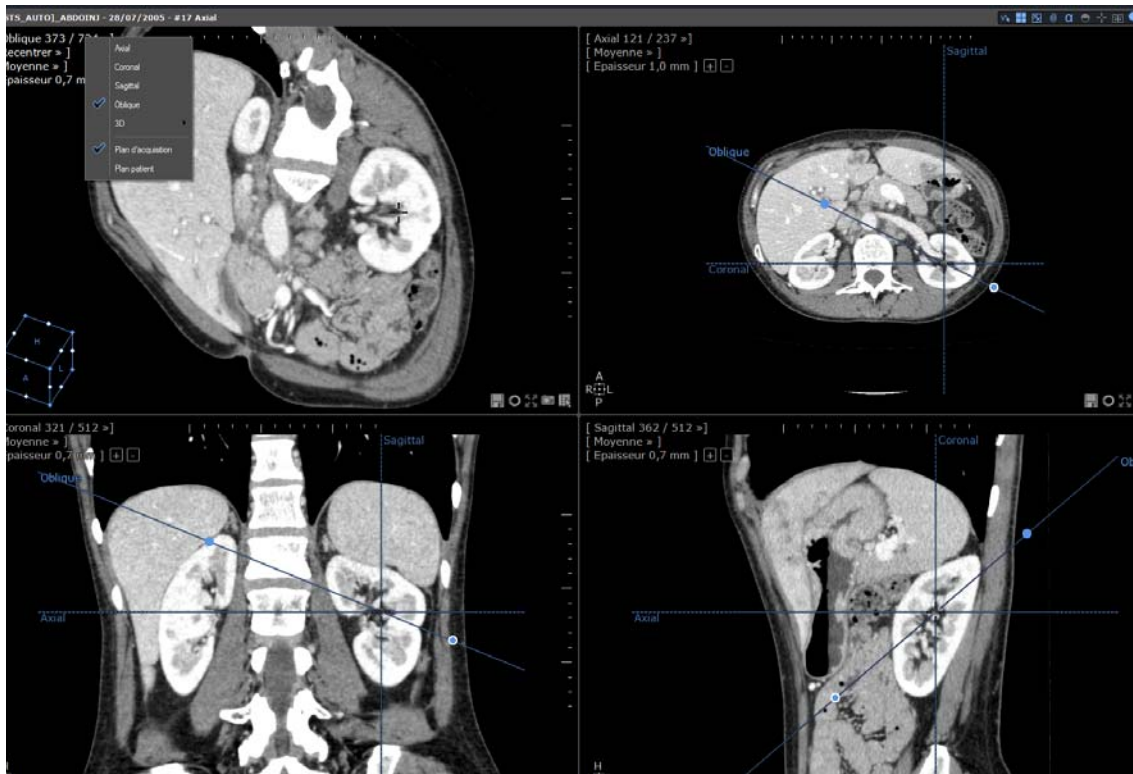


Figure 13-40 Example of coordinate system selection in MPR

In the Viewport orientation menu, the following coordinate systems are available:

- Acquisition Plane or Patient Plane

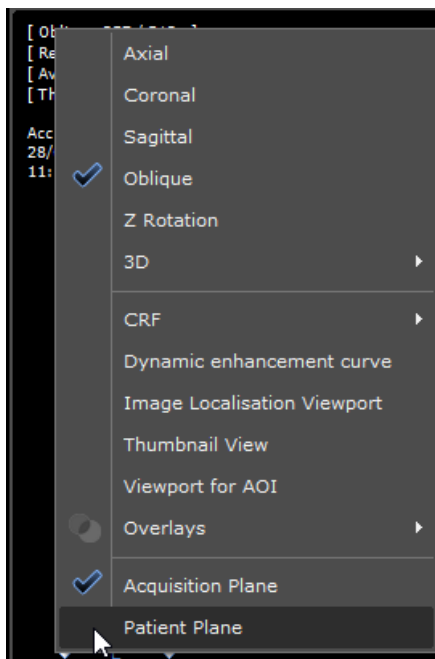


Figure 13-41 Select coordinate system

If you wish to set **manually** a custom coordinate system:

- Use the most dotted end of the Axial/Sagittal/Coronal reference line in any viewport (the mouse cursor will change form) as you would use an oblique rotation handle
- Drag a reference line and the corresponding plane will rotate as if it was an oblique viewport. The other MPR plane will also be rotated so as to maintain orthogonality.
- Release the reference line, the coordinate system is recomputed and applied to the reconstructed images. Axial/sagittal and coronal viewports will be displayed as new references.



Acquisition Plane is the default coordinate system.

## 13.4 MIP/MinIP Navigation

### 13.4.1 Overview

MIP/MinIP Navigation enables the use of intensity projection rendering modes.



The MIP rendering tool can be used on PET studies with FDG [18F] fluoro-2-deoxyglucose and may be suitable for use with other oncological probes. Some adjustments may be required to optimize performance with other radiopharmaceutical products.

### 13.4.2 Method of use

To modify Rendering Mode (by default set to 'Average' at Series load-up):

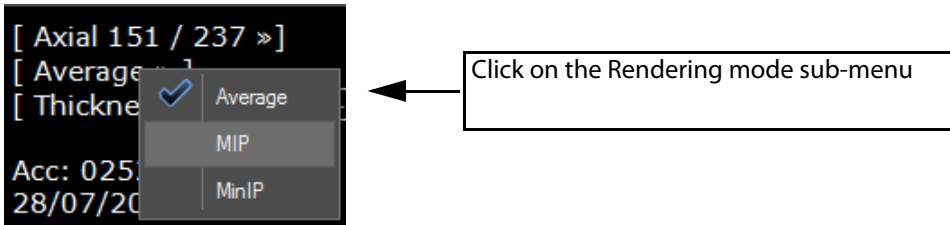


Figure 13-42 Rendering modes

- Select from one of the 3 available rendering modes:
  - 'Average' mode: accumulates images as if they were printed on transparent film and stacked on top of each other on a Viewing Box. Thickening slices in this mode has the effect of reducing grainy 'noise' sometimes present in very fine DICOM images.
  - 'MIP' (Maximum Intensity Projection) mode: displays the highest values from a set of stacked slices (useful for visualizing structures of high intensity such as bones or injected vessels).
  - 'MinIP' (Minimum Intensity Projection) mode: displays the lowest values from a set of stacked slices (useful for visualizing structures of low intensity such as airways in lungs or bile ducts). This feature can also be used in the Volume of Interest Mode.

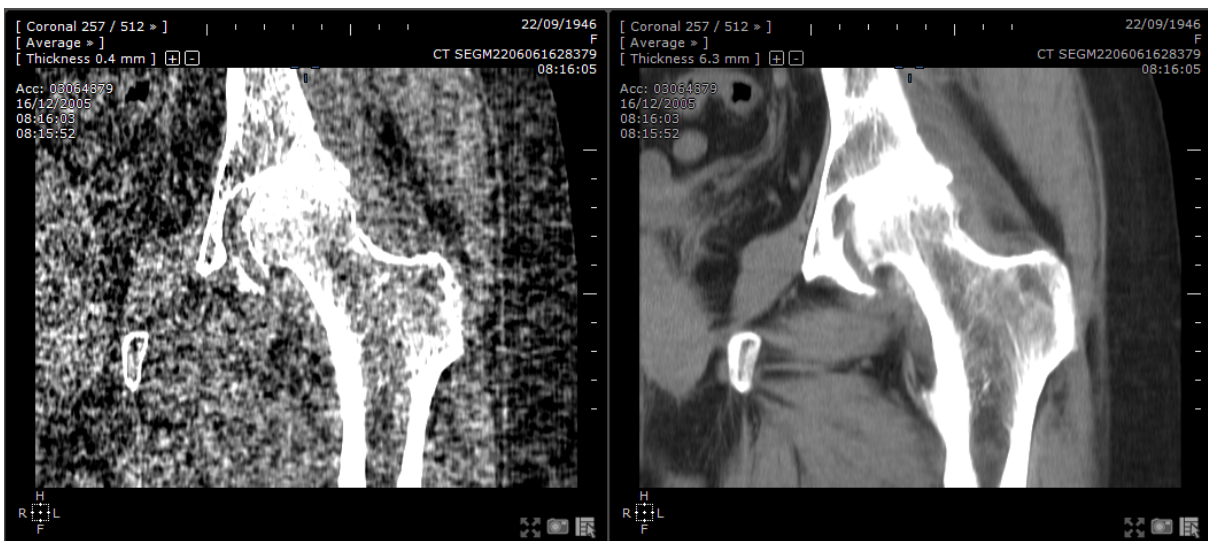


Figure 13-43 Example of slice thickening ('Average' rendering mode) to reduce image noise

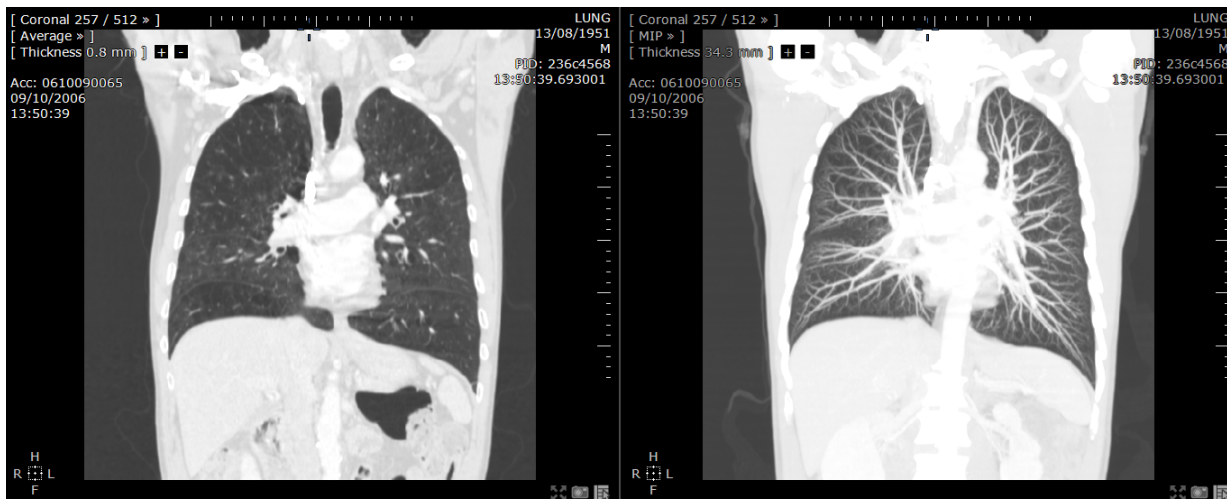


Figure 13-44 Example of slice thickening with MIP Rendering to view high intensity structures

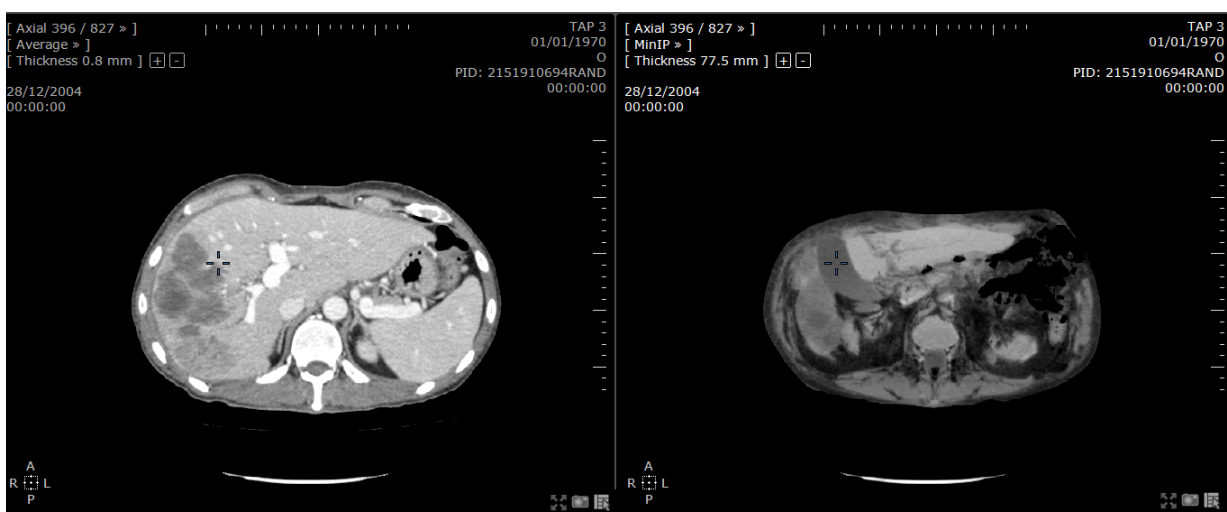


Figure 13-45 Example of Slice thickening with MinIP Rendering to view low intensity structures

## 13.5 CPR Navigation

### 13.5.1 Overview

The CPR feature activates CPR (Curvilinear MPR) viewport and displays the global view of a Path in a 2D plane to analyze curved or tubular-shaped organs such as vessels, airways, etc.

### 13.5.2 Method of use:


- Create a Path using the 'Path' tool  (see Section 4.6.4),
- Open the Orientation Menu at top-left of the Viewport,
- Click on 'Curvilinear' and select the desired path from the submenu.





Figure 13-46 Top-left Viewport orientation menu

- Modify the layout to your needs.

In the example below the following settings were applied:

- To the left and right of the 3-D frame, 2 CPR frames have been re-centered to display Coronal and Sagittal views of the volume. The Windowing has also been adjusted to enhance visibility of the aorta
- The center frame displays a 3-D rendering with a "Whole View" tissue coloration preset



Figure 13-47 Example of CPR usage (Stretched Mode)

Two types of CPR rendering are available:

- Stretched CPR Mode (as described above)
- Straightened CPR Mode (the Path/Vessel is a straight vertical line)

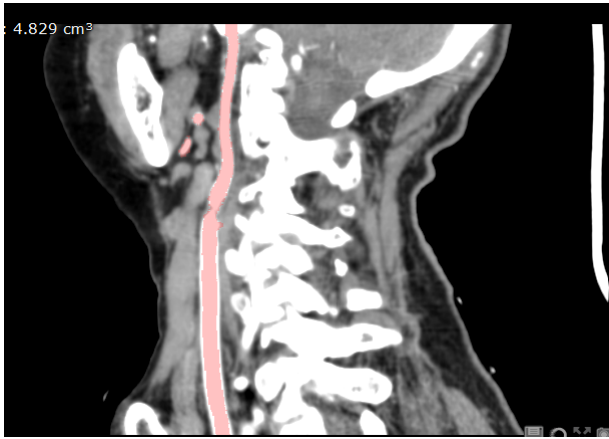


Figure 13-48 Stretched CPR Mode

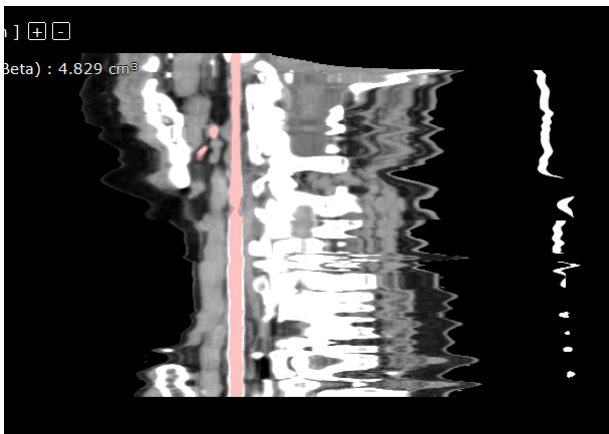


Figure 13-49 Straightened CPR Mode

After a path has been drawn, the type of CPR Rendering can be selected via the Rendering Mode Menu (top-left of the Viewports).

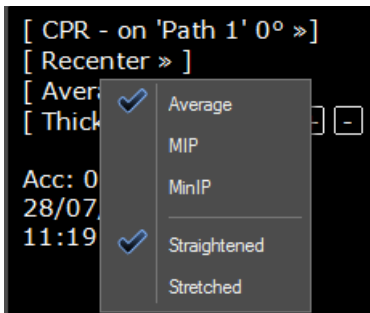


Figure 13-50 Selection of the CPR Reformation Mode



The Path does not appear in Straightened CPR Mode as it is implicit that it is a vertical line.



These types of CPR Rendering can also be activated via the Protocols in the optional XP-Vessel Add-on.



Curvilinear Mode can also be activated via the right-click menu on the Path or via the Anatomical center context menu.





You can click directly anywhere on a Path or one of its Branches in 2D or in 3D frames to select it.




The **orientation** of the CPR Viewport **auto adjusts to best-fit** the size and shape of the active Viewport.



Stenosis Measurements are displayed in both Stretch and Straightened CPR Mode.

### 13.5.3 Trace Path Section or Extension

To modify or redraw a Path:

- Select the 'Redraw Path' tool  at right in the Path floating menu
- Place the mouse cursor on the vessel Centerline (highlights Centerline)
- Click on the Path



Myrian® selects the closest Control Point and launches the Path Edition Mode automatically

- Click and hold the mouse button down to draw new Path line as desired
- Release the mouse button to complete the drawing your new Path line



Myrian® automatically finds the closest control point of the branch being edited and replaces the existing path between the Start and End point.

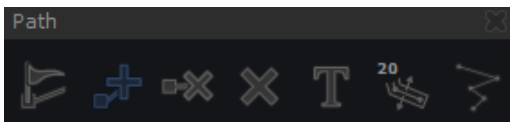


Figure 13-51 Trace Path Section or Extension



If the line you draw does not end on an existing Path Point, the following message appears to ask whether you wish to replace the existing Path, preserve it or abort the process.

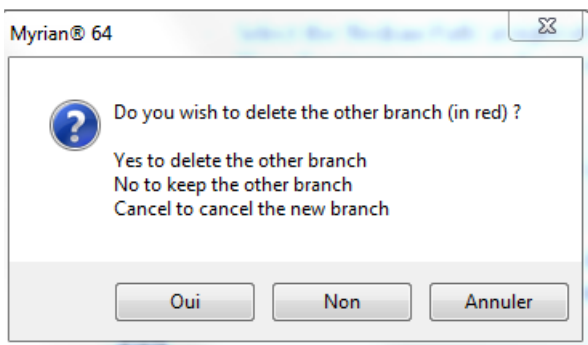


Figure 13-52 Path Redraw dialog window

## 13.6 Surfacic ROI

### 13.6.1 Overview

Surfacic ROI Mode presents an enhanced 3D Surfacic rendering of any or all ROI contained in the active Series.



Surfacic ROI Mode is not suitable for Diagnostic Purposes.

---



3D viewport rotation is synchronized between Surfacic ROI and Whole Volume viewports.

---

### 13.6.2 Method of Use

To use the Surfacic ROI mode, follow the steps below:

- Create one or more ROI using the '+' symbol in the Regions of Interest' Toolbar
- Select the Surfacic ROI option from the Views Menu at top right of any Viewport

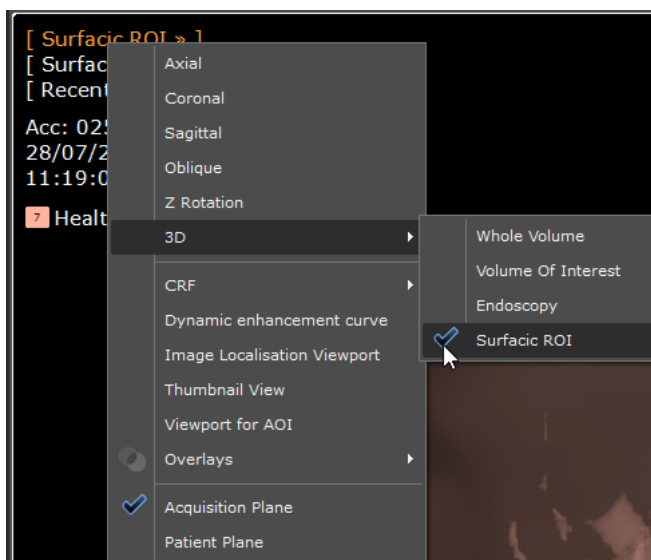


Figure 13-53 Surfacic ROI Mode option (Views Menu)

The following ROI Editing Tools 3D are usable in Surfacic ROI mode:

- Fill
- Fill Holes
- Inflate
- Deflate

Please refer to Section 7.16.3 for further detail on how to use the ROI Editing Tools.

### 13.6.3 Surrounding ROI

Several parameters of the ROI can be adjusted via the 'Parameters' screen, such as Name, Color, etc. (for further details about tuning ROI Parameters, please refer to Section 7.16.14).

Surrounding ROI are ROI that contain other ROI and that hence may at times hide them from view. In order to be able to see any 'contained' ROI:

- Right-click on the concerned ROI (that contain or hide other ROIs) in the Regions of Interest Toolbar
- Select 'Parameters' from the menu to open the ROI Parameters Screen

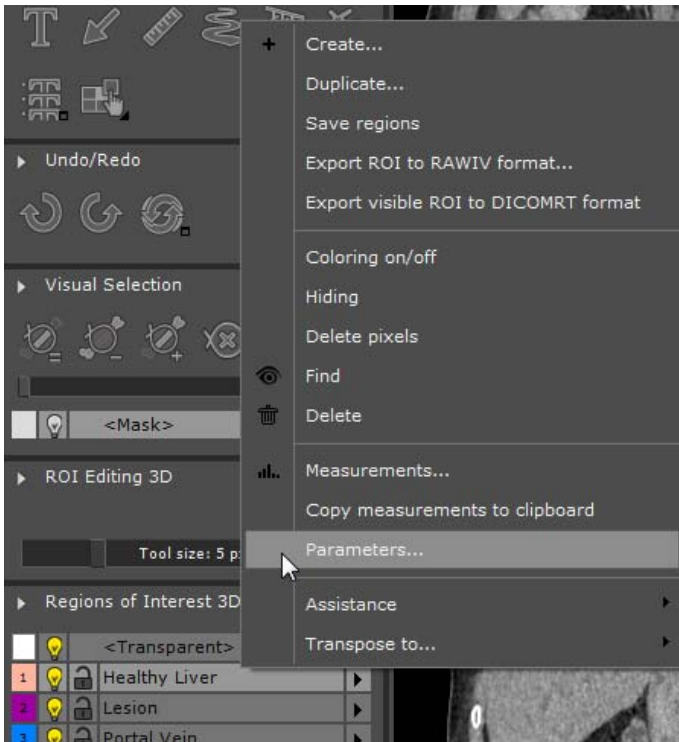


Figure 13-54 Parameters option in the ROI Context Menu

- Check the 'Surrounding ROI' checkbox
- Move the Opacity Slider to the desired level and click OK

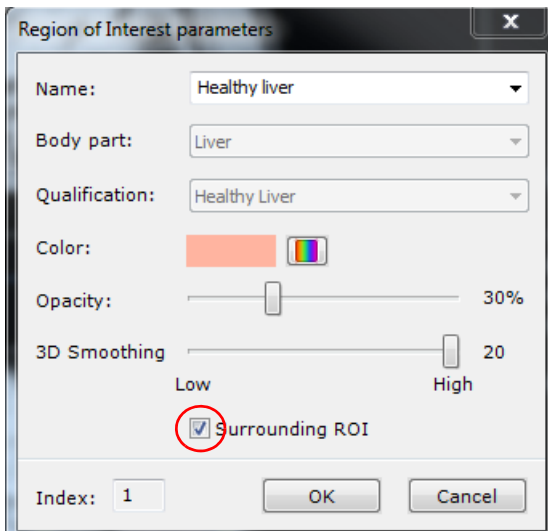


Figure 13-55 ROI Parameters Screen



If you are not entirely satisfied with the Surfacic ROI 3D rendering, you can adjust the ROI smoothing (see Section 7.15.18).

### 13.6.4 Example of Use

In the example below, a liver has been segmented into a full set of ROI including Vascularization. The Portal Vein ROI is made visible by tuning of the transparency level of the Surrounding ROI.

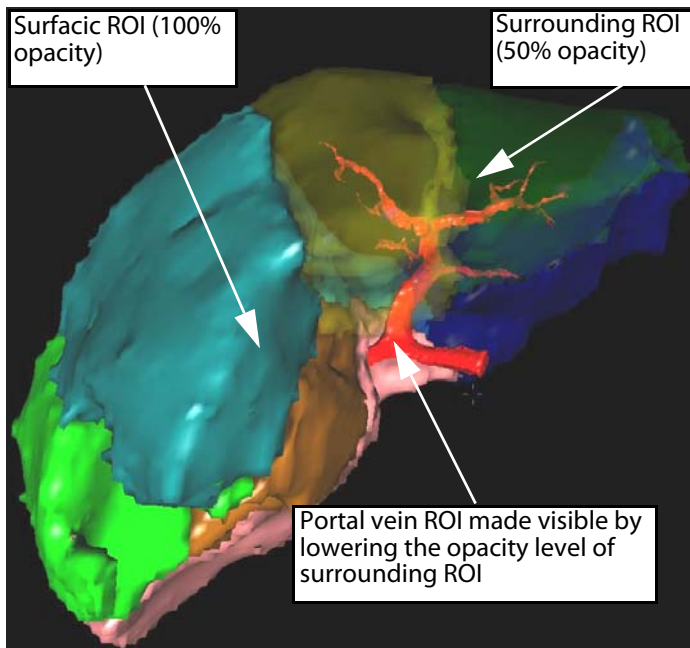


Figure 13-56 Example of use of Surfacic ROI to visualize Liver ROI

### 13.6.5 Quick ROI/ROI portion removal

In 3D Surfacic ROI mode, you can remove tissues from a selected ROI and adjust the ROI volume of interest.

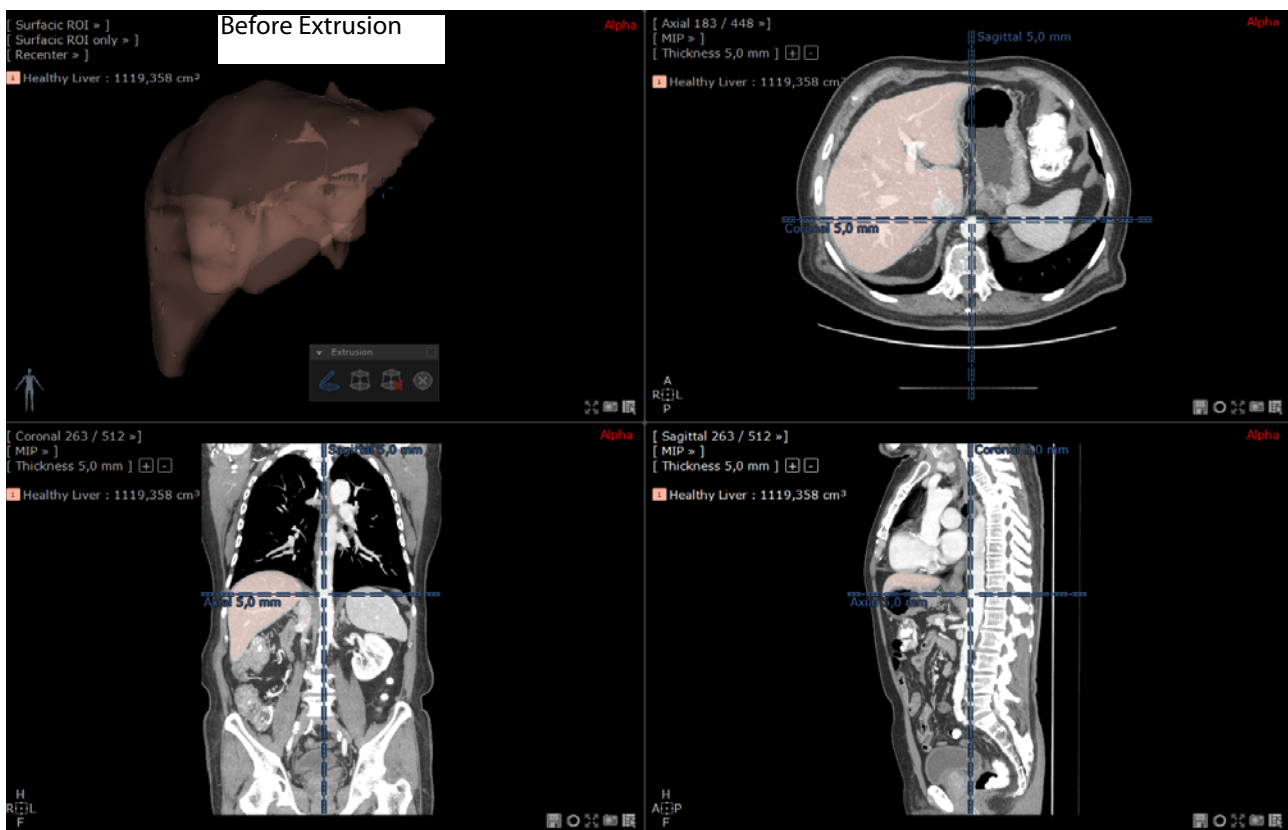




Figure 13-57 Selected ROI displayed in Surfacic ROI before extrusion

Follow these steps:

- Select the Surfacic ROI option from the view menu at top right of the selected viewport

- Click on the extrusion icon  from the ROI Editing 3D tools (see Section 7.15.3)

- Select the 'Add extrusion contour' icon  and draw a complete freehand contour around the portion of the ROI to be removed

Automatically, the contoured part of the ROI is suppressed and the volume adjusted.

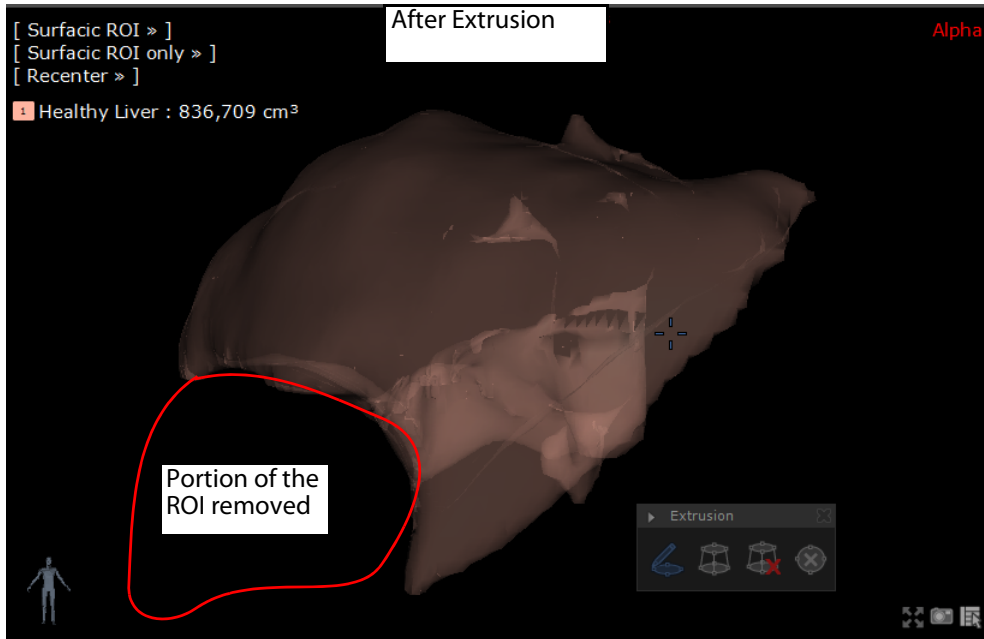


Figure 13-58 Using the extrusion tool in surfacic viewport protocol to remove portion of a selected ROI



In Surfacic ROI mode, the extrusion tool can either be visualized in Surfacic ROI only or mixed MPR (see following section).

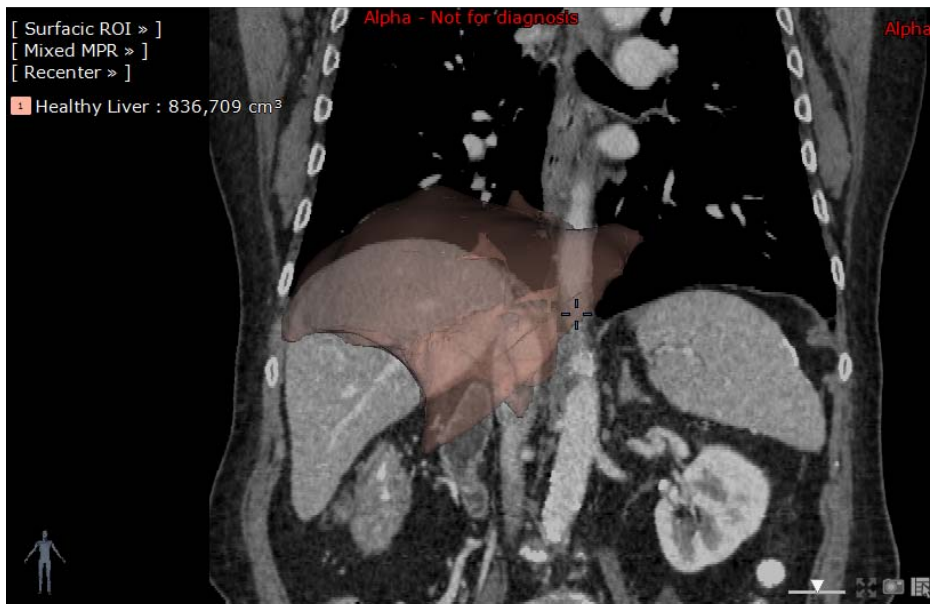


Figure 13-59 Mixed MPR in Surfacic mode



In Multiphase, the extrusion tool can only be performed on the 3D view when "All phases" is selected from the Multiple Phase menu.

### 13.6.6 2D distance measurement tool


You can perform distance measurements via two points positioned on one single ROI or between 2 distinct ROIs created in the Surfacic ROI viewport.



Be aware that the measurement calculation is performed from ROI surface to ROI surface. This means that the measurement is influenced by both factors:

- The ROI surface computation algorithm itself, that may adjust smoothing and precision according to ROI type
  - Any possible synchronization performed between multiple phases. In this case, if for instance, two ROI belongs to two different phases, activating the synchronization will deform ROI and thus have an impact on the measured distance.
- Therefore, this measurement tool must not be used alone and for diagnosis purpose. Consider this measurement as an indication only.

To do so, create a segment as follow:

- Select the measurement tool  from the Toolbox
- In the ROI Surfacic viewport, click on a desired surface to locate the first point
- Drag the created segment on the surface onto the second point and release the left mouse button

Myrian® calculates the distance between the 2 points and displays it next to the drawn segment. The measure is expressed in mm with 1 decimal.

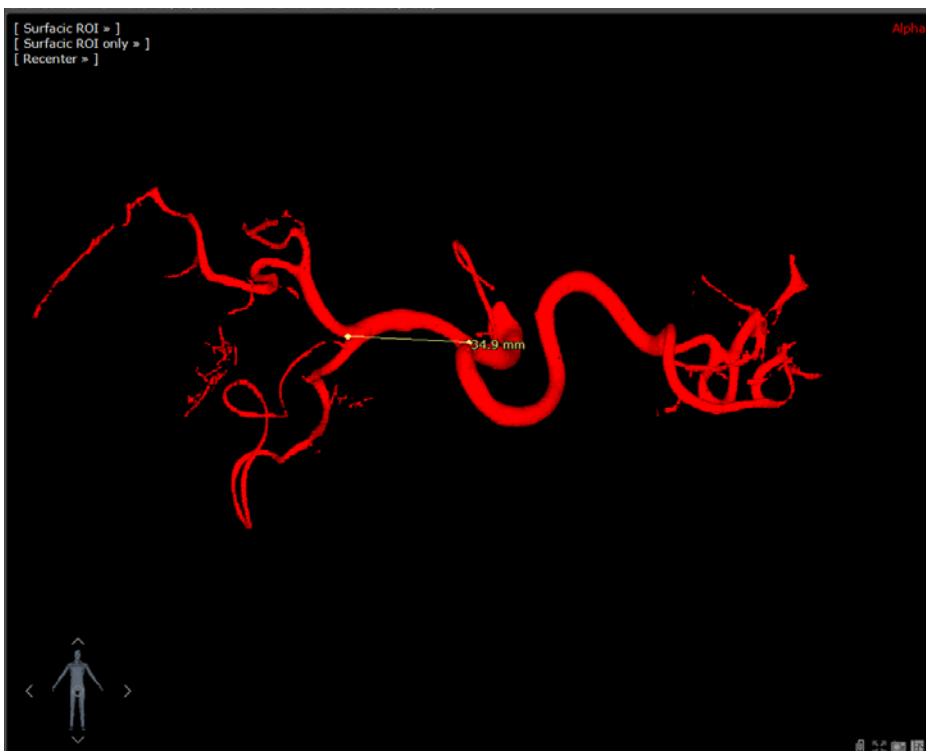


Figure 13-60 Measuring a segment in Surfacic ROI

You can create an indefinite number of segments.

A segment which has been created can be deleted via the right click menu and can also be repositioned and moved via the segment extremities.

The segment extremities can be positioned on any surface in the viewport including the cutting plane.



If a ROI is edited or even recomputed, existing segments are attached to the closest surface.



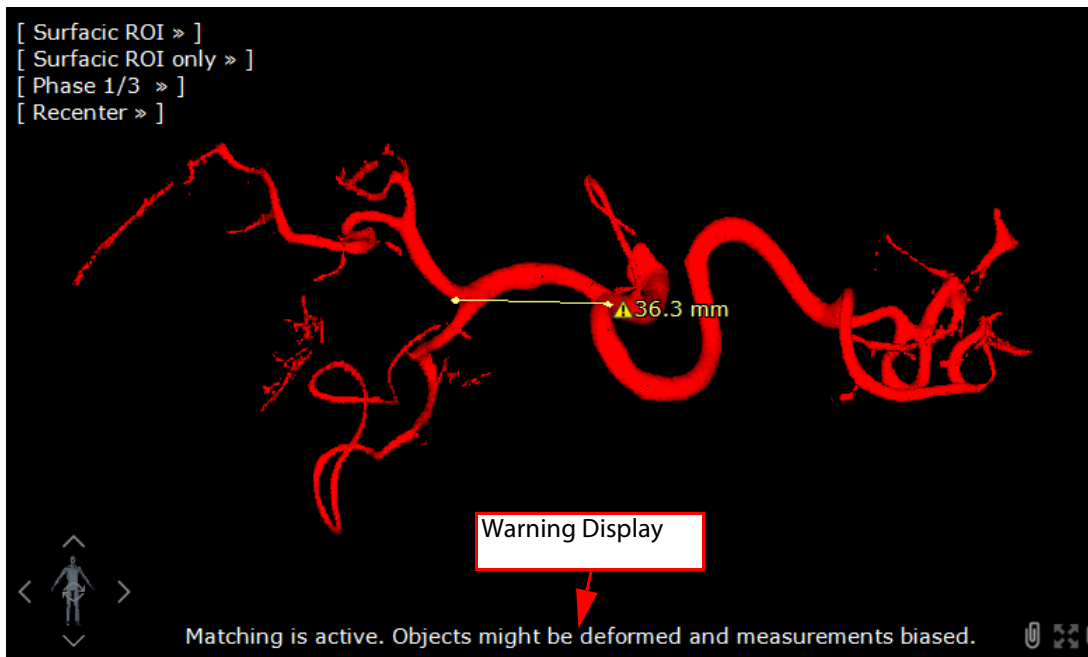
This measurement cannot be performed on surrounding ROI.



Measurements are not preserved when closing the series.



If a matching has been performed and is active (such as in multiphase mode), the ROIs might be deformed and the distance measurement biased. To inform you, a warning message is displayed at the bottom of the viewport and a warning symbol ⚠ is displayed next the measure. This warning is only displayed in case of matching.



### 13.6.7 Mixed MPR/3D rendering mode

This rendering mode is available from the Surfacic ROI viewport menu.

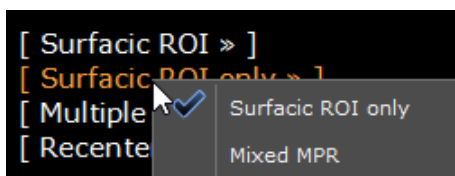


Figure 13-61 Surfacic ROI only/ Mixed MPR Rendering Mode menu

When mixed MPR is selected, an MPR plane of the Series is superimposed to the ROI.



There is no synchronization between the MPR plane and the other viewports.

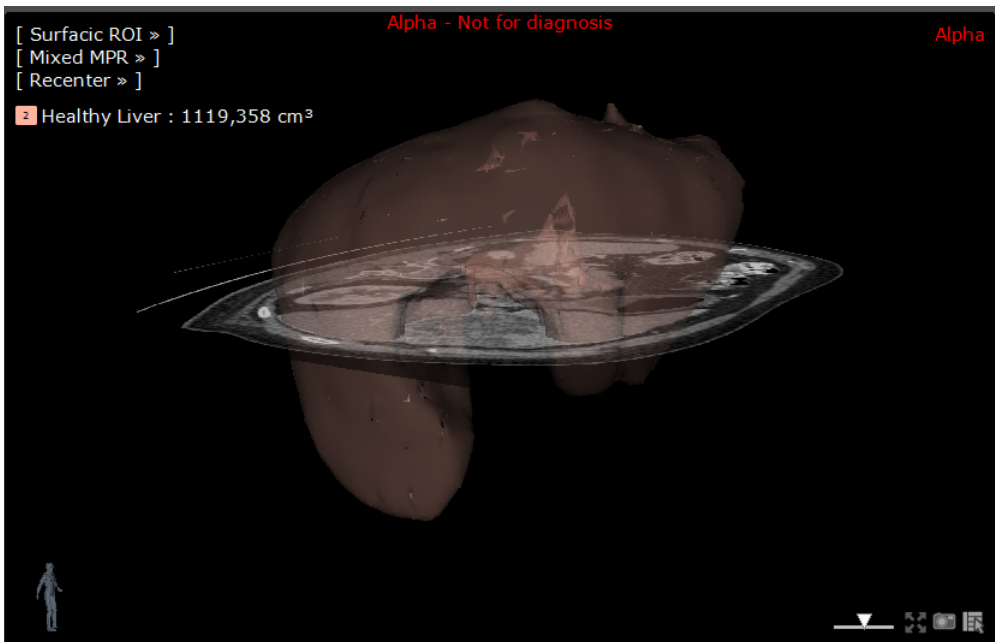




Figure 13-62 Superimposition of the MPR Plane with Surfacic ROI.

By default, the MPR plane is sagittal. It can be controlled by the Navigation Tool  (and can be performed on either plane).

Using the Image tools  on either of the viewports only apply to the selected viewport. When used on the Mixed MPR viewport, ROI are never affected.



Pressing the Shift key while using the Navigation tool restores the rotation capabilities of the viewport which is particularly useful in Cutting Surface where rotating is often needed to adjust the surface.

The orientation of the MPR Plane can also be changed through the “Recenter” Viewport Menu:

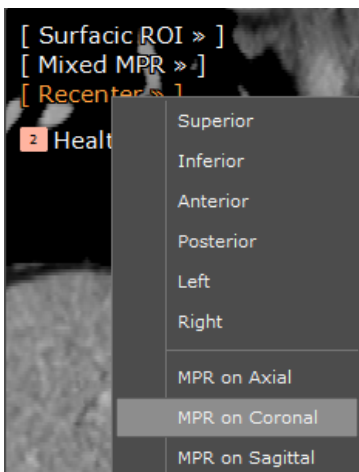


Figure 13-63 Recenter Viewport menu

Last, the MPR Plane transparency can be adjusted via a slider located at the bottom-right corner of the Viewport.



Figure 13-64 MPR plan transparency slider (without affecting the ROI)

- Move the transparency slider to the extreme left: the MPR plane becomes transparent



- Move the transparency slider to the extreme right: the MPR plane becomes opaque (black).



The MPR plane cannot be freely rotated as it is always aligned to the canonical planes.



The anatomical center can be repositioned on the MPR plane via the standard Navigation tool (activated beforehand) double-clicking on the red point.

## Multiphase mode

In MPR multiple phases (see Section 13.8.4 for detailed information), the displayed phase of the MPR plane is controlled by a dedicated “MPR Plane Phase Selection” viewport menu:

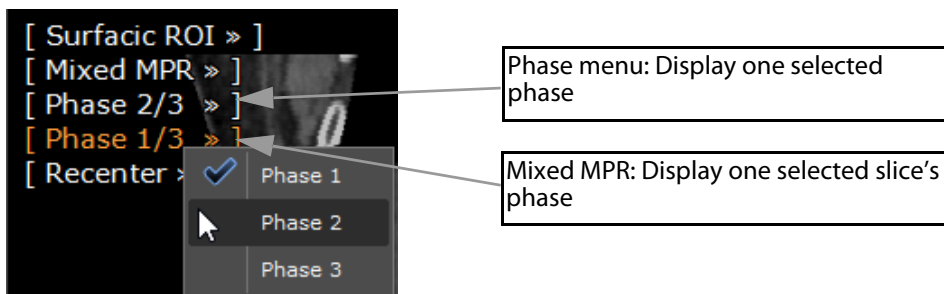


Figure 13-65 MPR plane phase selection Viewport menu

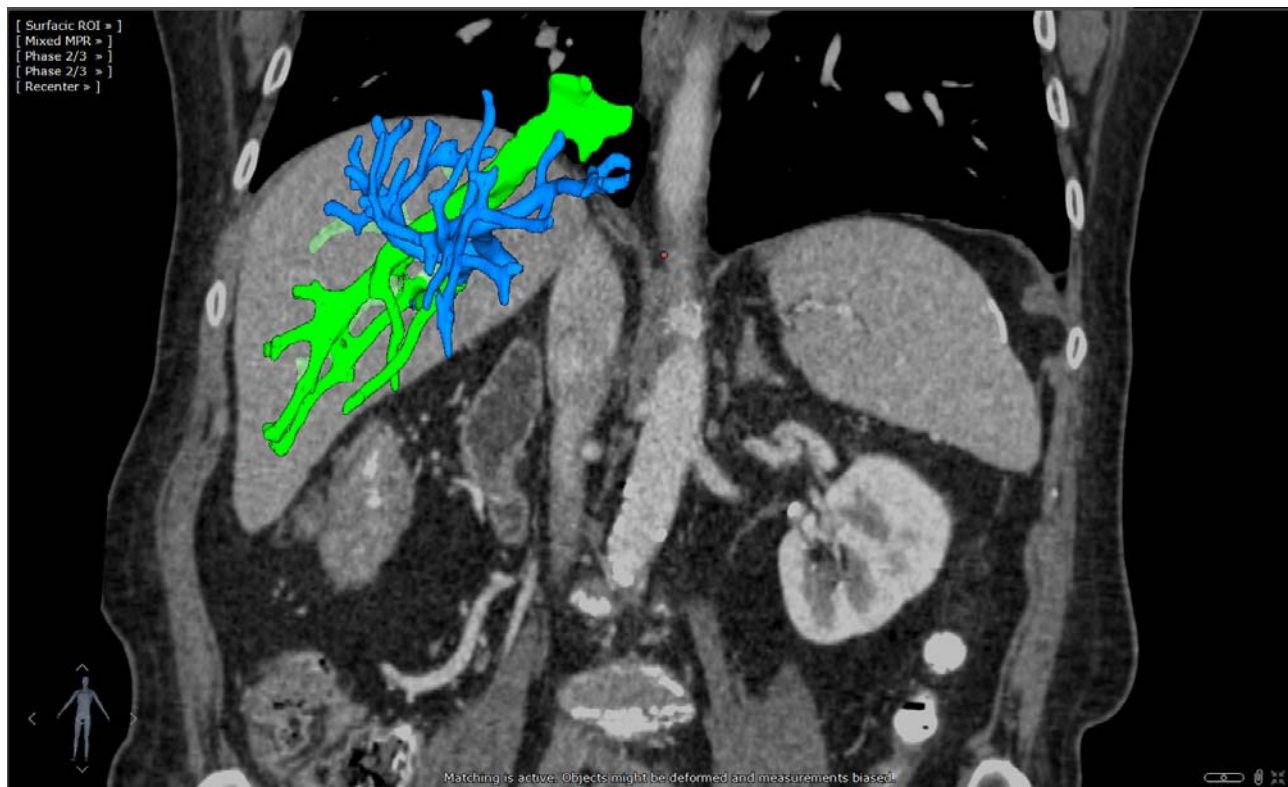


Figure 13-66 Multiphase Mixed MPR Rendering Mode: An MPR Plane of the Series (for a given Phase) is superimposed to the Surfacic ROI.

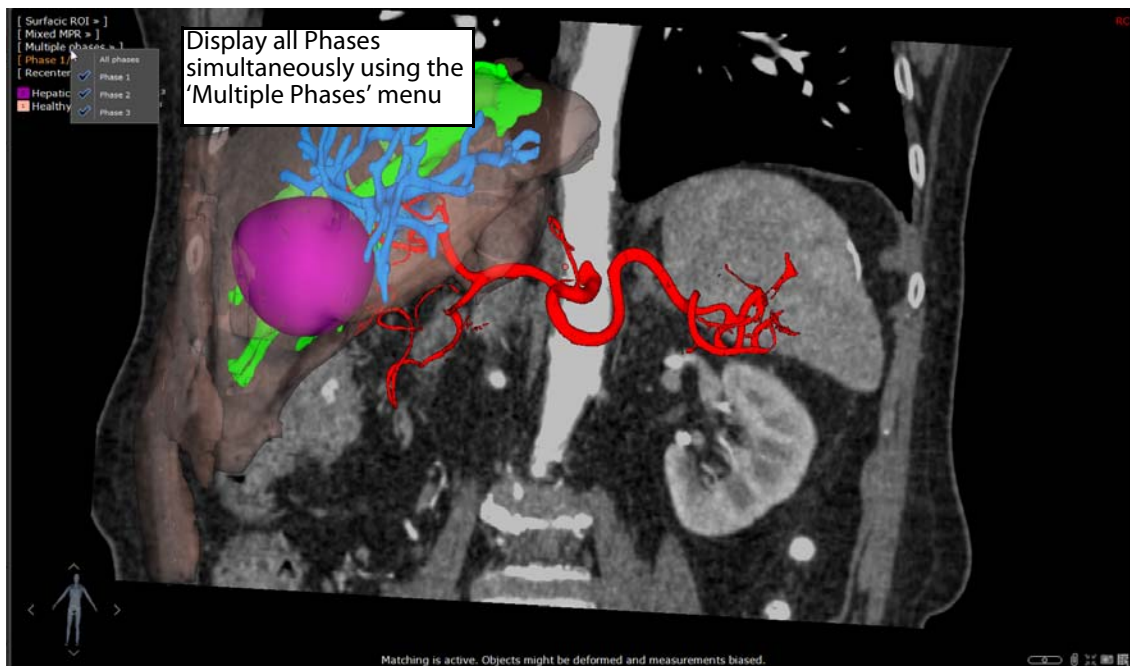


Figure 13-67 Multiphase Mixed MPR Rendering Mode: An MPR slice of the Series (all Phase visualization mode) is superimposed to the Surface ROI.

Whatever the visualization mode is selected (single or multiphase), the MPR plane remains unchanged in the Mixed MPR viewport.

## 13.7 3D Navigation



3D Volume rendering modes may be unavailable or incompatible with your workstation on which Myrian® is installed on account of insufficient hardware resources. Please contact Intrasure or the IT staff of your establishment to check and if necessary repair the configuration of your workstation.



Three-dimensional exploration is only available for DICOM images containing certain types of volumetric information.



Every time a 3D Viewport is opened, a memory check is launched automatically. If it is determined that not enough video memory is available, an error message is displayed and the User can choose another type of Viewport from the standard Viewport Menu.

### 13.7.1 Introduction

The 3D Navigation mode activates the 3D Viewports in the following visualization modes:

- Whole Volume and
- Volume of Interest

It also activates Tissue/Surface rendering modes (which can be applied to all 3 Modes) and a set of dedicated Protocols. 3D modes are activated via the Visualization Toolbar or the View menu at the top-left of each Viewport. They can also be activated at Series launch via the Protocols.



3D layout modes are based on orthographic projection model.



Standard image controls (grayscale Windowing, zoom, Pan, etc.) are also active in 3D Mode.



There is no limit to the number of 3D viewports you may have open at any one time. However, performance is subject to the memory limitations of your graphics card.

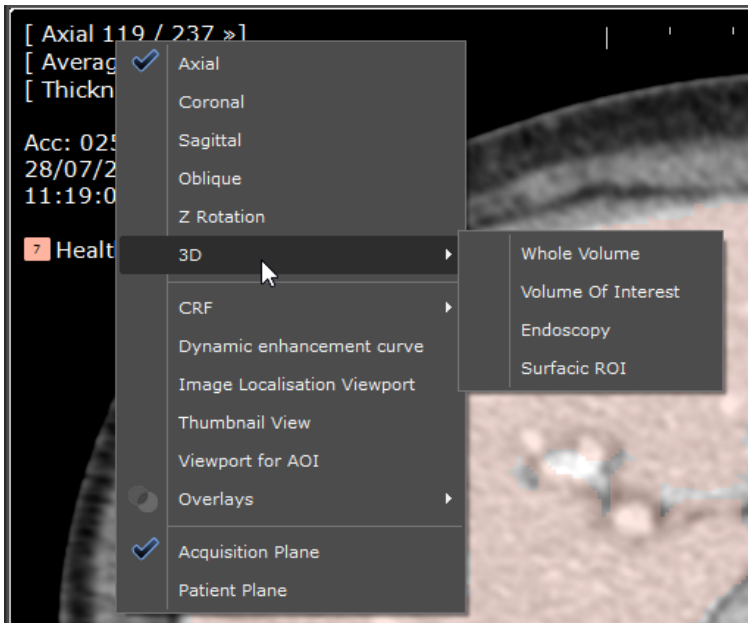


Figure 13-68 View Menu showing 3D visualization modes

### 13.7.2 Procedure

To activate 3D Mode via the Visualization Toolbar:

- Click on the MPR button 
- In the MPR Menu, select 3D Volume Mode  for a perspective 3D restitution of the Series, or

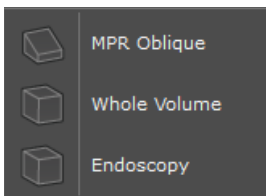


Figure 13-69 MPR Mode menu

Once 3D Mode is activated:

- The Series appears progressively in the 3D frame as slices are loaded.
- Loading progress is displayed as a percentage at the bottom center of the 3D frame.
- A little Mannequin appears at bottom left displaying:
  - Patient's Orientation

- Patient's gender (appears like a stick figure when gender is not specified)



During loading process, you may continue to work and use the 3D frame.



The speed at which 3D views are refreshed depend upon your hardware specs.

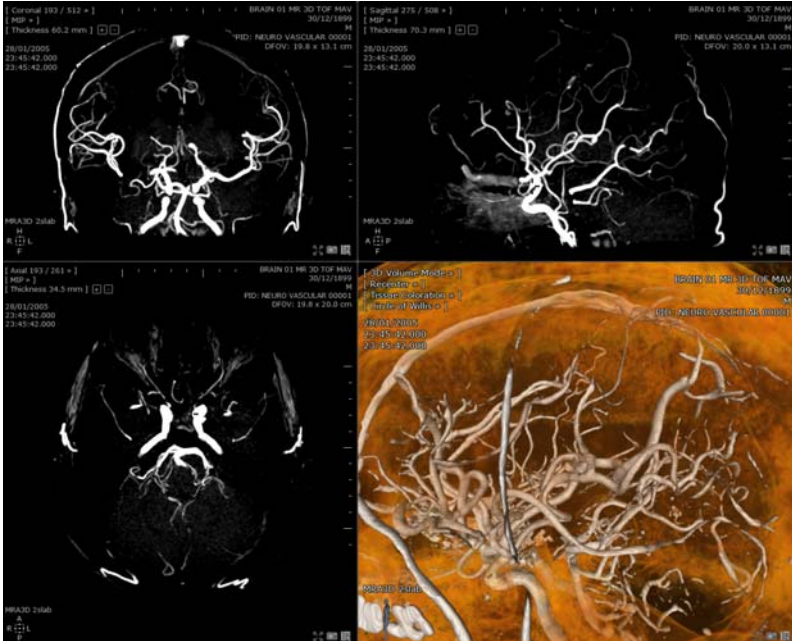


Figure 13-70 Thickened MIP + Tissue coloration

### 13.7.3 Whole Volume Mode

Whole Volume mode is a 3D representation of the entire Study as a perspective view.

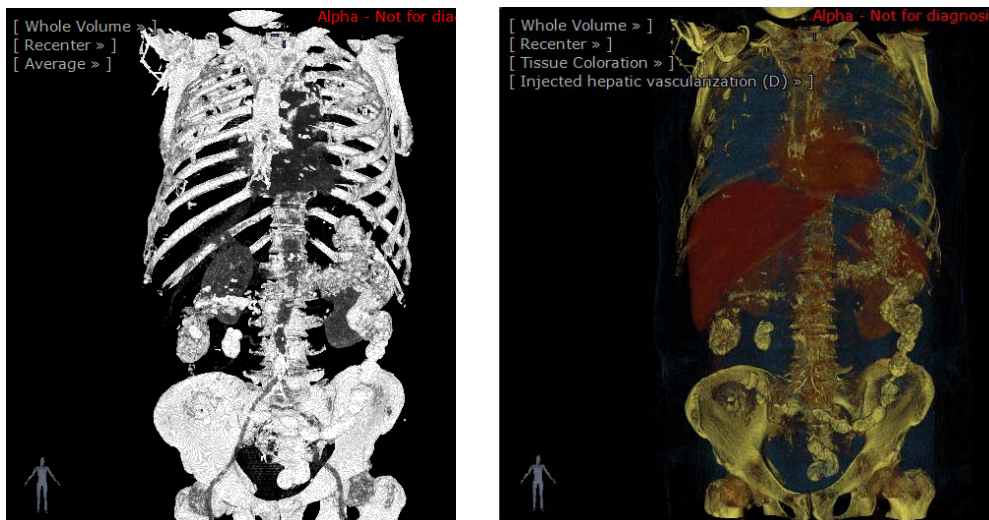


Figure 13-71 Example of 3D Volume Mode without/with Tissue Coloration



Whilst in Whole Volume mode, you can press the '3' key at the top of your keyboard to view/hide the inertia axis of the ROI. Note that the inertial axes disappear as soon as the ROI display is switched off.





The 'Invert colors' mode button  available in the top-right display mode button toolbar, inverts colors in Whole Volume mode, but does not invert ROI colors.

### 13.7.4 Volume of Interest (VOI) Mode

It is also possible to enlarge an area of the 3D view using the Volume of Interest (VOI) feature.

To activate VOI Mode:

- Select 'Volume of Interest' the view menu of any frame

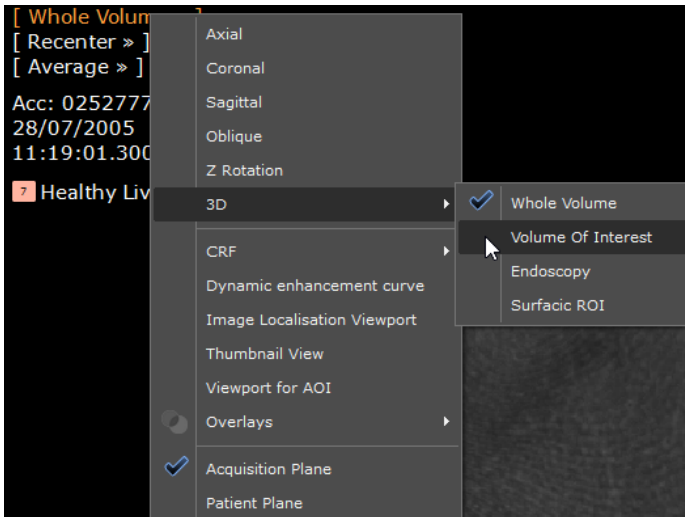



Figure 13-72 Volume of Interest Mode in the View Menu

The 3D VOI box outline is visible in all the orthogonal MPR frames.

You can adjust the size of the VOI box either directly in the Volume of Interest view:

- Click on the following icon  at bottom right of the VOI frame
- Drag the mouse cursor accordingly over the VOI frame to enlarge/diminish VOI size

Or, by click-and-drag using the handles which appear when you move the mouse over the VOI box outline in any of the MPR frames.

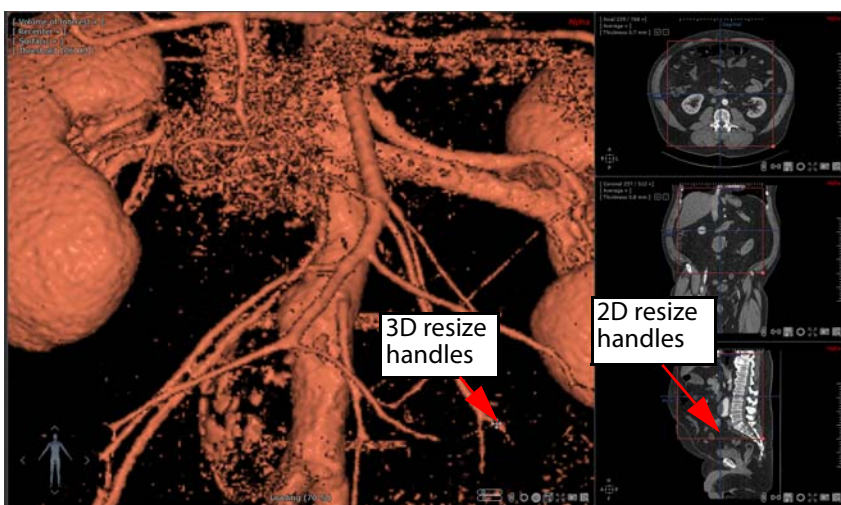


Figure 13-73 Resizing the VOI box in the MPR frames



Press 'Shift' during drag to resize proportionally in all three axes of orientation.

It is also possible to use one of the dedicated tissue Coloring presets for better rendering. In the example, a close-up of part of a colon was enlarged using VOI Mode, then enhanced using the dedicated 'Colon Wall' preset.



Figure 13-74 Example of Colon Wall rendering in VOI Mode



Rendering Modes are also available in Volume of Interest mode.

---



You can open several Volume of Interest viewports at the same time and manipulate them independently from each other.

---

### 13.7.5 Surfacic Mode

Surfacic Mode, available for CT images, displays ISO-density surfaces of which the threshold values can be modified by the User interactively.

If a ROI exists and it intersects the ISO-surface, then the surface takes on the color of the ROI. In the example below:

- A set of ROI were created in an ankle volume
- Surfacic Mode was selected to illustrate the bone structure of a foot

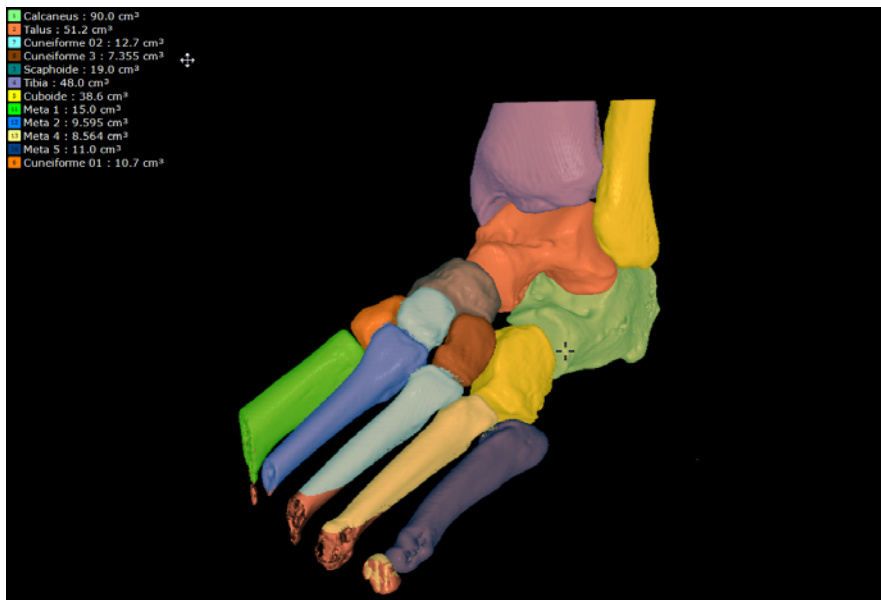



Figure 13-75 Example of usage of the Surfacic Mode

## 13.7.6 Synchronizing with the MPR views

### Windowing

In Tissue Coloration Mode, the mouse button assigned to the grayscale button  can be used for free rotation of the 3D view.



In Surfacic Mode, the Windowing tool affects the visibility of ROI.

## 13.7.7 Display modes

All rendering modes and filter presets are available in 3D Volume Mode.

## 13.7.8 Superimposed Menu

This menu is located at the top-left of the frame. When 3D Volume or any other three-dimensional reconstruction is selected, supplementary choices (with respect to MPR canonical frame) corresponding to specific settings for 3D view or Tissue Coloration mode appear in the command submenus.

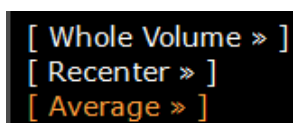


Figure 13-76 Default 3D superimposed menu

### 13.7.8.1 'Recenter' menu

The 'Recenter' menu in Oblique and 3D views is used to reset the active image to the following orientations:

- Superior
- Inferior
- Anterior
- Posterior
- Left
- Right

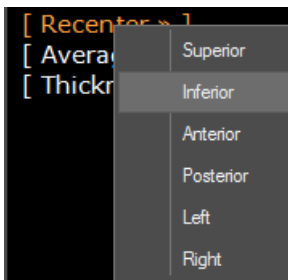


Figure 13-77 Recenter menu

### 13.7.8.2 'Render' menu

You can choose between the following rendering modes:

- Average
- MIP
- Tissue Coloration (which results in the display of the Tissue Coloration submenu)
- Surfacic (available for studies of CT modality only)

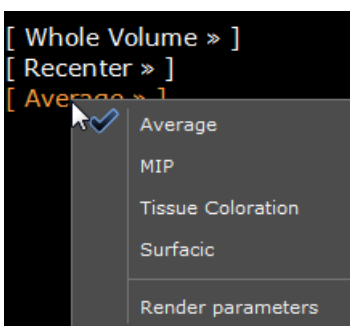


Figure 13-78 Rendering mode menu

For each rendering mode, render parameters can be edited.



The 'Tissue coloration' mode is an enriched representation of this 3D view, in which you may have certain tissues colored according to your needs. This and other enhanced visual aspects (such as shadowing, etc.) will increase your perception of the volume.

### 13.7.8.3 Edit 3D view rendering parameters

A dedicated configuration dialog box enables you to increase the visibility of specular lighting in the 3D view (Whole Volume, or Volume of Interest) whatever the rendering mode applied.

#### 13.7.8.3.1 Procedure

To adjust the **specular effects** of the current 3D view:

- Click on the Render menu (set to 'Average' by default)
- Then select 'Render parameters'

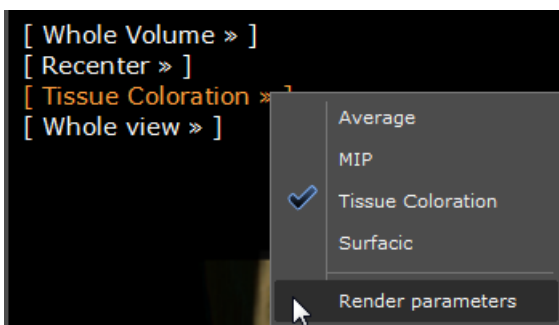


Figure 13-79 Opening render configuration dialog box for the 3D Tissue Coloration view displayed in Tissue Coloration mode



It opens the following parameter box:

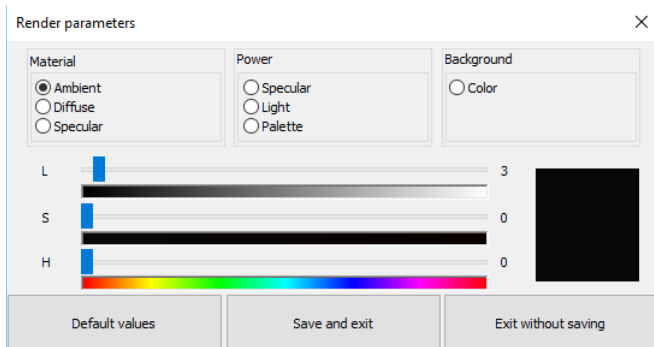


Figure 13-80 Render parameter dialog box (displaying the default values for the selected render mode)

Available parameters on which you can act are the following:

- Ambient, Diffuse, Specular lighting colors for **Materials**
- Specular, Light and Palette **Power** to apply:
  - The Specular power controls the zone where specular lighting applies; the higher the value (slider pushed to the right), the larger the parts where specular lighting applies
  - Lighting power acts like if surface normals were magnet to the camera, resulting in voxels getting more from light as they face it more
  - Palette power enables to boost palette colors as much as possible. If palette colors don't use the whole range of intensity, this parameter increases all palette color lighting value.
- **Background color**

When editing rendering parameters, the **3D view is refreshed real-time** to reflect the changes and visualize the applied render effects. The final specular result is the combination of each type of coloration applied.

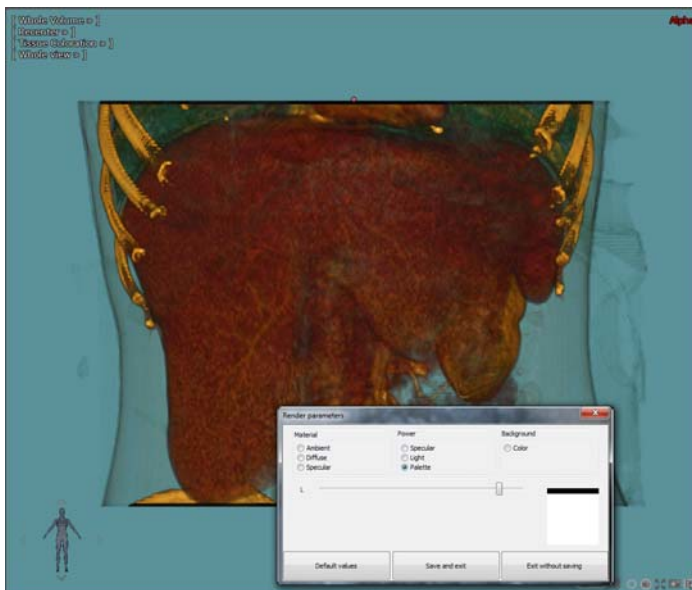


Figure 13-81 Render parameters edition for the 3D Tissue Coloration render mode

Finally when editing those parameters, you have the following options:

- **Reset all values** clicking on 'Default values' to reset the 3D view to its initial state
- **Save and exit**
- **Exit without saving**



Newly defined render values are persistent and saved from one session to the other.

In the above example, the edited render parameters apply for all tissue coloration palettes available as you can observe when

selecting 'Preview coloration palettes' from the 'Whole View' submenu as illustrated hereunder:



Figure 13-82 Coloration palette preview displaying the changes applied to the Tissue Coloration rendering mode



Lighting colors are additive. Therefore, pushing one lighting effect to the maximum combining **L** (Lightness)/**S** (Saturation)/**H** (Hue) cursors may prevent others to apply.



Depending on the selected render mode, all parameters don't apply. For example, parameters taking advantage of palette colors won't give any result in non palette render mode.

### 13.7.8.3.2 Palette mode render edition

In the same way as a palette render mode applied to a 3D view can be edited, the specular rendering can also be adjusted for one selected palette only from the (New or Legacy) Palette Editor window clicking on the 'Tweak render parameters' button



In order to edit one given palette render only, first open the Palette Editor (see Section 13.7.12):

- Select the palette to edit then click on the dedicated button 

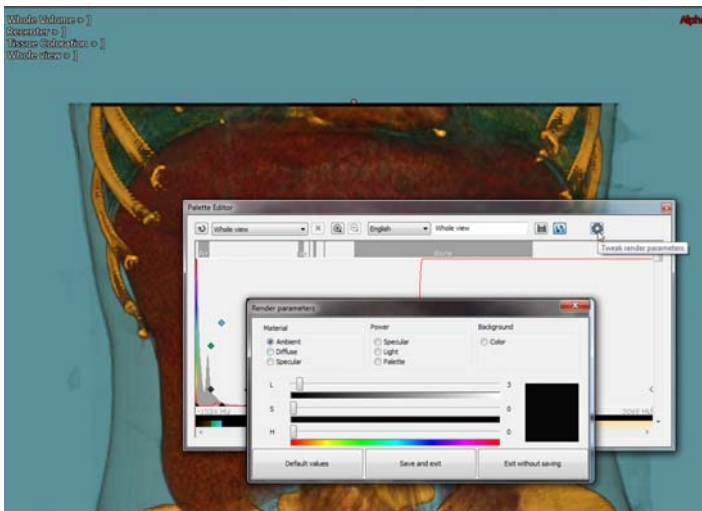


Figure 13-83 Opening the Render parameter configuration box for the 'Whole View' Coloration palette edition

- Edit render parameters as desired

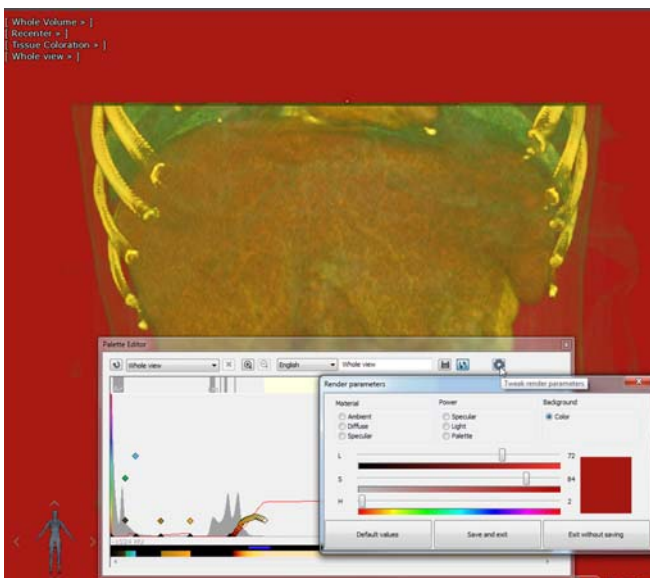


Figure 13-84 Editing the render parameters of the 'Whole View' palette

- Click on 'Save and Exit'.

As factory palettes cannot be modified, the following message is displayed:

- Confirm to create a copy of the edited palette

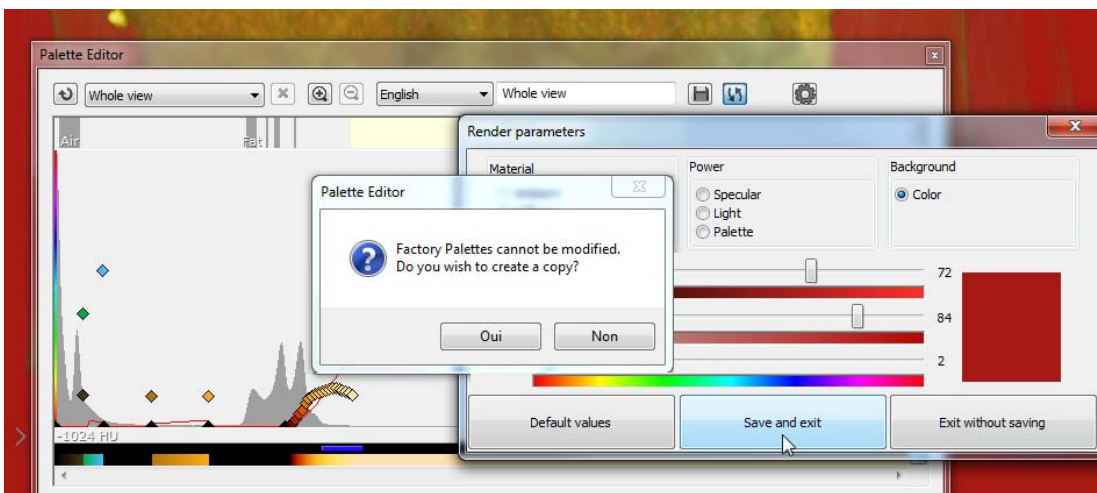


Figure 13-85 Saving the newly created Whole View palette

This new 'Whole View' palette will be saved and available from the 'Preview Coloration palettes' screen



When a palette has its own render parameters, the specular effects applied overwrite the render parameters of the current render mode.

### 13.7.9 MIP Mode (Maximum Intensity Projection)

This mode is accessible clicking on the dedicated command from the superimposed menu (by default, the activated mode is 'Average').

The 'M' key of the keyboard enables you to switch from 'Average' to 'MIP' mode.

The MIP mode enables to make visible only tissues of high intensities from the observer's direction. Therefore, you can isolate structures of high intensities (bones, injected tissues) while visualizing a study.

#### 13.7.103D MIP Rendering Mode

This mode enables you to highlight small vessels and enhance contrast in whole volume therefore revealing vascular system:

- Activate 3D mode
- In the Average menu, select MIP

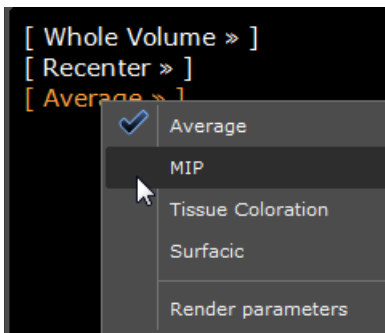


Figure 13-86 MIP contrast-enhancing mode

Once in MIP Rendering Mode, you can adjust the contrast (gamma correction) via the left-hand side slider.

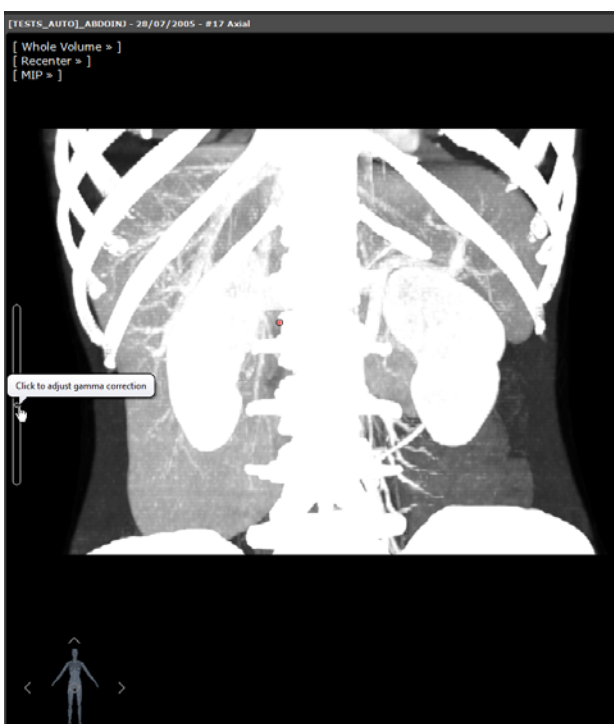


Figure 13-87 Adjust Intensity Projection in 3D MIP views



Gamma correction vertical slider should not be mistaken with the Windowing tool which remains linear.

---

### 13.7.11 Tissue Coloration mode

To view 3D images in Tissue Coloration mode:

- Activate 3D mode (see section above)
- Select 'Tissue Coloration' from the rendering menu

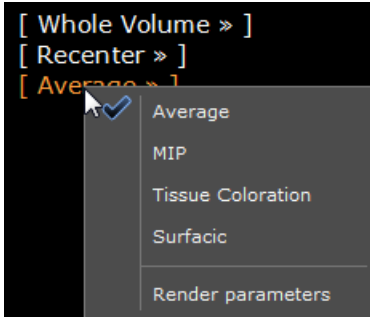


Figure 13-88 Whole Volume rendering menu (with 'Tissue Coloration' selected)

Coloration presets (by default, the 'Whole View' preset is applied to the study) become available as soon as the Tissue Coloration mode is selected.

Using those presets, you can color and isolate tissues according to their intensity by selecting the 'Tissue Coloration' mode in the render drop-down menu which by default is set on 'Average'.

- Click on 'Tissue Coloration' to display the list of presets available for the current study.
- 



Tissue Coloration palettes are intended to give Practitioners a quick yet approximate sample of various anatomical tissues/structures.

---



Tissue Coloration Palettes (or 'filters') are generally 'Static' (predefined). However some filters are 'Dynamic'. The latter are automatically re-calculated according to the density values of each image. Dynamic presets are marked with '(D)' mark to distinguish them from other palettes.

---



You can use the Windowing tool to manually adjust the active color palette settings whilst in Whole Volume and VOI Mode. When a palette is modified this way, it automatically displays a '\*' star beside it to mark it as having been changed.

---

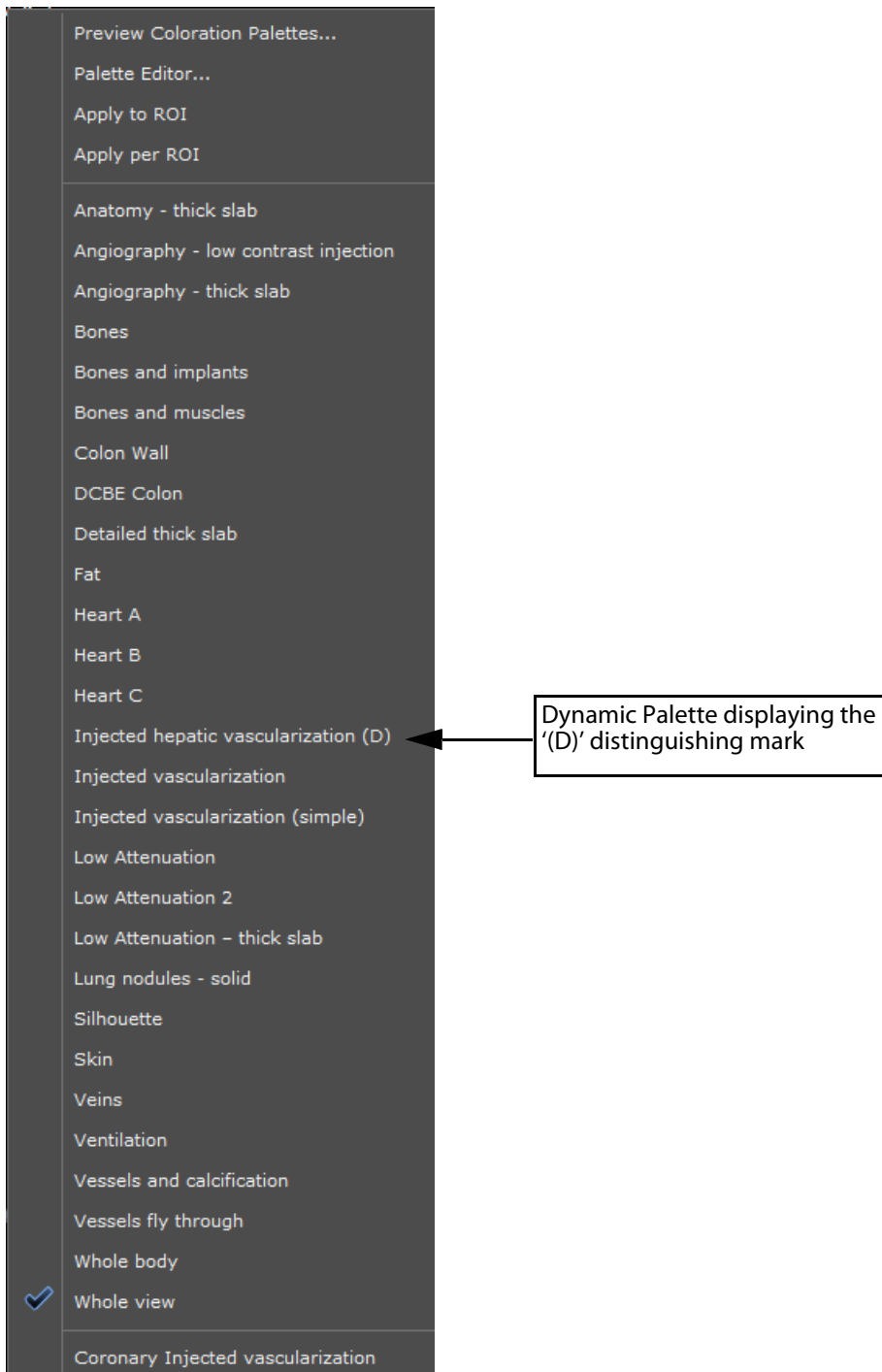


Figure 13-89 Tissue Coloration sub-menu

- Select your desired preset from the resulting Whole view menu

To view the Tissue Coloration preview screen:

- Activate a 3D Mode Viewport and
- Select 'Tissue Coloring' from the Rendering Menu
- Select 'Preview Coloration Palettes...!' from the ensuing menu to access a preview screen of all the tissue coloring thumbnails available for the current study
- Click on the thumbnail of your choice to select the desired tissue coloring



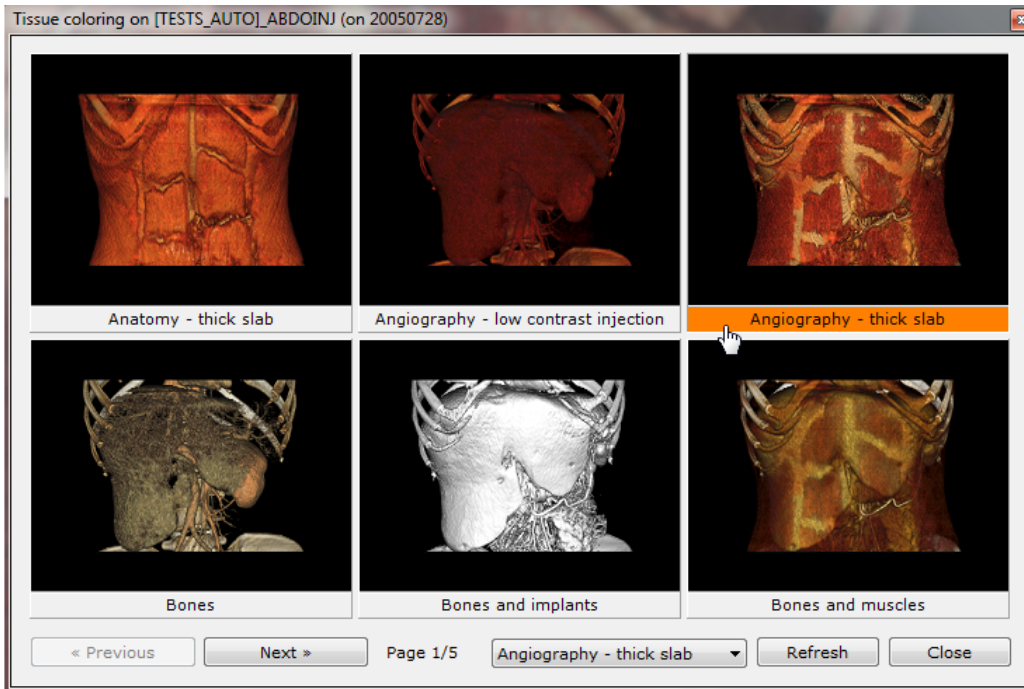


Figure 13-90 Coloration Palette preview menu

The name of the coloring associated to the currently selected preview thumbnail is highlighted in orange.

## 13.7.123D Coloration Palette Editor

### 13.7.12.1 Overview

The Palette Editor is an application enabling the creation of new Tissue Coloration Palettes or modification of existing ones available from a 3D Volume rendering viewport in Tissue Coloration rendering mode.

- Click on the Palette menu and select Palette Editor...

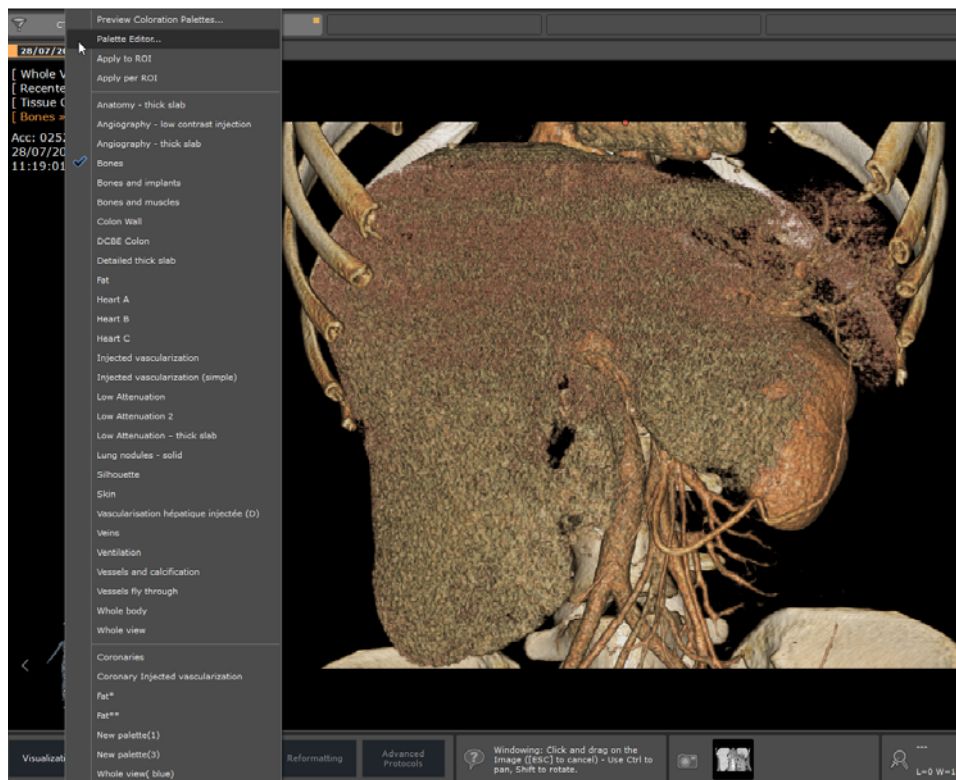


Figure 13-91 Open the Palette Editor window

### 13.7.12.2 Description



The Palettes allocate specific colors to each unit of intensity found in the Study.

The Palette Editor which allows you to define which color and transparency will be assigned to which intensity value in a compatible volume (CT, MR, etc.) consists of a single screen laid out as follow:

- The Editor titlebar at top of the window
- The Study Volume's curve display at center which includes:
  - Current volume histogram of intensities represented by a **gray curve**.
  - When available (CT palettes mainly), known intensities ranges are represented by colored zones. For example, yellow zone represents intensities range known to be part of bone.
  - Palette opacity curve which is represented by a **red line** between colored nodes: Currently selected node is drawn as a rounded square while other nodes are drawn as circles. Nodes are colored using palette color at their intensity.
- A Palette display mode bar
- A set of tools and menus at bottom of the window

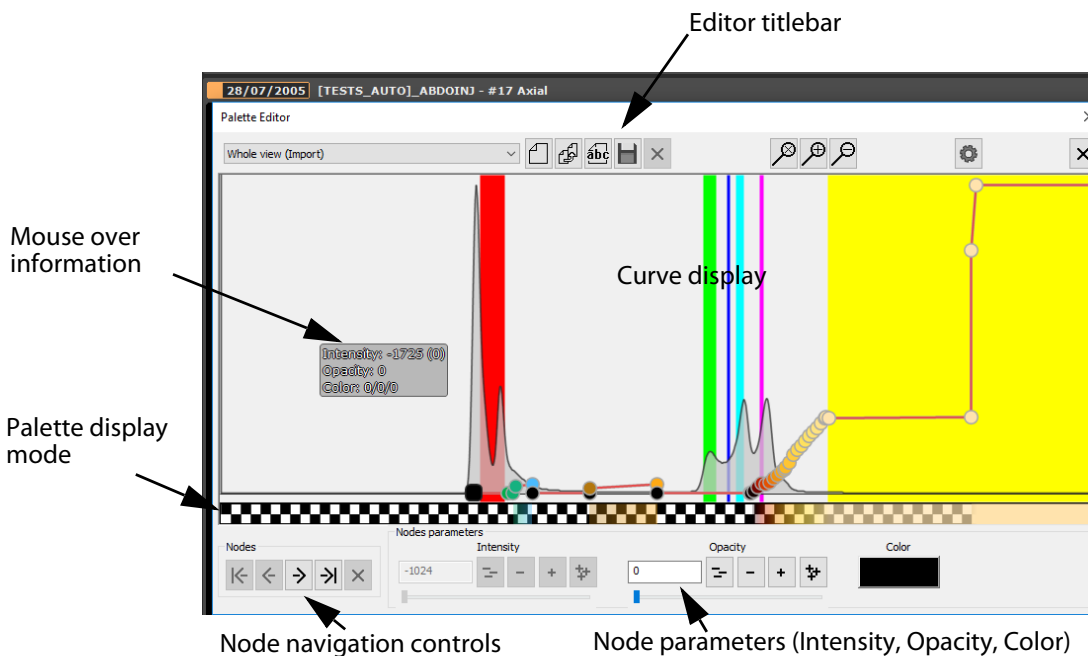



Figure 13-92 Palette Editor screen



The **X axis** represents **intensity** while **Y axis** represents **number of occurrences** for histogram curve and **opacity** for alpha curve

The tools in the **Palette Editor Titlebar** pictured below are (from left to right):

- Palette drop-down list (displays supported Palettes for current Study Modality): it lists all the palette available for edition using this palette editor

- 'Create a New Palette' button  : it creates a new, empty palette ready to be edited

- 'Create a Copy of the current palette' button  : factory palettes cannot be modified so changes made to a factory palette are saved as a copy (\*)








- 'Rename a current palette' button : it opens the rename dialog box in which you can set a new name for the current palette
- 'Save current Palette' button 
- 'Delete current Palette' button  (not effective on Factory Palettes)
- Reset Zoom/Zoom-in/Zoom-out buttons
- 'Tweak render parameters' button  to adjust the specular effects of the selected palette render mode (see Section 13.7.8.3.2)
- 'Quit palette editor' button 



Figure 13-93 Editor Titlebar

The **mouse-over information** on the curve view includes:

- Intensity at mouse position (X axis), and number of occurrences of voxels of that intensity in volume histogram.
- Opacity at current intensity.
- RGB color at current intensity.
- Eventually, the name of current intensity range when mouse hovers a known intensity range.

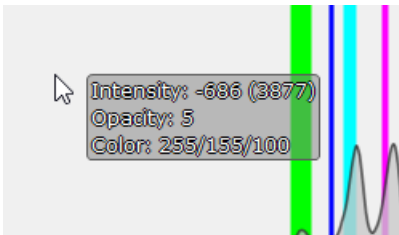
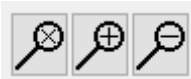


Figure 13-94 Mouse-over data

### 13.7.12.3 Curve display Controls

Zoom and Pan functions allow you to control the curve display.

**Zooming:**

- Use the dedicated zoom control buttons  to respectively reset zoom, increase zoom or reduce zoom or
- Click & drag the middle mouse button up and down or
- Press the CTRL key while using the mouse wheel.

**Panning:**

- Pan curve view left/right to visualize it in full by clicking & dragging the left mouse button left/right.

### 13.7.12.4 Palette display modes

To cycle through the following display modes, simply click on the palette view:

- **Normal view** (default intensity range) representing the palette colors for the currently displayed intensity range:



- **Amplified view** in which the opacity is amplified in order to visualize transparent color better



- **View without transparency** (i.e. colors use only RGB values without any transparency)



For each displayed intensity, a color is computed from the node colors and the curve opacity.

### 13.7.12.5 Node navigation and palette edition

The node edition allows you to customize your palette based on the three following parameters:

- Node intensity
- Node opacity
- Node color



Nodes on curve are sorted by their intensity. Curves include at least two nodes, first node corresponding to the lowest intensity and the last node to the highest.

**Nodes selection** can be done by panning the view and clicking on nodes, but it can also be done using the controls in node bar.

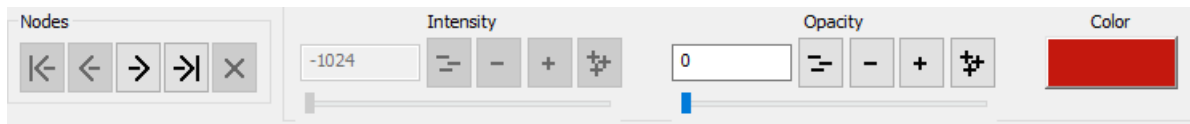







Figure 13-95 Node bar

The node navigation bar includes the following buttons:

- 'Go to first node' button  : Selects the first node of the curve which is not the one with lowest intensity
- 'Previous node' button  : Selects node with immediately lower intensity than currently selected one (i.e. if first node is not selected)
- 'Next node' button  : Selects node with immediately higher intensity than currently selected one
- 'Go to last node' button  : Selects the last node of the curve which is the none with higher intensity
- 'Remove current node' button  : Deletes current node



When switching from one node to another using the node navigation buttons, the curve view adapts to center view on the selected node.

**For each selected node**, you can tune in the following parameters:

- **Intensity:** Node intensity value bounds are its previous and next nodes intensity values. Two nodes can't have same intensity. First and last nodes intensity value can't be changed. Node intensity value can be changed by clicking and dragging the node in the curve view.

On the curve view, nodes can be dragged left or right to change their value inside their bounds (i.e. bounds being previous and next node intensity) but their intensity value can also be changed using node parameters controls related to intensity:





- Type-in intensity value in the dedicated field (value is clamped to bounds upon validation when pressing the 'Return' key) or

- Use intensity slider to set node intensity. Slider bounds are node intensity value bounds.



Once the slider is selected, the mouse wheel can be used to set value.

The node intensity value can be adjusting clicking on the following:

- 'Largely decrease current node intensity' button : Reduces selected node intensity value by 20.
- 'Decrease current node intensity' button : Reduces selected node intensity value by 1.
- 'Increase current node intensity' button : Increases selected node intensity value by 1.
- 'Largely increase current node intensity' button : Increases selected node intensity value by 20.

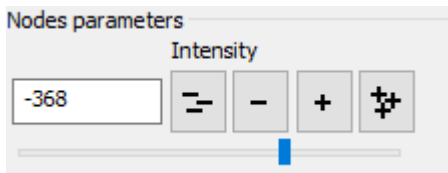


Figure 13-96 Setting node intensity





- **Opacity:** Node opacity value can be set from 0 to 100% opacity. No opacity value can be changed by clicking and dragging the node in the curve view.

On the curve view, nodes can be dragged up or down to change opacity value, but opacity value can also be changed using node parameters controls related to opacity:

- Type-in opacity value for selected node (value is clamped between 0% and 100% upon validation when pressing the 'Return' key).
- Use slider to set node opacity from 0% to 100%.



Once the slider is selected, the mouse wheel can be used to set value.

- 'Largely decrease current node opacity' button : Reduces selected node opacity value by 5.
- 'Decrease current node opacity' button : Reduces selected node opacity value by 1.
- 'Increase current node opacity' button : Increases selected node opacity value by 1.
- 'Largely increase current node opacity' button : Increases selected node opacity value by 5.

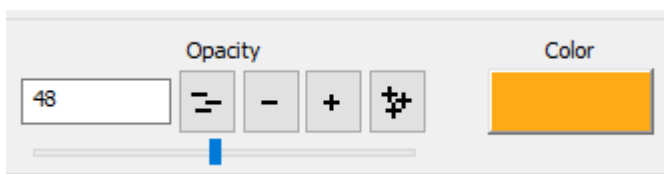


Figure 13-97 Setting node opacity

Finally you can edit the **node color**:

- Click on the Color button of the selected node or
- Double-click on the current node in the curve view to open the dedicated CLUT table allowing you to set your preferred node color definition.
- Then click OK.

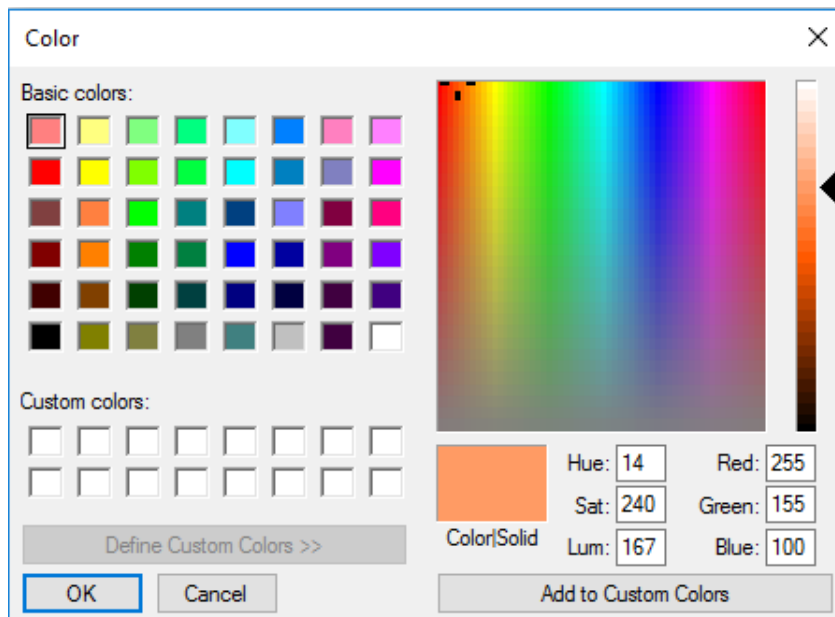




Figure 13-98 Node color selection and adjustment

### 13.7.12.6 Method of use



You can assess the rendering quality of the performed actions simultaneously on the view.

To create a new Palette:

- In Whole Volume Mode, click on the Tissue Coloration Palette menu which, by default, is 'Whole View'
- Select a Palette you wish to modify or click on the 'Create a new palette' button 
- Left double-click on a desired spot on the density view to place a new color node whose main color is the one corresponding to the color bar and select the desired color from the CLUT table that pops up
- To remove a node, right-click on an existing color node.
- Left-click on a color node while holding down the Shift key to change opacity (up and down) and/or intensity (left and right) of the color
- Drag the nodes up/down to set the Color value of your target anatomical structure
- Click on the 'Save' button  to save your new Palette



To increase mouse motion precision along the vertical axis, hold down the Shift key while moving the node.



The exam values increase horizontally and the vertical position of the curve acts on the transparency/opacity (a linear gradient from transparent at the bottom of the view to opaque at the top of the view).

The 3D view updates real-time upon each node parameter edition.

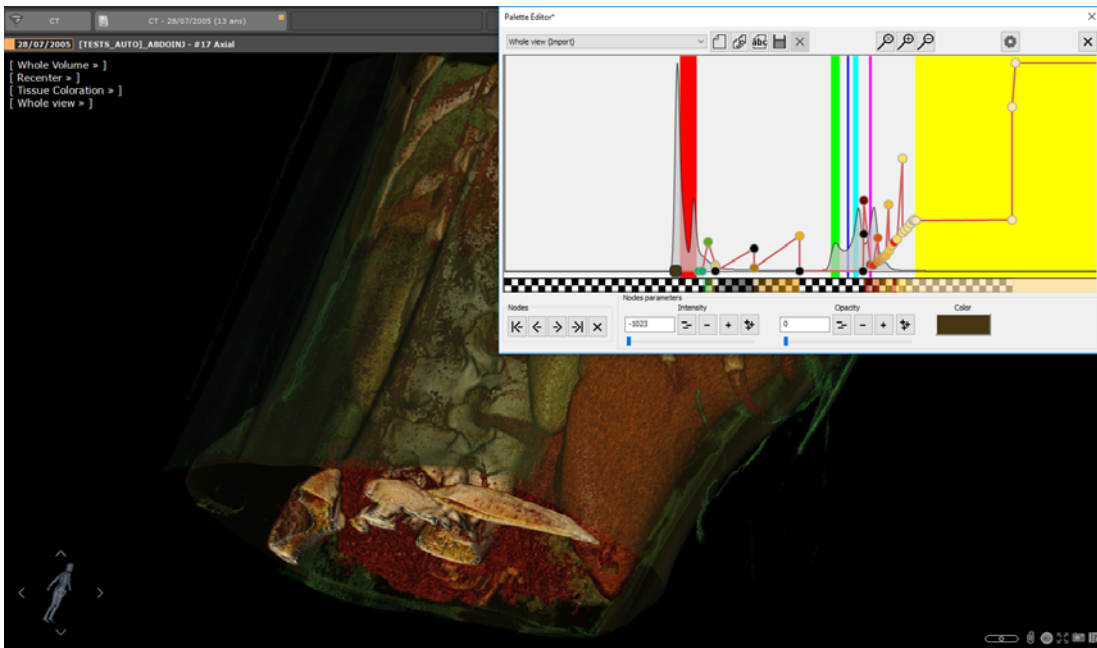


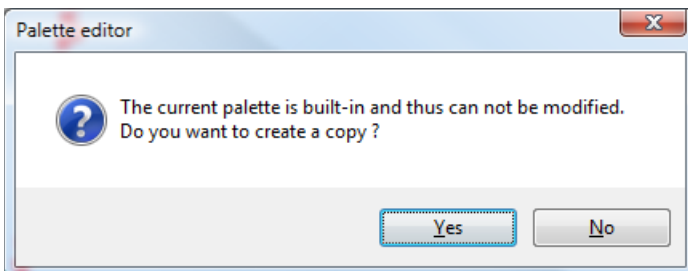




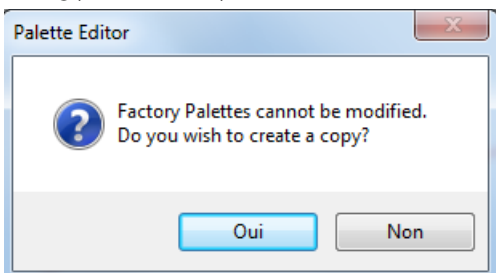
Figure 13-99 New palette

- Once your palette edition/creation is complete, click on . When you attempt to save modifications to an Existing User Palette, you will be prompted to either overwrite the existing Palette, create a new copy  or discard changes.



 Palette names with a trailing '(Import)' text indicate that this palette was created using old palette editor. Those palettes can be imported and modified by creating a copy.

 Factory Tissue Coloration Palettes cannot be modified. However if you attempt to modify one, a message pops up asking you whether you wish to create an editable copy of the Palette.



If you click on 'Yes', the software will create a copy bearing the same name with a '\*' star appended to it. You can rename it later if you wish.

### 13.7.13 ROI Interaction in 3D views



The contents of the present section only applies if the optional ROICreator module introduced in the Chapter 7 is installed and activated in your Myrian® version.

The Region of Interest (ROI) coloring can be visualized in the 3D view as well as in 'Tissue Coloration' mode.

Whenever ROIs are edited, they are automatically updated in the 3D view or in Coloration mode (a small delay might be observed).

The functionality enabling to activate/deactivate ROI coloring of the selected ROI in the Regions of Interest 3D toolbar is also enabled for both 3D view and 'Tissue Coloration', so is the 'R' key of the keyboard enabling to cycle through the ROI display modes (Filled, Contour, none) of all ROIs.

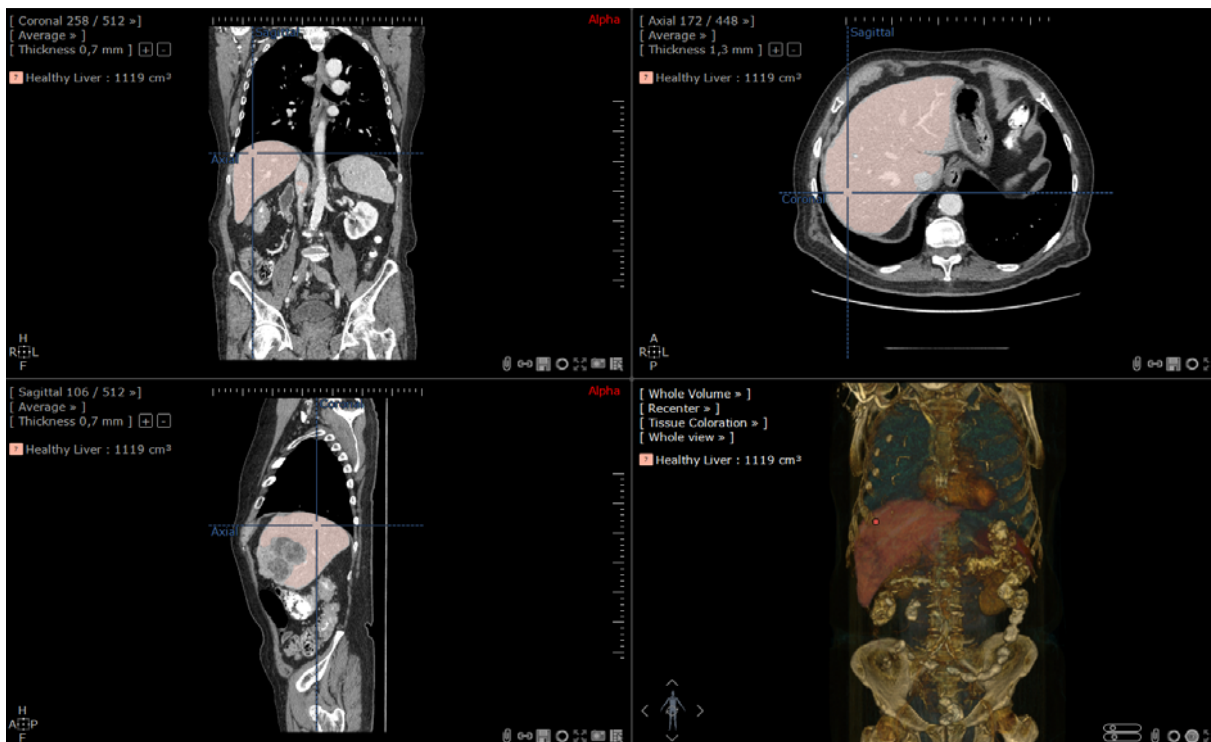



Figure 13-100 Example of ROI visualization in the 3D view

Besides, the functionality enabling to toggle ROI visibility On/Off of a selected ROI can also be used and visibility level adjusted. You can set an opacity level from 0 to 100% where a 0% value relates to the non-visibility of the selected ROI (which is therefore transparent).

This tool enables to visualize only the organ to study (provided a ROI has been allocated to this region) when setting at 0% the visibility value of the Transparent ROI (see Section 7.15.8).

### 13.7.14 The Mannequin

A Mannequin appears at the bottom-left of 3D Viewports. The Mannequin displays at all times and in real time the orientation of the Study.

When you hover over the Mannequin with the mouse, regardless of what tool is currently activated, the mouse automatically switches to "Rotation Mode" and the cursor displays a double-elliptic cross , signifying that you can manipulate the orientation manually by simply dragging the mouse over the Mannequin.

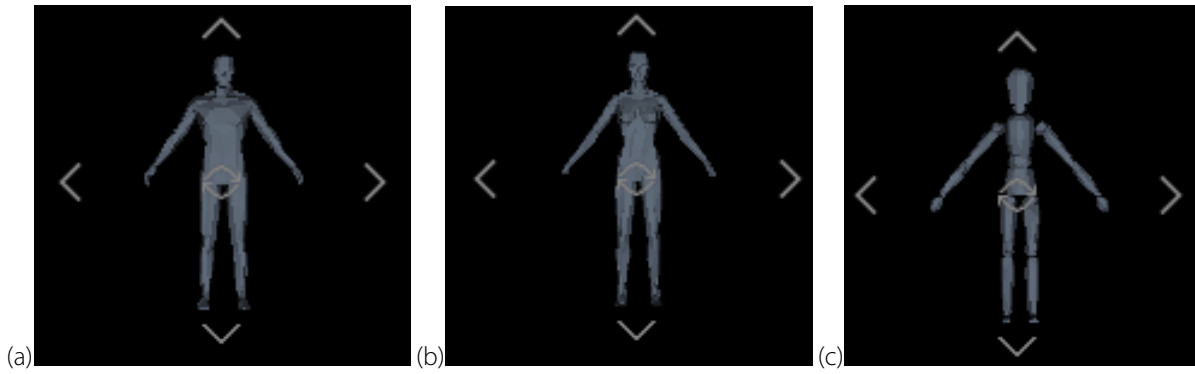


Figure 13-101 Masculine, Feminine and Indeterminate Mannequin



The Mannequin assumes the appearance of a male or a female figurine if the gender of the Patient is either masculine or feminine, and an undefined wooden dummy if the gender is indeterminate.

### 13.7.15 Manipulating the 3D View


Many of the functions that may be assigned to the mouse in the various MPR views may also be assigned for the 3D Modes, including:

- Zoom,
- Windowing,
- Pan and,
- Navigation (except for 3D Volume Mode).

#### 13.7.15.1 Free rotation

In 3D viewpoints, the camera rotates **around the anatomical center**.

You can rotate the 3D Volume views in any direction using click and drag action proceeding as follow:

- When you hover over the Mannequin with the mouse, regardless of what tool is currently activated, the mouse automatically switches to "Rotation Mode" and the cursor displays a double-elliptic cross . If you click and keep the left mouse button pressed down while dragging the mouse, you get a free rotation of the 3D volume.
- If a tool currently assigned to the mouse is unusable on the current 3D view the mouse pointer automatically assumes the 'Rotation' cursor shape (see figure below).

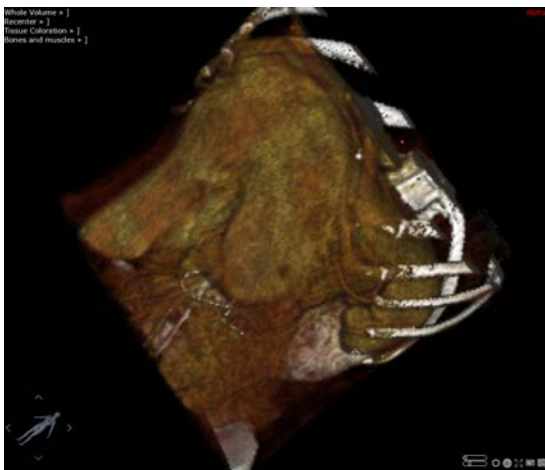


Figure 13-102 Free rotation



Press the CTRL key during rotation before releasing the mouse button to activate auto-rotation. In this mode, the 3D image carries on rotating around the same axis until you stop it by either clicking on the image or choosing another tool.

#### 13.7.15.2 Constrained rotation

If during a free rotation you hold down the 'X' keyboard key, crosshairs appear in the View Frame. Dragging the mouse then has the effect of forcing rotation of the 3D volume along the X/Y crosshair axis.

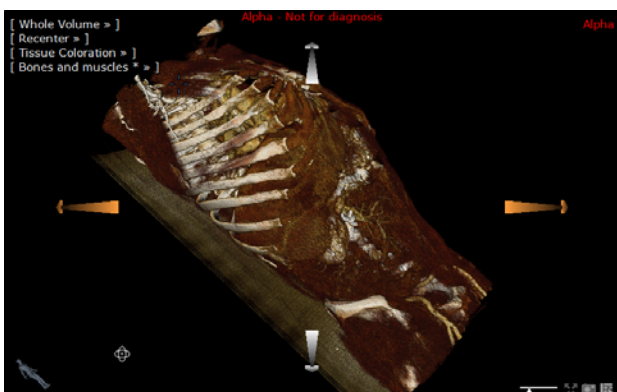


Figure 13-103 Constrained rotation with crosshairs






While pressing down the 'Inferior/Superior (<>)' keyboard key (generally located next to the left 'Shift' on your keyboard), simply click on a given crosshair axis and keep the left mouse button pressed down to select the crosshair of your choice (represented in orange on the image) and finally drag the mouse cursor: the rotation of the 3D volume is then forced along the selected axis.

When releasing the keyboard key, the constrained rotation crosshairs disappear and you can keep on manipulating the 3D volume in free rotation.

Another way to constrain the rotation along a given axis consists in positioning the mouse cursor over one of the arrows located around the mannequin.

According to the arrows browsed by the cursor, the rotation behaves differently:

- Left or Right arrows: rotation (illustrated by the  icon) is then **constrained along the horizontal axis** when dragging the cursor from left to right (horizontal crosshair axes appear on each side of the 3D volume).
- Up or down arrows: rotation (illustrated by the  icon) is then **constrained along the vertical axis** when dragging the cursor from bottom to top (vertical crosshair axes appear on each side of the 3D volume).
- Center of the mannequin (illustrated by the  icon): rotations are then constrained along the plane however the mouse cursor is dragged.



Use the 'Recenter' function (top-left superimposed menu) at any time to recenter the views: Axial (Superior/Inferior), Coronal (Anterior/Posterior) or Sagittal (Left/Right).

---



'Recenter' Shortcut Keys are "A/O", Anterior/Posterior, "L/R" Left/Right, and "T/B" Top/bottom.

---



You can also use the 2, 4, 6 and 8 number pad keys to rotate.

---



Use the left/right/up/down arrow keys on the keyboard to rotate the 3D volume by 10 degree steps.

---



The Mannequin figure at bottom-left of the 3D view refreshes in real-time to reflect the current orientation of the Study.

---

### 13.7.15.3 Visualize the rotation angles

When right-clicking on the mannequin in any 3D viewport, you can access a contextual menu enabling you to activate the following angle display:

- Absolute rotation angles from the **anterior position** of the patient
  - Relative rotation angle from the **position displayed** when clicking on the 'Reset' button.
- 



The rotation direction is defined using the following abbreviations:

- CRA: Cranial
  - CAU: Caudal
  - LAO: Left Anterior Oblique
  - RAO: Right Anterior Oblique
-

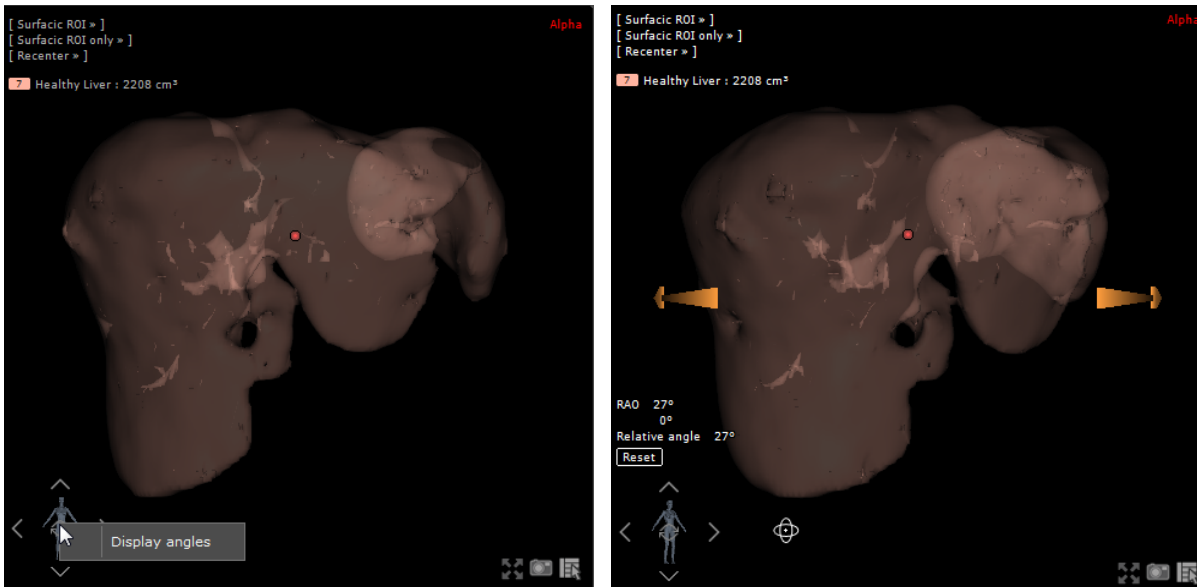


Figure 13-104 Rotation angle display

### 13.7.15.4 Synchronized 3D rotation

Rotation of any number of Whole Volume Viewports can be synchronized either within the same Series or across several different Series being viewed at the same time.

To set Whole Volume viewport synchronization:

- Select the 'Series Sync Settings' button  in the Series Layout tab of the Toolchest
- Check the '3D Rotation' checkbox

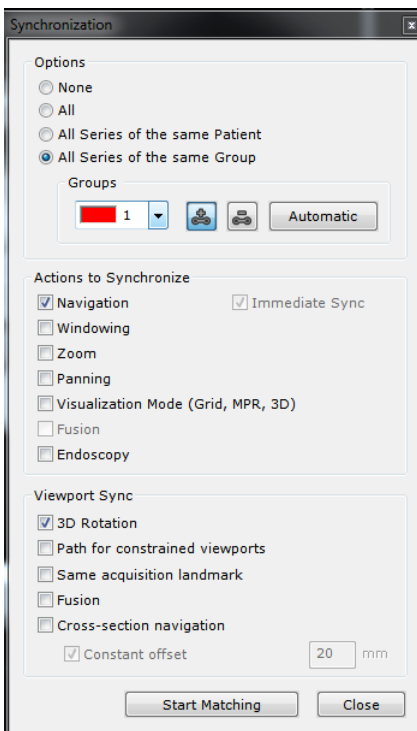


Figure 13-105 3D rotation synchronization checkbox

### 13.7.16 User-defined image degradation in 3D

Depending on the context, on your graphics card performance or your own perception, you may wish to define your own level of visual degradation **during interactive phases performed in the 3D viewport** (windowing, rotation, translation of the image).

A '3D visual degradation' slider located right under the '3D quality setting' slider, enables you to quickly and interactively

adapt the visual degradation level to your needs.



The '3D visual degradation' slider is **only** visible if the 'High-end 3D video card' option is **unchecked** in the Preferences>Display>Miscellaneous tab.



Figure 13-106 Image quality settings in the 3D viewport

It works as follow:

- Moving the slider to the left results in a high degradation of visual quality but a higher speed of the image display during interactive phases.
- Moving the slider to the right results in no degradation of the visual quality during interactive phases but less fluidity of the image display.



When moving the slider, the 3D image updates accordingly to display the intended level of degradation.



Figure 13-107 Adjusting the level of 3D degradation during interaction mode



The setting of the 3D degradation level is not persistent and only applies to the current 3D viewport.



Degradation policy:

- Rightmost levels put the viewport resolution reduction first (in order to preserve the color/luminance levels) to an acceptable (visual) limit
- Leftmost levels emphasize slice sub-sampling (acceptance of high visual impact).

## 13.7.173D Snapshots

### 13.7.17.1Overview

This option enables to generate automatic snapshots in 3D views.



The 3D snapshot option supports Volume Rendering (Whole Volume and Volume Of Interest) and Surfacic ROI rendering modes only.


When a 3D viewport is displayed in the Workspace (in one of the above mentioned rendering mode), a **right-click** on  located at the bottom-right of the 3D viewport opens a 3D snapshot parameter box enabling to launch the capture process. From this dialog box, you have access to the following parameters:



Figure 13-108 3D snapshot parameters box

- **The drop-down list:** contains a list of previously created presets.



Selecting one of the items in the list automatically updates the capture settings in the dialog box.



Note that an automatic name is assigned to the preset which cannot be modified.

- **Horizontal:** defines the total rotation angle around the vertical axis that will be applied during snapshot generation. Valid range is -360 to 360°.
- **Vertical:** defines the total rotation angle around the horizontal axis that will be applied during snapshot generation. The vertical rotation occurs AFTER the horizontal rotation. Valid range is -360 to 360°.
- **Steps:** defines how many images will be generated AROUND EACH OF THE AXIS (i.e.: if angles are specified for the vertical and horizontal rotations, then the total number of images is twice what is specified in the "images" box). Valid range is 1 to 180.
- **Reset view orientation:** automatically reinitializes the exam orientation in "anterior" mode, before starting taking snapshots.



If the 'Reset view orientation' box is unchecked, snapshots are generated starting with the orientation the exam was last set in.

You can define new presets using the '**Record**' button. The capture parameters are automatically retrieved from the current settings, and a new preset is created.

The active preset in the drop-down list can be removed by clicking on the '**Remove**' button.

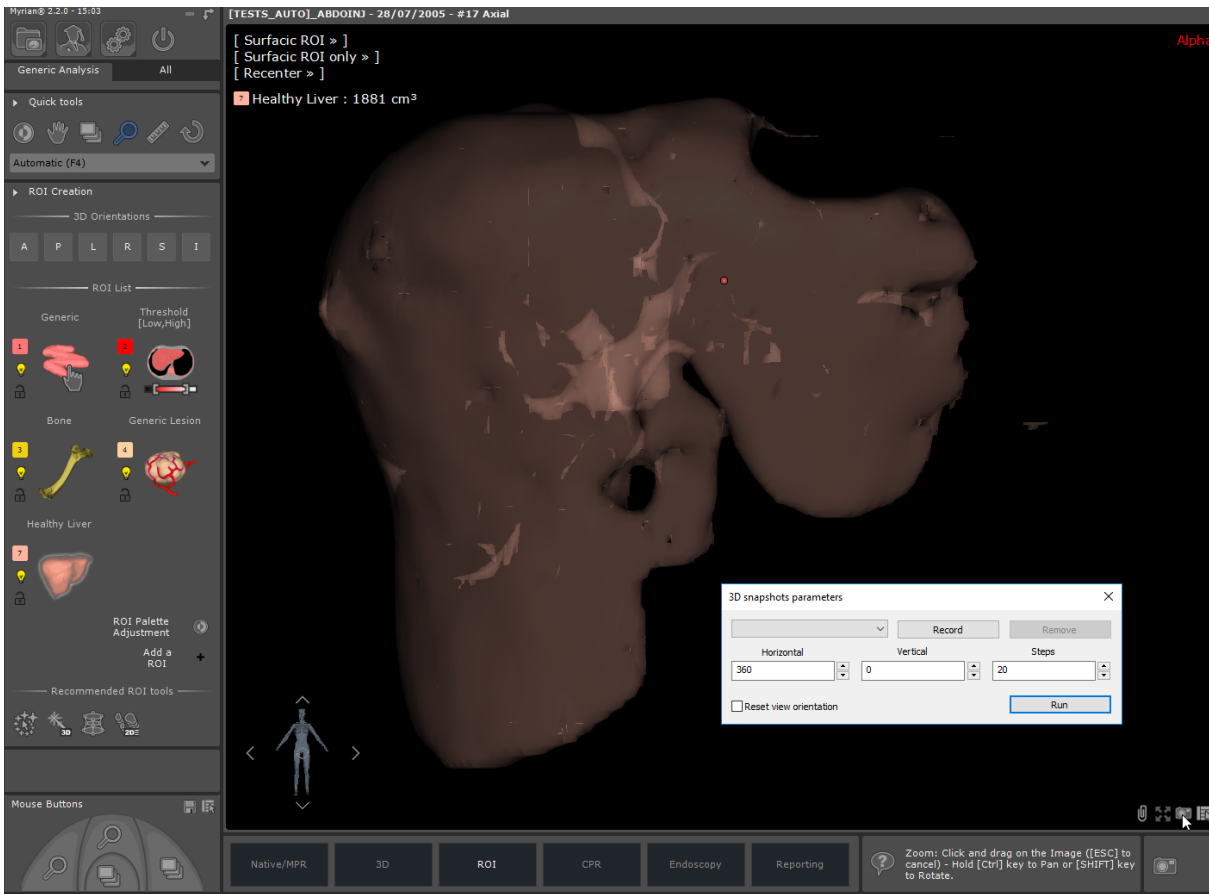


Figure 13-109 Access 3D snapshot dialog box from Surfacic ROI rendering mode



Clicking on the 'Rem.' button immediately deletes the preset without prior notice.

### 13.7.17.2 Method of use



- Right-click on the 'Capture' button at the bottom-right of the 3D viewport
- Modify the settings in the 3D snapshot parameter box as desired to create your new Presets.
- Then click on the 'Run' button.

A 3D Capture automatically launches generating snapshots of the 3D view.



The mannequin figure at the bottom-left of the 3D viewport starts rotating in real time according to the defined presets while the snapshot capture is on progress.

At the bottom-center of the main workspace under the image zone, the 'Scrapbook' panel displays the 3D snapshots as a set of thumbnails.

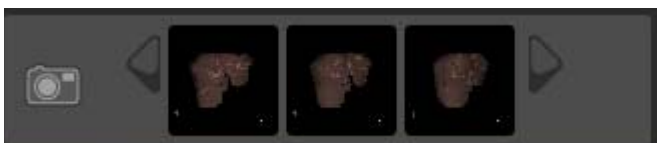


Figure 13-110 3D snapshot thumbnails

- Open the Scrapbook to visualize all 3D snapshots and eventually print them.

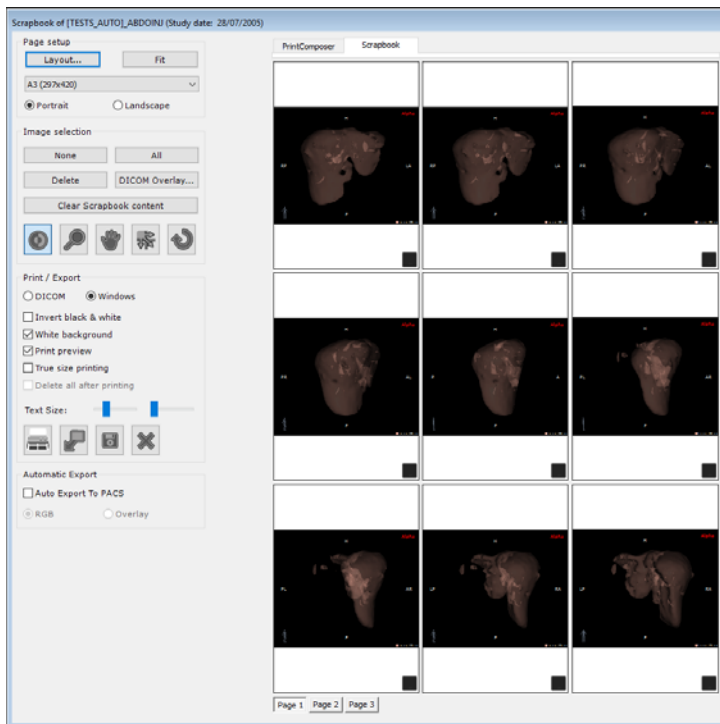


Figure 13-111 3D snapshots placed in the Scrapbook ready for printing



You can flip pages and easily rebuild the apparent movement of the rotation by setting the '1 image' layout "applying to all pages" and using the middle scroll button of the mouse.

## 13.8 Multiphase series viewer

The Multiphase Visualization Sub-Mode is comparable to the Fusion Visualization Sub-Mode as it allows the display of multiple Series in the same View. This mode is available from several protocols such as XP-Breast, XP-Prostate, Automatic Comparison CT or MR.



If you have activated the multiple "Patients in Workspace" option in Preferences > Display > Miscellaneous, whenever Series from different Patients are opened simultaneously a warning message is displayed.



Scrapbook contents are not saved upon exiting the Multiphase View.

### 13.8.1 Multiphase View

It consists of 3 basic functions:

- The Multiphase View enables the display of 2 or more datasets such as Arterial Portal and Late Phases in the same view, in Native or MPR mode
- The Temporal Navigation mode enables temporal navigation through phases, and
- A 3D Surfacic View (optional) where the ROI from each phase can be displayed all at once.

Each Viewport will show one Series, i.e. one Phase.

### 13.8.1.1 Method of Use



- Open a Multiphase Study from your Local Study List with any Multiphase-type protocol. The Workspace displays each Phase side by side within a single View.

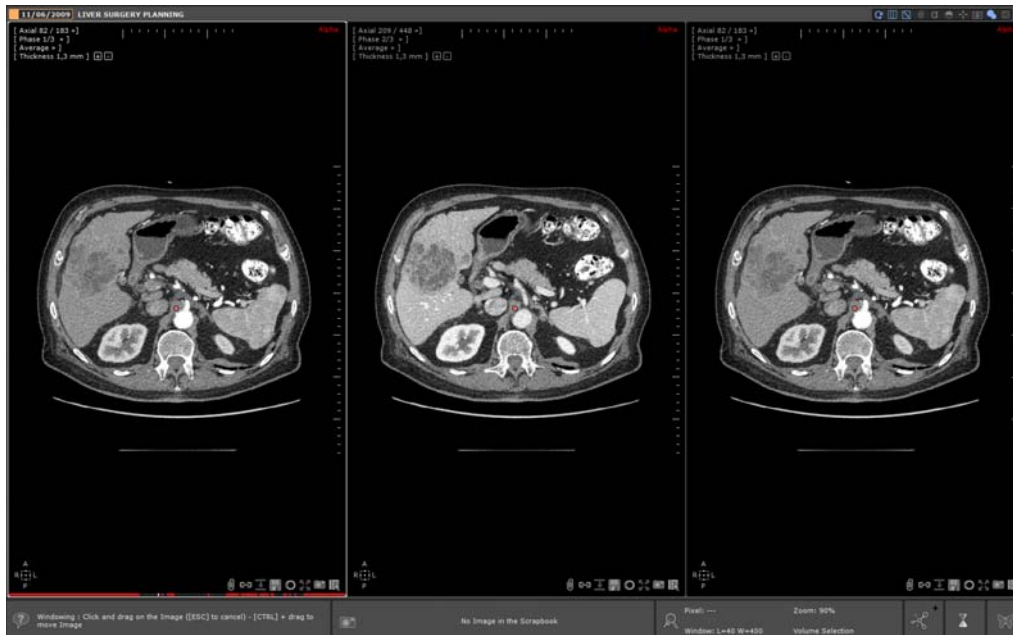


Figure 13-112 Multiphase View (MPR Phase Grid)

In a multiphase view, there are **two navigation modes** available from the Phase menu located at the top-left of any viewport:

- **'Spatial Navigation'**: the active Phase displayed Full-screen with a double slider at right: Spatial Navigation Slider on top to navigate through the slices of the Phase and Temporal Navigation Slider underneath to navigate through the Phases
- **'Temporal Navigation'**: the active Phase displayed Full-screen with a single Temporal Slider at right.



Series are loaded in increasing Acquisition Time order.

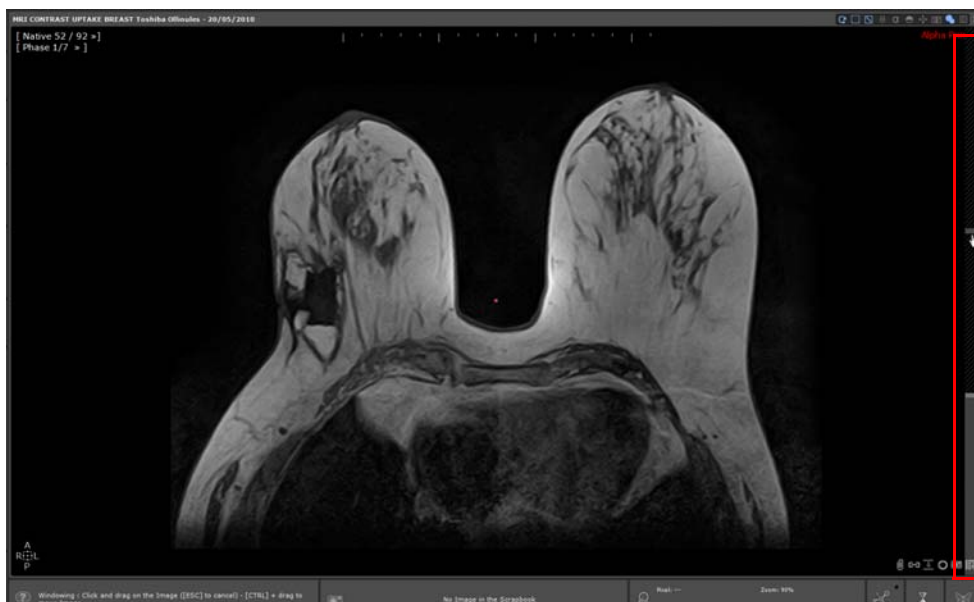


Figure 13-113 Spatial Navigation View with Spatial/Temporal Slider at right

### 13.8.1.2 Temporal Navigation

In a Multiphase View, the Temporal Navigation View navigates from Phase to Phase, i.e. through time, for any given position in the volume.



Figure 13-114 Temporal Navigation View with temporal Slider at right and Cinema view at bottom



Use the Cine Mode  (press the C keyboard shortcut) to navigate through the Phases automatically.

### 13.8.1.3 Controls

The following controls are available to navigate through the Phases:

- Moving the Temporal Navigation Slider upwards or downwards. This slider appears at the right of the Viewport (or the bottom-right if you are using the Spatial Navigation Layout)
- Rolling the mouse-wheel over the Temporal Navigation Slider

The different Phases can also be selected directly by clicking on the Viewport Phase Menu at the top-right of the Viewport:

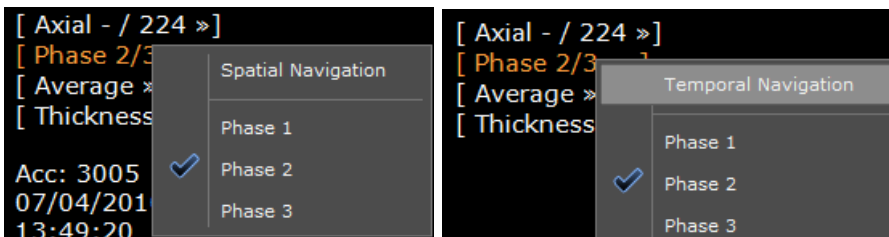


Figure 13-115 Switch between Spatial and Temporal Navigation in the Viewport Phase Menu

### 13.8.1.4 Synchronized Windowing between viewports

In a multiphase viewport, when performing windowing adjustments on one phase, those adjustments are automatically replicated on all other phases of the series. Additionally, those adjustments are also preserved when switching from one layout to another layout where that same series are displayed.



The whole windowing synchronization mechanism (performed per series category) cannot be applied if the protocol deactivates the synchronization, or if the <Shift> key is used.



This windowing setting is configurable.



## 13.8.2 Resynchronizing series loaded in a multiphase view

### 13.8.2.1 Overview

If you are not satisfied with how series are aligned with each other in the multiphase view, you have the possibility to **manually capture an offset** between those relevant proceeding as follow:




- 1 Deactivate the anatomical center synchronization in the viewport to realign
- 2 Search for an identical anatomical point using the Navigation Tool and/or moving the anatomical center over this point in the viewport to realign, in reference to the others
- 3 Capture the offset between the previous and the new anatomical center position.

Those steps can be performed viewport by viewport using the dedicated viewport buttons.



Figure 13-116 Realigning one series from one viewport within a multiphase view using dedicated viewport buttons



The capture offset icon representation changes according to the current position:

- **'No Offset with the current position'** : There is no offset between the viewport anatomical center position and the view anatomical center, meaning there is no user-defined alignment.
- **'Capture Offsets & Synchronize'** : There is an offset between the viewport anatomical center position and the view anatomical center. This offset resulting from the manual realignment of the series can be captured.
- **'Clear Offset & Synchronize'** : The manually defined alignment that has been set can be canceled. This is possible when a user alignment is defined and there is no offset visible between the viewport position and the view anatomical center.

### 13.8.2.2 Method of use

#### - Step 1: Deactivating the anatomical center synchronization from the relevant viewport

Once the relevant viewport is desynced from the view anatomical center:

- The anatomical center icon switches from  to 
- The anatomical center representation within the viewport turns from a **red spot** to a **gray spot** which indicates that it is no longer synced with the view anatomical center.

The 'Offset Capture' feature is now ready for use.



Navigating and/or moving the anatomical center inside the desynced viewport has no more impact on the anatomical center, meaning that those changes will not be reflected on other viewports belonging to the multiphase view.

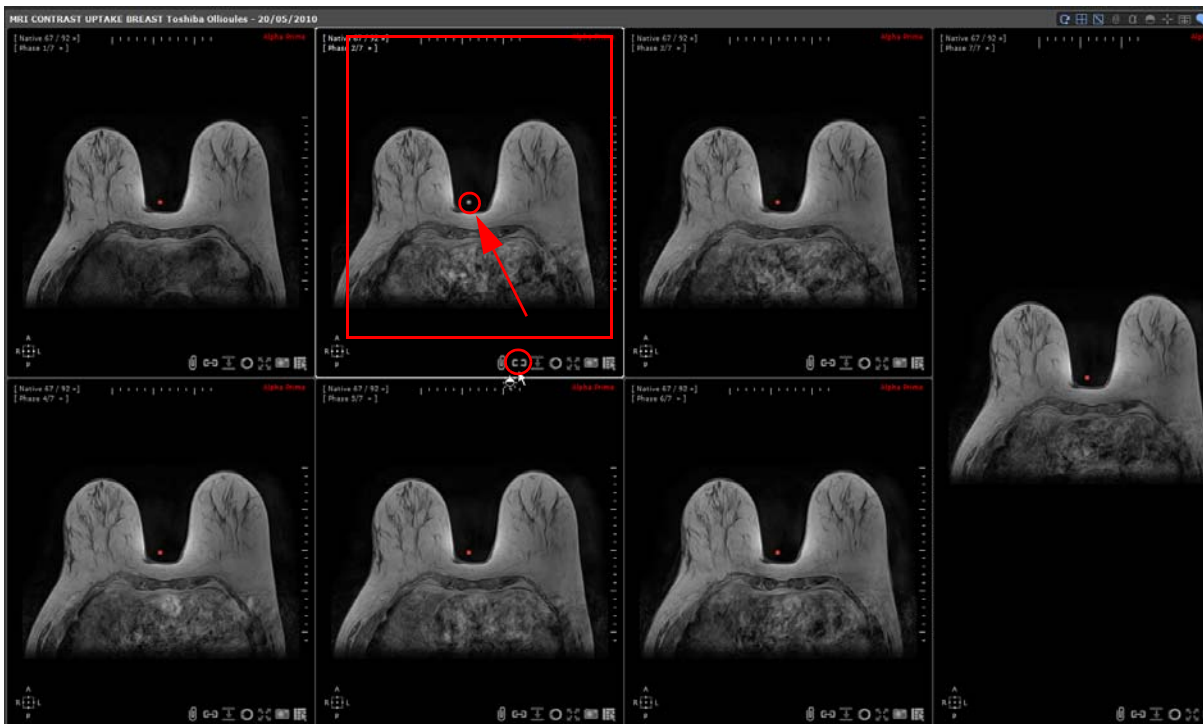


Figure 13-117 Deactivating the anatomical center in a given viewport

#### - Step 2: Capturing offsets between series and resynchronizing viewports in a multiphase view

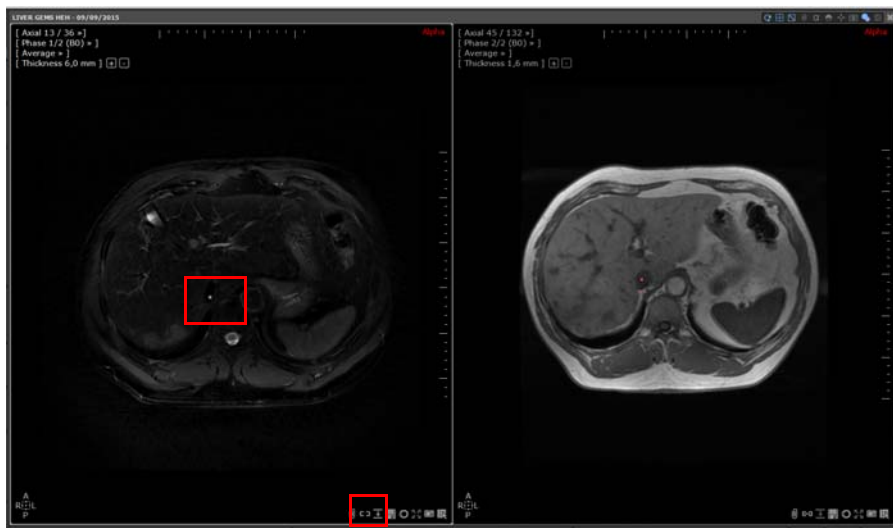
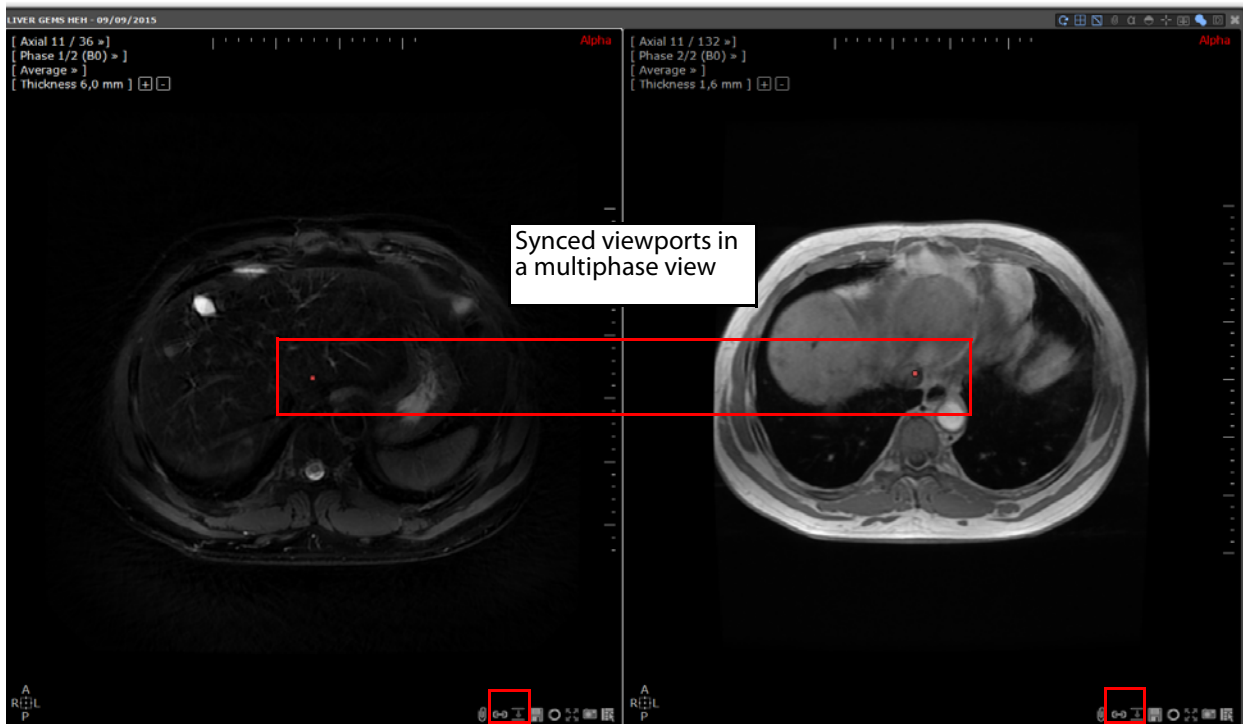


**Capturing offsets** between series loaded in a multiphase view is not available for view including a **soft matching** (see Section 4.6.9)


Realigning a series with another one can be done by moving the anatomical center onto a landmark in every series, each one in its own viewport. Off course, this can be performed only if the viewport displaying the series to be corrected is desynced.

As soon as you start navigating and/or moving the anatomical center in the desynced viewport, you automatically create an

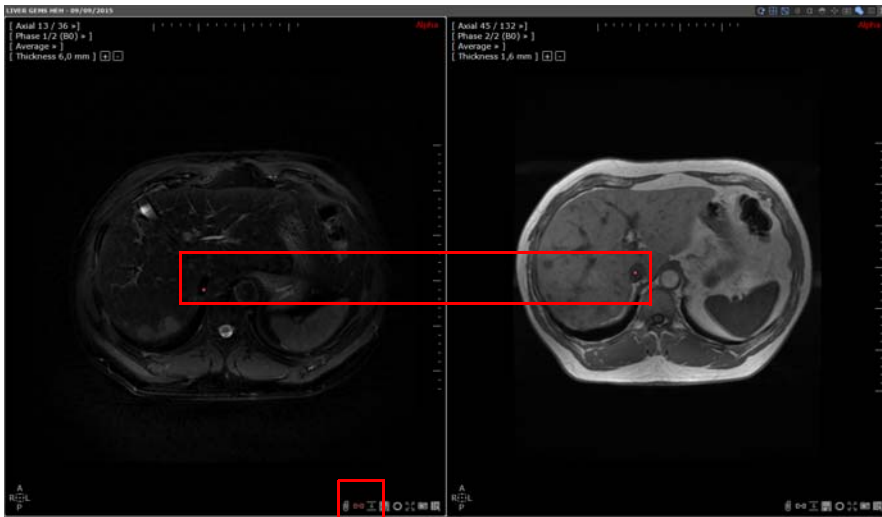
offset and consequently the 'Capture Offset' icon turns from the inactive mode  to the active mode .



The left viewport has been desynced and an offset has been created:  
There is now an offset between the position of the view anatomical center and the current viewport position (i.e. the gray spot)

Clicking on the 'Capture Offsets & Synchronize' icon  captures the defined offset and automatically reactivates the synchronization in the viewport.



Simultaneously, the anatomical center icon switches from  to  and the 'Capture Offset' icon  switches to  meaning that the series are now correctly aligned.




The left viewport has been re-synced to the right viewport taking into account the captured offset

- **Step 3: Clearing Offsets between series in a Multiphase view**

- Deactivate the anatomical center clicking on

The Capture offset icon switches from  to  meaning that the related viewport has a manual alignment and no offset visible between the viewport position and the view anatomical center.

- Click on  to remove the manually defined alignment and resynchronize the viewports belonging to the multiphase view reactivating the anatomical center in this viewport.



Defining an offset on a series used for the fused viewport results in modifying the volume alignment in the fused viewport.



Even if offsets have been defined between the series in one multiphase view, capturing offsets between views remain possible whether those views are single or multiphase.




**Except for series for which a rigid matching is performed**, offsets set for series in a multiphase view are **preserved upon closing** the series. Therefore, when the same series are reloaded again in a multiphase view, all previously captured offsets are applied (which also applies in the case of fused series alignment).

### 13.8.3 Manual resynchronization of two multiphase views

If you have two multiphase views opened in your workspace, whether those views have been opened with the same multiphase view protocol or not, you may not be entirely satisfied with the view synchronization navigation (which is automatically performed based on DICOM information).


Should this be the case, you can manually reset it:



If the Matching  is activated, make sure to deactivate the process in both views.

- Click once on the Sync button  at the top-right corner of a view to deactivate the current synchronization

performed between the views


- Search for an identical anatomical point in each view (using the Navigation Tool ) and move the anatomical center over this point in each view

- Click again  and select 'Capture Offsets & Synchronize' from the Synchronization contextual menu

Accordingly, both views are now correctly synchronized based on the anatomical center position.



Resetting the manual alignment defined between multiphase views using the 'Clear Offsets & Synchronize' option

from the synchronization menu  **also clears** all manually-defined offsets defined in a multiphase view (see Section 13.8.2)

### 13.8.3.1 Synchronized rotation in Z rotation Viewports

When **multiple views** are displayed in the workspace and that contain Z rotation viewports and provided those views are

synchronized , Z Rotation viewports are all synced by elevation when navigation  is initiated in one of these viewports.



There is no navigation synchronization between Z rotation and non Z rotation viewports.

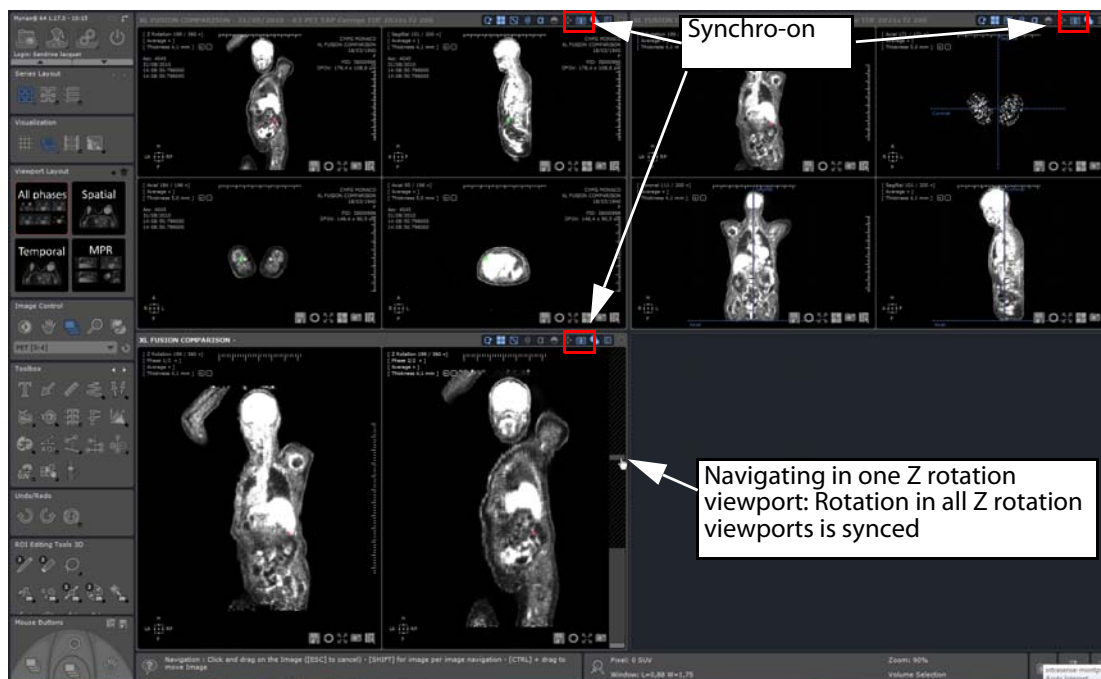


Figure 13-118 Workspace displaying 3 views (including one multiphase view) containing Z rotation viewports whose navigation is synced

## 13.8.4 Multiphase 3D Surfacic Viewport with registered ROIs

### All phase visualization mode

The 3D Surfacic Viewport can display all ROIs of all the phases simultaneously.

- Use the specific Phase Menu at top-left to view all Phases simultaneously:

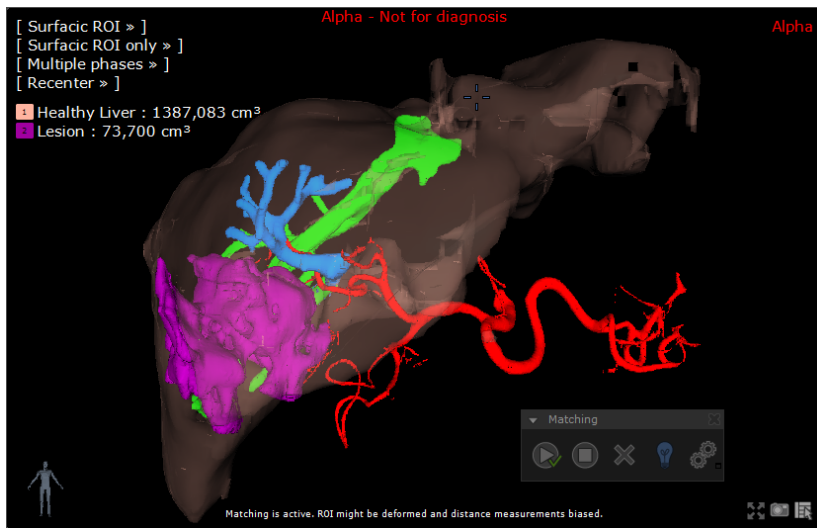


Figure 13-119 ROI Display in the 3D Surfacic ROI mode (Phase Menu set to "All Phases") with multiphase matching

### Phase per phase visualization mode

- Or select specific Phases

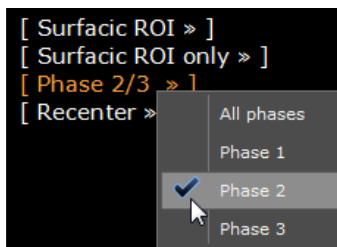


Figure 13-120 3D Surfacic ROI Viewport Phase Menu.



If a matching has been previously performed between phases and is still active, it is taken into account by the Surfacic ROI Exploration Mode:

- As ROIs and Annotations are repositioned so that they can be visualized in a unified space, be aware that their positions are modified to match this unified space. However, please be aware that annotations that suffer deformation will not be displayed.
- However the measurements attached to each ROI are NOT affected by this visualization mode (as they are always computed from the original ROIs in their original phase).

### 13.8.5 Adding Series using Drag & Drop in a multiphase protocol

Using the **QuickPatient** feature in a multiphase view protocol operates differently depending on whether the selected protocol requires the validation of identified and preselected series (i.e. category series selector window) before loading in the workspace or not.

For example, loading series in a multiphase protocol such as Liver Surgery Planning is automatic whereas loading series in a Fusion, Prostate or Breast protocol requires beforehand the validation of the series preselection into category, knowing that, in addition, some of those protocols enable the computation of new volumes resulting from a Volume Processor, as it is the case for the Prostate or the Breast MRI protocols.

No matter the protocol type that is used, the dropped series is always loaded in native orientation, native thickness and average mode (see Section 4.3.3.3 for detailed information)

## 13.9 Endoscopic Navigation

The Virtual Endoscopy tool reproduces the effect of a Camera Probe following a predefined Path. It can be activated at the series load stage via the Protocol presets, or during standard review by activating 'Endoscopy Mode' in the View Menu top-left of every frame as described below.

### 13.9.1 Overview

The Virtual Endoscopy tool is available for CT and MR modalities but with a different rendering to avoid any confusion:

- For CT, the rendering is done in orange/pink color
- For MR, the rendering is in grayscale



The Endoscopy tool in MR images is mainly used for **biliary duct exploration**.

---



When using the endoscopy tool with MR modality, the mannequin figure is displayed in the bottom-left corner of the 3D view.

---

### 13.9.2 Procedure

To activate Endoscopy Mode during Series review:

- Create a Path as described above in Section 4.6.4.3
- Select the 'Colon and Airways Endoscopy' Mode/viewport layout from the Advanced CT protocol (see Section 13.1.3) or use the drop-down menu by clicking on the overlaid Plane of View menu in any Frame

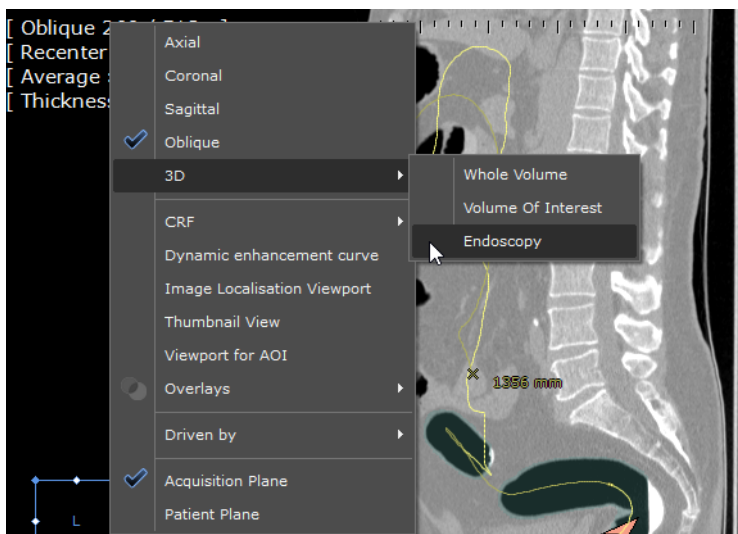


Figure 13-121 Endoscopy Mode selection in the View menu

The current selected Path is automatically affected to the Virtual Endoscopy module and the 'Camera' position is set to the last-created Point.

Navigation is controlled by the following commands:

- 'Play' to start navigation
- 'Flip' to perform an 'about-turn' in direction
- 'Stop' to stop navigation



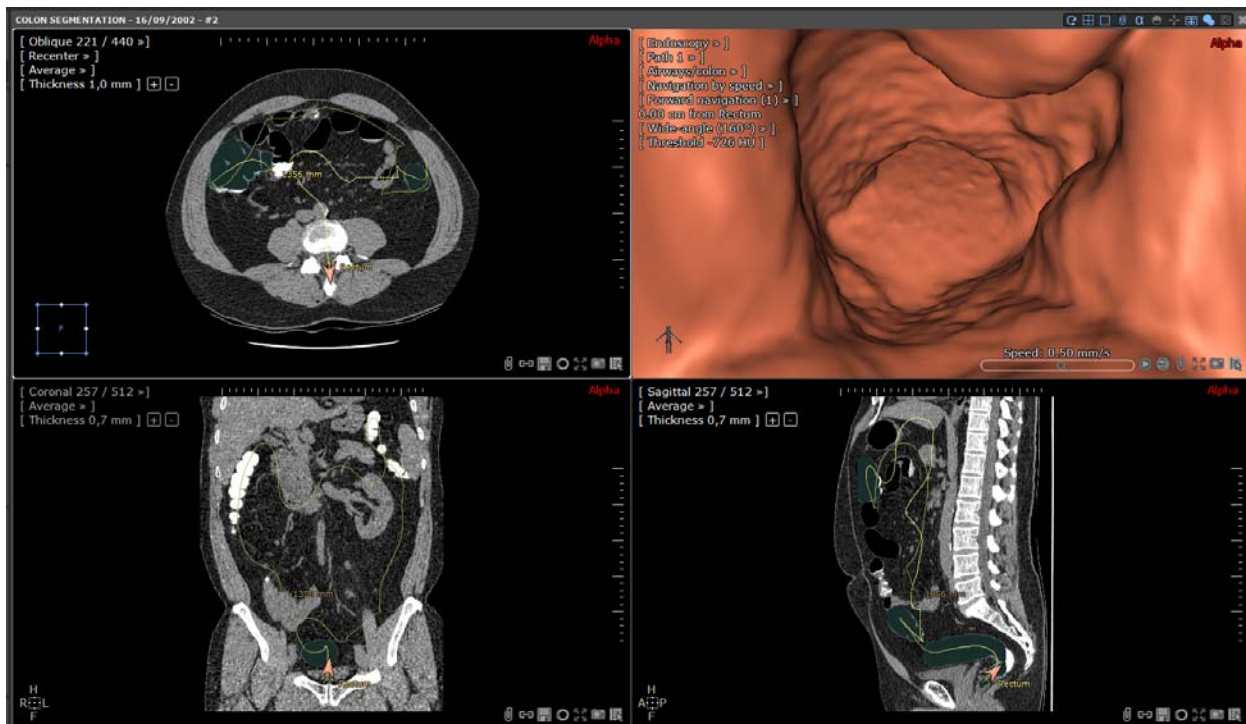


Figure 13-122 Create Path and activate Endoscopy Mode



In case of colon centerline edition, the anatomical center is synchronized in all viewports (either 2D or 3D) in the exact location where the seed point is created and for each click.



You can switch as many viewports as you wish to display Endoscopy Mode simultaneously, thereby simulating multiple camera probes.



If you open a 3D View then click anywhere on the 3D Path, the first Endoscopy to that was opened will refresh.



By default, to save on resource usage and optimize smoothness of navigation, the DICOM information is not displayed in the viewports during navigation, only after navigation stops). You can force DICOM information to be displayed at all times via the dedicated checkbox in the 'Miscellaneous' box of the Preferences>Display tab.



Check the 'High-end 3D video card' option in the 'Miscellaneous' box of the Preferences>Display tab to force optimal display quality of 3D images. When this option is off (not ticked), 3D display quality is reduced during navigation to improve the smoothness of movement (can be preferable for certain less powerful computers).



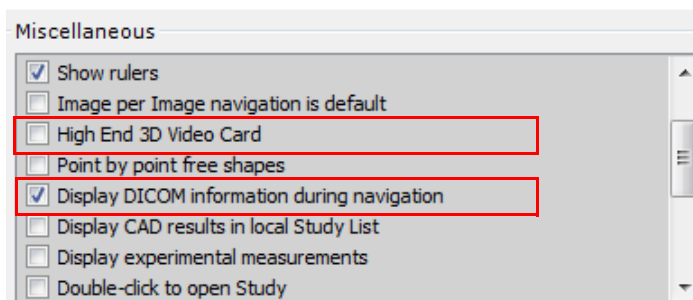


Figure 13-123 Display DICOM/High End 3D Video Card in the Miscellaneous box, Preferences>Display tab



The Anatomical Center may be hidden due to the Protocol setting. It can nevertheless be brought into view by double-clicking with the right mouse button on the desired spot in the Viewport.

### 13.9.3 Visualization controls

The 'Camera' position is represented in the MPR views by two pink line segments protruding from the central line. It can be repositioned manually by simply clicking on the Path in any view.

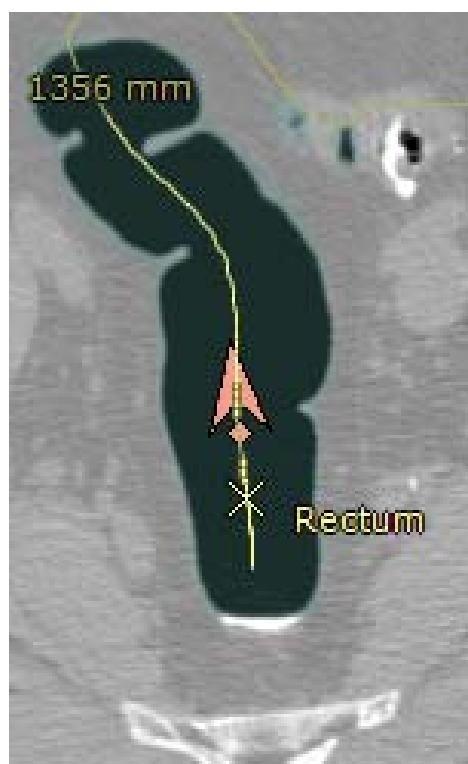


Figure 13-124 Path displaying camera position and orientation

Finally, both Camera orientation and navigation direction can be flipped in one click using the "Flip" button  (at the bottom-right of the Endoscopy Mode viewport).

#### 13.9.3.1 Rendering Modes

A choice of 3 Modes are available in the Rendering Menu (top-right of the Viewport):

- Airways: for visualizing airways or hollow tubular organs such as colon, trachea, bronchi, etc.
- Injected Vessels: for viewing tracer-injected vessels
- Full Sight: for a full perspective view of tubular vessels (including overlapped zones) enabling the visualization of colon polyps from different angles

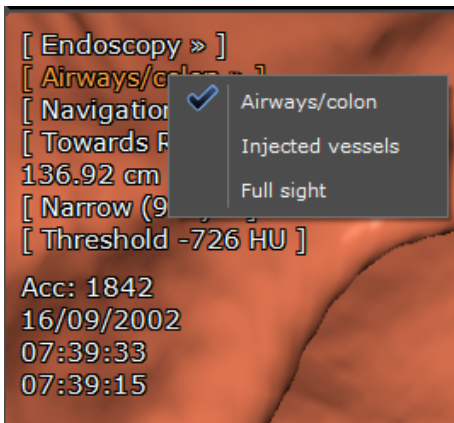


Figure 13-125 Endoscopy rendering modes

Full Sight Rendering Mode makes it possible to review the inner surface of a tubular volume around a Path. Structures on the surface are not hidden by folds.



Overlapped areas at top and bottom of the Endoscopy View (resulting from the angle exceeding 360 degrees) are shaded dimmer than the rest of the image.

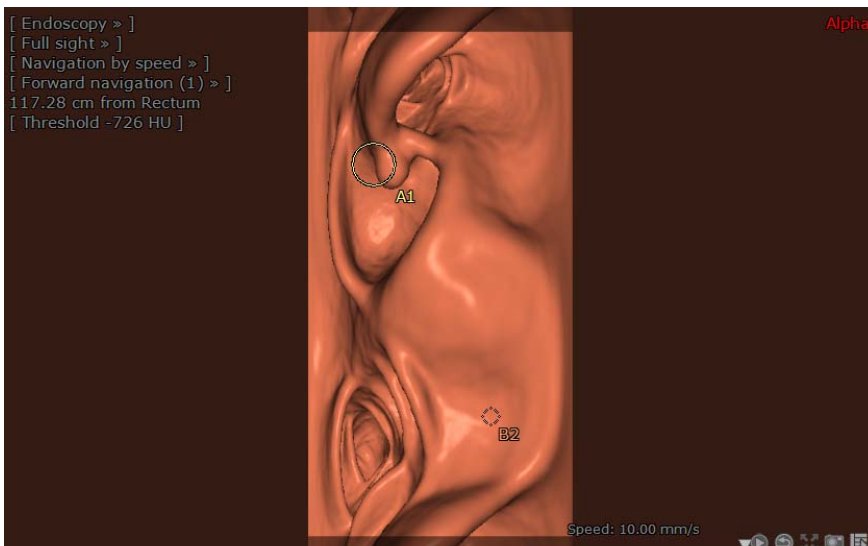


Figure 13-126 Example of a Full Sight Rendering Mode



Full-sight rendering mode shows a perspective view from the 'camera position' which angle is superior to 360° while remaining perpendicular to the vessel centerline.



These rendering modes can also be launched using the protocols.

### 13.9.3.2 Camera view angle

The width of the 'Camera Lens' can be modified via a drop-down menu available in the Endoscopy Mode frame.

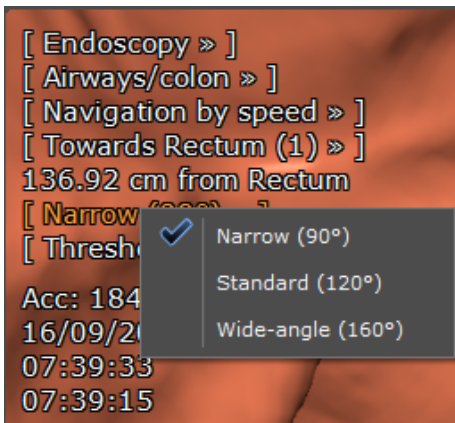



Figure 13-127 Camera scope drop-down menu

By default, the aperture angle is set to around 160 degrees in order to produce a full perspective view, not a flattened one

The Camera orientation and navigation direction can be changed by using the 'Flip'  button (bottom-right of the Endoscopy Mode viewport)



Default orientation and navigation direction of the Endoscope is Rectum to Caecum (Forward).



The direction is modifiable via the drop-down 'Towards' menu at top left of the Endoscopy frame.

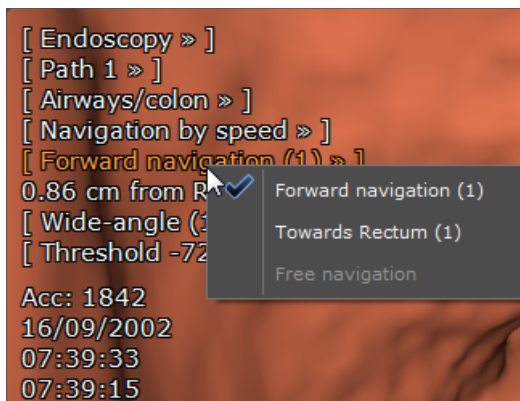


Figure 13-128 Colon Path direction menu

### 13.9.3.3 3D Anatomical Center

The Anatomical Center, which is visible in all MPR views and can be used to synchronize all MPR views on the same point, is also visible in 3D in the Endoscopy view.

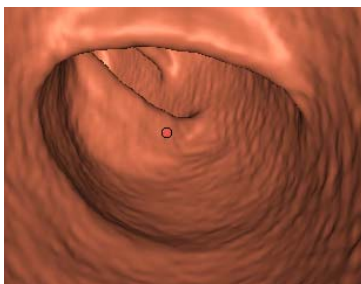



Figure 13-129 3D Anatomical Center in the Endoscopy Viewport

The 3D Anatomical Center is represented as a red-colored dot (or crosshairs) which do not actually intersect so as to leave the central point clearly visible.

## Manipulation

- Click on 'Navigation' mode  in the Image Control Toolbar to display 3D Anatomical Center
- Drag and drop the cross anywhere or
- Double-click on any spot to place the Anatomical Center directly where you wish



When the anatomical center is masked by surface (i.e. beyond the colon wall), its projection appears as a green dot.

---



Due to the fact that Windowing settings affect intensity levels and the way surfaces are perceived, they may also have an effect the positioning of the 3D Anatomical Center.

---



When you click on a thickened slice, the Anatomical Center is placed directly on the slice itself, not in the cumulated area.


---



Hold the ALT key while you click and drag to swivel around the 3D Anatomical Center.


---



You can reposition the 3D Anatomical Center freely on any MPR view by double-clicking on a desired location whilst in 'Navigation' mode ; all MPR frames reset to the new location automatically as does the Endoscope.

---



When the 3D Anatomical Center is repositioned in any MPR frame, it is also repositioned simultaneously in the endoscopy view. If you wish to move along the path while targeting the anatomical center (**using the mouse wheel only**), you can lock this target point of interest permanently clicking on the lock  that appears at the bottom of the endoscopic viewport. This targeting can be deactivated at any time unlocking the lock.

---



You can save the position of the Anatomical Center to User Protocols. When the Anatomical Center is placed on a POI, any Series loaded via this Protocol initializes on the first POI of the first POI List available. If the Protocol was saved with the Anatomical Center placed on a Path, the Series will open with the Anatomical Center placed on the first point of the first Path of the Series.

---

### 13.9.3.4 Threshold Parameters

The Threshold parameters for Airways and Injected Vessels Rendering Modes can be adjusted according to the context:

- For the Airways Rendering Mode
  - For the Injected Vessels Rendering Mode
- 



Threshold can be further modified using the "+" and "-" number pad keys (by steps of 20 HU) or by entering a value directly in the Threshold Field in the top-left Endoscopy Viewport menu.

---



Threshold values are preserved for Filet Mode, Endoscopy Mode and Surfacic Mode after modification and automatically saved to User Protocols.

---



All Threshold values and Rendering Settings are provided as examples and are not the result of any clinical specification. They should be used and considered accordingly. The Full Sight Rendering Mode produces a perspective view from the Endoscopy camera position which is greater than 360 degrees viewed perpendicular to the vessel centerline.

---

### 13.9.4 Navigation controls

---



When launching the Endoscopy Mode after automatic Colon segmentation, the default direction followed by the Endoscope is oriented from Rectum to Caecum (Forward Navigation). This setting is modifiable via the drop-down 'Towards' menu at top left of the Endoscopy frame.

---

The Endoscope is placed, by default, on the rectum of the Colon ROI. If this cannot be determined, default position is on the first point of the path or on the last point created (the default navigation direction depends on which point is placed the camera). Although, by default, navigation mode is 'automatic', 3 modes are available:

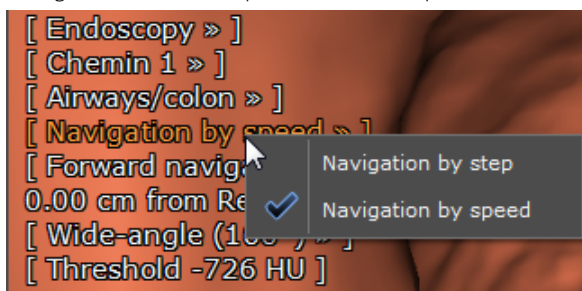
- **Automatic Mode:** whenever a new path is created/selected, or if you click on the 'Replay' button, this mode is activated by default. The 'Camera' is placed at the first point on the currently selected Path and direction of navigation can be toggled 'forward' or 'backward' along the axis of the Path via the overlaid menu at top-left of the frame.
- **Semi-automatic:** camera moves forward/backward along the axis of the path, but the orientation can be adjusted by means of the keyboard arrow-pad to look in any direction
- **Manual:** camera is placed in any location by yourself and made to move freely using the keyboard cursor arrows.

There are 2 types of Navigation Control:

- 1 **By Speed** (default method: a single slider at the bottom-right of the endoscopy viewport (see Figure a) hereafter) enables millimetre per second adjustment from -10mm (fast reverse navigation) to +10mm (fast forward navigation)
- 



Although Endoscopy navigation is, by default, set to 'By Speed', this mode can be switched to 'By Step' via the Navigation Menu at top left of the Viewport



- 2 **By Step:** transport is modified by 2 sliders, the 'Step' and 'Pause' sliders which enable:
    - Step: the 'size' or 'length' of each step forward/backward can be 0~10mm (default is 0.5mm)
    - Pause: the lapse of time from one step to another can be 0~1 second
-

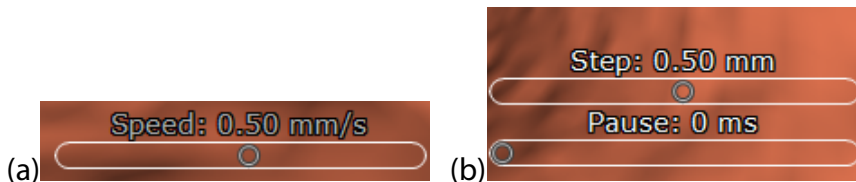


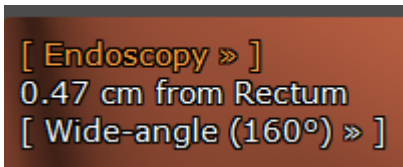
Figure 13-130 Transport Control: (a) 'Navigation by Speed' / (b) 'Navigation by Step'

- To reset speed navigation, right-click on the rounded cursor



When navigation starts, the fly-through menu is reduced to the following information:

- Distance from the rectum,
- Angle and field of view
- Acquisition date



When navigation stops, all the Canonical MPR viewports lock to the exact spot where the Virtual Camera stopped.



Move the mouse horizontally to navigate in Full-sight mode.




Use the 'Home'/'End' keys of your keyboard to navigate to the Start/End of the active Path or the Left/Right cursor keys to navigate between Path points.



As soon as the keyboard arrow keys are used, the Navigation Direction Menu switches to 'Free Navigation'.



Press the 'Alt' key when you click  to activate continuous play mode. In this mode, when the Endoscope reaches the end of the Path, it automatically flips back and continues the Fly-through in the reverse direction.

While in Endoscopy Mode, standard navigational functions apply:

- Zoom: moves the Camera view forward/backward
- Pan: moves the camera parallel to the view (Pan)
- Rotate: rotates the Camera view
- CTRL key + mouse click-and-drag: forces panning of the Camera view
- Shift key + mouse click-and-drag: forces rotation of the Camera view
- 'X' key + mouse click-and-drag: fixes rotation around the central axis of Camera view




Endoscopy Navigation parameters can be captured and saved in User Protocols.



Depending on the computing resources of the PC being used and the speed setting selected, the distance between two consecutive images might be greater than 10mm. In such cases, a warning is displayed to inform the user that some potentially important information might have been missed.

### 13.9.5 Endoscopy viewport synchronization

When several endoscopy viewports are opened in the workspace, you have the possibility to synchronize navigation.

- To toggle endoscopy viewport sync, open the synchronization window, right-clicking on  in the Layout option toolbar

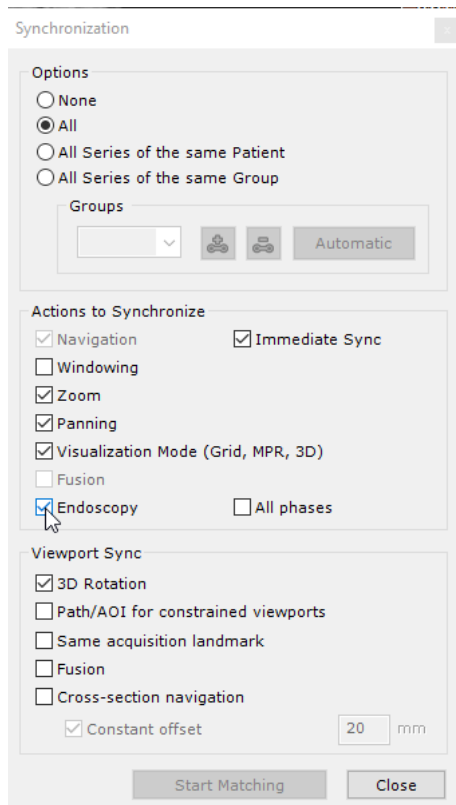


Figure 13-131 Activate endoscopy synchronization



toggling endoscopy synchronization automatically toggles navigation synchronization.



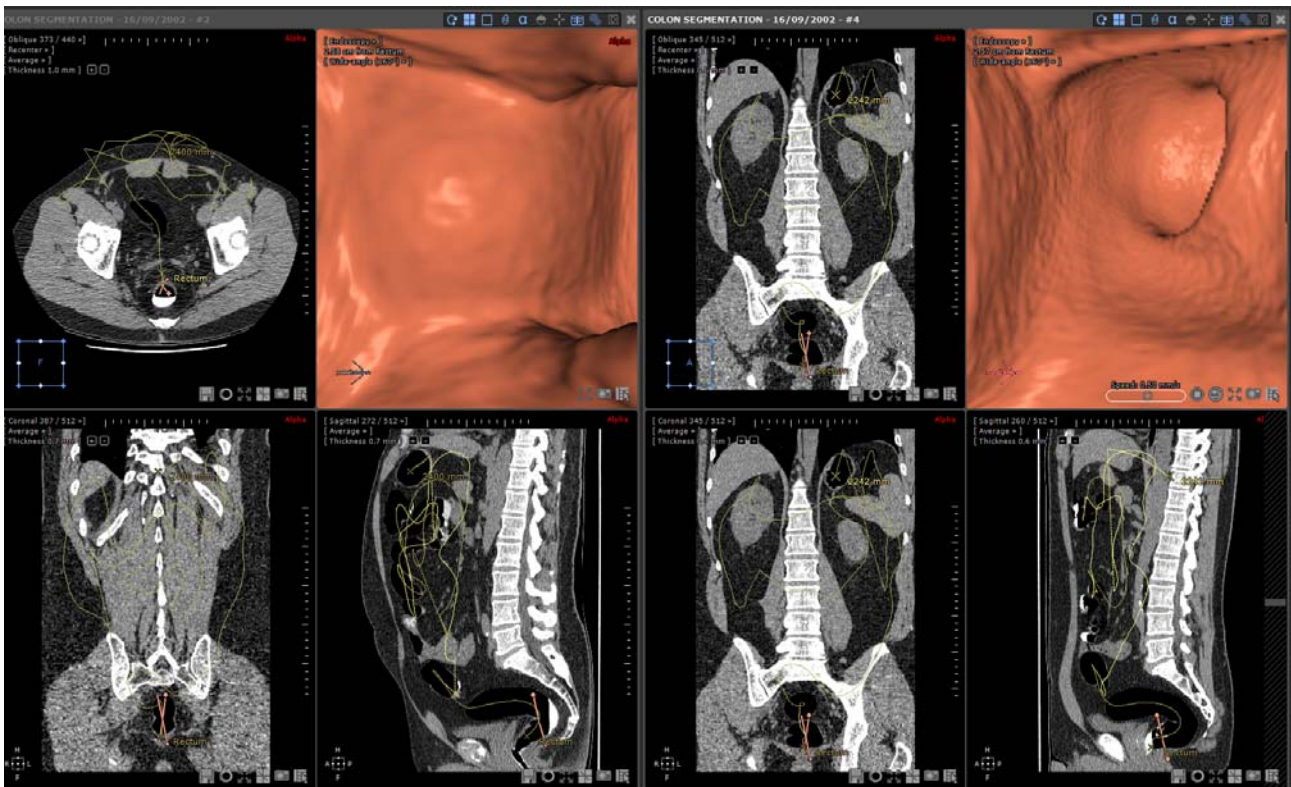


Figure 13-132 Navigation synchronization in endoscopy views

Whether you navigate using the mouse wheel or the fly-through camera, navigation is now synchronized.

- Click on the  button in the endoscopy viewport of your choice to start navigation



All viewports displaying images belonging to the same series in the same view are also synchronized (upon distance from synchronization start point, i.e. path beginning) according to the endoscopy camera (including a slight offset to have synchronization position in front of camera and not at camera position). It also applies in Multiphase mode.



In automatic fly through mode, the retained fly speed is the speed set in the viewport that initiated the automatic fly through. Fly through controls are disabled in other synchronized endoscopy viewports.



If you change fly direction clicking , the change automatically applies to other endoscopy viewports.

### Offset

Start point position is the offset from the beginning of the path where the synchronization was toggled.

- To change this offset, toggle synchronization off, set endoscopy viewport to desired offset, then toggle synchronization on again.

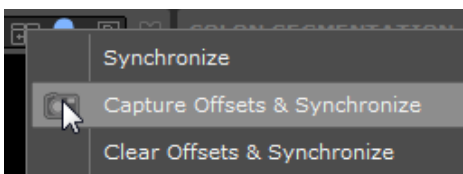


Figure 13-133 Set an offset in navigation synchronization for endoscopy views

Start offset will then be the current offset.



## Chapter 14

# 14 Additional Tools

### Introduction

The following chapter describes a number of additional tools, functions and modules that can be available in some Myrian clinical apps.

## 14.1 PDF ReportCreator

### 14.1.1 Overview


It generates interactive 3D PDF Reports. 3D Images are converted and embedded as 3D Objects which can be viewed and manipulated within a standard PDF.

Typical use can be to illustrate various Liver Resection scenarios.



All Measurement Data including 3D annotations (c.f.: Arrow Complex AOI) are exported with the 3D View.

### 14.1.2 Create a 3D PDF report

- Set any compatible View to 3D Mode
- Click on 'Create Report' button  in the Scrapbook/Reports Toolbar

The Report creation window opens:

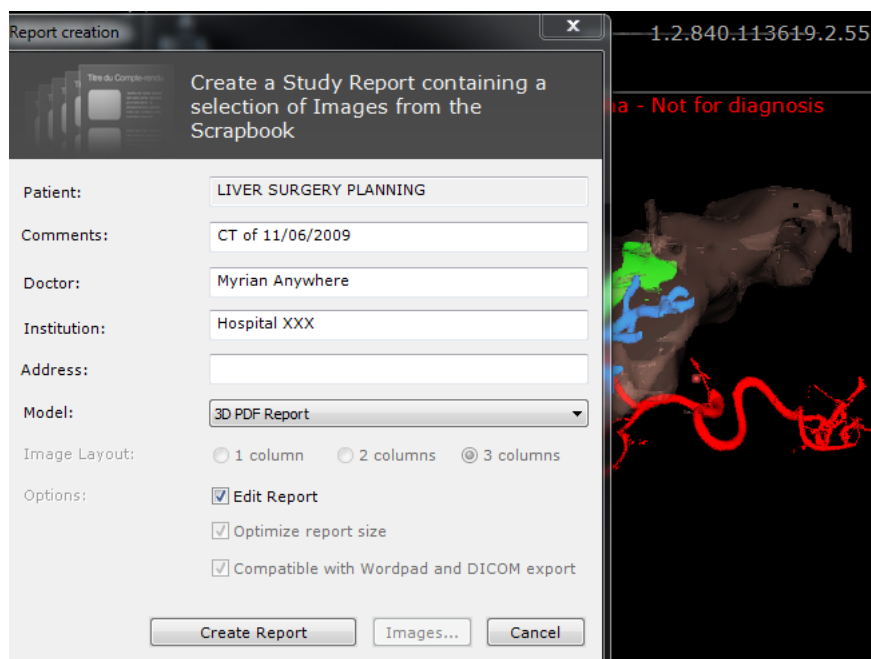
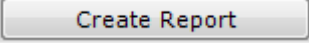


Figure 14-1 3D PDF Report option in the Report Creation Window

- Select '3D PDF Report' from the drop-down list
- Click  to launch Report Creation



Report Creation status is charted by the image processing progress bar in the Information Toolbar at bottom-right of



Myrian® Workspace

The 3D PDF report is automatically opened for visualization and stored in the 'Reports' Tab inside the Patient study (see Section 5.4.3).

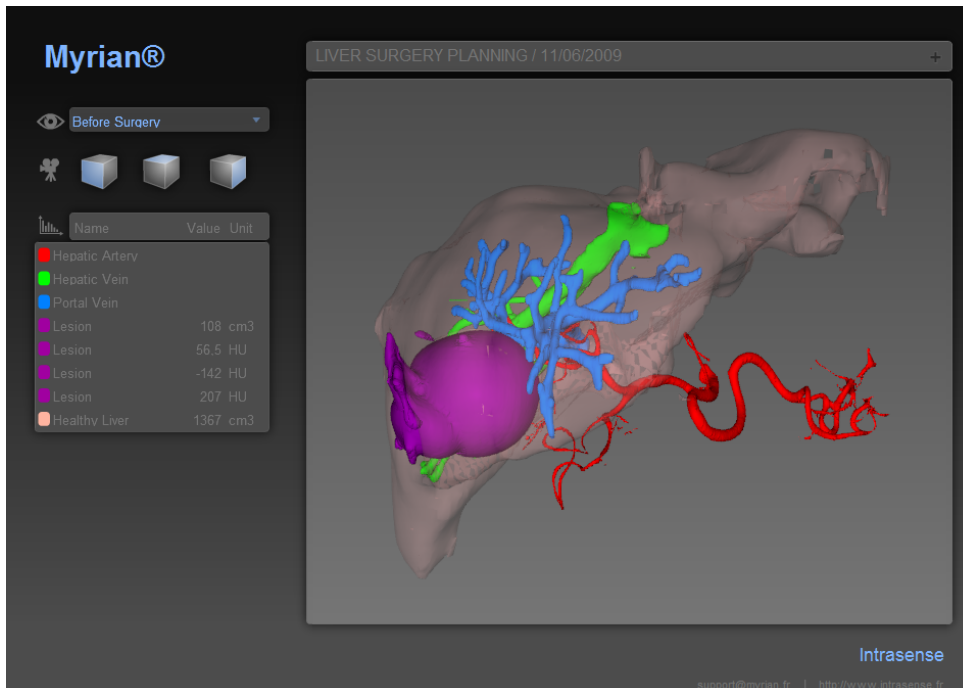


Figure 14-2 Interactive 3D PDF Report

Patient ID appears at the top of the Report:



Figure 14-3 Information field at top of PDF Report



All **Measurements** and **Combined Measurements** for every ROI (e.g. Volume, Ratio, etc.) **are exported** to the 3D PDF Report.



**Default ROI Set is exported** with all the defined ROI Groups if it is sole ROI Set.



Default ROI Set is NOT exported if more than 1 ROI Set exists.



If **no ROI Group** exists, **all ROI are exported**.

	Name	Value	Unit
	Hepatic Artery		
	Healthy Liver	1070	cm <sup>3</sup>
	Portal Vein		
	Hepatic Vein		
	Lesion	0.423	cm <sup>3</sup>
	Lesion	49.5	HU

Figure 14-4 ROI List with Measurements



To generate 3D PDF Reports, Myrian® 3D Navigation and 3D Graphic Card compatibility are not required.



For safety reasons, we strongly recommend you to upgrade to Adobe Reader X (10).

### 14.1.3 DICOMize a PDF report

PDF reports produced by Myrian® (either as a 3D PDF or based on a CRF report integrated in the Breast or the Prostate Protocol) can be DICOMized to be exported over the PACS and therefore imported and visualized by any of your colleagues.



E-CRF-based PDF reports are also automatically converted into DICOM Secondary Capture images (OT format) and added within the related patient study in the Study list. This file format can be opened using the Native Images Protocol.



DICOM PDF reports are compliant to DICOM standards for easy data import/export over the PACS.

- Select a Patient PDF report from the 'Reports' tab in the Study List



- Click on



Double-click on the PDF report to open it as a PDF file.

A message pops up:

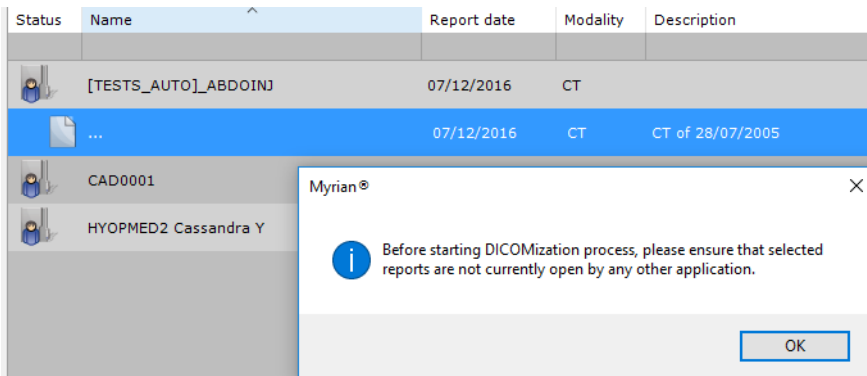


Figure 14-5 DICOMizing a PDF report

- Click OK

The PDF report is DICOMized and automatically added to the patient study in your Local Study List.

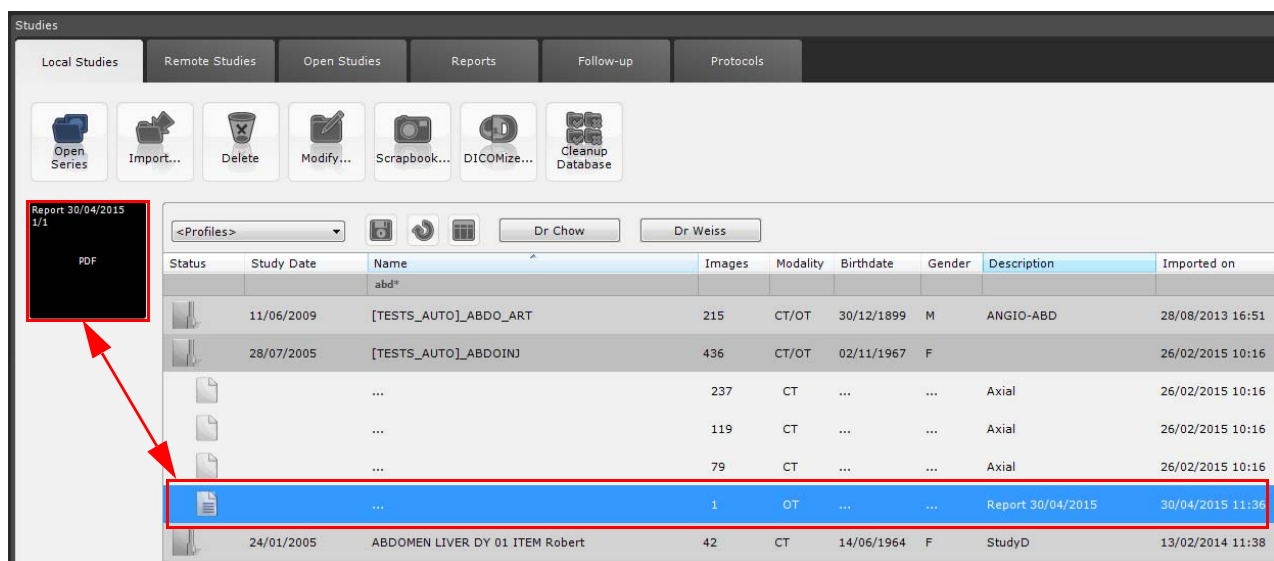


Figure 14-6 Dicomized report series



Dicomized PDF reports **are not** automatically exported to the PACS:

- To push a DICOMized report over the PACS, right-click on the selected report, then select 'Export Series', then 'To PACS, console...' and select your PACS system from the list.

#### 14.1.4 Extract a DICOMized PDF

- Import a DICOMized PDF report from the Remote Study tab (see Section 2.6).
- in your Local Study List, right-click on the imported DICOMized report in the appropriate patient study then from the Series Contextual menu, select 'Export Series' and 'Extract Report'.

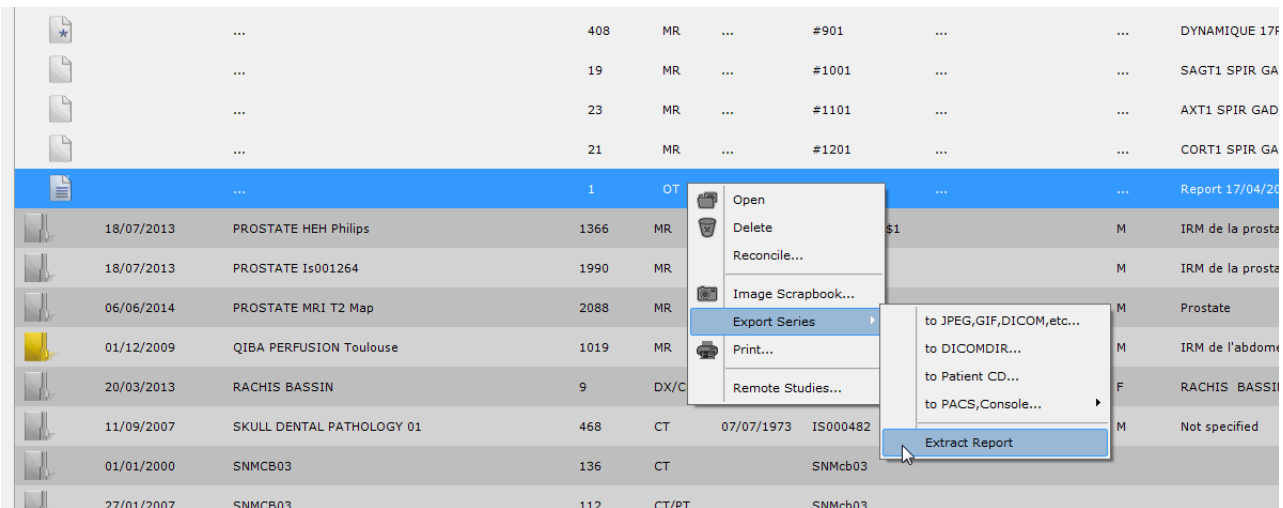


Figure 14-7 Extracting an imported DICOMized PDF report

A PDF version of the report, that is identical to the initially created one, automatically opens.



By default, the extracted PDF file is saved in C:\Users\\Documents\Intrasense\reports.

## 14.2 Stitching

### 14.2.1 Overview

This feature enables you to “Stitch” or combine multiple Data Sets so as to produce a single image or volume to facilitate navigation and review. This is particularly useful in cases such as MR imaging where, for instance, multiple Series of captures were required to achieve captures of large regions of the Patient’s body.

The “Stitching” is done within a single, specific viewport in which all the Images which require stitching are opened, displaying an automatically-generated stitching proposition.

You will nevertheless be able to readjust the images towards the top/bottom/left/right or forward/backward as well as modify the location of the stitching line.

### 14.2.2 Method of Use

- Select all the Series you wish to stitch together in the Local Study List

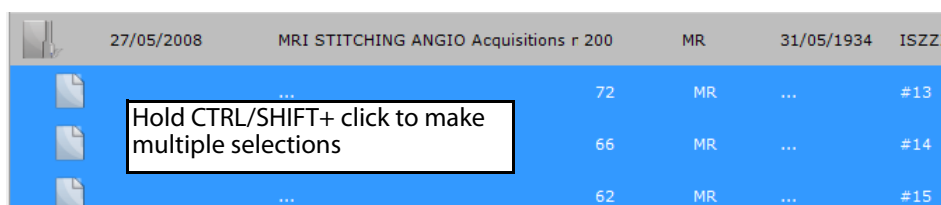


Figure 14-8 Select multiple Series to Stitch

- Select the ‘Automatic’ Protocol Loading Mode at top of the Study List and click on the ‘Open Series’ button at top-left of the Local Studies Tab
- In the Protocols Tab, click on the “Stitching” Family of Protocols at left of the Tab

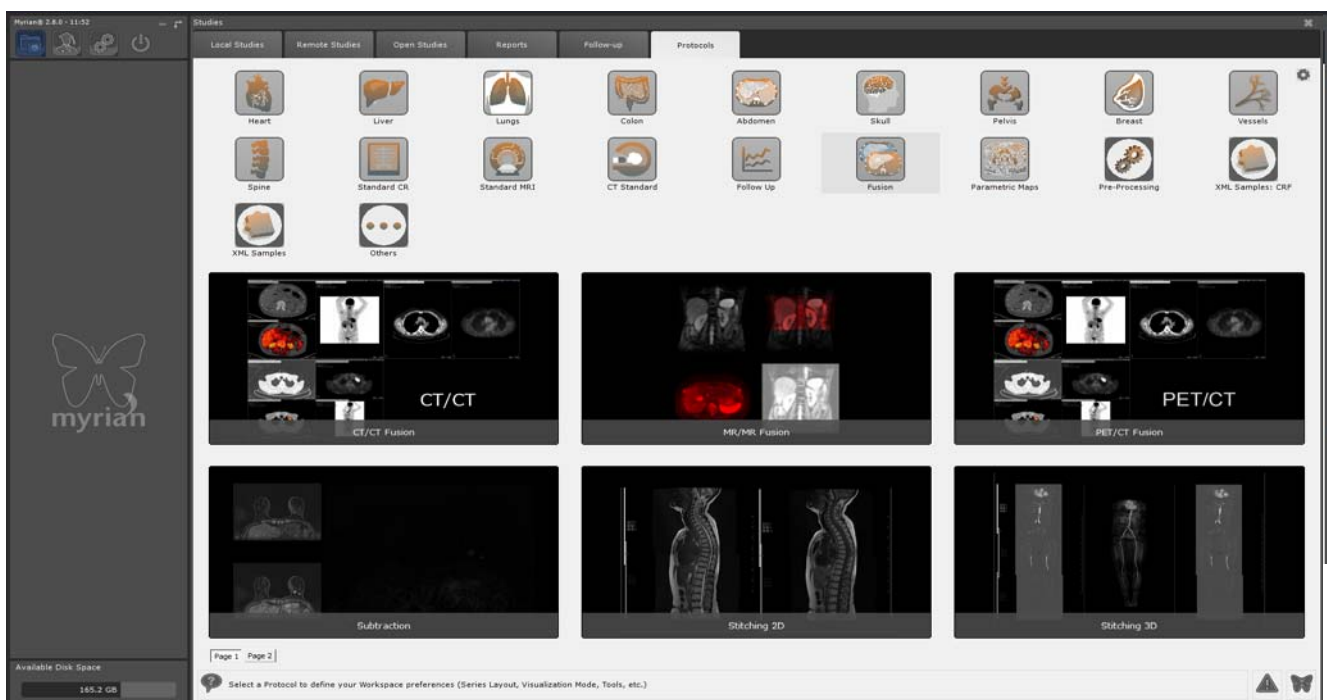


Figure 14-9 Select Stitching Protocol

- Double-click on a Stitching Protocol of your choice

The Series will open displaying a proposed initial alignment of the Series.



Figure 14-10 3D Stitching Protocol (Stitching viewport at left)

- Activate MIP Mode and increase the slice thickness to improve visibility

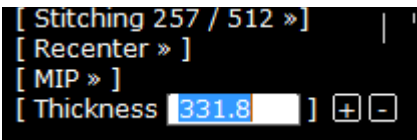
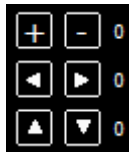


Figure 14-11 Modify Rendering and Slice Thickness

#### 14.2.2.1 Adjust alignment



- Click on the Alignment Button-Pad at left of the desired Series to activate it in order to be able to adjust the alignment



Figure 14-12 Select a Series to align

- Hold the 'CTRL+SHIFT' keys down and drag the mouse to realign the Series Left/Right or Up/Down to realign by dragging a Series with the Mouse

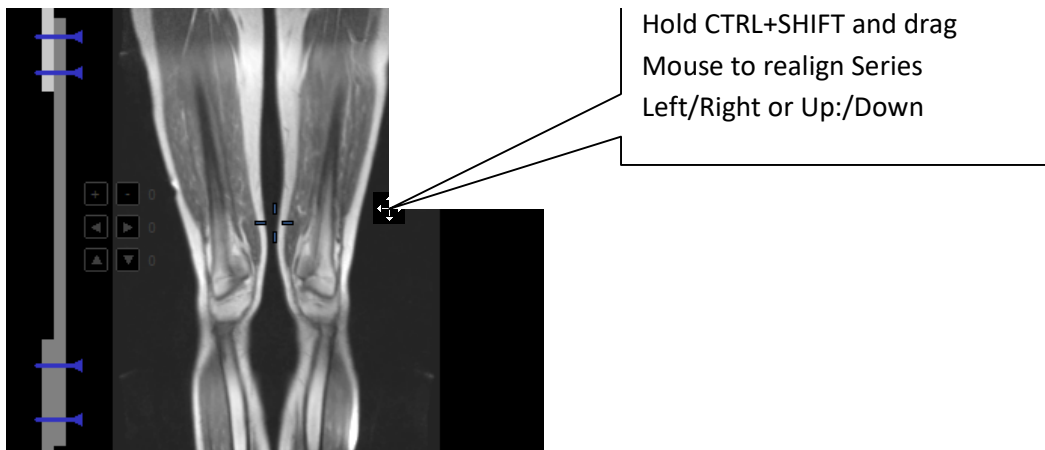




Figure 14-13 Realign by drag and drop



- Click on  at left of the Series to Move the Series Left/Right/Up/Down one step at a time
- Click on  at left of each Series to align the Series Back/Forward one slice at a time
- Right-click on any of the Alignment Buttons and click on 'Reset' to set the values back to 0

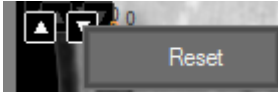


Figure 14-14 Reset alignment values

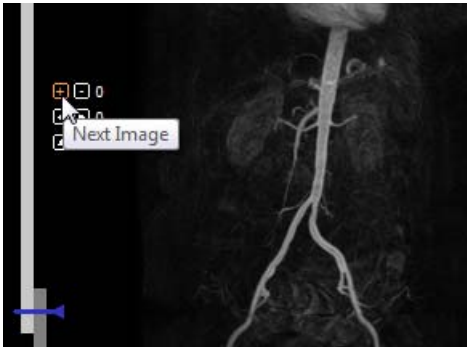


Figure 14-15 Align Slices

- Adjust the Overlap by dragging the blue-colored Stitching Seams at left up or down

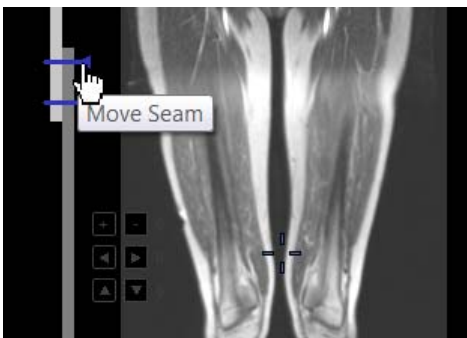


Figure 14-16 Adjust overlap seams





A progressive linear blending is applied to the Overlap Zone to ensure smooth transition between the images.



Use the Zoom  or activate a Volume of Interest Viewport to make fine alignment adjustments.

#### 14.2.2.2 Adjust windowing

There are two windowing modes available that can be performed on the stitching viewport:

- **Global windowing** which applies to the whole stitching volume (including all sub volumes)
  - Activate the windowing tool  then click anywhere on the stitching viewport: the windowing center/range values are modified accordingly for all sub volumes.
- **Sub-volume windowing** which applies solely on a given data set of the stitching volume
  - Activate the windowing tool  while holding down the <Alt> key. Only the windowing for the currently



selected sub volume is modified accordingly

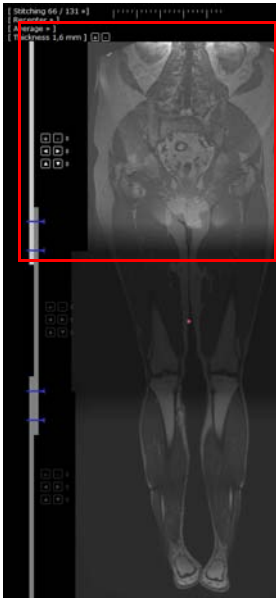


Figure 14-17 Applying sub volume windowing mode to upper sub volume



You can also modify the windowing in global and sub volume mode from the CLUT bar, keeping or not the <Alt> key pressed.



The current sub volume is the one whose alignment button pad is highlighted.



The sub volume windowing mode is accessible only when the viewport is in stitching mode. In all other cases, the windowing is modified for all the sub-volumes.

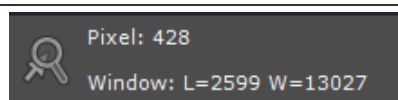


When a sub volume has different windowing settings, all adjustments performed in global windowing mode keep the shift between the sub volumes.




The flyover information toolbar is updated for both windowing modes.

By default, the windowing values of the upper sub volume are displayed. If the viewport is in stitching mode, pressing the <Alt> key displays the windowing for the current sub volume.



### 14.2.3 Saving Stitched Series

- When you are satisfied with your alignment settings, click on the 'Create a New Series' button  at bottom-right of the Stitching Viewport to save your work.



A pre-filled dialog box appears displaying a proposed name for the Stitched Series including the names of all the Series

contained in the Stitched Series.

- Modify the Series Description as desired and confirm by clicking on 'OK'.



Figure 14-18 Pre-filled Save dialog box



User-defined windowing settings applied to the stitched series are preserved.



ROI are not exported in the produced Series.

## Series Anonymization

You can anonymize the Series removing:

- Any identification relative to the Patient
- The orientation of the Patient
- The Name of the Hospital having produced the original Datasets

## Progress Bar

A progress bar will appear to chart the build status of the New Series.

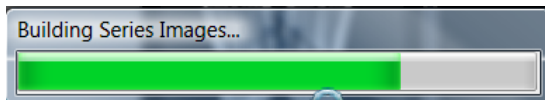


Figure 14-19 Processing Series progress bar

When the process is complete, the New Series will open alongside any other currently open Viewport in Native Mode (default setting).



The Stitched Series will be automatically added to the Study.

### 14.2.4 Stitching WBI protocol



The user should be aware that distortion effects on diffusion series may conduct to erroneous interpretation.

The Stitching WBI protocol enables you to stitch together each body part imaging of MR modality.

- Select a Whole Body Stitching study from your local study list.

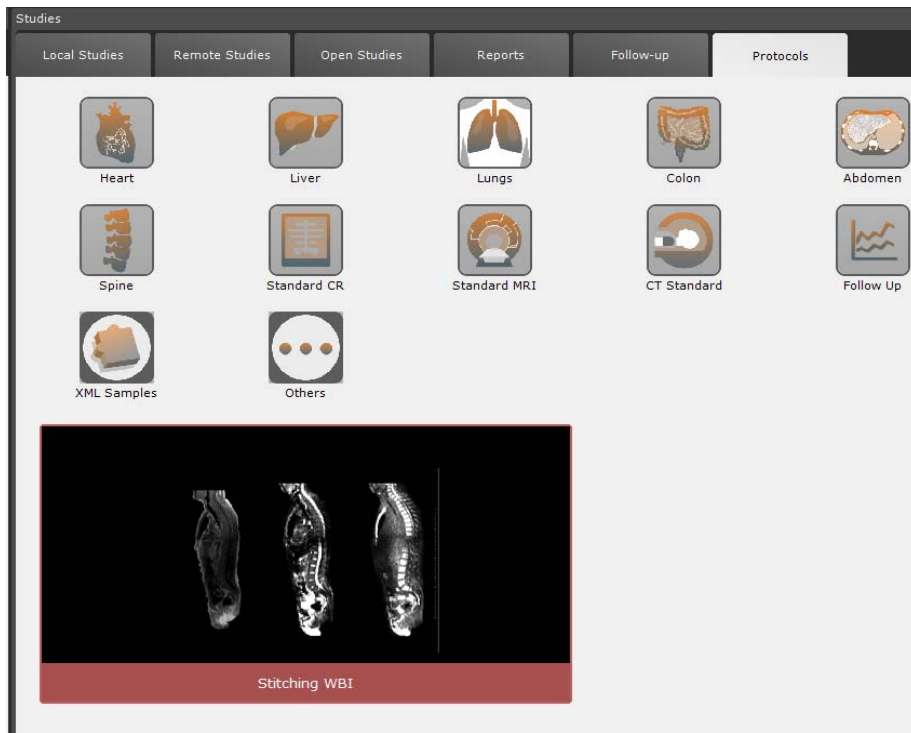


Figure 14-20 Stitching WBI Protocol

A Category selector window including 6 series categories opens:

- T1
- FFED3D
- T2
- Low B
- High B
- ADC

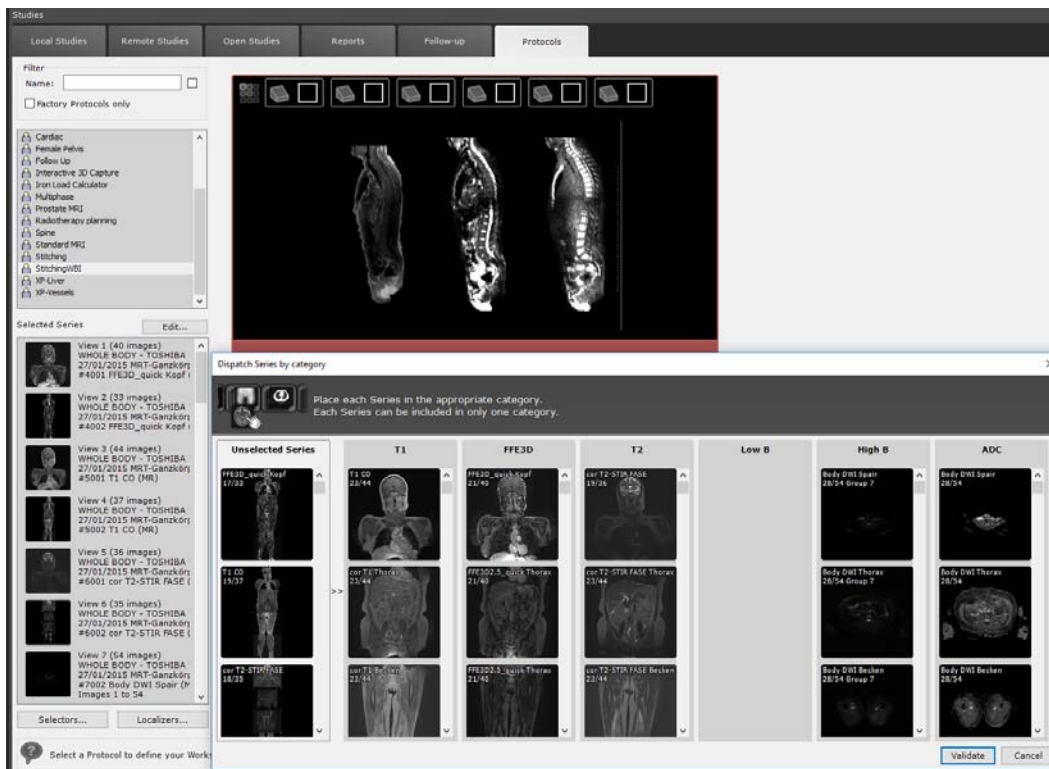
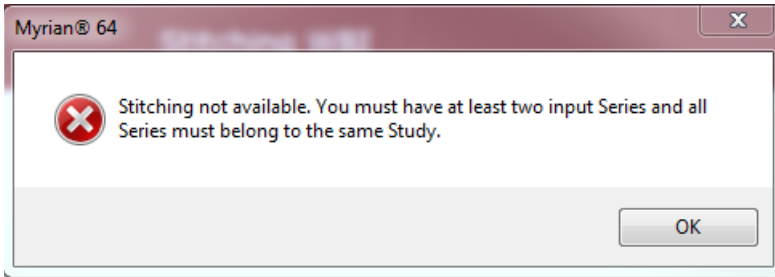


Figure 14-21 Stitching WBI 'Dispatch series' window



Upon validation, if the number of input series is insufficient, the following message is displayed:



- Once the series selection has been checked, and edited if required, click 'Validate'.



The Stitching WBI protocol is protected by an activation bit.

Stitched series are automatically opened in a dedicated multiphase view including two views:

- One view displaying the stitched series in the same orientation plane (one series category per viewport)
- One ADC view



Stitched series are either opened in Coronal or Axial orientation.



Figure 14-22 Visualization of the stitched series in coronal plane

**Navigation** is synchronized between viewports of the **same orientation** only whereas the anatomical center is always **synchronized for all viewports**.

As for **windowing**, it is synchronized between viewports displaying **series of same category only**. Windowing is preserved even after changing viewport layouts.

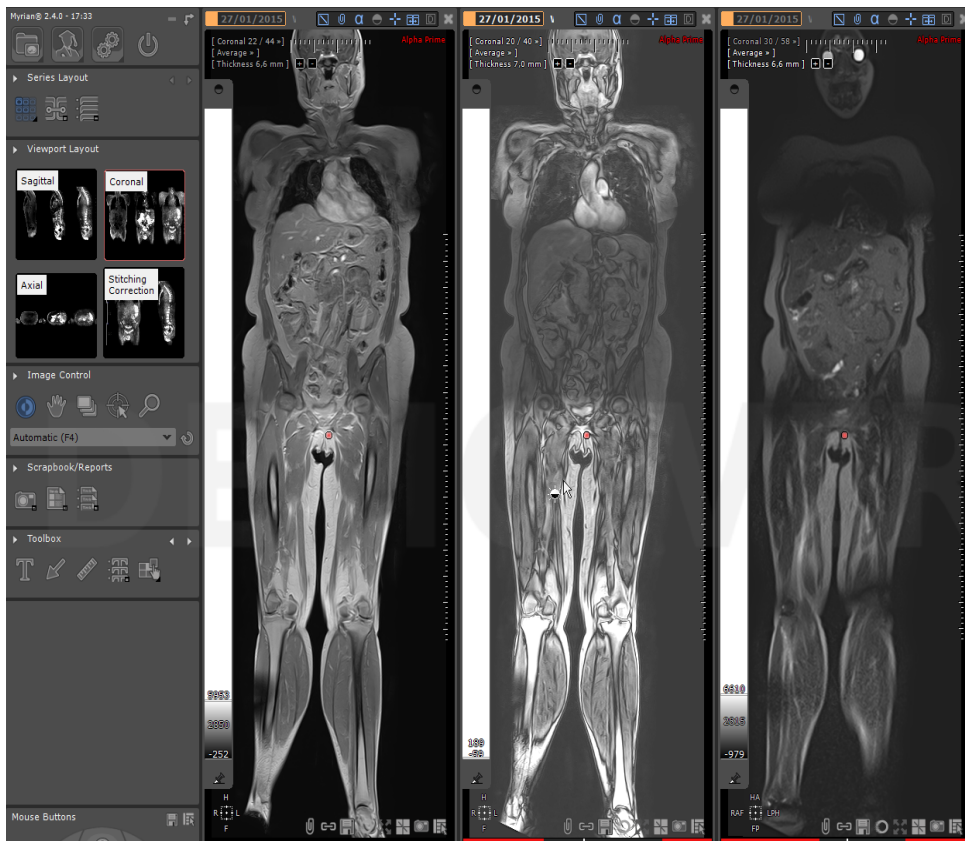


Figure 14-23 Performing windowing adjustment on the middle viewport only

The Stitching WBI protocol also includes 4 viewport layouts, three of them dedicated to a specific orientation and the fourth one to Stitching correction.

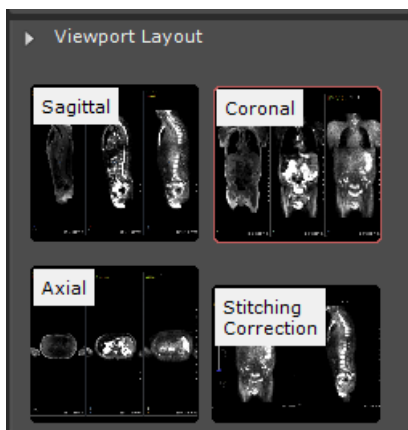


Figure 14-24 WBI Stitching viewport layouts

- To edit the stitched volumes, click on dedicated viewport
- Use the data alignment buttons for each of the stitched views (see Section 14.2.2.1)

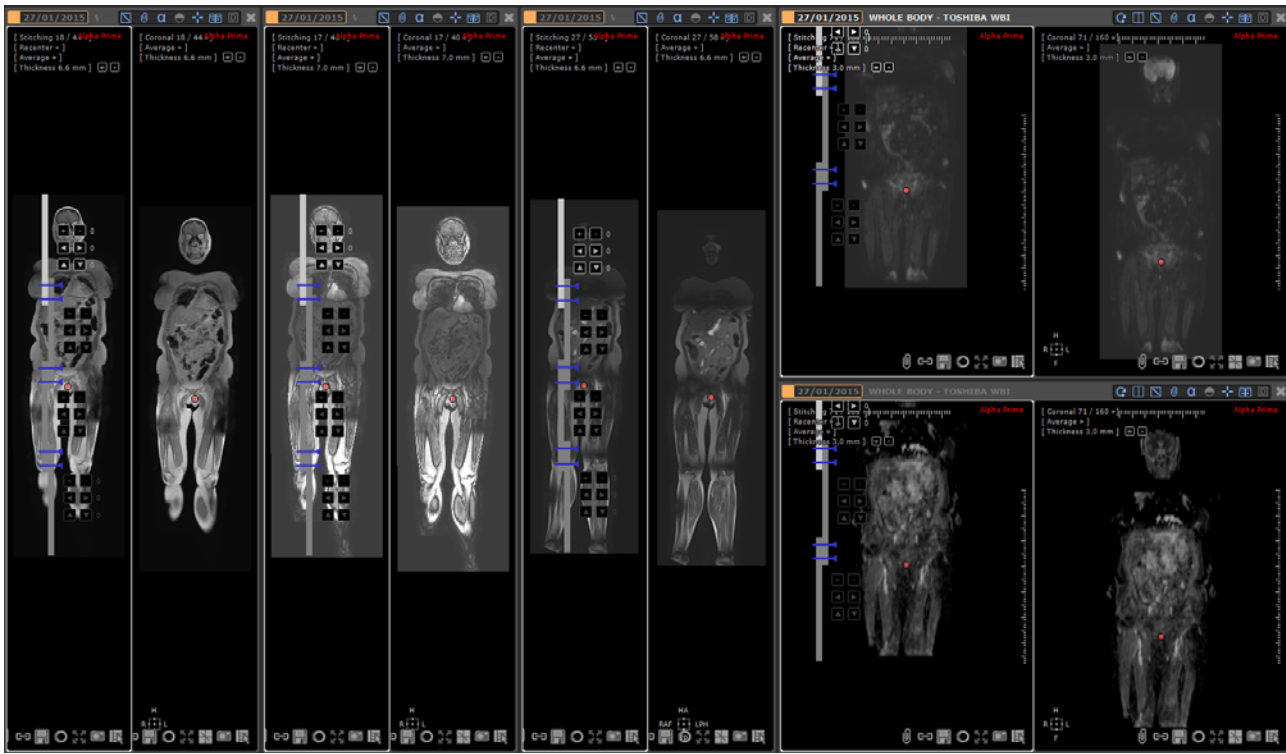


Figure 14-25 Realigning stitched volumes



If a stitched volume is re-aligned, all changes apply for the corresponding category of all stitched views, even after changing viewport layouts.

## 14.3 QuizCreator

### 14.3.1 Overview

QuizCreator enables creation and usage of DICOM Study-based quizzes for the purpose of:

- Learning to use Myrian® software
- Self-evaluation
- Medical Education in general

Quizzes are interactive exercises which contain a list of questions, images and annotations. You can use the software to create either open-ended or multiple-choice questions and use images that can be Study material contained in the software's database.

### Basic Workflow:

#### Tutorials

- The Teacher uses Myrian® to create a Quiz
- The Teacher issues copies to the Students
- The Students complete the Tutorial and return their copies to the Teacher
- The Teacher corrects and marks the copies
- The Teacher returns the corrected copies to each student, as in the case of any standard file-exchange examination ring.



The Teacher decides freely on the content, marking and assessment of each Quiz.

---

#### Self-evaluation

The Quiz can also be used as a 'Self-evaluation' tool. In this case, the Teacher incorporates both questions and answers within the Quiz. The answers are 'Locked' by a Password so as not to be seen by the Student until he has completed the test. Once completed, he simply 'Unlocks' the Quiz using the Password provided by the Teacher.

#### Management

Teacher/Student transfer of Quiz files is not managed by the software itself. Similarly, if a Quiz is based on a DICOM Study which is located on the database of the Teacher's workstation, it is up to the Teacher to ensure that Students have access to the Study.

To do this:

- Create a shared folder
- Place the required DICOM Studies in the shared folder
- Indicate the file path for Students to download the required images before starting the Quiz

### 14.3.2 Quiz Creation

To create a New Quiz:



- Click  to open the Quiz page

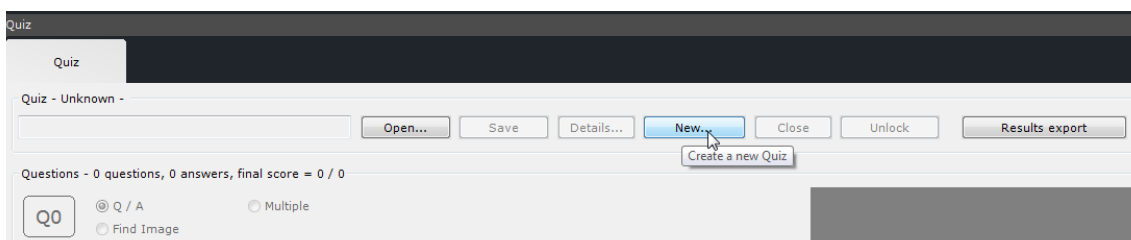


Figure 14-26 Create a new Quiz



Clicking  enables you to access later the already created quiz properties.

- Click on 'New' to open the 'New Quiz' window

Fill-in the following fields:

- Title
- Description
- Author
- Institution name
- Passwords (+ confirmation)

Figure 14-27 New Quiz window

The **Administrator password** is used by the author of the Quiz to lock writing access to the Quiz.

This password is required:

- To create a new Quiz
- To correct a student copy of a Quiz

The **'View Corrections' password** is required to **lock access** to exact answers. If this field is left **blank**, all Teacher Answers, images and Annotations are accessible to students. This password can be provided to students to reveal correct answers.

- Click on OK to save using a name and location of your choice.



You can continue to work normally in Myrian® (return to any screen, load Studies, etc.) without closing a Quiz, which remains in a 'Current' state as long as the session is open, the Quiz has not been closed using the 'Close' key, or another Quiz



has not been opened/created. You can return to the current Quiz by clicking

### 14.3.3 Question types

There are 3 types of questions to choose from:

<b>Q/A (Question/Answer)</b>	Open question requiring a written answer from the student
<b>Multiple</b>	Multiple Choice question requiring the selection of one answer from a predefined set of answers
<b>Find image</b>	Requires that the student locate/annotate an image provided

Images can also be linked to questions (see section below) or imported from various other sources. Supported image formats are:



- JPEG,
- GIF,
- TIFF,



- PNG,
- BMP,
- DICOM.

### 14.3.4 Questionnaire creation

There are 2 ways to create questions:

- Click on the  icon which appears bottom-right of a view in the main Myrian® workspace when a Quiz is open
- Click on the 'Add a new question' button  at bottom-left of the Quiz screen or right-click on the Image zone enabling to display the contextual menu and select 'Add new question'.

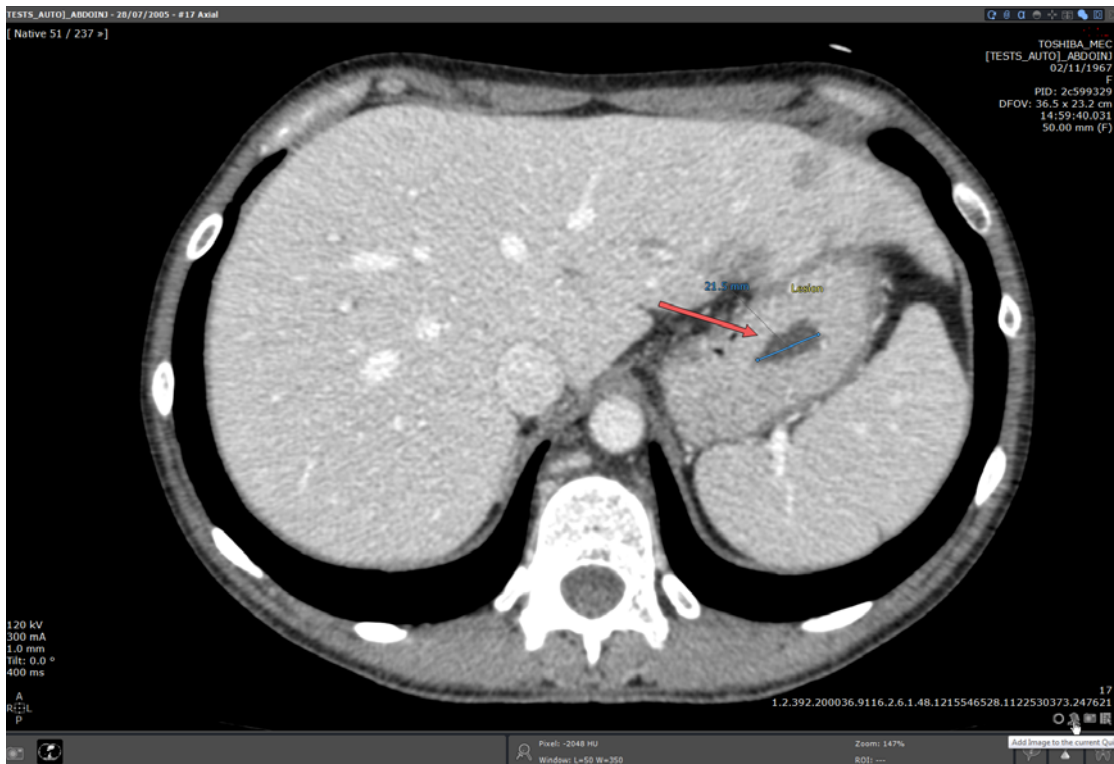



Figure 14-28 Add image to the current quiz

When you click :

- If there are no questions yet in the questionnaire, the first question will automatically be created and the captured image (whether 2D or 3D) will be linked to this question (several images can be added to one question).
- If a questionnaire contains questions, a context menu appears to prompt as to whether a new question should be created using the image or whether it should be added to the current question as an 'Add on'.

When you click on 'Add a new question':

- Select the type of question of your choice

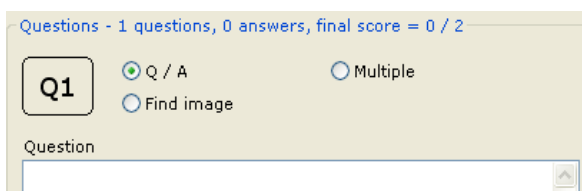


Figure 14-29 Question type option buttons

- Type-in the text of your choice in the 'Question' field
- Add the maximum score of your choice in the 'Score max' field (bottom-left of the Quiz screen)

Multiple choice questions are created in the following way:

- Add the question of your choice to the 'Question' field
- Define the list of answers. Each 'answer' must be preceded by a user-defined number/letter between 'braces' (square '['] brackets) as in the example below.
- Add the maximum score of your choice in the 'Score max' field (bottom-left of the Quiz screen)

The screenshot shows a quiz creation interface with the following elements:

- Question ID:** Q1
- Question Type:** Multiple (selected), Q / A, Find image
- Question:** Which answer best describes an 'Artery'?
- Answers:**
  - [1] A muscular blood vessel that carries blood away from the heart
  - [2] A sport using a bow to shoot arrows
- Student answer:** Two radio buttons corresponding to the answers above, both unselected.
- Teacher answer:** An empty text input field.
- Correction:** An empty text input field.
- Score:** 0
- Score max:** 2
- Buttons:** Create, -> Series, <, >

Figure 14-30 Example of creation of a Multiple Choice question

#### Mouse functions:

- Click on an image with the left-mouse button to add an Arrow Annotation
- Click again with the left-button to select and move it (use the 'Delete' keyboard key to delete a selected Annotation)
- Right-click on the Annotation to modify the direction it points towards
- Left-click on the Annotation to select it and shift it on the image.
- Left double-click on the Annotation to access a color palette dialog box enabling to customize the annotation color.
- Right-click on an image elsewhere than on the Annotation to open the context menu described in Table 14-1
- Right-click on an empty frame (no image) to open a context menu which is described in Table 14-2



All text and arrow annotations as well as ROIs or measurements (density or distance) **added to a quiz image from the workspace as a question or a add-on** are preserved. When the 'Annotation locked' option is checked, all those will **not be visible** to the student when answering the quiz.

#### Context menus:



When you click on an image, the context menu that appears groups both Tables 7-1 and 7-2. When you click on an empty frame, only the Table 14-2 menu appears.



<b>Delete image</b>	Deletes the current image
<b>Image locked</b>	Locks/unlocks the current image
<b>Annotations locked</b>	Locks/unlocks the current Annotations (to enable/disable student access)
<b>Open Series</b>	Opens the Study which contains the current image (not applicable for imported images)
<b>Full size</b>	Toggles the image size to stretched/original size
<b>Delete Annotations</b>	Deletes all Annotations for the current image

Table 14-1 Top part of the Quiz image frame context menu

<b>Next question</b>	Opens the next question
<b>Previous question</b>	Opens the previous question
<b>Delete question</b>	Deletes current question
<b>Import an image</b>	Imports an external image (.jpg, .gif, .tiff, .png, .bmp, .dcm) to the current question
<b>Add question</b>	Creates a new question
<b>Save</b>	Saves the current Quiz

Table 14-2 Bottom part of the Quiz image frame context menu (and empty frame context menu)

To navigate through the questions:

- Use the  and  buttons at bottom, or
- Click on the question number at top (left-click to go to next question, right-click to go to previous question), or
- Use the slider at the right, or
- Use the context menu as described above

To load a study associated to the question and the image, click on the 'Open DICOM series linked to the current image'

button  or select the 'Open series' option from the image contextual menu.

### 14.3.5 Student answer to a Quiz

To 'sit' for a Quiz test:

- Click on the 'Open' key to locate the Quiz files (\*.quiz extensions in the 'file types')
- Click on the desired file to select it
- Click on 'Open'

A prompt 'Open as' screen will appear:

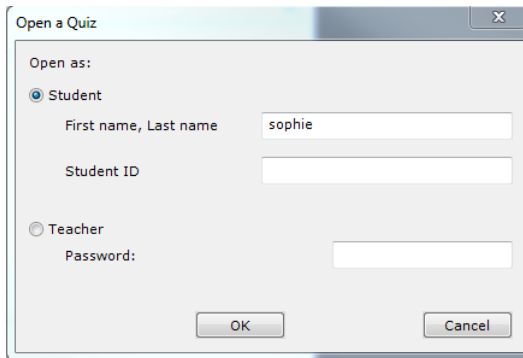


Figure 14-31 Open Quiz prompt screen

- Type-in the student name in the corresponding field and click 'OK' to open the quiz. The student name will be automatically logged in the \*.answers file and sent to author/teacher.



You can use this screen you log on as Teacher to modify the Quiz (add further questions, images, modify text, Annotations, scoring criteria, etc.). To log on as Teacher, you will be required to enter the Administrator password which was used at the Quiz creation stage.

Once logged on, students simply fill in the answer fields as required, save under a '\*.answers' file type and submit their copy for revision. Once corrected, the student copy can be unlocked and opened by the student to review corrections using the 'Corrections' password described above.



All text and arrow annotations as well as measurements **added to a quiz image from the workspace as an answer or a add-on** are preserved.

### 14.3.6 Unlocking a Quiz (to review corrections)

To unlock a Quiz:

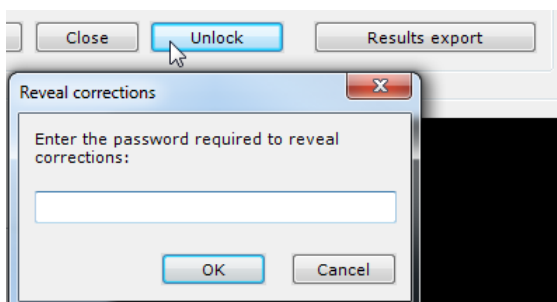


Figure 14-32 Unlock Quiz to reveal answers

- Click on the 'Unlock' key at top of the Quiz window
- Enter the 'Corrections' password

### 14.3.7 Quiz review & correction (teacher)

To review and correct a Quiz:

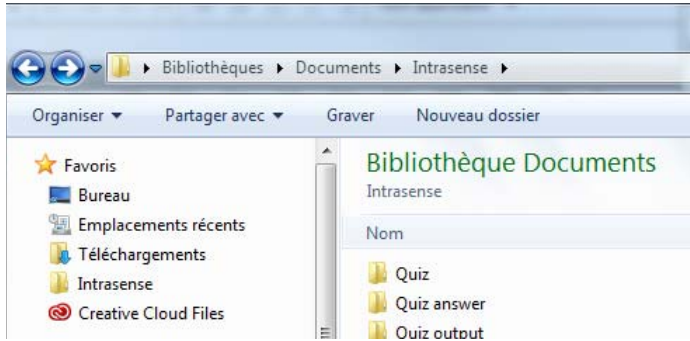
- Locate and select the desired student \*.answers copy
- Click on 'Open'
- Enter the 'Teacher' password
- Fill-in the 'Teacher answer', 'Correction' and 'Score' fields.
- Click on 'Save'

### 14.3.8 Quiz mass treatment (teacher)

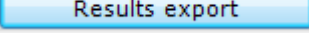
Myrian® quiz mass treatment feature lets you automatically generate reports from quiz answers once the student answer copy have been manually corrected. **Two types of report** are then created, one per student and one global condensed overview file.



In your C:\username\Documents\Intrasense\directory, you need to define in the first place a folder containing all student answer files to be treated and an output folder where output files will be stored.



#### 14.3.8.1 Method of use

- To generate those files, click on  located at far right of the quiz toolbar (see Figure 14-26) to open the following dialog box:

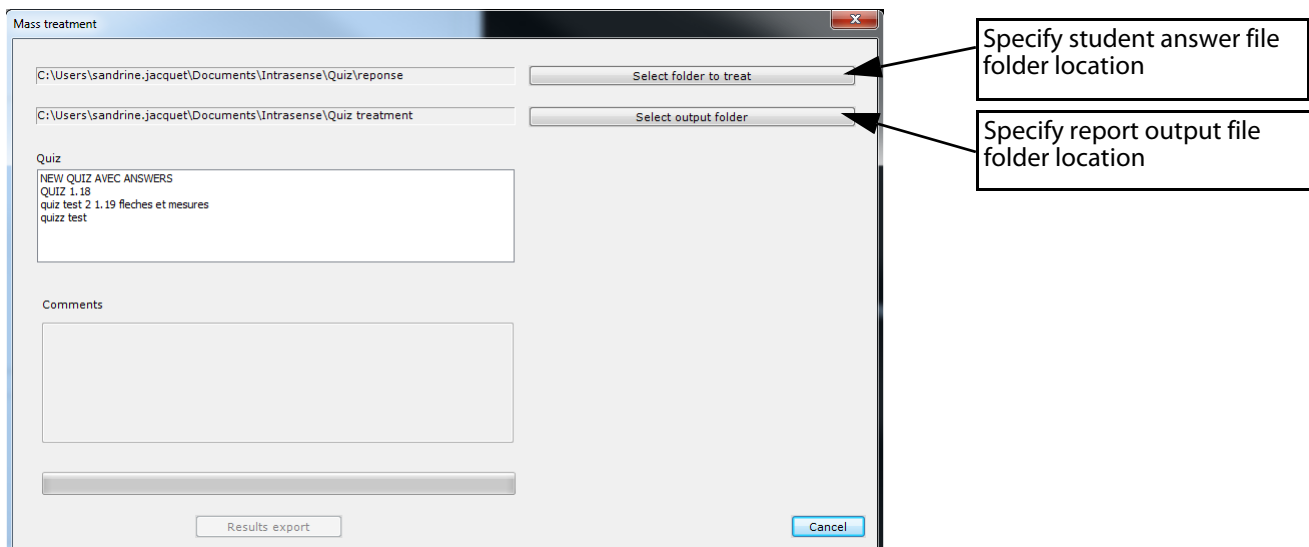
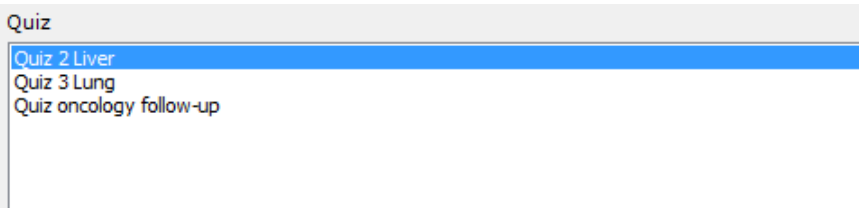


Figure 14-33 Quiz mass treatment window



All answer files are scanned and the examination to which they belong is displayed in the box.



- Select the quiz you wish to treat simply highlighting it
- Add any remarks in the 'Comments' section (optional)

- Click **Results export** to launch quiz mass treatment process.

A dialog box automatically pops up asking you for the quiz protection password.

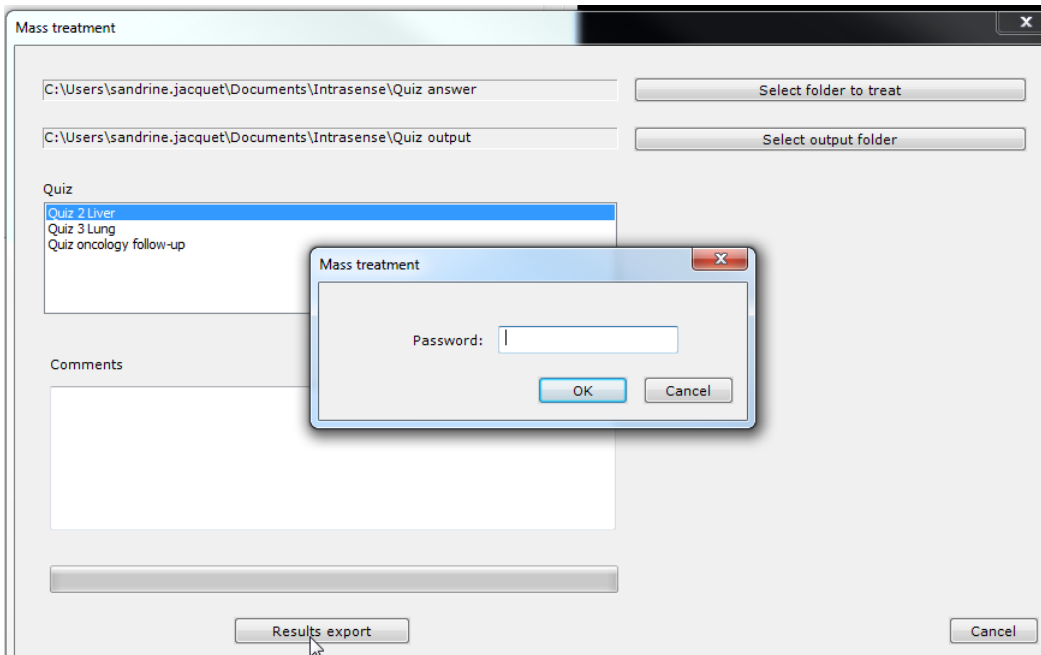
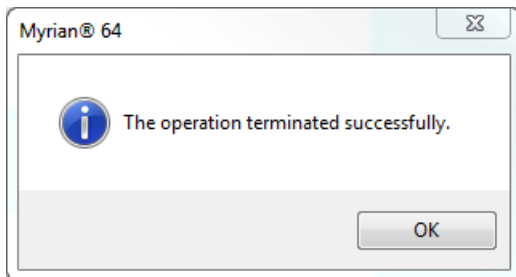


Figure 14-34 Quiz data protection prior to Quiz mass treatment

Once you have typed it in and pressed OK, the process starts.



A progress bar starts running until the process is complete and a message is displayed indicating you that it has been completed successfully.



### 14.3.8.2 Generated files

- Go to your output folder

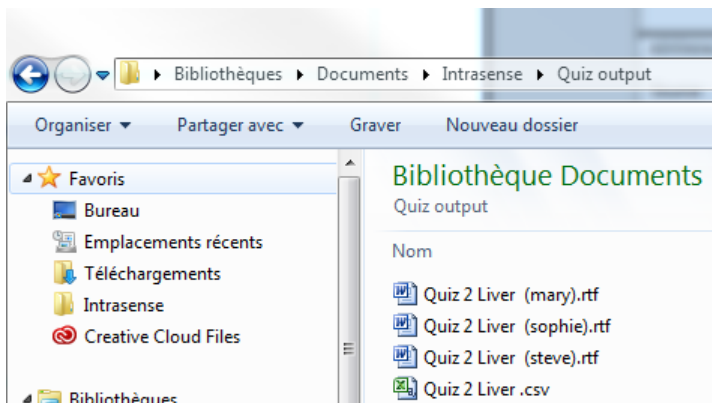


Figure 14-35 Mass treatment output files

The Mass treatment process generates the two following types of file:

- **One .rtf file per student**, generated from the student .answer file and a language dependent template file.

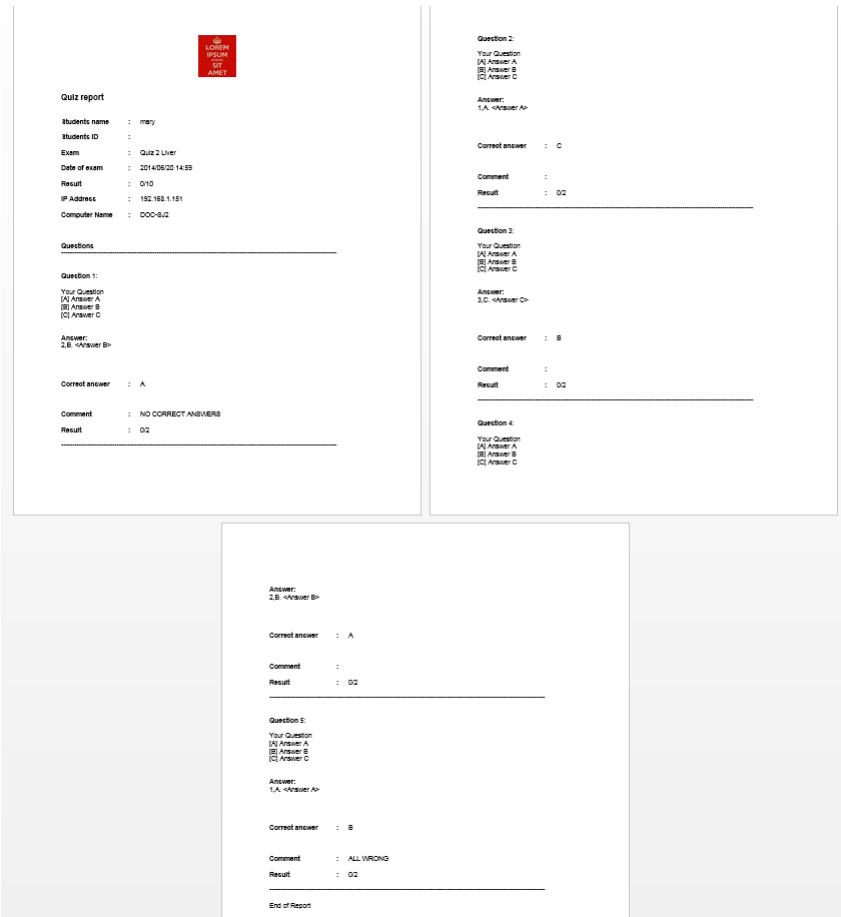


Figure 14-36 Example of a Quiz report template (per student)



A template based version resides in Intrasense/Template folder. You can edit this template file and store your new user-defined template version in the folder /My Documents/quiztemplate/. Make sure that the file name is the same as the original template file.

### Template file content:

The first part of the template file that acts as a header contains all the following student and global quiz information:

- Quiz name
- Time and date at which the test was finished
- Student name/last name
- Student ID
- Computer AE
- Computer IP address
- Student results (if possible)
- Final score (if any .answer file have been corrected)



You have the possibility to edit this template and add your logo or any other textual information of your choice.

The second part of the template file relates to every question in the quiz and contains the following:

- Question number

- Question
- Students answer
- Correct answer
- Teacher/PhD comment (if any)
- Image from the question (if any)
- Student selected image (if any)
- Score or emplacement for score if scoring is not automatic / quiz has not been corrected

This part will be added to the final document once for each question in the quiz.

- **One .csv (Comma Separated Values) condensed file** generated from all the questions in the quiz opening with Excel.

	A	B	C	D	E	F
1	Quiz 2 Liver			20/06/2014		
2						
3	mary		0\10	20/06/2014 14:59	192.168.1.151	DOC-SJ2
4	sophie		2\10	20/06/2014 14:59	192.168.1.151	DOC-SJ2
5	steve		2\10	20/06/2014 14:59	192.168.1.151	DOC-SJ2

Figure 14-37 Example of a Quiz condensed file

### Condensed file content:

The file contains:

- Quiz name
- Date of examination
- A comment made by the Teacher/PhD (if any)

And for each student:




















- Name/Last Name
- Student ID
- Score (if possible)



## 14.4 Complex annotations and orthopedic measures

### 14.4.1 Overview


These annotations which are also referred to as “complex AOI”, consist in a group of Orthopedic Angle and Length Measurement tools as they combine lines, points, circles, texts etc. They are the following:

- Non-secant Angle 
- 3-point Angle 
- Right HKA Angle Measurement 
- Left HKA Angle Measurement 
- Cobb's Angle 
- Neonatal Pelvis 
- Coxometry, Anteroposterior View 
- Coxometry, Lateral View 
- Hip Tilt 
- Biometric Angles of the Right Knee (only available for RF & CR modalities) 
- Biometric Angles of the Left Knee (only available for RF and CR modalities) 
- Prosthesis Wear 
- Caliper One Shot 
- Caliper Step by Step 
- Collapsed Vertebra 
- Orthogonal Diameters 
- Pelvic Incidence 
- Hip Dysplasia 
- TT-TG 

AOI share most behavioral characteristics with other annotations, such as:

- They can be moved about freely by the user

- They are persistent (they are saved from one session to another)
- They are listed in the 'Annotations' List'

These tools are accessible via the Toolbox clicking on the active 'AOI' icon . The following menu appears:

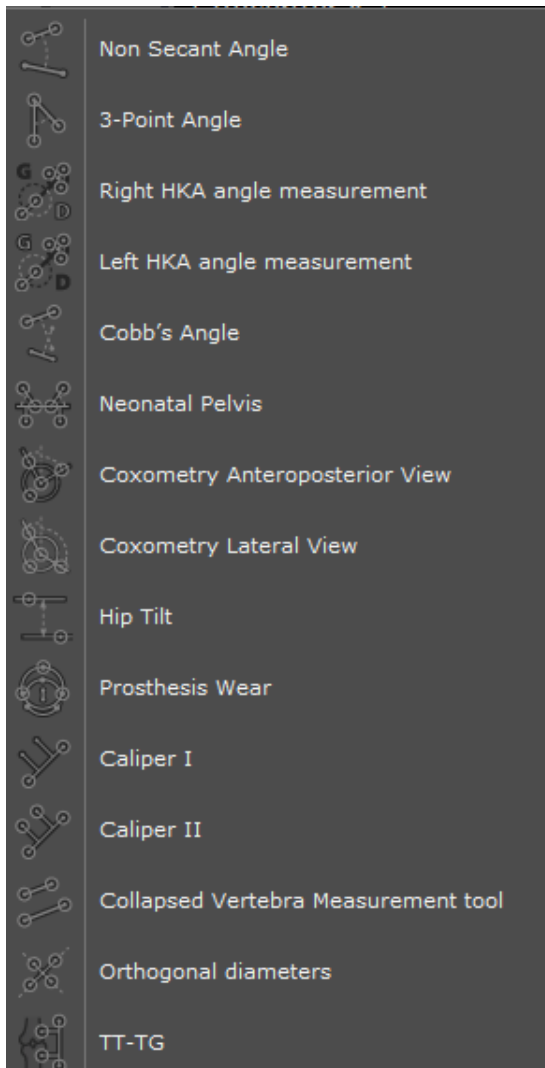


Figure 14-38 AOI creation menu



AOI Measurements are automatically included in Reports (requires the ReportCreator add-on).

## 14.4.2 Method of use



A segment can be modified, moved or extended by drag and drop. The percentage value is immediately updated.

### 14.4.2.1 Non-secant and Cobb's Angles

- Click on the 'AOI' button in the Toolbox.
- Depending on your needs, select either "Non-secant" or "Cobb's Angle" from the resulting menu



By default, the "Non-Secant Angle"  is active at the start of each session.



Click on the desired starting point, drag and release on the end point of the first segment

Figure 14-39 Draw first segment (Non-secant Angle)



The second segment automatically appears after you have dragged and clicked to complete the first segment.



Click and drag anywhere on the segments to adjust their position or size freely

Figure 14-40 Manipulate segments to calculate desired angle

The resulting angle appears.





If the text annotation appears in a position which, for any reason, is not suitable (for instance if it covers an important part of the image, etc.), drag it around freely to the location of your choice.



Figure 14-41 Drag to move text

### 14.4.2.2 3-Point Angles

- Click on the active 'AOI' button  in the Toolbox
- Select "3-point Angle"  from the resulting menu
- Click on the desired starting point, drag and release on the end point of the first segment
- Drag and click to place the end point of the second segment where you wish.

The second segment appears as well as the resultant inner-angle measurement



Drag the angle arc to the other side of the angle to display the opposite angle.

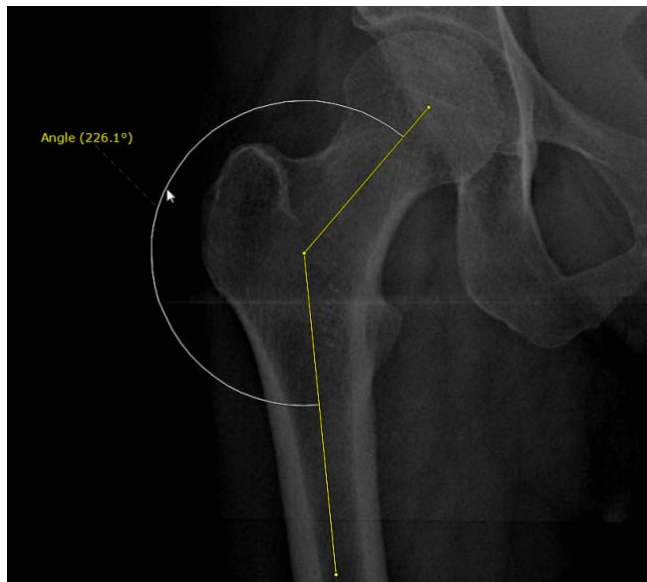
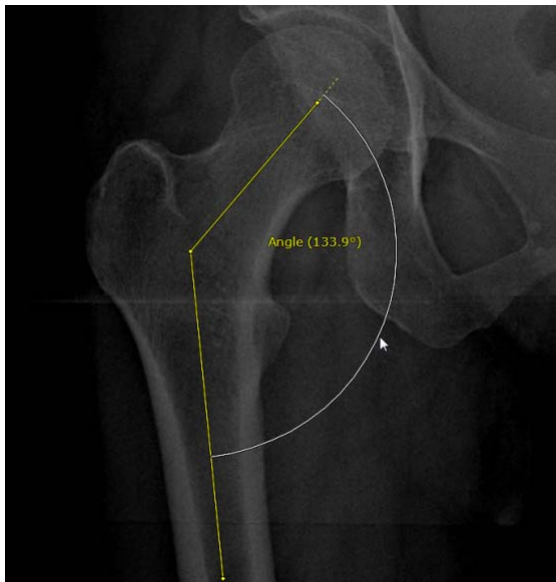


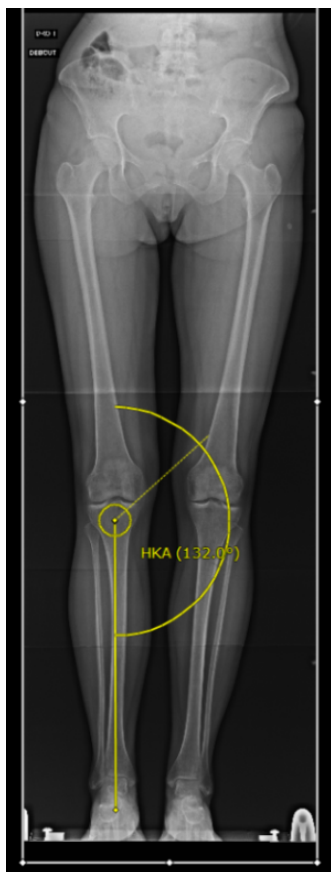


Figure 14-42 Displaying inner and outer 3-point Angle measurements

### 14.4.2.3 HKA Angle Measurement (Hip-Knee-Ankle alignment)

- Click on the active 'AOI' button  in the Toolbox
- Select the "Right or Left HKA angle measurement"  from the corresponding menu

The interactive wizard guides you through the three-stage creation process of the HKA angle measurement:



1. Click on any 3 points (3) on the edge of the Femoral Head
2. Click on 1 point at the knee center
3. Click on 1 point at the ankle talus



Figure 14-43 HKA angle measurement display

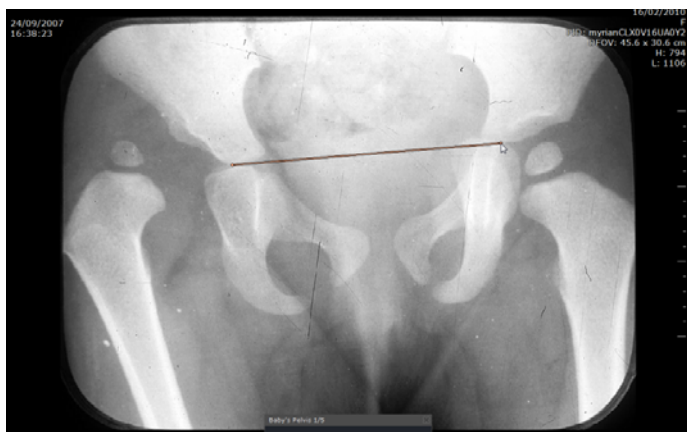
The HKA angle measurement is automatically displayed on the view as well as the angle value (stated in °).

#### 14.4.2.4 Neonatal Pelvis

This measurement tool is used to calculate CHD (Congenital Hip Dislocation).

The AOI launches a step-by-step Wizard to assist you.

- Click on the active 'AOI' button 
- Select the Neonatal Pelvis  AOI in the resulting menu
- Follow the step-by-step instructions described in the Wizard:



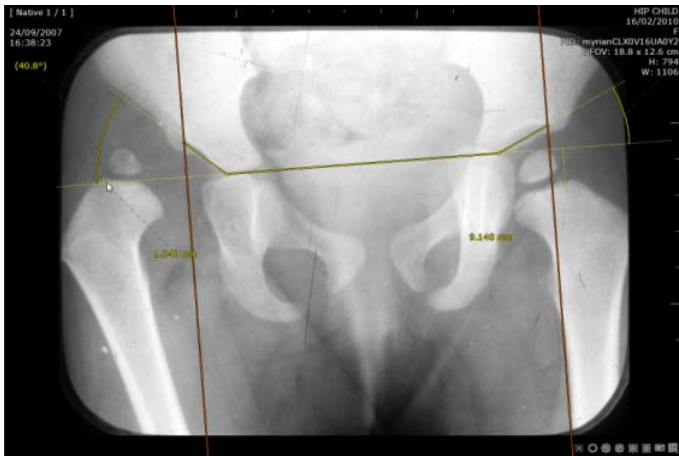
1. Click on the two lowermost points of the Ilium to draw the "Y-line" (Triradiate Cartilage Line)

Figure 14-44 Connect lowest points of Ilium



2. Click on each Talus (most lateral point of the Acetabular Roof) to define the "Acetabular Index" on each side

Figure 14-45 Define Acetabular Index



3. Click on the uppermost point of each Femoral Metaphysis to define the Perkins-Ombredanne Line

Figure 14-46 Click on the highest Metaphyseal Points

It is thus possible to analyze Congenital Hip Dysplasia in six steps.





At any time, click on the 'x' cross  at left of the Wizard step to abort the construction of the AOI.

#### 14.4.2.5 Coxometry

The Coxometry module enables you to analyze and evaluate pathological and non-pathological hip joint situations, such as Hip Dysplasia, using a number of different measurable angles and distances.

##### Anteroposterior View


- Click on the active 'AOI' button  in the Toolbox
- Select 'Coxometry, Anteroposterior View'  from the resulting menu

Follow the Step-by-step Wizard to:


- Click and drag on the image from the edge of the Femoral Head to define its circumference with a circle
- Place one end of the "Protractor" on the most lateral point of the Acetabular Roof
- Place the other end of the "Protractor" on the most medial point of the Acetabular Roof

##### Lateral View

- Click on the active 'AOI' button  in the Toolbox

- Select 'Coxometry, Lateral View'  from the resulting menu
- Click and drag on the image from the edge of the Femoral Head to define its circumference with a circle
- Place one end of the "Protractor" on the most anterior point of the Acetabular Roof
- Place the other end of the "Protractor" on the most posterior point of the Acetabular Roof

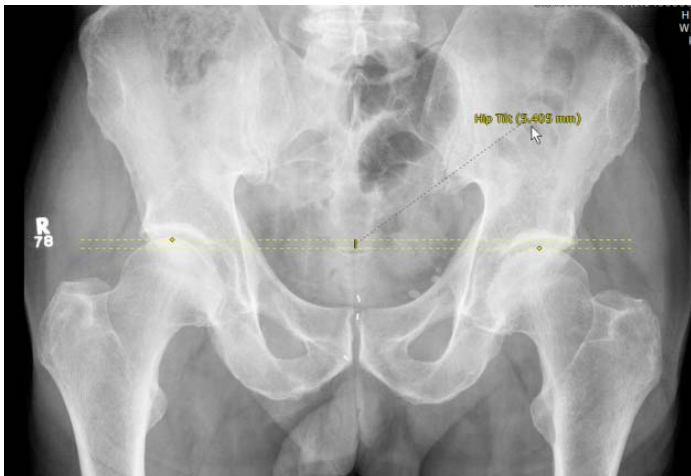
#### 14.4.2.6 Hip Tilt

- Click on the active 'AOI' button  in the Toolbox
- Select the "Hip Tilt" AOI



1. Place the first point on the highest point of the right Femur Head

Figure 14-47 Hip Tilt: place first point



2. Place second point on the corresponding point of the left Femur



Figure 14-48 Hip Tilt: place second point



AOI measurements appear gradually as they are being built.

#### 14.4.2.7 Biometric Angles of the Left and Right Knees

The Pangonogram module activates a Wizard assistant to guide you through the steps required to calculate accurate biometric angle measurement:

- Click on the active 'AOI' button  in the Toolbox
- Select the "Biometric Angles of the Left/Right Knee"  from the corresponding menu



Follow the step-by-step instructions described in the Wizard which will then appear.

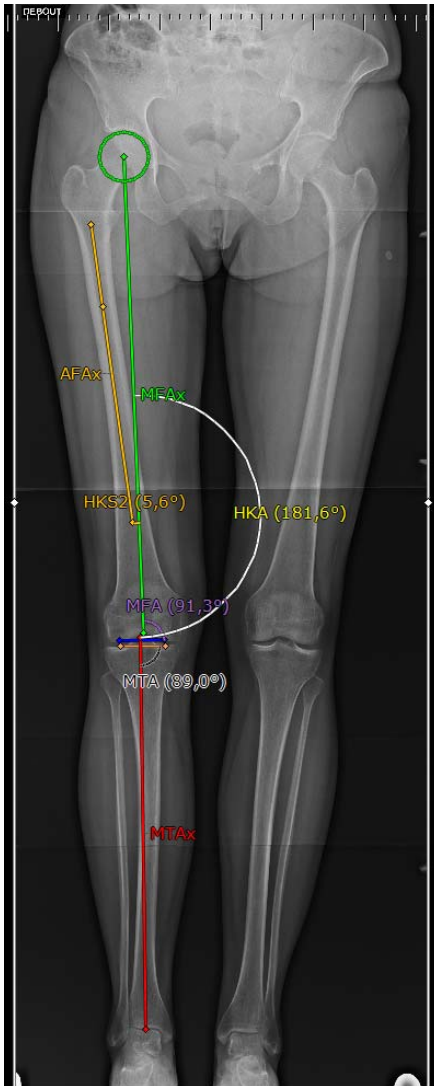


Figure 14-49 Biometrical angle measurements of the Right knee




Once the Annotation has been created, it can be modified by dragging the Points, Segments, or Text Annotations. Angle Arcs can be moved nearer to or further from the vertex or in or out to display the inner angle or the outer angle.



With the manual engine, use the Zoom  and Panning  tools to help you place the points as accurately as possible.



With the Automatic engine , when you click near a bone, the point is automatically repositioned as close as possible to the bone for improved accuracy and productivity.





The 2 Biometric Knee Angle measurements are assisted by wizards which provide the user with step by step operational guidelines.



### 14.4.2.8 Prosthesis Wear

To measure Prosthesis Wear in Total Hip Replacement (THR):

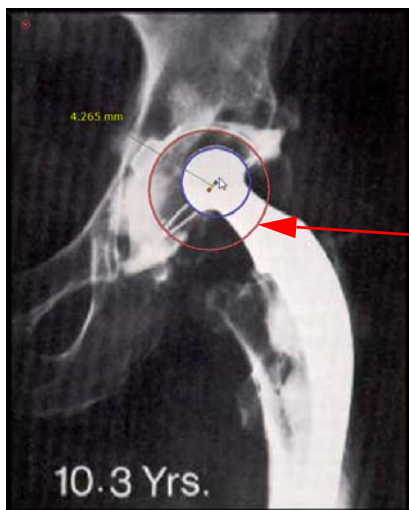
- Click on the active 'AOI' button in the Toolbox 
- Select Prosthesis Wear 

In the corresponding menu:



1. Click on 3 points around the Prosthetic Femoral Head

Figure 14-50 Trace a circle around the Femoral Head



2. Click on 3 points around the inner surface of the Acetabular Component to define a circle matching the cup of the roof

Figure 14-51 Define the Acetabular Roof

The resulting measurement automatically appears.

### 14.4.2.9 Caliper I/II



Calipers can be used to make measurements such as Anterior or Posterior Drawer Tests in the context of physical examination for tears of the Anterior or Posterior Cruciate Ligaments.

There are two types of Caliper:

- The "One Shot" type, whereby the Caliper is drawn all at once then manipulated and adjusted by hand, or
- The "Step by Step" Caliper which is drawn segment by segment

To use the Calipers:

- Click on the active 'AOI' button  in the Toolbox
- Select "Caliper One Shot" or "Caliper Step by Step" in the corresponding menu.

- Depending on whether you have selected “Caliper One Shot”  or “Caliper Step by Step”  draw your Caliper either segment by segment or all at once, then manipulate each segment to place the Calipers as desired





H1H2 is the measurement of the distance between the jaws of the Caliper

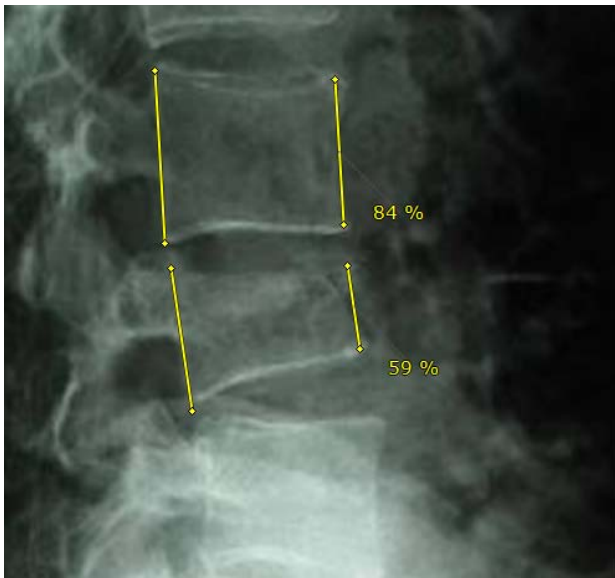
Figure 14-52 Caliper measurement

#### 14.4.2.10 Collapsed Vertebra

This tool is used to evaluate compression fractures in X-ray images.

##### Usage:

- Open your desired Study
- Click on the active ‘AOI’ button  in the Toolbox
- Select Collapsed Vertebra  from the resulting menu.



1. Click on the top/bottom corners of your target vertebrae to quantify the amount extent of compression as a percentage

2. Trace 2 lines on the anterior and posterior vertebral walls to calculate their ratio expressed as a percentage

Figure 14-53 Quantify the extent of vertebral compression as a percentage

#### 14.4.2.11 Orthogonal Diameters

This measurement tool enables to perform manually two orthogonal segments on a lesion from a CT image called long axis and short axis.

- Click on the active ‘AOI’ button  in the Toolbox


- Select 'Orthogonal Diameters'  from the resulting menu.
- Click on 4 points at each axis extremity of the lesion to obtain the longest and largest transverse diameters (in mm).





Figure 14-54 Orthogonal diameter measurements

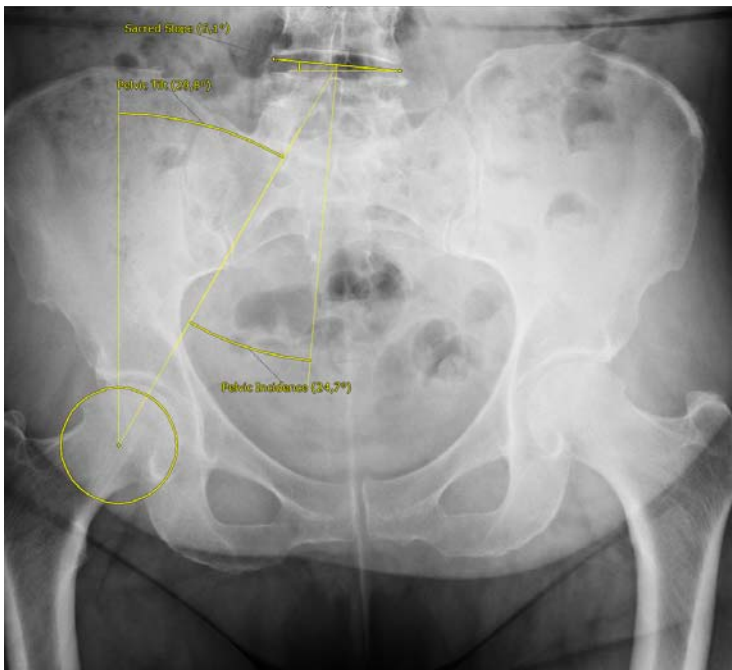


Both segments have to be performed on the same CT slice.

#### 14.4.2.12 Pelvic Incidence

- Click on the active 'AOI' button  in the Toolbox
- Select "Pelvic Incidence"  from the resulting menu

The Pelvic Incidence angle measurement is created in two steps:



1. Click on any three points on the edge of the Femoral Head
2. Click on two points at each extremity of the Sacral Slope



Figure 14-55 Automatic computation of the Pelvic incidence

The Pelvic Incidence, Pelvic Tilt and Sacral Slope angles are displayed as well as their respective values (stated in °).

#### 14.4.2.13 Hip Dysplasia



This measurement tool is available for any modality and any orientation plane.

- Click on the active 'AOI' button  in the Toolbox
- Select Hip Dysplasia  from the resulting menu

The interactive wizard guides you through the four-stage creation process of the HKA angle measurement:



1. Click on any 3 points (3) on the edge of the first Femoral Head.  
A first circle is displayed.
2. Trace the first angle segment
3. Click on any 3 points (3) on the edge of the second Femoral Head  
A second circle is displayed.
4. Trace the second angle segment

Figure 14-56 Display of the angle measurements in the detection of hip dysplasia



The resulting angle measurements automatically appear.



Once created, the Annotation can be modified by dragging the Points, Segments, or Text Annotations. Angle measurements are automatically updated.

#### 14.4.2.14TT-TG: Superimposed Image Measurement Function

This feature enables the use of various AOI on several superimposed images.

- Open any multi-image series using the MPR or Native Image protocol and select a Native grid with at least two viewports
- Click on the active 'AOI' button  in the Toolbox
- Select TT-GT  from the corresponding menu

The following Floating Toolbar appears:

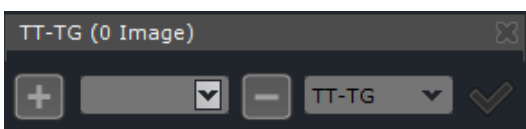




Figure 14-57 TT-TG Floating Toolbar

- Navigate to the slice you wish to use as the first image of your combined measurement
- Click the "+" button  to select the first image
- Navigate to the slice you wish to use as the second image of your combined measurement
- Click the "+" button  to select the second image
- Repeat the same process to select as many images as desired to be superimposed

All added images are displayed in the Image combobox.



When an image is selected in the list, the viewport is automatically refreshed to display the related slice.



The TT-TG title bar always displays the total number of selected images to be averaged.

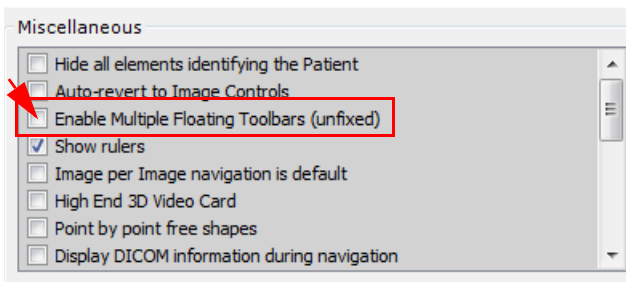


Only images with the same orientation can be averaged. So the image list is automatically refreshed each time the current viewport changes in order to reflect the images selected for the viewport orientation (i.e. in MPR mode).

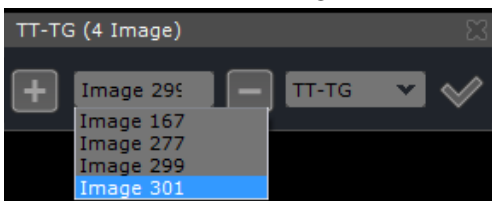


In docked mode, the current viewport is the one on which the floating bar is docked. Otherwise it is the last viewport overflow by the mouse (with highlighted text).


To undock the floating toolbar, go to User Preferences>Display>Miscellaneous and select 'Enable Multiple Floating Toolbars (unfixed)'



Click the "-" button  to delete the current image from the Image combobox in which are displayed the slice number of each selected image.



Images/Slice numbers can be modified at any point whilst the floating toolbar is still open and the slice selection has not yet been validated.

- Use the pull-down menu on the right-hand side of the floating toolbar to select one of the following AOI Measurements:
  - TT-TG → Caliper
  - LTI → Non Secant Angle
  - Patellar Tilt Angle → Non Secant Angle
- Click on the 'Superimpose Images' button  to validate the combined image and selected AOI



The validation button  requires at least two selected images to be active.

---



You can make more than one AOI measurement on the same image.

---



You can Combine Images in more than one Viewport at the same time, e.g. use the three different Measurements in three different Viewports.

---

The floating toolbar is then automatically closed and the display mode of the target Viewport is automatically modified to display a combination of the selected images.

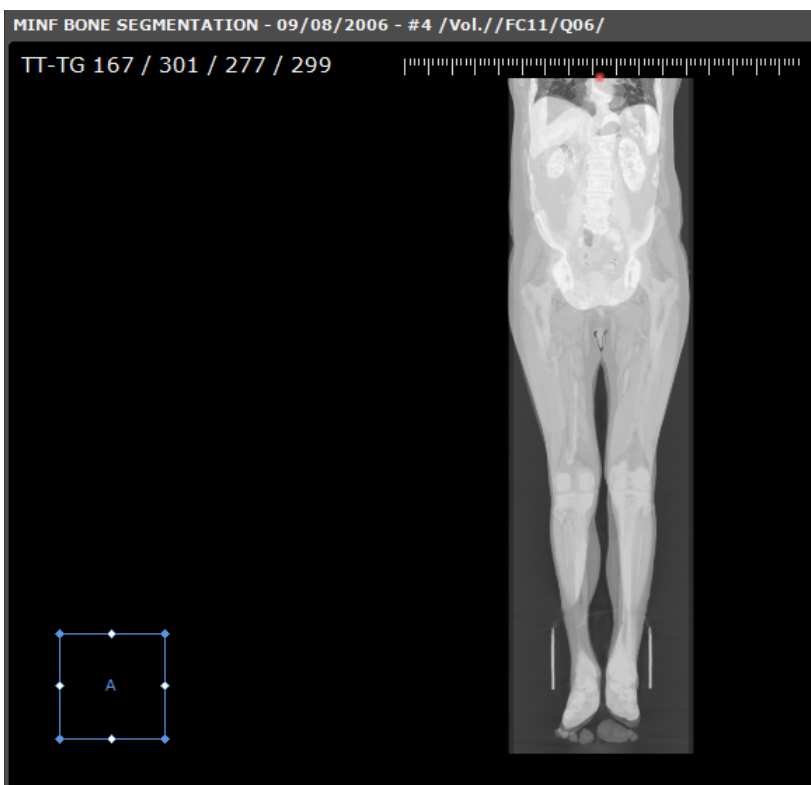


Figure 14-58 Superimposed image viewport

The corresponding AOI is automatically activated and can be used directly from this point (see above for directions to use Calipers or Non-Secant Angle calculation).

- The viewport menu displays the selected measurement instead of all other Rendering Menu in the top left-hand corner
- The Superimposed Image can be captured in RGB to the Scrapbook/PrintComposer as any other Viewport and will include the AOI

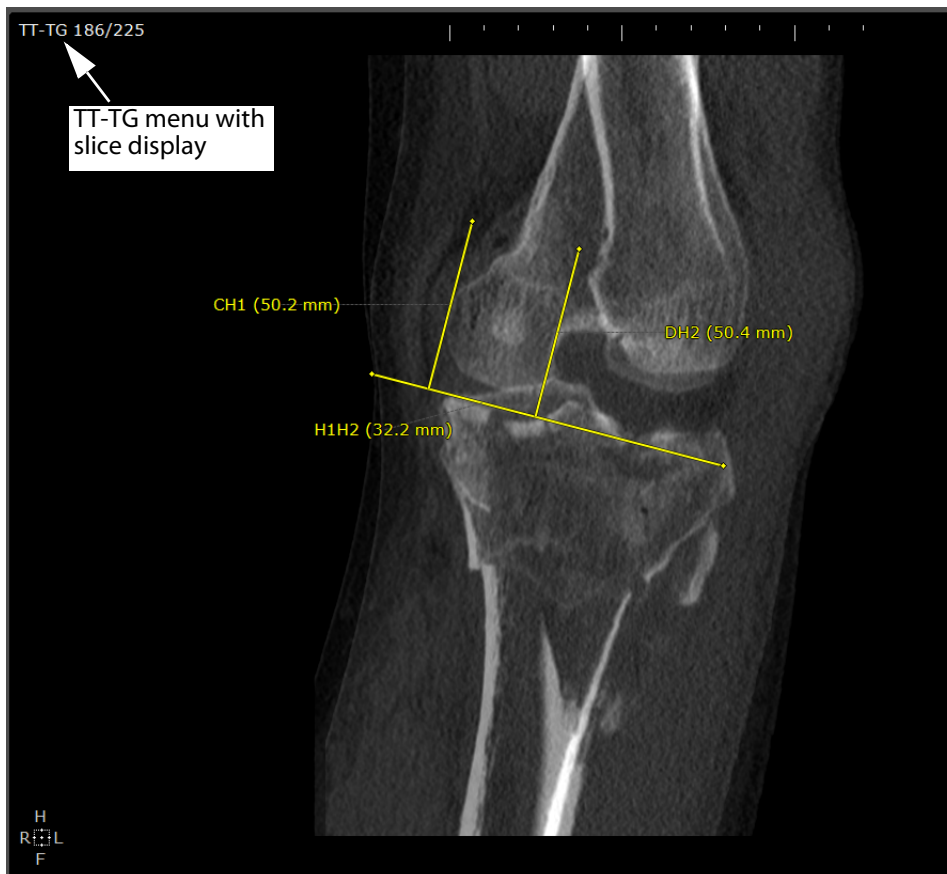


Figure 14-59 Caliper AOI on Superimposed Images



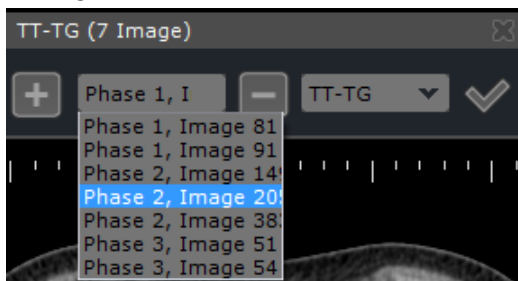
In the viewport displaying superimposed images, the intensity information is not displayed (in the hovering information or by pressing the 'Alt' key).



Both the image and the AOI are "volatile", i.e. they disappear as soon as you navigate in the Combined Image Viewport.



The Superimposed Measurement feature is also active on 2D or 3D multiphase views, allowing to average images coming from different series.



To select another measurement tool, click and hold for a while on  to reopen the menu.

## 14.5 Cardio-Thoracic Ratio measurement

### 14.5.1 Overview

This AOI tool allows you to calculate the Cardio-Thoracic Ratio (CTR) and determine the enlargement of the Heart. When it is

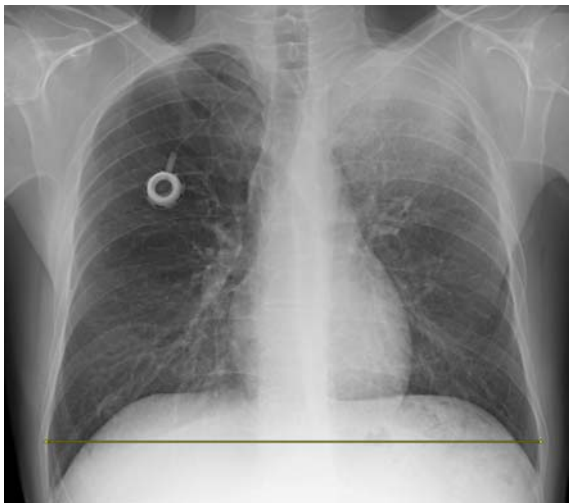
activated, the CTR AOI button  appears in the toolbox.

The CTR AOI is created in 2 steps:

- Thorax Measurement Line: to measure the widest transverse diameter of the Thoracic Cavity
- Heart Measurement Line: to measure of the widest transverse diameter of the silhouette of the Heart

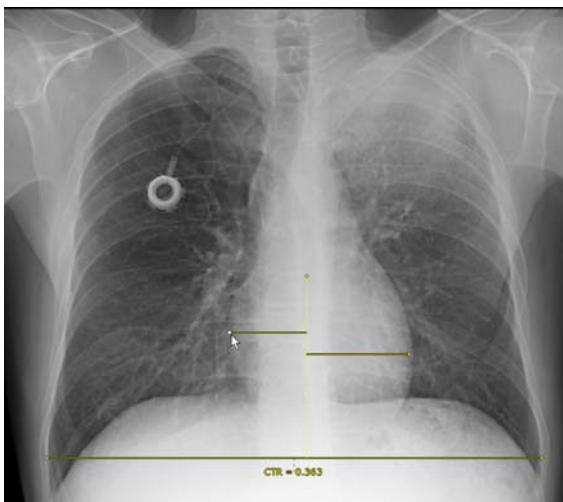
### 14.5.2 Method of Use

- Click on the CTR button  in the Toolbox



1. Click on the left and right edges of the widest part of the Thoracic Cavity to draw Thorax Measurement Line

Figure 14-60 Draw Thorax Measurement Line



2. Click on the left and right edges of the widest part of the Heart silhouette to draw the Heart Measurement Line

Figure 14-61 Draw the Heart Measurement Line

The CTR Ratio appears underneath the Thorax Measurement Line




## 14.6 ADC Calculation

The ADC (Apparent Diffusion Coefficient) Calculation Tool referred to as a 'complex AOI' is used to measure the magnitude of diffusion of water molecules in brain tissues from **MR studies**.



A dedicated ADC protocol is available with the appropriate activation option enabling you to create ADC mapping image (see Section 14.10.7 for detailed information)

---

The 'ADC ROI AOI' tool is accessible from the toolbox clicking on the 'Measure ADC' icon .

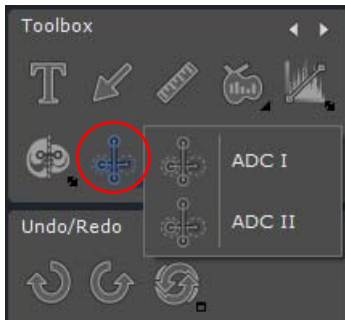


Figure 14-62 Activating ADC measurement tool

There are two ADC measurement options available:

- 'ADC I' AOI
- 'ADC II' AOI

### 14.6.1 ADC I

- Select the 'ADC I' calculation tool so that it is now activated
- Draw a vertical symmetry line on the brain view by click-drag-release to define two opposite points (A and B)

A yellow dashed line is displayed.

- On the right side of the symmetry axis, draw a ROI (C)

A circular ROI (referred as D) perfectly symmetric to hand drawn ROI C is immediately displayed on the left side of the view (see Figure 14-63).

Only the hand drawn circle is editable.

---



Left click on the circular ROI to enlarge or reduce it.

---



You can reposition the circular ROI clicking on the yellow point in its center and move it up and down or from right to left.

---



Whether you enlarge or reduce the diameter of the circle or move the circle horizontally or vertically, its opposite clone image is automatically updated (with respect to the AB vertical axis) so that they remain totally identical and symmetrical.

---



When active, any selected line becomes orange.

---

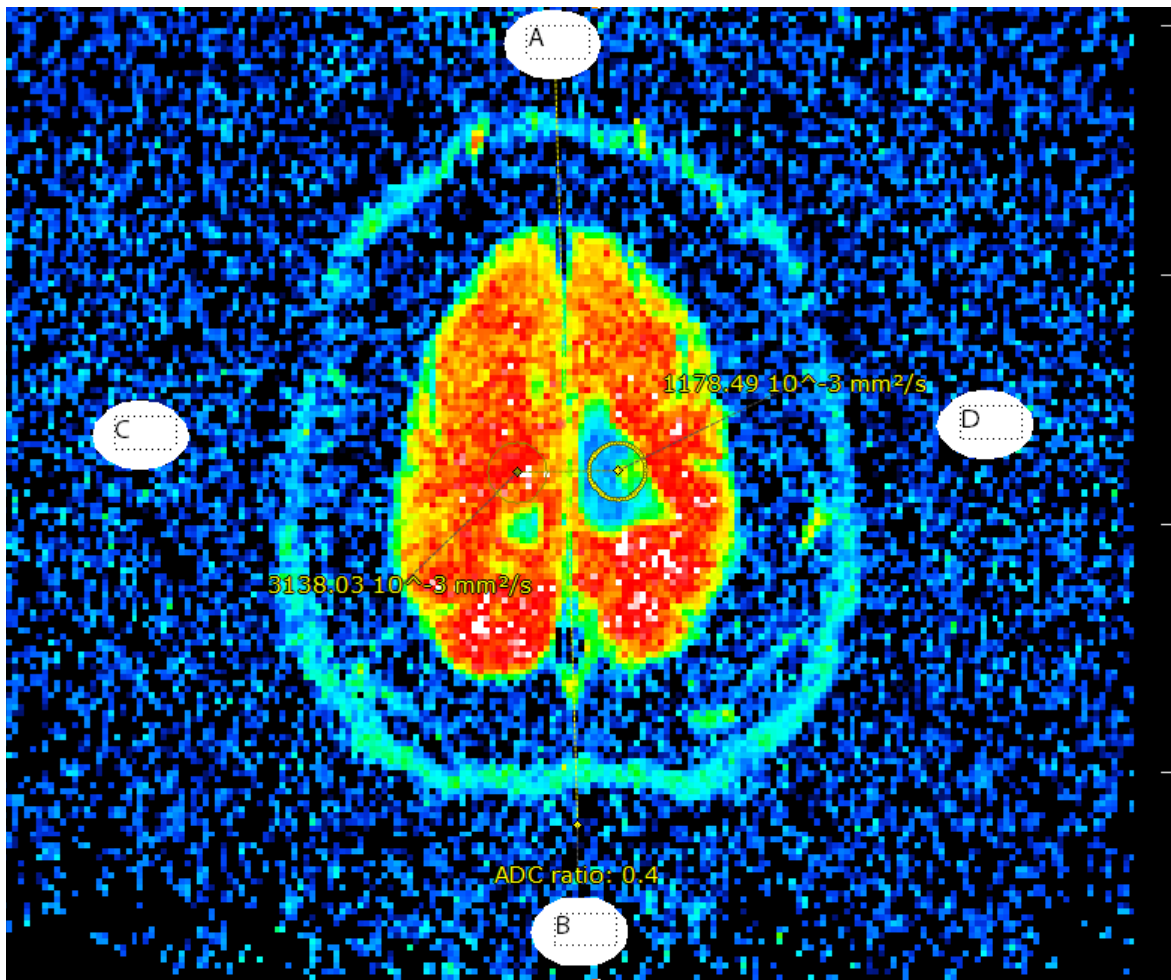


Figure 14-63 Creating 'ADC I' AOI ROI

Myrian® automatically provides you with the following calculations:

- The average ADC value of the voxels related to each circle which is displayed next to the ROI. The measurement unit is  $10^{-3} \text{ mm}^2/\text{s}$
- The ratio between the two circles which is displayed below the vertical dashed line

## 14.6.2 ADC II

- Select the 'ADC II' calculation tool so that it is now activated
- Create a first circle (lesion ROI) on a first slice of the ADC map
- Navigate then click on the view (on any slice) where you wish to locate the second circle (muscle ROI)

A symmetrical circle is created (see Figure 14-64) with displayed next to the lesion and muscle ROI, the ADC average value and below the ratio in percentage between the lesion ROI and the muscle ROI according to the following formula:

$$\text{ADC ratio (\%)} = (\text{average value of ROI}_{\text{lesion}} / \text{average value of ROI}_{\text{muscle}}) \times 100$$



When using the ADC II tool, you can choose to define the ROI circles (lesion and muscle) on two different slices of the ADC map.

Both lesion and muscle circular ROIs can be resized and translated and displayed values are updated accordingly.



Figure 14-64 Creating 'ADC II' AOI ROI

### 14.6.3 Launching the ADC protocol by drag & drop



A dedicated ADC protocol is available from the Protocols Tab from the main screen in the Standard MRI family (see Section 14.10.7 for detailed information)

- Load a study containing 2 diffusion series in the workspace in Native or MPR mode
- Click on the title bar of any view and drag and drop one of the diffusion series onto the other one
- Select ADC from the displayed combined protocol menu (see Section 2.4.2)



When a **drag & drop** is performed from one series to another one, the combined protocol menu displays **all protocols compatible with both series**.



ADC protocol can also be launched **right-clicking** on the title bar of any view. In that case, the right-click combined protocol menu displays all protocols compatible with **all series** opened in the workspace. Thus, the right-click combined protocol menu is particularly adapted when you have more than two series opened in the workspace that you wish to load in the ADC protocol or any available compatible protocol.

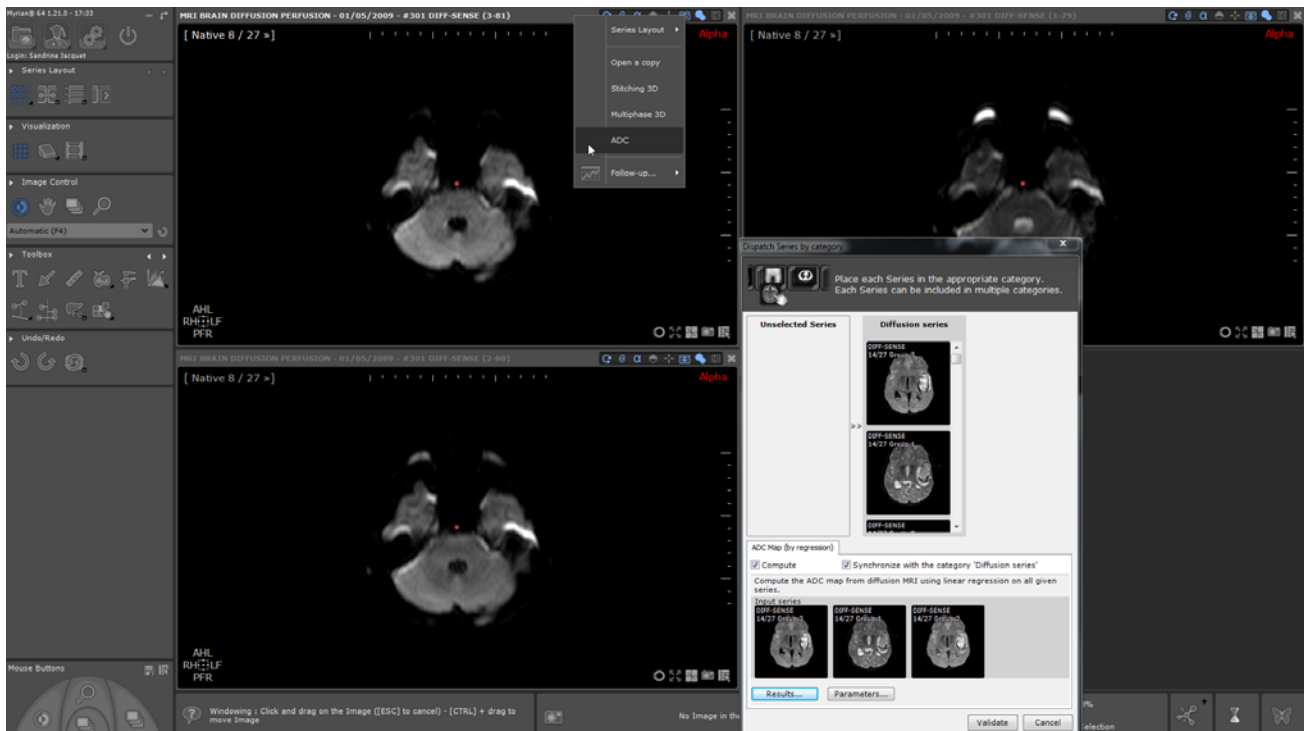


Figure 14-65 Loading diffusion series displayed in Native mode into the ADC protocol via Drag & Drop

Consecutively, a 'Dispatch series by category' window (see Section 14.10.2.1) appears prompting you to adjust series selection by drag & drop.

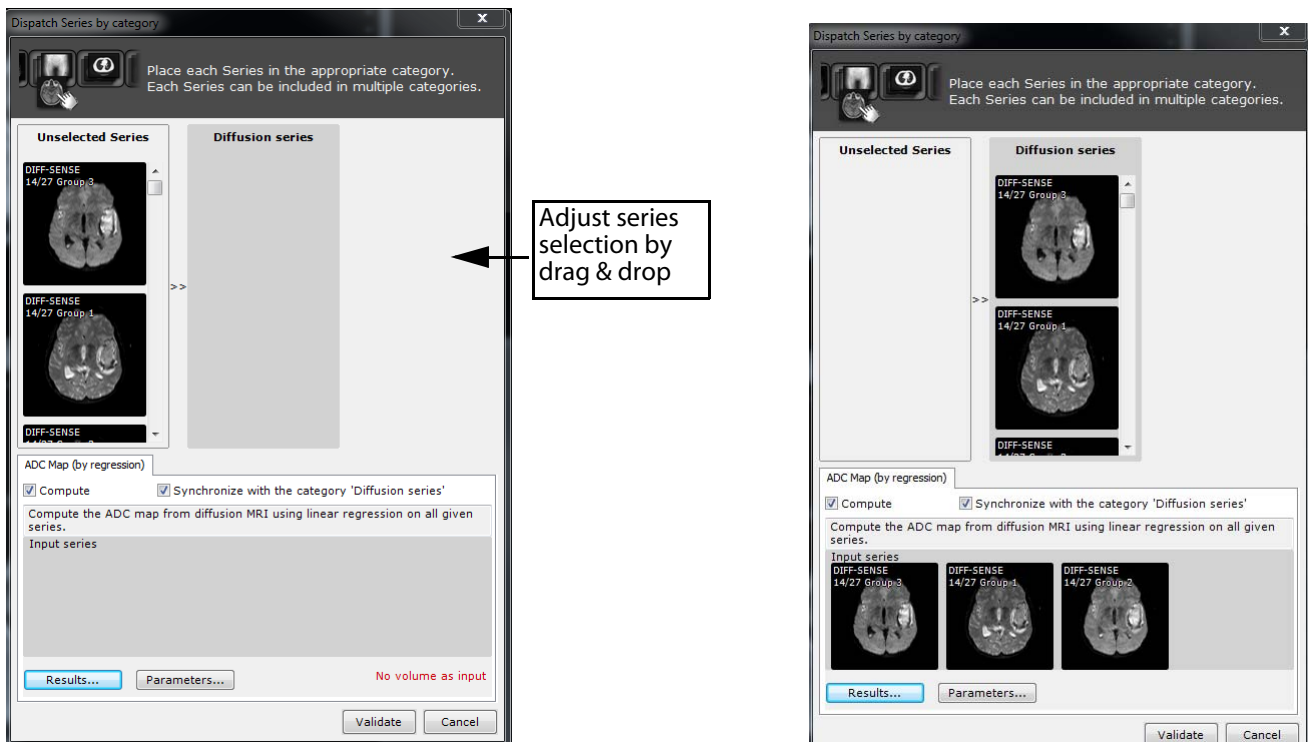


Figure 14-66 Adjusting series selection

- If required, adjust B values (see Section 14.10.2.1.2)
- Click OK

Myrian® loads the two series in a view using the ADC drag & drop protocol.

The ADC map computation is launched and once over, displayed in a specific ADC map view.

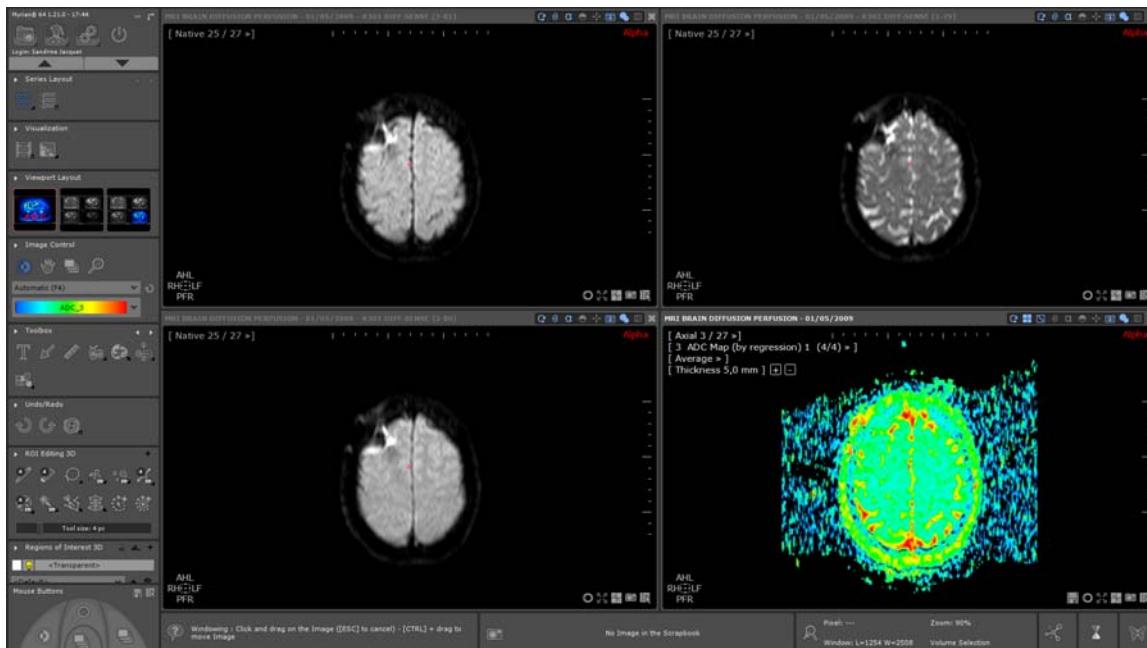


Figure 14-67 ADC map computation and display in the ADC protocol

## 14.7 ROICreator

### 14.7.1 Overview



The tools and functions presented in this chapter are only available if your Myrian® installation includes the corresponding modules.



ROI edited in canonical coordinates on tilted exams superior to 8.6° in Myrian® 1.7 and older versions are not compatible with Myrian® 1.8 and following and are not reproduced during software update. Updating to version 1.12 solves this incompatibility.

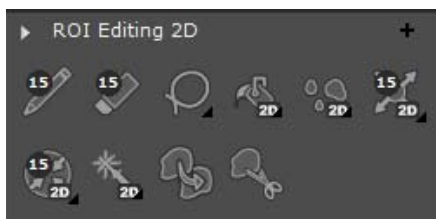


Figure 14-68 ROI Editing toolbox tab


ROICreator enables the creation and editing of Regions of Interest (ROI). ROI can be used to analyze and make measurements of the **volumes of various tissues**. By defining ROI in Studies having been made at different periods, it is thus possible to **Study the evolution** through time of certain target volumes of interest.

### 14.7.2 Presentation and use of the ROI editing tools (2D/3D)

The following tools use the same **color/parameter settings** as the **active ROI**.

In **'Overwrite Mode'** (see table below), if the active ROI is transparent, color-fill/drawing tools **hide pixels by 'painting' them 'transparent'**.

A **small white digit** at the top-left of a tool indicates its modifiable **stroke size**. Size is user-definable via a click on the

number at top-left of  Pen and/or  Eraser tools, which induces the appearance of the **tool dimension slider**.

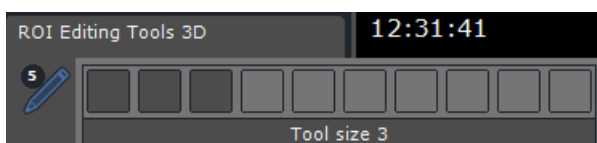
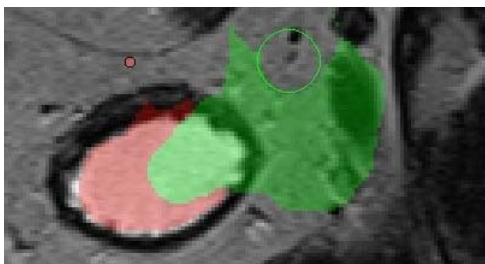


Figure 14-69 Tool dimension slider



When clicking-and dragging on the image using either the Draw or the Eraser tool, a colored circle matching the color of the selected ROI surrounds the mouse cursor. In the same way, the colored circle takes the size of the stroke size assigned to the tool that is used.





When pressing the **SHIFT key** while using the '**Draw**' tool, the 'Draw' tool starts behaving like the '**Erase**' tool



When pressing the **SHIFT key** while using the '**Erase**' tool, the 'Erase' tool starts behaving like the '**Draw**' tool

Icon	Tool	Usage (Overwrite Mode)	Usage (Preserve Mode)
	Global ROI Preserve/Overwrite toggle	Toggles all displayed ROI that were 'Overwrite' mode back to this state	Toggles all displayed ROI in 'Overwrite' mode to 'Preserve' mode
	Freehand <b>Draw</b> tool	Draw contours/lines by hand <b>anywhere</b> (can draw over other shapes/contours)	Draw contours/lines by hand anywhere <b>except</b> over existing contours/shapes
	Freehand <b>Erase</b> tool	Erase <b>any existing</b> contours/lines/shapes	Erase contours/lines/shapes of <b>the active ROI</b>
	<b>Lasso</b> tool:	Create freehand color-filled shapes (auto-completes) <b>anywhere</b>	Create freehand color-filled shapes (auto-completes) anywhere <b>except</b> over existing contours/shapes
	<b>Paint bucket</b> tool (2D/3D)	Click on any contour/shape to replace its Color	Click on <b>an empty space/shape</b> within a ROI to fill-in.
	Slice-by-slice auto <b>Hole-fill</b> tool (2D/3D/auto slice-by-slice)	Click on any shape to <b>fill-in the hollow spaces</b> within the shape	Click on an active ROI shape to <b>fill-in the hollow spaces within the shape not belonging to any other ROI</b>
	Slice-by-slice auto <b>Inflate</b> tool (2D/3D/auto slice-by-slice)	Click on any shape to <b>expand/inflate</b> it (overwrites any existing ROI)	Click on any shape to <b>expand/inflate</b> it (preserves any existing ROI)
	Slice-by-slice auto <b>Deflate</b> tool (2D/3D/auto slice-by-slice)	Click on any shape to <b>contract/deflate</b> it (overwrites/clears any existing ROI)	Click on any shape to <b>contract/deflate</b> it (preserves any existing ROI)
	<b>Magic wand</b> (2D/3D)	Automatically selects/paints <b>all</b> bordering pixels of similar intensity (overwrites any existing ROI)	Automatically selects/paints <b>all</b> bordering pixels of similar intensity (preserves any existing ROI)
	<b>Merge ROI</b> tool ((2D/3D/	Merge a clicked ROI with a selected ROI in the list (overwrites any existing ROI)	Merge a clicked ROI with a selected ROI in the list (preserves any existing ROI)
	<b>ROI cut</b> tool	Select this tool then click and drag on a zone to remove it from the active ROI. The removed zone is based on the tool size	

Table 14-3 2D/3D ROI editing tool functions

The following tools open a floating menu when they are activated:

- **Paint bucket** (2D/3D)
- **Hole-filler** (2D/3D/auto slice-by-slice)
- **Inflate** (2D/3D/auto slice-by-slice)
- **Deflate** (2D/3D/auto slice-by-slice)
- **Magic wand** (2D/3D), which enables to paint and assign to a selected ROI a bordering region of similar intensity by one click or by click and drag on one slice (2D viewport) or on the whole volume (3D viewport), respectively playing with windowing or the applied color code.

The floating menus enable the choice of the following modes:

- **Two dimensions** (2D), e.g. treating the holes on a single slice,
- **Three dimensions** (3D) e.g. treating three-dimensional **holes found in a volume** and finally,
- **'Auto slice-by-slice'** which **automatically applies a 2D fill to each slice**, which has the advantage of filling in, for example, those regions that would have been left out by a 3D fill due to being 'open' at the end-most slices.



Hold down the Shift keyboard key during manipulation of most ROI editing tools to toggle between next/previous or opposite action tools



Some ROI editing tools may only be applied on 2D views (Axial, Sagittal, Coronal, Oblique and Native slice views). They are visible in the 3D view but cannot be edited directly in 3D.



A small white digit at top-left of any tool indicates its stroke size or size of increment/decrement.



Right-click on the small white number to induce the Tool-size slider to appear.



If a Study size exceeds the limit of the workstation's memory resources, ROI editing tools presented in this section may not be available. In such a case, a pop-up warning will appear to indicate this. Viewing will nonetheless still be available.

### 14.7.3 3D ROI editing tools

The ROI editing toolbox also includes the following tools, which are only available in MPR Mode:

Icon	Tool	Function
	<b>Cutting Surface</b>	Opens the <b>Cutting Surface</b> floating toolbar to enable virtual cutting operations on ROI in 2D or 3D
	<b>Extrusion</b> tool	Opens the <b>Extrusion</b> floating toolbar to enable extrusion
	<b>Assign to ROI</b>	Select this tool then <b>click on a zone to add it</b> to an active ROI
	<b>Perform automatic recognition</b>	Launches the automatic Tissue Recognition tool (requires the corresponding Expert Module to be installed)

Table 14-4 Advanced 3D ROI editing tools




The 'Assign to a ROI'  tool is also available in Whole Volume Mode, Volume of Interest Mode and Endoscopy Mode



The 'Lasso' (auto-filled freehand)  is available in Whole Volume Mode and Volume of Interest Mode.




## 14.7.4 Assisted 2D contour drawing mode

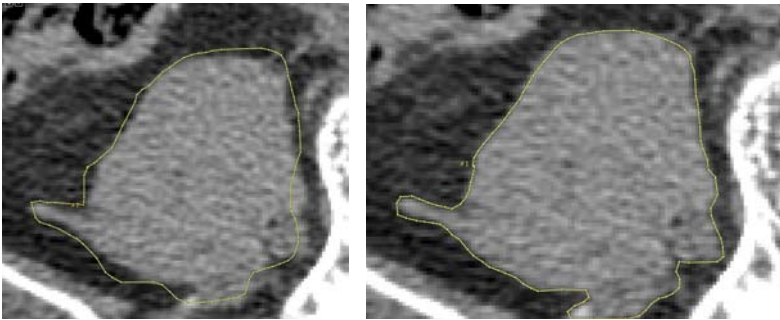
When drawing a freehand contour, you can activate from the Viewport layout toolbar the assisted 2D contour tool .

Depending on the windowing, this assisted contour engine works for any ROI edition tools (i.e. contrast curve, visual selection, extrusion, free shape AOI, lasso) based on **freehand contours** and enable to automatically adjust the user-defined contour to the targeted structure



Windowing adjustments enabling an improved visualization of the anatomical structure are required prior to use this tool.

- Click on the drawing mode icon  to activate the assisted 2D contour tool.
- Draw a freehand contour (selected in any of those above-mentioned ROI edition tool menu) around the target anatomical structure



The user-defined contour is automatically adjusted to better fit to the contoured target zone.



If the resultant contour does not suit you entirely, you can still edit the contour manually (pressing the ALT key): the correction of the contour only applies to the edited portion of the contour



When the assisted 2D contour tool fails to refine the freehand contour, the original contour is maintained.

## 14.7.5 Morphological Extrusion Tool

### Tool Description

**Extrusion** generates 3D ROIs by **interpolation of user-defined contours**.



### Usage

Used for volume measurement and 3D visualization of pertinent anatomical structures.

### Method

As in the case of the Cutting Surface tool described above, clicking on the Extrusion tool button  induces the opening of a Floating Toolbar which has three buttons:

- 'Add an extrusion contour'  to draw contours freehand
- 'Launch extrusion'  to create a 3D ROI

- 'Launch extrusion using Erase mode'  from contours drawn in **2D only**
- 'Delete all targets'  to remove all Extrusion contours

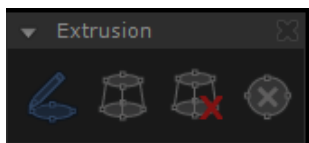






Figure 14-70 Extrusion tool Floating Toolbar

## Procedure



- Choose/add relevant ROI to which you wish to add the extrusion.
- Select the 'Add an extrusion contour' button 
- Locate the first slice containing the target anatomical structure in the desired plane of view
- Draw the **first ROI** contour
- Navigate to another pertinent slice and draw the **next contour**

---


 You can activate the 2D assisted contour tool  to automatically adjust the freehand contour around the outlined target zone (see Section 14.7.4)

- 
- Repeat process as required from first slice to central point to last slice (each contour is **numbered automatically**)
  - Click on  'Launch extrusion' to **generate the new ROI**

---

 If the extrusion is unsatisfactory, click on  'Delete all extrusion contours', the 'Undo' (in the Undo/Redo tab) or use the 'CTRL + Z' keyboard shortcut. This will remove the extrusion but retain the contours.


---

 If you want to carry out a new extrusion, be sure to remove the previous contours first.


---

 Use the handles to modify selected contours as desired

---

 Once a contour has been drawn in one plane of view, a small rectangle appears in every other viewport to indicate its precise location. The rectangles, which are yellow if the contour is currently selected, and orange if it is not, contain an initial and a number to indicate which plane of view they are in and their order if there are several contours in the same viewport

---

 Click on a 'rectangle' contour representation to refresh all other views to the contour's position and to automatically select it

## Example

In the following example, the extrusion tool was used to create a 3D ROI isolating a cyst of the kidney. Six contours were drawn by hand on different slices in the Axial plane and the extrusion was launched. Figure 14-73 illustrates the end result with **clear 3D visualization** and the **volume measurement display**.

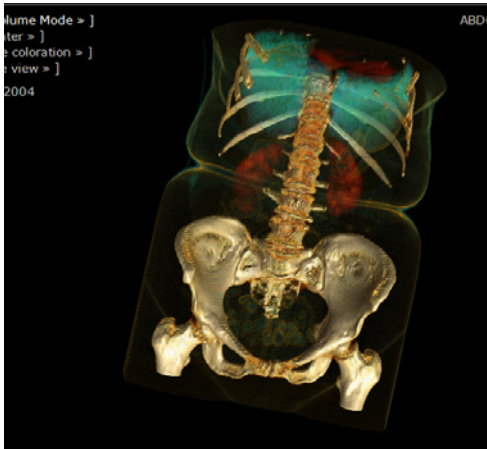


Figure 14-71 Example: Extrusion Tool –'Before'

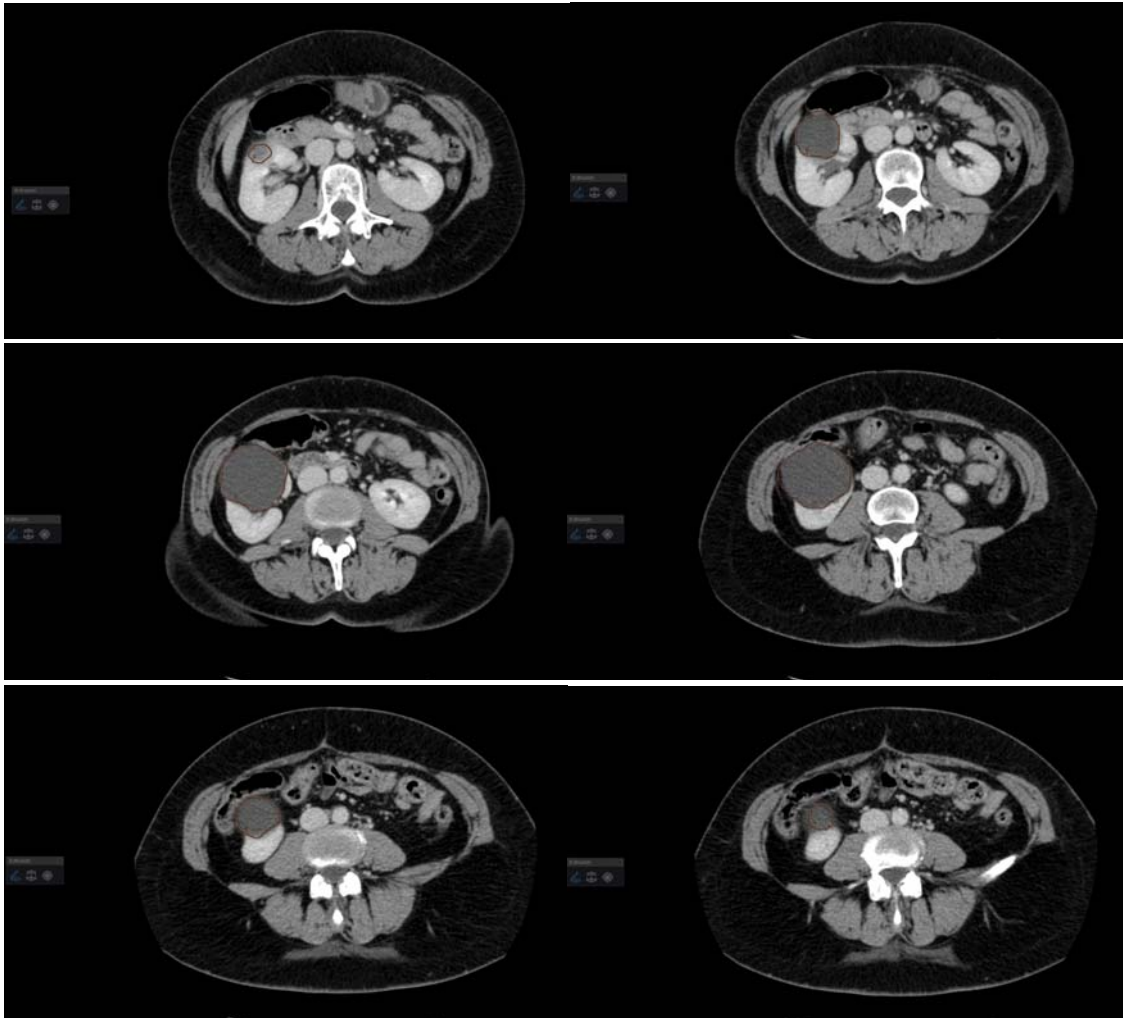


Figure 14-72 Example: Extrusion tool –'Add contours'

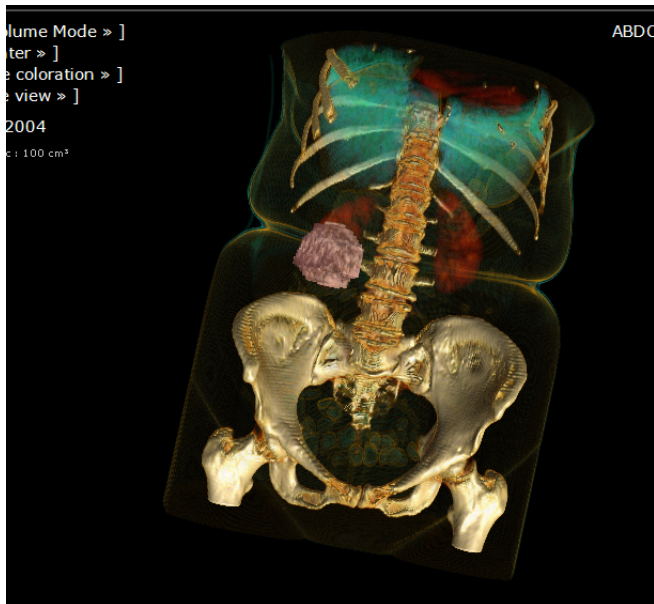


Figure 14-73 Example: Extrusion tool –‘After extrusion’

## 14.7.6 Automatic tissue recognition



The tools and functions presented in this chapter are optional. They are only available if the corresponding add-on modules have been installed and activated.

### Introduction

Available in **Native Mode or MPR**, both in 2D and 3D, the **tissue recognition tool** enables **ROIs to be defined rapidly** for a number of different anatomical regions.

Once **verified and validated**, ROI may be edited if they need to be corrected or adjusted with the help of a set of editing tools.

This complementary information may be added to/included in the Study report.



Only a qualified medical practitioner can discriminate healthy tissue from a lesion and identify the true nature of any suspected pathology. Myrian® software’s ROI Creation tool is intended to help radiologists isolate and highlight tissues with similar/homogeneous density properties. Its intended use is to assist professional interpretation of Studies by qualified medical staff.

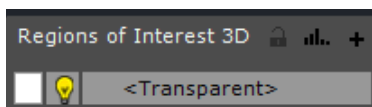


Figure 14-74 Region of Interest tab

## 14.7.7 Create ROIs

You can create up to 127 ROI for a single Series. To create a ROI (Region of Interest):

- **Click** on the ‘**Create a New Region of Interest**’, ‘+’ button at the top-right of the Region of Interest tab to open the **list of available recognition engines**

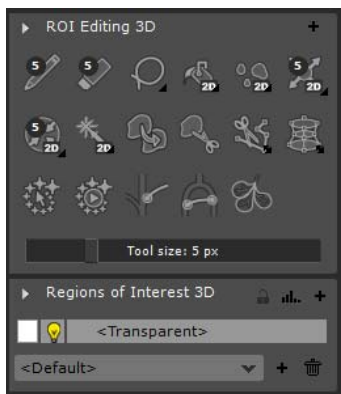


Figure 14-75 Create and Edit ROI toolbars

This action opens the ‘**Create one or multiple ROIs**’ screen which lists available tissue recognition engines grouped by type of anatomical structure.

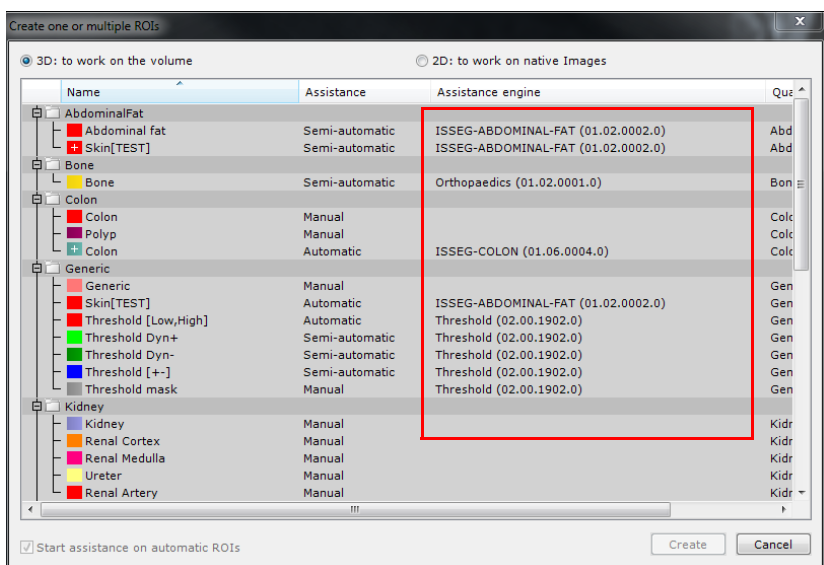
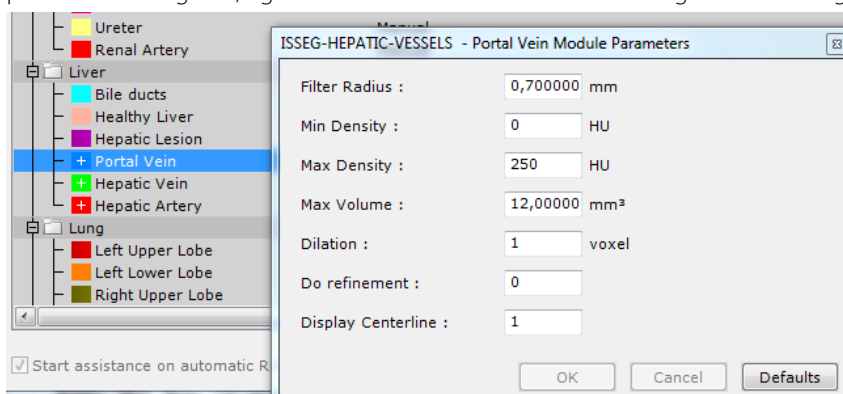


Figure 14-76 Example of a list of available tissue recognition engines ('Create one or more ROIs' screen)




The behavior of several tissue recognition engines (i.e., portal vein, hepatic vein, hepatic artery, abdominal fat, colon, low attenuation, aortic vessels and left coronary artery) can be modified by editing their parameters. To access dedicated parameter dialog box, right-click on one of those concerned segmentation engines as illustrated hereafter:



Modifying those parameters is to be performed by **advanced users only**.

- **Select** the desired tissue of interest (or make multiple selections to create several ROIs simultaneously using the 'CTRL/Shift+click' command)
- Click on '**Create**' to launch the automatic recognition tool and to return to the main Study screen

If the recognition mode of a segmentation engine is 'semi-automatic', **after clicking on 'Create'** and returning to the main workspace:

- Click on the **'Assign to a ROI'** button  in the Editing Regions of Interest tab)
- **Click on the zone** in the image which corresponds to the relevant anatomical structure to launch the engine.

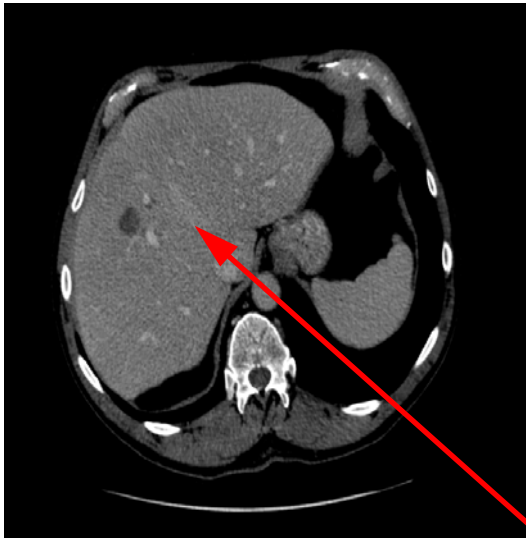


Figure 14-77 To create a semi-automatic ROI, click on desired zone



Figure 14-78 View after ROI is obtained

While the recognition process is in progress, a progression bar appears in the active ROI entry(s) in the list of ROIs

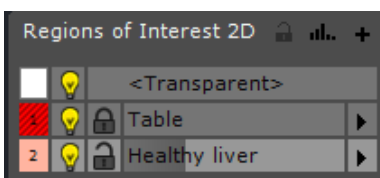


Figure 14-79 Example of ROI creation (processing in progress)

Simultaneously, the hourglass displayed in the right-end of the information panel gets animated.

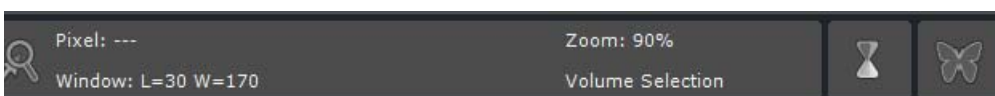


Figure 14-80 Animated hourglass during the segmentation process

The selected ROI is automatically added to the list of ROIs in the Region of interest tab.



If the segmentation engine mode is 'Automatic' processing begins instantly after engine is launched.

---



Once ROI have been created, the volume and Color information pertinent to each ROI is displayed top-left of every viewport (or bottom-right of Scrapbook and PrintComposer snapshots).

---



ROI are persistent: they are saved from one session to another and are loaded with their containing Series once the Series has been loaded.

---



If no ROI Creation engine is available or specifically adapted to the type of ROI required, use the Magic Wand to select zone.

---



The segmentation results should be a complete segmentation of the target structure only without any part belonging to other tissues. If, for any reason, the segmentation is incomplete or it includes erroneous parts, you can refine/complete the segmentation by using the Magic Wand or other ROI editing tools for further details on editing ROI).

---



You can configure the optional 'Lung Tissues' segmentation engine by right-clicking on it in the ROI creation list. The available parameters to select are the 'High' and 'Low' intensity limits of tissue (expressed in HU).

---

### 14.7.8 Transparent ROI

The **Transparent ROI** is the first ROI in the list of ROIs. It is a special ROI in that:

- It includes every part of the 2D/3D image that is not already assigned to another ROI
- It is always present
- It has a reduced right-click menu via which it is possible to:

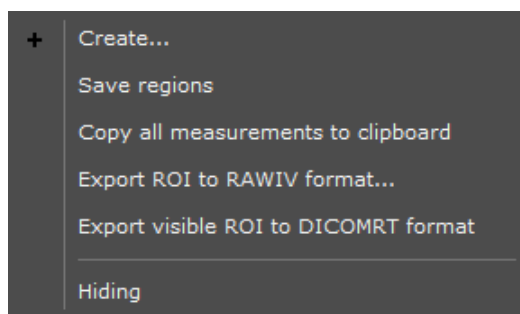


Figure 14-81 Transparent ROI right-click menu

- Save all ROIs at once
- Copy all advanced measurements to the Windows® Clipboard
- Hide/Reveal transparent ROI



	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Healthy liver	(RENAL1 - 20/12/2007 - #6 Recon 2: ABDOMEN INJECTE (1-171))												
2	Measurement Unit	Value												
3	Volume	cm <sup>3</sup>	243,42											
4	Slice-by-slice area	N/A												
5	Mean density HU		301,05											
6	Min, Max	HU	101	1221										
7	Standard-dev HU		179,75											
8	Density histo -		35,87	101	213	34,97	214	325	13,68	326	437	5,95	438	
9	Inertia Axis -		142,19	144,19	84,12	-2,06	-2,99	111,7	-8,72	57,91	1,39	51,97	7,8	

Figure 14-82 Example of copy-paste measurements to MS Excel



You can hide the Transparent ROI to reveal any other existing ROIs.



Figure 14-83 Visibility slider

### 14.7.9 Create Generic Threshold ROI

By default, the threshold assistance engine available in the 'Generic' section of the ROI creation window when working in 3D enables you to create 5 types of ROI.



Except the threshold mask, all other threshold-type ROIs can be created in 2D.

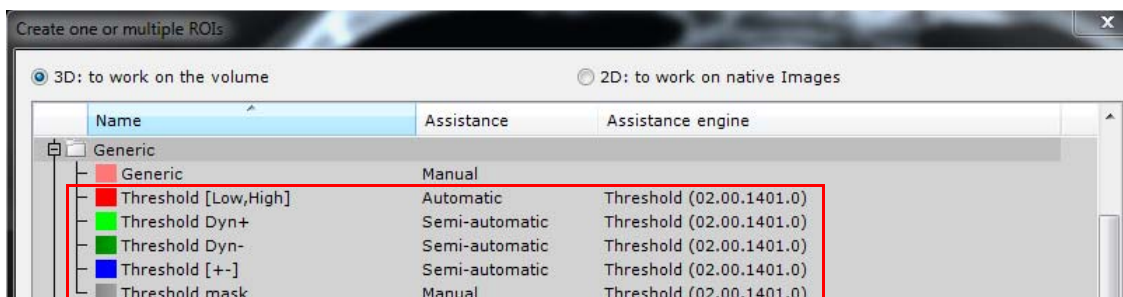


Figure 14-84 Available threshold assistance engines

These ROIs have their own threshold specifications described here after



Before launching any threshold-type ROI segmentation, always make sure that the default intensity thresholds are adapted to your needs.

### Threshold [Low/High]

This ROI is automatic. It comprises all voxels ranging between a low limit (set to 300 by default) and a high limit (set to 4096 by default).



These parameters may be manually defined via the threshold 'parameters' box.




When a mask ROI exists and is not empty, the computation is done only within the mask ROI. Otherwise the whole



volume is taken in account.

---

Once the ROI is created, there are two options:

- Either the ROI is automatically calculated
- Or the ROI does not appear and in that case, you need to assign it to the ROI clicking on 

### Threshold Dyn+


This semi-automatic ROI requires a click on the view to activate the assistance engine. It comprises all voxels of intensity superior or equivalent to the intensity of the clicked voxel.

---



When a mask ROI already exists and is not empty and if you click on the mask, the computation is done only within the mask ROI. Otherwise the whole volume is taken in account.

---

- Once the ROI created, assign it to the ROI clicking on  and click on the view to start computation. The threshold detection is launched and the voxels appear (the value used as a "low limit" is the one of the clicked voxel)

### Threshold Dyn-


This semi-automatic ROI requires a click on the view to activate the assistance engine. It comprises all voxels of intensity inferior or equivalent to the intensity of the clicked voxel.

---



When a mask ROI exists and is not empty and if you click on the mask, the computation is done only within the mask ROI. Otherwise the whole volume is taken in account.

---

- Once the ROI created, assign it to the ROI clicking on  button and click on the view to start computation. The threshold detection is launched and the voxels appear (the value used as a "high limit" is the one of the clicked voxel)

### Threshold [+/-]

This semi-automatic ROI requires a click on the view to activate the assistance engine. It comprises all voxels of intensity close to the intensity of the clicked voxel.


Here, "Close" means the intensity of the clicked voxel including a range +/- set to 25 by default.

---



When a mask ROI exists, is not empty and the user clicked on the mask, the computation is done only within the mask ROI. Otherwise, the whole volume is taken in account.

---

- Once the ROI created, assign it to the ROI clicking on  and click on the view to start computation.

The threshold detection is launched and the voxels appear (the value used as a "high limit" is the one of the clicked voxel)

---



The 'Range +/-' as well as the 'high limit' parameters can be customized in the Threshold 'Parameters' window.

---



Any parameter modification is preserved at the opening and closing of the session. To restore parameters by default, click on 'Defaults' in the threshold parameter box.

---

Finally, the last ROI is an input mask enabling to define a specific region to work within (see following section).

### 14.7.10 Create a Threshold mask ROI

This detection engine enables you to create a user-defined ROI based on a specific volume and specific voxel intensity range



The threshold mask assistance engine only works on 3D ROIs.

#### Procedure:

- Click on the '+' button in the 'Regions of Interest 3D' Toolbar
- In the 'Create one or multiple ROIs' screen, select the 'Threshold mask' in the group of 'Generic' ROIs.

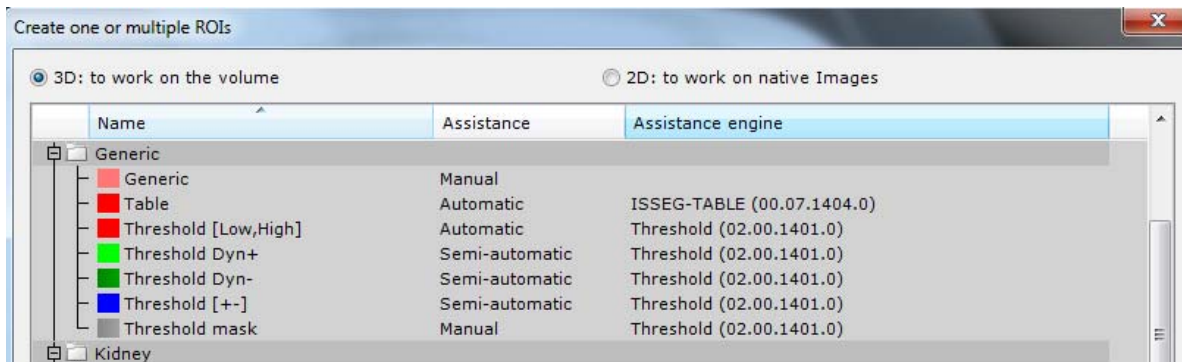


Figure 14-85 Initiating the threshold mask engine

- Click on the 'Create' button at the bottom of the window to initiate the computation engine.

The 'Threshold mask' is automatically displayed in the ROI list.

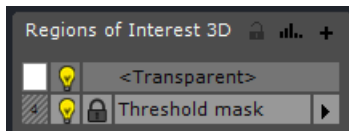




Figure 14-86 Creation of the Threshold mask ROI

- In the 'ROI editing tools 3D' toolbox, click on the lasso icon and activate the type of mask ROI you wish to create from the displayed menu, either a filled shape  or a sphere 

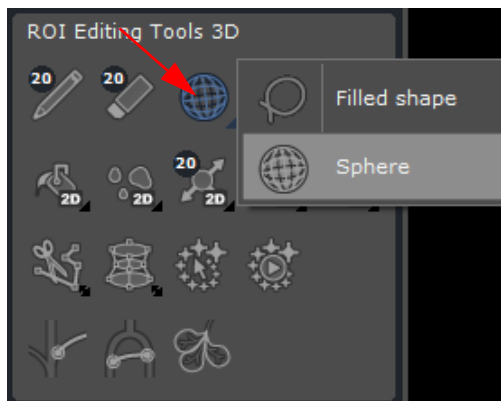


Figure 14-87 Defining a threshold mask

- Draw manually the mask ROI on the view

The Threshold mask assistance engine automatically launches and creates the threshold mask

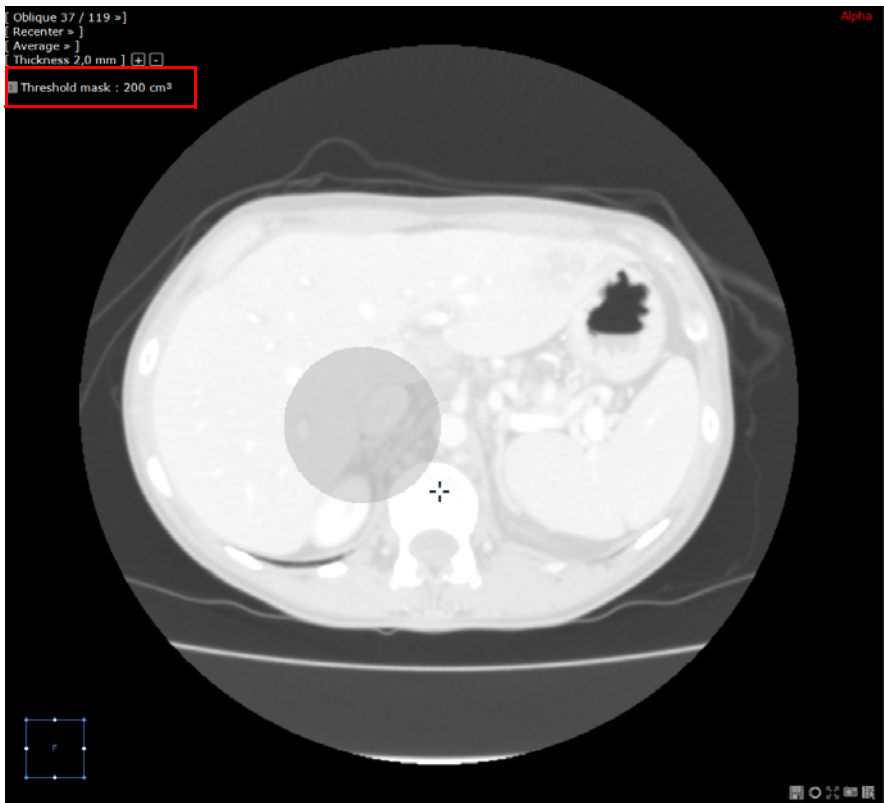


Figure 14-88 Drawing a sphere shape as a threshold mask



The properties of the threshold mask ROI can be edited via the ROI parameter box (see Section 14.7.18).

- If you wish to access the Threshold mask 'Measurements' window, click on the Histogram icon .

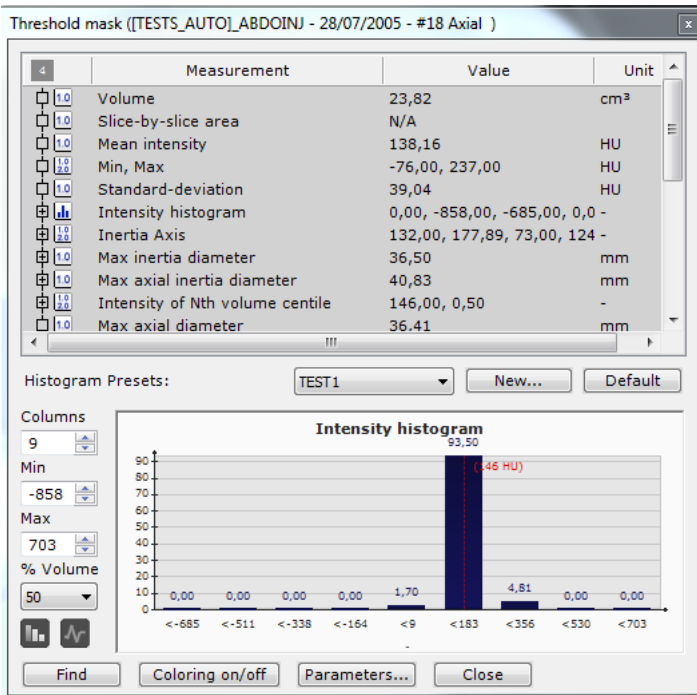


Figure 14-89 Threshold mask advanced measurement & Histogram window

### 14.7.11 Resetting the predefined threshold parameters

By default, the **threshold high limit** is set to 4096 while the **threshold low limit** is set to 300. However, these parameters can be adjusted to your preferred values.

Another editable parameter is the **threshold range** which by default is set to 25.



The threshold setting window is accessible only when the threshold mask has been created.

- To access this configuration dialog box, right-click on the Threshold mask ROI from the list, click on 'Assistance' and then 'Threshold'

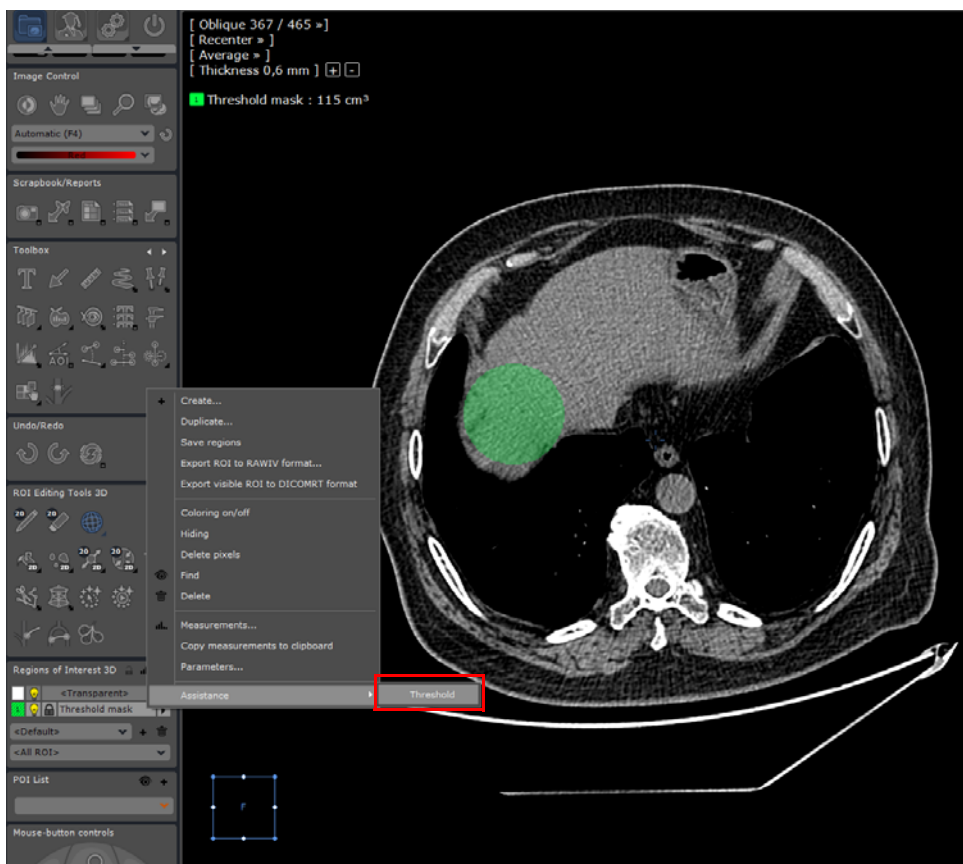


Figure 14-90 Opening the threshold configuration dialog box

- Enter your preferred values

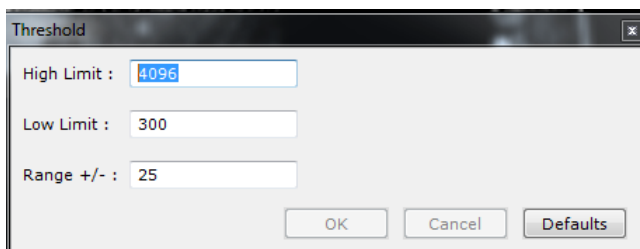


Figure 14-91 Setting your preferred threshold values


- Click on OK to confirm and apply these new settings.



To restore factory parameters, click on 'Default' from the threshold configuration dialog box.

### 14.7.12 Cancel segmentation in progress

Sometimes, segmentation takes a very long time to complete and results in an incorrect ROI. In that case, you have the possibility to cancel the segmentation.

- Click on the hourglass  to interrupt the process, or
- Right-click on the ROI entry in the list to which the segmentation engine applies in order to cancel automatic assistance

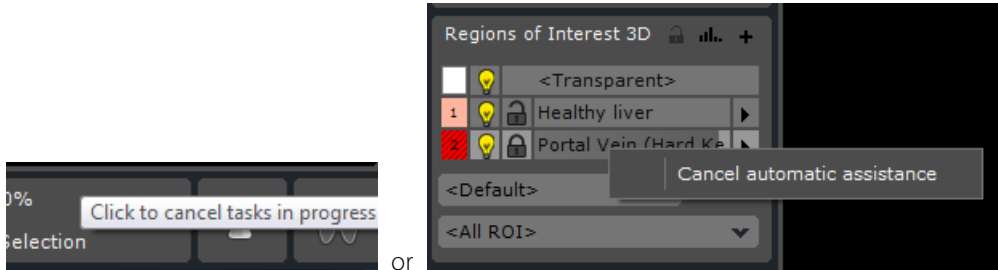


Figure 14-92 Interrupting the ROI detection

### 14.7.13 Delete ROI

- To delete a ROI, simply right-click on the target ROI name in the ROI Toolbar List and select 'Delete' from the resulting context menu.

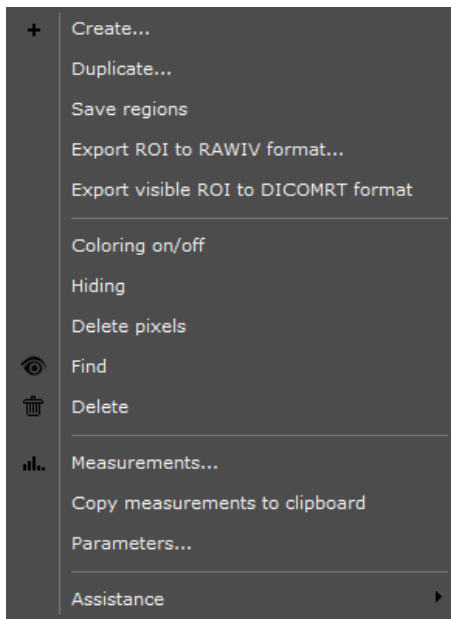


Figure 14-93 Delete ROI in the ROI List Context Menu



If you delete a ROI to which a Path is associated, the Path too will be deleted.



You can also undo a segmentation by clicking on



in the Toolchest or simply by pressing "CTRL+Z".

### 14.7.14 ROI Stacking/Volume Sharing

ROI can coexist in the same volume. However, when multiple ROI coexist in a volume, only one ROI is displayed: the display priority is determined by the order in which the ROI were created, with the most recently created ROI having higher priority over the oldest (i.e. from bottom-to-top, in the ROI toolbar list).



Non-Surrounding ROI always take display priority over Surrounding ROI.

When using a ROI Editing Tool on any region, only the displayed ROI can be modified. However, whether or not it is modified is dependent upon the Preserve/Overwrite/Lock setting of the displayed ROI (see Section 14.7.16).



Mouse-over information does not display the fact that multiple ROI are present on the same voxel. Only the visible ROI is described.

### 14.7.15 ROI display adjustment

You can modify the appearance of ROI via both right and left-click commands to enhance, isolate, highlight and illustrate any lesion or pathology of Interest.

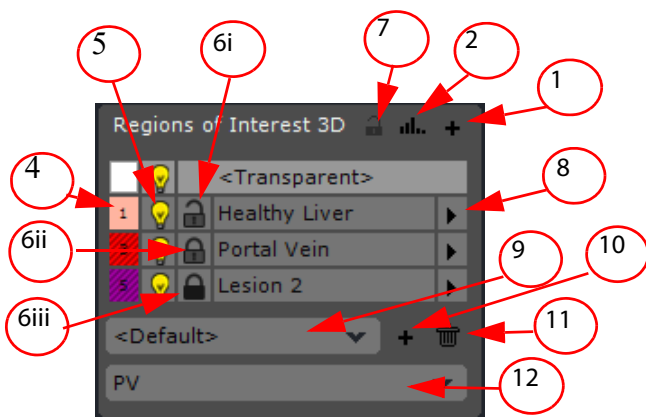


Figure 14-94 ROI display adjustment commands

Functions are:



- 1 Create a ROI button
- 2 Advanced Measurements & Histogram window
- 3 List of ROIs (right-click to open context menu)
- 4 Toggle ROI Color On/Off
- 5 Toggle ROI pixel/voxel visibility On/Off
- 6 Individual Protect ROI status:
  - Overwrite Mode (6i)
  - Preserve Mode (6ii)
  - Locked Mode (6iii)
- 7 Global Preserve/Overwrite Mode toggle switch
- 8 Locate the ROI: Position the anatomical center in the center of the active ROI
- 9 Current ROI Set
- 10 Create New ROI Set
- 11 Delete ROI Set
- 12 ROI Groups

### 14.7.16 ROI Lock/Preserve/Overwrite modes

Each ROI can be individually locked against accidental modification or deleting. There are 3 modes you can choose from:

-  Overwrite: In 'Overwrite' Mode, ROI can be modified, reduced, stacked or deleted, etc. When new ROI are



created in the same location as displayed ROI, all corresponding voxels are assigned to the new ROI.

-  Preserve: in this mode, ROI are protected against being deleted. All voxels contained in such ROI can also be assigned to new ROI, i.e. shared, however the 'Preserved' ROI are not reduced in volume.
-  Locked: all voxels contained in a 'Locked' ROI are exclusively assigned to this ROI and cannot be shared with other ROI. Locked ROI can be neither overwritten, deleted nor reduced.
- Click on the padlock icon to cycle through the different modes and select the most appropriate.



The locking status for each ROI is stored when closing the Series and restored when the Series is opened again.

#### 14.7.16.1 Global Lock

Furthermore, a 'Global Preserve'  / 'Overwrite'  function is available at the top right of the ROI Toolbar. Clicking on this icon will toggle any ROI in Overwrite Mode to Preserve Mode and back.



ROI already in Preserve or Locked Mode will not be affected.



Whenever the individual Preserve/Overwrite Mode of a ROI is modified, the Global Preserve Mode is automatically deactivated and all ROI retain their current Mode.



If multiple ROI are selected, Global Lock/Unlock settings will affect only the group of Selected ROI.

#### 14.7.17 Set the ROI Volume precision

You can adjust the number of decimal points of the ROI volume displayed on viewports according to your ongoing needs.

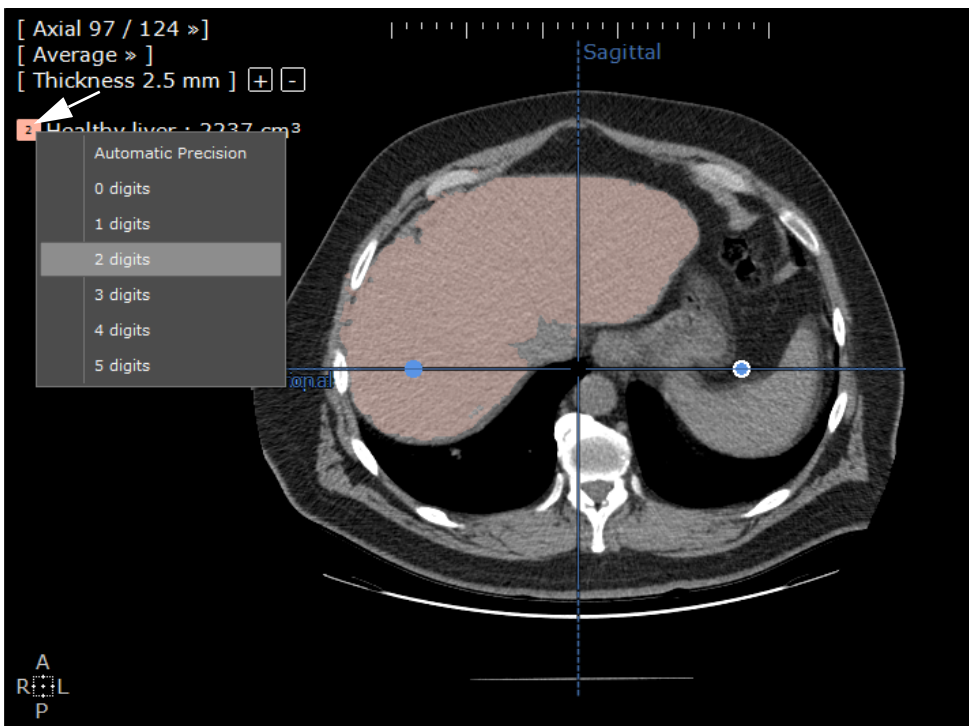


Figure 14-95 Modify the number of decimals of a displayed ROI volume



To change the number of decimal points displayed, click on a ROI volume index **2** and select the required option in the contextual menu.

### 14.7.18 Customize ROI parameters

By default, the software automatically completes fields and color/opacity/smoothing settings for Region of Interest. These are however user-definable using the Region of Interest parameters screen available via the right-click menu described in the table above. Customizable fields are:

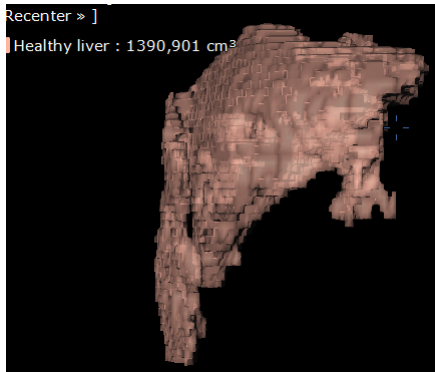
- Name
- Color
- Opacity
- Smoothing



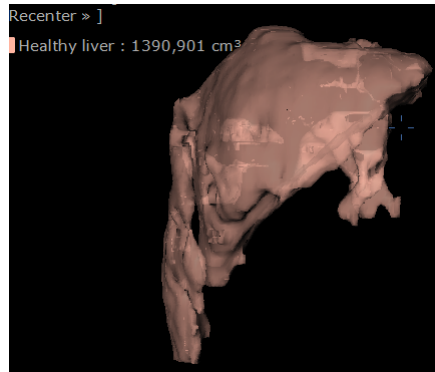
The default smoothing level (between 1 to 20) is based and depends on the class/qualification of each ROI. These parameters are configurable.

When modifying the ROI, the corresponding smoothing is applied to all ROIs sharing the same class/qualification.

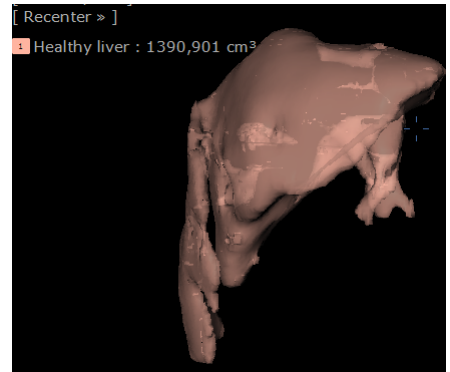
When creating the ROI, the smoothing level of ROIs will be set as a user setting, **only if a user setting does not exist yet for this class/qualification**. Once default parameters modified, these new parameters are saved in the user settings.



a) Smoothing level = 0



b) Smoothing level = 10



c) Smoothing level = 20

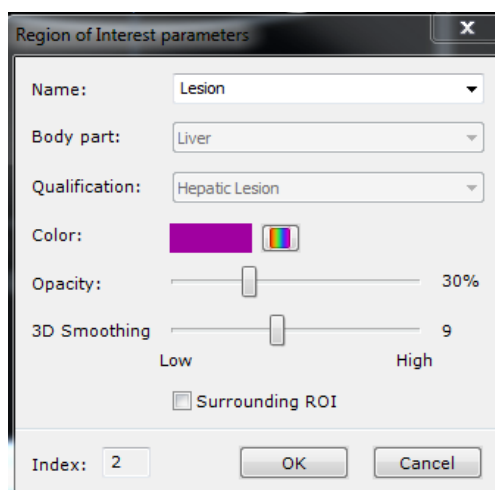


Figure 14-96 Basic ROI parameter customizing screen



The ROI parameter screen is also accessible via the Measurements and Histogram screen.





Tissue Recognition is carried out as a 'background task'. Other tasks may be carried out in the application during its progress. General performance and responsiveness may however be slowed down depending on the hardware resources of the workstation.



The predefined qualifications are merely a suggested default nominative value aimed at saving time for the specialist. They must systematically be edited and corrected and should in no way be interpreted as more than a recommended name.

### 14.7.19 Opacity of the Study

The opacity of the Study may be adjusted with a slider as follows:


- Locate the 3D Regions of Interest tab at left of main workspace
- Locate the <Transparent> ROI in the list of the ROI displayed in the tab
- Right-click on the 'Masking On/Off' button  at left of the <Transparent> ROI
- Set the slider to the desired transparency level:



Figure 14-97 Setting the opacity

### 14.7.20 ROI contextual menu

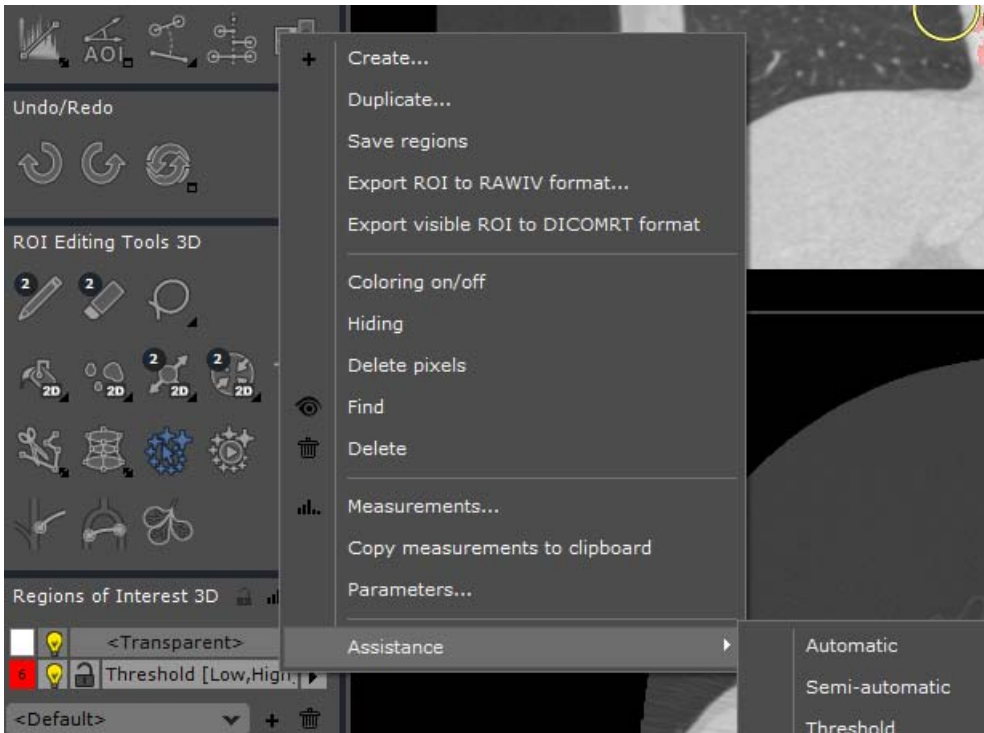


Figure 14-98 Right-click menu (existing ROI)

All these commands are available via the **listed ROI right-click menu** (see above), as well as the following:

Command	Function	
Duplicate	Duplicates the current <b>ROIs attributes</b> whilst <b>automatically</b> proposing a <b>different Color</b> and <b>incrementing its number</b>	
Save Regions	Saves all Regions of Interest regardless of Preference settings (useful in a multi-user situation or in case of an unexpected session crash-out)	
Find	Positions <b>anatomical center on the center</b> of the active ROI	
Copy measurements to clipboard	Copies the advanced Measurements to Windows® clipboard to make them available for pasting in a word processing application	
Parameters	Opens the <b>ROI Parameters display editing</b> screen (see fig 9-7)	
Segmentation	Automatic	ROI are created by the Engine alone
	Semi-automatic	ROI creation is assisted by the Engine
	Engine name	Launches the corresponding Segmentation Engine

Table 14-5 Right-click menu commands

General image smoothing settings in the Preferences>Display tab are also applied to ROI when they are highly magnified ('Zoomed-in'), as in the example below.



Figure 14-99 Smoothing parameters in the Preferences>Display tab

### 14.7.21 ROI Groups

The ROI Groups function enables you to define then display or hide custom made groups of ROI in one click via the drop-down menu at the bottom of the ROI Toolbar. Until you have created ROI Groups, the basic default menu provides 2 choices:

- <All ROI> to display all existing ROI
- <...> to create New ROI Groups

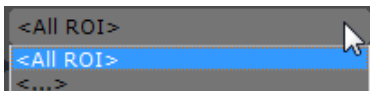


Figure 14-100 ROI Group drop-down menu in the ROI Toolbar

Whenever you create new ROI Groups they are added to the ROI Group drop-down menu.



ROI Groups are stored with the ROI in the local Database Folder at the close of the Series and reappear with the ROI at the reopening of the Series.



ROI Groups are created either manually or automatically by various Protocols (see Protocol Addendum).

#### 14.7.21.1 Create ROI Group



To create a ROI Group you must have already created at least one ROI. The ROI Group drop-down menu will not appear until you have done so.

- Create at least 1 desired ROI
- Click on the ROI Groups drop-down menu

- Click on '<...>'
- Type a name value in the 'New' field
- Click 'Create'. The New Group name is added to the ROI Group List
- Initially, no ROI is selected in the New Group. In the 'ROI' area on the right-hand side of the window, click on the corresponding checkboxes to select the ROI you wish to add to the New Group
- If you wish to create other groups, repeat the previous steps
- Click 'Close' to exit the ROI creation window.

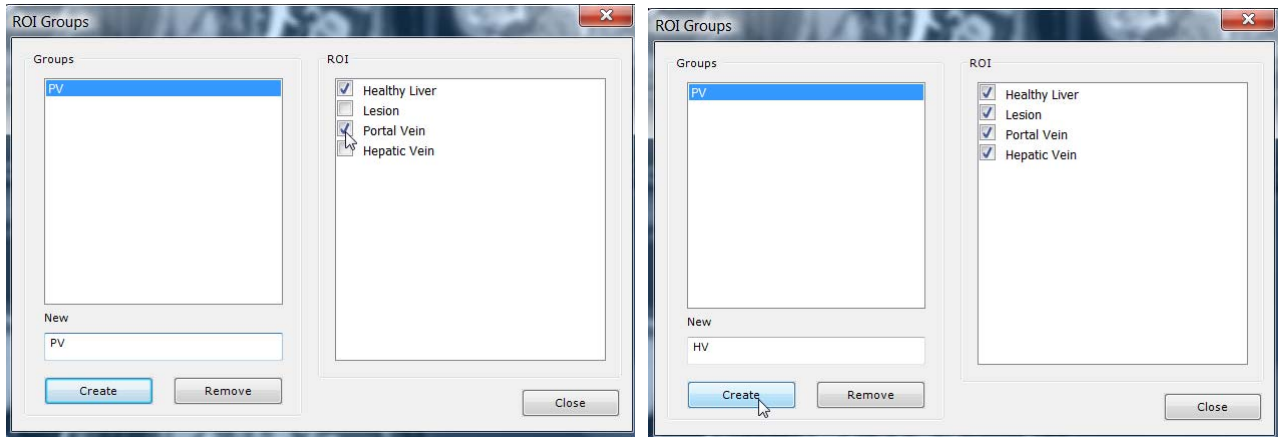


Figure 14-101 Create several ROI Groups

#### 14.7.21.2 Selecting ROI Groups for display

- To select a ROI Group, click on your desired Group in the ROI Group drop-down menu.

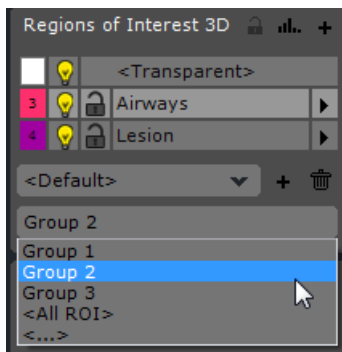


Figure 14-102 Select ROI Group



When you select a ROI Group, only the ROI contained in the selected Group are displayed. All other ROI are masked both in the Workspace and in the ROI List

- If a ROI is not selected in any group, select <All Regions> in the drop-down menu to display it.
- If a ROI is created while a group is selected, it is automatically added to the current ROI Group.



ROI Groups can be created, deleted or modified at any time, before or after having created the ROI.

#### 14.7.21.3 Delete ROI Group

- Select '<...>' in the ROI Group drop-down menu
- Select the desired group in the Groups list
- Click on the Remove button.

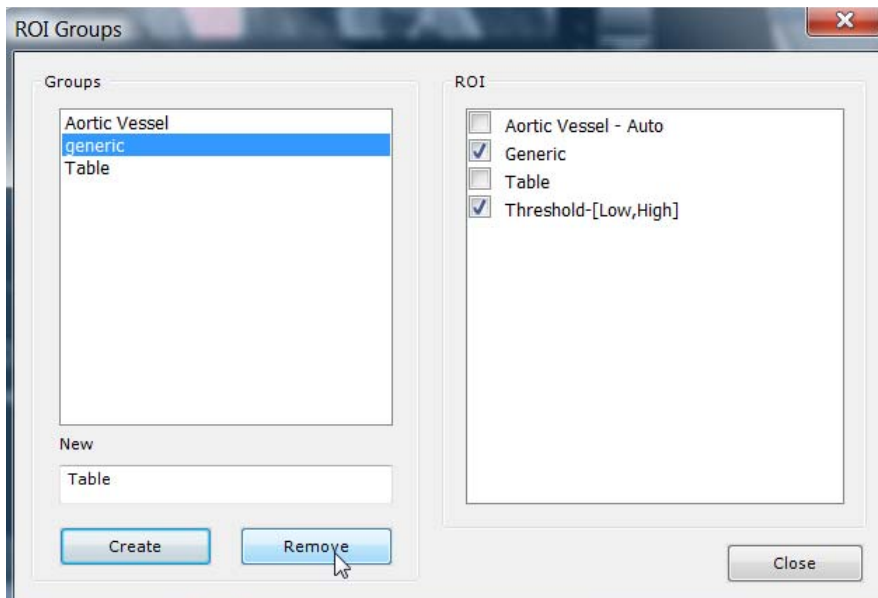


Figure 14-103 Remove ROI Group

### 14.7.22 ROI Sets: Saving and Uploading Resection Scenarios

The 'ROI Set' Feature enables you to store the state of ROI and Annotations "on-the-fly". The Feature is located in the ROI Toolbar underneath the ROI List. It consists of a pull-down menu, a '+' Create button and also a Delete function.

It can be used in the context of Liver Surgery Planning to save and view different scenarios.

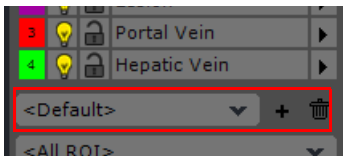


Figure 14-104 ROI Set pull-down menu and create/delete tools

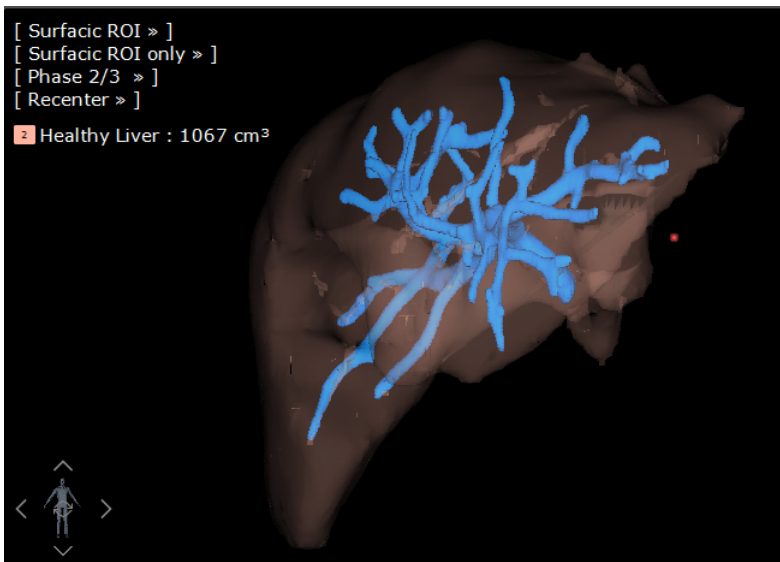


Figure 14-105 Segmented ROI

- When you are satisfied with the state of your ROI Segmentation, click the '+' Create New ROI Set button at right of the ROI Set pull-down menu.

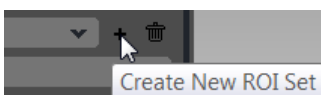


Figure 14-106 Create New ROI Set

- Type the name of your choice in the Name field at the top of the ROI Set creation window.

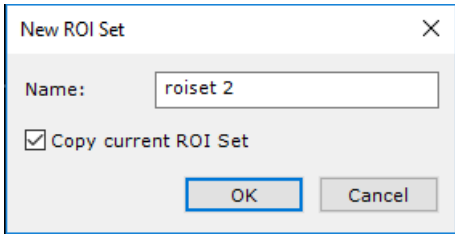


Figure 14-107 ROI Set creation window

#### 14.7.22.1 Copy current ROI Set checkbox

In the ROI creation window:

- Check the 'Copy current ROI Set' checkbox to copy all **the current ROI and Annotations** to the New ROI Set,
- Uncheck the 'Copy current ROI Set' checkbox to create a New ROI Set which contains **no ROI nor annotation**.
- Click OK to exit the ROI Set creation window.




The new ROI Set you create is, by default, not selected so you can carry on working on a 'Default' ROI Set without modifying the state of the ROI Set you have saved.



All modifications are automatically updated in the ROI Set which is currently selected in the ROI Set menu. If you do not wish to modify the currently selected ROI Set, select '<Default>' or the ROI Set of your choice in this menu.

#### 14.7.22.2 Delete ROI Set

To delete a ROI Set:

- Select the desired ROI Set in the ROI Set drop-down menu
- Click on the delete ROI Set button  at right of the ROI Set Menu
- Click 'Yes' at the next window to confirm the delete action

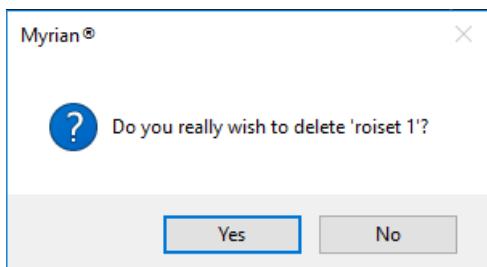


Figure 14-108 Confirm delete ROI Set

#### 14.7.23 Combined ROI Measurements

Once ROI have been created, you can use the Combined Measurements feature to compute values resulting from combinations of multiple ROI. For example, when doing liver surgery, you may wish to compute the percentage of the remaining healthy liver.



You can define customized "Fields" via XML files then have them automatically displayed and computed in Myrian® at will.

- Right-click on the Toolchest and select 'Combined Measurement'  to activate the Combined Measurement Toolbar.

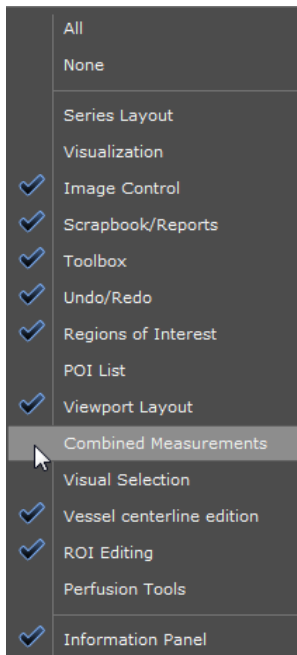


Figure 14-109 Activate the Combined Measurements Toolbar

- Click on the “+” button at top-right of the Combined Measurements Toolbar to open the Combined Measurements List

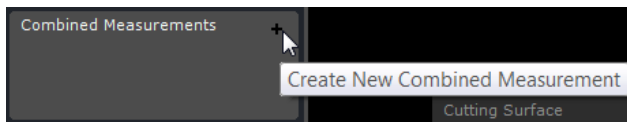



Figure 14-110 Open Combined Measurement List

- Select desired Combined Measurement in the List and desired type of measurement and click  to launch the measurement tool

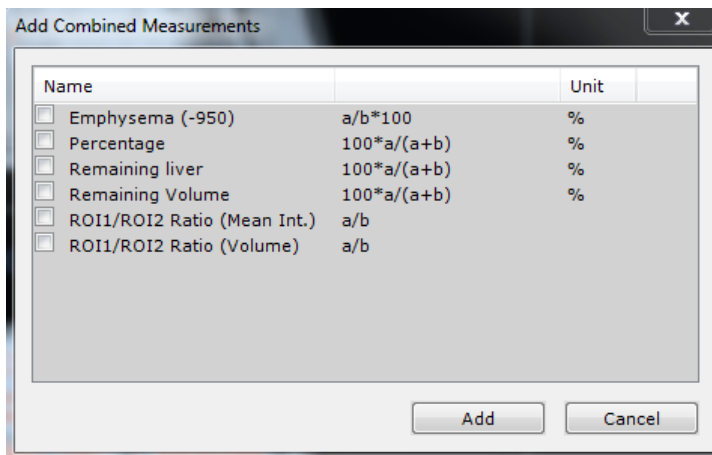




Figure 14-111 Select desired Combined Measurements

---

 The software attempts to automatically determine which ROI are linked with the ‘variable’ values contained in each field, however this may not always be possible in case where there are several ROI matching the same variable or ROI linked to a variable are not present.

---

 If the software fails to link a ROI to a variable, a question mark (“?”) is displayed next to the Combined Measurement

concerned. In such cases you must manually designate ROI in the Combined Measure Parameter dialog box.

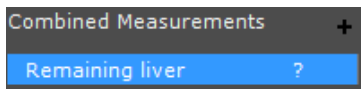


Figure 14-112 Error linking ROI to variable

The Combined Measurement Parameters dialog box enables configuration of the Combined Measurement by double clicking on the Combined Measurement, or using the context menu of the list of Combined Measurements.

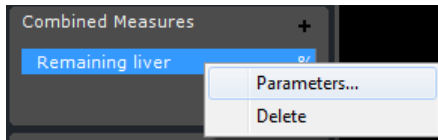


Figure 14-113 Access to the Combined Measure Parameters

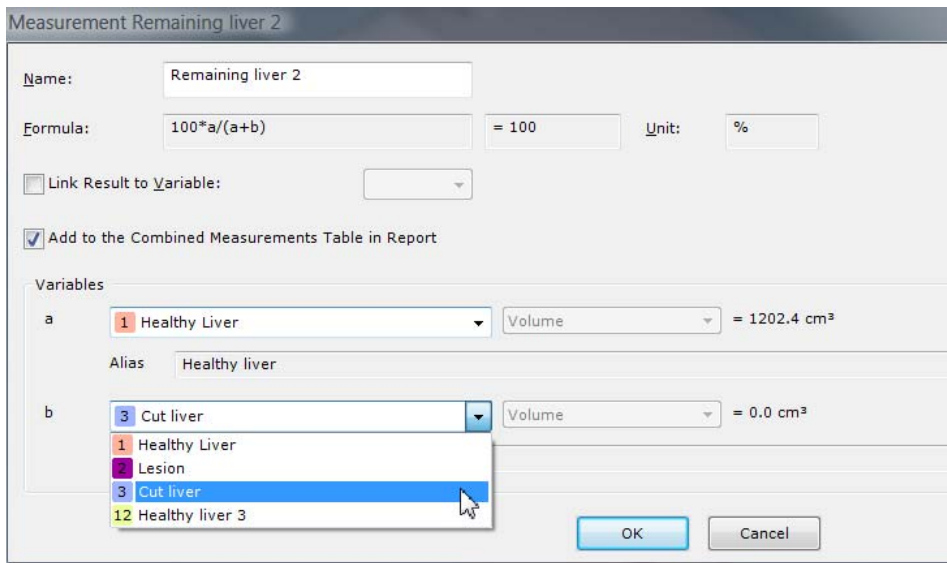


Figure 14-114 Select appropriate ROI in Combined Measurements Parameters Window

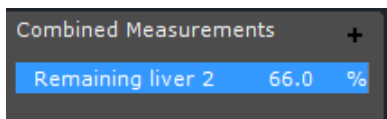


Figure 14-115 Combined Measurement Result



All the measurements defined in the 'Combined Measurements' screen are stored with the ROI data whenever the Series is closed.



If any Series containing Combined Measurements are closed they be reloaded at the next reopening of the Series concerned.



When using Combined Measurements, you must be aware that errors, inconsistencies or mistakes may arise due to the fact that they are configurable. It may therefore occur that a given factory preset may no longer be configured according to its original parameters.

### 14.7.23.1 Advanced and Combined ROI Measurements

You can view a comprehensive list of Advanced and Combined ROI Measurements in the Advanced Measurements and Histogram Window.

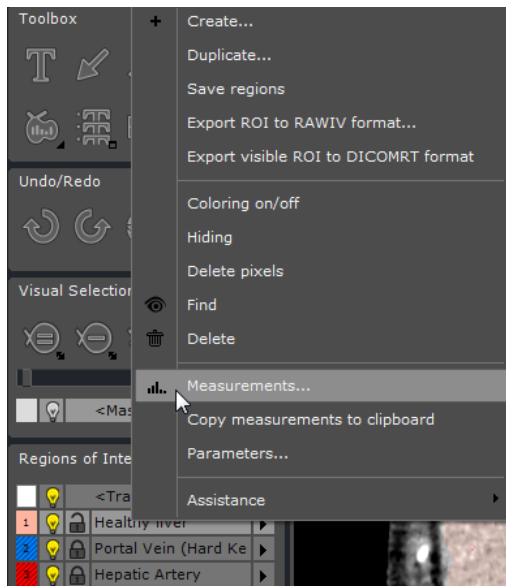


Figure 14-116 Display Advanced Measurements Option in the ROI List Context Menu

The Advanced Measurements and ROI Histogram window opens listing all available advanced and combined ROI measurements.

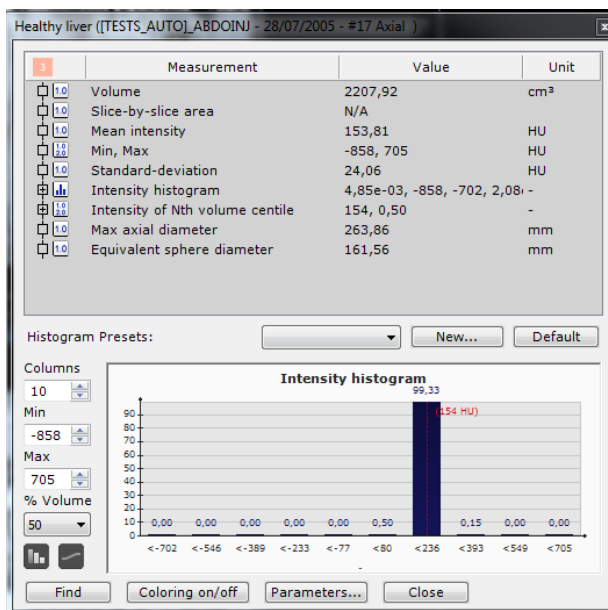


Figure 14-117 Advanced ROI Measurements



Use the scrollbar at right of the Measurement List to view hidden parts of the List.



Drag the resize arrows which appear when you hover over the sides of the Window to resize the ROI Histogram screen.

### 14.7.23.2 Combined Measurements in Reports

Combined Measurements are also included to the "Measurements" section of Reports



## MEASUREMENTS

Series 3/ Arterial and Portal Phases

ROI	Volume (cm <sup>3</sup> )	Average Intensity
Healthy Liver	772 (96.0 % / 804)	73.3
Lesion	5.782	44.4
Cut liver	398	72.6
Healthy liver 4	32.4 (4.0 % / 804)	72.7

Combined Measurements	Result	Formula
Remaining liver 2	66.0 %	$100 * a / (a + b)$
		a = Healthy Liver [1], Volume (cm <sup>3</sup> )
		b = Cut liver [3], Volume (cm <sup>3</sup> )

Figure 14-118 Combined Measurement result in Report



Only computable Combined Measurements are included in Reports.

### 14.7.24 Updating ROI

- **Regions of Interest (ROI)** are automatically updated and displayed in the 3D views. Changes in ROI Color or visibility are automatically updated.



Press 'R' keyboard key to toggle ROI display on/off.



Press the 'F2' keyboard function key to force update of the 3D view after any change has been performed.

### 14.7.25 Multiple ROI Selection

You can select multiple ROI in the Regions of Interest Toolbar and apply various commands to all selected ROI simultaneously. To select one or more ROI in the ROI list:

- Click on a ROI in the ROI Toolbar to make it active.
- Hold CTRL and click on the desired ROI to select multiple ROI.



The Active ROI is affected by all ROI Edition Tools.



Only one ROI is active at any one time.



The background color of the Active ROI is light gray in the ROI Toolbox.



The text color of multiple ROI selection is in white in the ROI toolbox.



Click again on a selected ROI while holding down the CTRL key to deselect it from the group.

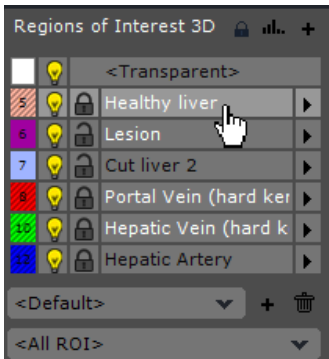


Figure 14-119 Multiple ROI selection: 'Healthy Liver' is the active ROI



Whenever you select multiple ROI, the Active ROI is also selected by default. Hold CTRL+click to deselect it.



When ROI are deselected, the text appears in black.

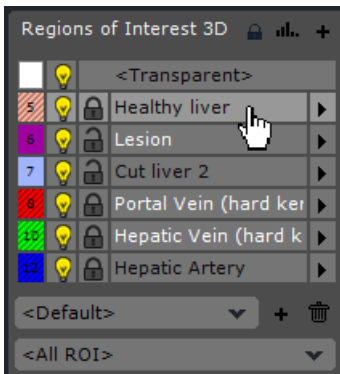


Figure 14-120 Multiple ROI selection: the active ROI ('Healthy Liver') is deselected

- Right-click on any ROI in the multiple ROI selection to access the following options in the context menu:

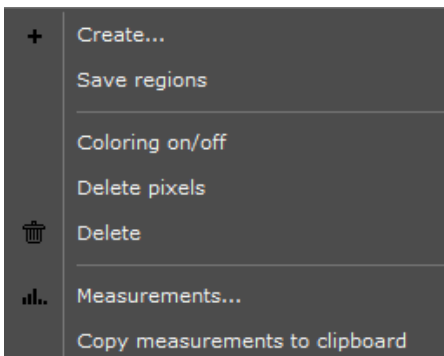


Figure 14-121 Multiple ROI selection context menu

### 14.7.25.1 Multiphase multiple ROI selection

If any "Undetermined" Multiphase ROI are selected as "Multiple ROI", the context menu is the following:

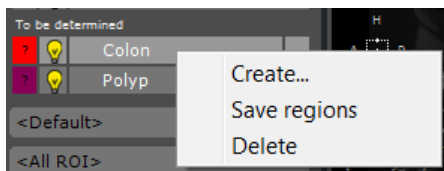


Figure 14-122 Context options available for Undetermined ROI

### 14.7.26 Apply to ROI

The 'Apply to ROI' feature which can be accessed via the Coloration Palettes menu Coloration Palettes menu showing 'Apply to ROI' feature, enables adjustment of how the Tissue Coloration presets affect display of ROI in the following ways:

- All ROIs except the transparent ROI are colored according to the active coloration preset
- The transparent ROI remains in 'Average' rendering mode
- All attached ROIs are in Surfacic mode

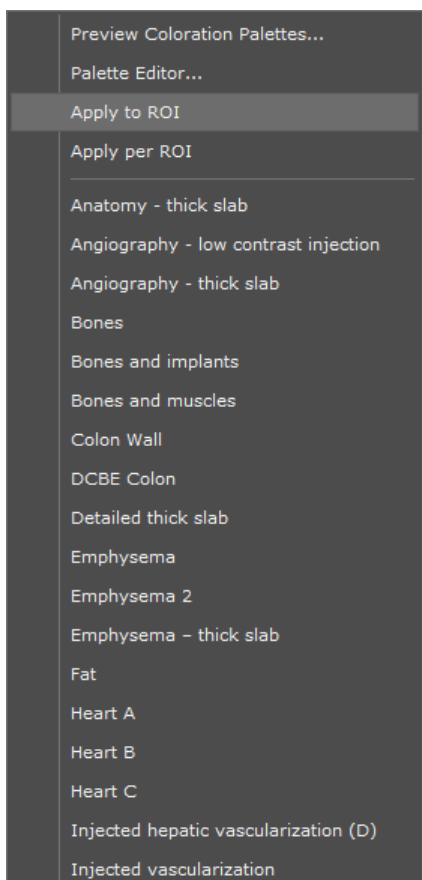


Figure 14-123 Coloration Palette menu showing the 'Apply to ROI' feature



In 'Apply to ROI' mode, the tissue coloration palette applied to the ROI can be modified by holding down the ALT key while using the Windowing tool.

### 14.7.27 Apply per ROI

A feature named "Apply per ROI" is available for 3D Views from the Tissue Coloration menu immediately below "Apply to ROI" in the Coloration Palette Menu when in Tissue Coloration Mode

This mode renders each ROI with its own Palette selected from the Coloration Palette Menu and associated to the active ROI in the ROI list. This mode is available in Whole Volume and Volume of Interest Mode.

Each Palette can be set and/or adjusted via the ROI Parameters dialog box. By default, if no palette or an invalid palette is assigned to a ROI, the "Global View" Palette is used.

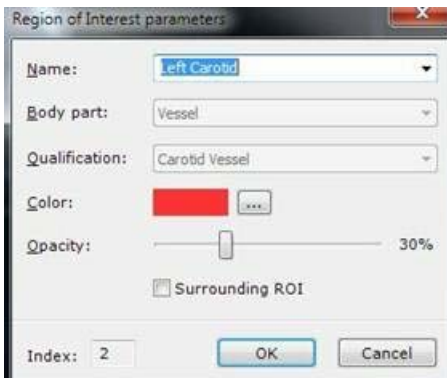


Figure 14-124 ROI Parameters screen



The active Palette is applied to the currently selected ROI.

---



Whenever a ROI is selected in the ROI List, the corresponding Palette is displayed in the Palette Menu of the 3D Viewport and the name of the ROI is indicated.

---



Whenever a Palette is modified, the Parameters are updated accordingly.

---



The Apply per ROI parameters can be set and adjusted in the Protocols.

---



The maximum number of individual Palettes is dependent upon the hardware specification of the workstation running Myrian®.

---



Palettes can be windowed separately.

---



Windowing applies to the active ROI Palette.

---

## 14.8 ROI Transposing

### 14.8.1 Overview

ROI Transposing enables you to transfer 3D ROI from one Series to another.

Typical use can be:

- Bone masking in CTA, between the non-injected and the injected Series
- ROI defined in Ytrium-perfused MR Studies transferred to CT Studies for surgery planning
- Transfer of a Late Phase Hepatic Vein ROI to a Portal Phase in order to compute Vascular Territories in the same Series for both Portal and Hepatic Vein Territories).

ROI Transposing takes into account DICOM Series alignment as well as both Rigid and Non Rigid Synchronization (Manual or Automatic).



ROI can be transferred between Views and between Phases in a Multiphase View.

---



Transposed ROI preserve the same properties as the original ROI.

---



The User should verify the pertinence and exactitude of transposed ROI and all attached information (name, dimensions, measurements, etc.).

---



Single or multiple ROI selection are both supported.

---



Only 3D ROI are supported.

---

### 14.8.2 Usage

- Open at least two series either two different Views or a Multiphase View
- Right-click on the ROI of your choice in the Regions Of Interest 3D Toolbar
- Select the desired Target Series in the "Transpose to..." submenu

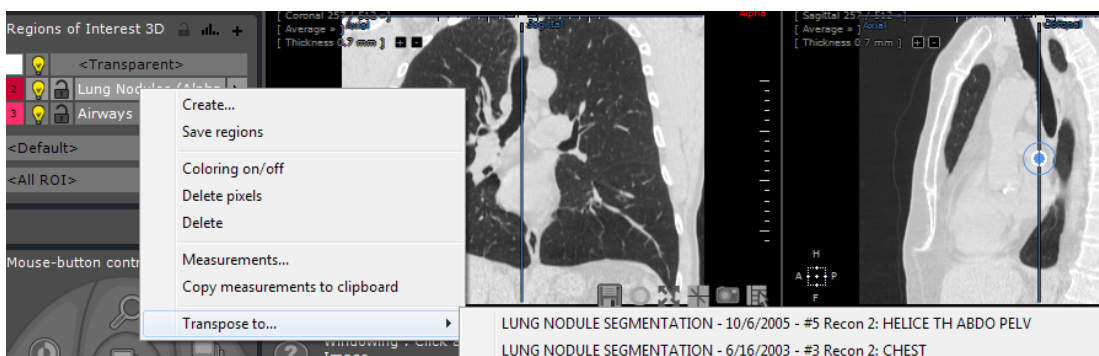


Figure 14-125 "Transpose to" option in the Context Menu

### Result

A new ROI is created in the Target Volume bearing the same Name, Color and Properties as the original.

## 14.9 Cut Simulation

### 14.9.1 Overview

This tool enables you to simulate surgical action by splitting ROI and to retrieve vital measurement data. It allows you to evaluate results of operations such as Hepatectomy after which the resulting sections can be studied as separate ROI. The tool can be used in 2D or in 3D using the Surfacic ROI Viewport.



The Cutting Surface can be used on Axial, Sagittal and Coronal Views in 2D or in 3D using the Surfacic ROI Viewport.



The Cutting Surface is not active in Oblique, CPR, Endoscopy and Filet Viewports.










3D Cutting Surface can only be traced and adjusted in the 3D Surfacic ROI Mode.



The Cutting Surface can be used to cut away anatomic zones that have been erroneously added to any ROI.



The width of the incision is adjusted by setting size of the Pen or Eraser tools.

- Click on the CutSimulator  icon to open the Cutting Surface Floating Toolbar with the following buttons:
- **'Trace a Cutting Surface'** , to draw a line freehand
- **'Perform the splitting according to the defined Cutting Surface'**  to perform the cutting
- **Display/Hide** the Cutting Surface 
- **Translate** the Cutting Surface in 3D\* 
- **Deform** the Cutting Surface in 3D\* 
- **Stretch** the 3D Cutting Surface in 3D\* 

\* Only available in the 3D Surfacic ROI Viewport

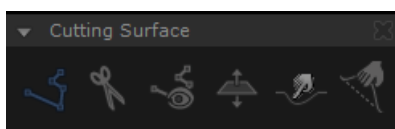



Figure 14-126 Cutting Surface Floating Toolbar

## 14.9.2 Procedure

- **Locate the range of images** within which cut should be made.
- **Select the 'Trace a Cutting Surface' tool** .
- On the first and last slices of the chosen range, **outline the surface of the cut** by drawing a line (orange colored).



The Pen stroke size defines the width of the incision line (click on the white number to modify it).

---



Both anchors (line endpoints) can be moved freely to adjust the line. Move the midpoint which then becomes an inflexion point to turn it into a curve (this creates a new anchor). By moving the center of one of these two new line segments, further points of inflexion are created which can be adjusted as desired.

---

- Once curves have been defined on any slice, the procedure can be repeated on any other slice. The application will interpolate lines across slices. You can correct a line curve at any time by dragging points freely or continue to add new inflexion points by moving the midpoints.
- 



Keep the cutting curves as simply as possible to avoid that the overall Cutting Surface representation and subsequent manipulation become overly complex or cumbersome.

---



To increase/decrease the Cutting Surface to a greater/smaller number of slices, navigate to the first or last slice of the current cutting range and use the Left and Right Keyboard Arrow keys to augment/diminish the slice range of the cutting zone by moving the selected cutting line up one slice or down one slice.

---



To select and jump to the first/last solid surface line, use the Home Key or End Key on your keyboard.

---



To jump to the previous/next cutting line, use the Up/Down Arrow Keys.

---

- Repeat the above steps as desired
  - Click on 'Perform the splitting according to the Cutting Surface defined'.
  - You may now remove one of the split parts from the current ROI by using the fill tool with the transparent ROI selected, or by assigning it to another ROI.
- 



If you draw a single orange line, the cut will be executed performed on all slices along this same line.

---

## Example

An example of Cutting Surface usage is illustrated in the following figures. The split sections (ROI) have been isolated and defined.

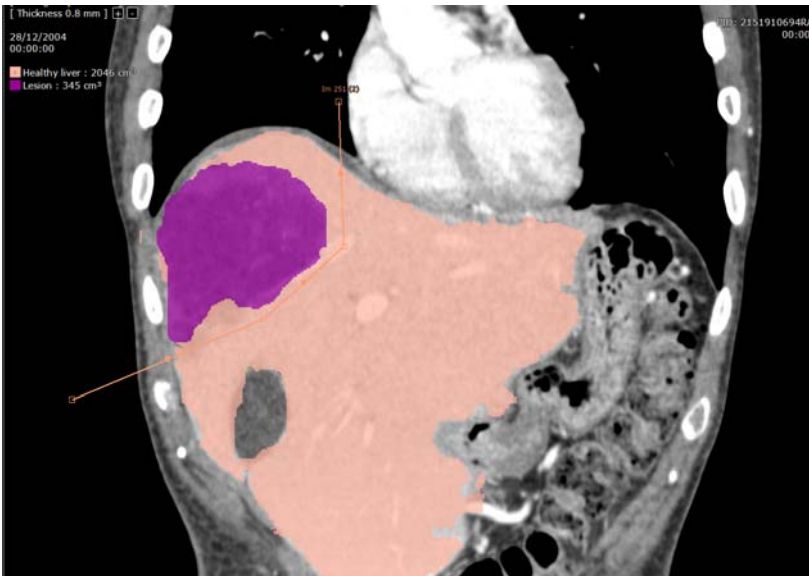


Figure 14-127 Example of Cutting Surface: describing the intended cut

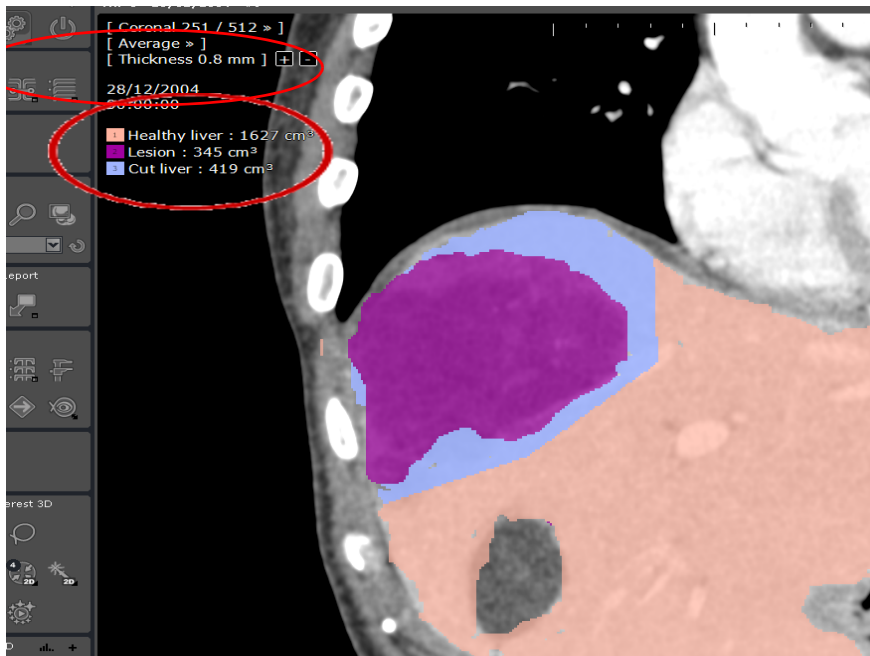




Figure 14-128 Example of Cutting Surface tool: after performing the cut

Once the cut has been performed, the volume of the cut anatomical structure is displayed top-left of the screen (circled red in the above illustration).

### 14.9.3 3D Cutting Surface

The Cutting Surface can also be used directly in 3D. It can be entirely created or adjusted in the 3D Surfacic ROI Mode:

- Select "Surfacic ROI" mode in the views menu at top-left of any Viewport
- Select Liver ROI in the ROI list
- Click on the CutSimulator button 
- Click on 'Trace a Cutting Surface'  in the floating menu (if not already active)
- Trace a line describing the approximate line of desired cut
- Use the SHIFT key to rotate your anatomical zone as desired trace the line around completely around the volume of your target zone





Press the 'Backspace' key to cancel a line tracing.

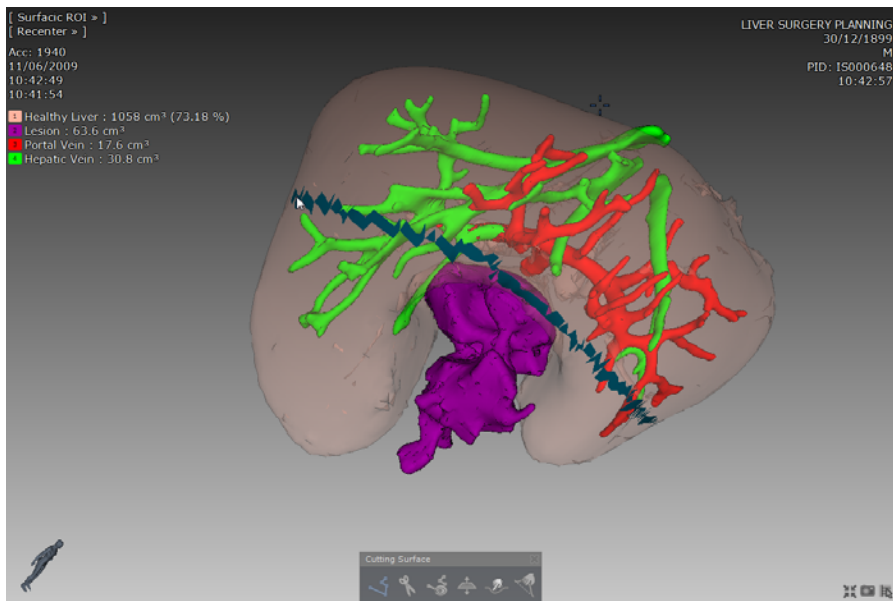


Figure 14-129 Trace the desired line of Cut

- Press 'Enter' to validate the 'cut'

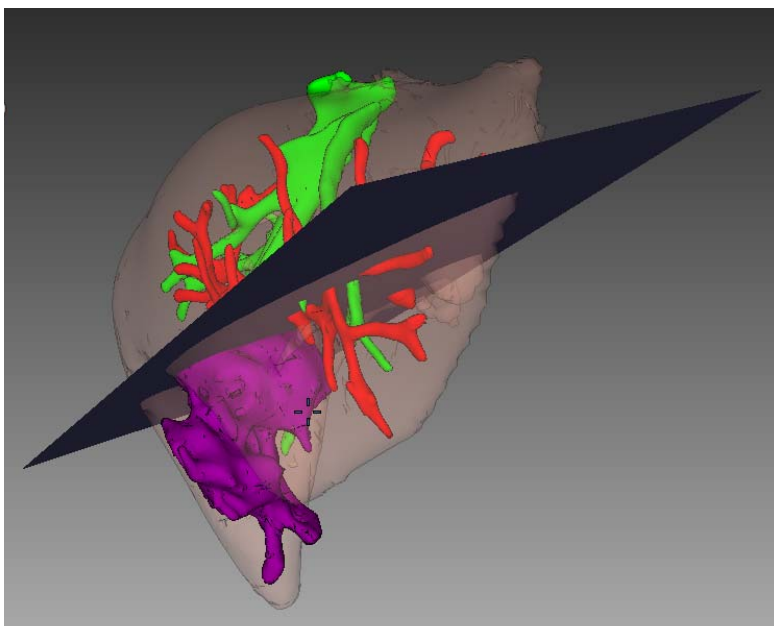


Figure 14-130 Initial 3D Cutting Surface calculated



The average line of cut is computed.

### 14.9.3.1 Adjustment of a 3D Cutting Surface

There are 3 tools available to adjust your Cutting Surface in 3D:

- Translate Cutting Surface (3D)
- Deform Cutting Surface (3D)
- Stretch Cutting Surface (3D)



Once the Cutting Surface has been modified in 3D, it can no longer be modified in 2D and vice-versa.



Both in 2D and in 3D you must make sure that your Cutting Surface line passes the whole way through your target ROI.

### 14.9.3.2 Stretch/Translate the Cutting Surface (3D)



- Select the Stretch Cutting Surface (3D) tool to resize the cutting surface
- Click and drag on any edges that do not pass the whole way through your ROI to stretch it or reduce it all the way across

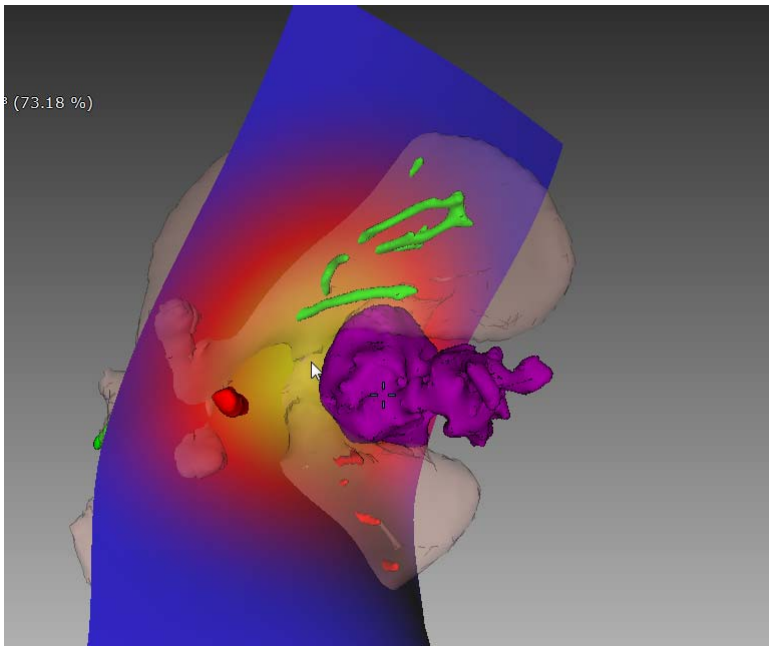


- Select the Translate Cutting Surface (3D) tool to move the Surface to adjust its position

### 14.9.3.3 Deform the Cutting Surface (3D)



- Click on the Deform Cutting Surface (3D) button

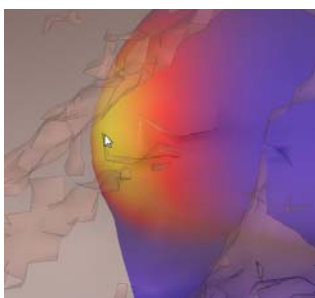


1. Hover over the portion of the Cutting Surface you wish to deform. The Deformation Zone color changes to orange to display the size of the Zone that will be modified
2. Drag the mouse to Push/Pull the Deformation Zone in your desired direction.

Figure 14-131 Deform Cutting Surface (3D)



Press the ALT key and drag the mouse to increase/decrease the size of the Deformation Zone.



3. Adjust Deformation Zone

Figure 14-132 Fine adjust Deformation Zone

### 14.9.3.4 Simulate the hepatectomy

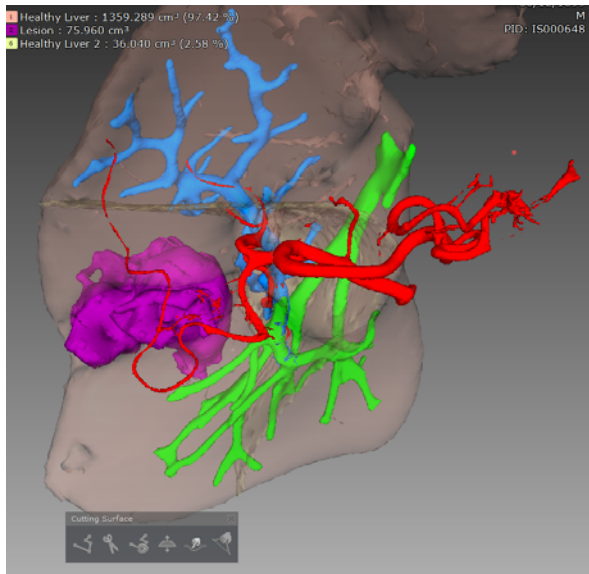



Figure 14-133 Split ROI

4. Click the 'Split ROI' button  to simulate the Surgical Action

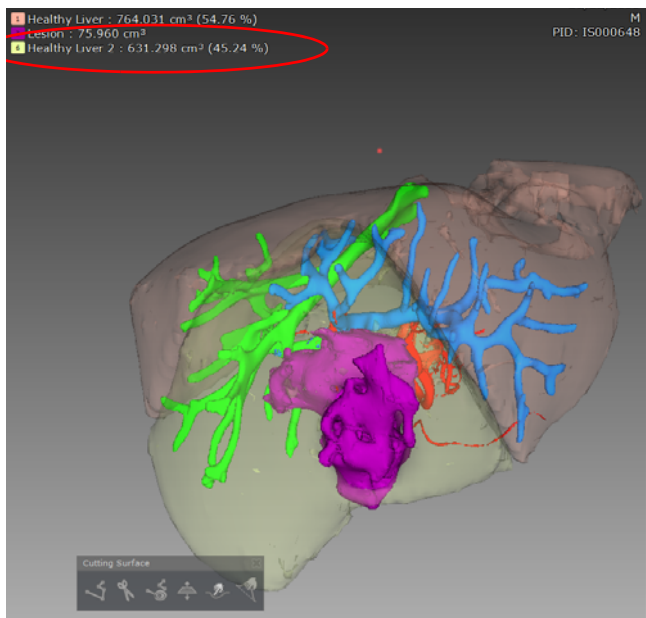



Figure 14-134 After splitting the ROI: the volumes of both Healthy Liver and cut liver (Healthy Liver 2) ROI are displayed both in cubic centimetres and as a percentage

5. Click in the liver part to reset (select the Liver ROI in the ROI list beforehand) using the automatically selected 'Fill 3D' button 



If you have the ROI Set option activated, create a ROI Set to save your Resection Scenario for later reference (see Section 14.7.7 for further detail).

## 14.10 Advanced MRI protocol functionalities

Unlike the Standard MRI protocol, some MRI dedicated protocols offer optimized viewing and analysis capabilities and output volume calculation.

These viewers include advanced common functionalities such as:

- **Preselection of Input volumes** within a category selection window
- **Specific Volume processor** which according to the selected protocol and the required input series category, enable to generate new volumes or parametric maps. All Sequence post-processing operations which are listed in the bottom part of the category selection window of the selected protocol are performed by those Volume Processors (VOP).
- **Specifically adapted visualization modes and layouts**



Each VOP has its own parameter window and specific settings and some of these VOPs have their own dedicated protocol.

These features apply to the following protocols:

- Subtraction protocol (available in the Standard MRI family)
- ADC Protocol (available in the Standard MRI family)
- WI\_WO\_TTP\_AUC protocol (available in the Standard MRI family)
- Liver MRI protocol (available in the Standard MRI family)
- Ovarian masses and Cervix protocols (both protocols are available in the Female Pelvis protocol family)

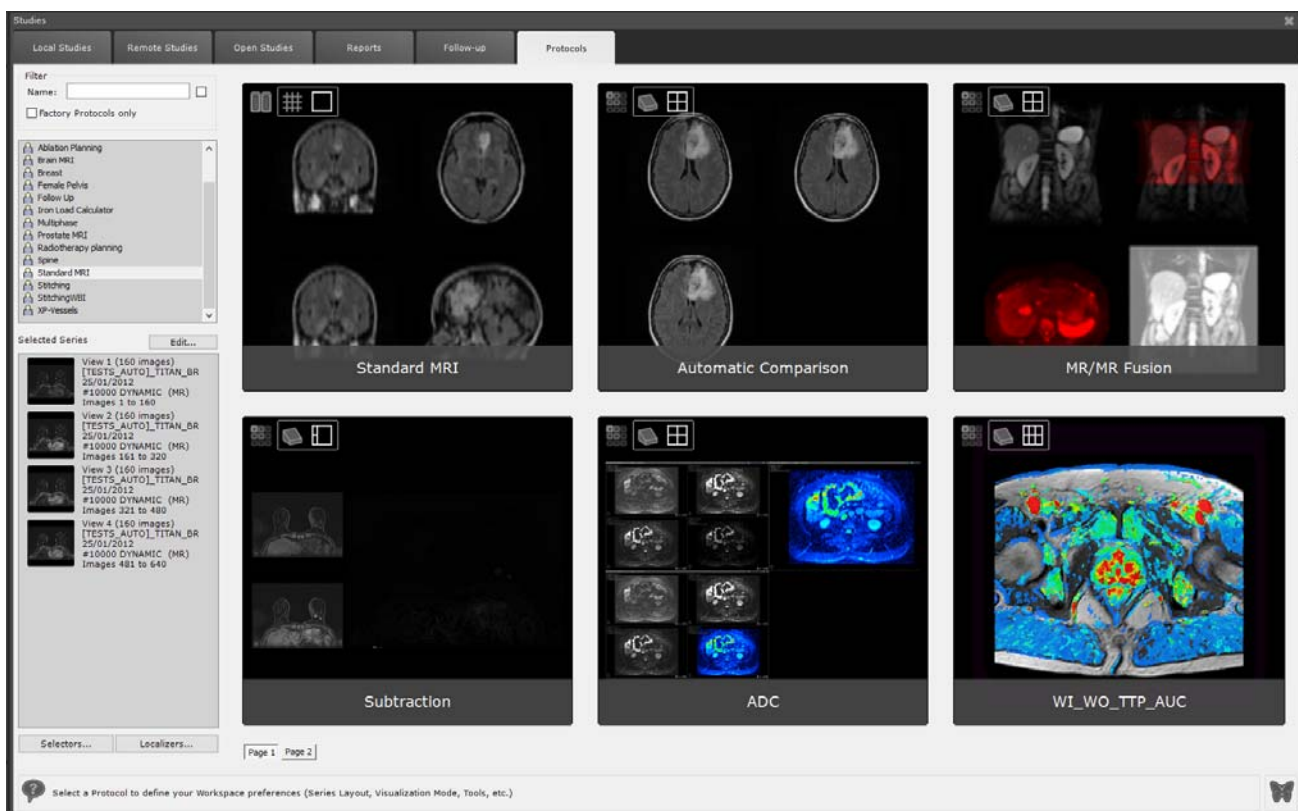


Figure 14-135 Standard MRI protocols

Some of these protocols will be described in the following sections of this chapter.

### 14.10.1 Series preselection

- Select a MRI study from the study list

When loading MRI series with any of the here-above mentioned protocols, a **category selector window** appears on the screen in which input series extracted from the selected study have been pre-identified and dispatched according to the

available preset category.

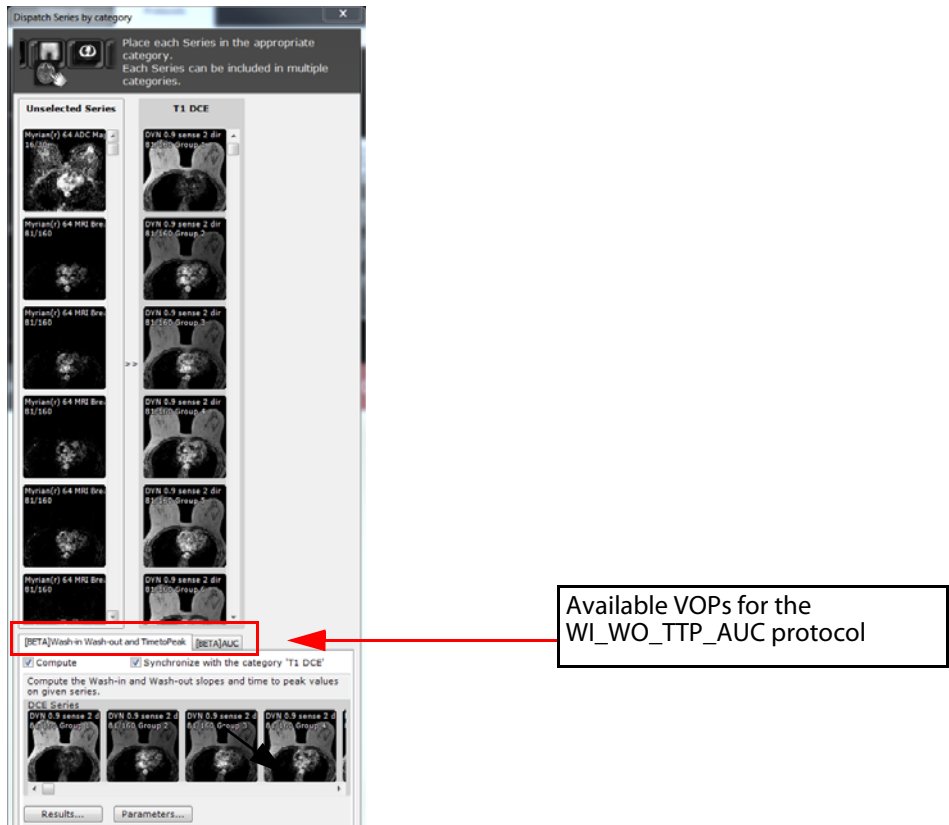


Figure 14-136 Validate series selection for the WI\_WO\_TTP\_AUC protocol

- Check that these pre-identified input series are correctly dispatched in the preset category for the selected protocol and associated VOP
- Where applicable, adjust series selection by drag-and-drop
- Click 'Validate'



The VOP always checks that the series match the VOP requirements. If the selected series are inappropriate, a message is automatically displayed and the protocol cannot open.



Each preset column includes a description field indicating the series type (diffusion, dynamic T1, T1, T2...)



It may happen that series dispatch does not occur requiring a manual operation: to save time, if applicable, you can select multiple series simultaneously from the 'Unselected Series' category: press **CTRL + click** on the first series of your choice then scroll down the list until the last series you wish to select and press **SHIFT + click**: all series in between will be highlighted and selected at once, ready to be dragged and dropped into desired category



- If you wish to perform any do-it-yourself selection of the series to be taken into account in any calculation, do as follow:
- Uncheck the "Synchronize with the category..." checkbox
  - Drag and drop the series from the above section to the Unselected series

## 14.10.2 Sequence post-processing

All Sequence post processing operations which are listed in the bottom part of the category selection window are performed by specific Volume Processor (VOP). Those are:

- Wash-In Wash-Out and TimeToPeak
- AUC (Area Under the Curve)
- Raw Subtraction
- ADC map (by linear regression)

By default, all computation options (i.e. ADC Map, Raw Subtraction...) are activated when those have not been previously performed on the selected series.

---



For each sequence post processing, parameters defined within the protocol are applied. Nevertheless, you can modify those default parameters at that stage or later in your workflow.

---

Once the series selection and VOP parameters are validated, the series are loaded.

### 14.10.2.1 DWI sequence post-processing

---



Diffusion series are series which verify the following conditions:

- Series are of MR modality
  - Series from which a B value can be retrieved from the DICOM fields
  - Series are not ADC map (although ADC maps often contain a B value)
- 



Before proceeding to the workspace, always check that all Diffusion series have been adequately detected and that their associated B value is relevant. Myrian® integrates a set of security and checking mechanisms to limit errors but a systematic control by a trained professional is mandatory.

---

#### 14.10.2.1.1 Compute the ADC map

If, when loading the MR study into for example the ADC protocol, diffusion series (encoded with a B-value) have been pre-identified and the 'Compute' option of the 'ADC map' is activated, the ADC map is generated when clicking 'Validate'.

---



At least **two diffusion series** are required to compute an ADC map. If the Diffusion column does not contain at least two series, uncheck the 'Compute' option in the ADC map tab.

---

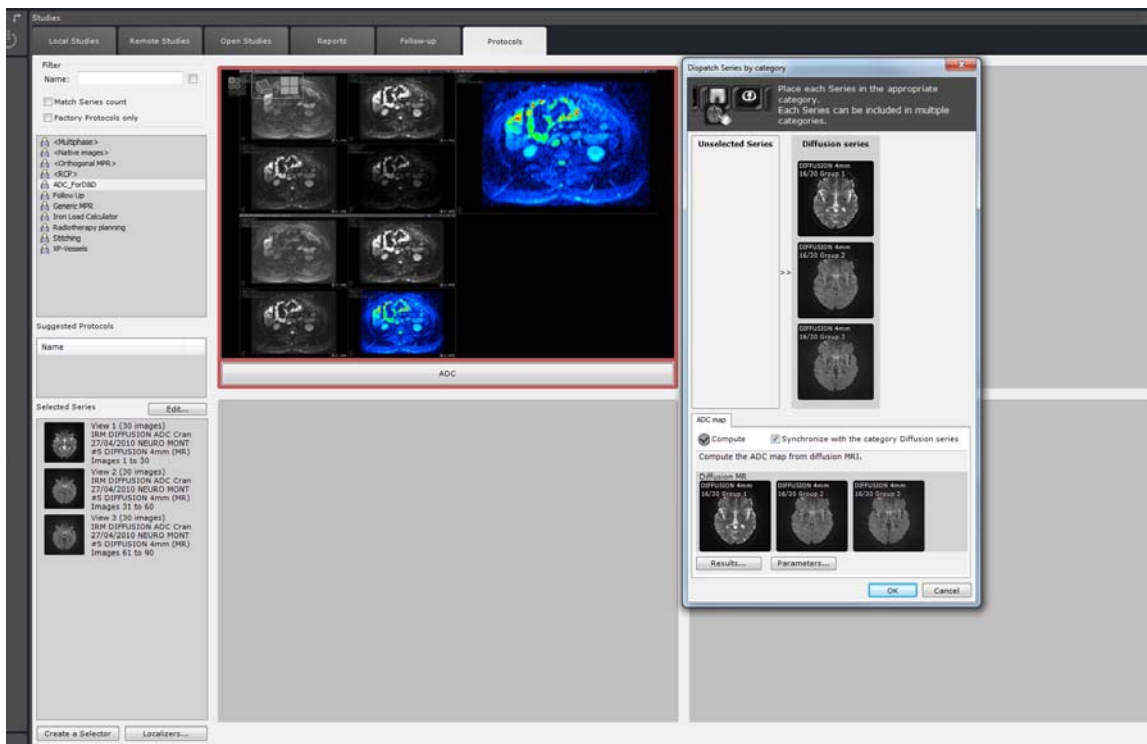
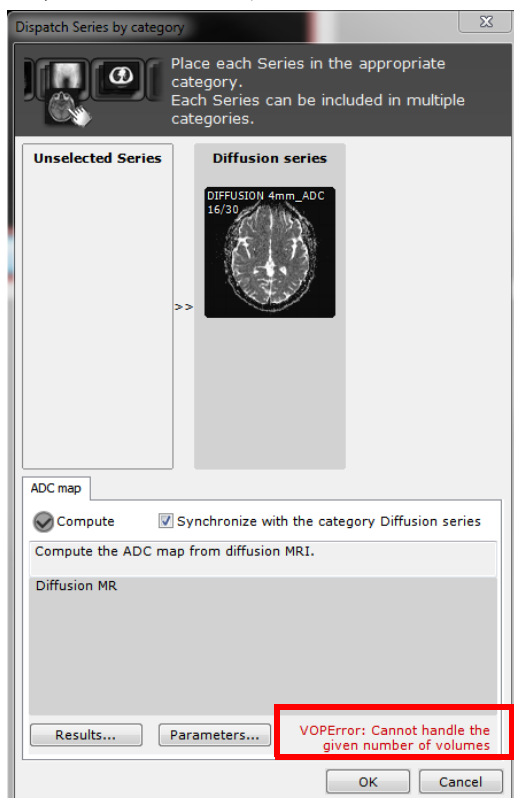


Figure 14-137 Opening ADC protocol

However, if applicable, drag & drop series from the 'Unselected series' column to the 'Diffusion series' column.



Whenever an error is detected (i.e. missing or invalid B value, or insufficient number of series), an informative error or warning message is generated preventing the computation of the ADC map and requiring an action from you to solve it. Only then will the computation launch.



Display of an error message indicating that ADC computation requires at least 2 diffusion MR series

In order to proceed with the ADC map computation, you need to **modify manually the input series parameters** (see Section 14.10.2.1.2) **and/or the selected series**.





If one input series is detected as an ADC map, the following message is displayed: 'An ADC map is not a Diffusion MR'. If that occurs, you need to remove the ADC map wrongly selected as diffusion series from the input series.



Inappropriate series which are not recognized as diffusion MRI cannot be opened in the ADC protocol



By default, series from the 'Diffusion' Category are preselected in the Diffusion MR section for the ADC Map calculation

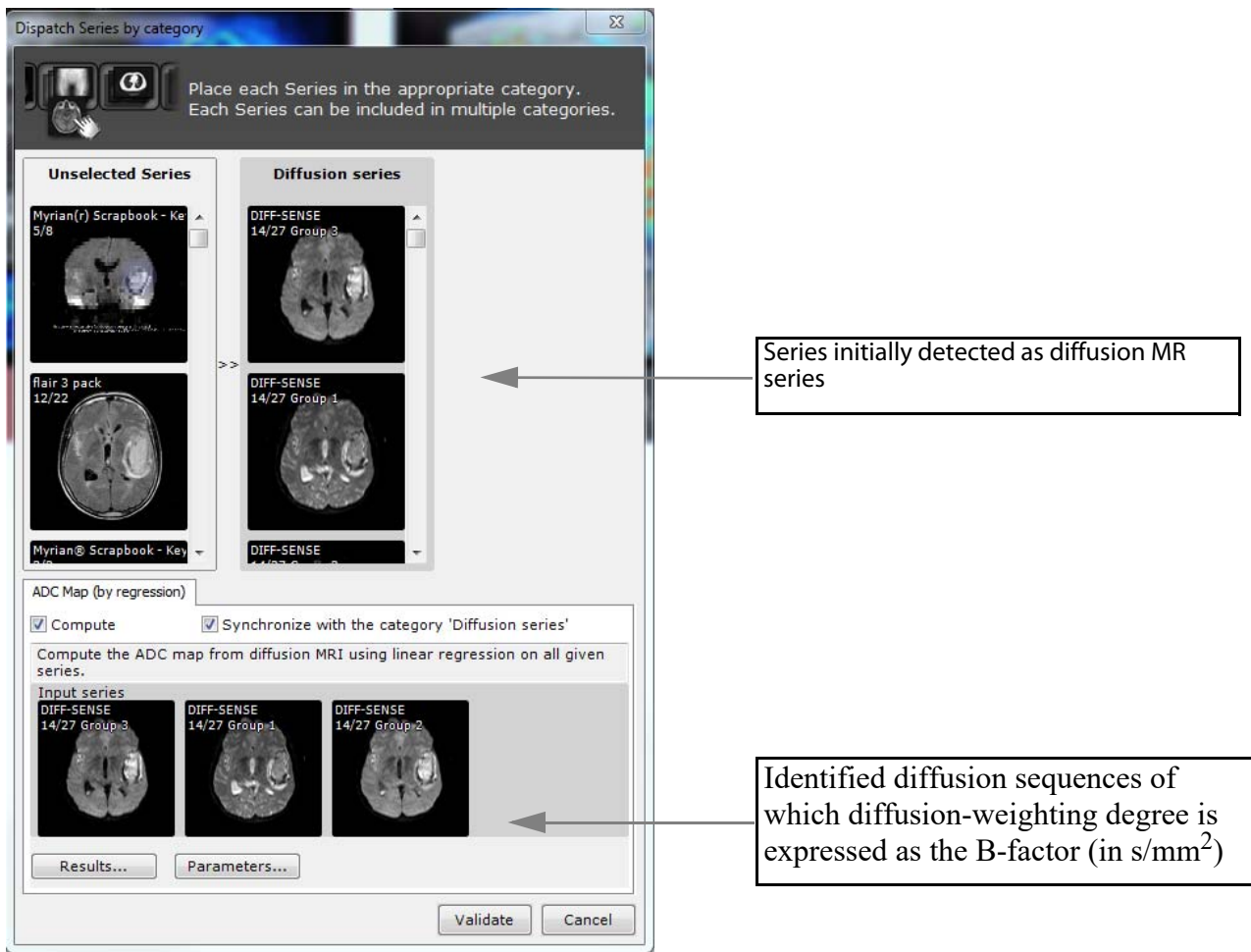


Figure 14-138 Launching ADC map calculation

#### 14.10.2.1.2 Edit ADC map input parameters

Before proceeding with the ADC mapping of the selected MR diffusion series, you can if required, edit the ADC map parameters from the 'Dispatch Series by category' window:



B value parameters are automatically initialized from the DICOM fields when possible. However it may occur that B values are incorrect or cannot be initialized.

- Click on 'Parameters'

The following window opens:



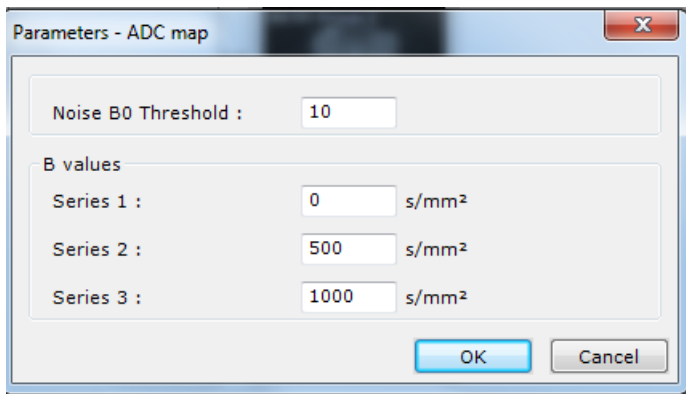


Figure 14-139 Defining B values for each selected input series

- Manually enter the correct B values of the selected input series then click OK



The number of displayed B value fields depends on the current number of selected series.

Once series have been selected and configured:

- Click '**Validate**' in the 'Dispatch by category' window to generate the ADC map.



Perform the following actions if the ADC Map series have been previously generated: In the ADC Map tab, click on the 'Results...' button and in the Existing results window, unselect the series previously generated then press OK.

#### 14.10.2.2 DCE sequence post-processing



According to the manufacturer, it may happen that the correct acquisition times of dynamic MRI series cannot be read in DICOM tag AcquisitionTime (0008,0032). In that case, a 'Check the Acquisition Times' dialog box pops up (see Section 4.6.9.5 for detailed information) as soon as a computation involving those series is invoked.

##### 14.10.2.2.1 Compute Raw subtraction



A dedicated protocol called **Subtraction protocol** is available from the Standard MRI protocol family.

Computing the subtraction between series is particularly relevant when several acquisitions have been done after the injection of a contrast agent. In this context, the subtracted series will allow better visualization of the tissues that take contrast.

If, when loading the MR study, Dynamic series have been pre-identified and the 'Compute' option of the 'Raw Subtraction' is activated, the Volume Processor generates the Subtracted series when clicking 'Validate'.



At least **two DCE MRI series** are required to compute Raw Subtraction.



By default, series from the 'T1 DCE' category are preselected in the Input series section for the Raw Subtraction calculation.

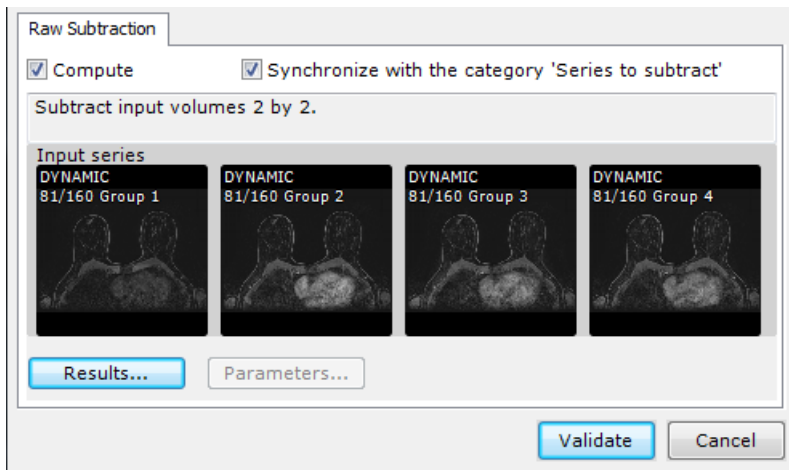


Figure 14-140 Computing Raw Subtraction from T1 DCE series

#### 14.10.2.2.2 Compute WI\_WO\_TTP parametric maps



The WI\_WO\_TTP\_AUC protocol is specifically dedicated to parametric map computation



Inappropriate series (see Section 14.10.2.2.3) which are not recognized as MRI-DCE series cannot be opened in the WI-WO-TTP-AUC protocol

#### Description

Time-Intensity parametric maps constitute semi-quantitative perfusion measures particularly useful for quickly identifying suspect lesions.

Those color maps which are generated for each voxel of a given Dynamic-Contrast-Enhanced series of **MR modality** (T1-weighted) allow the visualization of the dynamic enhancement of tissues (i.e. kinetic curve) over time by categorizing the Wash-out pattern of the injected contrast product.

The following parameters are calculated:

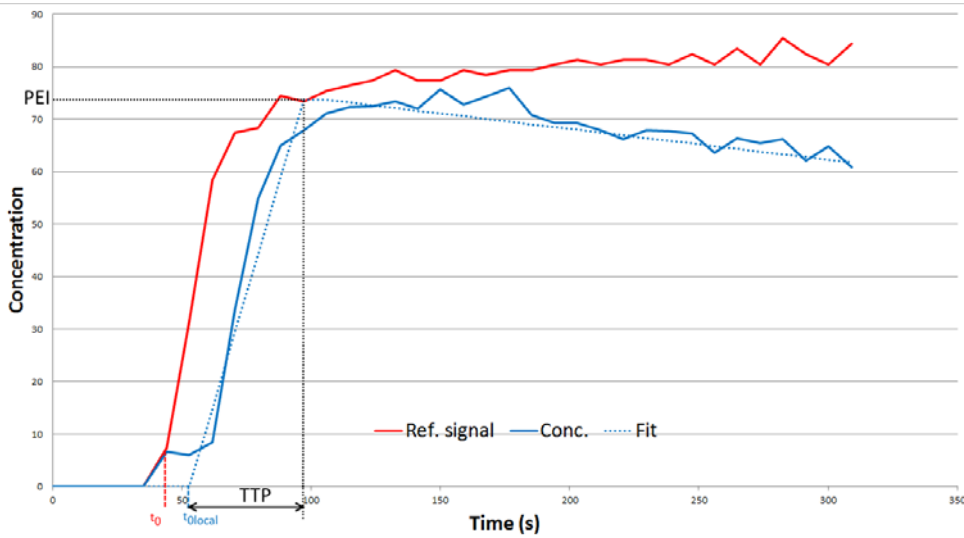
- Wash-In (WI)
- Wash-Out (WO)
- Peak Enhancement Intensity (PEI)
- Time to Peak (TTP)
- Area under the Curve (AUC)

Those perfusion parameters are calculated from the enhancement curve corresponding to the average signal intensity over time of the region of interest or pixel-by-pixel. For each parameter, a parametric map is created.



The WI, WO and TTP values are computed between  $t_0$  and the end of the acquisition

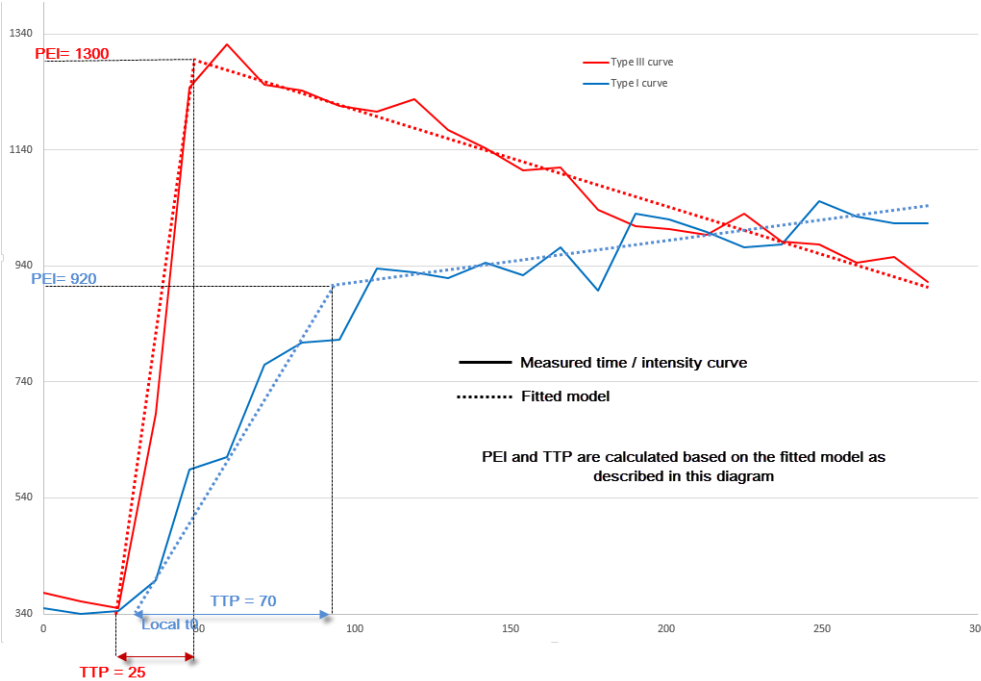
- The  $t_{0local}$  time that defines the beginning of the injection at any given point/region is computed. It may differ from the  $t_0$  on the reference signal.
- The 2 lines that best fit the concentration between  $t_{0local}$  and the end of the injection are computed.
- The Peak Enhancement Intensity (PEI) is the intersection of these 2 lines.
- The Wash-In is the slope between  $t_{0local}$  and the PEI.
- The Wash-Out is the slope after the PEI.
- The Time to Peak is the difference between  $t_{0local}$  and the PEI time.



The reference signal over time is shown in solid red, the concentration is shown in solid blue and the model fit on this concentration is shown in dotted blue.



TTP and PEI calculation methods are represented hereafter for Type III and Type I curves:



There are three types of curve pattern classified as:

- Type I (blue-coded), persistently enhancing (progressive), which is suggestive of benignity
- Type II (yellow-coded), plateau type, which has an intermediate probability for malignancy
- Type III (red-coded), washout type, which is indicative of malignancy.

The type of contrast enhancement kinetic curve (i.e., persistently enhancing, plateau, or washout) seen on dynamic contrast-enhanced MRI (DCE-MRI) is predictive of malignancy. Qualitative estimates of the type of curve are most commonly used for interpretation of DCE-MRI.

Comparing those resulting dynamic enhancement curves calculated on pixel-by-pixel or ROI basis, enables to analyze the

type of time-signal intensity curve (where the signal increases with the concentration of contrast agent after injection) and therefore to better characterize the lesion through the interpretation and analysis of the kinetic curves.

### Input series parameters

To generate those parametric maps, **at least 4 input series** are needed.

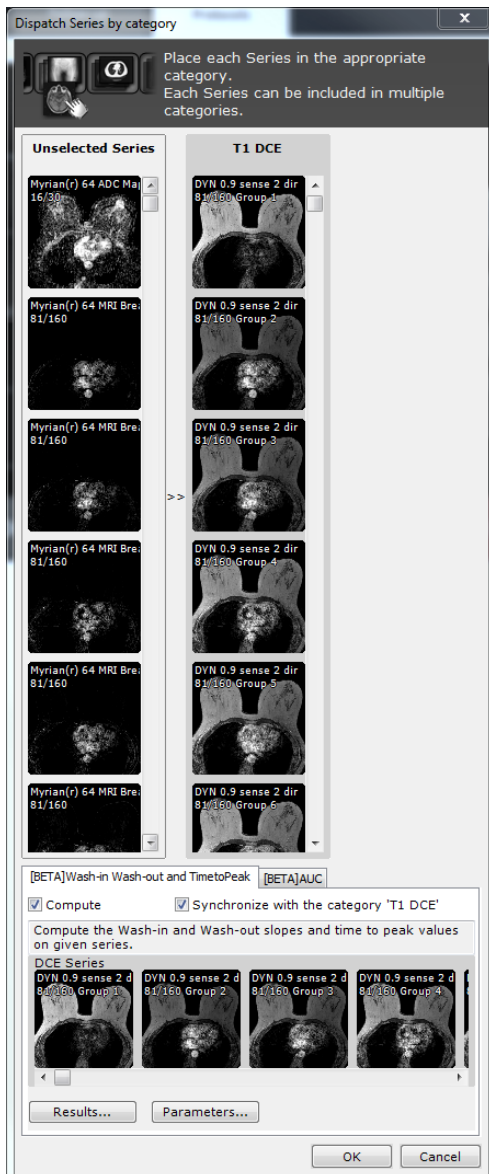


Figure 14-141 Launch Wash-In Wash-Out and Time to Peak parametric map computation from dedicated protocol



By default, series from the 'Dynamic' Category are preselected for Wash-In Wash-Out and TimeToPeak tab.

- Click on the 'Parameters...' button to open the Wash-In Wash-Out and TimeToPeak parameter window.

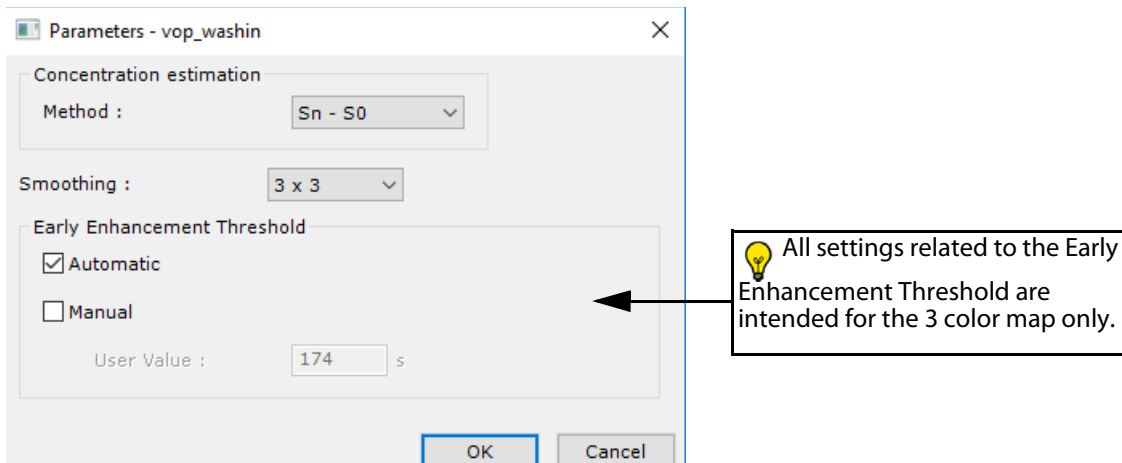


Figure 14-142 Wash-In Wash-Out and Time to Peak parameter window

From this window, you can edit the concentration computation method used by the Volume Processor to generate those parametric maps among the following:

- Sn - S0 (default method used by the protocol)
- (Sn - S0)/S0,
- Raw signal.

The Volume Processor also allows for 3 methods of spatial smoothing of signal:

- None,
- 3x3 voxels,
- 5x5 voxels.
- Press OK to validate.



Whenever an error is detected (i.e., acquisition time issue or insufficient number of input series), an informative error or warning message is generated preventing the computation of those parametric maps and requiring an action from you to solve it. Only then will the computation launch.

### 14.10.2.2.3 Compute the AUC map

#### Description

The Area Under the Curve is calculated from given Dynamic Contrast-Enhanced Imaging of **MR modality** which are automatically preselected in the AUC tab.

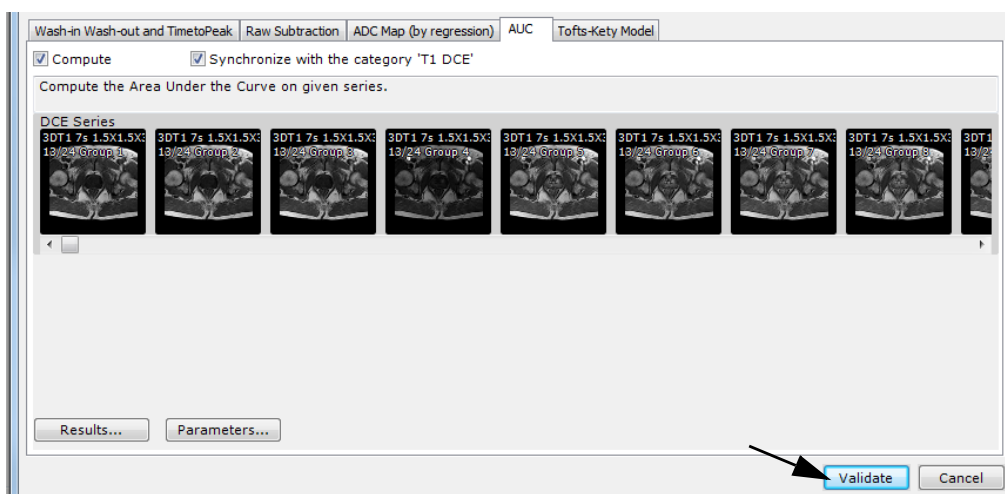


Figure 14-143 Launch AUC parametric map computation

The AUC is defined as the Area Under the Enhancement Curve between 2 times:

- The  $t_0$  time defines the beginning of the part where the area is computed. This time corresponds to the injection of the contrast product.
- The  $t_{AUC}$  time defines the end of the part where the area is computed. This time depends on the organ, the acquisition protocol...

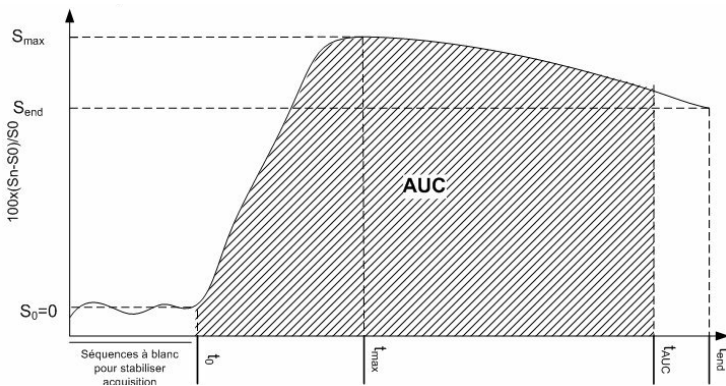


Figure 14-144 AUC value: computation definition



At least **3 input series** are required to calculate the Area Under the Curve

### Input series parameters

An AUC parameter window is available clicking on the 'Parameters...' button.

You can choose from two methods of concentration computation:

- $S_n - S_0$  (default method used by the protocol)
- $(S_n - S_0)/S_0$ .

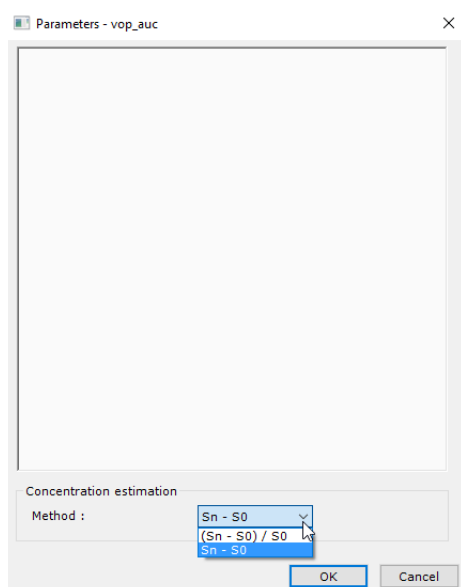


Figure 14-145 AUC parameter window

### 14.10.3 Setting Result storage

Setting options are also available from each computation tab:

- Click on the 'Results...' button from the desired computation to access the results storage configuration dialog box.
- Modify storage settings as wanted.



By default, the 'Store all computed series in the database' option is always preselected for ADC map and Raw Subtraction options.

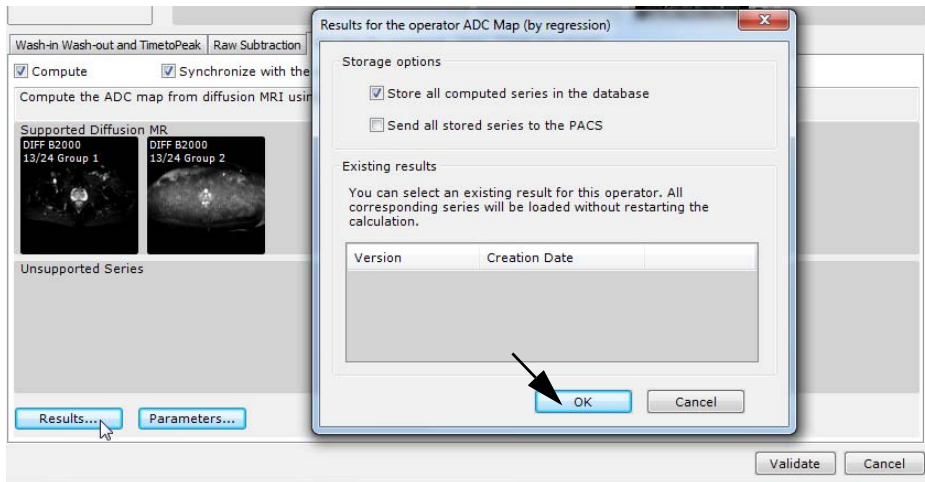


Figure 14-146 Set storage options

- Click OK

When the computation process is over, the generated series are automatically stored into Myrian® database and displayed in the 'Dispatch Series by category' window.

- Back on the 'Dispatch Series by category' window, press 'Validate' to load selected series into the selected protocol.

#### 14.10.4 Reopening the same study

- Open again the selected MRI study with the same protocol.

The Dispatch Series by Category window is displayed again.

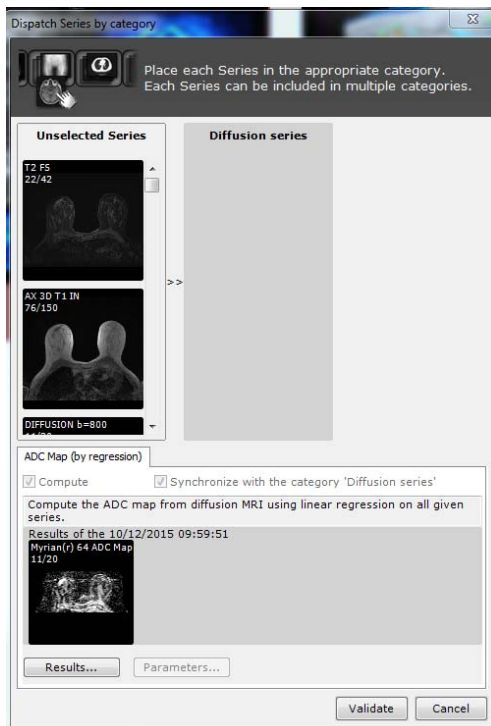


Figure 14-147 Reloading the MRI study (including pre-computed ADC map)

By default, ADC map results have been stored and come preloaded in dedicated tab.



As computations have already been performed and the corresponding results stored in the reuse table accessible from the Results button, when the same set of computations has to be performed again in the future, the (most recent) previously calculated result is reused and the actual computation options are deactivated.

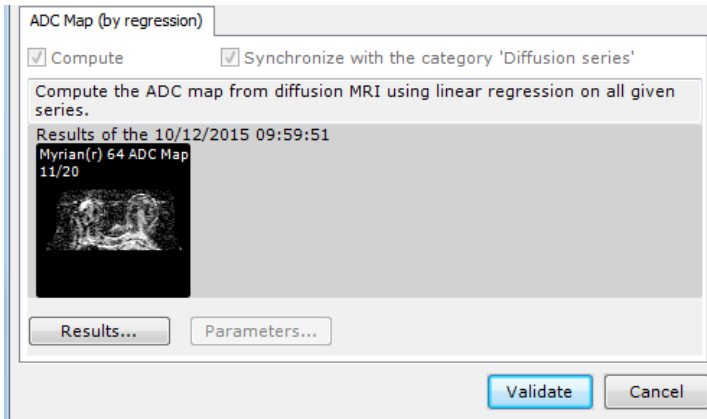


Figure 14-148 Display of pre-computed volume results

- Click  to open these preloaded volumes in the workspace without restarting the calculation.

If you are not satisfied with these precomputed volumes, you can restart a new computation for each one:

- For example, go to the ADC map tab and click on the 'Results...' button
- Then in the 'Existing Results...' section, uncheck the 'Version' checkbox that enables to select previously generated series

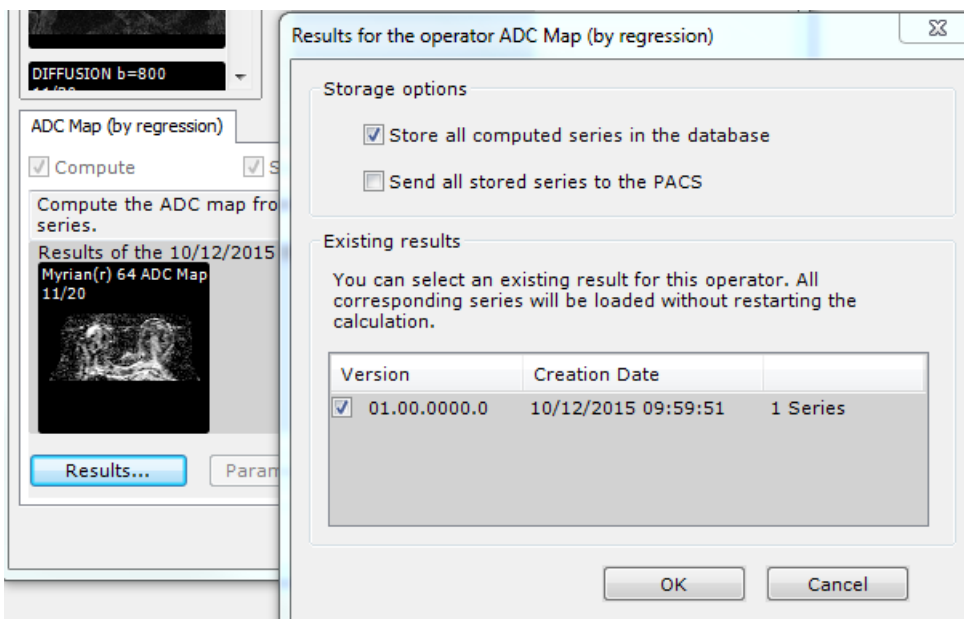


Figure 14-149 Uncheck existing results disabling preloading

- Click OK.



If target annotations are already listed, delete them via the target ROI contextual menu and start the lesion localization process all over again



## 14.10.5 Protocol key features



By default, the following image level DICOM fields are displayed in the viewports for MRI modality in all the protocols showing non native MRI images:

- EchoTrainLength
- RepetitionTime
- EchoTime
- FlipAngle

### 14.10.5.1 Visualization modes

In each advanced MRI protocol, factory viewport layouts providing you with various adapted visualization modes associated to the different series categories, are available for you to improve your workflow during imaging review and analysis.

#### 14.10.5.1.1 Navigation

##### Phase menus

The phase menu at the top-left of any Dynamic series Viewport enables you to navigate through the various phases of the dynamic series.

- Display the selected phase simply clicking on it.

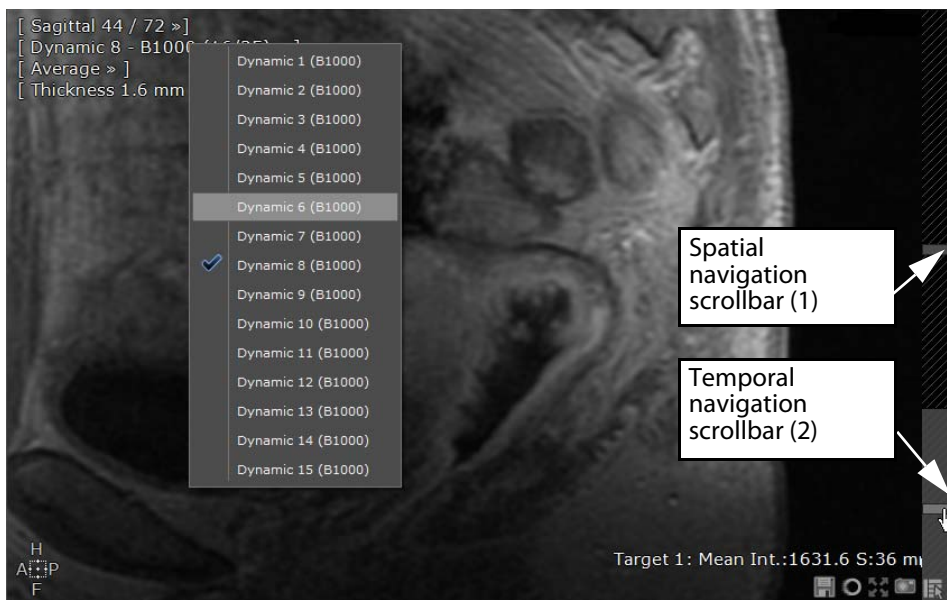


Figure 14-150 'Dynamic Series' viewport phase menu and available navigation toolbars

##### Navigation Controls

- At the right side of **any viewport** is located a spatial navigation scrollbar (1) enabling you to navigate through the series slices. The spatial navigation is synchronized for a slice-by-slice comparison of images in all viewports of the same plane of orientation.
- An additional temporal navigation scrollbar (2) is available in the **Dynamic, Dixon and Diffusion viewports** enabling you to navigate from Phase to Phase (same behavior as the Viewport Phase Menu described here-above) for an interactive visualization of the contrast injection.

## 14.10.6 WI\_WO\_TTP\_AUC Protocol

### 14.10.6.1 Overview

The WI\_WO\_TTP\_AUC protocol provides you with two workflow interfaces:

- A Structured Reading mode for a streamlined workflow approach specifically adapted to beginners
- And the Legacy workflow, giving access to all tools

You can freely move back and forth between these two synchronized modes at any time by simply clicking on the desired

tab in the Toolchest.

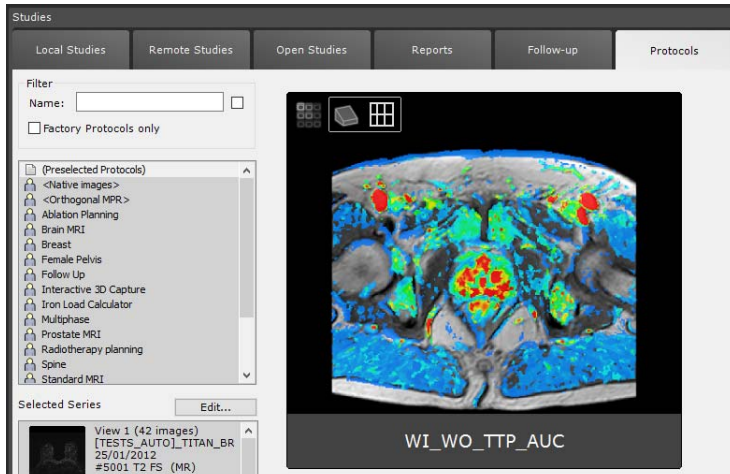


Figure 14-151 WI\_WO\_TTP\_AUC protocol



The WI\_WO\_TTP\_AUC protocol which requires the **activation** of the **dedicated option** is available from the Protocols Tab in the **Standard MRI family**.

### 14.10.6.2 Time-Intensity map analysis

#### 14.10.6.2.1 Activation mode

- Click 'All' to access the Workspace including all toolbars corresponding to the 'Legacy' workflow.

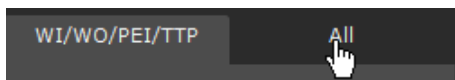


Figure 14-152 Open Legacy workspace

You can go back and forth between 'Legacy' workflow and WI/WO/PEI/TTP reading mode.

#### 14.10.6.2.2 Multivolume

Series are loaded in a multivolume view in a workspace displaying only the relevant tools. This user-friendly interface with clear options enables to simplify your workflow.



By default, upon loading the series, the 'Parametric maps' layout is automatically displayed in the workspace

The workspace includes two viewport layouts:

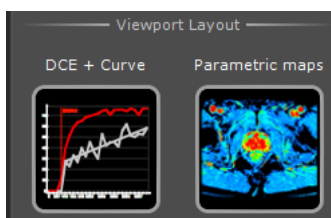
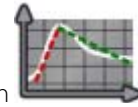
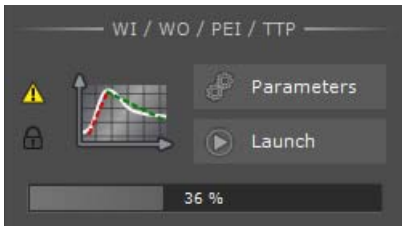



Figure 14-153 WI\_WO\_TTP\_AUC available layouts

Upon loading series in the workspace, the second layout is opened displaying automatically the map computation in progress and associated WI-WO model curve and fitted model.



In the WI/WO/PEI/TTP section of the Toolchest, a progress bar associated to an alert symbol  indicates the computation status.



At the end of the process, a green check mark  is displayed on the left side of the graph icon to indicate that WI/WO/PEI/TTP maps have been correctly generated.

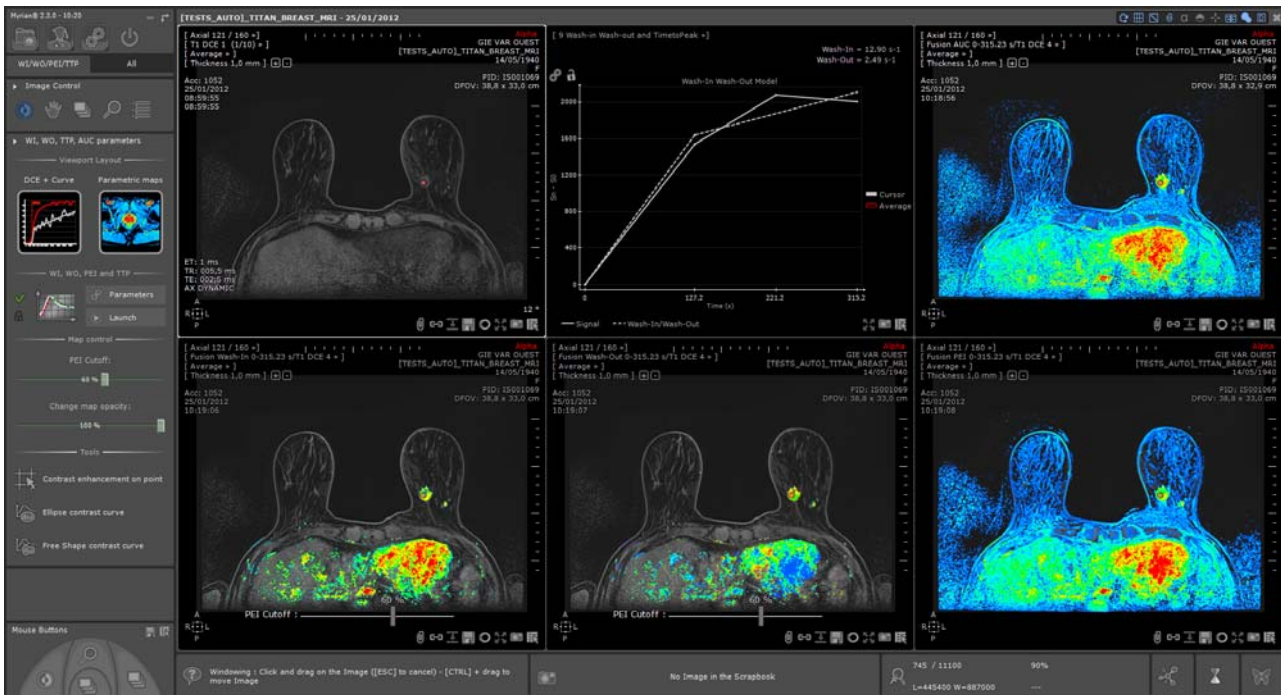


Figure 14-154 Visualization of the computed WI/WO/PEI/TTP maps in fusion mode (T1 overlay)

### 14.10.6.2.3 Semi-quantitative and qualitative analysis via contrast-enhanced kinetic curve interpretation


- Switch back to the first layout for in-depth analysis of the T1 Dynamic series/sequences
- **Adjust windowing, navigate and zoom** in the Dynamic series to localize a suspect area and for which the enhancement kinetic curve shows a significant pattern for a lesion

In the time-intensity curve viewport, the Time-Intensity curve related to the cursor's position is displayed and updated in real-time as you move the cursor, enabling you to visualize the kinetics of the desired region based on Wash-In Wash-Out model. The 'Average' curve (in red), hidden by default, relates to the intensity profile.




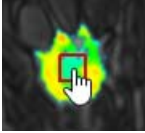

By default, the Intensity profile curve in dedicated viewport is hidden. To visualize the curve, click on the 'Average' square button outline  Average



- Place the anatomical center over any suspect lesion on the T1 DCE series  
 From the Perfusion toolbar, you can adjust the area of interest (1x1, 3x3, 5x5 voxels, etc...) clicking on the 'Dynamic intensity curve around point' tool 


 The default neighboring size is set to 3x3.

- To visualize this neighboring area, press the Shift key while holding down the left mouse button and drag the mouse in the Dynamic series (or any other viewports) over a suspect lesion or a desired region to move the anatomical center simultaneously.

  A red square representing the area of interest you have previously defined is displayed over the anatomical center while the mouse cursor changes to 

In the Time-Intensity curve viewport, the WI WO model curve displays dynamically the signal intensity averaged over the defined area of interest.

- If needed, activate the target annotation clicking on  in the Toolchest and draw the annotation around the suspect area to create a contrast curve.

 Press the **Shift key** while creating the annotation to keep the anatomical center over the point of interest.

Each target annotation is automatically reported in the time-intensity curve viewport displaying the WI-WO model curve. For each target as well as for the cursor (in gray) are displayed at top right of the viewport in the allocated color (see Figure 14-161):

- WI value (expressed in s-1)
- WO value (expressed in s-1)

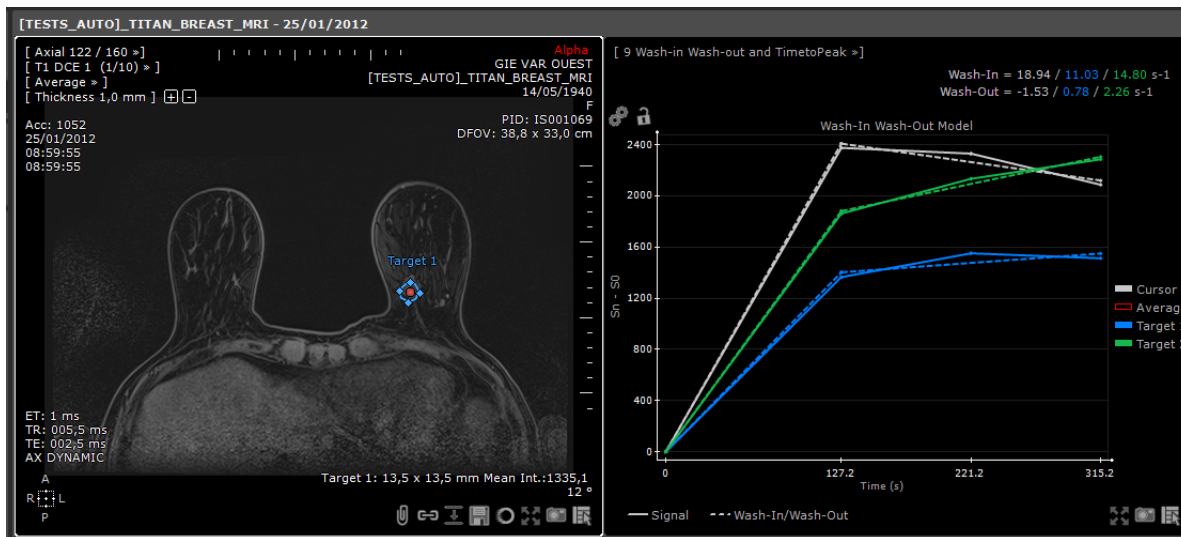


Figure 14-155 Visualization of the time-intensity curves (WI-WO model) related to all created annotations of interest

### Display options:

You can switch back to the dynamic enhancement curve (**raw signal intensity-time** graph) clicking on the Wash-In Wash-Out menu.

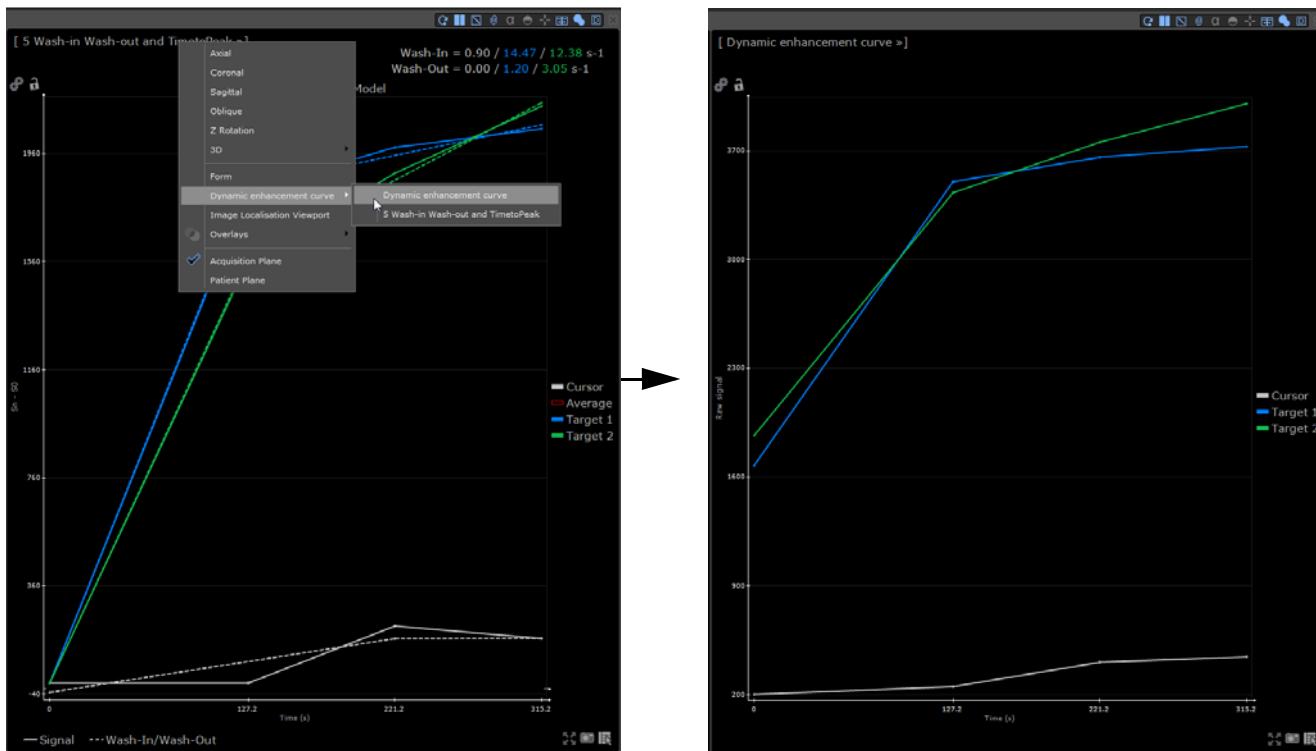


Figure 14-156 a) Wash-In Wash-Out model curve menu

b) Contrast enhanced curve (raw signal)

In both cases, you can choose whether to display/hide one specific curve simply clicking on the corresponding target icon. When one target display is deactivated, its associated square switches from solid color to a simple outline.

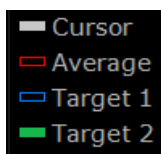
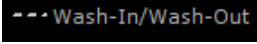




Figure 14-157 Enable/Disable Target display



You can also choose to activate/deactivate the curve display associated to the cursor. In that case, the contrast curve reflecting the dynamic position of the cursor in the time-intensity curve viewport is masked.

You can also hide WI and WO fitted model slopes clicking on  at the bottom of the time-intensity curve viewport.

The 'Axis parameters' button  enables you to set the scale of the graph so that the different curves when defining targets or moving the cursor in the exam are exactly comparable in scale. When clicking on , a floating parameter window pops up:

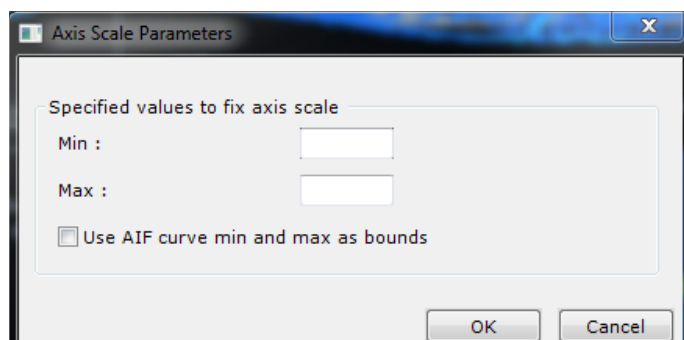




Figure 14-158 Set Enhancement curve min and max value of the intensity axis

- Type your chosen min and max values, or
- Check the 'Use AIF curve min and max as bounds' to automatically fit the scale to the min and max values of the AIF curve (i.e: only apply in the Prostate protocol for Tofts-Kety model curve)
- Click OK




Whenever axis values are modified, the scale is automatically locked  by default. However you can unlock the scale at any time.

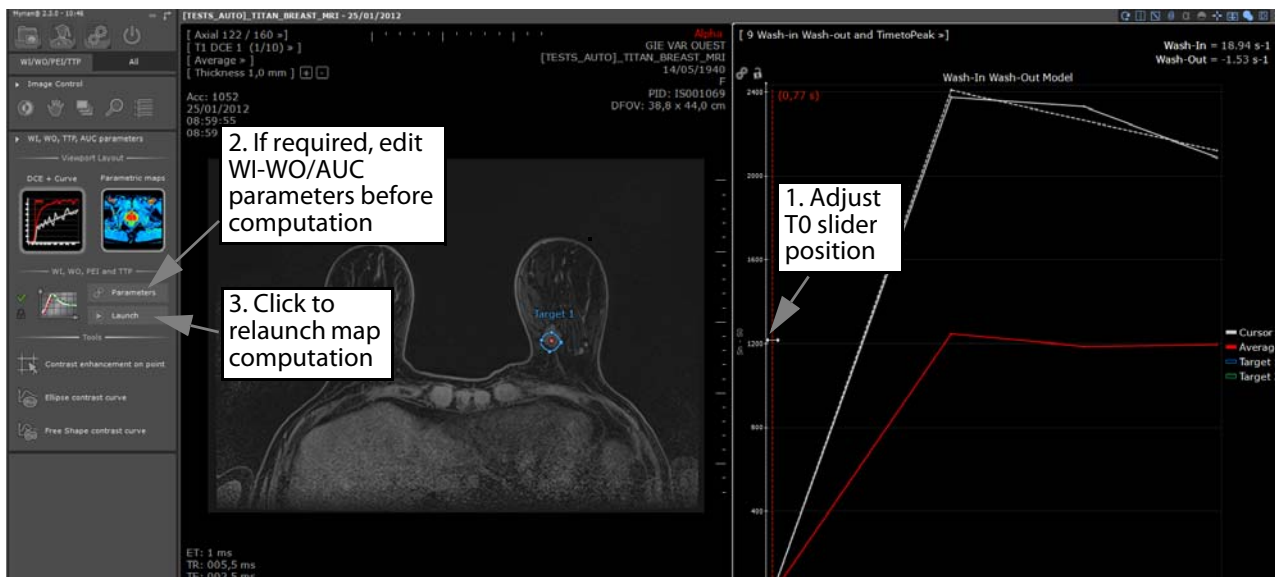
- To add the graph to the Scrapbook/PrintComposer, click on  in the bottom-right of the Time-Intensity curve viewport to open dedicated menu and click on 'Selected Image' (« P» keyboard shortcut)



If required:

- Adjust T0 slider's position related to the Intensity profile curve (passing the mouse over the red dashed line when the 'Average' time-intensity curve display is enabled) to the point where the signal intensity starts increasing significantly which corresponds to the beginning of the contrast enhancement.
- In the Toolchest, click on 'Launch map computation' icon  to restart computation so that any changes of input parameters are taken into account.





T0 is the arrival time of the contrast agent in the tissue after injection.

#### 14.10.6.2.4 Visual assessment using generated parametric maps

- Switch back again to the second layout to visualize the target annotation(s) on the computed parametric time-intensity maps displayed in fusion mode (with DCE MRI overlay series).

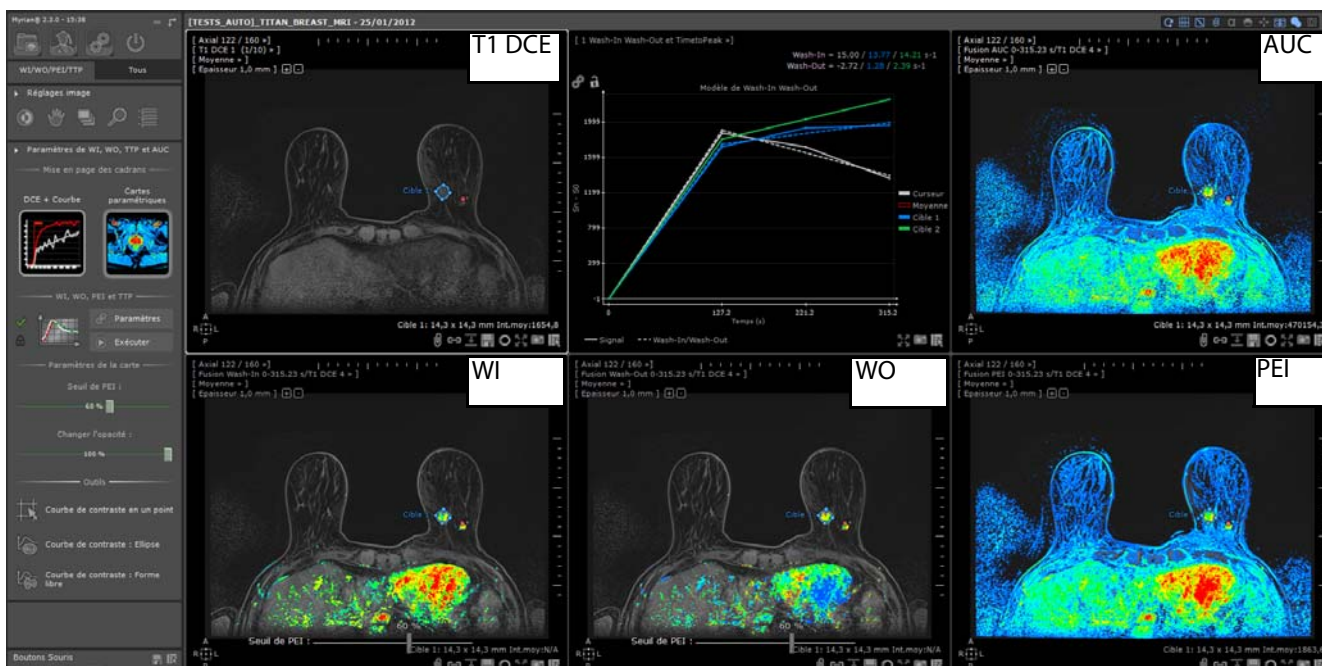
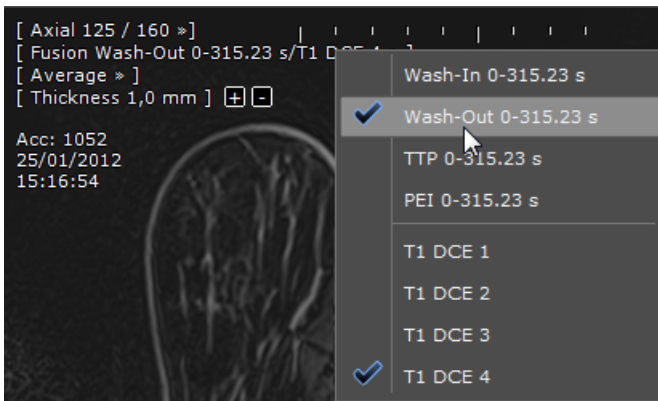


Figure 14-159 Visualizing and analyzing parametric maps

The anatomical center which is synchronized on all viewports, is still located on the area of interest.



To modify the phase to be fused with a given parametric map, click on the fusion viewport menu of your choice and select preferred T1 Dyn sequence.



Then, if required, adjust the CLUT for each parametric map.

- Observe simultaneously the WI-WO curve related to the cursor position or to previously created targets.

A region of interest is significant of malignancy (Type-3 curve) when combining and showing simultaneously all the following factors:

- High Wash-In (rapid initial contrast uptake on the curve)
- Low Wash-Out (wash-out of the contrast agent)
- High AUC

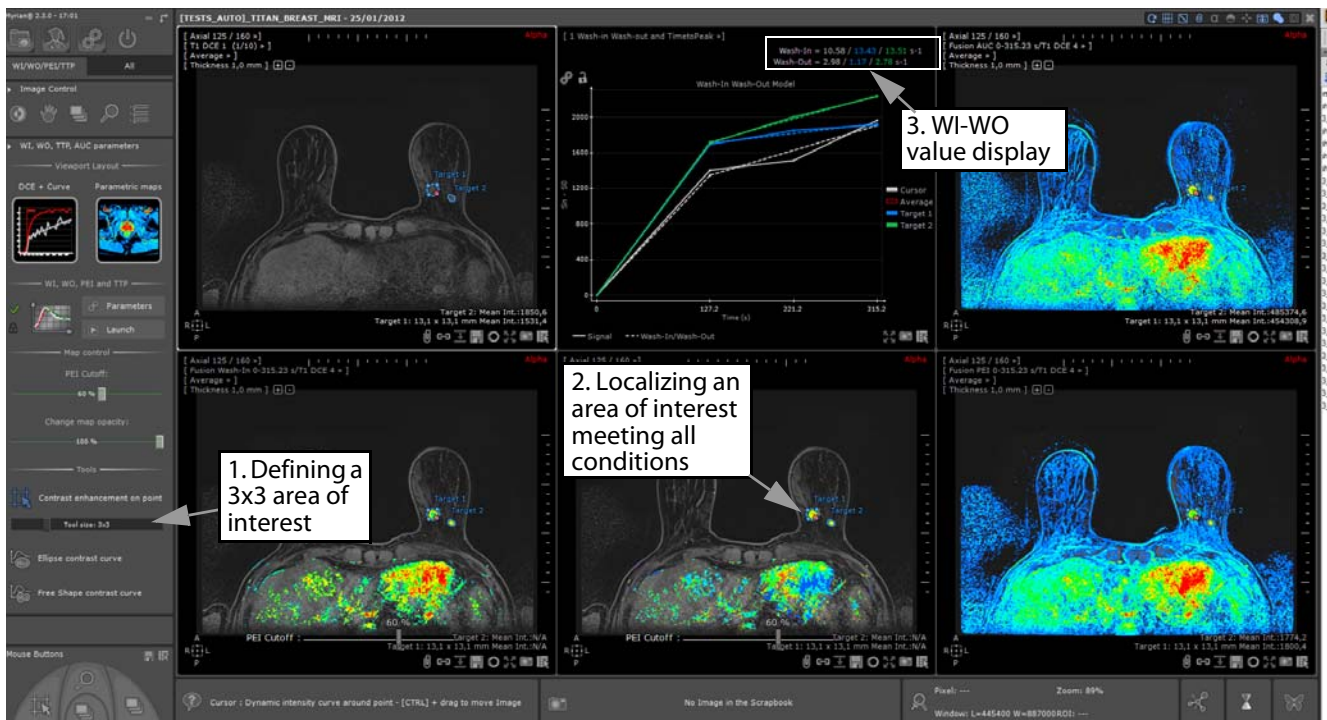


Figure 14-160 Localizing a hot spot with high WI (red), low WO (blue) but low AUC (blue)

- if you localize a new spot matching all previously laid out conditions, select the annotation of your choice in the Perfusion toolbar and draw the annotation on the located spot in the viewport of your choice.



The calculated and displayed values on the map only apply for contrast-enhanced voxels of tissue.



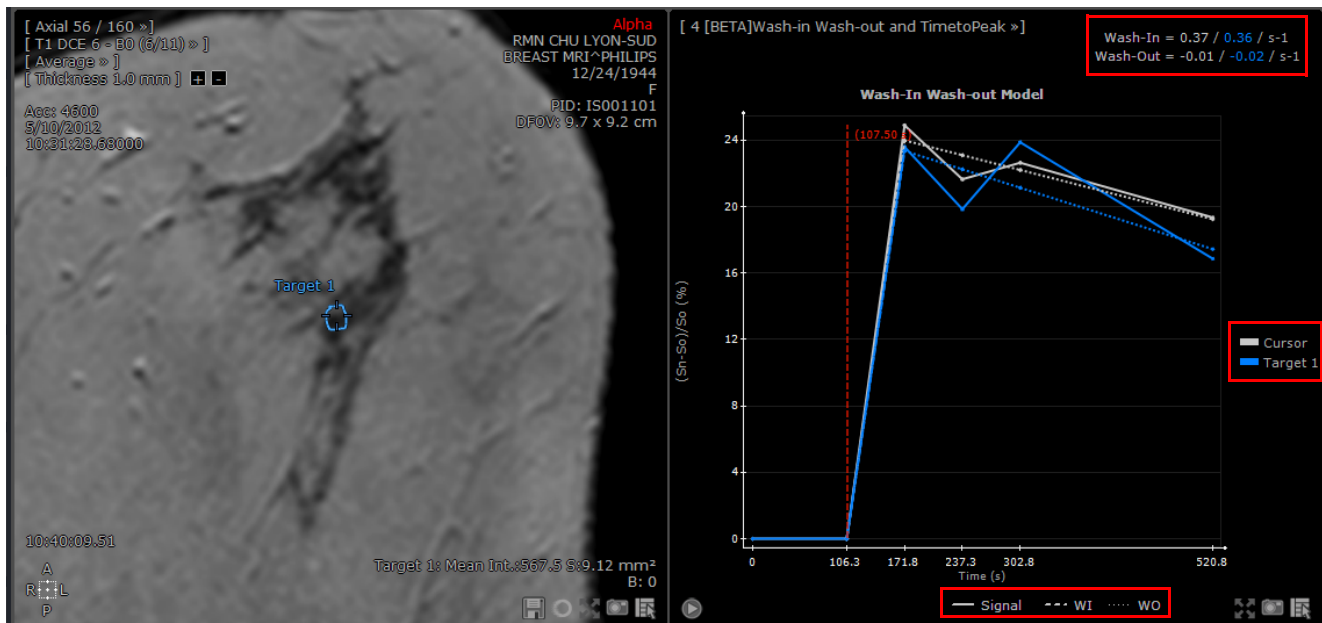


Figure 14-161 Create target annotation and observe the associated WI-WO model curve

You can draw **as many target annotations as you wish**. Each target annotation is allocated a specific color that also matches the contrast curve color. The graph is dynamically updated.

#### 14.10.6.2.5 Modify parametric map parameters



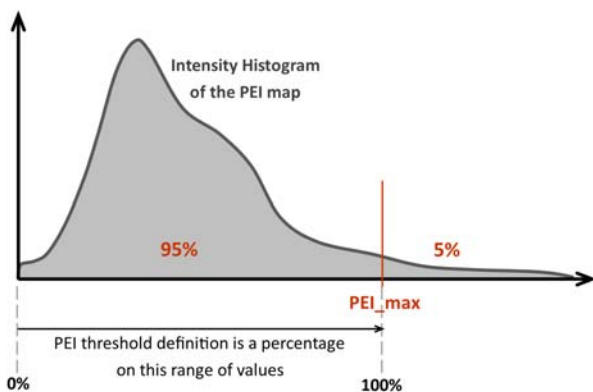
These advanced settings apply for the Wash-in and the Wash-out parametric maps only.

Outside CLUT adjusting or customizing (see Section 4.3.2.11), you can also adjust the following parameters simply moving the dedicated slider:

- The PEI (Peak Enhancement Intensity) threshold percentage using the PEI cutoff slider from the WI and WO parametric maps



The threshold on the PEI is a percentage value of a PEI max. This maximum is calculated as the 95 first centile of the whole PEI map histogram to exclude abnormal points.



By default, the PEI display cutoff is set to 60%.



You can also proceed to the threshold adjustment using the PEI cutoff sliders located in the WI and WO parametric map viewports

- Map opacity (i.e. adjustment of the mixing level for the WO or WI parametric maps displayed in fusion mode on DCE-MRI Series)

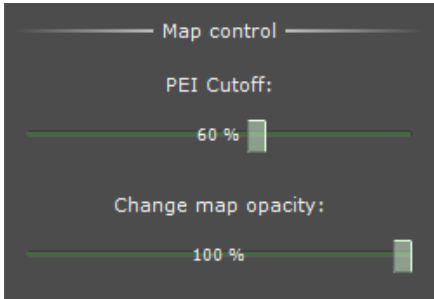


Figure 14-162 WI-WO Map controls



Default map opacity is set to 100%.

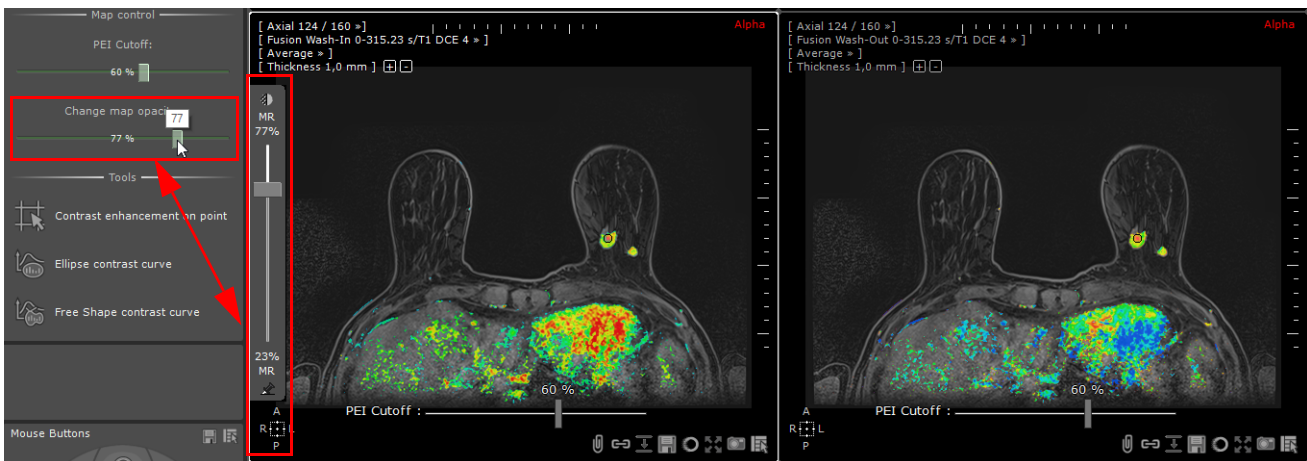


Figure 14-163 Adjusting map opacity



You can also use the Fusion slider located on the left side of the Fusion Viewport to adjust map opacity.

## 14.10.7ADC Protocol

### 14.10.7.1Overview

This protocol which requires the **activation** of the **dedicated option** enables to generate an ADC map fitting any measured signal intensities (referred to as signal attenuation expressed by the B value factor) in diffusion-weighted imaging.



The ADC protocol is available from the Protocols Tab from the main screen in the Standard MRI family

Accordingly, the Volume Processor (VOP) that generates an ADC map for **several diffusion MR series** using **linear regression**, requires **at least 2 input series** with no upper bound and no limitation in number of selected series.

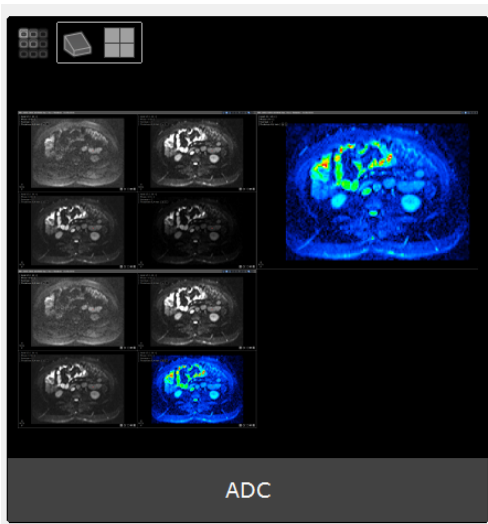


Figure 14-164 ADC protocol

### Reference and model

The signal attenuation  $S(b)$  enabling to compute the ADC map using linear regression is expressed as  $S(b) = S_0 \exp^{-bD}$  where  $D$  is the Apparent Diffusion Coefficient (ADC)



This same model is used when computing ADC maps with **only 2** different B values. However, in the case of the ADC map using linear regression, the signals available for any B values are used in order to offer more precise results.



The higher the number of input diffusion series, the higher the precision of the ADC map.

### Calculation method

In both cases, ADC maps are computed pixel by pixel using **the raw DICOM intensities** of acquisitions; no filter is applied prior to ADC computation, whether it be the homogenization filter, or a denoising one. **No registration is used**; this is a voxel by voxel computation.



When the value  $S_0$  is below a predefined threshold (Noise B0 Threshold), the ADC value is replaced by 0 in order to provide less noisy ADC maps.



This threshold can be modified through the parameter interface (see Section 14.10.2.1.2).



**The values in the ADC map are clamped.** ADC values below 0 are clamped to 0.  $65535 \mu\text{m}^2\text{s}^{-1}$  is the upper bound for ADC values.



Current limits of the ADC map (by linear regression) computation:  
 - No signal de-noising of inputs is applied.

- Diffusion direction is ignored


### 14.10.7.2 Display diffusion MRI series B value

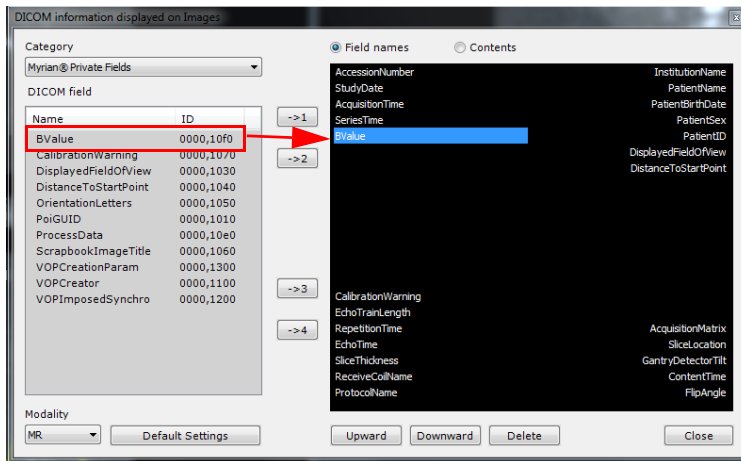
Series are recognized as Diffusion MRI series when a B value can be retrieved from the DICOM fields. The B value of the Diffusion Weighted Imaging exam is displayed in **native mode** but **also in 3D mode** (MPR, 3D,.) and is prefixed with the letter B.



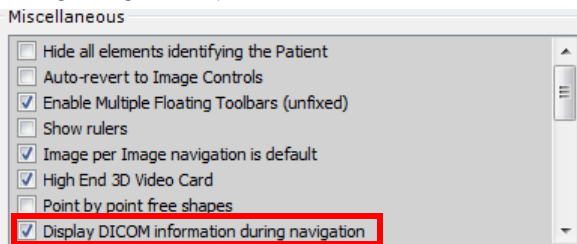
B values can mainly be found in the DICOM header of the supported machines. The main MRI constructors are supported but please bear in mind that the B value of a diffusion MR might be stored at a different location but should be retrievable via the XML file (./protocols/dicom\_query.xml). These .xml files can also be edited **upon request** in order to support site specific machines or modalities.



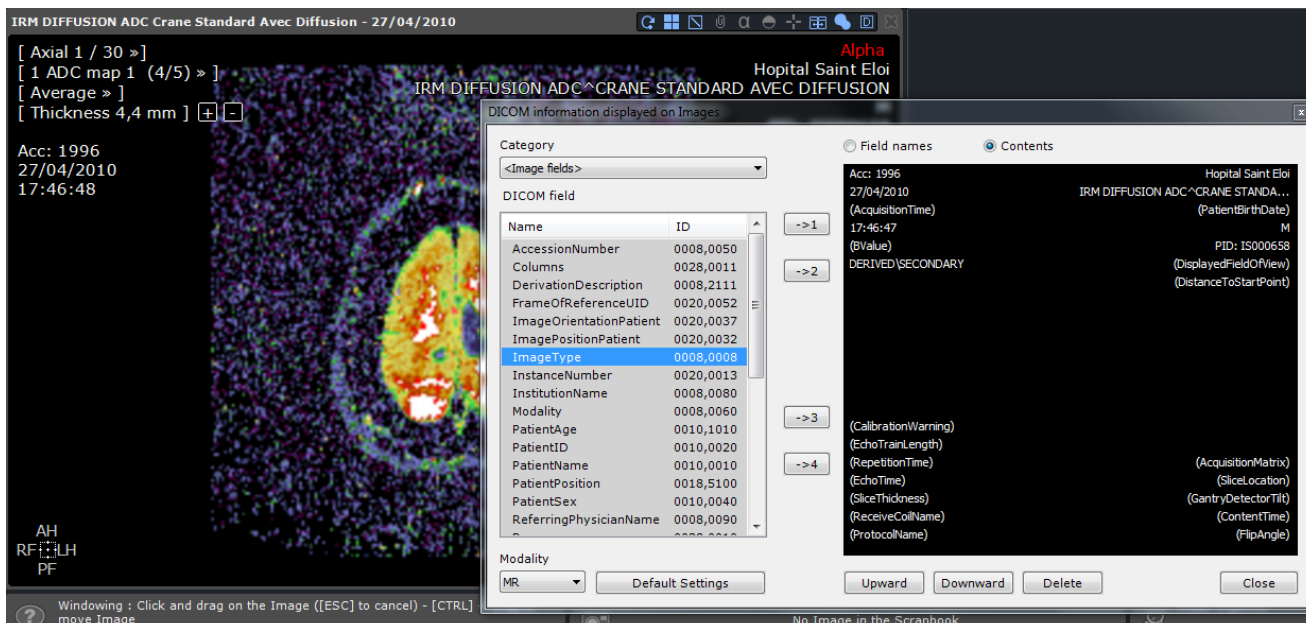
To check that the B value is contained in the series and get the information displayed on the view, open the series in one of the above mentioned mode and click on the DICOM icon  from the image Display Function Toolbar in the main workspace at the top-right of the view. In the 'Category' field, select Myrian® @Private Fields then 'B Value' in the list, define its location on the view then close the window.



To have any DICOM information displayed on images, make sure beforehand that the 'Display DICOM information during Navigation' option is activated in the User Preferences>Display>Miscellaneous.

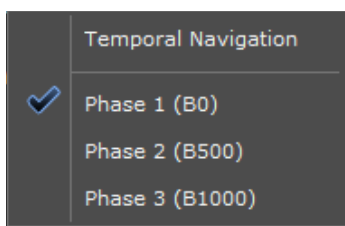


ADC map series cannot be selected in ADC protocol although they often contain a B value. The 'ADC' chain of a series can be checked in the DICOM screen via the ImageType field (value 0008,0008).

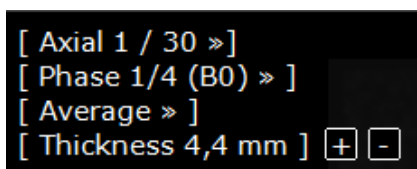


On the view, B values are displayed as follow:

- in the phase menu (multiphase views)



- in each phase menu item (multiphase views)



- in DICOM overlay (typical display for series loaded in single view)



### 14.10.7.3 ADC map visualization

Once the computation process is complete, the ADC map is automatically generated and displayed in the default CLUT.

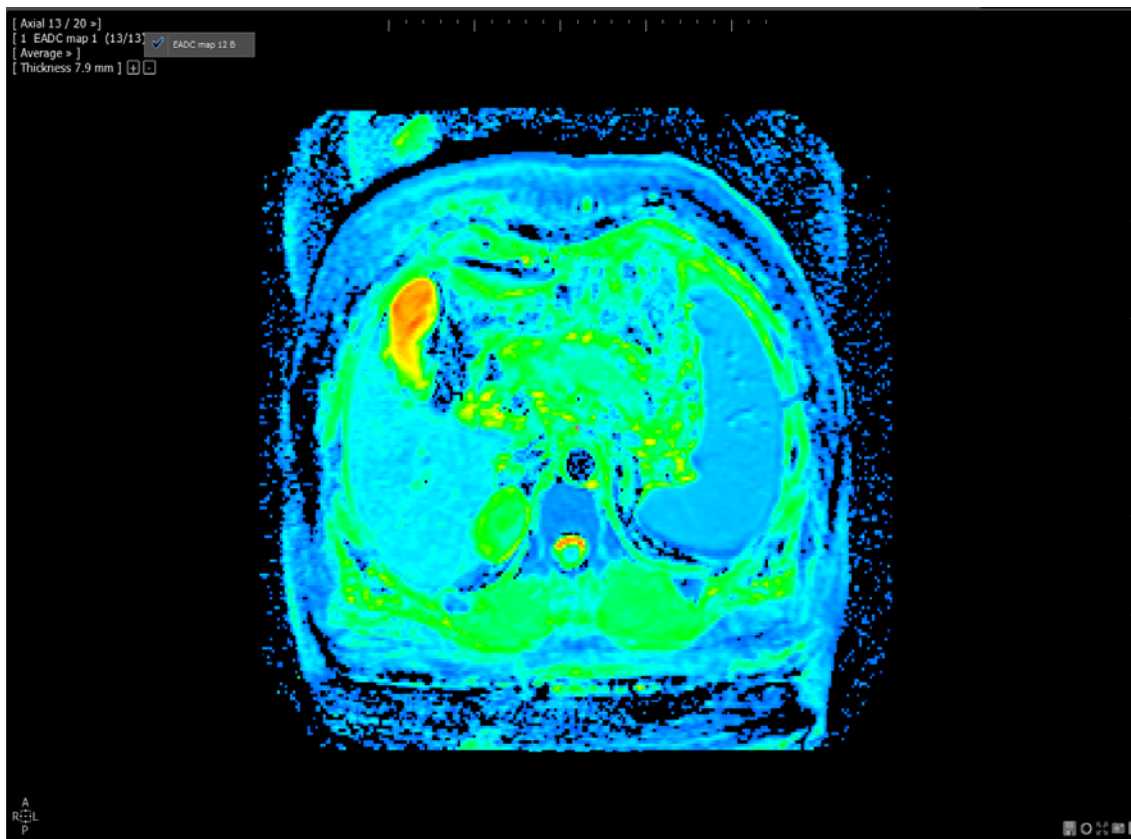


Figure 14-165 Computed ADC map display



Click on the ADC map menu to display the number of B values on which the computation of the ADC map is based.

The ADC protocol user interface includes 3 possible layouts:

- ADC Map
- ADC Map\_2
- ADC Map\_3

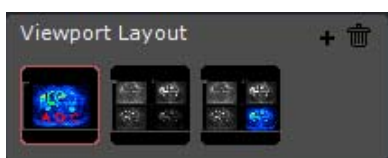



Figure 14-166 Available ADC map Layouts

You can modify or adjust the CLUT to improve the ADC map display respectively selecting the preferred CLUT preset in the Fusion Toolbar or using the CLUT slider which appears on the left side of the ADC map view to adjust color settings.

The 'Measure ADC' tool  can either be used on MRI studies or on the computed ADC map.



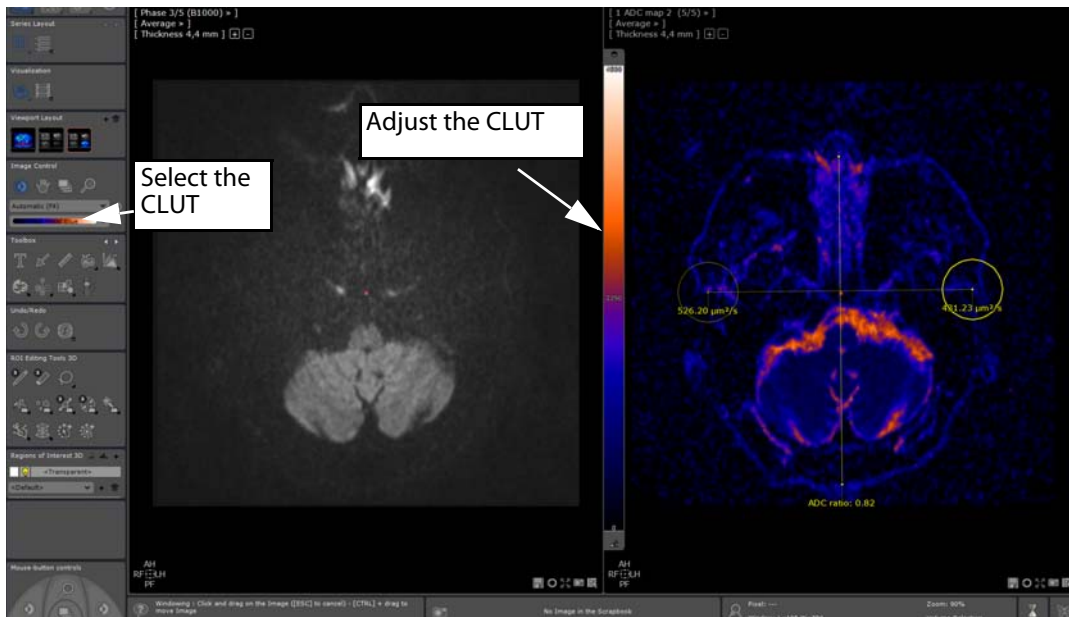


Figure 14-167 Example of use of the 'ADC' ROI AOI tool on the generated ADC map (ADC map\_3 layout)



According to standards in force, the regions in the brain (example above) which appear in yellow-red color are those with the highest water diffusion (high ADC) whereas those in blue-green color reveal a drop in the water diffusion (low ADC).

## 14.10.8 Female Pelvis protocols

### 14.10.8.1 Overview

The Female Pelvis protocol family is designed for the visualization and analysis of **female pelvis magnetic resonance images**. Each dedicated protocol offers optimized viewing capabilities for Dynamic Contrast Enhancement imaging and different acquired MRI sequences in a workspace configuration specifically designed for the staging of pelvic pathology.

This Female Pelvis protocol family includes 5 Display Protocols.

Each of the following protocols loads Series into specifically adapted work environments with different visualization layouts:

- **"Myometrial masses analysis"** → Localize, characterize and evaluate the treatment efficiency of myometrial masses
- **"Endometrium"** → Review images of the endometrium, stage endometrial cancer and search for lymph nodes
- **"Ectopic endometrium analysis"** → Visualize, characterize and localize endometrial cells inside and outside the uterine cavity
- **"Ovarian masses"** → Localize, characterize and stage Ovarian masses.
- **"Cervix"** → Localize, characterize and stage Cervix lesions

Moreover, **the Ovarian masses, Cervix and Myometrial mass analysis protocols** also contain the following tools:

- Contrast Uptake Curve computation for the analysis of the contrast uptake of injected MRI Series
- Automatic ADC map calculation from diffusion-weighted imaging for qualitative and quantitative analysis.

Additionally, **both the Ovarian Masses and the Cervix protocols** include the Comparison and fusion of Diffusion-weighted functional and anatomical MRI series

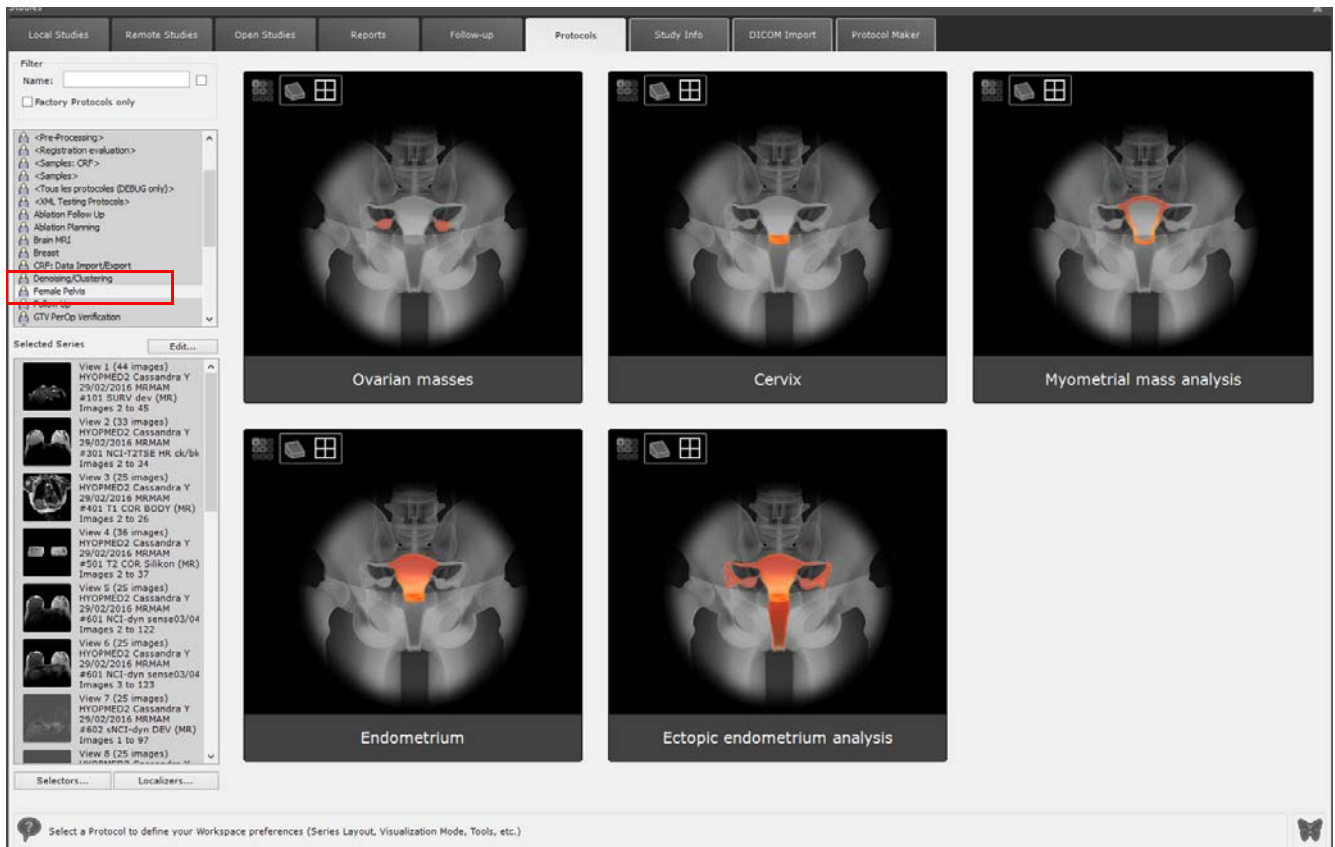


Figure 14-168 Female Pelvis protocol family



## 14.10.8.2 Key features

### 14.10.8.2.1 Contrast uptake tool

The Contrast Uptake Curve tool  enables the **analysis of the dynamics of Contrast-Enhanced MRI Series** (see Section 4.6.9).

### 14.10.8.2.2 Double monitor configuration

MRI Female Pelvis protocols support dual monitor workstation provided the option has been activated beforehand in Myrian® Preferences>Display tab clicking on the 'Multimonitor...' button.

In that case, a second icon indicating that the Multimonitor option is on, appears on each Female Pelvis protocol thumbnail.

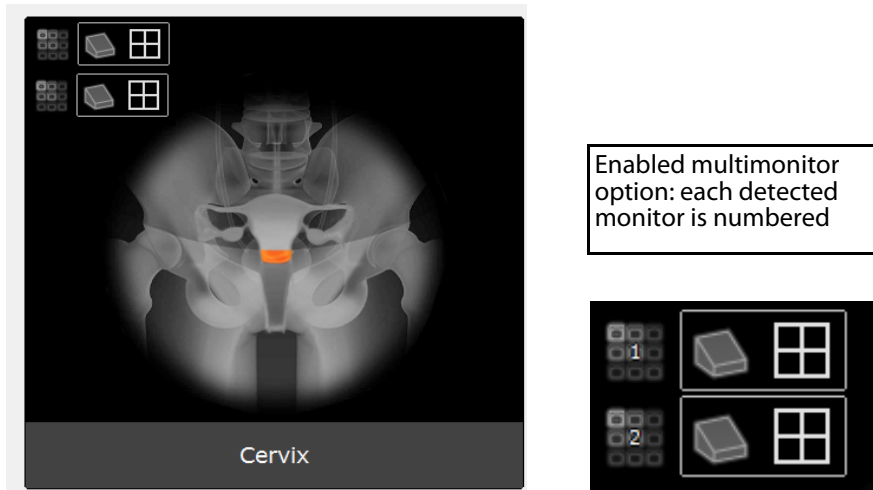


Figure 14-169 Multimonitor enabled mode

When opening MRI series, the Multimonitor option spreads your Myrian® workspace over the dual monitor configuration. By default, the first layout allowing to characterize the lesion is displayed on the main monitor while the second layout enabling to localize the lesion is displayed on the secondary monitor.

According to your needs, you can allocate any viewport layout to the monitor of your choice.

- Click on one of the monitor view titlebar first to activate the monitor then select the viewport layout you wish to allocate to the monitor from the Layout toolbar.



You can take snapshots of the whole Workspace displayed over both monitors:

- Click on the Capture button  at the bottom-right of any viewport and select 'Screen Capture' from the contextual menu

---

## 14.10.8.3 Cervix protocol

### 14.10.8.3.1 Tissue characterization and lesion localization

By default, the following series are loaded in a workspace dedicated to **tissue characterization and lesion localization**:

- Sagittal T2
- Axial T2
- Diffusion series
- DCE sequences

The other available layout is dedicated to the **Treatment follow-up**.

All views are synchronized on navigation, zoom and pan for viewports sharing the same orientation.



Windowing is not synced in between viewports

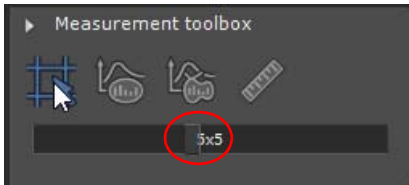
- Navigate, zoom, pan and modify the windowing as required



- Use the 'Dynamic intensity curve around point' tool to define an area of interest (1x1, 3x3 or 5x5 voxels, etc...) via the toolsize slider.



The default cursor neighboring size is set to 5x5 but can be adjusted moving the slider



- When localizing any suspected lesion, place the anatomical center on it in one viewport to locate it on others.

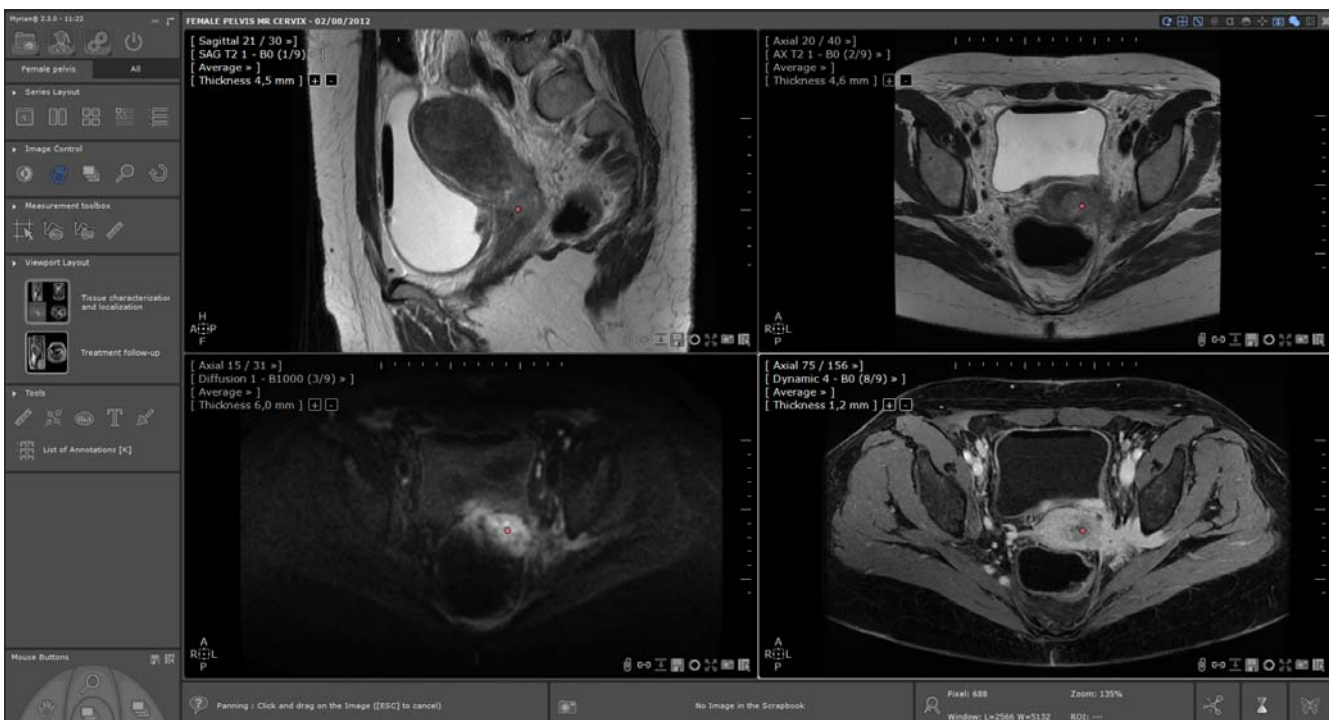





Figure 14-170 Placing the anatomical center on the target region of interest

- From the Measurement toolbox, select the 'Add length' tool  to measure the lesion each canonical viewpoints

You can also create target annotations  /  over the Regions of Interest on the Dynamic series viewport.

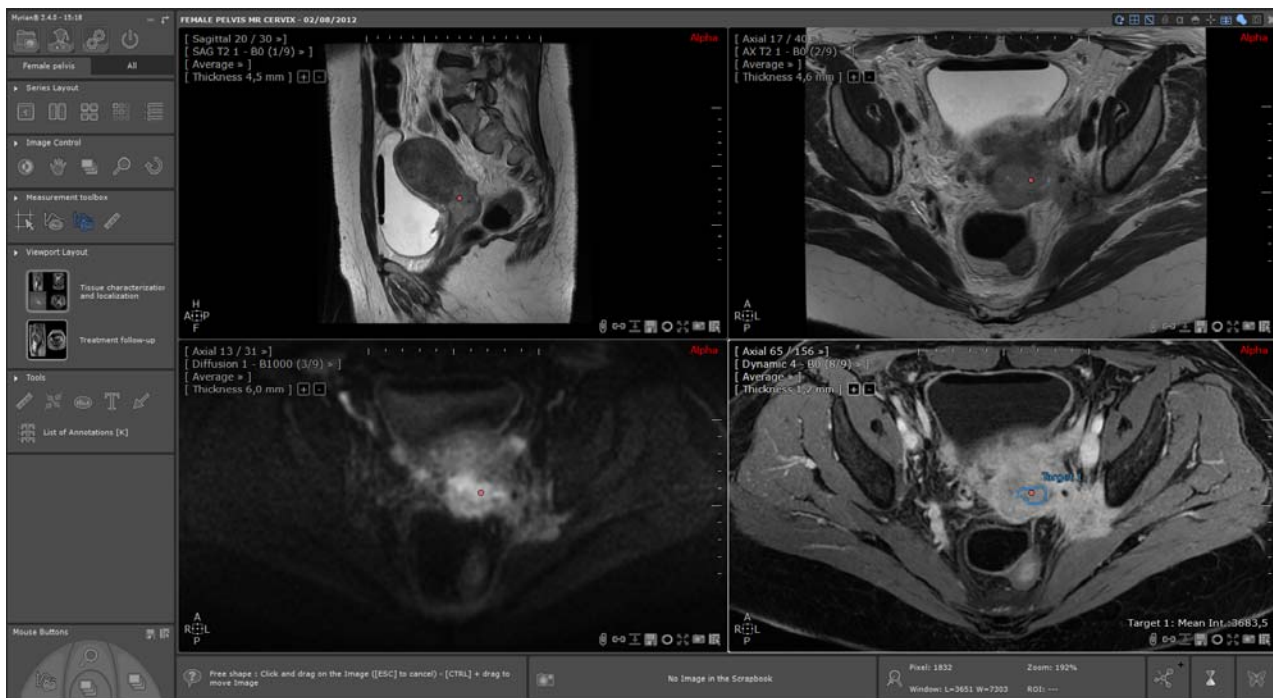


Figure 14-171 Drawing a contrast curve annotation on the target ROI on the DCE series

- To visualize the contrast curve graph associated to the annotation or to the cursor position, click on the viewport menu of your choice and select 'Dynamic Enhancement Curve' from the ensuing menu.

It opens the Dynamic Enhancement curve viewport.

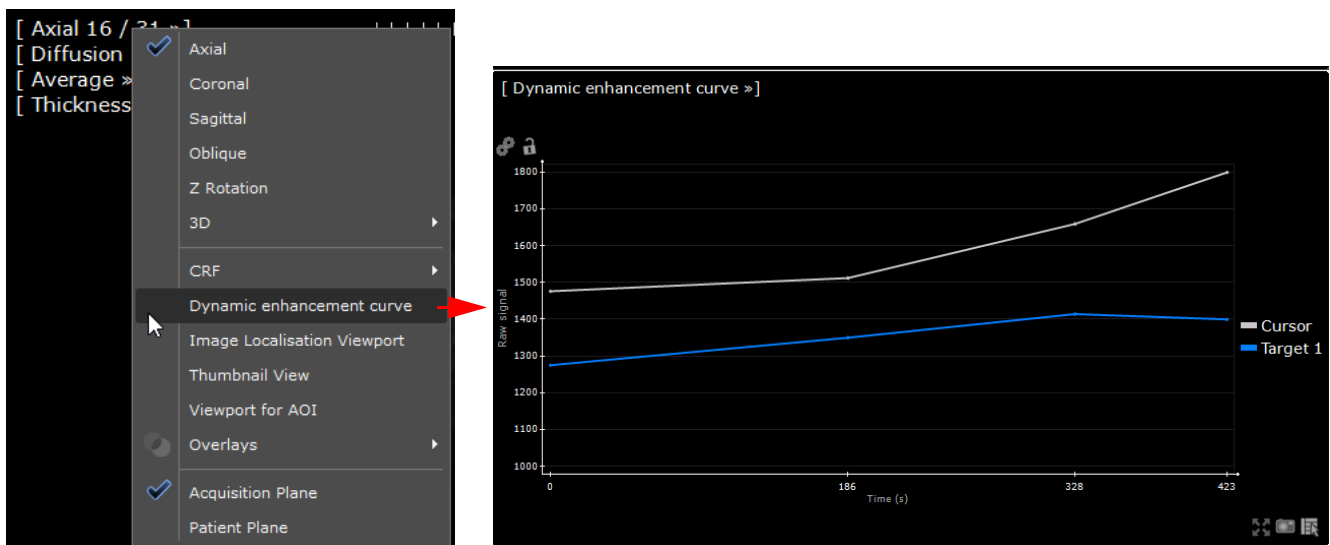



Figure 14-172 Opening the Dynamic Enhancement curve viewport from the viewport menu

All contrast curve annotations are duplicated on each dynamic phases of that same viewport at the same position.



It is recommended to draw a reference annotation on healthy tissue

- Add to the Scrapbook all relevant images clicking on the 'Capture' button 
- Add a combined image in the Scrapbook



All annotations are saved when the session is closed

### 14.10.8.3.2 Treatment Follow-up

- Select the 'Treatment Follow-Up' layout which contains the following viewpoints:
  - Sagittal T2 series,
  - Dynamic series,
  - Fusion Diffusion/Axial T2,
  - ADC map.

This viewport layout is dedicated to the **search of any residual lesions**.



All image control tools are synced for viewports sharing the same orientation with the exception of the Windowing tool.

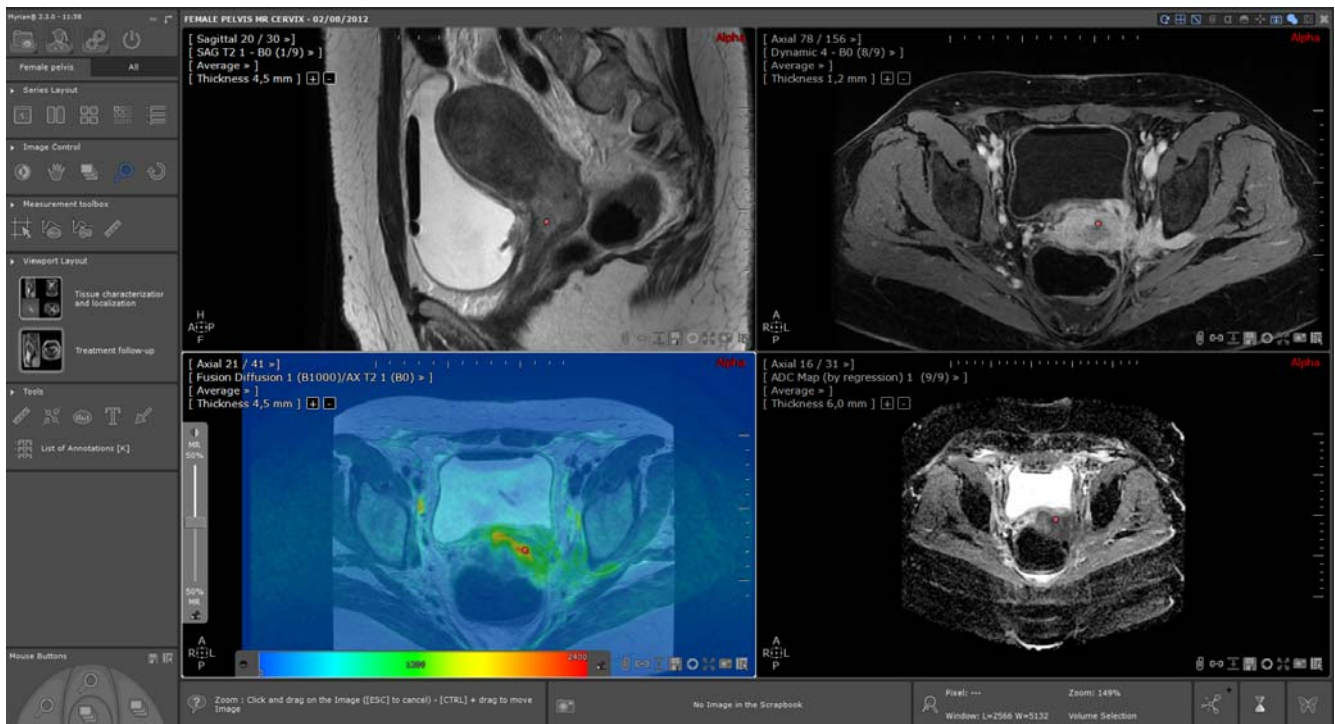



Figure 14-173 Treatment follow-up viewport layout

### ADC map display

- Hover your mouse pointer over the left side of the ADC map viewport to make the CLUT slider visible and dock it pressing the pushpin 
- To activate the CLUT, right-click on the CLUT slider to display the following contextual menu and select 'Activate the CLUT'

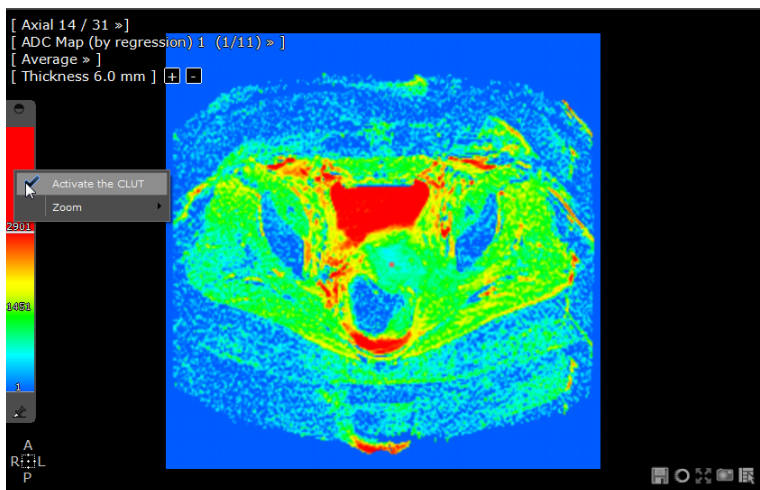



Figure 14-174 ADC map analysis

## Fusion viewport

- In the Fusion Toolbar, click on the 'Data Alignment' button  to display the image alignment pad in the Fusion viewport
- Use it to align the Series manually Up/Down, Forward/Backward or Left/Right
- Select the most adapted CLUT preset in the CLUT Drop-down menu in the Fusion Toolbar

In the Fusion viewport:

- Use the Fusion slider located on the left side of the Fusion Viewport to adjust the mixing levels between CT and PET Series.
- Hover your mouse pointer over the bottom of the Fusion viewport so that the CLUT slider is visible and dock it pressing the pushpin



The docking status for both toolbars (CLUT and/or Fusion) is a configurable parameter.

- Adjust the CLUT level

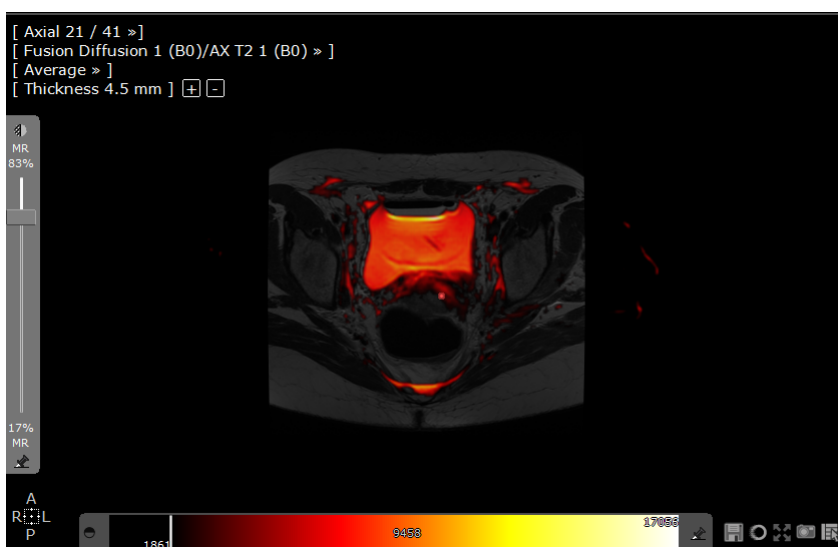


Figure 14-175 Fusion View using Diffusion and Axial T2 series

- Open the Fusion Diffusion drop-down menu to change Diffusion sequence



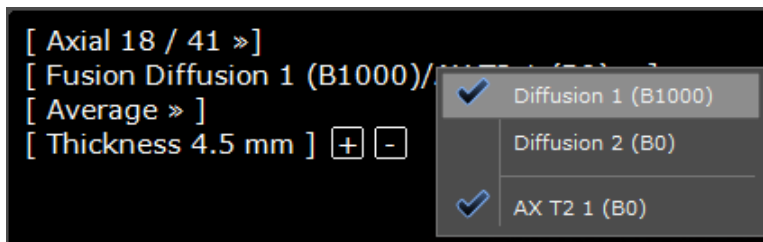


Figure 14-176 Fusion drop-down menu

- Add Fusion and ADC images to the Scrapbook (see Section 5.4.2 for detailed information about how to generate a report).

### 14.10.8.4 Ovarian mass protocol

#### 14.10.8.4.1 Lesion characterization and localization

By default, the workspace opens displaying the Tissue Characterization and Localization dedicated viewport layout.

This layout enables you to analyze the following input sequences and detect any potential lesions:

- Axial T1 series
- Axial T2 series
- Sagittal T2 series
- Axial T1 Fat Saturated series (when available)

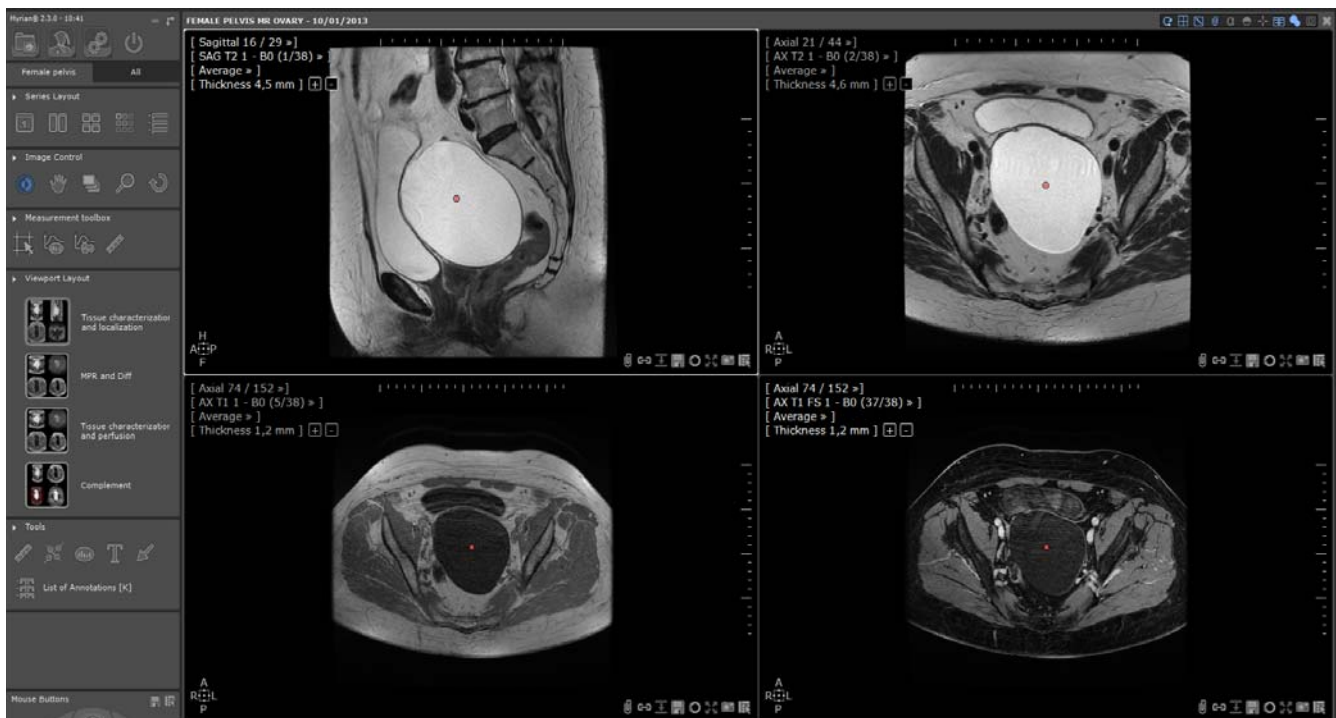







Figure 14-177 MR imaging review for tissue characterization in the ovaries

- Use the Navigation , Zoom , Windowing  and Panning  tools in the displayed viewports in order to better visualize the pelvic content
- Use the 'Dynamic intensity curve around point' tool  to define an area of interest (1x1, 3x3 or 5x5 voxels, etc...) via the toolsize slider.
- Localize a suspect area scrolling through the images of any viewport and place the anatomical center over the anatomical structure of interest to easily locate and focus on it on all other available viewports

During this tissue characterization process, you can add to the Scrapbook all images of Interest clicking on the 'Capture'

button  located at the bottom-right of any viewport



Navigation, Zoom and Panning actions are synchronized for viewports sharing the same orientation.

#### 14.10.8.4.2 Create Target lesion

- From the Measurement Toolbox, select the Target annotation of your choice

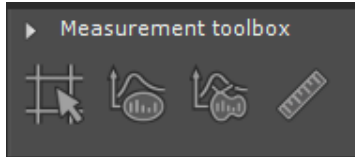


Figure 14-178 Measurement Toolbox

- Draw the annotation over the suspected lesion in the Dynamic series viewport.
- Repeat the same process for any other suspect lesion

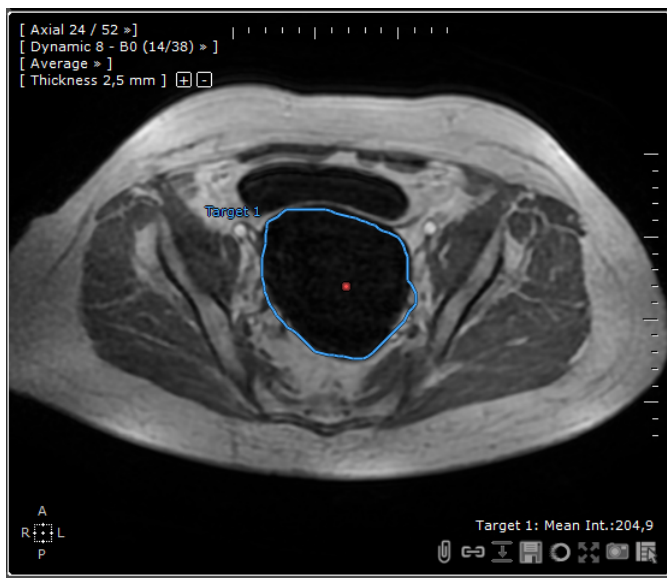


Figure 14-179 Tracing outlines around the target ROI



The annotation is duplicated on each phase of that viewport at the exact same position.

You can adjust the contour of a target, modify its shape or position.

- To display the dynamic enhancement curve related to the annotation or to the cursor position, click on the viewport menu of your choice and select 'Dynamic Enhancement Curve' from the menu or switch to the 'Tissue Characterization and perfusion' layout.

#### 14.10.8.4.3 Measure localized lesions

- Switch to the 'MPR and Diff' layout

- In the Measurement Toolbox, select the 'Add Length' tool  or the 'Orthogonal Diameters' tool  to measure the localized lesion in each canonical viewport.
- Add to the Scrapbook any relevant images from each viewport

#### 14.10.8.4.4 Tissue characterization and perfusion

- Switch to the third layout dedicated to the tissue characterization by perfusion-weighted magnetic resonance imaging.

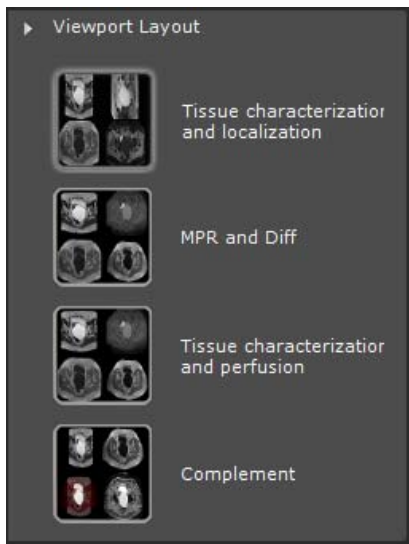


Figure 14-180 Available Ovarian masses viewport layouts

The workspace is automatically refreshed, displaying among others, ADC, diffusion and dynamic viewports and more specifically, the dynamic enhancement curve viewport

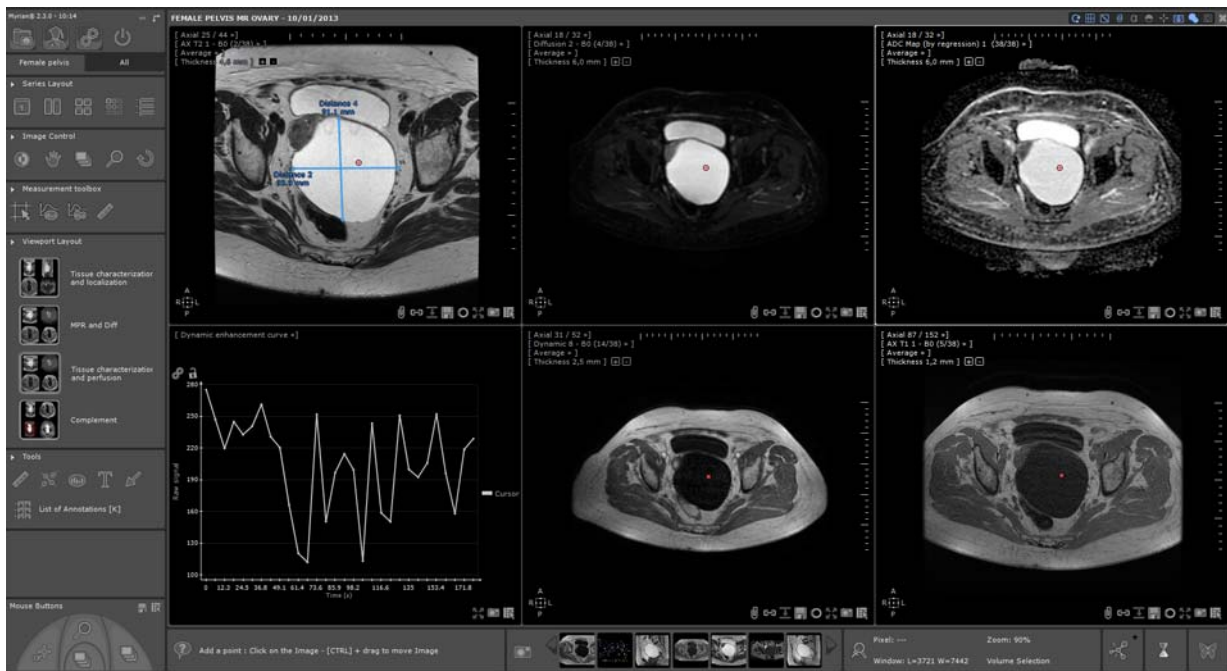


Figure 14-181 Tissue characterization through perfusion-weighted imaging analysis

#### 14.10.8.4.5 Complement

- Select the 'Complement' layout in which you can visualize Dynamic, Axial T2, Axial T1, Fusion Diffusion/Axial T2, Dynamic Enhancement Curve and ADC map viewports



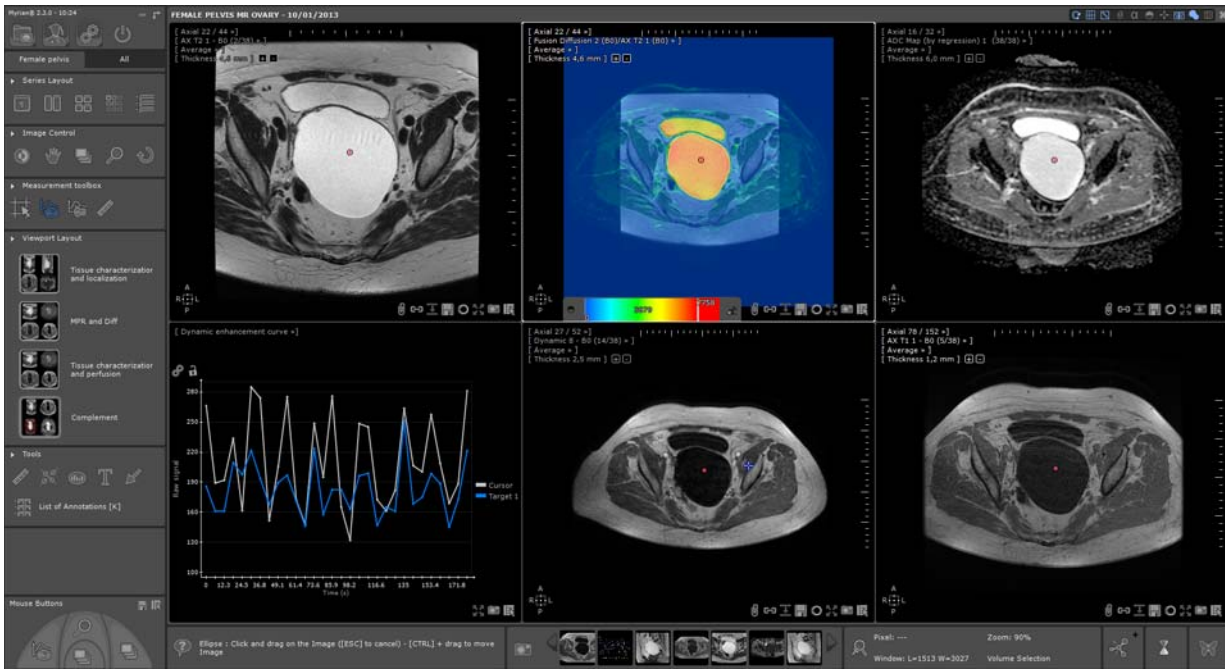



Figure 14-182 'Complement' layout

- Add to the Scrapbook any relevant images from each viewport



Select the most adapted CLUT preset in the CLUT drop-down menu in the Fusion toolbar.

- To create a Report for the active study, switch to the 'All' tab from the Toolchest then from the Scrapbook/Report toolbar, click on the  button (see Section 5.4.2 for detailed information about how to generate a report).

## 14.11 Histogram

The histogram represents different volumes in the segmented areas in the lungs. The curve is a representation of quantities of pixel by Hounsfield unit.

The histogram representation: on x axis it represents the Hounsfield unity; the y axis represents the pixel quantity.

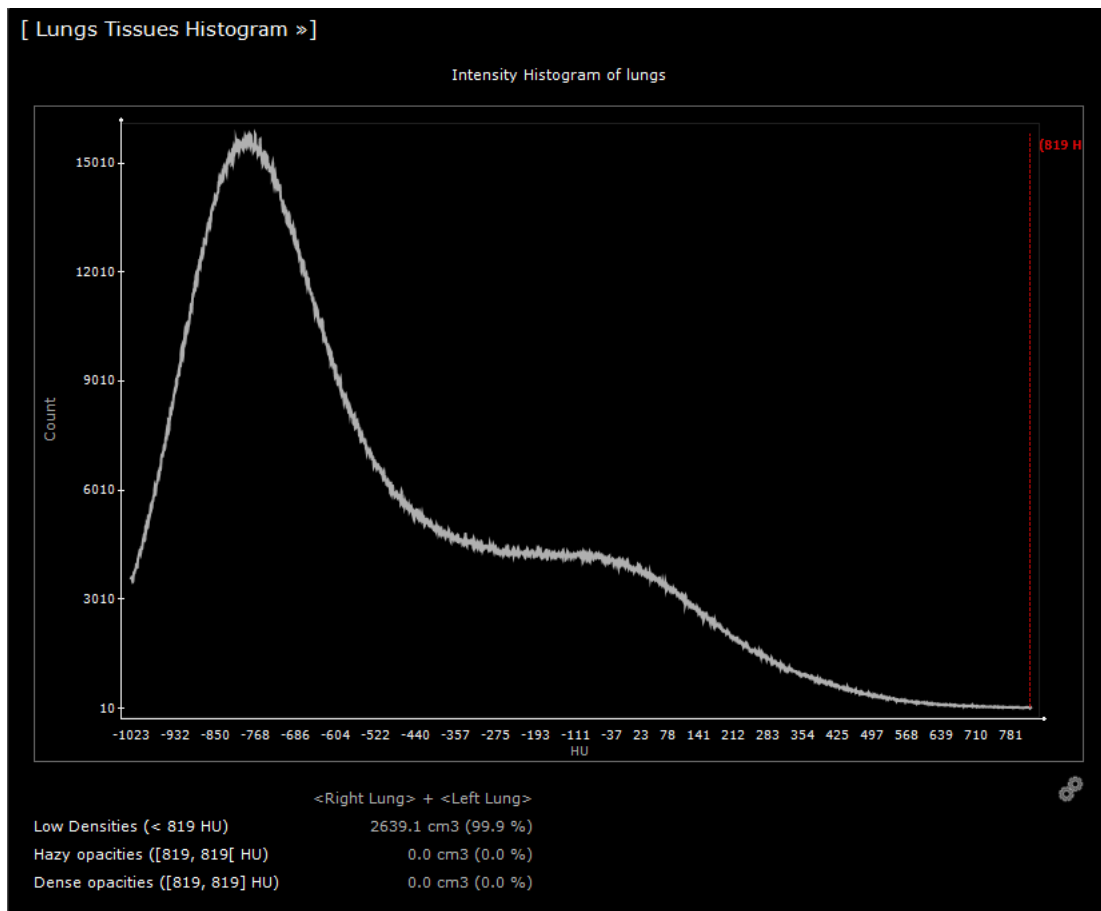


Figure 14-183 Histogram viewport used in the COVID-19 application

### 14.11.1 Adjust the thresholds with the sliders

Thresholds are used in order to isolate specific structures in the lung tissues according to their densities. Each isolated structure is colored in specific overlay in the native images.

- First slider moved is to threshold the Hazy densities.
- Second slider moved is to threshold the dense opacities.



Dense opacities volume could include a part of vascular volume as both structures have similar intensities. Please check carefully the results of the threshold on the native images.

- 
- Third slider moved is to threshold the vascularization.



Vascularization volume could include a part of dense opacities volume as both structures have similar intensities. Please check carefully the results of the threshold on the native images.

---

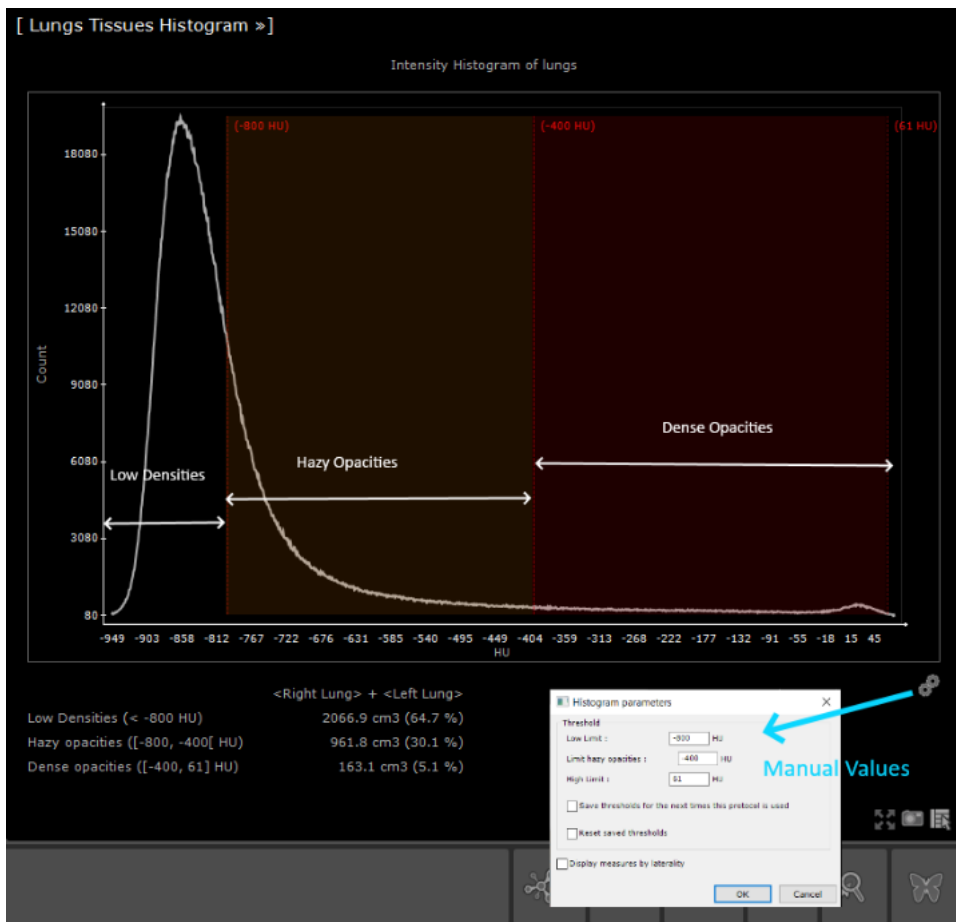


Figure 14-184 Lung tissues Histogram and parameters window

It's possible to insert manually the threshold values.

### 14.11.2 Histogram available parameters

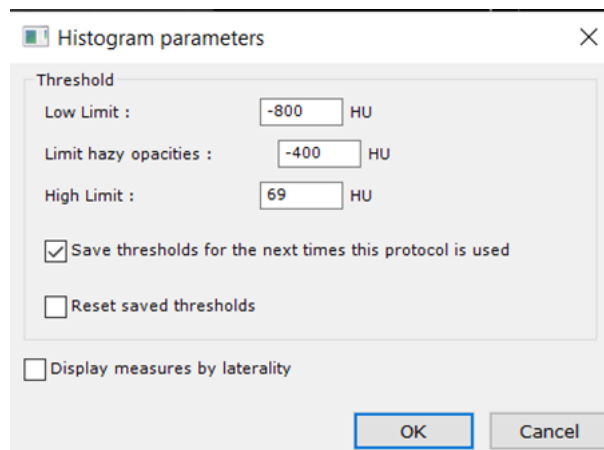


Figure 14-185 Histogram parameters window: save and reset thresholds

Check the box to save threshold for the next time, it will save those thresholds for next studies. You can also reset saved threshold by checking the box.

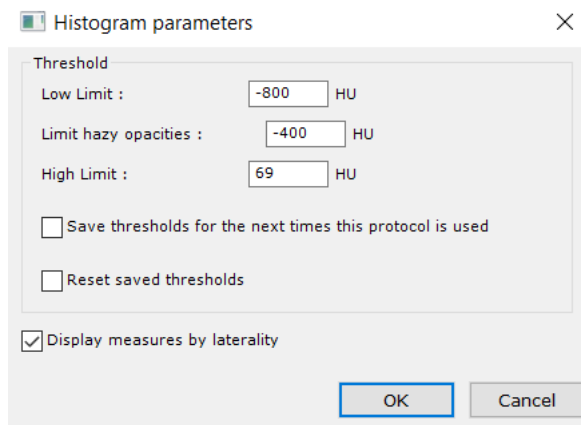


Figure 14-186 Histogram parameters window: display measures by laterality

Check the box to display measures by laterality right and left



Figure 14-187 Lung tissue histogram and real time visualization

When moving sliders, real time colorization is done. In orange the hazy opacities, in red the dense opacities, in white the vascular tree.

### 14.11.3 Volume visualization

Volumes displayed in the histogram are updated according to the different thresholds selected.

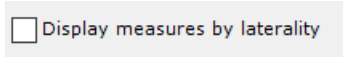


Figure 14-188 display measures by laterality: unchecked

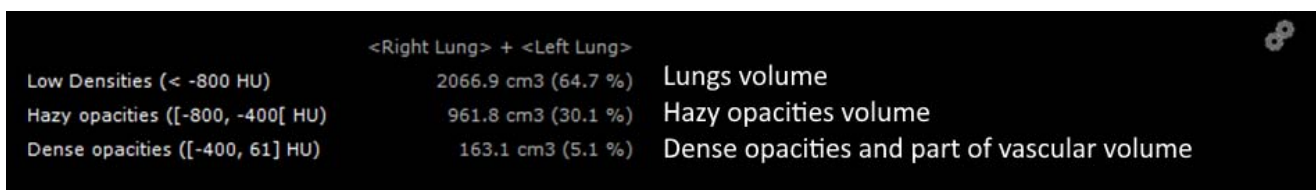


Figure 14-189 Volume displayed for both lungs

If the display measures by laterality box is unchecked you can read the global volume and percent in both lungs

Display measures by laterality

Figure 14-190 display measures by laterality: checked

	<Right Lung> + <Left Lung>	<Right Lung>	<Left Lung>
Low Densities (< -800 HU)	2066.9 cm3 (64.7 %)	1189.3 cm3 (65.6 %)	877.6 cm3 (63.4 %)
Hazy opacities ([-800, -400[ HU)	961.8 cm3 (30.1 %)	541.1 cm3 (29.9 %)	420.7 cm3 (30.4 %)
Dense opacities ([-400, 69] HU)	164.2 cm3 (5.1 %)	80.0 cm3 (4.4 %)	84.3 cm3 (6.1 %)

Figure 14-191 Volumes displayed per lung

If checking the display measures by laterality box you can read the different volumes and percent in right and left lungs. You have the curves in the histogram for all the different volumes, global for both lung (white), right lung (green) and left lung (blue).

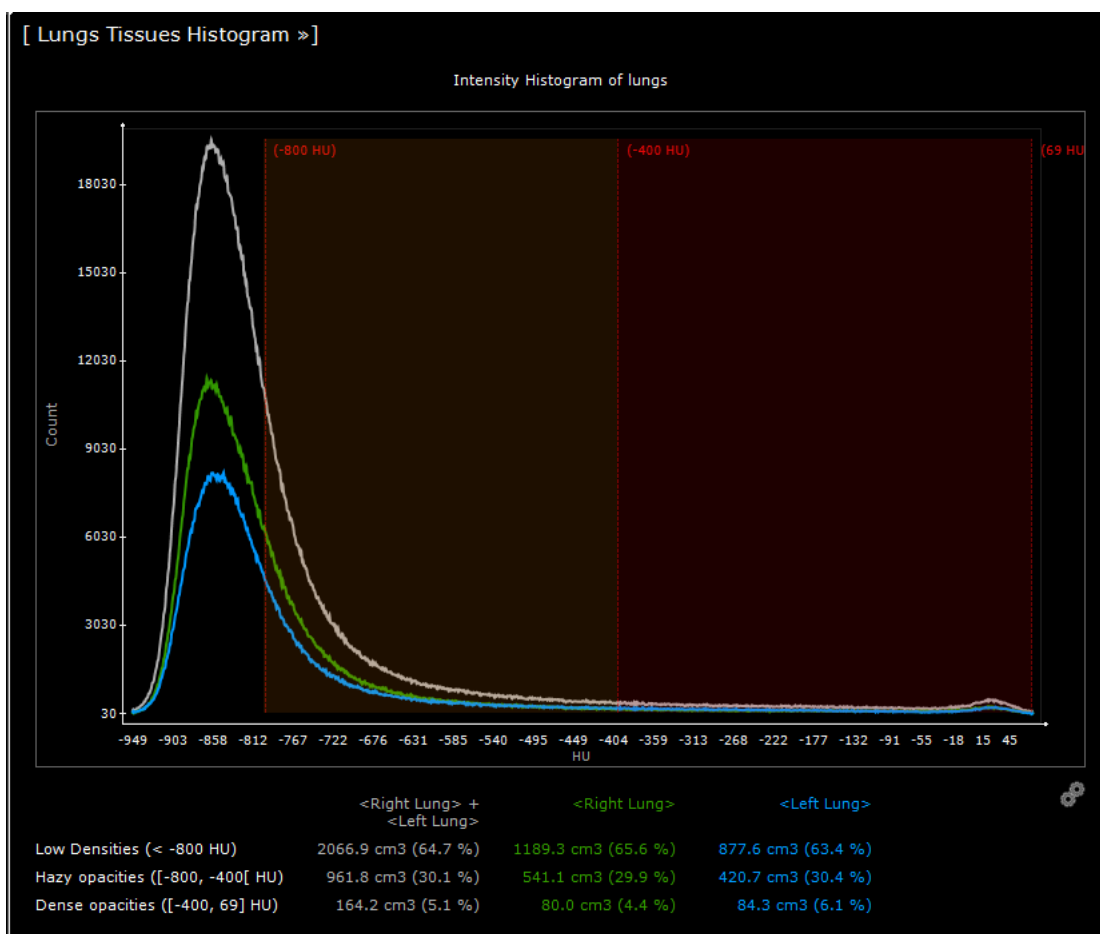


Figure 14-192 Histogram displayed per lungs

## 14.12 Préparation for Radiotherapy Planning

### 14.12.1 Presentation

This optional module is dedicated to the preparation of radiotherapy treatment planning.

This tool, dedicated to the visualization of CT or MR modality series, allows the detection of lesions and the precise definition of their location, shape and volume with the creation of Target Volume Regions of Interest (i.e. part of the body that should be

irradiated for therapeutic purposes)

This Target Volume is divided into three subsets which are :

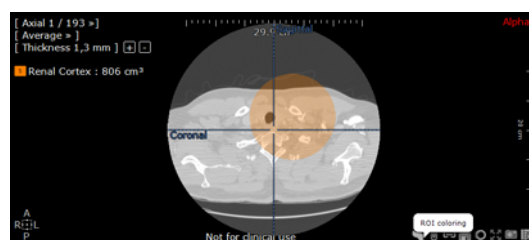
- Macroscopic Target Volume (MTV)
- Anatomical-Clinical Target Volume (CTV)
- Planned Target Volume (PTV)



The Radiotherapy Planning module is not a Treatment Planning System and should not be used as such; therefore, it does not allow the direction of the beam or the size of the field to be determined. This tool is only dedicated to the preparation of lesion targeting and segmentation.

Independently enable overlapping ROI in separate windows.

It is possible to manage the coloring of the ROI overlay independently in separate windows. So you can also use it on an active window.



## 14.12.2 Usage

The Radiation Therapy Planning module includes the following two Radiation Therapy Planning protocols :

- "RT Structures" → dedicated to the review of CT images
- "RT Structures MP" → adapted to the review of dynamic MRI sequences injected in multiphase acquisition for simplified analysis and matching

These protocols integrate tools allowing the creation and export of 3D Regions of Interest in DICOM RT format for the preparation of radiotherapy planning.

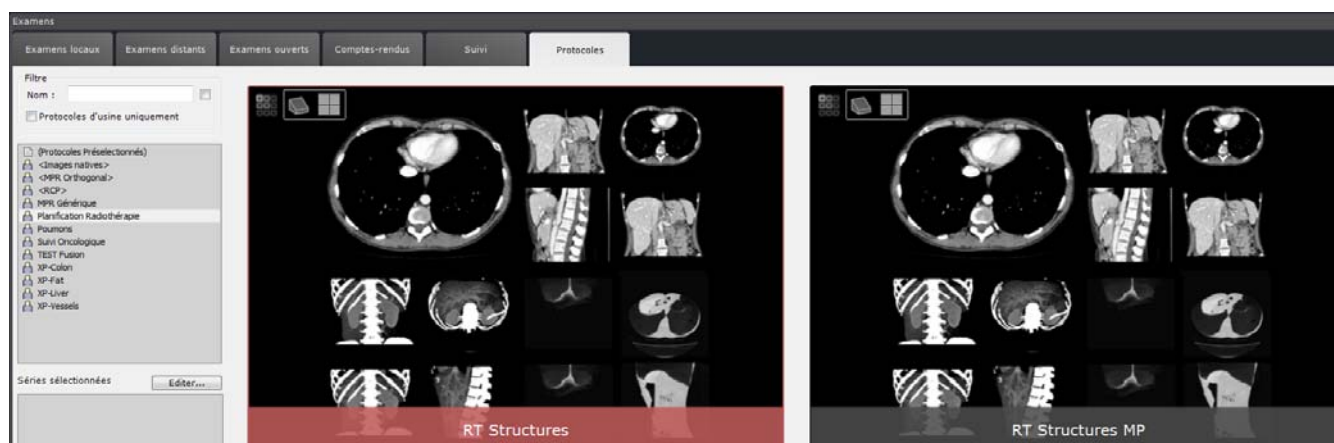


Figure 14-193 Open the selected series with the RT Structures Protocol

When opening the exam in the dedicated workspace, the series is loaded in 4 dials by default. Empty ROIs of the Target Volumes are automatically created in the Regions of Interest toolbar, ready to be segmented

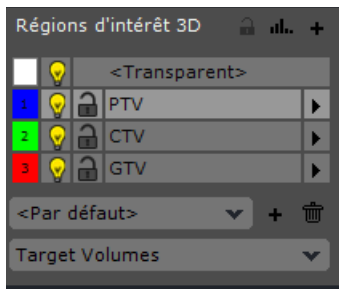


Figure 14-194 Displaying the list of Target Volume ROIs

- Navigate through the cuts to locate the lesion and then use the Manual ROI Editing Tools (extrusion, solid shape...) to segment each Target Volume



Click on the "Image Layout" button  to select the desired dial layout and optimize the visualization of the anatomical structure

Results can be displayed in both 2D and 3D mode.

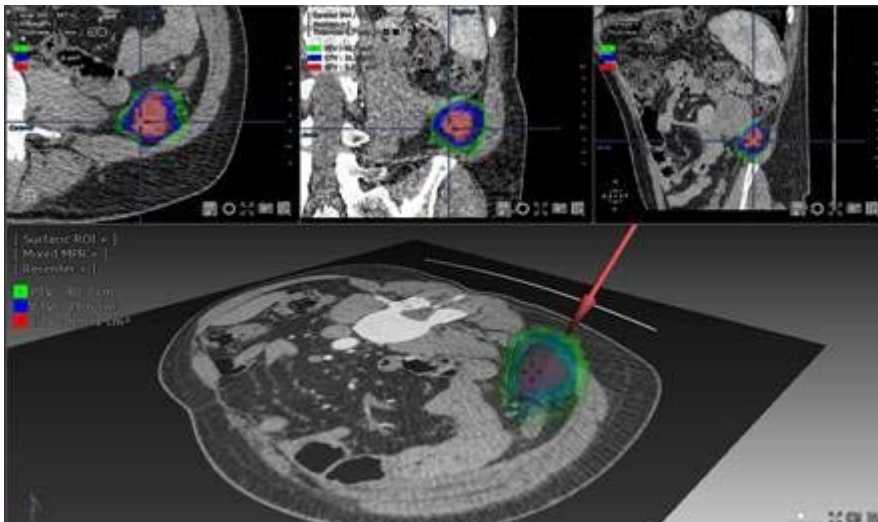


Figure 14-195 Target Volume ROI Creation

Volume measurements (in cm<sup>3</sup>) are automatically calculated and displayed at the top left of each view.



Myrian® allows to combine 3D visualization with Multiplanar Reformating (MPR) to allow a precise localization of the lesion.

Depending on your needs, you can also create ROI sets per segmented organ.

The default menu offers you the following options :

- Group of ROI classified by anatomical regions (brain, abdomen...)
- <All regions> to display all existing ROIs
- <...> to create new ROI groups

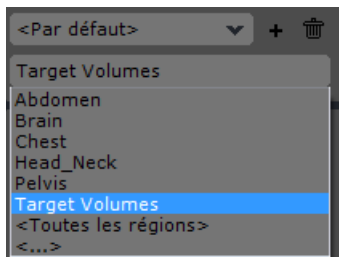


Figure 14-196 ROI group drop-down menu

Each group is made up of a selection of the most frequent ROI for each part of the body.

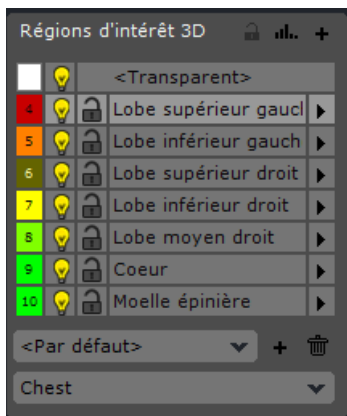


Figure 14-197 Thorax ROI Group

You can also modify existing ROI groups by selecting the ROIs you want to display for each anatomical structure, or create new ones.

- Select <...> to access the Edit ROI Groups window (see Section 7.7.26)

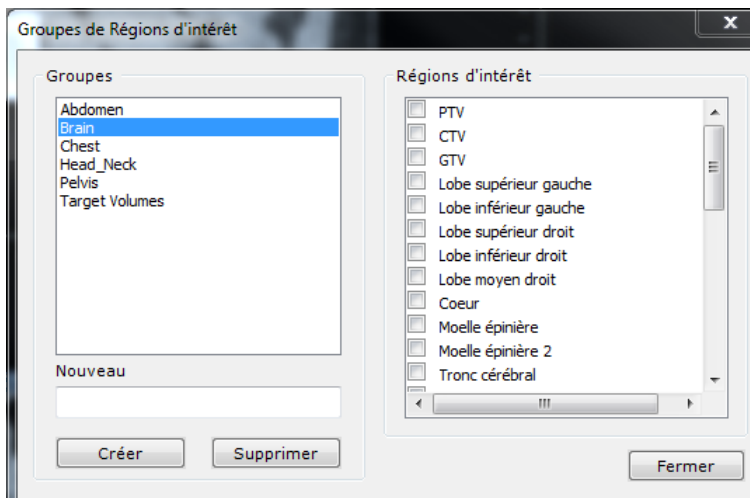


Figure 14-198 Editing window for ROI Groups

Each ROI can then be exported in DICOMRT format (see Section 5.3.6) to or from a Treatment Planning System.



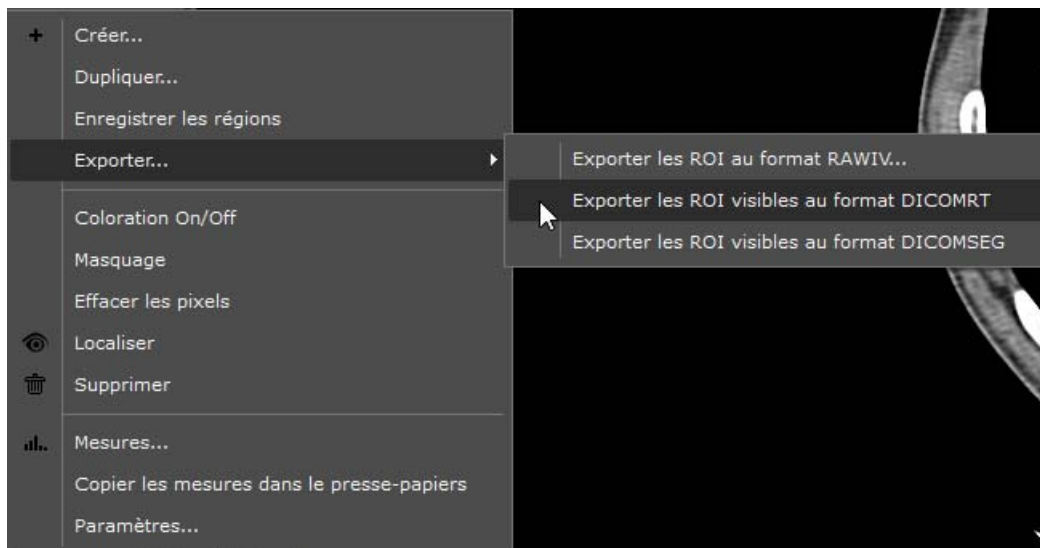


Figure 14-199 Export of ROI in DICOM RT format

## 14.13 Lung CAD

If the Lung CAD option is activated, a medical diagnostic aid is integrated into the Standard CT and Standard CTAP protocols.

Automatic detection of lung nodules is performed by the Veolity medical device developed by Mevis. The detected nodules are then automatically integrated in Myrian and displayed on demand.

### 14.13.1 CAD button

#### Standard CT

A CAD button  is available in the button bar in the visualization step.

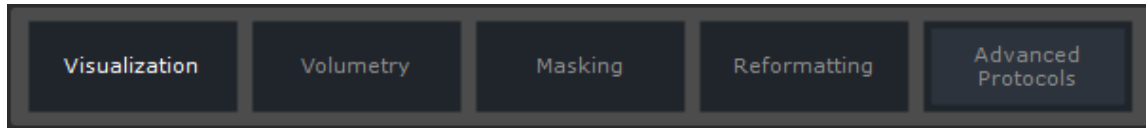
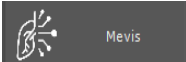


Figure 14-200 Steps in Standard CT

#### Standard CTAP

A CAD button  is available in the button bar at the «Lungs» step.

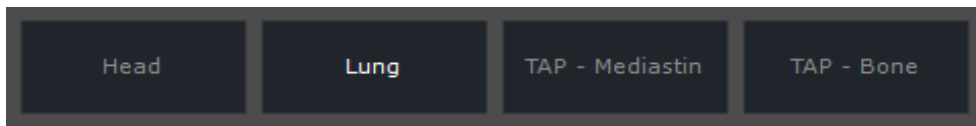


Figure 14-201 Steps in Standard CTAP

### 14.13.2 Functionalities

Click on the CAD button to display the suspected lesions.

The number of detected findings is displayed below the button.

Blue squares surrounding the suspected lesions are displayed on the exam.



Figure 14-202 Display of findings

You can navigate from one finding to another by using the arrows or by using the drop-down list.

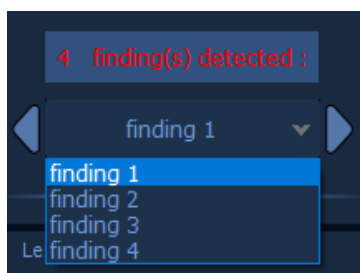


Figure 14-203 Navigation between findings

To hide the findings, click on the CAD button again.

A button allows you to switch to the XP-LungNodule protocol to deepen your analysis.

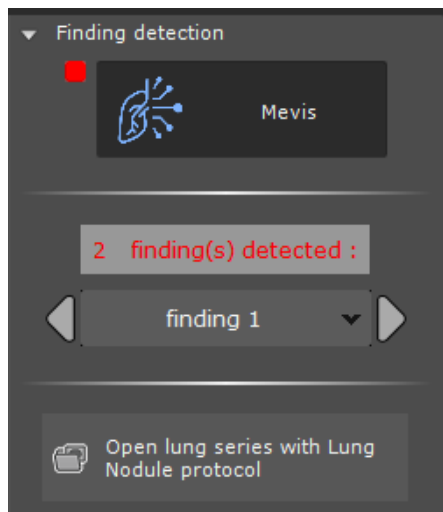


Figure 14-204 Open lung series with Lung Nodule protocol

## Chapter 15

# 15 User Preferences


- Click on  in the Main Screens tab at top-left to open the Preferences screen.



Figure 15-1 Preferences button

Via this screen you can access the seven following configuration tabs to modify your User Preferences:

- DICOM tab: DICOM configuration
- Users tab: List of registered users and associated privileges
- System tab: global operational software settings (activation code, server settings, automatic database cleaning setting via DBManager, etc.)
- Display tab: workspace Color scheme, image Resampling, hide/reveal patient details, mouse button tool assignment settings, screen calibration etc.)
- Support tab: for contacting Intrasure
- Protocols tab (see Section 7.3.2 for detailed information)
- About tab: Myrian® license and 3rd party license agreements

The user has the possibility to show or hide these different tabs. The tab displayed at the opening of Myrian can also be chosen.

Please contact Intrasure's support to implement the modifications (see Section 1).

## 15.1 DICOM settings

The DICOM setup screen is divided into three parts:

- A list of known DICOM servers
- The DICOM connection status panel
- Configuration of the Series reception service

These parameters largely depend upon your establishment's DICOM network configuration and are usually set by the person responsible for the installation of Myrian®. It is however possible to test connection to the displayed DICOM network easily thanks to the 'Echo' function.

To test connection to DICOM servers:

- Select the server(s) of your choice in the list.
- Click on the 'Echo' key at right of the 'Port' field



To select more than one server at a time, hold down either the Shift or Control keyboard key and click on your choice. You may also use the Arrows pad whilst holding down one of these keys).



You must have administrator rights to change these parameters.

---



As long as DICOM parameters have not been set-up, it will not be possible to either list or retrieve Studies from a remote DICOM server.

Figure 15-2 DICOM configuration



Myrian® filters DICOM Application Entities, such as PACS, Servers, Printers, CD/DVD Recorders, etc., according to the type of DICOM entity which was specified via a drop-down menu in the DICOM properties screen which appears when you create new or edit an existing DICOM entity profile. The type is then displayed in the 'Service' column.



Remote DICOM entities sending Studies to Myrian® require both the local IP address and TCP/IP of the host machine, which must be provided to enable module to retrieve Studies.



DICOM images are retrieved via the listening port.



In cases where the host computer has more than one IP address (several network adapters, OpenVPN, etc.), it is possible to select the desired choice from a drop-down menu.



Any DICOM "AE" (Application Entity) must be authorised to connect Myrian® to distant servers, modalities or printers.

Contact your establishment's appropriate personnel to configure remote connectivity authorisation.

If you are using Microsoft® Windows® XP SP2, make sure that outgoing and incoming DICOM request ports have been authorized (contact your establishment's IT personnel to verify or adjust these settings).

## 15.2 System parameters

The System screen contains a detailed list of settings.



Please make sure to include these information whenever you need to contact Intrasure Technical Support ([support@intrasense.fr](mailto:support@intrasense.fr)).

Parameter	Value
Activation Key	4637:1FC8:F62D:2B18:1616:1463
Activation Server (1/2)	
Activation Server (2/2)	
Centralized Configuration	Disabled
Certification Zone	CE
Current user data	pf_ro / Admin+Operator+Observer / Windows
Downloaded Files	Preferences:0 Protocols:0
Local IP address.	192.168.56.1 / 192.168.1.18
Network connection	Ok/17/9/2020/local/04
OS	Windows 10 Professional (Build 18363)
Package	Myrian 2.8 / 0502
Percentage of physical memory used	73%   2138 Mb/8077 Mb   2670 Mb/15245 Mb
Serial number	CUC6-J7EH-LIAC-9F9A-SE11-YZTC
Version	Myrian® 2.8.0 (Build 105) / DBMS Ok

Figure 15-3 System settings tab

This screen provides access to a number of functions:

- The 'Refresh' key updates Parameter and Value fields
- The 'Copy key' button copies the product's activation key to the clipboard
- The 'System' radio-button at top-right of the tab activates the display all the information relative to the System (date and time of installation, version of the Software, Activation key, etc).
- The 'Modules' radio button beside the System button displays all the modules that are installed with your software and can, if needed, be activated.
- The 'Activated options' radio button displays the list of activated products and their UDI number

System     Modules     Activated options

Figure 15-4 'System', 'Modules' and 'Activated options' radio-buttons

### 15.2.1 Files

You can switch between Local Study Lists in Myrian® by changing the Database directory in the 'Files' section of the System Tab.

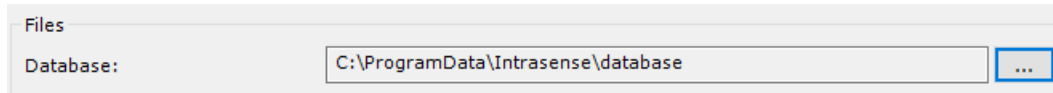



Figure 15-5 Database Directory

This can be particularly useful if you are working on several different Study Lists such as, for example, a research database and an everyday clinical database.



Changing Local Database  is done 'on the fly' and does not require a software reboot.

---



You can copy both the 'System' and/or 'Modules' information to the Clipboard via a right-click menu.

---



Some information contained in this tab can be requested by the Intrasense Technical Support Team during Helpcall (see Section 15.5).


---

### 15.2.2 Activation

This section indicates the way the product was activated by the Intrasense license provider (locally or by network). The installation guide found on the application CD includes a product activation guide.

- Check the 'Connected' box to make the license server operational.

### 15.2.3 SvcManager

Double-Click on 'SvcManager' icon  enables you to access the database management system window for the configuration of the following parameters:

- DICOM SCP
- Database
- Declared Users

A list of authorized users is provided in this screen. The current user is shown in the 'Connected Users' section at right.

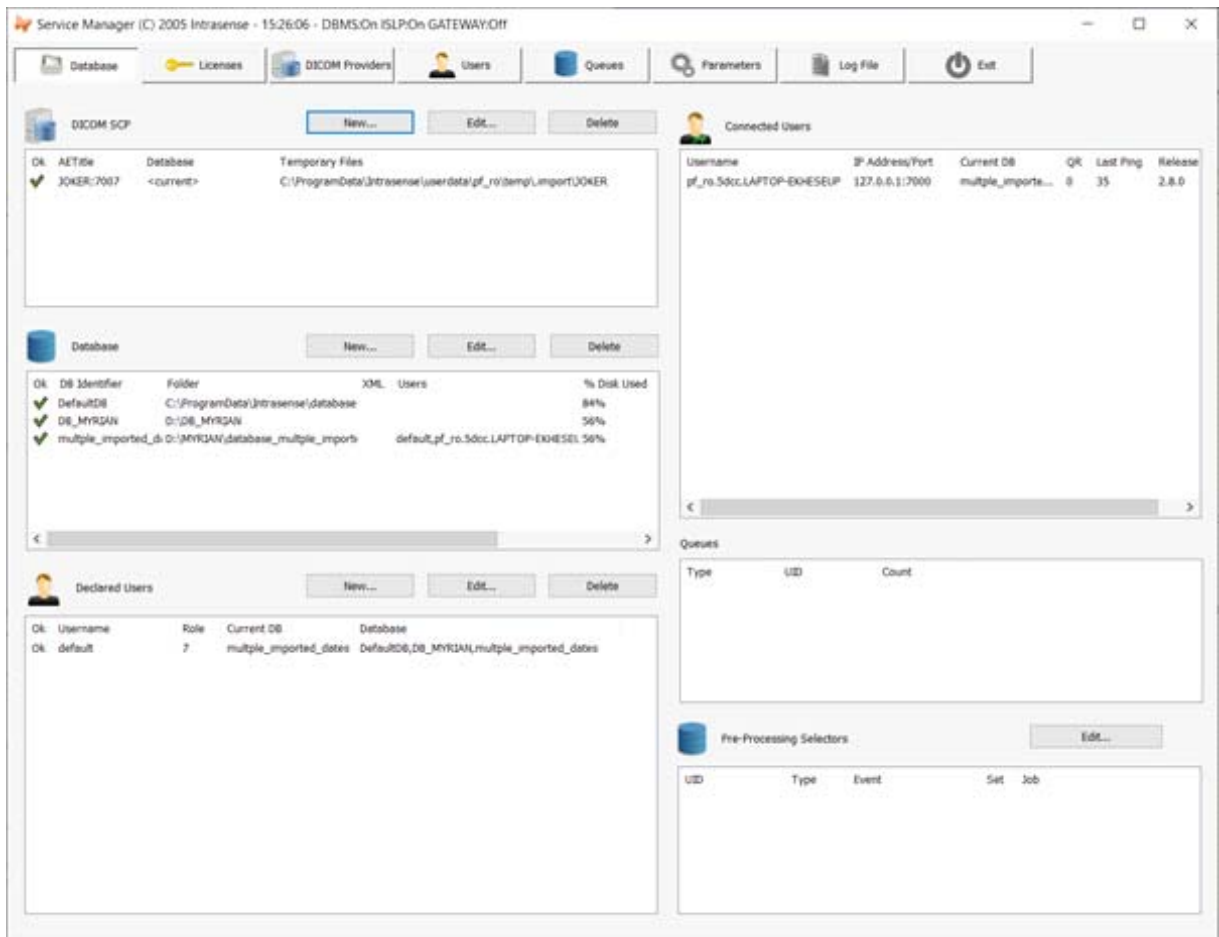


Figure 15-6 Service Manager main screen



Only the Administrator can create and/or delete user accounts and databases and modify the privileges and password.

## 15.3 Display settings

### 15.3.1 Color theme

This part of the screen provides a choice of user-definable Color themes for your Myrian® workspace. It is also possible to customize the color of the text information display (DICOM fields, etc.)



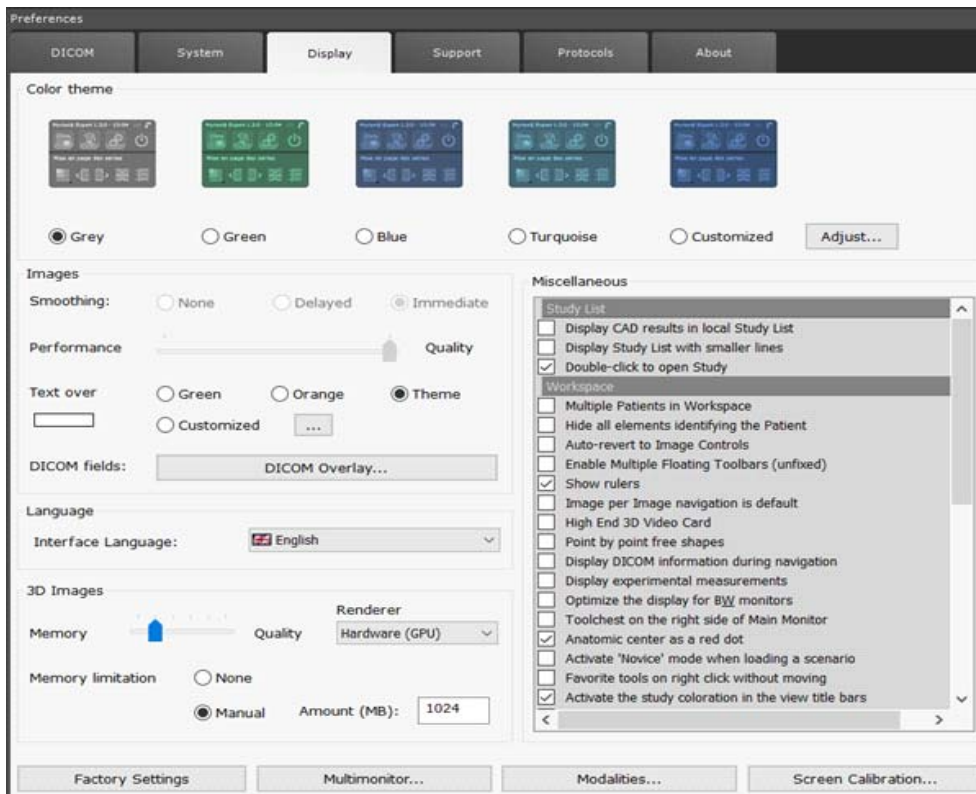



Figure 15-7 Display settings

### 15.3.2 DICOM Overlay

- Click on **DICOM Overlay...** to open the 'DICOM information to be displayed on images' screen (can also be accessed using the DICOM key  from the image Display Function Toolbar in the main workspace, see Section 4.4.4.2).

This screen enables the configuration of overlay DICOM fields to appear on images generated by any modality.

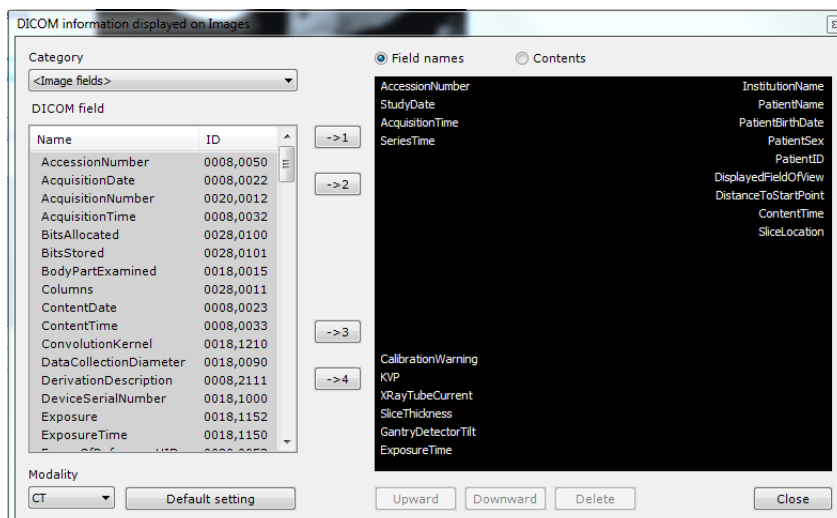


Figure 15-8 DICOM information displayed on images screen

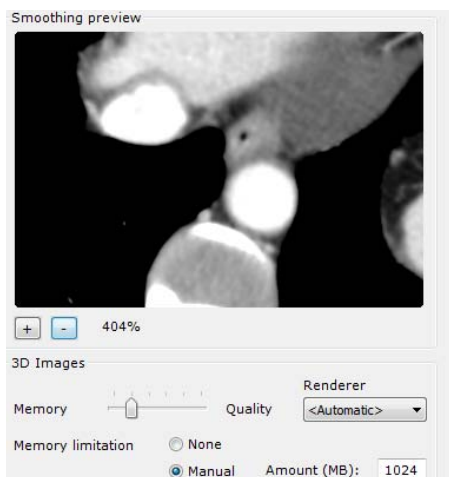
### 15.3.3 Image Smoothing

'Smoothing' is a 'Resampling' process aimed at improving the appearance of images in Myrian®.

You can adjust **Smoothing** by selecting one of 3 filters:

- **None**: no alteration to the image originating from the modality
  - **Delayed**: Smoothing is applied after mouse/keyboard activity stops: allows faster navigation and is more appropriate for slower machines
  - **Immediate**: Smoothing is continuously applied (requires more computer resources)
- Use the 'Performance > Quality' slider to modify the Smoothing (higher settings reduce computer performance).

A zoomable preview window displays the current settings.



Use the '+' and '-' keys to zoom in/out or drag the mouse over image whilst holding down the left mouse-button to Pan the image around

Figure 15-9 Smoothing preview thumbnail and '3D Images' quality slider



Use the 5-point '3D Images Memory/Quality' slider to modify the quality of 3D rendering



Smoothing settings also apply to ROIs when they are highly zoomed-in



The Smoothing settings and preview are only available once a Study has been opened.



When interpreting images, you should bear in mind that Resampling may affect the original image. Please experiment with this tool to acquire the appropriate technique.



As for all images, Native Images are by default smoothed to improve their visual aspect. This filter can however be removed by selecting the 'No Smoothing' setting

### 15.3.4 Language

- Use the drop-down menu to select a language for Myrian® interface.

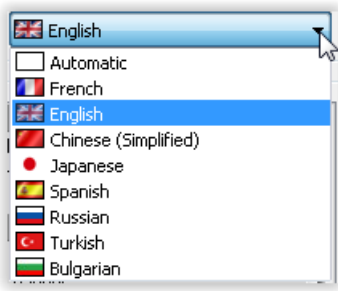


Figure 15-10 Language drop-down menu



Choose 'Automatic' to select the host PC's default OS language.

### 15.3.5 'Miscellaneous' - Advanced User Options

This menu has checkboxes to switch on or off the following functions:

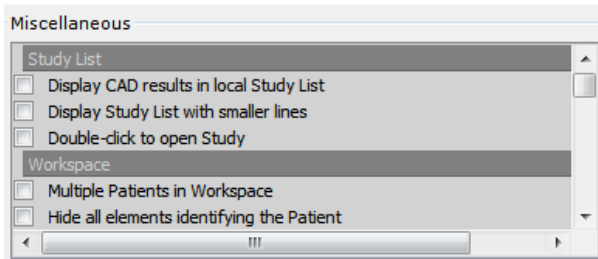


Figure 15-11 Miscellaneous tab

- Hide all elements identifying the patient - Patient Name will be blanked out on all screens (in viewer titles, the 0010,0010 DICOM field) which could appear as an overlay, in the Scrapbook title, etc.
- Auto-revert mouse-buttons to Image Controls - Toggles mouse-buttons to revert to last assigned Image Control ('Primary Tool') after just one use of an assigned 'Secondary Tool' (see Section 4.9)
- Enable Multiple Floating Toolbars (unfixed) - Several Floating Toolbars may be opened at the same time, moved around freely and placed anywhere in the workspace ('unfixed'). Default setting is unchecked: only one Floating Toolbar can be opened at a time and it snaps to the bottom-center of the active view
- Show Rulers - Toggles display of viewport rulers on/off
- Image per image navigation is default - The 'Shift' key must be held down during rapid mouse-action to activate speed-navigation (factory setting), otherwise default navigation setting at load-up is set to rapid mouse-action and the 'Shift' key must be held down during navigation to force slice-by-slice navigation
- High End 3D video card - activates/deactivates the maximum quality of 3D rendering (highest Level of Detail) during actions such as panning, rotating, zooming
- Point by point Free shapes - any freehand contour tracing may be done point by point as opposed to drawing in one whole movement
- Display DICOM information during navigation - activates display of DICOM information during navigation or Fly-through
- Display CAD Results in Local Study List - activates display in the Study List of 'CAD Result'
- Display experimental measurements - activates display of the following measurements in the Advanced Measurements window:
  - Greatest diameter of inertia (3D)
  - Greatest diameter of inertia of all slices in the Axial Plane
- Double-click to open a Study - toggles the double-click action on a Study icon between expand the Study and open directly
- Optimize the display for B&W Monitors - enhances the display on Black and White Monitors
- Display Study List with smaller lines - toggles icon display for Studies and Series between large and small to optimize

the display for large lists

- Toolchest on the right side of Main Monitor - places the Toolchest on the right-hand side of the Workspace in the Main Monitor (does not appear in the list if the Mutimonitor option is activated)
- Verify conflicts on Patient CD - checks for Name, Date Of Birth and PID conflicts when importing Studies into the Local Study List.
- Multiple Patients in Workspace - enables Series belonging to different Patients to be loaded in the Workspace at the same time
- Anatomical center as a red dot (by default): toggles display of the anatomical center as a red dot and a light blue cross
- Favorite tools on right-click without moving
- Allow selector capture and edit



The 'Hide all elements identifying the patient' option does not delete any identifying information that incorporated natively in DICOM images (as can be the case in certain ultrasound environments for example).

---



CAD Results are Series which have been generated via dedicated computation servers. Such Series are not directly viewable in the Workspace, although they are required by certain processing engines to generate some types of ROI such as the Colon or Polyp ROI.

---

### 15.3.6 Restore Factory Defaults

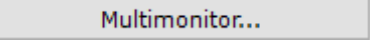
- If you wish to undo all user-modified settings, click on  under the Miscellaneous tool box.

### 15.3.7 MultiMonitor

#### 15.3.7.1 Overview

The Multimonitor option enables you to spread your Myrian® workspace over as many monitors as your system is configured for. When it is activated, a button appears in the Preferences>Display Tab beneath the Miscellaneous tools box (see Figure 8-7).

#### 15.3.7.2 Method of use

When you click on the  button, the Multimonitor Settings screen appears:

- Use all monitors: click on this to activate Multi-monitor functionality
- Left-to-right ordering: click on this to toggle (1) the Toolchest either left or right and (2) Primary monitor either left or right of all Secondary monitors
- Automatic Series distribution: a drop-down menu enables you to choose whether when you load multiple Series, they are evenly distributed (automatically) on all screens or on any one screen in particular



These settings require application reboot to take effect.

---



You can modify the size of the font of all the annotations/overlaid DICOM information on the image by modifying each respective "Font scaling" percentage 

---

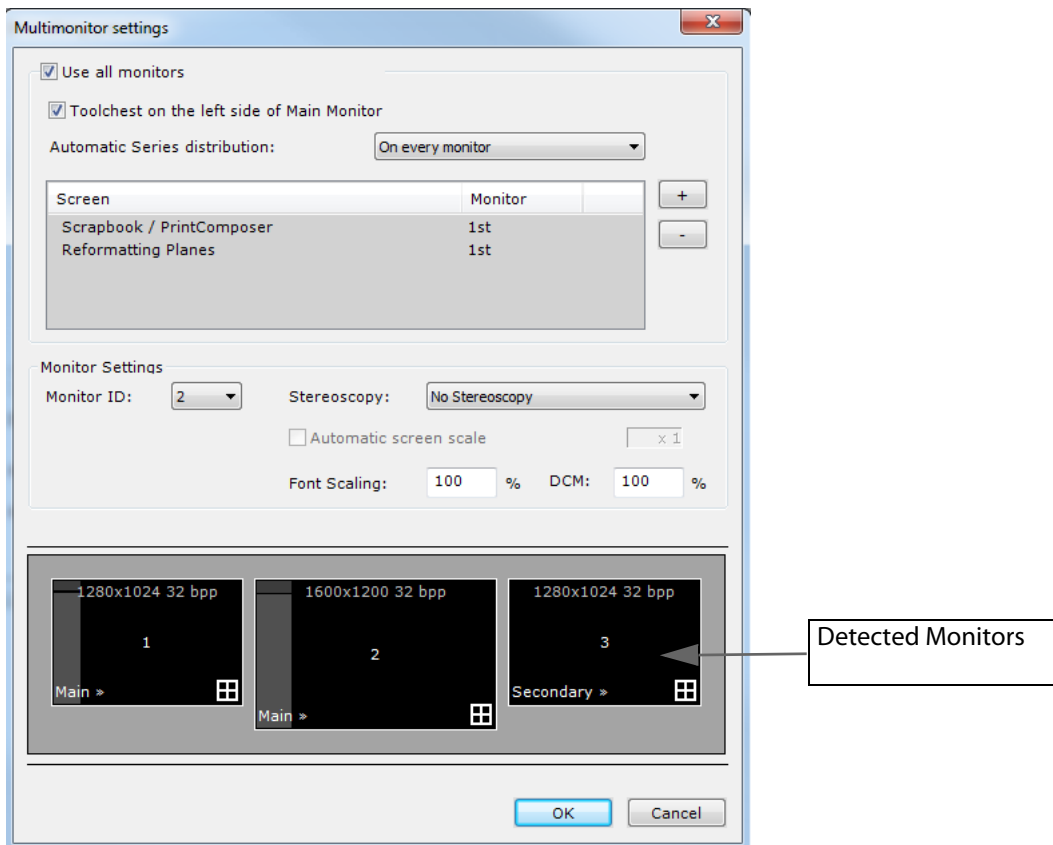


Figure 15-12 Multimonitor setting screen

You can also select items in the box above the 'Detected Monitors' area (Scrapbook/PrintComposer, etc), then using the '+'/'-' buttons, you can choose which monitor will display each item.



This function can also be modified via the context menu on the title bar of the Secondary Screens.



This function does not require an application reboot.

Moreover:

- Click on the bottom-left corner of the detected monitors to determine their status: either 'Main', 'Secondary' or 'Not used'

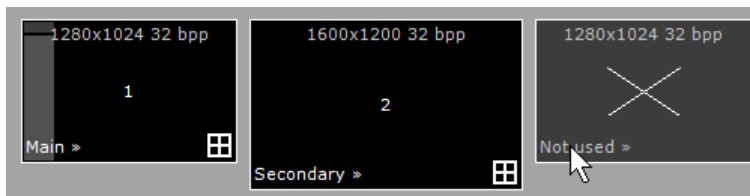


Figure 15-13 Toggle monitor status

- Click on the little white square at the bottom-right of any **secondary monitors** to set that monitor as "part of the Main Workspace", i.e. it can display clinical images as well as the Scrapbook, PrintComposer, etc.

This monitor will also be used to display multiple Series when multiple Series are opened in automatic distribution mode.



Figure 15-14 Workspace to secondary monitor toggle



Series can be moved from one monitor to another by drag & drop from the view title bar of the view containing the series to move. When drag & dropping the series on top of an existing one on the other monitor, series swap from one monitor to another.



The selected series can be added into the other monitor (instead of swapping) by clicking on CTRL while performing the drag & drop. The other monitor adjusts to the new view.

You can also configure the Multimonitor mode to visualize simultaneously the **Study list on one monitor** and **your workspace on the other**. In that display configuration, the Study list always remains visible and usable on the first monitor as illustrated hereunder:

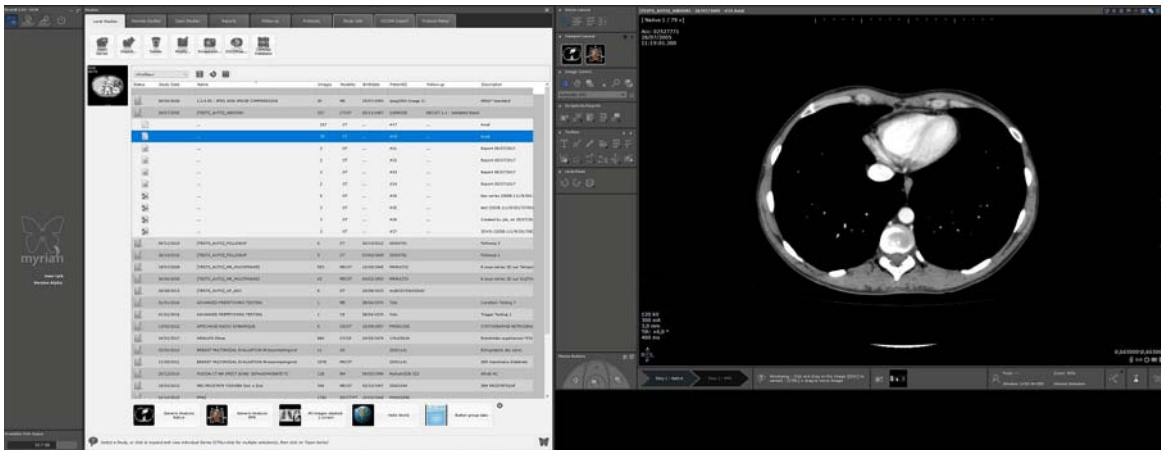




Figure 15-15 Multimonitor mode combining display for workspace and Study list

- To set Myrian® in such configuration, gray out the workspace icon  on the main monitor by clicking on it
- Make sure that there is an active workspace (white icon ) for any other monitor

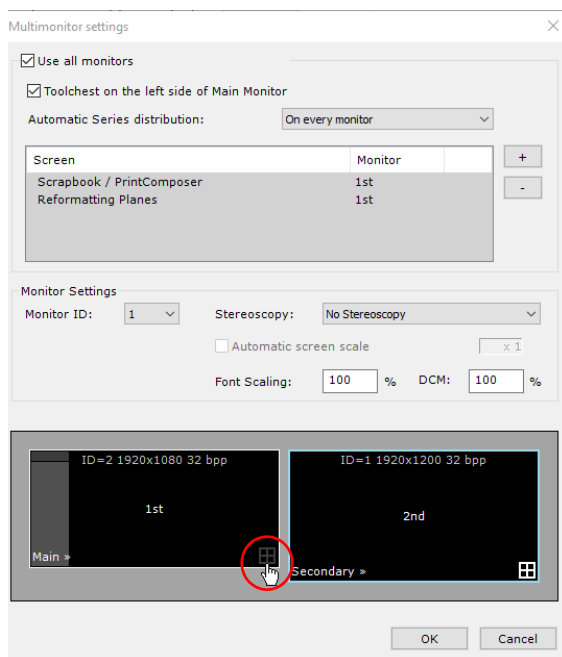


Figure 15-16 Configuration for Multimonitor combining display for workspace and study list

### 15.3.7.3 Distribution

#### 15.3.7.3.1 Auto-grid mode

When you open multiple series simultaneously in Multimonitor mode, the auto-grid mode behaves in the following way:

- If the **resolution and page layout (portrait/landscape) configuration varies for each screen**, the Workspace on each monitor is managed independently: **Series will open alternately on one monitor then the next, one by one in maximum size**
- If the **resolution and page layout is identical for each monitor**, the global display area is considered as a single Workspace and the series will open from **left to right across all monitors in a single autogrid layout**

When opening multiple series simultaneously in Multimonitor mode, select a customized grid mode.


Whatever layout is applied to visualize the multiple series (grid 2x1, 3x3, etc.), series display splits in the selected layout among both screens supporting at the same time synchronization for page navigation between the two monitors.

- Use the series layout navigation control buttons to scroll series.


To navigate through series pages on active screens:



Figure 15-17 Dual monitor navigation toolbar

- Click on the left page navigation control  to scroll series from right to left (series disappear from the left screen while displaying new series are displayed on the right and so on as you go along with series navigation).



The right page navigation control  enables you to proceed with series display the other way round.

#### 15.3.7.3.2 Customized grid mode

When opening multiple series simultaneously in Multimonitor mode, select a customized grid mode.

Whatever layout is applied to visualize the multiple series (grid 2x1, 3x3, etc.), series display splits in the selected layout among both screens supporting at the same time synchronization for page navigation between the two monitors.

- Use the series layout navigation control buttons to scroll series.



To enable synchronization, make sure that the display settings (page layout and grid size) for both monitors are identical.

#### 15.3.7.4 Stereoscopy rendering mode via the Alioscopy screen plugin



Stereoscopy rendering mode must not be used for diagnostic purposes.



Stereoscopy usage is subject to option activation.

This feature which requires a stereo-capable monitor (Alioscopy Screens) enables to visualize 3D viewports in stereoscopy 3D rendering mode in the following exploration modes:

- Volume Rendering (all render modes i.e. MIP, tissue coloration, etc)
- Surfacic ROI
- Endoscopy

#### Connecting Alioscopy screen to computer

- Plug in the Alioscopy 3D screen and connect the DVI cable from the computer to the 3D screen



Computer must be shut down and powered off before connection.

---



The connection cable from the computer to the 3D display screen must be DVI/DVI only.

---



For better 3D performance, we recommend NVIDIA graphics cards (although ATI cards can be used).

---

- Connect the power supply cord
  - Turn on the computer then the Alioscopy 3D screen
  - Modify monitor settings to Multimonitor display in your system 'Display Settings'
- 



Monitor native resolution is required: Open 'Screen Resolution' by clicking the Start button, click Control Panel and then, under 'Appearance and Personalization', check that your monitor screen resolution is set to 'Recommended'.

---

- Open Myrian® application and go the User Preferences> Display Tab.
  - Click on the 'Multimonitor' button
  - In the 'Stereoscopy' area, set both monitor status (Main, Secondary) via the Monitor ID combo-box then select your preferred stereoscopy mode to apply to the appropriate monitor via the 'Mode' drop-down menu:
    - Alioscopy 5 View points
    - Alioscopy 8 View points
    - Anaglyphic (wearing standard Green/Red glasses is required)
- 

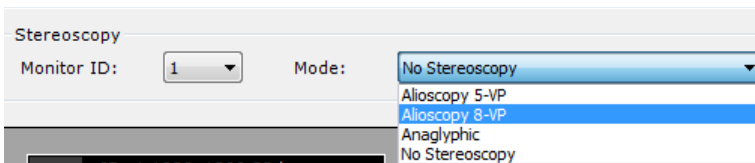


Figure 15-18 Setting Alioscopy display parameters

---



Whatever stereoscopy mode is selected, it fully works both in OpenGL and DirectX.

---

According to the selected Alioscopy mode, the abbreviation corresponding to the chosen mode is displayed (in red capital letters) at the bottom-right of the selected monitor:



Figure 15-19 All 3D viewports opened on Monitor 2 will be displayed in Alioscopy 8-VP stereoscopy rendering mode

---

- Click OK to confirm.
  - Go back to Myrian® main screen and open the desired series from the 'Local Studies' list to be visualized in one of the supported 3D exploration modes.
- 



The Stereoscopy Rendering Mode may affect performance display (such as 3D display speed) as it requires one rendering per viewpoint.


In 'Whole Volume' Exploration mode, the Stereoscopy Rendering Mode can be deactivated during interactive phases unchecking the 'high end graphics card' option in the Preferences/Display tab. Note that the other supported Exploration




Modes always keep the Stereoscopy Rendering Mode during interactive phases.

At the opening of the 3D view on the allocated monitor, the appropriate stereoscopy mode is automatically activated.

 Capturing a 3D Viewport in the Scrapbook keeps the Rendering Mode.


 Proper visualization of such images via an external viewing application requires the use of appropriate display device. Make sure that the image export is:

- Lossless (only BMP or TIF),
- And viewed at exact image size in the external viewing application.

 Changing Stereoscopy settings in the Preferences>Display>Multimonitor Tab automatically requires the closing and reopening of the view for the change to be taken into account.

### 15.3.7.5 Printing a snapshot in Multimonitor environment

To take a snapshot of the whole Workspace displayed over both monitors:

- Click on the Capture button  at the bottom-right of any viewport and select 'Screen Capture' from the contextual menu

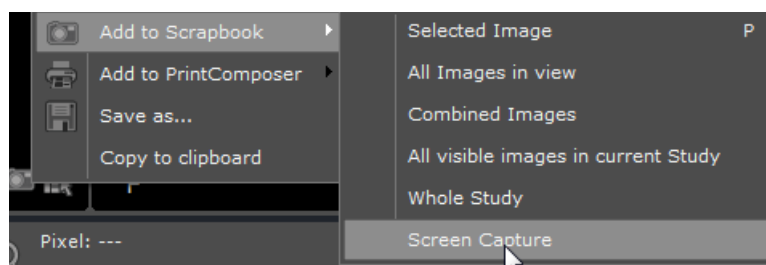


Figure 15-20 Capture a snapshot of all views displayed over both monitors

A global screen capture is created displaying the capture of each screen in a row (in the same order as the monitors).

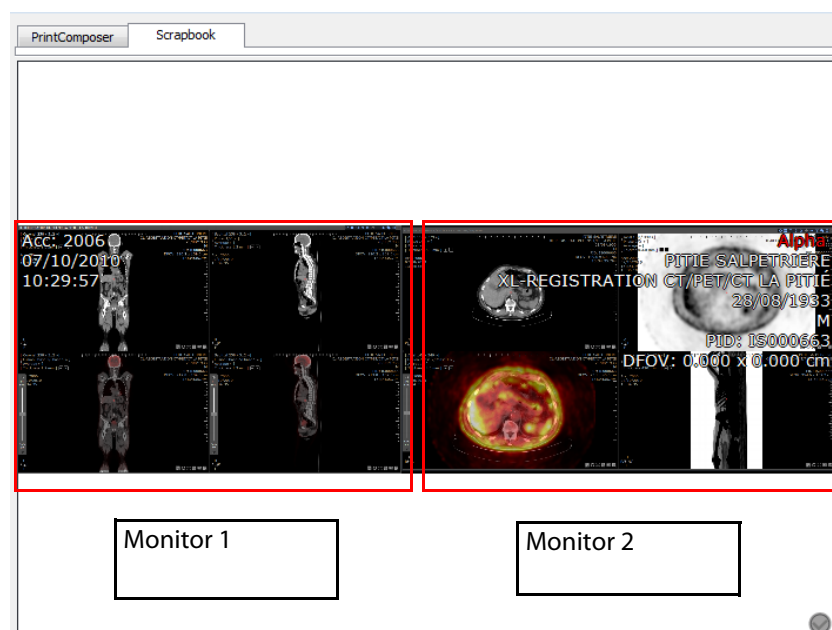
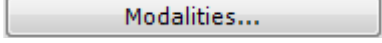


Figure 15-21 Single screen capture in Multimonitor configuration (Fusion PET/CT protocol)



Multimonitor support enables you to capture all screens for both PrintComposer and Scrapbook.

### 15.3.8 Modality Selection

Clicking on  at the bottom of the Preferences>Display Tab (beneath the Smoothing Preview) opens a list of Modalities which enables selection of which Modalities are listed in the 'Modalities' Filters of the Local Study List, the Remote Studies Tab and the Reports Tab (see Section 2.1).

By default, the Modalities listed are CR, CT, MG, MR, NM, PT, PX, RF, SC, US, OT and XA.

- Check the checkbox at left of any desired Modality to add/remove it from these lists.

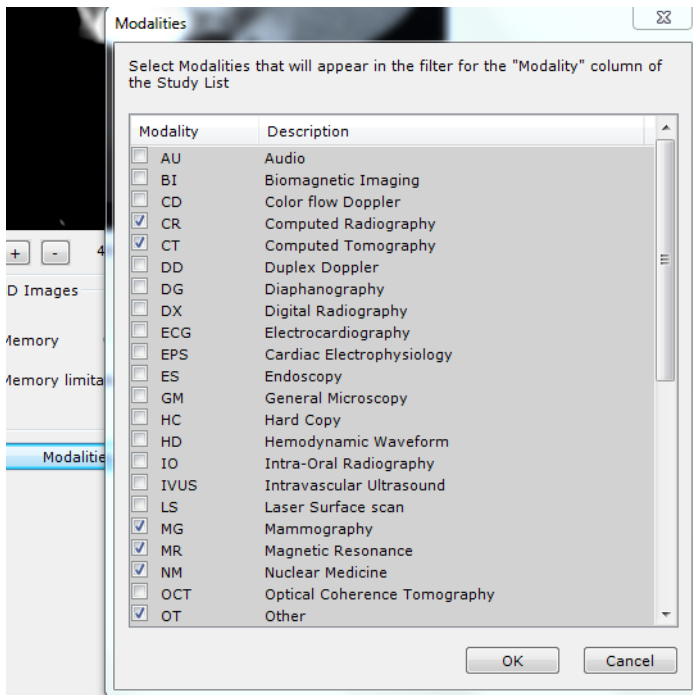


Figure 15-22 List of Modalities

### 15.3.9 Screen Calibration

The 'Screen calibration' key launches the 'ISCalibrator' Myrian®'s screen calibration tool. Please refer to Appendix 8. for further details on using ISCalibrator



ISCalibrator calibration procedure is quick and simple to perform. It is strongly recommended that you should carry it out as working with a screen that is badly or not at all calibrated may reduce your ability to analyse and interpret medical images correctly.

## 15.4 Keyboard shortcuts tab

The preference menu contains the keyboard shortcut tab.

In this tab, the shortcutable actions are displayed in 10 Shortcut Category tabs : Image settings, Workspace, Workflow, Layout, Annotations, Tools, 3D, Endoscopy, Key images, Others. For each action, the description of the action is displayed (1), including the key shortcut by default (between brackets), and the context (kind of viewport) if applicable (2). The shortcut can be edited by modifying the corresponding field (3). Once you have completed your changes, click on "save all changes".

It is possible to revert to the default value of a shortcut by clicking on  or clear the associated shortcut by clicking on .

To restore all keyboard shortcuts to their default values, click on "Reset to default values".



Figure 15-23 Keyboard shortcut tab

## 15.5 Support Tab

To contact Intrasense:

- Access the Preferences>Support Tab
- Use this screen to contact Intrasense technical support directly.

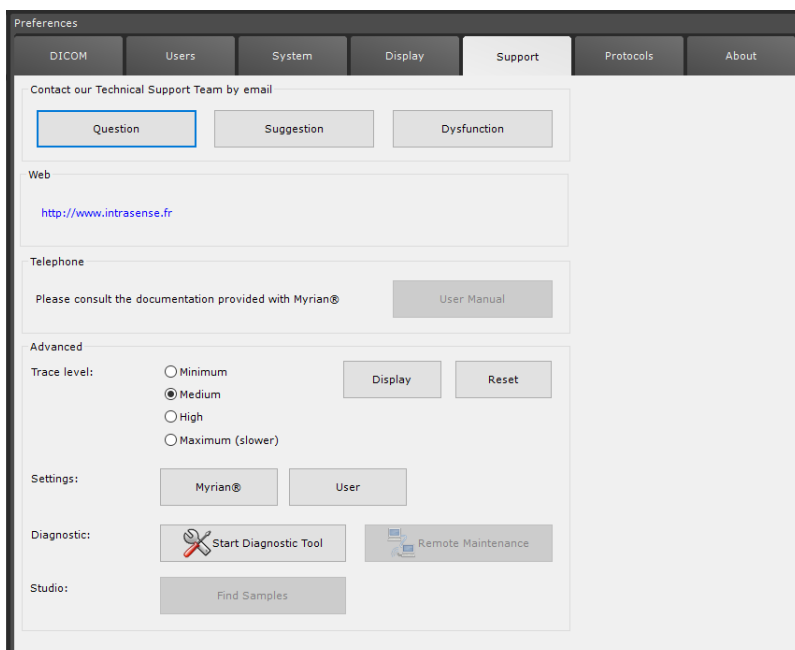


Figure 15-24 Support

- Click on 'Question', 'Suggestion' or 'Dysfunction' (generates an auto-filled email)

- Complete the message with your request or suggestion

- Click on 'Send'.



Requires an internet connection and a properly configured email client, e.g. Outlook, etc)



Technical information about your Myrian® installation is automatically included at the end of this preformatted email.

### User Manual

- Click on the 'User Manual' button at center-right of the Support Tab to access a manual in PDF format.

If supported, the User Manual will be provided in your own language. If however this version of the manual is not available, the User Manual will default to the English version.

### System Diagnostic

At the bottom of the page are a set of four buttons which launch settings and system diagnostic buttons. These buttons are intended for Intrasense Technical Support use only. An Intrasense Support technician may ask you to launch these tools during a help call.

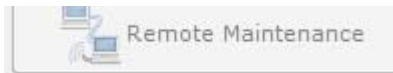
## Remote Maintenance

Intrasense does not perform preventive or regular maintenance. However, if necessary, Intrasense offers a remote maintenance service. Technical support will be able to launch a remote maintenance session from your Myrian® using the external Teamviewer® application.

Please request assistance from an Application Engineer from Intrasense for Teamviewer® installation and configuration on your machine.



The 'Remote maintenance' button



is disabled until Teamviewer® application has been successfully installed.

---

## 15.6 Protocol Tab

### 15.6.1 Overview

Protocols define the way your Workspace is organized. They predefine layouts, available tools, active viewports, use of monitors, auto-launch of segmentation engines, Study selection and loading criteria, etc.

Depending on your version of the software, it can contain various Factory Protocols adapted to the visualization and manipulation of the different forms of medical images.

Protocols can also be used to launch Series in other applications or modules which are installed on your machine and compatible with Myrian®.



Optional Expert Modules such as XP-Colon and XP-LungNodule have their own sets of Factory Protocols, some of which also create ROI automatically.

---

### 15.6.2 Protocol management

The Preferences>Protocols Tab lists all the Protocols, Protocol Families, Protocol Selectors which are present on your machine.

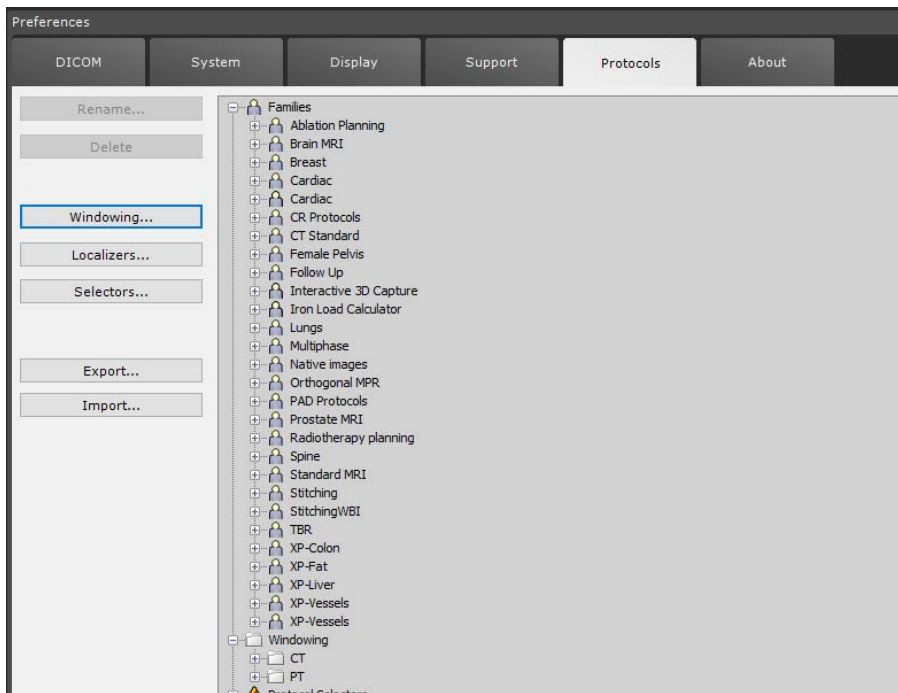


Figure 15-25 Preferences>Protocols Tab

- Expand each Family by clicking on the '+' symbol at left of the Family.
- For each Protocol Family, the following settings are listed:
- Values such as:
    - Which modalities the Protocol is available for,
    - Whether the Protocol in question is a Factory or a User Protocol
    - Which body part the Protocol concerns,
    - Etc.
  - The Name of the Family in all the supported languages
  - Each Protocol contained in the Family

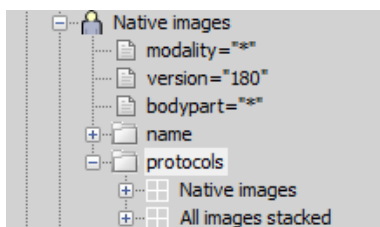


Figure 15-26 Expand User-defined 'Native Images' Protocol Family



The '(\*)' symbol indicates that the Protocol or Protocol Family has been modified or created by the User.

A set of command buttons at left of the Protocol List enables you to:

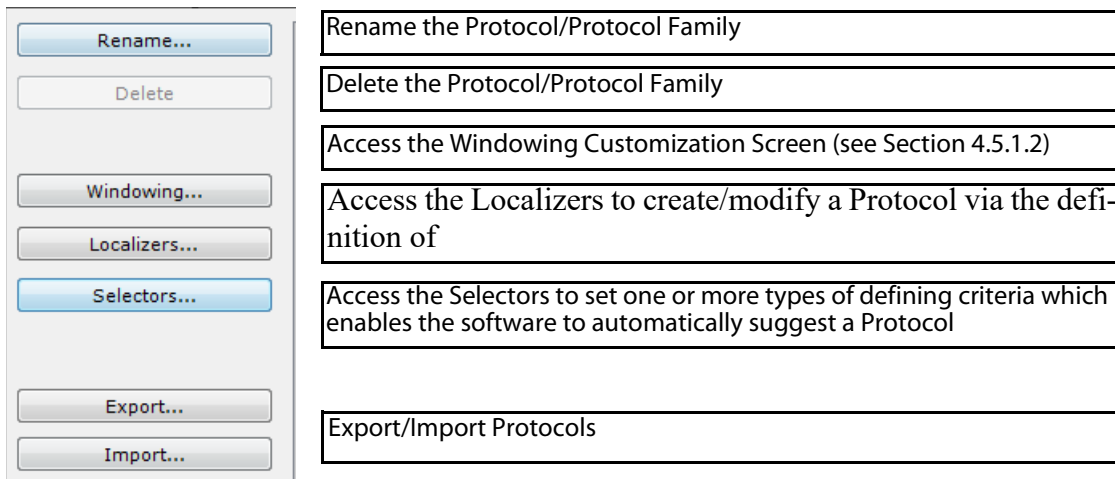


Figure 15-27 Command Buttons

### 15.6.3 Screen areas

The Protocol Tab is divided into several basic work areas:

- 1 Available/suggested protocol area
- 2 Protocol preview area

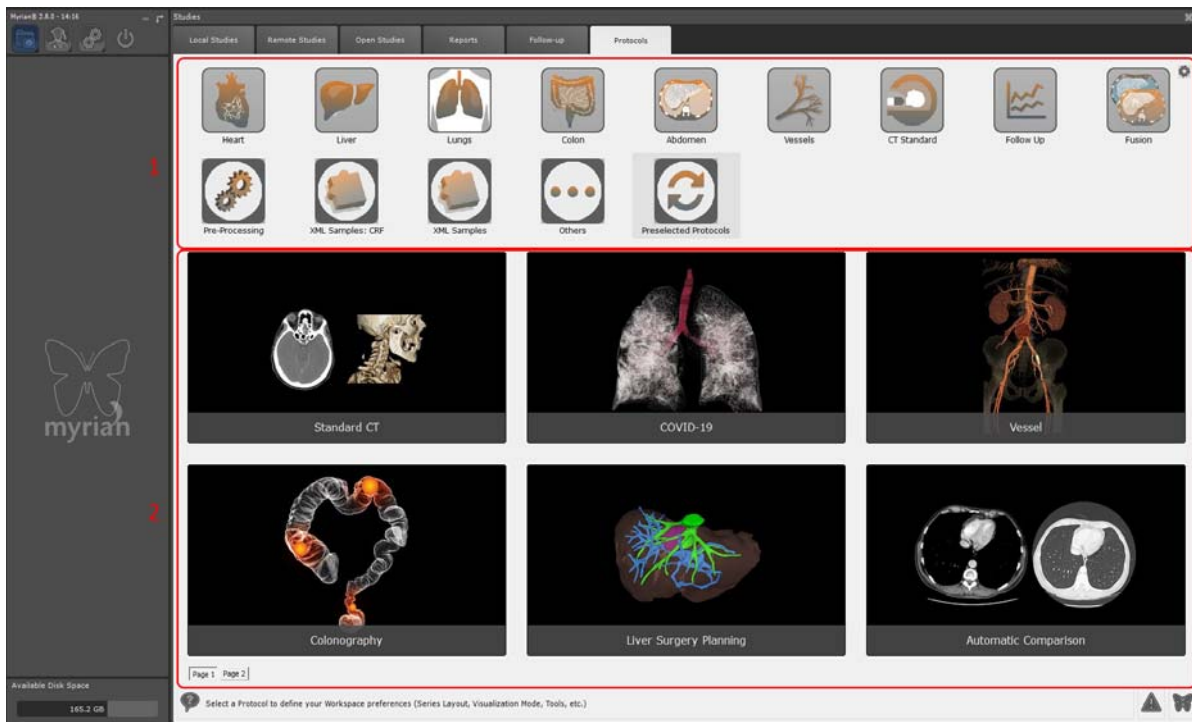


Figure 15-28 Protocol Tab

The software automatically suggests the most appropriate available Protocol, and outlines it in red.

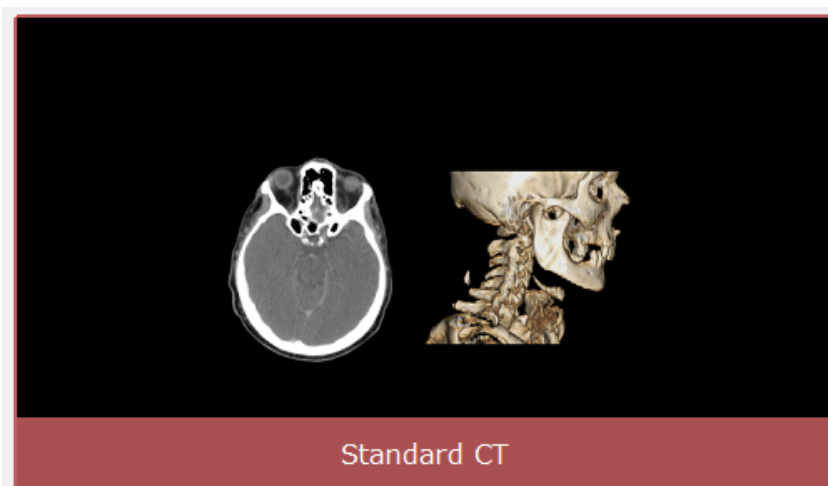


Figure 15-29 Suggested Protocol

Besides, right-clicking on a protocol thumbnail opens the following menu:

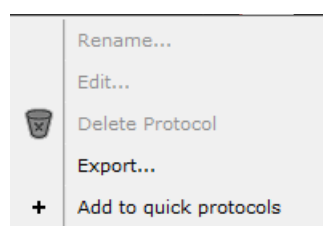


Figure 15-30 Protocol thumbnail context menu

## 15.6.4 Protocols which launch External Tools

Some Protocols automatically launch internal or external tools, such as segmentation engines or other applications installed on your machine.

For example, the 'Cardiac' Protocols load Series in the Workspace within the "Medis Suite MR" dedicated heart analysis application.

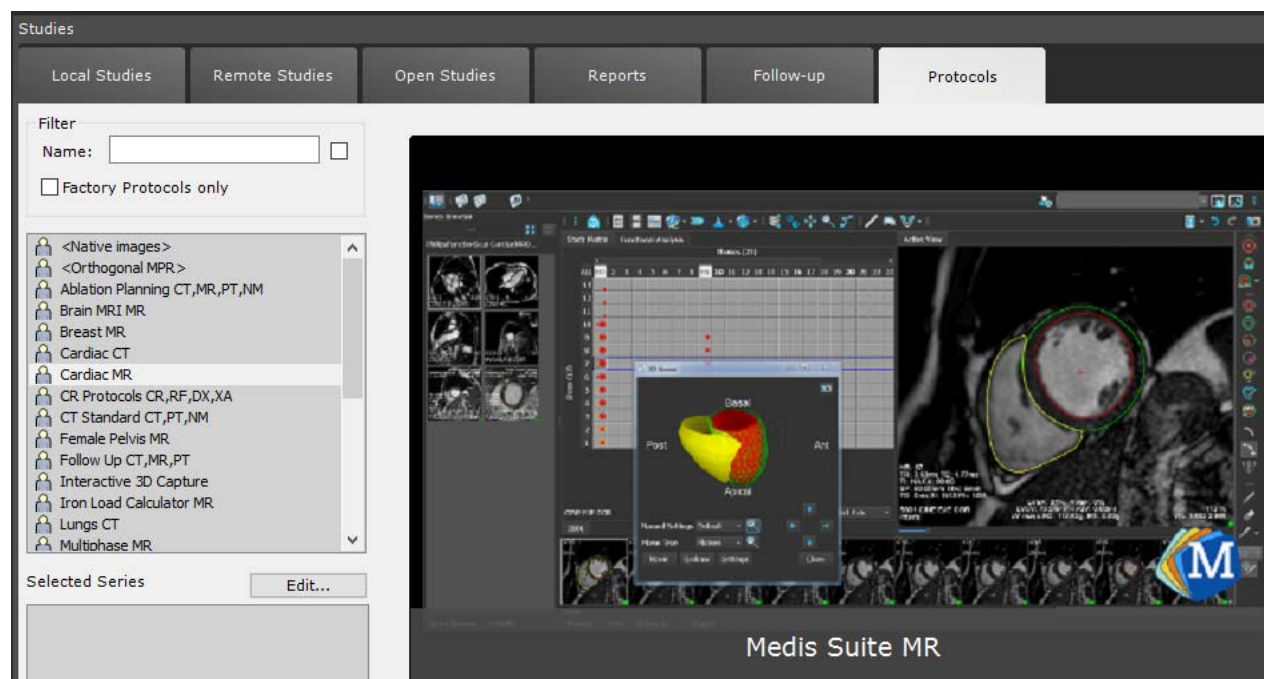


Figure 15-31 Medis Suite MR dedicated Cardiac Analysis application launching Protocol



The “Medis Suite MR” Protocol requires the corresponding Medis Software to be installed and activated.

### 15.6.5 Preview area

The Preview area displays large thumbnails of available Protocols. The software groups Protocols by ‘Family’ and by default displays the most pertinent family, highlighting the most appropriate.

A set of icons at top-left of the Protocol thumbnails indicates how the selected Protocol displays the Series (Series Layout, Visualization, Image Layout, Series count, etc). In the example below, the Series are loaded via the ‘Native Images’ Protocol with the following settings:

- Page Layout: Auto-grid
- Visualization: Grid Mode
- Image Layout: 1 Image, Full-screen
- Series count: All (opens all compatible Series among the selected Series)



Figure 15-32 Example of Protocol thumbnail icons

### 15.6.6 Filter and available/suggested Protocol area

#### 15.6.6.1 Filter area

Use this area to refine your search for the most appropriate Protocol using the ‘Filter’ field and/or checkboxes. As for other filter fields in the software, you can activate/deactivate the filter via a checkbox to the right of it. Furthermore, 1 checkbox is available:

- Factory Protocols only: only displays Factory presets

#### 15.6.6.2 List of Protocols

The box immediately below lists all Protocols present on your machine, grouped by ‘Family’.

- Click on one Family to view the Protocol thumbnails at right in the Preview area.

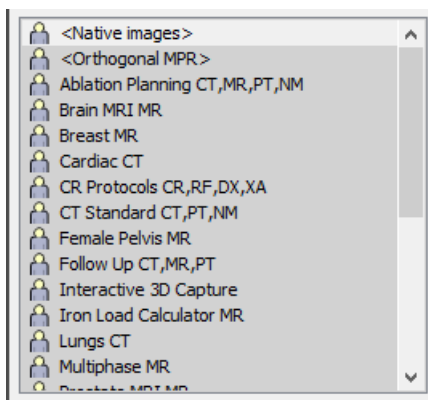


Figure 15-33 List of Protocol Families

### 15.6.7 Suggested Protocols

Below the list of Protocols is the ‘Suggested Protocol’ box, which proposes the choice of available Protocols compatible with any existing ‘Selectors’ created for the type of Study/Series you are opening.

#### 15.6.7.1 Create a Selector

Selectors can be defined either at the time of creation/modification of a Protocol (see Section 5.1.5) or in via the ‘Selector’ button located under the Selected Series area.





Figure 15-34 Create Selector button

You can set one or more types of defining criteria which enables the software to automatically suggest a Protocol:

- Select the Series you wish to open (if you have selected more than one Series, you specify the Series to which each Selector applies by clicking on 'Other Series' in the Selectors screen),
- Choose the types of criteria in the first 2 drop-down menus,
- Type-in the precise values in the 3rd column (must be done for each new Selector).

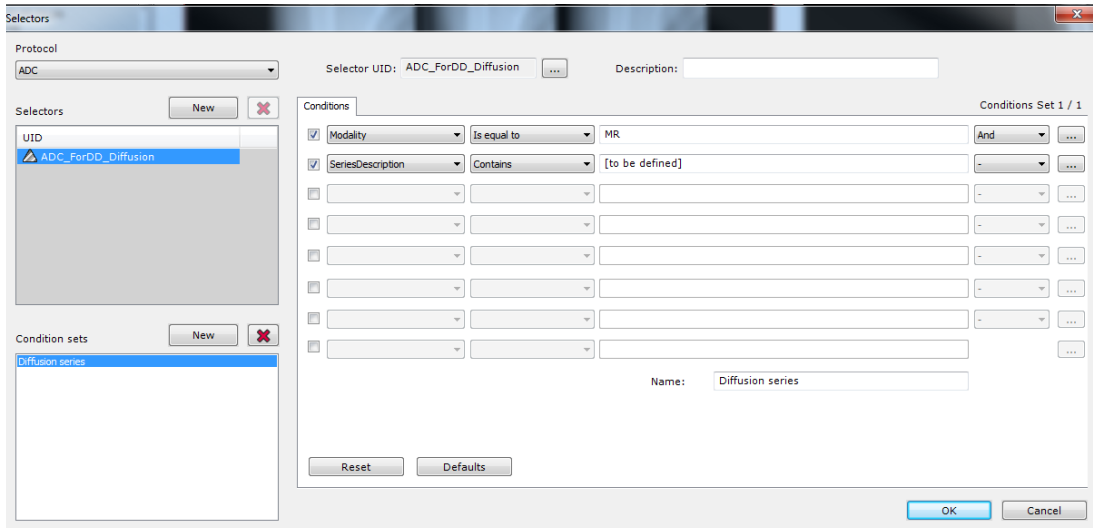


Figure 15-35 Define a Selector

### 15.6.7.2 Selector capture and edition for protocol series dispatching categories

Some protocols includes category selectors at series loading (i.e., Breast MRI protocol, Prostate protocol, PET/CT Fusion protocols, etc.). You can capture/edit a set of conditions (based on DICOM tags) for certain types of exam enabling you to customize protocol selectors without modifying factory protocol layouts.

- In order to enable selector capture on-the-fly and/or edition, go to User Preferences>Display>Miscellaneous and activate 'Allow selector capture and edit' option.

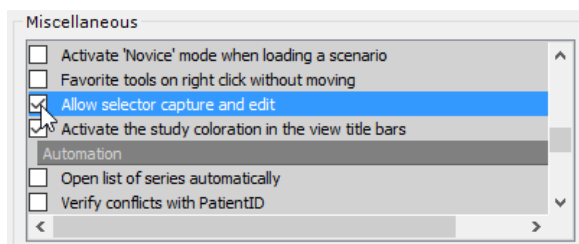


Figure 15-36 Activate Selector capture and edition in the Miscellaneous options

When loading series in a protocol including category selectors, a 'Capture...' and 'Edit' button will appear at the bottom-left of the window.

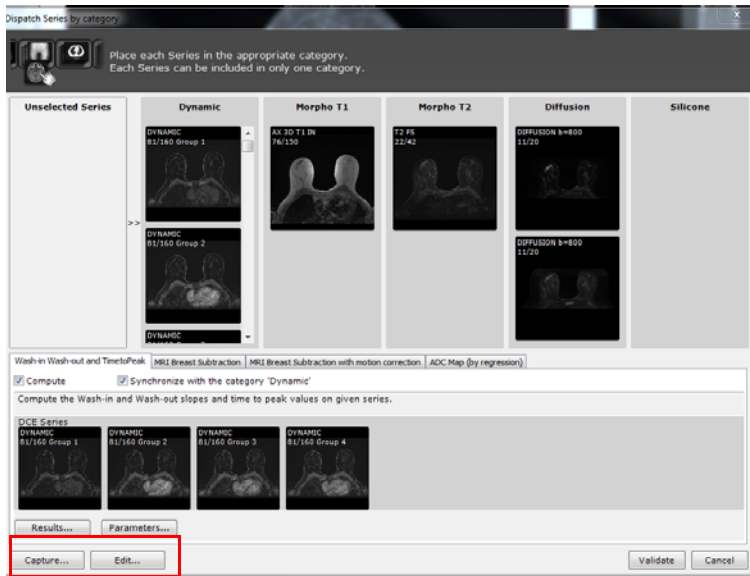


Figure 15-37 Selector 'capture' and 'edition' button in the category series selector window of the Breast MRI protocol

For detailed information about how to proceed, please refer to Myrian® App Clinical Toolkit 2.13.chm manual ('Selectors' section), located in the Documentation folder of Myrian® package installation.

### 15.6.7.3 Localizers

Localizers are Selectors which are used to exclude certain types of Series, such as "Localizer" or "Scout" Series, when opening Studies. They can also be used to discard such Series in the QuickPatient Toolbox.

To create a Localizer, click on the 'Localizers...' button at bottom-left of the Protocols tab and follow the steps for the creation of a standard Selector described in the previous Chapter (see Section 15.6.7.1 above).

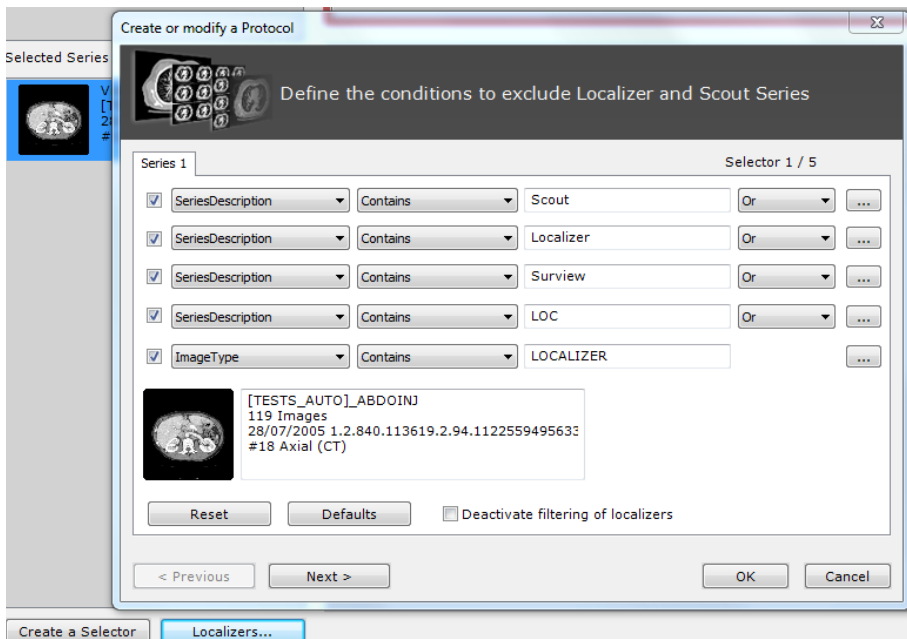


Figure 15-38 Create Localizers of exclusion rule



Series are automatically excluded when opening one or more **Studies**.



Series are not excluded when opening one or more **Series** or **Sub-Series**.



Localizers are global Selectors, not linked to any given Protocol.

## 15.6.8 Edit user preferences for Standard protocols (CT, MR, CR, PET/CT Fusion, Native images)

Some User preferences can be configured for all Standard protocols.

- For those Standard protocols, the 'User preferences' dialog box can be accessed directly from the workspace, right-clicking on the view titlebar:



Figure 15-39 Edit user settings for the Standard CT protocol from the workspace

Click on 'Edit user settings...'

The user preferences dialog box dedicated to the selected protocol opens.

**Layout selection**  
Choose the default layouts for the reading

Main monitor : Axial

Secondary monitor : MPR and Oblique

**Series layout**  
Maximum count of series open by study

Series count : 4

Activate the automatic loading of previous studies with the selected study

Count of previous studies to open : 1

Study organization of view by group in the Workspace

Organization : By Study / Rows

Synchronize navigation between views.

**Automatic processing**

Automatic masking of the table in 3d viewports

PET SUV normalization method : Patient Weight (g/ml)

Activate the series matching

Choice of default layouts on main or secondary monitors: these preferences are available for Standard CT; PET/CT Fusion. The secondary monitor is only available if Myrian® has been configured to use two monitors.

Choice of number of series open by study. Available for all Standard protocols.

Choice of number of previous studies. Available for all Standard protocols.

Choice of organization of the studies in the workspace. Available for all Standard protocols.

To save time, the masking of the table should not be activated to avoid the automatic computation at series opening when 3D viewport is not used. Available for Standard CT protocol.

Choice of normalization method. Available for PET/CT Fusion

This preference launches automatically the series matching during the loading process. Available for all Standard protocols.

Figure 15-40 User preferences edition screens for Standard protocols.

In the user preferences of the Standard CT protocol, in addition to the five windowing buttons selected by default, the user has the possibility to add, or hide, other windowing buttons in the workspace (see Figure 15-41).

**Add windowing preset buttons**

Windowings

- Automatic
- Chest
- Abdomen
- Pelvis
- Brain
- Lung
- Colon
- Bone
- Head and Neck
- Mediastinum
- Lung Fly Vessels
- Larynx
- Calcified Vessel
- Vertebra
- Pelvis Bone
- Soft
- Internal Auditory Canal
- Orbits
- Liver
- Cord
- CTC
- 2D Vessels
- 3D MIP Vessels
- 3D Average Bones

Figure 15-41 Screen to add/hide windowing buttons in the workspace

The Standard CT protocol loads previous studies in the workspace with the same modality as the selected active study, except for Standard CR protocol which loads previous studies of CR, DX and RF modalities.



According to the standard protocol to edit, the configuration options displayed in the dialog box can be different as well as the default settings.



For detailed information about user setting configuration related to the PET/CT protocol, please refer to Section 4.3.2.11.

To access the edition dialog box, you can also right-click on any of those above-mentioned protocol thumbnail in the Protocol screen to visualize the following context menu:

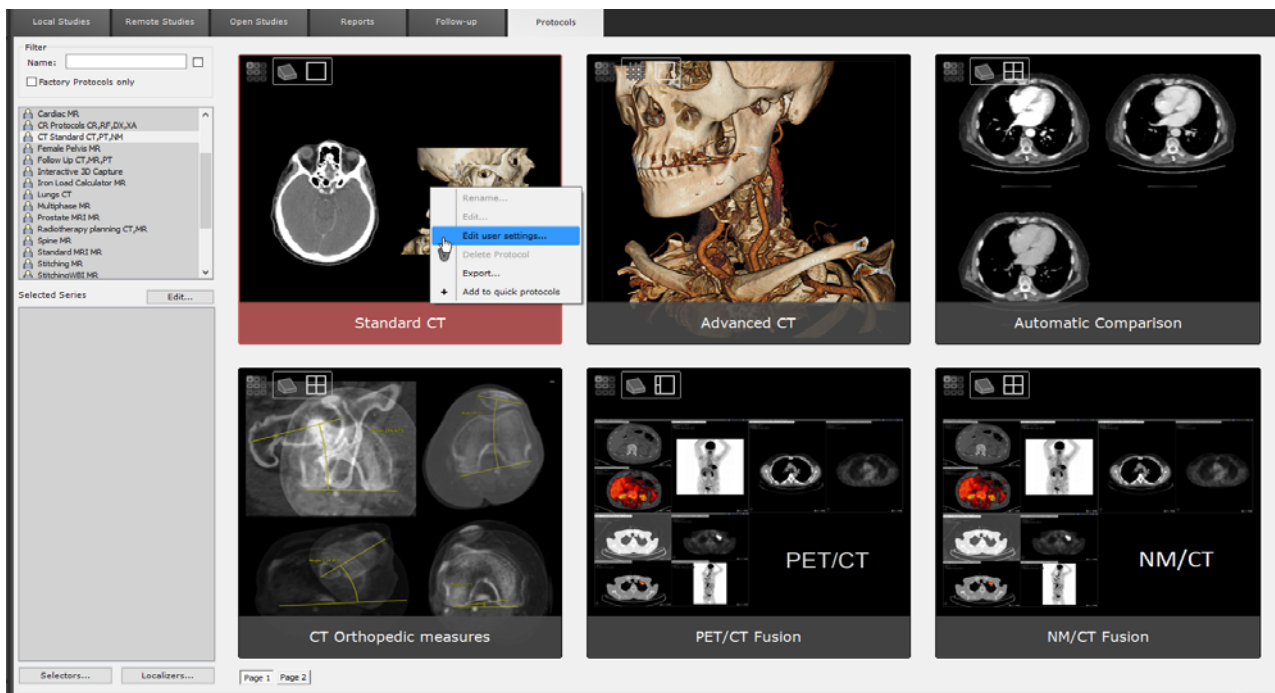


Figure 15-42 Edit user settings for the Standard CT protocol from the Protocol tab



The edited settings are preserved upon closing Myrian® and will be applied whatever series is opened with the relevant standard protocol

# 16 Appendices

## Appendix 1

### 1. Guide to the buttons





Button	Function
	Toggles display between List of Studies (local Myrian® database) and the currently open Study (in main Workspace)
	Current Quiz (optional add-on)
	Shows user preferences and global options
	Closes the current session

Tableau 16-1 Main buttons














Button	Function
	All Series are automatically laid out side-by-side (up to 16 Series may be displayed at a time)
	All Series are laid out on top of one another (up to 16 Series may be displayed a time)
	Full Screen layout: a single Series takes up the entire image zone (default load-up layout)
	2 Series laid out side-by-side
	4 Series in a 2 by 2 grid layout
	9 Series in a 3 by 3 grid layout
	16 Series in a 4 by 4 grid layout
	Auto-grid: automatic optimal layout for all Series (up to 16 Series may be displayed a time)
	One or more Series laid out across 2 screens
	Displays the <b>next Series</b>
	Displays the <b>previous Series</b>
	Adjusts the <b>Series synchronization settings</b>
	Displays the <b>current Study's Series list</b>

Tableau 16-2 Series page layout buttons




Undo/Redo	
Button	Function
	Undoes the last action
	'Redo' - restores the last canceled action as if it had not been canceled (i.e. the opposite of undo)
	Displays a list of undoable actions

Tableau 16-3 Undo/Redo buttons





Image visualization modes	
Button	Function
	Opens the Grid layout menu
	MPR + Oblique Mode
	MPR + 3D Mode
	Opens the Cinema Mode transport bar to view slice animation

Tableau 16-4 Buttons for selecting the image visualization mode








Image adjustment	
Button	Function
	<b>Grayscale</b> Windowing
	<b>Zoom</b> in/out
	<b>Pans</b> image sideward
	<b>Navigates</b> through the images in the Series
	Move the anatomical center to a new position clicking on the 2D/3D image to focus on a target
	Opens zoomable <b>Magnifying lens</b> tool
	Restores <b>Default</b> Grayscale Windowing settings

Tableau 16-5 Image control tools















Buttons available on an image	
Button	Function
	Edge enhancement
	Annotation display deactivated
	Annotation display activated (by default)
	Anatomical center synchronization de-activated
	Anatomical center synchronization activated
	Context menu (can be assigned to a mouse button)
	Selects/Unselects the image for the Report (flash green icon indicates its selection for the report)
	Adds the image to Reprographics bay
	Toggles Full-screen on/off
	Activates inter-Series cross-reference line for current frame
	Adds to current Quiz
	Flips current frame

Tableau 16-6 Iconic buttons found on an image


























Image Scrapbook and Reports tab	
Button	Function
	Opens the <b>Image Scrapbook</b>
	<b>Creates a report</b>
	Displays the <b>list of reports for the current Study</b>
	<b>Exports the current Series</b>
	<b>Export Images to the operating room</b>

Tableau 16-7 Scrapbook, Export and Reports tab buttons

Annotations	
Button	Function
	Makes a <b>Text Annotation</b>
	Makes an <b>Arrow pointer</b> to indicate a point of interest
	Makes a <b>length measurement</b> . Two length measurements determine an angle.
	Opens the <b>"List of Annotations" screen</b>
	Pixel calibration tool
	Linear reformatting rake
	Curved reformatting rake
	Radial reformatting rake
	Freeform measurement shape
	Elliptic measurement shape
	Rectangular measurement shape
	Ellipsoid
	IsoContour 3D
	ROI Contour
	Threshold
	Selects/displays previous object
	Selects/displays next object
	Preserves as Visual Selection
	Excludes from the Visual Selection
	Includes into the Visual Selection




























	Clears Visual Selection
	Masking tools
	Manual Bone Masking
	Vessel correction (progressive)
	Vessel correction (two-clicks)
	Displays Visual Selection only
	Displays whole Study
	Displays Study without Visual Selection
	Visibility Slider
	Drag and Drop Viewport
	Drag and Drop a View

Tableau 16-8 Toolbox buttons

Icon	Tool	Usage (Overwrite Mode)	Usage (Preserve Mode)
	Global ROI editing tool <b>Preserve/Overwrite</b> mode	Each new ROI tool action <b>overwrites</b> any existing ROI it comes into contact with	New actions add to existing ROI but existing ROI are not undone by any new ROI tool action.
	Freehand <b>Draw</b> tool	Draw contours/lines by hand <b>anywhere</b> (can draw over other shapes/contours)	Draw contours/lines by hand anywhere <b>but not</b> over existing contours/shapes
	Freehand <b>Erase</b> tool	Erase <b>any existing</b> contours/lines/shapes	Erase contours/lines/shapes of <b>active ROI</b>
	<b>Lasso</b> tool	Create freehand color-filled shapes (auto-completes) <b>anywhere</b>	Create freehand color-filled shapes (auto-completes) anywhere <b>but not</b> over existing contours/shapes
	<b>Paint bucket</b> tool (2D/3D)	Click on any contour/shape to replace Color	Click on <b>an empty space/shape</b> within a ROI to fill-in.
	Slice-by-slice auto <b>Hole-fill</b> tool (2D/3D/auto slice-by-slice)	Click on any shape to <b>fill-in the hollow spaces</b> (adds filled-in spaces to active ROI)	Click on an active ROI shape to <b>fill-in the hollow spaces not belonging to any other ROI</b>
	Slice-by-slice auto <b>Inflate</b> tool (2D/3D/auto slice-by-slice)	Click on any shape to <b>expand/inflate</b> it (overwrites any existing ROI)	Click on any shape to <b>expand/inflate</b> it (preserves any existing ROI)
	Slice-by-slice auto <b>Deflate</b> tool (2D/3D/auto slice-by-slice)	Click on any shape to <b>contract/deflate</b> it (overwrites/clears any existing ROI)	Click on any shape to <b>contract/deflate</b> it (preserves any existing ROI)
	<b>Magic wand</b> (2D/3D)	Automatically selects/paints <b>all</b> bordering pixels of similar intensity (overwrites any existing ROI)	Automatically selects/paints <b>all</b> bordering pixels of similar intensity (preserves any existing ROI)
	<b>Merge ROI</b> tool	Enables to Merge a clicked ROI with a selected ROI in the list	
	<b>ROI cut</b> tool	Select this tool then click and drag on a zone to remove it from the active ROI. The removed zone is based on the tool size	
	<b>Cutting Surface</b>	Opens the <b>Cutting Surface</b> Floating Toolbar to enable virtual cutting operations on 2D and 3D ROI	
	<b>Trace Cutting Surface</b>	Enables freehand drawing and modification of a projected surgical operation simulating a Cutting Surface cut	
	<b>Split ROI</b>	Splits ROI with the Cutting Surface	
	<b>Display/Hide Cutting Surface</b>	Toggles display of Cutting Surface on/off	
	<b>Translate Cutting Surface (3D)</b>	Moves the 3D Cutting Surface	
















	<b>Deform Cutting Surface (3D)</b>	Deforms the 3D Cutting Surface (press the ALT key and drag the mouse to modify the size of the deformation zone)
	<b>Stretch Cutting Surface (3D)</b>	Stretch the edges of the 3D Cutting Surface to enlarge/diminish it
	<b>Extrusion tool</b>	Opens the <b>Extrusion</b> floating panel to enable extrusion
	<b>Draw extrusion contours</b>	Enables freehand drawing of extrusion contours
	<b>Launch extrusion</b>	Creates interpolated 3D ROI
	<b>Remove extrusion contours</b>	Deletes extrusion contours
	<b>Create path</b>	Opens the Path toolbar
	<b>POI Toolbar</b>	Opens the POI toolbar
	<b>Assign to ROI</b>	Select this tool then <b>click on a zone to add</b> to active ROI
	<b>Perform automatic recognition</b>	Launches automatic Tissue Recognition tool (requires corresponding Expert Module to be installed)
	<b>Add a diameter measurement (3D)</b>	Creates a Diameter Measurement (3D)
	<b>Create a new vascular tree</b>	Create a new branch
	<b>Connect a vessel to a vascular tree</b>	Add a branch to an existing tree
	<b>Fuse two vascular trees</b>	Fuse two vessels
	<b>Vessel labeling</b>	Opens the vessel labeling toolbar

Tableau 16-9 ROI editing buttons





<b>ROI contextual buttons</b>	
<b>Button</b>	<b>Function</b>
<b>+</b>	'Create a new region of interest' – opens list of available Tissue Recognition engines
	'Display Advanced Measurements and Histogram screen of selected ROI' – opens an information window providing volume, density, a histogram, etc.
	Toggles Coloring of the currently selected ROI on/off (right-click to display Color intensity slider)
	'Hide/Show currently selected region of interest' (right-click to display visibility/transparency slider)
	Positions the anatomical center in the center of the currently selected ROI

Tableau 16-10 ROI contextual buttons

Display Function Toolbar	
Button	Function
	Switches ROI freehand drawing mode (point by point, continuous or assisted mode)
	Adds image to PrintComposer module
	Basic MPR mode page layout
	Cycles Crosshair display settings
	Toggles Annotation display on/off
	Toggles 'Invert Colors' Mode on/off
	Recenter on Anatomical Center
	Toggles inter-Series navigation sync on/off
	Toggles ROI coloration on/off
	Toggles DICOM info display on/off (right-click to open displayed info customisation screen)
	Closes Series (right-click to close all currently open Series)

Tableau 16-11 Display information buttons

Cinema mode buttons	
Button	Function
	Launches Cinema Mode
	'Reverse Play' transport button – animates towards the beginning of the Series
	'Play' transport button – animates towards the end of the Series
	'Stop' transport button – stops the animation

Tableau 16-12 Cinema mode buttons

Miscellaneous buttons	
Button	Function
	Small folder used in lists of Series for the current Series
	A non-interpreted Study
	An interpreted Study
	A locked Study




	Used for accessing the upper hidden portion of the toolbar
	Reduces a zone of buttons when the toolbar is at the top
	Click on this Arrow to scroll a functional toolbar (or use the mouse wheel)

Tableau 16-13 Miscellaneous buttons

## Appendix 2

### 2. Mouse cursors

According to the **selected function** or that which is associated to the mouse, the **cursor** (the 'pointer' that is controlled by the mouse) **changes its appearance**. An icon may appear beside the Arrow or the pointer or may change entirely. This is to help **visually verify the action** that a mouse click will cause.













Cursor	Current function
	Sets the grayscale Windowing (with the mouse button held down, move horizontally to adjust the Windowing size and vertically to set the center)
	Sets the grayscale Windowing center to that of the next pixel that is clicked on
	Zooms on the image (with the mouse button held down, move horizontally for a rapid zoom and vertically for a slow zoom)
	Pans an image or Annotation Moves the center point of four frames, thus resizing them
	Navigates within a Series (move horizontally or vertically) Checks a checkbox on an image in order to select that image
	Places an Annotation (in text form)
	Activates buttons Places an Arrow Annotation
	Places a distance measuring rule Changes the length of a distance measure or an Arrow that has already been placed (go to one of its endpoints to do this)
	Resizes image frames (go to their borders to do this)
	Rotation when in mode 3D mode/Orientation Cube
	Rotation by an obliqueness cube's edge
	Rotation by an obliqueness cube's face

Tableau 16-14 Mouse cursors

# Appendix 1

## 1. Keyboard shortcuts

General User Interface (GUI) and 2D Viewports	
Key	Function
-	Reduce the slice thickness in MPR mode (identical to the '-' button in the viewports), or Reduce the length of the Filet Section by 1 mm (number pad only)
+	Increase the slice thickness in MPR mode (identical to the '+' button in the viewports), or Increase the length of the Filet Section by 1mm (number pad only)
1,2,3 ... 0	Select corresponding ROI
C	Cine Mode
D	Toggles DICOM information display on/off
Enter	Cycle back through last 3 tools assigned to left mouse button
Espace	Cycle forward through the 4 Image Control tools: Windowing, Panning, Navigation, and Zoom
F	Windowing tool
R	Cycle through the ROI Display Modes (Filled, Contour, none)
F4, F6, F10, F8, F3, F2, F11, F9, F7	Activate Windowing presets using the following "F" Function Key: Automatic: F4 Abdomen: F6 Bone: F10 Brain: F8 Chest: F3 Colon: F2 (Note: WW=1500 and WL= -200 Windowing) Head Neck: F11 Lung: F9 Pelvis: F7
Left Arrow (Cursor Key) / Right Arrow (Cursor Key)	Moves a Cutting Surface line forward/back
Left Cursor Key Right Cursor Key Top Cursor Key Bottom Cursor Key Home End	Locate and Activate Previous/Next Annotation, Contour, etc., or Navigates through Slices in Native Mode
Up/Down Cursor Arrows	In the Study List to select previous/next/first/last line
Left/Right Cursor Arrows	In the Study List to scroll across table columns slightly left/right (+ hold "CTRL" to go directly to the far end at left/right of the list)
PageUp PageDown	in the Study List to select first/last line of the page (or first/last line of previous/next page)
G	Grid Mode
H	Automatically selects the distance tool for an immediate usage



I	Switches the underlying frame to full screen mode (when in Grid mode or 'MPR + other mode')
K	Toggles Annotation list display on/off
L	Opens the Series Synchronization Window
M	MPR Mode
P	Adds the active image to the Scrapbook. Whether the image has ROI or Annotations such as Path or not, it will be captured in RGB or in Native mode
S	Opens the QuickPatient Window
Del	Deletes active Annotation e.g. Text, Arrow, Length/Angle measurement, Path points, POI, Quantification Shapes, Complex AOI, Cutting surface mid-points, mask and extrusion contours)
T	Assigns Panning tool to the left mouse button
Tab	Displays Next Page (when several pages are open)
Z	Restores Zoom to its original value

Table 17-1 Keyboard shortcuts: GUI and 2D Viewports



Combo Keys are combinations of Keyboard Keys

Combo Keys	
Combo Keys	Function
ALT+C	Clear all voxels of all existing ROI
ALT+I	Switches large or primary viewports with the viewport under the cursor for "3+1", "3+2", "2+1" and "6"-frame preset layouts
ALT+M	Cycles through available Viewport layouts
ALT+P	Adds the active image to the PrintComposer. Whether the image has ROI or Annotations such as Path or not, it will be captured in RGB or in Native mode
ALT+CTR+P	Add image in RGB format to the PrintComposer
ALT+SHIFT+P	Add image in Native format to the PrintComposer
ALT+X	Opens the Study List (form the Workspace)
CTRL+ '+'	Sets the Slice Thickness to maximum thickness in MPR mode, or Sets the Filet Section length to maximum (number pad)
CTRL+ '-'	Sets the Slice Thickness to minimum thickness in MPR mode, or Sets the Filet Section length to minimum (number pad)
CTRL+1,2,3 ... 0	Switch to NxN Grid Mode (e.g. 'CTRL' + '4'= 4x4 Grid)
CTRL + I	Switch to full screen display
CTRL+Z	Undo previous action
CTRL+Y	Redo previous action
CTRL+P	Add an image in RGB format to the Scrapbook
CTRL+SHIFT+P	Add an image in Native format to the Scrapbook
SHIFT+Enter	Cycle forward through 3 three tools assigned to left mouse button
SHIFT+Spacebar	Cycle back through the 4 Image Control tools: Windowing, Panning, Navigation, and Zoom
SHIFT +Tab	Displays Next Page (when several pages are open)
SHIFT + Z	Assign Zoom to left mouse button
SHIFT+Up/Down/ Home/End/Page Up/ Page Down	In the Study List to select multiple Studies

Table 17-2 Combo Keys: GUI, all Viewports

### 3D, VOI, Whole Volume Viewports

Key	Function
CTRL	forces the translation of the image
E	Forces the ROI export as 3D Objects in .obj format file
X	forces the constrained rotation of the volume along the X or Y axis contained in the view plane
Click/Drag over the Mannequin	Rotation
Navigation Tool	Rotate in VOI and Whole Volume Mode (hold CTRL during navigation as you release the moused button to switch to auto-rotation)
M	Cycle through "Average", "MIP" and "MinIP" Intensity Rendering Modes
3	Display/Hide 3D Axes of Inertia in Whole Volume Mode only
CTRL + 3	Opens the 3D preview screen for 3D capture

Table 17-3 Keyboard shortcuts: 3D Viewports

### Endoscopy Viewport

Key	Function
+	Increase the Threshold by 20HU (hold the Shift Key for fine adjustment) (number pad only)
-	Decrease the Threshold by 20HU (hold the Shift Key for fine adjustment) (number pad only)
ALT key during fly-through	Activate "Ping Pong" Mode (fly-through goes back and forth continuously when it reaches the end of the current Path)
Home End	Go directly to the start or end point of the current Path
Left Cursor Key	Move the Camera Left (hold Shift for finner adjustment)
Right Cursor Key	Move the Camera Right (hold Shift for finner adjustment)
Top Cursor Key	Move the Camera Forward (hold Shift for finner adjustment)
Bottom Cursor Key	Move the Camera Back (hold Shift for finner adjustment)
PageUp	Move the Camera Up
PageDown	Move the Camera Down
SHIFT	Activates Rotation Tool
CTRL	Activates Panning Tool
X + Rotation Tool	Constrains Rotation about the axis of the horizontal or vertical plane of view
Click/drag over the mannequin	Constrains Rotation from the mannequin

Table 17-4 Keyboard shortcuts: Endoscopy

## Toggle Commands

Toggle Commands are combinations of Keys and Tools which can override or modify standard behaviors “on the fly”.

Tool or action	+ Key	Behavior
Inflate ROI	SHIFT	Deflates ROI (opposite tool)
Deflate ROI	SHIFT	Inflates ROI (opposite tool)
Length Measurement Tool	SHIFT	Constrains the tracing of the line to vertical or horizontal
Draw	SHIFT	Eraser (opposite tool)
Eraser	SHIFT	Draw (opposite tool)
Fill Zone	SHIFT	Empty Zone (opposite tool)
Zoom and Pan	SHIFT	Synchronizes all MPR Viewports
Ellipse	SHIFT	Reshapes an ellipse without rotation
Navigation	SHIFT	Toggles between High-speed Navigation Mode and Image per Image Navigation Mode NB: press SHIFT and mouse button simultaneously
Drag and Drop	CTRL	Pan image
Ellipse	CTRL	Constrains to a Circle
Rectangle	CTRL	Constrains to a Square
Double-click on a part of the Study List or Reports List	CTRL	Expand/Collapse the open folders
Mouse over an image	Alt	Displays the HU Value of the Pixel immediately underneath the cursor
Anatomical Center and Reference Lines	SHIFT	Gives access to the area directly underneath the Anatomical Center or Reference Lines

Table 17-5 Keyboard commands



SHIFT key can be used to alter the priority of objects during a click on any Viewport.

# Appendix 1

## 1. Glossary

**AVG** ('Average') – display mode consisting of thick slices calculated in terms of their native images

**DICOM** (*Digital Imaging and Communications in Medicine*) – a communications and archiving standard for medical imagery. Also refers, by extension, to a specific medical imagery file format that adheres to this standard

**DICOM AE** (AE Title) – an application's identity, necessary in achieving communication between diagnostic stations, DICOM servers, PACS consoles, etc.

**DICOMDIR** – a file describing a collection of DICOM images in the form of patient(s) / Study(ies) / Series

**Study** – a collection of Series that constitutes the complete set of images taken for one patient in a certain modality on a given date

**HU** (*Hounsfield Unit*) – a unit of intensity for tomodensitometric Studies, corresponding to tissue density. By convention, water has a value of 0, air or fatty tissue have negative value and bone has a large positive value

**ISB** (*IntraSense Binary*) – a proprietary image file format designed for viewing operating room image collections, by virtue of the Intrasense Myrian® Viewer

**MiniP** (*Minimum Intensity Projection*) – Thick slice display mode calculated by taking the minimal value from the native images in the slice (conceived to aid observation of low intensity structures such as bile ducts)

**MIP** (*Maximum Intensity Projection*) – Thick slice display mode calculated by taking the maximal value from the native images in the slice (conceived to aid observation of high intensity structures such as injected vessels)

**Modality** – apparatus dedicated to the acquisition of medical images (Scanner, MRI, Echography, etc)

**MPR** (*Multi Planar Reformatting*) – a display mode where native images are transformed into axial, coronal and sagittal plane views

**PACS** (*Picture Archive and Communication System*) – an infrastructure allowing for the management and manipulation of digital medical images

**PPID** – a unique identifier attributed to a patient by an establishment. Be aware that this identifier is only valid within the scope of the establishment in question

**ROI** (*Region Of Interest*) – a geometric zone defined by a user, corresponding to an anatomical or pathological structure (or some part of it) with a view to determining certain properties (size, volume, spread, type etc.) or to apply some 3D visualization to it (hide, color, etc.)

**Series** – a Study is composed of one or more Series of images. The plurality of Series generally corresponds to the various phases of the Study (before and after injection of a contrast product, for example)

**Subseries** – an identical concept to that of a 'Series', occurring when a modality 'forgets' to differentiate between Series

**TCP/IP** – a widely-spread communications network protocol

**UID** – a globally unique DICOM identification number

# Appendix 1

## 1. DICOM Modalities

The meaning of terms corresponding to DICOM modalities are presented below.

The term **SC** (for 'Secondary Capture') is sometime encountered, designating that which is not acquired by any particular modality.

<b>CR</b> = Computed Radiography	<b>CT</b> = Computed Tomography
<b>MR</b> = Magnetic Resonance	<b>NM</b> = Nuclear Medicine
<b>US</b> = Ultrasound	<b>OT</b> = Other
<b>BI</b> = Biomagnetic Imaging	<b>CD</b> = Color flow Doppler
<b>DD</b> = Duplex Doppler	<b>DG</b> = Diaphanography
<b>ES</b> = Endoscopy	<b>LS</b> = Laser surface Scan
<b>PT</b> = Positron emission Tomography	<b>RG</b> = Radiographic imaging
<b>ST</b> = Single-photon emission computed Tomography (SPECT)	<b>TG</b> = Thermography
<b>XA</b> = X-Ray Angiography	<b>RF</b> = Radio Fluoroscopy
<b>RTIMAGE</b> = Radiotherapy Image	<b>RTDOSE</b> = Radiotherapy Dose
<b>RTSTRUCT</b> = Radiotherapy Structure Set	<b>RTPLAN</b> = Radiotherapy Plan
<b>RTRECORD</b> = RT Treatment Record	<b>HC</b> = Hard Copy
<b>DX</b> = Digital Radiography	<b>MG</b> = Mammography
<b>IO</b> = Intra-Oral Radiography	<b>GM</b> = General Microscopy
<b>PX</b> = Panoramic X-Ray	<b>SM</b> = Slide Microscopy
<b>PR</b> = Presentation State	<b>XC</b> = External Camera Photography
<b>ECG</b> = Electrocardiography	<b>AU</b> = Audio
<b>SR</b> = SR Document	<b>EPS</b> = Cardiac Electrophysiology
<b>HD</b> = Hemodynamic Waveform	<b>IVUS</b> = Intravascular Ultrasound

Table 19-1 DICOM Modalities

## Appendix 2

### 2. DICOM Fields

This appendix lists the **DICOM fields** for the more common modalities (to display them in Myrian®, see Section 4.4.4)

#### CR (Computed Radiography)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Study Description	(0008,1030)	
Image and Fluoroscopy Area Dose Product	(0008,115E)	X-ray dose, measured in dGy*cm*cm, to which the patient was exposed for the acquisition of this image plus any non digitally recorded fluoroscopy which may have been performed to prepare for the acquisition of this image.
Body Part Examined	(0018,0015)	
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-2 DICOM fields in the CR modality

NB: The value of the Area Dose Product DICOM field expressed in dGy\*cm<sup>2</sup> unit can be displayed on CR studies as specified in the X-Ray Radiation Dose DICOM module (cf. Dicom Standard, section C.8.7.8)

#### CT (Computed Tomography)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Plane	(0020,0032)	The calibration plane (i.e. Axial, Coronal, Sagittal)
Image Dimensions	(0028,0010), (0028,0011)	The number of rows and columns in the image
Voltage	(0018,0060)	The machine's peak voltage (in kilovolts)
Current	(0018,1151)	Current of the X-ray tube (in mA)
Slice Thickness	(0018,0050)	Ratio between slice spacing and slice thickness
Gantry Tilt	(0018,1120)	Gantry Tilt
Exposure Time	(0018,1150)	Exposition time in milliseconds
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-3 DICOM fields in the CT modality

## DX (Digital Radiography)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Laterality	(0020,0060) and/or (0020,0062)	Indicates the image's orientation (left to right and top to bottom)
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-4 DICOM fields in the DX modality

NB: The value of the Area Dose Product DICOM field expressed in  $\text{dGy}\cdot\text{cm}^2$  unit can be displayed on DX studies as specified in the X-Ray Radiation Dose DICOM module (cf. Dicom Standard, section C.8.7.8)

DICOM field name	Identifier	Notes
Image and Fluoroscopy Area Dose Product	(0008,115E)	X-ray dose, measured in $\text{dGy}\cdot\text{cm}\cdot\text{cm}$ , to which the patient was exposed for the acquisition of this image plus any non digitally recorded fluoroscopy which may have been performed to prepare for the acquisition of this image.

## ES (Endoscopy)

DICOM field name	Identifier	Notes
Study ID	(0020,0010)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-5 DICOM fields in the ES modality

## MG (Mammography)

DICOM field name	Identifier	Description
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Laterality	(0020,0060)	Indicates the image's orientation (left to right and top to bottom)
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast
View Position	(0018,5101)	The acquisition's point of view

Table 19-6 DICOM fields in the MG modality

## MR (Magnetic Resonance)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Plane	(0020,0032)	The calibration plane (i.e. Axial, Coronal, Sagittal)
Acquisition Matrix	(0018,1310)	The resolution at which the image acquired
Echo Train Length	(0018,0091)	The k-space acquisition length per excitation and per image
Repetition Time	(0018,0080)	The time between impulses (in ms)
Echo Time	(0018,0081)	The time between the middle of the excitation impulse and the peak in resulting echo (in ms)
Slice Thickness	(0018,0050)	Ratio between slice spacing and slice thickness
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-7 DICOM fields in the MR modality

## NM (Nuclear Medicine)

DICOM field name	Identifier	Notes
Study ID	(0020,0010)	
Manufacturer Model Name	(0008,1090)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-8 DICOM fields in the NM modality

## OT (Other)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-9 DICOM field in the OT modality



## PT (Positron Emission Tomography)

DICOM field name	Identifier	Notes
Study ID	(0020,0010)	
Manufacturer Model Name	(0008,1090)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-10 DICOM fields in the PT modality

## RF (Radio Fluoroscopy)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-11 DICOM fields in the RF modality

## US (Ultrasound)

DICOM field name	Identifier	Notes
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Plane	(0020,0032)	The calibration plane (i.e. Axial, Coronal, Sagittal)
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-12 DICOM fields in the US modality

## XA (X-Ray angiography)

DICOM field name	Identifier	Notes
Manufacturer Model Name	(0008,1090)	
Study ID	(0020,0010)	
Study Description	(0008,003E)	
Series Number	(0020,0011)	Identifies the Series in the Study
Instance Number	(0020,0013)	Identifies the image in the Series
Frame Number	(0028,0008)	Total number of images
Image Comments	(0020,4000)	
Window Width	(0028,1051)	The image's brightness
Window Center	(0028,1050)	The image's contrast

Table 19-13 DICOM fields in the XA modality

# Appendix 1

## 1. Deactivated Mode/Offline Mode

### Deactivated Mode

If the software has not been activated, it automatically switches to 'Deactivated Mode'. In this mode, although the user may access his/her database, certain limitations are applied, such as the importing/exporting function being disabled.

List of functions disabled

- Image export
- Local and remote export
- Add/remove users
- 3D
- Segmentation
- ROI editing
- Reformatting Planes
- Education module
- Pack select
- DICOM printing
- Dicomization
- Series reconciliation
- Study and patient modification
- Clear database

### Offline Mode

If network connection is lost while the software has been configured for ISLP network activation, Myrian® goes into Offline Mode. Whilst in Offline Mode, the same restrictions apply as in Deactivated Mode (see above). After a few minutes, the following screen appears.

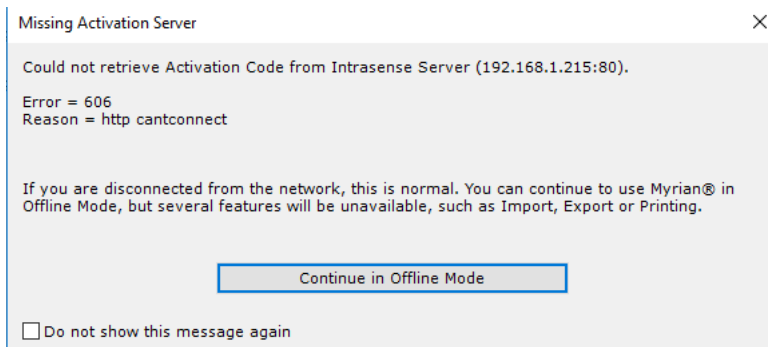


Figure 20-1 Offline Mode screen



You can choose to ignore this screen by clicking on the 'Don't display this message again'

### Connection lost

If the software has been activated correctly over the network, connection is automatically checked and updated every few minutes. If connection fails, the software goes into Disconnected Mode and an error message pops up.

### Automatic Disconnection

When the software uses a network connection, depending on the user-licence bought, users dispose of a certain number of

'user-tokens'. If a user leaves his/her post, or for some reason his/her workstation becomes inactive for more than 5 minutes, the token must be handed in order for another user to connect. In such cases, the software goes into Disconnected Mode and the following screen appears.

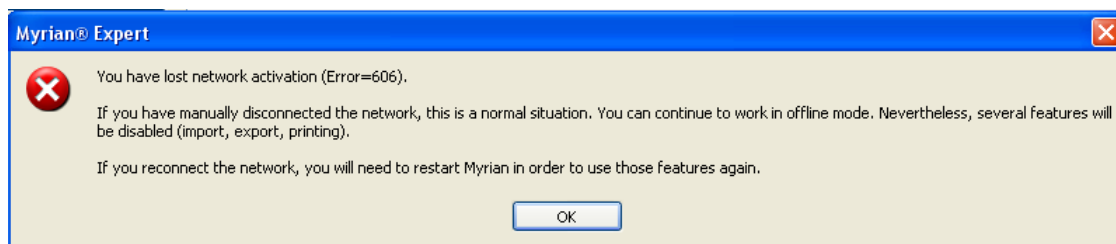


Figure 20-2 Disconnected Mode screen



The software must be rebooted to reconnect via ISLP.

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## Appendix 1

### 1. About geometric distortion: known issues with CR et RF modalities

Due to interference caused by magnetic fields (including the earth's magnetic field) as well as image intensifier input screen curvature, CR and RF modalities are potentially subject to 3 types of geometric distortion:

- Pincushion distortion
- Parallax errors
- Unequal magnification

Pincushion distortion, which is more pronounced near the image boundaries, causes image centers to be 'pinched' and edges to be curved inwards.

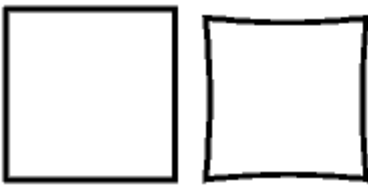


Figure 21-1 Example of Pincushion distortion: normal image at left, and distorted image at right

#### Parallax errors and unequal magnification

In conventional radiology, the refraction of x-ray beams may cause parallax errors as well as unequal magnification.

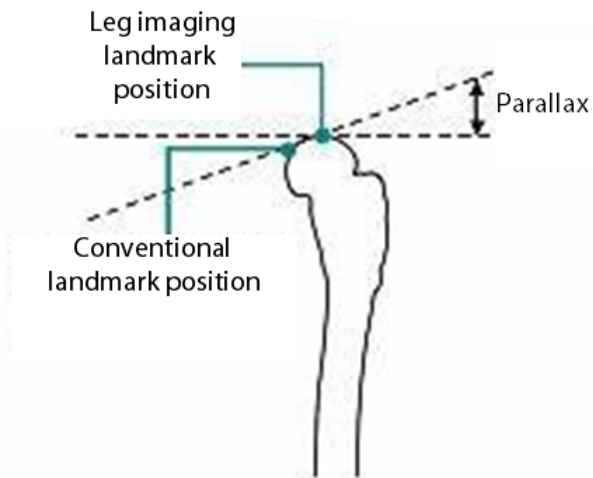


Figure 21-2 Landmark shifting

Parallax errors are caused by distance shifts between landmark and input screen resulting in varying sizes of distances between refracted beam paths and 'true' beam paths.

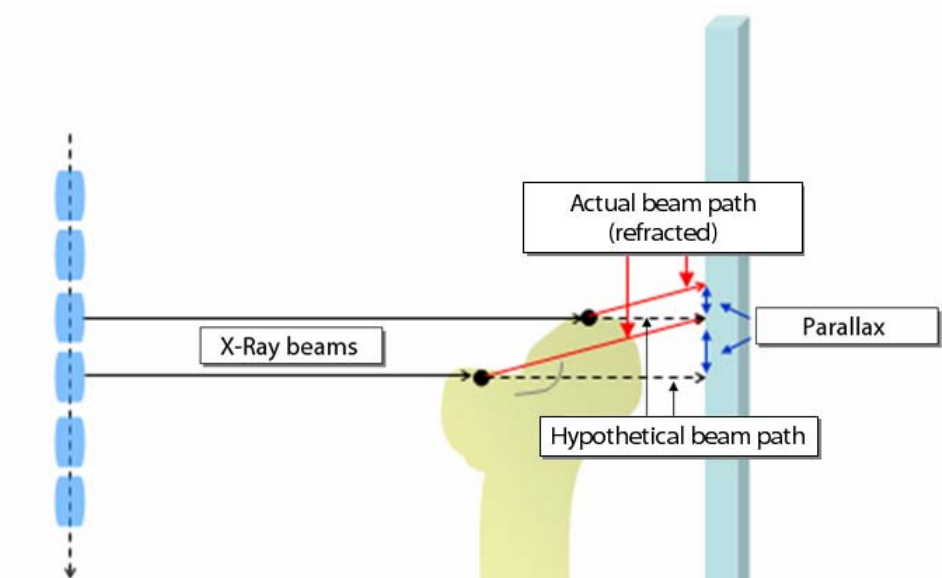


Figure 21-3 Parallax error


Unequal magnification is the small remaining parallax error caused by different parts of imaged subject being positioned in different planes relative to the detector and the receptor. This means that:

- The further the imaged zone is from the input screen, the greater its magnification will be.
- Certain areas may be more out of focus than others.

As a result of the potential existence of geometric distortion, it is strongly recommended that, during manual calibration, users should calibrate images as near as possible to image centers and over distances of at least 200 mm.

## Appendix 1

### 1. Launching external applications via Myrian®

In some cases, the following icon  may appear at bottom-right of the screen next to Myrian® icon.

The presence of this icon indicates that the version you are using has been configured by your establishment's IT personnel to enable other applications to be launched directly via this button.

In such cases, please request assistance from a qualified member of your establishment's IT department for instructions pertaining to this configuration.

#### Caution

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Whenever an external application is used to handle Patient Data, there is a potential safety risk. Because such data management is performed outside of Myrian®, it is impossible to guarantee that Patient Data displayed in Myrian® corresponds exactly to that which is displayed in external applications. Whenever such methods of data management are used, users should be duly warned and made fully aware of all the risks involved. Be sure to consult with your establishment's IT personnel to get all appropriate warnings regarding these aspects.

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## Appendix 1

### 1. AuditTrail - in compliance with HIPAA Security and Privacy requirements

In conformance with HIPAA (Health Insurance Portability and Accountability Act) security regulations and FDA's 21 CFR Part 11, Myrian® logs any action performed by users that can access to PHI (Protected Health Information) or give access to them.



The 21 CFR Part 11 regulations provide criteria for acceptance by the FDA, of electronic records, electronic signatures, and handwritten signatures executed to electronic records as equivalent to paper records and handwritten signatures executed on paper.

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#### Local AuditTrail data storage

The AuditTrail events are stored and encrypted in the user local database (SQLite)

The process records the information system activity by logging any relevant user actions that are:

- Opening/Closing a session
- Reviewing a given series
- Deleting a study/series
- Anonymizing a study/series
- Modifying patient or study data (including name, birth date and gender): A copy of the initial patient demographic data is recorded.
- Copying patient data to Windows® clipboard (ROI parameters, contrast uptake curve data, ironload concentration data...)
- Drag & dropping a workspace screenshot to another application
- Saving new Objects of Interest
- Undoing/Redoing any action
- Creating Volume Processor series, rake series and any series via a floppy disk or the Album
- Performing measurements,
- Creating a report,
- Closing a study without validating
- Validating a follow-up study (measurements performed are also saved as a .xml format file provided Myrian® settings have been configured accordingly)
- Closing a follow-up with or without validation
- Devalidating a whole follow-up or a follow-up study
- Deleting a follow-up
- Importing or exporting data to/from DICOM entity, CD-Rom or network.
- Unsuccessful login attempt including the user name that failed to be authenticated.
- Modifying the system configuration (DICOM,...)

For any of these actions, the following information are recorded:

User / Application / ApplicationVersion/Computer (IP Address) / EventID / Action / Status / Event Date / Patient Name / Patient ID / Transaction Source / Transaction Destination / Transaction initiator / Description / Data Type / Data Size / Data.

#### Report example:

Description category:

- User: The user that was logged in when the action was done.

- Application: Name of the application where the event happened.
- Application version: Version number (and build number) of the application involved
- Computer: IP of the computer that initiated the action.
- Event ID: A unique ID for the event being logged.
- Status: The status code of the action involved in the event (0 = no error).
- Event Date: Timestamp of the event according to the ISO 8801 Standard (YYYY-MM-DD-THH:MM:SS+HH:00)
- Patient name (Last name and First name)
- Source: AET of the source for any DICOM transaction
- Destination: AET of the destination of the transaction.
- Initiator: AET of the initiator of the transaction
- Description
- Data Type: Type of additional data (for example, .xml, .txt or .bmp file)
- Data Size
- Data: Additional data for a given event (description)

Example: Modality A asks B to move a series to C. In this case, source is B, destination is C and initiator is A

#### Action category supported:

- ACTION\_ACCOUNT\_PASSWORDCHANGED: A user password has changed.
- ACTION\_ACCOUNT\_PERMISSIONSCHANGED: A user permissions have changed.
- ACTION\_ACCOUNT\_USERADDED: A new user account have been created.
- ACTION\_ACCOUNT\_USERDELETED: A user account have been deleted.
- ACTION\_ACCOUNT\_USERMODIFIED: A user account have been modified (ex: user name changed).
- ACTION\_PHIACCESS\_DICOMQUERY: System have received a FIND or MOVE query.
- ACTION\_PHIACCESS\_INSTANCESCREATED: New images have been added to the database.
- ACTION\_PHIACCESS\_INSTANCESMODIFIED: Instances data have been modified
- ACTION\_PHIACCESS\_INSTANCESSTORED: New instances have been added to the database.
- ACTION\_PHIACCESS\_INSTANCESDELETED: Instances have been removed from database.
- ACTION\_PHIACCESS\_CLIPBOARD: Data have been copied to the clipboard (text only)
- ACTION\_PHIACCESS\_EXPORT\_PRINT: Instances have been sent to a printer.
- ACTION\_PHIACCESS\_EXPORT\_STORE: Instances have been exported to external storage (ex: local export/dicomdir), for example measurements associated to ROI and annotations
- ACTION\_PHIACCESS\_EXPORT\_BURNCD: Instances have been burned to a CD.
- ACTION\_PHIACCESS\_USERACTION: All actions triggering an undo/redo event.
- ACTION\_PHIACCESS\_VALIDATION: Generated by a study validation.
- ACTION\_SYSACCESS\_USERLOGIN: A user have logged in.
- ACTION\_SYSACCESS\_USERLOGOUT: A user have logged out.
- ACTION\_SYSACCESS\_USERLOCK: A user have locked workstation.
- ACTION\_APPLICATION\_STARTED: An application have started.
- ACTION\_APPLICATION\_ENDED: An application have ended.
- ACTION\_LOGGING\_STARTED: Logging system started
- ACTION\_LOGGING\_ENDED: Logging system ended

## Remote storage on Myrian® AuditTrail Server

Another storage possibility is to send all the AuditTrail information on a remote server called Myrian® AuditTrail Server (MATS). In that case, local storage becomes only temporary.

#### How does it work?

The AuditTrail (Myrian®) sends the audit trail notification messages through a TCP/IP socket over the network (using a DICOM connection) to the AuditTrail server which collects the audit trail notifications.



Myrian® AuditTrail Server writes all the actions performed in Myrian® in a dedicated global audit trail database. All the relevant audit trail information as described hereabove is stored.



Data is received as a DICOM dataset. This dataset is used to create the record that will be stored in a global database.

Besides, the MATS which is developed as a MS-SQL server hosted application, takes advantage of the following built-in key features:

- Backup of the audit trail database
- Access control on the database to authorised users
- Integrity check of the registered data.
- Encryption of the registered data
- Perenity of the data



The MATS can be installed either on a MAS or on a dedicated machine which receives notifications from one or multiple standalone Myrian® workstations.



The installation procedure requires the assistance of an Application Engineer. Please contact Intrasure for detailed information regarding setup and configuration.

## Measurement data export

Myrian® can be configured to export/trace any measurements performed by the user in the workspace. This piece of information is recorded in the AuditTrail process.



When there is no export configuration, measurement data can only be traced via the 21CFR mode (creation of an .xml format file only accessible via the AuditTrail Server)

The exported/traced data which then include all measurements associated to ROI and annotations (distance, general, combined measurements, contrast curve-associated measurements...) can be automatically exported at the series closing in the Workspace in two different ways:

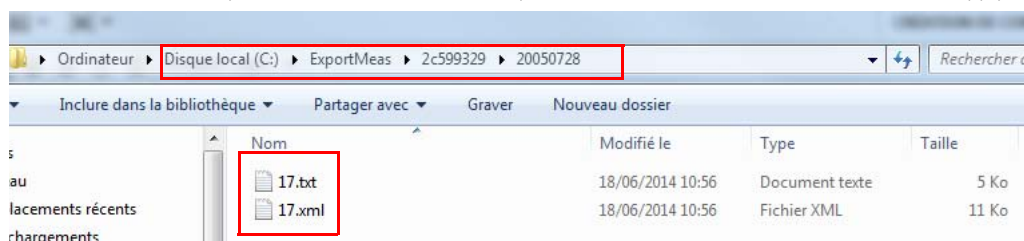
- **To a third party system** using a TCP/IP connection
- **To a local directory**, in a user-defined folder



Inside the export folder defined in Myrian® settings, measurements are exported according to the following arborescence:

Exportfolder/PatientID/Exam date/seriesnb.extension.

For each patient with measurements, a folder is created (named after corresponding patientID) and for each exam, a subfolder is created (named after the exam date). The file names match the series number(s) (SeriesID)





When exporting data to a local folder, if the same content is exported several times, the new file does not erase/replace the previous one.

Both ways require specific configuration in Myrian® settings.

Similarly, the measurement file format can also be configured in Myrian® settings: available file types include .xml and/or .txt files.

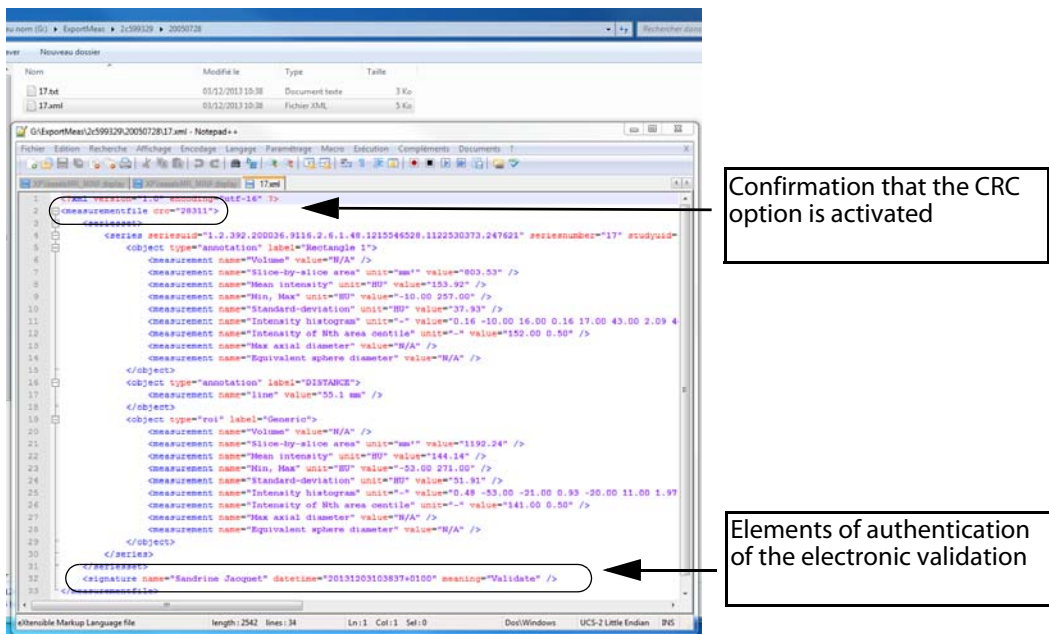


Even though a .txt measurement file has been configured to be exported locally, this format is **not traced** in the ISAudittrail (.xml format only)

Examples of measurement export to .xml and .txt files recorded in local mode are illustrated hereafter.

In accordance with the 21 CFR Part 11, when the electronic signature is performed, the following information are stored together with the signed record:

- The name of signer,
- Signature date and time
- And the reason for the signature ('validate'), here in the context that the signer has validated all measurements performed.



Confirmation that the CRC option is activated

Elements of authentication of the electronic validation

Figure 23-1 Measurement export and traceability .xml file

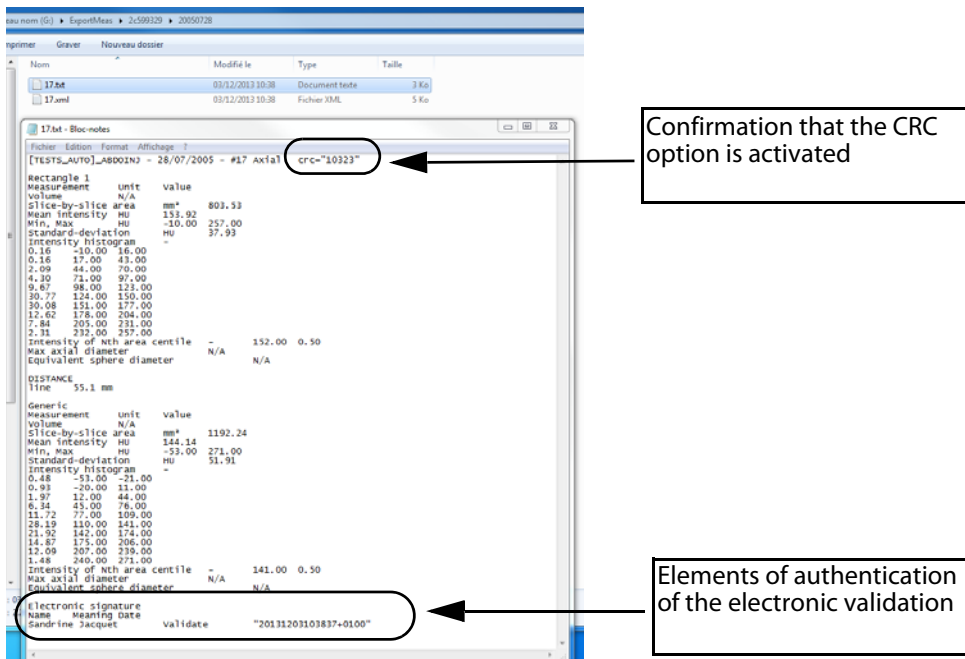


Figure 23-2 Measurement export and traceability .txt file

In addition to the measurement reporting, the file automatically includes the following identifying data:

- Series description
- Study date
- Study UID
- SeriesNumber
- Series UID



Units of measurement and referring tools or measurement types are also reported on.



The accuracy of exported distance measurements (in terms of measurement unit and depending on the value, whether positive or negative as well as number of digits) can be configured. Please request assistance from an Application Engineer from Intrasure.



There is **one distinct measurement file per view** (whether the closed view is single or multiphase):

- when a single view, the file contains the measurements of only one series
- when a multiphase view, the file contains the measurements associated with all the series in the view

The export, measurements and the user electronic signature (name of signer, signature date and time and "validate" value meaning) are traced in the AuditTrail and reported on the measurement file regardless of format (Figure 23-1 and Figure 23-2) provided the CFR21 part 11 option is activated.

**Whether the Study is closed with or without validation, the information is always traced in the AuditTrail.**

In the case that the study is closed without the « Signature meaning: Validate », the information does not appear in the AuditTrail.

On the other hand, in the case of a Follow-up where a Time Point or the Whole Study is devalidated, the **devalidation action is also traced** in the AuditTrail with the reason invoked at the time the devalidation occurred **whether the 21 CFR option is activated or not** (although, when not activated, the reason for devalidation is optional).

## How does the CFR21 mode work?



This mode is triggered with an activation bit (CFR21 part 11) available in the New Features 2.13 within Myrian® Platform package.

In accordance with FDA regulations, when the CFR21 part 11 compliance bit is set, a validation window is displayed on closing any series whenever measurements have been performed. It is extended with an electronic signature certificate, to be authenticated by the user.

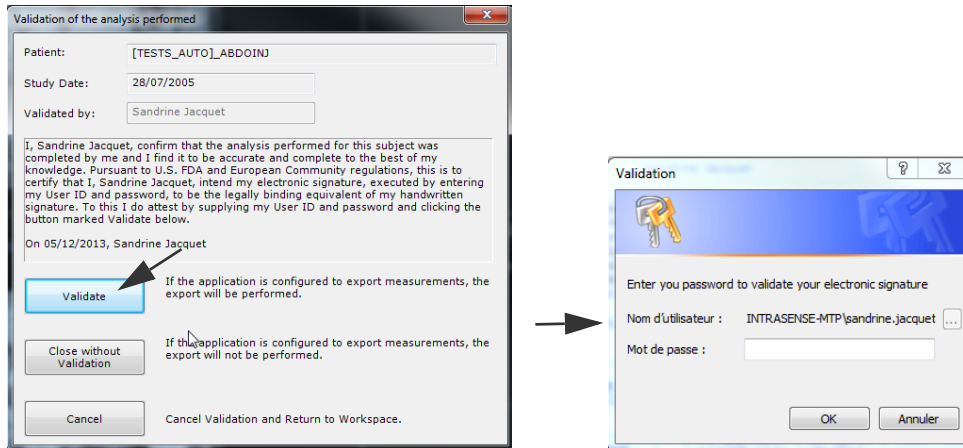


Figure 23-3 Authentication and validation process

Upon validation, a Windows® validation dialog box pops up asking you to enter your Windows® password in order to authenticate your electronic signature.



If you close a single view among all the views in the workspace, you will be prompted for its signature if Myrian® is to save data to the database.



By default, measurements performed in a follow-up view are not exported/traced as the Follow-Up manages and exports its own measurements. However, if you perform measurements that are not related to the follow-up inside a view (i.e. simple distance annotation), these won't be included in the follow-up. To export Follow-Up measurements, Myrian® settings have to be configured accordingly.

## Data integrity checking using CRC

A Cyclic Redundancy Check (CRC) is an error-detecting method enabling to control data integrity. A tool called ISCRC that is generated when the CFR21 activation bit is triggered, is provided for you to check that the validated data has not been modified since the user electronically signed in the validation window.

This command-line tool (iscr.exe) is located in your local disk (C) in Program Files>Intrasense>Myrian®

To run this executable, you need to start a command prompt from your console (cmd.exe) with the following command:

- Type in C:\Program Files\Intrasense\Myrian®>iscrc.exe and enter the file path to be verified.

```
C:\Windows\system32\cmd.exe
Microsoft Windows [version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation. Tous droits réservés.

C:\Users\sandrine.jacquet>CD C:\Program Files\Intrasense\Myrian>
La syntaxe de la commande n'est pas correcte.

C:\Users\sandrine.jacquet>CD C:\Program Files\Intrasense\Myrian

C:\Program Files\Intrasense\Myrian>iscrc.exe G:\ExportMeas\2c599329\20050728\17.
txt
The CRC is correct.
C:\Program Files\Intrasense\Myrian>iscrc.exe G:\ExportMeas\2c599329\20050728\17.
txt
```

Figure 23-4 Launching ISCRC tool

When no modification is detected, a message is displayed indicating that the CRC is correct.



If Myrian® is not executed in CFR21 mode, it is to be noted that the export files will not contain the CRC and therefore the following error message will be generated: 'Impossible to check the CRC for this file'

---

# Appendix 1

## 1. Working at a computer workstation

The correct organization of a computer workstation and its monitor will improve the general comfort of its users and reduce visual constraints as well as physical stresses and pains that a user is typically subjected to when working at a computer console.

When preparing the working environment of a computer console and monitor the following should be taken into account:

- The **lighting** of and around the workstation
- The **characteristics of the human body** and the specific physical details of the relationship between a user and a computer console
- The way in which equipment is organized and physically configured in an office
- The type of tasks that are performed and the way in which they are organized

The person that uses a workstation and monitor is the one best suited for adjusting its use and adapting it to his or her own physical characteristics.

Assuming and maintaining an appropriate posture reduces tensions and risks of lesions. Setting up a working area does not necessarily imply buying new furniture, but if office furniture is acquired, it is recommended that it be adjustable to the user's individual needs.

### The ambient lighting

Glare occurs when the eyes receive too much light, despite the compensating reaction of the eye's pupil. To avoid this type of visual fatigue during work at a computer console, all light, be it direct or reflected, which washes out or otherwise disturbs the user's vision should be avoided or reduced as much as possible (see Figure 24-1 and Figure 24-2).

To do this, the monitor should be placed in such a way that **light sources**, including windows, should be **parallel to the line of sight**, that is, to one side with respect to the screen. Light sources should not be found immediately in front of the user's eyes, thereby washing the vision out, nor behind, which would create a disturbing reflection. White clothing may also be a source of reflection on the screen.

To identify light sources, switch off the monitor and observe any reflections on the glass front of its screen. Unwanted light sources will become evident.

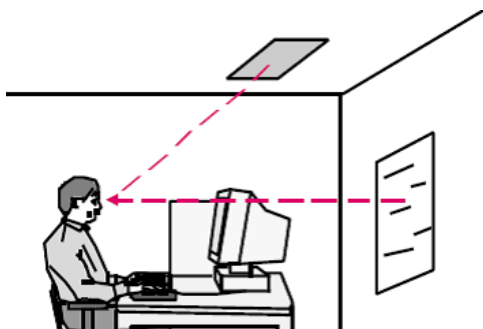


Figure 24-1 Direct light

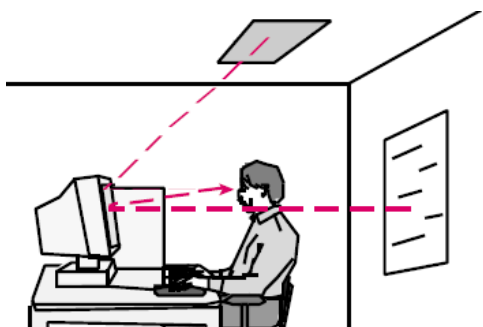


Figure 24-2 Indirect light

## To avoid visual fatigue and troubled vision

- Avoid direct or indirect glare
- Be sure of a **sufficiently well lit working area**, which should be less than that required for reading documents
- Make use of a angle-poise or other directional lamp for the working area in order to read documents comfortably (500 - 750 lux)
- If necessary, equip the working area with a document holder which should be installed at the same height and distance from the eye as the monitor and at the same angle
- Ensure the use of diffusers for any light sources
- Control natural light by use of curtains or blinds which should be used as necessary during the day
- **Avoid bright or shiny work surfaces.** Opt for surfaces that are matt and avoid large contrasts
- Avoid the use of shiny paper

## Replace fluorescent tubes that flicker in any way

- If necessary, add an **anti-reflection filter** to the monitor. Clean the screen and filter regularly
- Make a **visual pause** from the screen regularly and whenever necessary by alternating office tasks. Let the eye muscles rest regularly by gazing in a direction that is unobstructed over at least 6 meters
- Adjust the brightness of the screen with respect to the amount of ambient light during the day. Ensure that the 'focusing' of the screen itself is correct

## The human body and its postures when working at a computer console

The **postures** that a user adopts whilst working at a computer console tend to be **static** and held over a **long period of time**. Working in a static way at a computer console implies a constant muscular contraction at various parts of the body. The position of the body tends to be **fixed with very little joint movement** or other release from muscular contraction. It is therefore of the utmost importance that office equipment be **adjusted to the user's morphology** in order to avoid fatigue, tension and **musculo-skeletal difficulties**.

The physical characteristics of a user at a computer console are central factors to be considered when adjusting the various components of a work station to a monitor (chair, table, screen, keyboard, mouse). Just as each body has its own characteristics, so too should a working area be adjusted correctly so that it be suited to that person.

Adopting this posture implies that the user will reduce to a minimum the tensions and musculo-skeletal demands resulting from working at a computer.

These tensions are primarily found in the neck, shoulders, arms and elbows, wrists and fingers and the back, whereas pressures tend to be found around the waist and in legs, thighs and calves.



Figure 24-3 Muscular load

To identify sources of discomfort and to correct the working area one should, whilst in a typical working position, **locate points of muscular tension**, body **pains** and if possible, **points in the body that are under pressure**.

One would then configure equipment by **adjusting its position** or by correcting its configuration as part of a revision of the entire office layout in such a way as to reduce the physical constraints caused by a ill-adapted work area.

Note that all the elements that make up a working area are related to each other and that adjusting one piece may put into question the adjustment of another.

# To adjust the working area of the computer console

## The chair and footrest

The **chair** should come with some system (based on a screw or a pneumatic cylinder) that **allows the seat and backrest to be adjusted** to the dimensions of the user.

It is also preferable that the height and angle of the chair's seat, backrest and armrest may be adjusted.

A firm and fabric upholstery is recommended since this allows for a good grip and ensures a better circulation of air. The base should have 5 feet with wheels, suited to the type of the floor's surface to guarantee easy movement. A pivoting system eases movement of the trunk and upper members.

The foot rest is used to keep the feet firmly pressed down whilst leaving sufficient space under the thighs to allow for blood to circulate through the legs.

Too great a pressure under the thighs makes the legs feel heavy and can eventually lead to the appearance of varicose veins.

## Adjusting the chair

- Set the **height of the seat** in such a way that when seated with the feet planted firmly down, the angle of the thighs and calves are at roughly 90 degrees
- There should be practically no pressure under the thighs
- Set the **height of the backrest** (if adjustable) in such a way that the concave part of the backrest supports the base of the back (lumbar support)
- Adjust (if possible) the **angle of the backrest** whilst respecting an angle of 90 to 110 degrees between the trunk and the thighs when pressing against the backrest
- Adjust the depth of the backrest, being careful that the edge of the seat does not apply any pressure on the calves. If this pressure does not stop when supported, the seat is too deep
- If the chair has armrests, they should not prevent the chair from being manoeuvred under the desk, nor disturb movement of the forearms while entering data at the keyboard

## The desk

The **desk**, which may have an adjustable or folding keyboard / mouse area, should be of **moderate height** allowing the user to work within recommended angles, heights and distances once the chair and footrest are correctly adjusted and the console is head on.

If a table is set too high, the chair will also be set too high, leading to pressure under the thighs or having to continuously hold the shoulders in a raised state. On the other hand, a table set too low will lead the user to lean forward and tilt the neck, leading to neck pain and other problems of the shoulder and back.

Note also that when the keyboard and mouse are not being used, the height of the desktop should allow for the forearms to rest upon it without raising the shoulders.

- Remove anything from under the table that prevents you from adopting a natural posture that is comfortable for the legs and feet
- Leave sufficient space around the table to allow you to pivot the chair, move it forwards and backwards and access other equipment and items around the office
- Avoid bending, twisting or lifting anything heavy whilst in a seated position

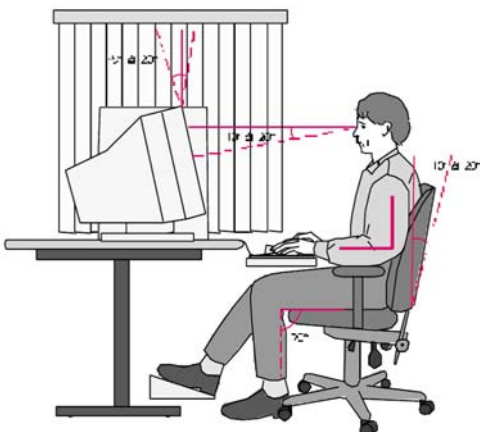


Figure 24-4 Adjusting the computer's working area



## The keyboard-mouse-screen ensemble

- Place the keyboard **straight in front of you**, at a height that allows the following angles to be respected:
  - The **angle of the elbows should be at roughly 90 degrees** when working at the keyboard or the mouse. The arms should be parallel with the trunk and the shoulders should be relaxed, as should the neck muscles

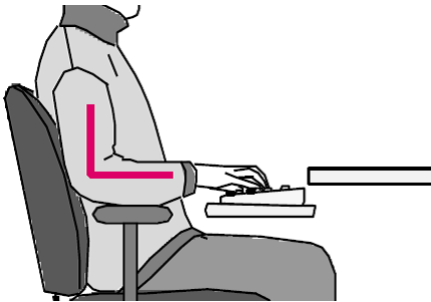


Figure 24-5 Elbow angle

- The angle of the wrists should be 180 degrees, a direct extension of the forearms
- Place the mouse next to the keyboard and at the same height

**Avoid working at the keyboard or the mouse with the arm extended, the shoulders raised or the wrists at an angle either opened or closed with respect to the forearm. Maintaining any of such posture will rapidly lead to pains.**

- Place the **screen directly in front of you** to avoid any torsion in the neck or excessively solliciting the eye muscles. Placing the screen to the left or the right of the desk may lead to pain around the eyes, the neck, the shoulders and the back. Adjustable screen-holders and monitor stools are available to correctly reposition the screen
- The **height of the screen** should be at the **height of the eyes**. The angle of view, at the center of the screen, should be 10 to 20 degrees to the horizontal. The neck should not tilt forward nor backward but should instead be seated naturally as an extension of the spinal column;
- The angle of the screen (if adjustable) should be  $-5$  to  $20$  degrees with respect to the vertical
- The brightness and contrast of the screen should be adjusted regularly according to the varying level of ambient lighting of the office
- Any document holder should be kept at the level of the screen, at the same angle as the screen and as near to it as possible. The document itself should be clearly legible



Figure 24-6 180 degree wrist angle

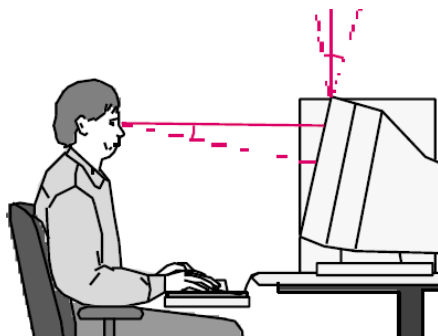


Figure 24-7 Positioning the screen

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