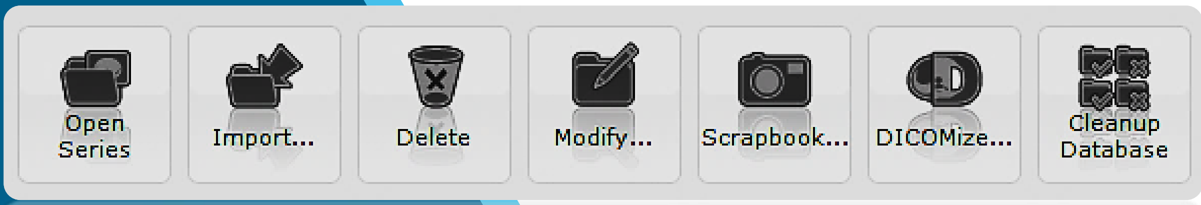
intrasense®

Myrian®

Quick User Guide



www.intrasense.fr

About Myrian®

Manufacturer:

intrasense

1231 Avenue du Mondial 98
34000 Montpellier
France
Tel : +33 4 67 130 130Fax : +33 4 67 130 132

Contact : support@intrasense.fr

Web site : www.intrasense.fr

CE 0459

The Myrian® suite is software intended to provide information which is used to take decisions with diagnosis or therapeutic purposes. Myrian® is CE mark as class IIa medical device

Intellectual property:

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⚠ Copies of this software and/or functionalities bearing the labels “Alpha”, “Alpha-Prime” or “Beta” must under no circumstances ever be used for diagnostic purposes.

Key to symbols

In this document, you will see the following symbols:

⚠ Caution or safety warning related to the use of the software.

❓ 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.

Contents

Myrian®Introduction

About Myrian®

Myrian® is a software suite intended for the **visualization**, **storage**, **reproduction** and **exporting** of **medical images**. Image data may originate from standard DICOM modalities (CT, MR, US, CR, PT, NM, etc.) or digital photography (jpeg, tiff, bmp).

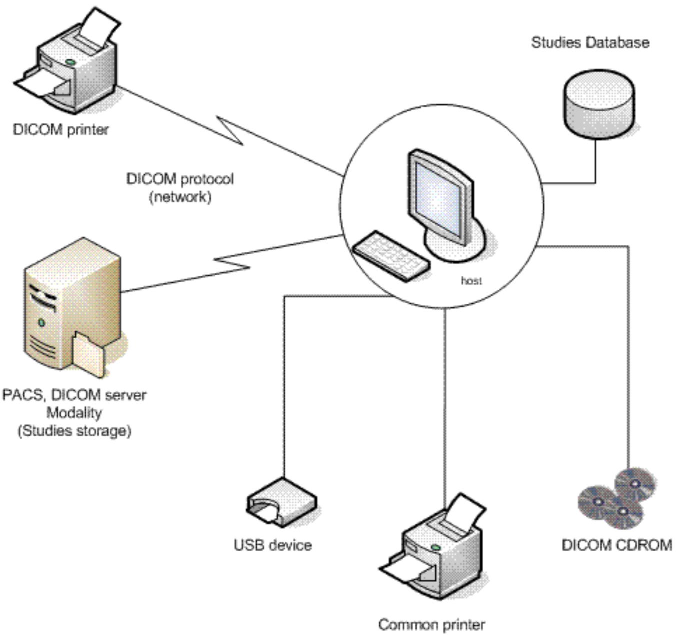
Myrian® is adapted to **3D imaging**. It enables **Multi-Planar Reconstruction (MPR)** of native images as well **as real-time modification of the thickness of slice reconstruction**.

Furthermore, this software supports **MIP** and **MinIP** display modes as well as highly detailed **volume rendering**.

The modular architecture of Myrian® software means it can be expanded to house the optional **Expert Modules**, a comprehensive range of specialized add-ons such as the XP-Liver module for the automatic detection of anatomical and pathological structures of the liver.

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

Myrian® functional diagram



Myrian® functional diagram

Myrian®Intended Use

Myrian® is a medical device software for processing, management, advanced visualization and analysis of multimodality medical images. Myrian® is intended to provide information which is used to take decisions with diagnosis or therapeutic purposes.

It provides Users with the following features:

- Import and export of DICOM files from/to any DICOM-compliant modality, workstation or PACS.
- Visualization of DICOM images in various standard visualization modes (e.g. MPR, 3D…etc.) with optional image-alignment feature;
- Creation of Objects Of Interest ("OOI") for analysis and measurement purposes;
- Generation of medical reports;
- Virtual Cutting surface tool for preoperative evaluation of surgery strategies;
- Longitudinal Follow-up of patient, designed to support the oncological workflow by helping the user to confirm the absence or presence of lesions, including evaluation, quantification, follow-up and documentation of such lesions.

Common Users are trained medical professionals, including surgeons, radiologists, clinicians and technicians.

Myrian® is designed to be run:

- On standard Standalone Platform, through the installed operating system. The hardware of such platform consists in "off-the-shelf' standard PC computer components and may be purchased independently by the end 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".

Warning! Please read carefully before use

⚠ 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 European Council Directive 93/42/EEC. Before use, please make sure that you have thoroughly read and fully understood all the safety and regulatory considerations outlined in this section.

⚠ 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.

⚠ 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.

⚠ 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 artifacts 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.

⚠ 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 behavior 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

⚠ 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.

⚠ Prior to performing medical diagnosis on images created by Computed Radiography (CR in DICOM terminology), please ensure the screen used is CE marked in compliance with Council Directive 93/42/EEC concerning medical devices.

⚠ 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 accuracy of the measurements displayed in Myrian® depends on the image resolution.

⚠ 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. Initially opening a 3D PDF does not show 3D content but it can be enabled by simply setting the menu checkbox at "Preferences – 3D and multimedia – 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

⚠ This product should only be used with approved hardware and software. Please refer to the Hardware and Software Configuration section for further details.

⚠ If using ATI graphic cards, the User may need to change its Renderer settings into Hardware GPU instead of Software CPU for better performance in Endoscopy Mode.

⚠ If the LOD (Level of Detail) is activated, the image may be degraded.

⚠ It is the responsibility of the User to ensure that the image datasets inputted to the Module are complete and that no image or information is missing, otherwise results may not be reliable.

⚠ 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.)

⚠ 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.

⚠ 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.

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

⚠ 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.

⚠ Myrian® considers as low attenuation all regions which density is below -950 HU although this threshold value can be configured by the User. Prior to use of the CT modality, the User should always make sure that it is properly calibrated to ensure low attenuation calculation correctness

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

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.

Geometric distortion such as unequal magnification, pincushion distortion and parallax errors is known to exist in conventional radiography, such as CR and RF radiography. In order to minimize errors, it is recommended to calibrate such imagery as near as possible to image centers and over at least 200 mm.

All series that are compatible with MPR reconstruction can be loaded directly in volume mode, however the filters applied to the image may affect the image quality whenever the displayed series is subject to one or both conditions described below:
- Series where the inter-slice gap is greater than 10% of the slice thickness
- Series containing various voxel dimensions (Voxel Anisotropy) where the dimension of the largest voxel is more than 5 times greater than the dimension of the smallest voxel
In such cases, a warning message appears at the bottom of any of the viewports using these filters indicating that the image is not suitable for diagnostic purposes.

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 of the colon 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.

⚠ Surfacic ROI Mode is not suitable for Diagnostic Purposes.

⚠ To prevent any diagnosis errors, please check that the Centerline, the accuracy of the position of the lumen and outer wall boundary contours, as well as the position of lesions and reference points all match-up to the exact anatomical positions.

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

⚠ The Fusion feature is designed for use as a visualization tool only.Therefore it is the responsibility of the User to determine if the results of image fusion are satisfactory for visualization.

⚠ 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”).

⚠ In order to allow measurements to be performed, image data from CR or XA/XRF or DX modalities are automatically calibrated according to DICOM standards (ftp://medical.nema.org/medical/dicom/final/cp586_ft.pdf). Accordingly, Myrian® calibrates images in the first place on the basis of the PixellSpacing value retrieved in the DICOM fields, and where applicable, on the ImagerPixelSpacing attribute. In that case, a message pops up to inform the user.

⚠ Measurement performed on the projection images, as is the case for DX, CR, DR, DX, RF and XA imagery, do not reflect the real size of the object that is measured in the patient’s anatomy.

⚠ When using SUV calculation during PET assessment, certain assumptions are made with regard to the reference time for the acquisition of the data series. Variability in the interpretation of requirements outlined in the DICOM Standard with regard to determination of the start reference time during acquisition and the time of tracer injection may result in variability in the SUV values calculated by different vendors. It is important to note that due to inconsistency of approach throughout the industry, the acquisition time used in SUV calculation may be any of the acquisition times presented in the DICOM data.

⚠ It is equally important to note that SUV is affected by a number of physiological factors which may cause variability. Taking these two factors into account, SUV can be thought of as a simplified measure of radio-pharmaceutical uptake which has a complimentary rather than directive role in the assessment, treatment and staging of disease.

⚠ 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 radio-pharmaceutical products.

⚠ 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.

⚠ Automatic Vessel Measurements require Contrast-enhanced CT images. Measurements can only be calculated on contrast-enhanced lumen.

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

⚠ 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.

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

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

⚠ It is essential that the radiologist examines all images in the CTC examination, not only the images with segmentation engine marks. The User should examine the entire colon. A 3D read should examine the colon in both directions.

⚠ It is essential that the User check the colon segmentation thoroughly if using a primary 3D reading.

⚠ The distance from rectum calculation should not be used for diagnostic purposes as it should only be used as a guide to locate the ROI in the colon. The distance from rectum measurement should not be used as a guide for Optical Colonoscopy (OC) examinations.

⚠ The computer operator must click on a polyp to launch segmentation.

⚠ The PEF has been designed to highlight regions with a diameter in the range 5-20mm.

⚠ Failure to comply with scanner specific protocols may result in inaccurate results for the identification, segmentation and measurement of ROIs. Scans must comply with good practice for CT Colonography.

⚠ Segmentation may be suboptimal for pedunculated polyps, polyps arising from folds and flatter regions.

⚠ Reproducibility of the PSM output cannot be guaranteed.

⚠ It is not recommended that PEF be used with prepless (no colonic cleansing) or poorly insufflated cases as this may affect the product’s sensitivity. The colon should be well distended. Performance of the PEF may be less than optimal in cases where faecal or fluid tagging has been used.

⚠ It is not recommended that FT be used with prepless (no colonic cleansing) or poorly insufflated cases as this may affect the product’s sensitivity.

⚠ Users should visually check that the polyp segmentation is correct. If not correct, users should re-segment the polyp.

⚠ When calculating the total volume of the Healthy Liver ROI, Myrian® takes into account every existing instance of “Healthy Liver” ROI, regardless of any modifications to the “Name”. This is also the case for “Kidney” ROI.

⚠ To avoid any potential errors, verify the accuracy of all existing “Healthy Liver” ROI as well as that of any ROI volume calculated relative to the Healthy Liver ROI. The same applies to the “Kidney” ROI.

⚠ Whenever the “Healthy Liver” ROI is modified, verify the pertinence of any relative ROI. The same applies to the “Kidney” ROI.

⚠ This device is indicated for mammography only with the proper module XM-MG. This module isn’t marketed on the American territory.

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

⚠ 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.

Installation guidelines

Hardware and software configuration

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

? 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 Intrasense.

⚠ 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.

⚠ The End-user should ensure that the machine 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.

? Upgrading Myrian® from versions of Myrian® which are older than the 1.5 might require hardware upgrades to maintain the same level of performance.

? Any configuration with performances similar or above the recommended configuration should be suitable to run Myrian®, taking into account notes 2, 3 and 4 below.

? For Computed Radiography (CR) Studies, the internal memory (RAM) requirements are: 2 GB (minimum) and 4 GB (recommended).

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

Screen Calibration

To set screen resolution parameters:

- Right-click on the Windows® desktop
- Select 'Properties' from the resulting context menu
- Select 'Parameters'
- Modify the 'Parameters' section as required

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

⚠ 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.

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.

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.

1 Importing Studies

1.1 From a Hospital PACS

- Select the “Remote Studies” tab
- Type the patient Name and/or the PPID in the relevant field by clicking on the corresponding part of the bar underneath the Column Headers

- Filter your search according to **Study Type** (Modality) or leave the field empty

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.

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

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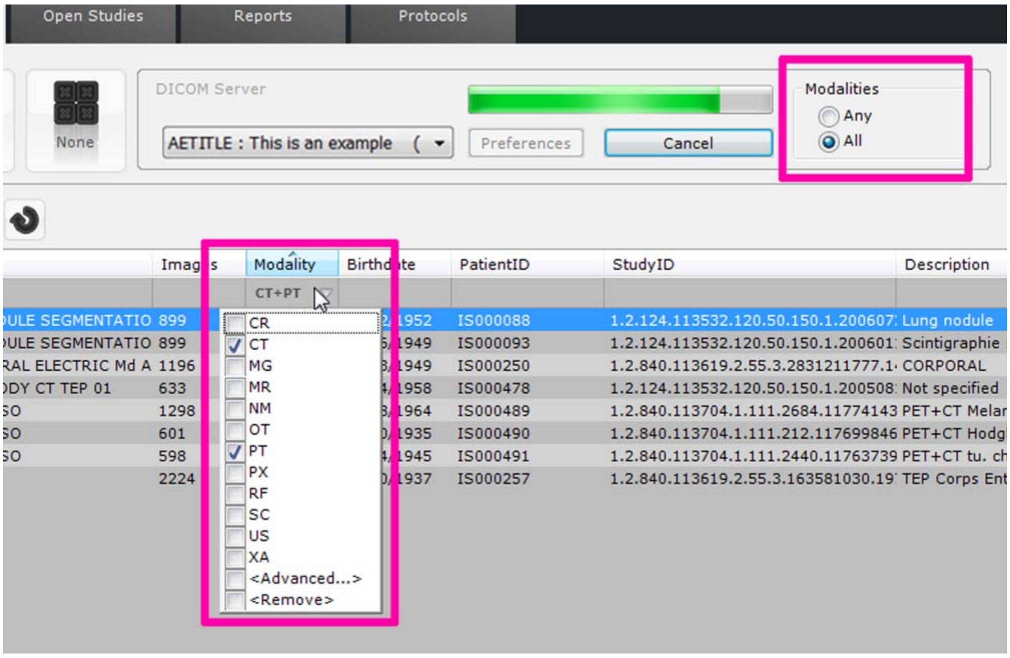
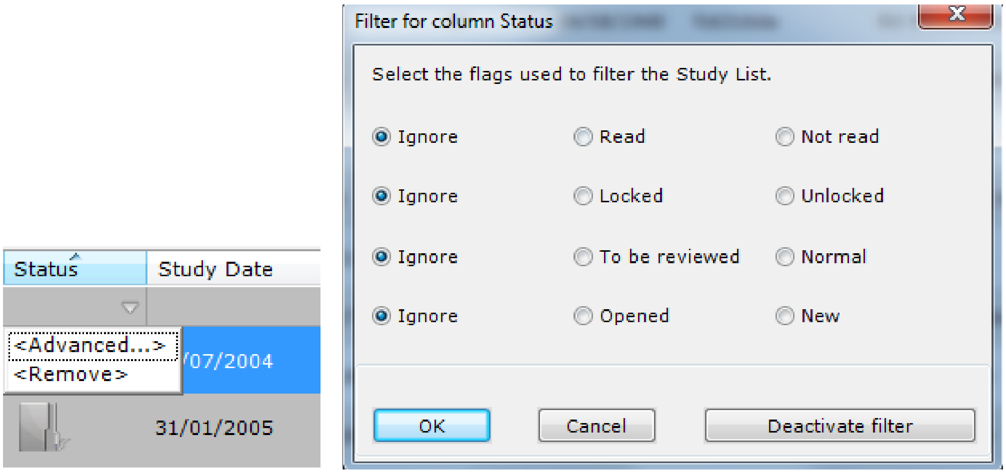


	Images	Modality	Birthdate	PatientID	StudyID	Description
		CT+PT				
ULE SEGMENTATIO	899		1952	IS000088	1.2.124.113532.120.50.150.1.200607	Lung nodule
ULE SEGMENTATIO	899		1949	IS000093	1.2.124.113532.120.50.150.1.200601	Scintigraphie
RAL ELECTRIC Md A	1196		1949	IS000250	1.2.840.113619.2.55.3.2831211777.1	CORPORAL
DY CT TEP 01	633		1958	IS000478	1.2.124.113532.120.50.150.1.200508	Not specified
SO	1298		1964	IS000489	1.2.840.113704.1.111.2684.11774143	PET+CT Melar
SO	601		1935	IS000490	1.2.840.113704.1.111.212.117699846	PET+CT Hodg
SO	598		1945	IS000491	1.2.840.113704.1.111.2440.11763739	PET+CT tu. ch
	2224		1937	IS000257	1.2.840.113619.2.55.3.163581030.19	TEP Corps Ent

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 retrieve.

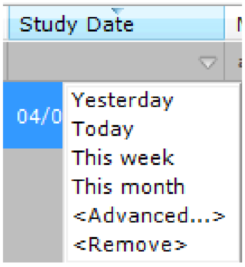
- Filter the Study List according to the ‘New’ or ‘Opened’ status via the Status Column Filter Window by clicking on the ‘Advanced’ Option in the Status Column Menu



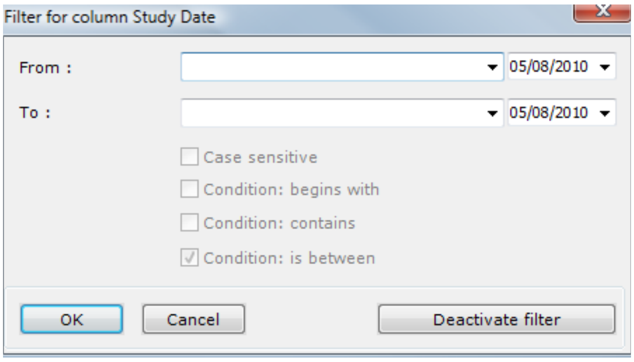
Select the flags used to filter the Study List.

● Ignore ○ Read ○ Not read
● Ignore ○ Locked ○ Unlocked
● Ignore ○ To be reviewed ○ Normal
● Ignore ○ Opened ○ New

- Filter your choice by selecting Study Dates

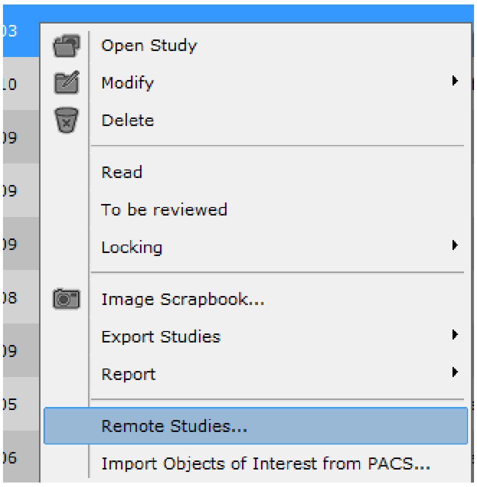


- Or more specific Dates by clicking on '<Advanced>' and selecting your choice of Dates in the resulting Menu

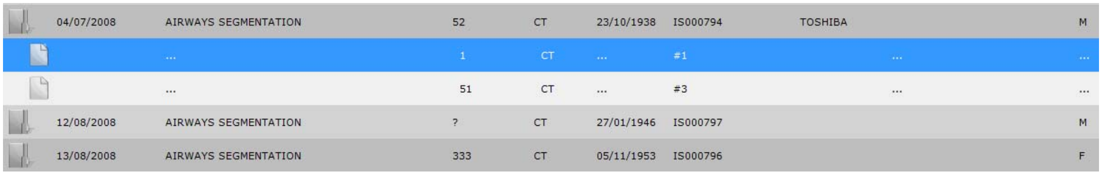


From : 05/08/2010
To : 05/08/2010
☐ Case sensitive
☐ Condition: begins with
☐ Condition: contains
☑ Condition: is between

You can also click on "Remote Studies" in Context Menu by right-clicking on your desired Study to automatically launch a Query/Retrieve on your Main PACS according to the corresponding PatientID



- Click on Retrieve
- Click on the desired Patient line to select the whole study, or
- Click on the folder icon itself to expand the list and select your choice of Series



04/07/2008	AIRWAYS SEGMENTATION	52	CT	23/10/1938	IS000794	TOSHIBA		M
	...	1	CT	...	#1		...	...
	...	51	CT	...	#3		...	...
12/08/2008	AIRWAYS SEGMENTATION	?	CT	27/01/1946	IS000797			M
13/08/2008	AIRWAYS SEGMENTATION	333	CT	05/11/1953	IS000796			F

- To finish, click on to import the Series to your Local Study Database

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You can double-click on a **Series/Subseries** to import it directly

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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

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Select a Study in the Local Study List then click on ‘Remote Studies’ to automatically launch a Query/Retrieve on your Main PACS according to the selected PatientID. The results will then be displayed in the Remote Studies tab

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Importing is done “in the background” which enables other tasks to be carried out at the same time in the interface. You can check the import status by clicking on the ‘Background Jobs’ button (butterfly icon) located at bottom-right of the screen

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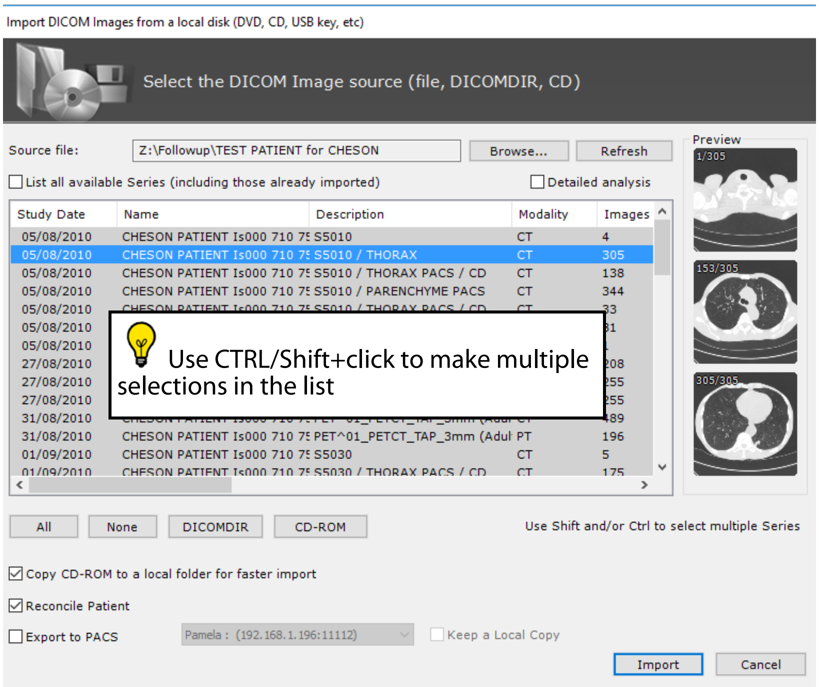
1.2 From a CD or DVD

- Select the **‘Local Studies’** tab
- Click on in the Tools menu at the top of the Local Studies Screen

- Then CD-ROM

The following screen appears in which you can select any Series, multiple Series or all Series:



Import DICOM Images from a local disk (DVD, CD, USB key, etc)

Select the DICOM Image source (file, DICOMDIR, CD)

Source file: Z:\Followup\TEST PATIENT for CHESON

☐ List all available Series (including those already imported)

☐ Detailed analysis

Study Date	Name	Description	Modality	Images
05/08/2010	CHESON PATIENT Is000 710 7!	S5010	CT	4
05/08/2010	CHESON PATIENT Is000 710 7!	S5010 / THORAX	CT	305
05/08/2010	CHESON PATIENT Is000 710 7!	S5010 / THORAX PACS / CD	CT	138
05/08/2010	CHESON PATIENT Is000 710 7!	S5010 / PARENCHYME PACS	CT	344
05/08/2010	CHESON PATIENT Is000 710 7!	S5010 / THORAX PACS / CD	CT	33
05/08/2010				31
05/08/2010				1
27/08/2010				208
27/08/2010				255
27/08/2010				255
31/08/2010				489
31/08/2010	CHESON PATIENT Is000 710 7!	PET^01_PETCT_TAP_3mm (Adul	PT	196
01/09/2010	CHESON PATIENT Is000 710 7!	S5030	CT	5
01/09/2010	CHESON PATIENT Is000 710 7!	S5030 / THORAX PACS / CD	CT	175

Use CTRL/Shift+click to make multiple selections in the list

Use Shift and/or Ctrl to select multiple Series

☑ Copy CD-ROM to a local folder for faster import

☑ Reconcile Patient

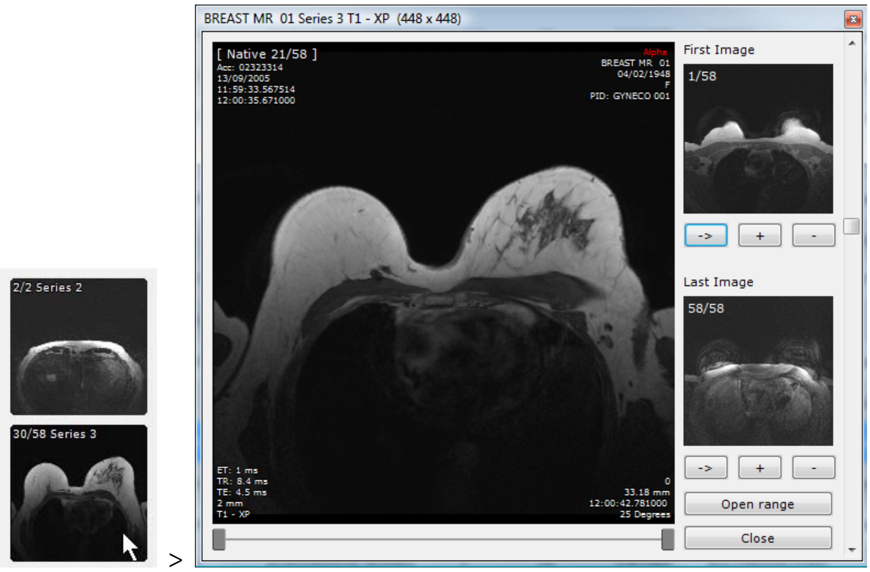
☐ Export to PACS Pamela : (192.168.1.196:11112) ☐ Keep a Local Copy

- Click on Import to import the Study to your Local Database

If you browse for a new location clicking on Browse..., 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.

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

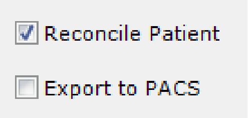
Click on a Series thumbnail to open the Preview Screen before import



- Navigate through the slices by turning the mouse-wheel (or click-and-drag the mouse over the thumbnail)
- Double-click on the image to import the Series

Whenever a Myrian® session is open, inserting a CD or DVD into the PC's CD/DVD player opens a dialog box displaying the contents of the disk.

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



☑ Reconcile Patient

☐ Export to PACS

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

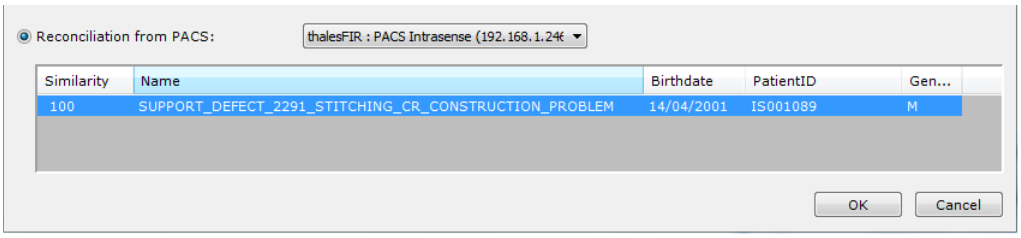
If you activate the 'Use Patient Data from Imported Series' radio button, the Patient Reconciliation process will be overridden and the Patient Information from the Imported Series alone will be used.

Patient Reconciliation

● Use Patient Data from Imported Series (no Reconciliation):

Name: HING_CR_CONSTRUCTION_PROBLEM Date of Birth: 14/04/2001 Gender: M

If you activate the 'Reconciliation from PACS' radio button, Myrian® will automatically launch a query for all Studies stored on the PACS bearing the same Patient Name.



● Reconciliation from PACS: thalesFIR : PACS Intrasense (192.168.1.24€

Similarity	Name	Birthdate	PatientID	Gen...
100	SUPPORT_DEFECT_2291_STITCHING_CR_CONSTRUCTION_PROBLEM	14/04/2001	IS001089	M

- Press OK to launch Reconciliation

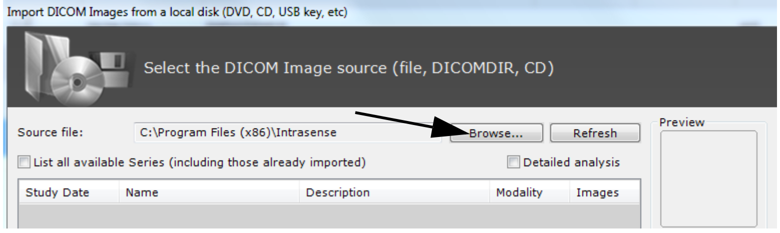
The Reconcile Patient feature is not available for Follow-ups.

The Reconcile Patient feature changes Patient Info of Series only.

1.3 From external storage devices (USB keys, etc.)

- Click on the Local Studies button
- Click on Import... in the toolbar at the top of the Local Studies Tab

- Click on Browse... in the resulting screen


Import DICOM Images from a local disk (DVD, CD, USB key, etc)

Select the DICOM Image source (file, DICOMDIR, CD)

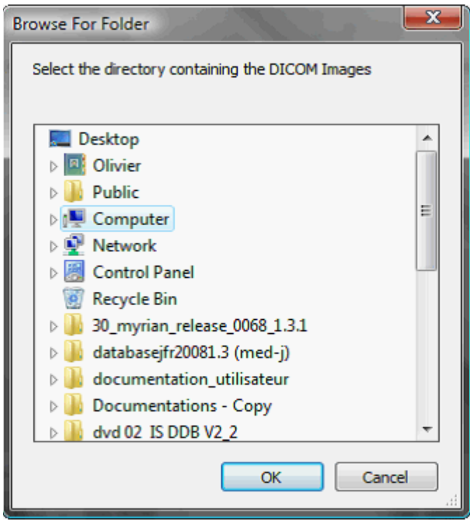
Source file: C:\Program Files (x86)\Intrasense

☐ List all available Series (including those already imported)

☐ Detailed analysis

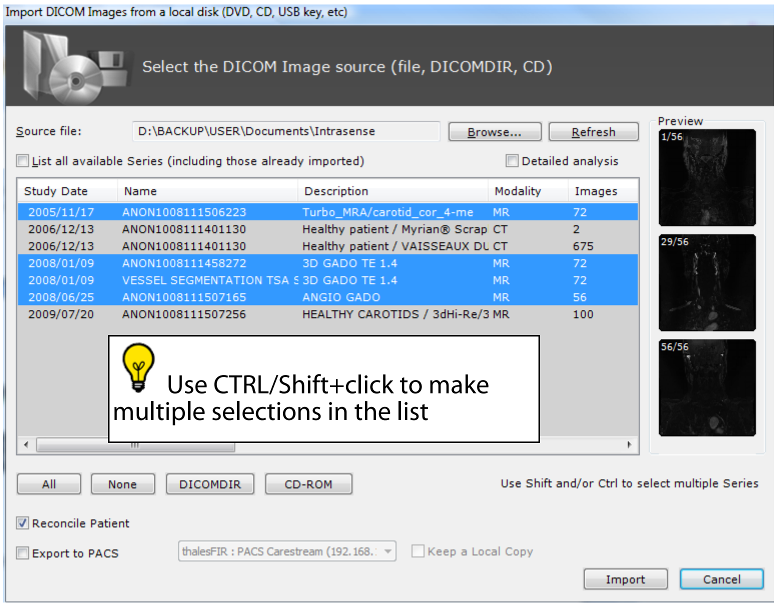
Study Date	Name	Description	Modality	Images

- Use the Windows browser to locate and select the desired folder then click OK


Browse For Folder

Select the directory containing the DICOM Images

- In the resulting window, select one or more Studies/Series (using Ctrl/Shift button + mouse-click for multiple selections)


Import DICOM Images from a local disk (DVD, CD, USB key, etc)

Select the DICOM Image source (file, DICOMDIR, CD)

Source file: D:\BACKUP\USER\Documents\Intrasense

☐ List all available Series (including those already imported)

☐ Detailed analysis

Study Date	Name	Description	Modality	Images
2005/11/17	ANON1008111506223	Turbo_MRA/carotid_cor_4-me	MR	72
2006/12/13	ANON1008111401130	Healthy patient / Myrian® Scrap	CT	2
2006/12/13	ANON1008111401130	Healthy patient / VAISSEAUX DU	CT	675
2008/01/09	ANON1008111458272	3D GADO TE 1.4	MR	72
2008/01/09	VESSEL SEGMENTATION TSA S	3D GADO TE 1.4	MR	72
2008/06/25	ANON1008111507165	ANGIO GADO	MR	56
2009/07/20	ANON1008111507256	HEALTHY CAROTIDS / 3dHi-Re/3	MR	100

Use CTRL/Shift+click to make multiple selections in the list

Use Shift and/or Ctrl to select multiple Series

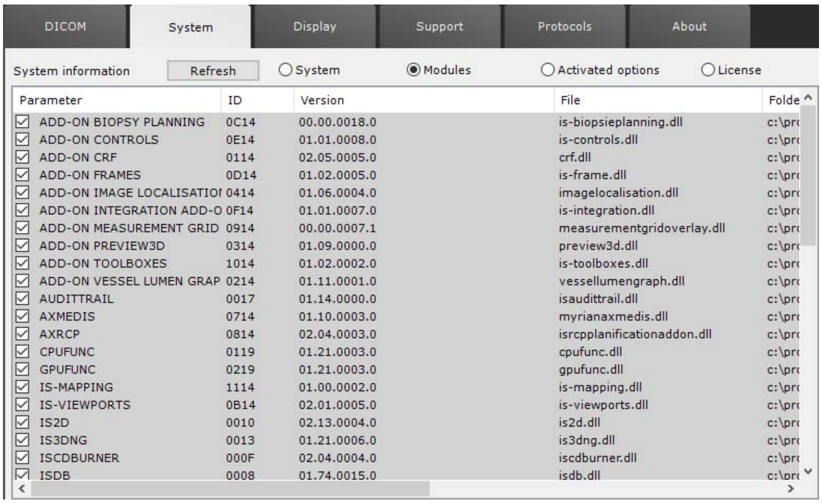
☑ Reconcile Patient

☐ Export to PACS thalesFIR : PACS Carestream (192.168. ☐ Keep a Local Copy

- Then Import

Click on a thumbnail to preview a Series before importing

Note : In the settings, in the system tab and in module space, using the checkbox you can select which DLL Myrian should load or not. Removing some unused DLL will speed up Myrian startup.



System information ○ System ● Modules ○ Activated options ○ License

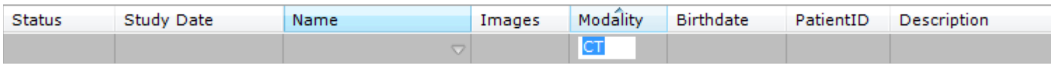
	Parameter	ID	Version	File	Folde
☑	ADD-ON BIOPSY PLANNING	0C14	00.00.0018.0	is-biopsieplanning.dll	c:\pr
☑	ADD-ON CONTROLS	0E14	01.01.0008.0	is-controls.dll	c:\pr
☑	ADD-ON CRF	0114	02.05.0005.0	crf.dll	c:\pr
☑	ADD-ON FRAMES	0D14	01.02.0005.0	is-frame.dll	c:\pr
☑	ADD-ON IMAGE LOCALISATIO	0414	01.06.0004.0	imagelocalisation.dll	c:\pr
☑	ADD-ON INTEGRATION ADD-O	0F14	01.01.0007.0	is-integration.dll	c:\pr
☑	ADD-ON MEASUREMENT GRID	0914	00.00.0007.1	measurementgridoverlay.dll	c:\pr
☑	ADD-ON PREVIEW3D	0314	01.09.0000.0	preview3d.dll	c:\pr
☑	ADD-ON TOOLBOXES	1014	01.02.0002.0	is-toolboxes.dll	c:\pr
☑	ADD-ON VESSEL LUMEN GRAP	0214	01.11.0001.0	vessellumengraph.dll	c:\pr
☑	AUDITTRAIL	0017	01.14.0000.0	isaudittrail.dll	c:\pr
☑	AXMEDIS	0714	01.10.0003.0	myrianaxmedis.dll	c:\pr
☑	AXRCP	0814	02.04.0003.0	isrcpplanificationaddon.dll	c:\pr
☑	CPUFUNC	0119	01.21.0003.0	cpufunc.dll	c:\pr
☑	GPUFUNC	0219	01.21.0003.0	gpufunc.dll	c:\pr
☑	IS-MAPPING	1114	01.00.0002.0	is-mapping.dll	c:\pr
☑	IS-VIEWPORTS	0B14	02.01.0005.0	is-viewports.dll	c:\pr
☑	IS2D	0010	02.13.0004.0	is2d.dll	c:\pr
☑	IS3DNG	0013	01.21.0006.0	is3dng.dll	c:\pr
☑	ISCDBURNER	000F	02.04.0004.0	iscdburner.dll	c:\pr
☑	ISDB	0008	01.74.0015.0	isdb.dll	c:\pr

2 The Study List

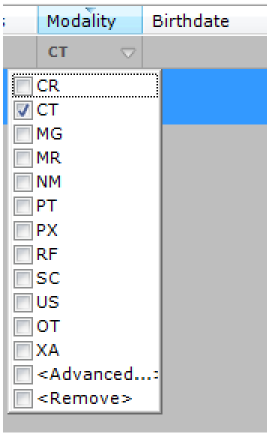
2.1 Filters

1. Click on the Study List tab
2. Type a name in the 'Name' field or select a Study in the Local Study List

The Local Study List can be **filtered** using Name, Study Type (Modality) or any other criteria by clicking on the line immediately beneath the desired criterion and typing-in your filter condition



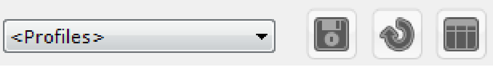
You can also use the **drop-down menus** below the column title fields



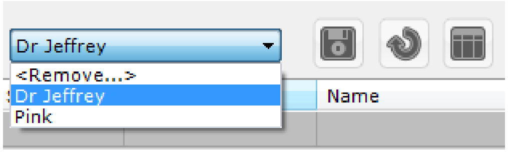
Press ✖ Deactivate Filters to deactivate all column filters. Note that this button appears at the top-right of the Study List Tab **only if a filter is activated**

2.2 Profiles

You can click on the "Capture or Modify current Profile" button (floppy disc icon) in the Column Configuration Profiles toolbar above the Local Study List to save or configure your filter settings



- To select a Profile, use the Column Profiles drop-down list



To delete a Profile you must first select it in the drop-down list, then click on "<Remove>" at the top of the same drop-down list

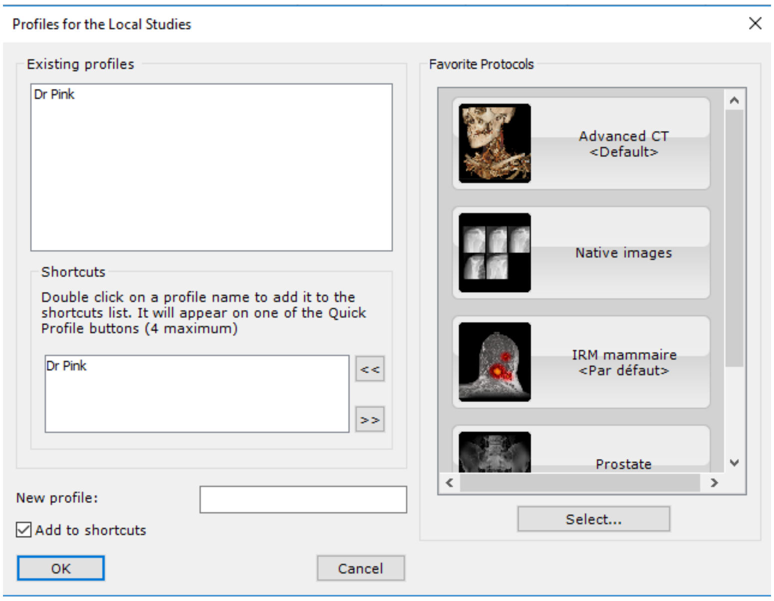
---

You can also create or modify Column Configuration Profiles by clicking on in the same toolbar, or use to restore the user set Default Column Configuration

2.3 QuickProfiles

You can use the "QuickProfiles" function to create quick access buttons at the top of the Study List for your favourite 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, click on the "Capture or Modify current Profile" button to open the Current Profile modification window



Existing profiles: Dr Pink

Shortcuts

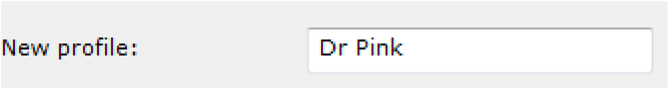
Double click on a profile name to add it to the shortcuts list. It will appear on one of the Quick Profile buttons (4 maximum)

Dr Pink

New profile:

☑ Add to shortcuts

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



New profile: Dr Pink

- 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

---

Tick the checkbox ☑ Add to shortcuts at the bottom-left of the Profiles window to automatically add any selected new Profile to the QuickProfiles list

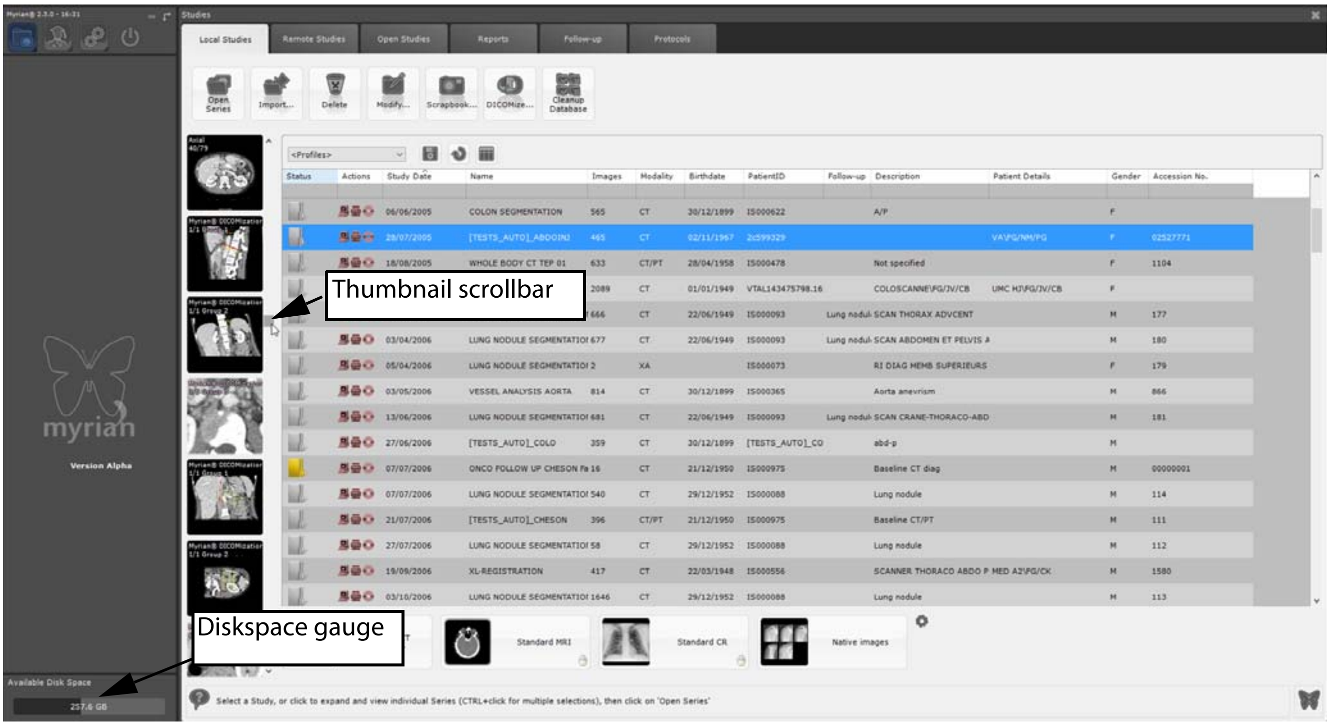
---

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

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

2.4 Preview Thumbnails

1 Click on the study folder icon to expand the list of Series contained in a Study



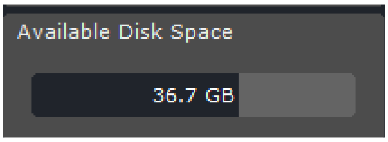
Select a Study, or click to expand and view individual Series (CTRL+click for multiple selections), then click on 'Open Series'

A Thumbnail of each Series/Subseries you select is displayed at left of the Study List (use the scrollbar at left to view any hidden thumbnail).

Click on a thumbnail to open a preview screen in which you can preselect the specific range of slices you wish to open

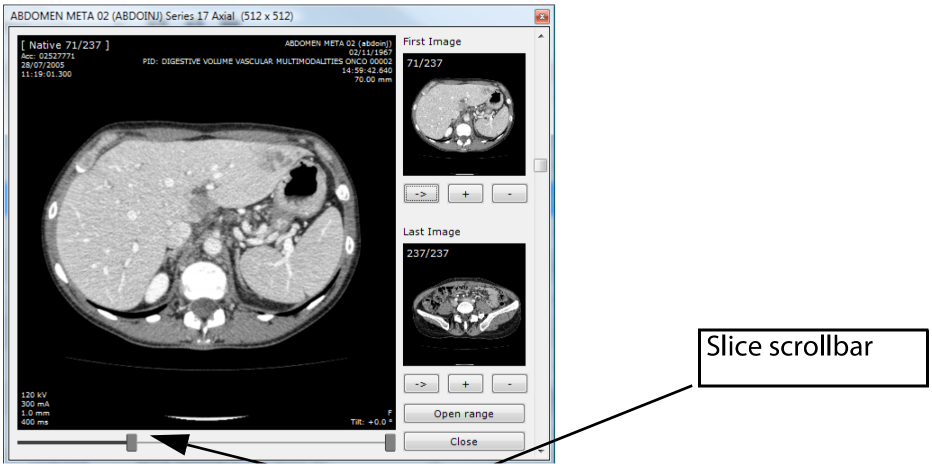
---

At any time, you can check the available disk space of Myrian® database system at the bottom-left of the main screen.

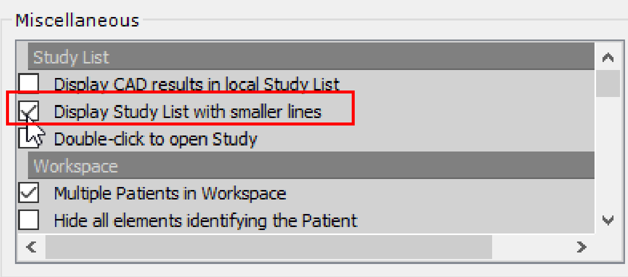

Available Disk Space

36.7 GB

You can double-click on thumbnails to open Studies directly



You can modify the size of Study List icons and lines in the Preferences>Display>Miscellaneous menu


Miscellaneous

Study List

☐ Display CAD results in local Study List

☑ Display Study List with smaller lines

☐ Double-click to open Study

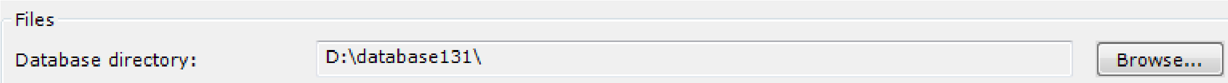
Workspace

☑ Multiple Patients in Workspace

☐ Hide all elements identifying the Patient

2 Select one or more Series then click on the 'Open Series' button at far left of the toolbar

You can switch between Local Study Lists in Myrian® by changing the Database directory in the 'Files' section of the Preferences>System Tab. 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

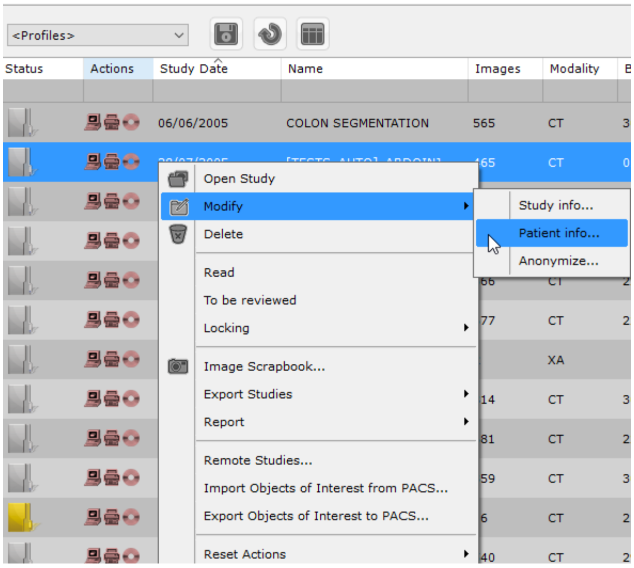

Files

Database directory: D:\database131\

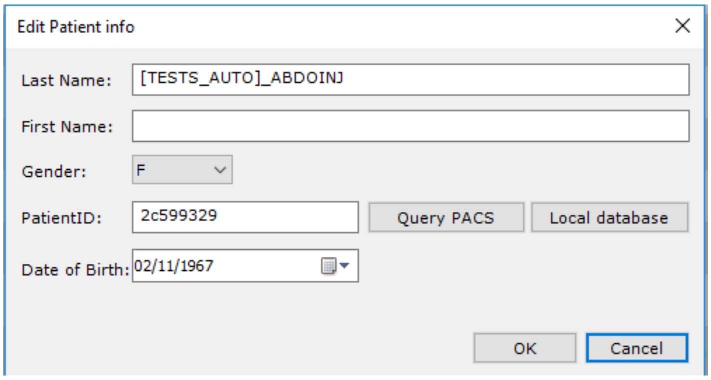
Changing Local Database is done 'on the fly' and does not require a software reboot

2.5 Modify Patient Information

1 Right-click on the Study of your choice and select 'Modify' from the context menu



2 Select 'Patient Info in the ensuing sub-menu



Edit Patient info

Last Name: [TESTS_AUTO]_ABDOINJ

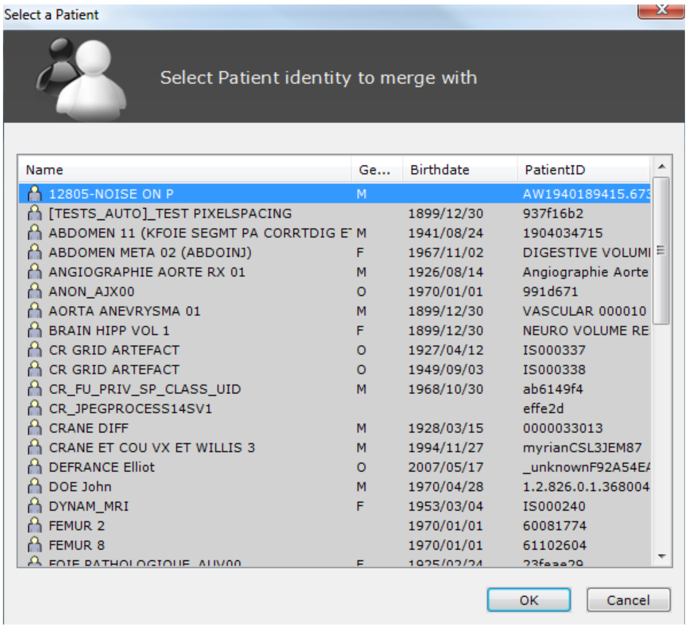
First Name:

Gender: F

PatientID: 2c599329

Date of Birth: 02/11/1967

3 Click on Local database to open the Local Study Database Reconciliation Window and select a Study of your choice



Select a Patient

Select Patient identity to merge with

Name	Ge...	Birthdate	PatientID
12805-NOISE ON P	M		AW1940189415.673
[TESTS_AUTO]_TEST PIXELSPACING		1899/12/30	937f16b2
ABDOMEN 11 (KFOIE SEGMT PA CORRTDIG ET	M	1941/08/24	1904034715
ABDOMEN META 02 (ABDOINJ)	F	1967/11/02	DIGESTIVE VOLUMI
ANGIOGRAPHIE AORTE RX 01	M	1926/08/14	Angiographie Aorte
ANON_AJX00	O	1970/01/01	991d671
AORTA ANEVRYSMA 01	M	1899/12/30	VASCULAR 000010
BRAIN HIPP VOL 1	F	1899/12/30	NEURO VOLUME RE
CR GRID ARTEFACT	O	1927/04/12	IS000337
CR GRID ARTEFACT	O	1949/09/03	IS000338
CR_FU_PRIV_SP_CLASS_UID	M	1968/10/30	ab6149f4
CR_JPEGPROCESS14SV1			effe2d
CRANE DIFF	M	1928/03/15	0000033013
CRANE ET COU VX ET WILLIS 3	M	1994/11/27	myrianCSL3JEM87
DEFRANCE Elliot	O	2007/05/17	_unknownF92A54E
DOE John	M	1970/04/28	1.2.826.0.1.368004
DYNAM_MRI	F	1953/03/04	IS000240
FEMUR 2		1970/01/01	60081774
FEMUR 8		1970/01/01	61102604

4 Press Query PACS to open the Patient Reconciliation Window and select a Study of your choice

from the PACS

It is possible to modify Patient Information of Patients that have one or more Follow-ups in progress

---

This operation changes the Patient Information of all Series for the Patient concerned simultaneously.

If the Patient being modified has one or more Follow-ups in progress, the Patient Information is updated to the new values in each Follow-up.

Patient Info modifications in Reports created prior to the modifications are not updated.

It is not possible to reconcile Series that belong to a Follow-up

---

2.6 Display Protocols

1. Select a Study or Series and click on the “Open Series” button

---

Use the CTRL/SHIFT key + click to select multiple Series or Studies

---

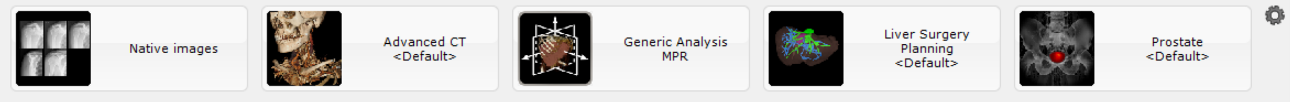
This action opens the Protocols tab

2. Double-click on your choice to launch the Series
3. in the settings, by checking the opening by double click you can open this way an exam in the study list by clicking directly on the study

Sélectionnez un protocole. Le protocole définit l'organisation de l'espace de travail, c'est à dire la mise en page des séries, le mode de visualisation, les outils disponibles, etc.

2.7 QuickProtocols

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



1 Click on the “Configure QuickProtocols” button (cogwheel icon) ⚙ at the bottom-right of the Study List

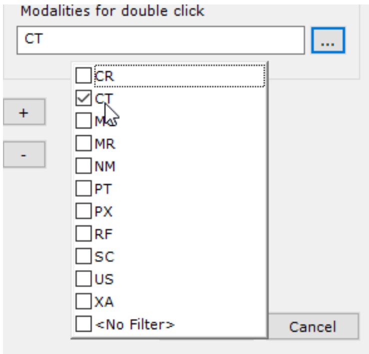
2 In the QuickProtocols Configuration Window, select a Protocol in the QuickProtocols Box at left and modify its properties via the fields at right.

3 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 button (you can rename any Protocol freely).

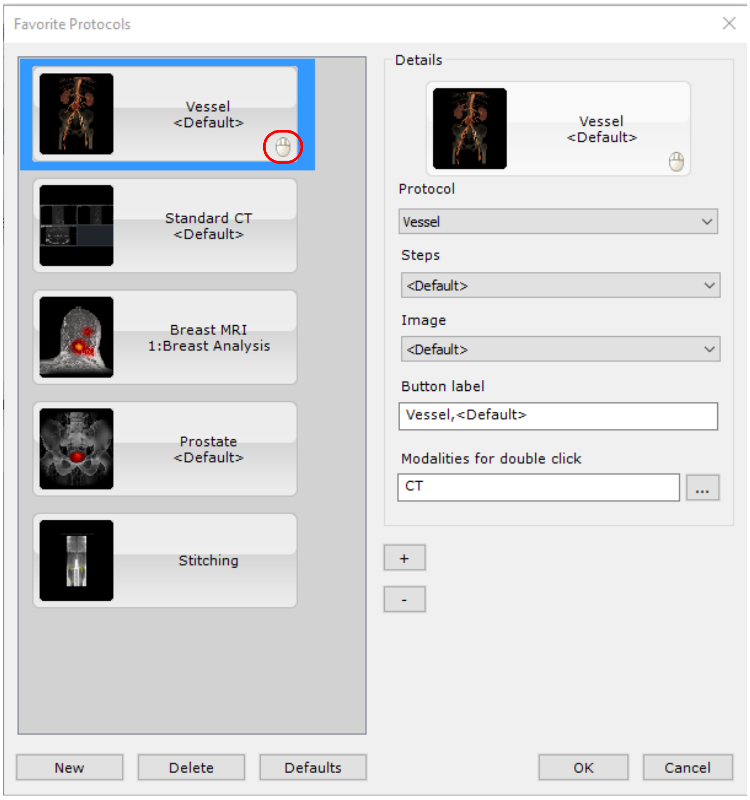
4 You can also associate the double-click to a given protocol associated to the requested modality(ies).

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


Modalities for double click: CT

- ☐ CR
- ☑ CT
- ☐ MG
- ☐ MR
- ☐ NM
- ☐ PT
- ☐ PX
- ☐ RF
- ☐ SC
- ☐ US
- ☐ XA
- ☐ <No Filter>

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


Favorite Protocols

Details

Protocol: Vessel

Steps: <Default>

Image: <Default>

Button label: Vessel,<Default>

Modalities for double click: CT

You can select any QuickProtocol and modify it freely

---

5 Use the Move Up/Down buttons + / - to modify the order the QuickProtocols appear in

6 Click on New under the QuickProtocol 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

---

7 To remove a QuickProtocol, first select it then click on Delete to the right of the Create New QuickProtocol button

---

Click on Defaults to restore Factory Settings for QuickProtocols

---

3 The Workspace

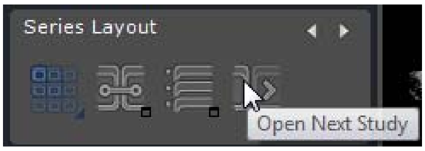
3.1 Opening Studies from the Workspace

The “Open Next Study” function 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, this feature will load only those types of Studies).

This option enables you to close all open Series and open the next Study in the Study List directly from the ‘Series Layout’ Toolbar in the Workspace by clicking on the ‘Open Next Study’ button

---

- Click on the ’Local Studies’ button
- Open a Study/Series using the desired Protocol
- When you find yourself in the Main Workspace, click on the ‘Open Next Study’ button to launch the next Study in your Local Study List automatically closing the current Series



The Study List is reviewed taking into account any active filtering or sorting

---

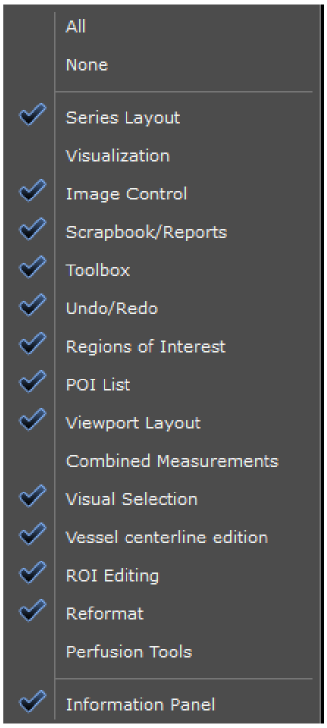
If a Study is opened via a QuickProtocol, the next Study will be opened with the same Protocol.

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.

3.2 Image adjustment

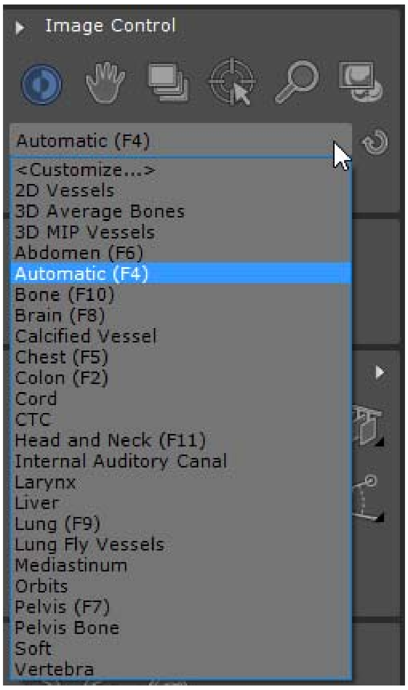
Once the Series is loaded, you are ready to view the Images

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

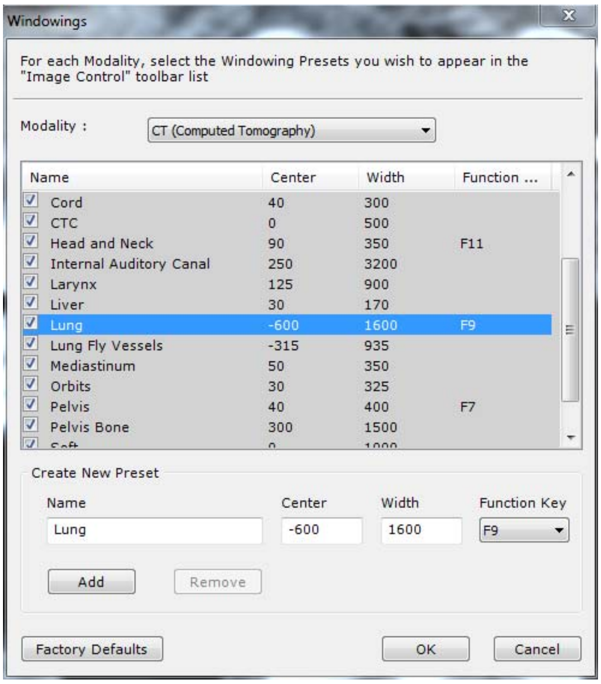


You can hide all toolbars and the bottom information panel if you wish to toggle the image display to full screen mode: press **CTRL + I**
To restore overall layout mode back to normal, simply press CTRL + I again.

- Press to activate the Windowing tool and modify **Windowing** settings manually,
  or,
- Use the Presets (Bones, Lungs, etc.) from the drop-down menu:



- Click on “Customize” to modify the Windowing Presets to your own needs



For each Modality, select the Windowing Presets you wish to appear in the "Image Control" toolbar list

Modality : CT (Computed Tomography)

	Name	Center	Width	Function ...
☑	Cord	40	300	
☑	CTC	0	500	
☑	Head and Neck	90	350	F11
☑	Internal Auditory Canal	250	3200	
☑	Larynx	125	900	
☑	Liver	30	170	
☑	Lung	-600	1600	F9
☑	Lung Fly Vessels	-315	935	
☑	Mediastinum	50	350	
☑	Orbits	30	325	
☑	Pelvis	40	400	F7
☑	Pelvis Bone	300	1500	

Create New Preset

Name	Center	Width	Function Key
Lung	-600	1600	F9

- Customize the list of Presets available for each Modality

- To sharpen the definition of any image, click on the Edge Enhancement button at the bottom-right of the corresponding Viewport and choose the desired setting from the menu:

- Click on the Grid Filter 'On' button to remove artefacts caused by Anti-Scattering grids used on CR Modalities.

- Click on the Grid Filter 'Off' button to remove the Grid Filtering

---

Filtering settings are persistent. Filters are active from session to session until they are removed

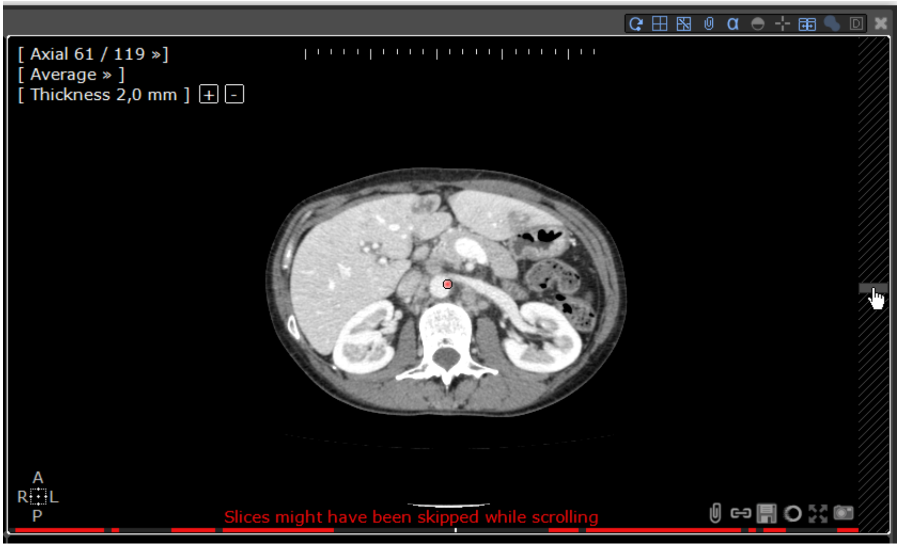
---

- Use to zoom in and out on any specific point in an image

- Move the image using the Pan tool

- Click on to navigate through the image slices

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 scrollling' as illustrated hereunder:



[Axial 61 / 119 »]
[Average »]
[Thickness 2,0 mm] + -

Slices might have been skipped while scrolling

If navigation seems too slow, uncheck the **'Image per Image navigation is default'** option in the Preferences> Display>Miscellaneous menu

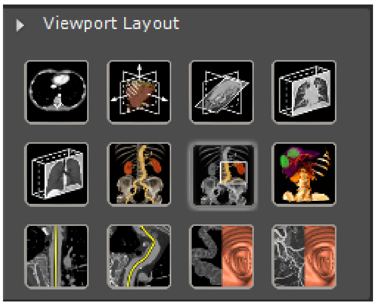
---

- Use the Grid Mode button to display the Native Images in the Series

The Movie Mode and Magnifying Glass can be effective presentation tools during Medical Staff Meetings, Case Reviews, Seminars, Grand Rounds, etc.

Press the 'M' key shortcut to switch to MPR (if both the 'ObliqueNavigator' and 'MPRNavigator' options have been activated in your version of the software)

Click on the desired Layout in the Viewport Layout Toolbar to instantly change the Display Protocol

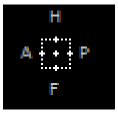


- Double-click anywhere in the image **while in Navigation Mode** to move the Anatomic Centre to that location
- **If you are in Oblique mode**, press the ALT key to place the Anatomic Centre automatically to the mouse

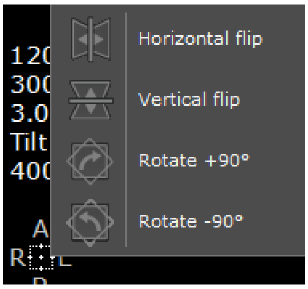
position

- While holding down the ALT key, click-and-drag the mouse within the Oblique Viewport to swivel the view around the Anatomic Centre

Projected images can be flipped horizontal/vertical 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**



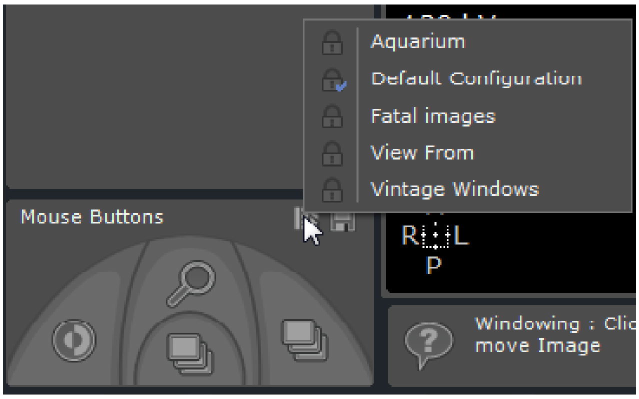
For all other modalities, use the Flip/Rotate menu which appears when you click on the orientation square at bottom-right of each Viewport



3.3 Mouse-button function settings and profiles

3.3.1 Factory mouse profiles

By default, the applied mouse button profile is the default configuration

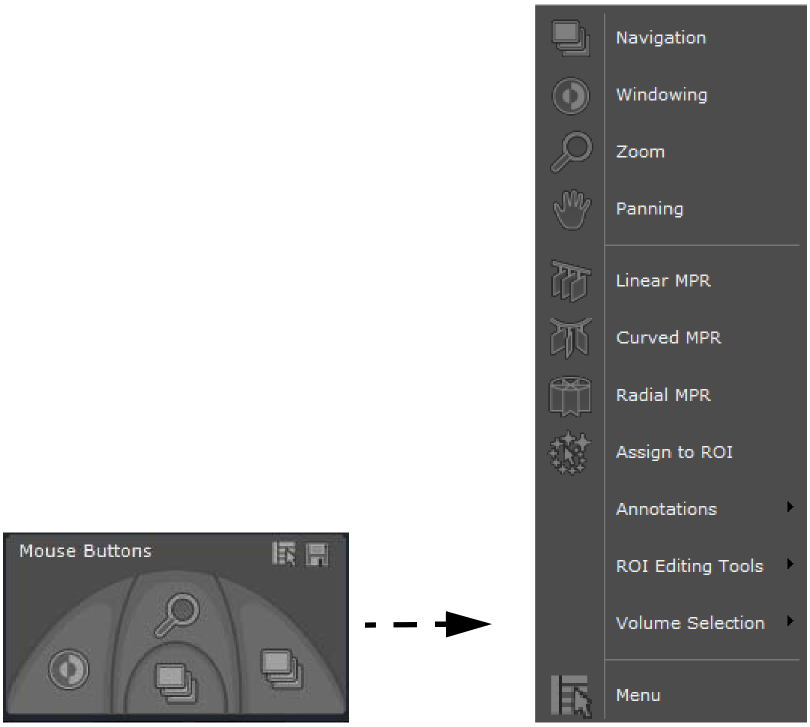


- If you wish to switch from the mouse default configuration to another mouse factory profile, click on and select a mouse button profile among those listed.

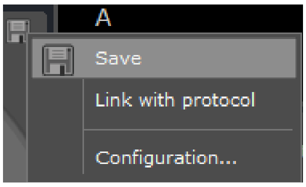
3.3.2 Modifying a factory mouse profile

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

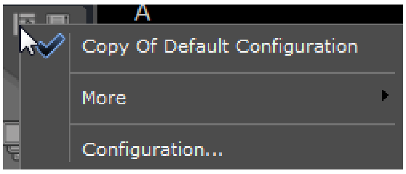


- To save it, click on 💾 then select 'Save' from the resulting contextual menu.



This customized profile becomes the default configuration profile and is automatically:

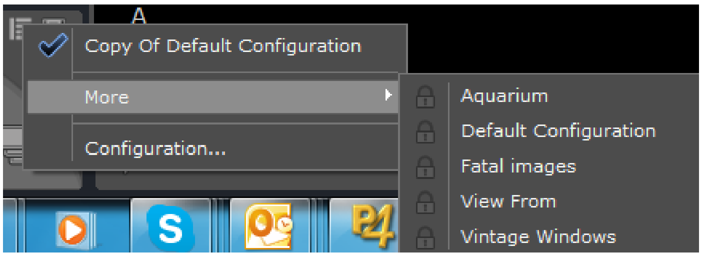
- Updated with the new added tools when opening a view in the workspace
- Named 'Copy of (factory name)'



You can rename this 'Copy of (factory name)' profile via the 'Configuration...' button

---

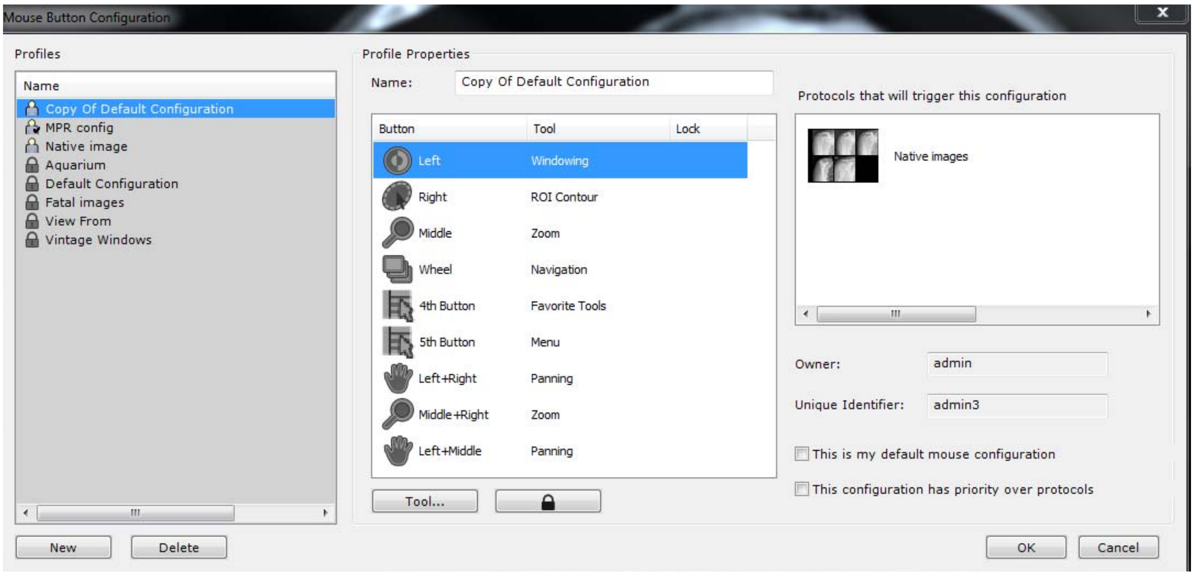
To switch from the customized mouse profile to one of the existing factory mouse profiles, click on 'More' to display the mouse profile list



3.3.3 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:



Name: Copy Of Default Configuration

Button	Tool	Lock
Left	Windowing	
Right	ROI Contour	
Middle	Zoom	
Wheel	Navigation	
4th Button	Favorite Tools	
5th Button	Menu	
Left+Right	Panning	
Middle+Right	Zoom	
Left+Middle	Panning	

Owner: admin

Unique Identifier: admin3

☐ This is my default mouse configuration

☐ This configuration has priority over protocols

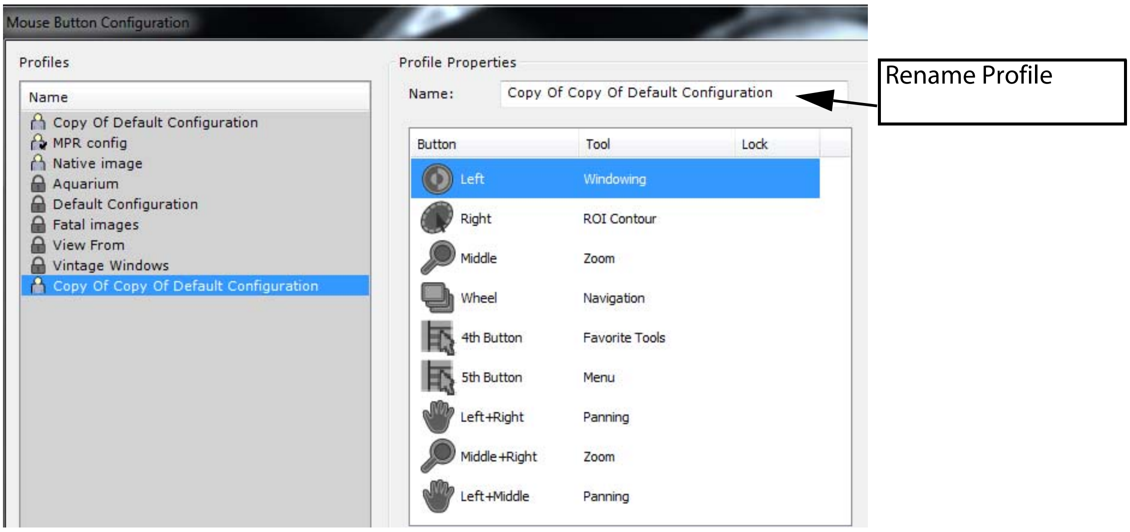
Factory mouse profiles (represented by the padlock icon 🔒) **cannot be edited** nor **deleted**.

Only user-defined mouse profiles can be removed clicking on Delete

---

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 on New
- Rename this new mouse profile in the Name field

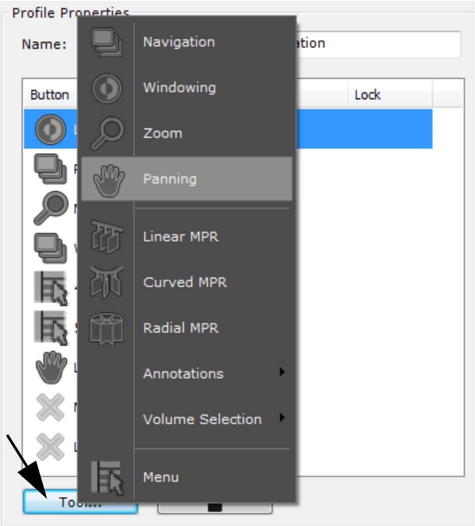


Rename Profile

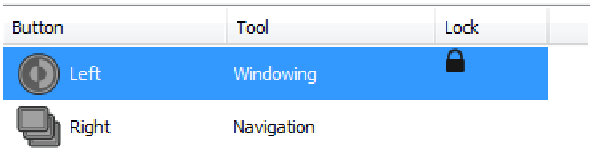
Name: Copy Of Copy Of Default Configuration

Button	Tool	Lock
Left	Windowing	
Right	ROI Contour	
Middle	Zoom	
Wheel	Navigation	
4th Button	Favorite Tools	
5th Button	Menu	
Left+Right	Panning	
Middle+Right	Zoom	
Left+Middle	Panning	

- Assign the mouse buttons to the tools of your choice, selecting the default assigned tool then clicking on ’Tool...’ (or simply double-clicking on the default assigned tool) to open the ’Tool’ contextual menu.

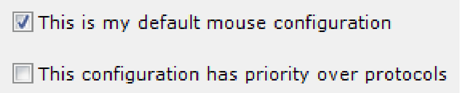


To prevent any modification of the assigned button in a given mouse button profile, you can lock any of those tools clicking on the 🔒 padlock icon



Button	Tool	Lock
Left	Windowing	🔒
Right	Navigation	

- Define the following profile properties:



☑ This is my default mouse configuration

☐ This configuration has priority over protocols

- 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 they 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.

3.3.4 Associate any mouse profile to the current protocol

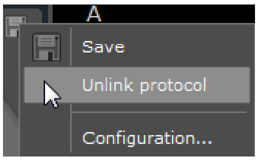
- Click on 'Link with protocol' from the disk icon 💾 contextual menu

---

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 on 💾 and select 'Unlink with 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.

3.4 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

---

3.5 QuickTools

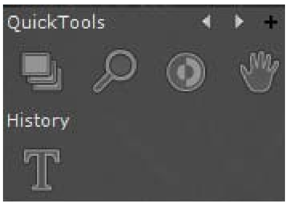
This feature requires a 5-button Mouse

The QuickTools function enables you to configure sets of Favourite 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

If you have used any tools before calling up the QuickTools Toolbox, a ‘Recent’ palette displays the most recently used tools (up to 3 maximum)

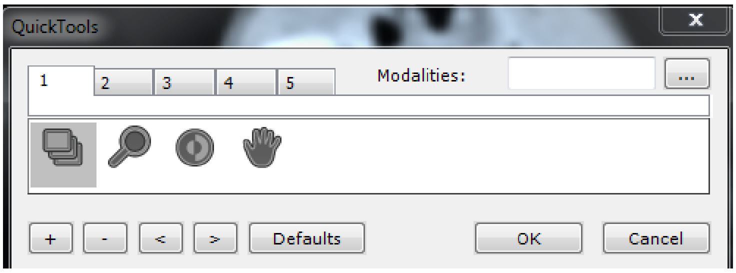
- Use the “forward” ▶ and “back” ◀ arrows at the top of the QuickTools Toolbox to cycle through the various existing palettes



By default, there are 3 available QuickTools palettes: 1 Image Control and 2 Measurement palettes

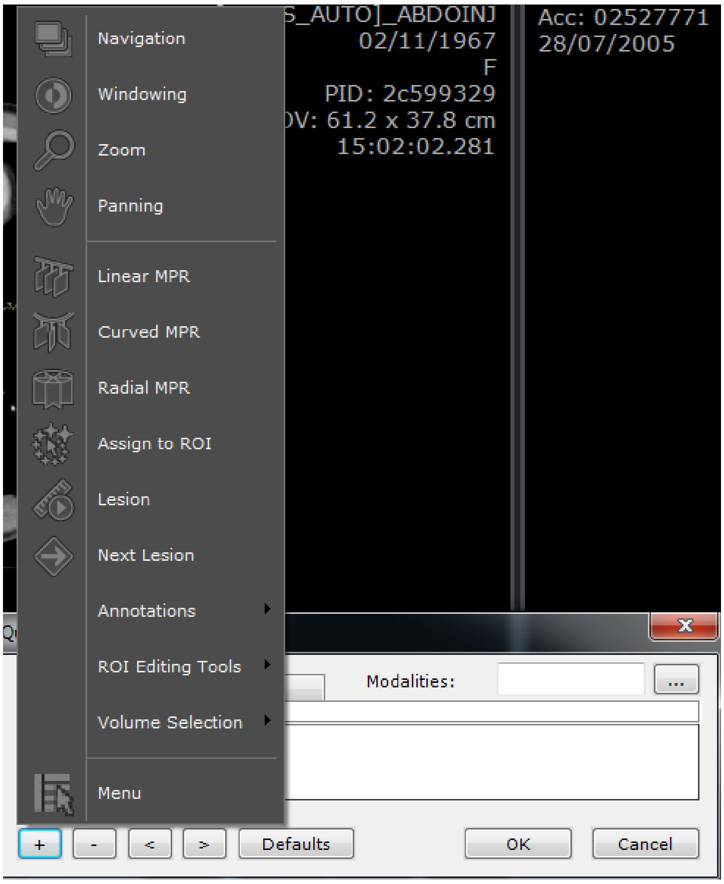
---

- Click on the “Create New Palette” button ‘+’ at the top-right of the Palette to open the Palette Configuration Window



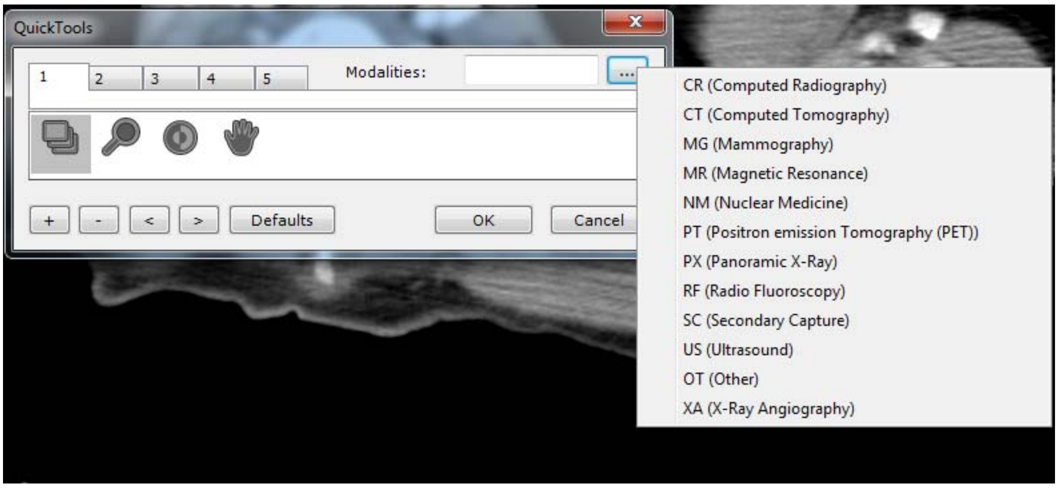
The QuickTools Palette Editor enables you to create up to 5 different palettes, each of which is represented by a separate tab. Tabs are numbered 1 to 5

- 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



You can remove elements from the palettes using the ‘Remove Selected Tool’ button - beside the Add Tool button, or rearrange them by using the ‘Move Left/Right’ buttons < > to the right of the Add/Remove buttons

For each set, you can define a list of modalities for which the set is designed by clicking on the Browse button ... at right of the ‘Modalities’ field (at the top-right of the QuickTools Editor). The modalities can be further edited directly in the ‘Modalities’ field.



QuickTools 'Modality' settings default to that of the active view

---

You can use the mouse wheel to cycle through the sets

Click on Defaults to restore factory settings

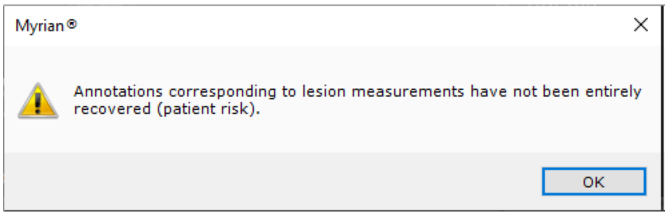
3.6 Warning box:

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



Annotations corresponding to lesion measurements have not been entirely recovered (patient risk).

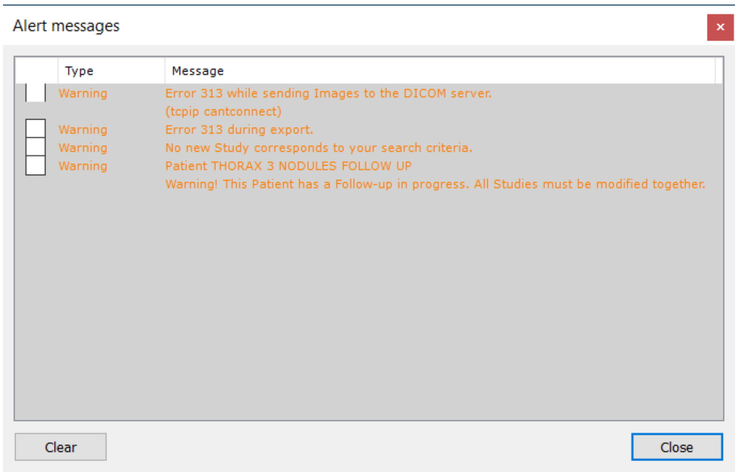
All displayed messages are listed in the toolbox, composed of three columns:

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

The second column is the message type; two different type 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.



	Type	Message
☐	Warning	Error 313 while sending Images to the DICOM server. (tcpip cantconnect)
☐	Warning	Error 313 during export.
☐	Warning	No new Study corresponds to your search criteria.
☐	Warning	Patient THORAX 3 NODULES FOLLOW UP Warning! This Patient has a Follow-up in progress. All Studies must be modified together.

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.

4 Viewing several Series/Studies simultaneously

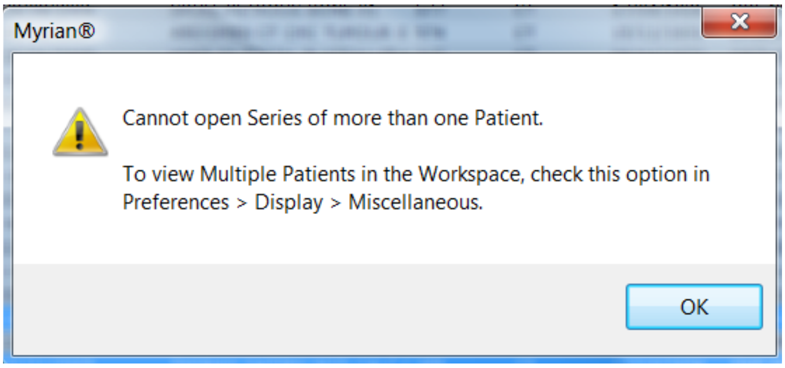
This function is designed to aid in the analysis of multiphase contrast-enhanced Studies or in Patient Follow-up

4.1 Study comparison

- Click on the 'Local Studies' button
- Select from the Local Study List several Studies/Series belonging to the same patient you wish to compare (using CTRL/Shift + click to select multiple items)

- Click on the 'Open Series' button

By default, the software does not allow you to open Series belonging to different Patients (*) with the same Workspace. If you attempt to open Series of different Patients simultaneously from the Study List, the following warning message will appear.



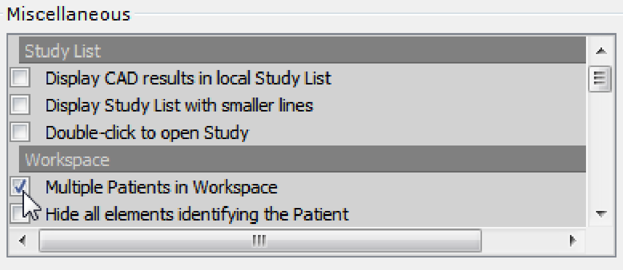
Cannot open Series of more than one Patient.

To view Multiple Patients in the Workspace, check this option in Preferences > Display > Miscellaneous.

(*) e.g. due to discrepancies in the Name, date of birth or PatientID
If you open a Study belonging to one Patient whilst the Study of another Patient is already open, the Software will automatically close the Study which is currently open

---

- If however you do really wish to open multiple Patient Studies simultaneously, you must activate the 'Multiple Patients in Workspace' option in the Miscellaneous list of the Preferences>Display tab

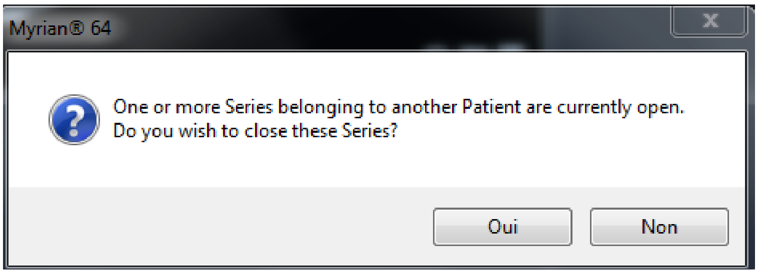


Miscellaneous

Study List
☐ Display CAD results in local Study List
☐ Display Study List with smaller lines
☐ Double-click to open Study

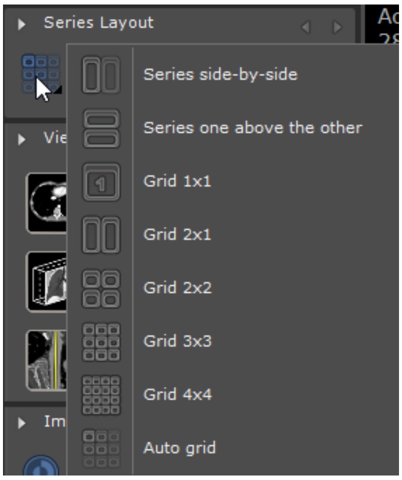
Workspace
☑ Multiple Patients in Workspace
☐ Hide all elements identifying the Patient

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.



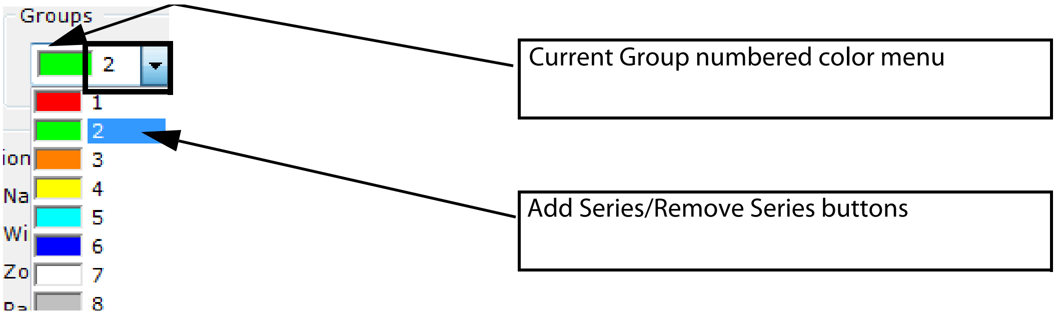
One or more Series belonging to another Patient are currently open.
Do you wish to close these Series?

The 'Layout' menu proposes a set of Page Layouts

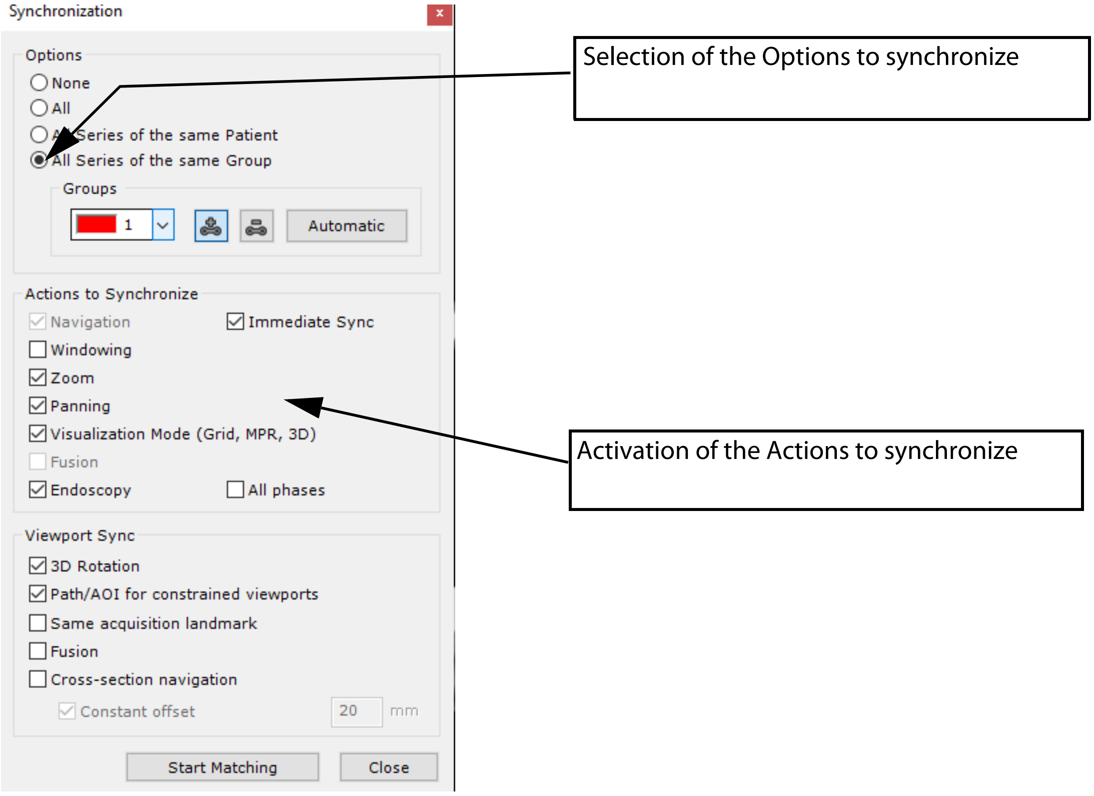


4.2 Setting up synchronization

- Click on in the Series Layout toolbox to open the Series Synchronization window:
- Select the Options to synchronize (for example, activate the 'All Series of the same Group' option) and check the Actions to synchronize (Navigation, Zoom, etc)
- Click on the **'Add Series' button**



By default, the current synchronization group is displayed. You can choose to define another group via the drop-down menu. A distinctive color and number are automatically allocated to each Group.



Synchronization

Options
○ None
○ All
○ All Series of the same Patient
● All Series of the same Group

Groups
🟥 1 | Automatic

Actions to Synchronize
☑ Navigation ☑ Immediate Sync
☐ Windowing
☑ Zoom
☑ Panning
☑ Visualization Mode (Grid, MPR, 3D)
☐ Fusion
☑ Endoscopy ☐ All phases

Viewport Sync
☑ 3D Rotation
☑ Path/AOI for constrained viewports
☐ Same acquisition landmark
☐ Fusion
☐ Cross-section navigation
☑ Constant offset 20 mm

Selection of the Options to synchronize

Activation of the Actions to synchronize

All Series that can potentially be linked together with the active Series are automatically highlighted

---

- Click successively **on an image** of a Series you wish to compare in Synchronized Mode with another Series

A frame corresponding to the color of the predefined group is displayed around the ⊞ icon on each selected image, indicating you that synchronization is now activated.

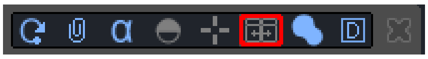
- If you wish, repeat this procedure to create multiple synchronized Groups.

You can also click on Automatic at right of the Groups zone in the Synchronization Window to automatically define all the Synchronized Groups of Series that can potentially be created

---

- To remove any or all Series from any group, first select the Group in the drop-down Menu, then click on the "Remove Series" button and click directly on the image of the Series you wish to desynchronize from the Current Group

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

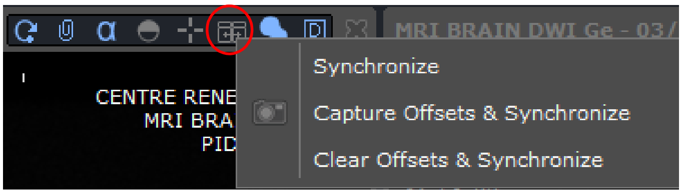


- To resynchronize Series, click on the Sync button again

4.3 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:

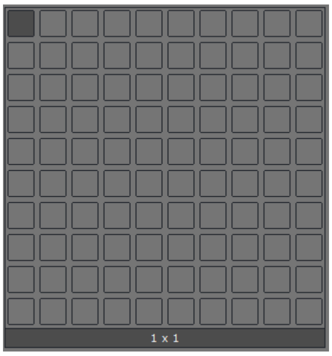


  - Synchronize: Reactivate synchronization between views (as initially configured, see Section 4.2)
  - Capture Offsets & Synchronize: Maintain all offsets between views and reactivate Synchronization (in the case you have navigated through one of the image slices and that they are no longer aligned but 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

You can synchronize images in any 2D frame (Axial, Sagittal, Coronal and Oblique)

4.4 Synchronizing the Anatomical Centre

- Navigate through the slices to place them at the same location using anatomical landmarks
- **Place the Anatomic Centre** (red dot) on a recognizable anatomic structure which is common to all the Series you wish to synchronize, such as the Carina Trachea. All images which are synchronized with the Anatomic centre are refreshed allowing you to **easily locate** an anatomical structure of interest in each plane of view **simultaneously**.
- Click on then to force Native Mode



If you cannot see the Anatomic Centre, select the Navigation tool and double-click anywhere in the image

Multiple Series of the Same Patient can be synchronized in Native Mode or even between MPR and Native Mode as long as they have the same Frame Of Reference UID. The Anatomic Centre is then visible in all synchronized series and refreshes during navigation

If you activate the "Centre on Anatomic Centre" option and then zoom-in on a specific point in an image, the image remains centred on the Anatomic Centre; this option can be found in the Display Options at top-right each Series window

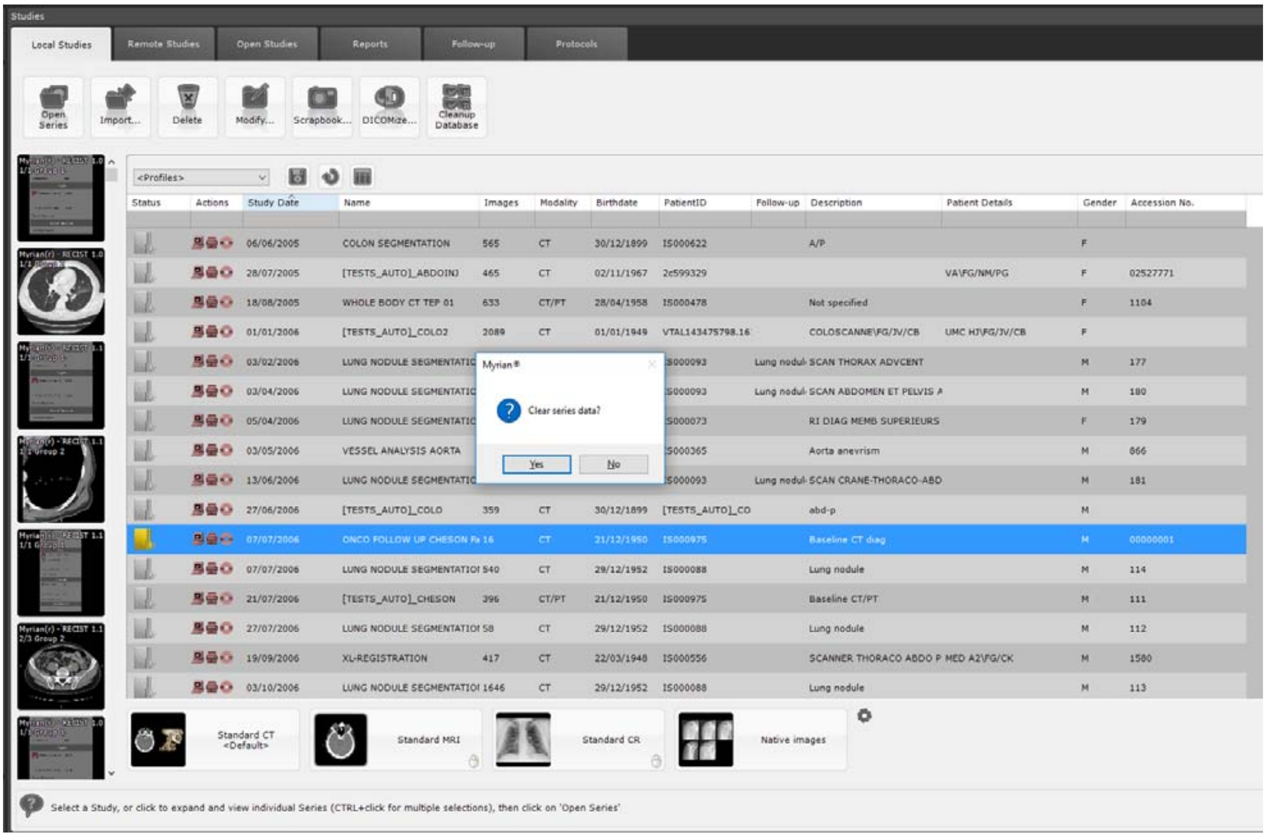
5 Data Cleanup

5.1 Clear Series Data

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 following dialog box pops up:



Clear series data?

Status	Actions	Study Date	Name	Images	Modality	Birthdate	PatientID	Follow-up	Description	Patient Details	Gender	Accession No.
		06/06/2005	COLON SEGMENTATION	565	CT	30/12/1899	IS000622		A/P		F	
		28/07/2005	[TESTS_AUTO]_ABDOINJ	465	CT	02/11/1967	2e599329			VA\FG/NM/PG	F	02527771
		18/08/2005	WHOLE BODY CT TEP 01	633	CT/PT	28/04/1958	IS000478		Not specified		F	1104
		01/01/2006	[TESTS_AUTO]_COLO2	2089	CT	01/01/1949	VTAL143475798.16		COLOSCANNE\FG/JV/CB	UMC HJ\FG/JV/CB	F	
		03/02/2006	LUNG NODULE SEGMENTATIC				S000093	Lung nodul	SCAN THORAX ADVCENT		M	177
		03/04/2006	LUNG NODULE SEGMENTATIC				S000093	Lung nodul	SCAN ABDOMEN ET PELVIS A		M	180
		05/04/2006	LUNG NODULE SEGMENTATIC				S000073		RI DIAG MEMB SUPERIEURS		F	179
		03/05/2006	VESSEL ANALYSIS AORTA				S000365		Aorta anevrism		M	866
		13/06/2006	LUNG NODULE SEGMENTATIC				S000093	Lung nodul	SCAN CRANE-THORACO-ABD		M	181
		27/06/2006	[TESTS_AUTO]_COLO	359	CT	30/12/1899	[TESTS_AUTO]_CO		abd-p		M	
		07/07/2006	ONCO FOLLOW UP CHESON Fa	16	CT	21/12/1950	IS000975		Baseline CT diag		M	00000001
		07/07/2006	LUNG NODULE SEGMENTATIOI	540	CT	29/12/1952	IS000088		Lung nodule		M	114
		21/07/2006	[TESTS_AUTO]_CHESON	396	CT/PT	21/12/1950	IS000975		Baseline CT/PT		M	111
		27/07/2006	LUNG NODULE SEGMENTATIOI	58	CT	29/12/1952	IS000088		Lung nodule		M	112
		19/09/2006	XL-REGISTRATION	417	CT	22/03/1948	IS000556		SCANNER THORACO ABDO P	MED A2\FG/CK	M	1580
		03/10/2006	LUNG NODULE SEGMENTATIOI	1646	CT	29/12/1952	IS000088		Lung nodule		M	113

Select a Study, or click to expand and view individual Series (CTRL+click for multiple selections), then click on 'Open Series'

- Click 'Yes' to confirm

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

5.2 Clear Patient/Series/Study Data

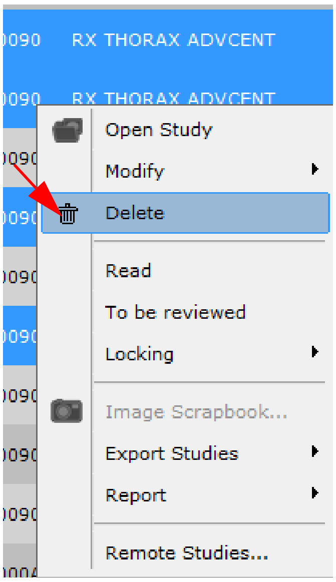
This alternative tool can also be performed from your Local Study list but opens up a dialog box displaying the following elaborate cleanup data options:

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

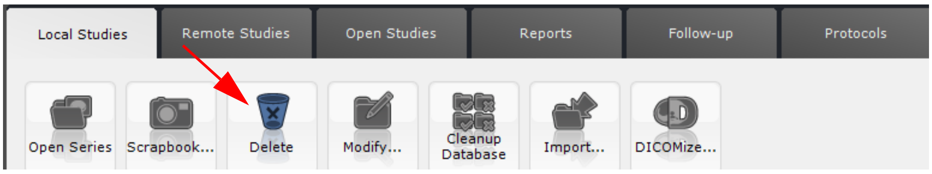
Referring to (according to selection):

  - 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.
- Delete only ROI, Annotations and Visual Mask' (see Section 5.1) - shared option by all types of selection.

Right-clicking on the selected series/studies then selecting 🗑 from the popup 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

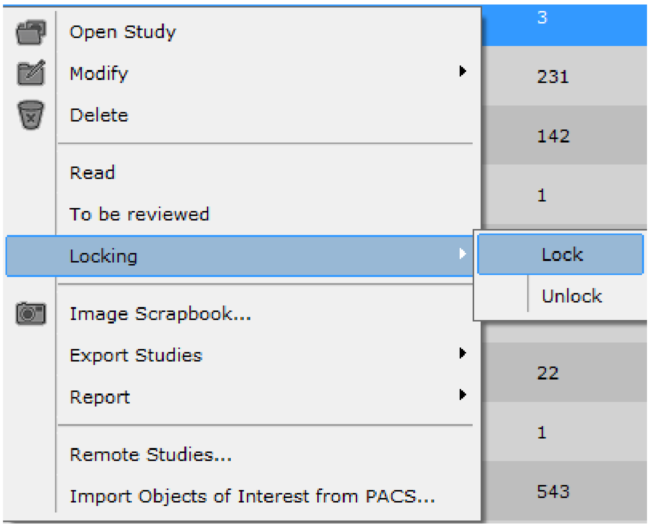


The displayed options in the 'Delete' dialog box depend on whether you have selected one or several studies/series from your Local Study list

---

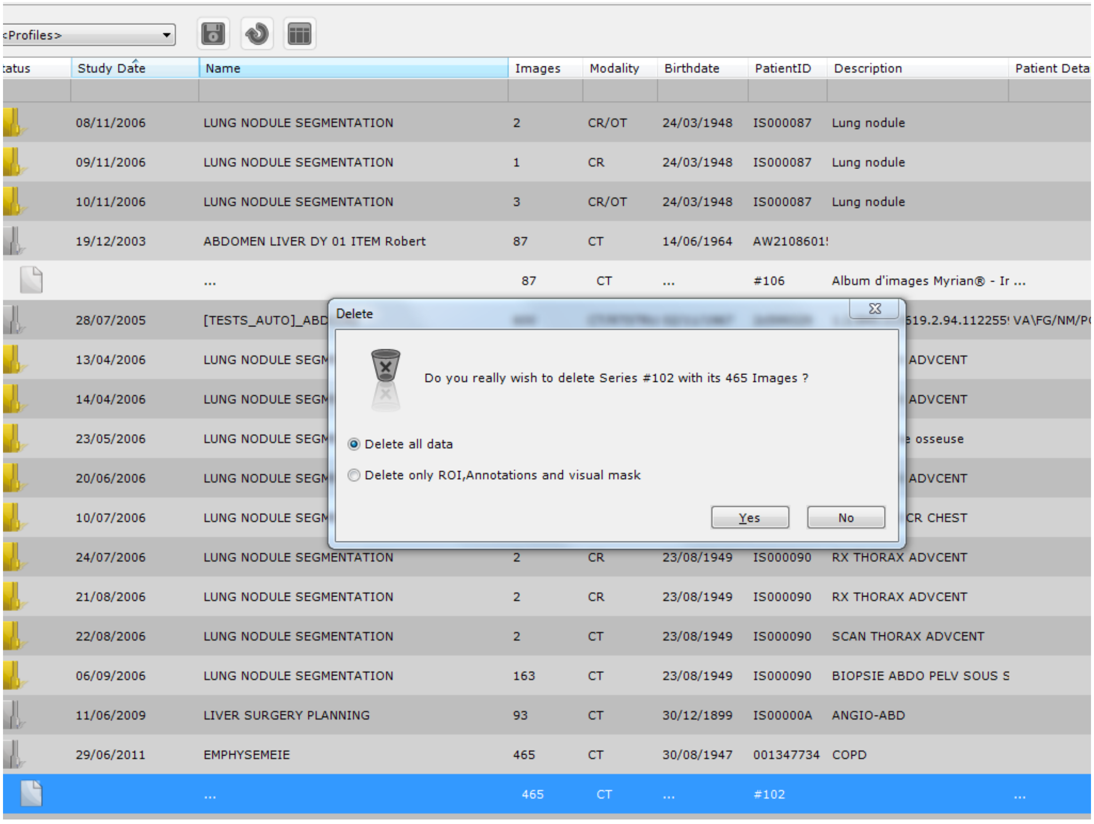
To perform a 'Clear Series data' on all the studies belonging to a same patient, select them in the study list (holding down the CTRL key) and click on the 'Delete' button from your keyboard.

Series cannot be deleted if a Study status has been set to either 'Locked' or 'To be reviewed'. To **prevent** a Study from being unintentionally deleted, **select "Lock"** from the 'Locking' Sub-menu of the Study List Context Menu



Method of use:

- Select the desired series/studies from the Study list:



atus	Study Date	Name	Images	Modality	Birthdate	PatientID	Description	Patient Deta
	08/11/2006	LUNG NODULE SEGMENTATION	2	CR/OT	24/03/1948	IS000087	Lung nodule	
	09/11/2006	LUNG NODULE SEGMENTATION	1	CR	24/03/1948	IS000087	Lung nodule	
	10/11/2006	LUNG NODULE SEGMENTATION	3	CR/OT	24/03/1948	IS000087	Lung nodule	
	19/12/2003	ABDOMEN LIVER DY 01 ITEM Robert	87	CT	14/06/1964	AW2108601!		
		...	87	CT	...	#106	Album d'images Myrian® - Ir ...	
	28/07/2005	[TESTS_AUTO]_ABD					619.2.94.112255! VA\FG/NM/P	
	13/04/2006	LUNG NODULE SEGM					ADVCENT	
	14/04/2006	LUNG NODULE SEGM					ADVCENT	
	23/05/2006	LUNG NODULE SEGM					osseuse	
	20/06/2006	LUNG NODULE SEGM					ADVCENT	
	10/07/2006	LUNG NODULE SEGM					CR CHEST	
	24/07/2006	LUNG NODULE SEGMENTATION	2	CR	23/08/1949	IS000090	RX THORAX ADVCENT	
	21/08/2006	LUNG NODULE SEGMENTATION	2	CR	23/08/1949	IS000090	RX THORAX ADVCENT	
	22/08/2006	LUNG NODULE SEGMENTATION	2	CT	23/08/1949	IS000090	SCAN THORAX ADVCENT	
	06/09/2006	LUNG NODULE SEGMENTATION	163	CT	23/08/1949	IS000090	BIOPSIE ABDO PELV SOUS S	
	11/06/2009	LIVER SURGERY PLANNING	93	CT	30/12/1899	IS00000A	ANGIO-ABD	
	29/06/2011	EMPHYSEMEIE	465	CT	30/08/1947	001347734	COPD	
		...	465	CT	...	#102		...

Delete

Do you really wish to delete Series #102 with its 465 Images ?

● Delete all data

○ Delete only ROI,Annotations and visual mask

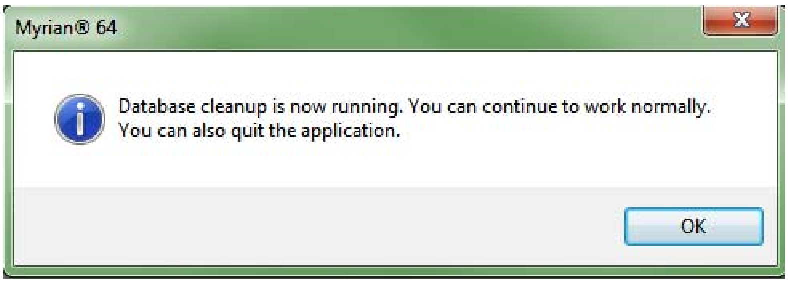
- Check the radio button related to the type of data you wish to remove
- Confirm clicking 'Yes'

5.3 Automatic cleanup database

The database cleaning process is administered within ServiceManager and performed according to preconfigured cleanup settings. By default, automatic database clean-up is configured to delete studies older than 30 days (including studies which are 'Not Read') taking into account disk drive occupation rate.

However, you can still manually launch an automatic cleanup database clicking on the 'Cleanup Database' tool particularly if the disk gauge 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:

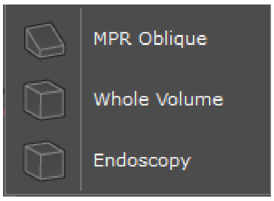

Myrian® 64

Database cleanup is now running. You can continue to work normally.
You can also quit the application.

6 MPR and CPR Reconstruction

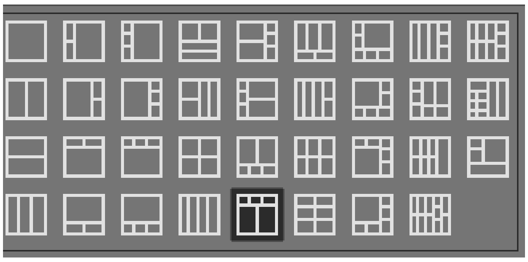
6.1 Multi Planar Reformatting (MPR) Mode

- Click on in the 'Visualization' toolbar to open the following menu



- Select your choice of Volume reconstruction (MPR+Oblique/Whole Volume/Endoscopy)
- Click on Page Layout in the 'Display Options' (top-right in the Titlebar)

- and select your preferred layout setting from the following menu



Immediately to the right of the Page Layout button in the Display Options is the 'Reference Lines' button

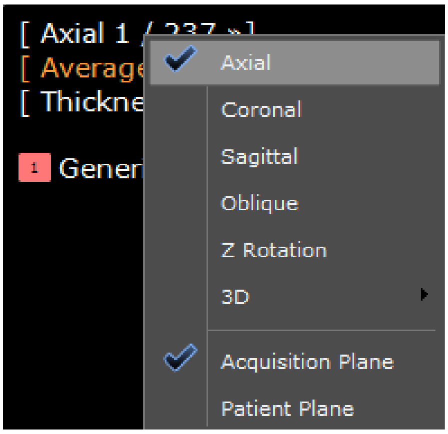
- Use this button to display the desired set of Reference Lines:
  - None
  - Only Oblique
  - Only Orthogonal
  - All

You can navigate to any point in the image volume by any of the following:

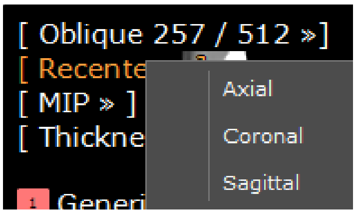
- Dragging the Anatomic Centre to this point
- Double-clicking on the point
- Manipulating each reference line so that it intersects the point

The Menu at **top-left** of every Viewport enables:

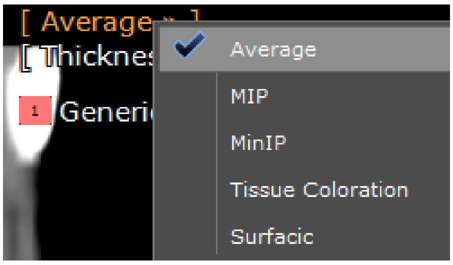
- Choice of Plane of View



- ‘Recenter’ to refresh to orientation (Oblique or 3D Views)



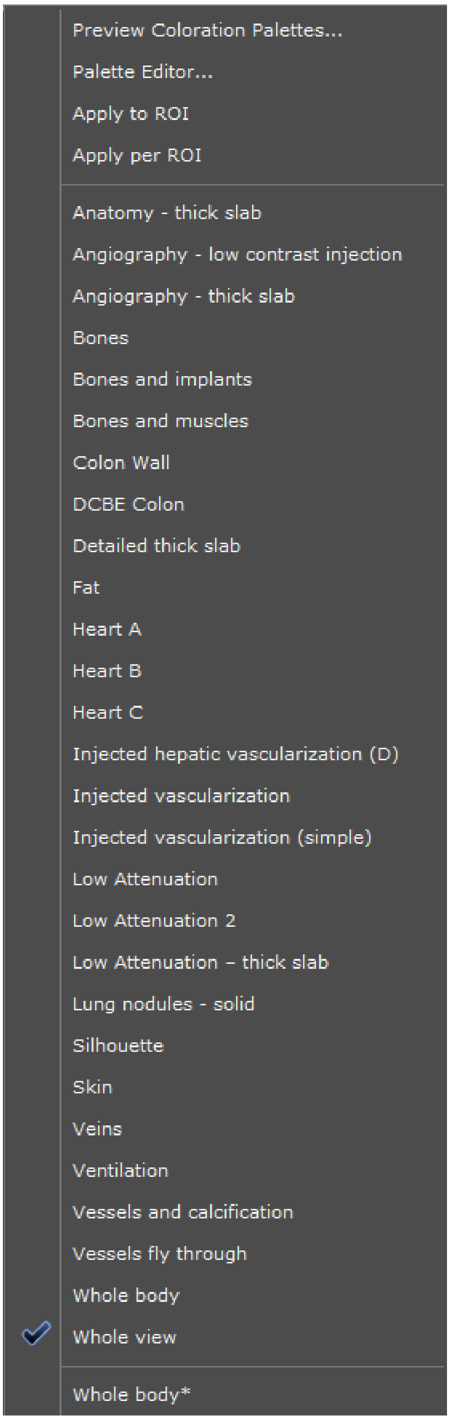
- Choice of Rendering Modes



- Increase/Decrease Slice Thickness via ‘+’ or ‘-‘ buttons or by entering a numeric value directly

Increase thickness [CTRL+Click] for max thickness

- Tissue Coloration/Surfacic Rendering’ presets in 3D Modes



The Windowing tool ◐ can be used on 3D Volume Rendering views to highlight structures of interest

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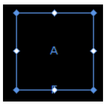
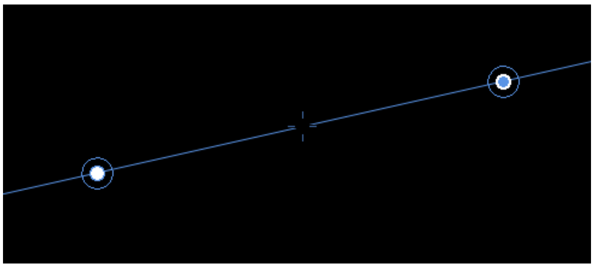
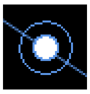
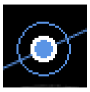
6.2 Oblique View

You can manipulate the Oblique View using the handles of the Orientation Cube  ->  or the 'Oblique' Reference Line

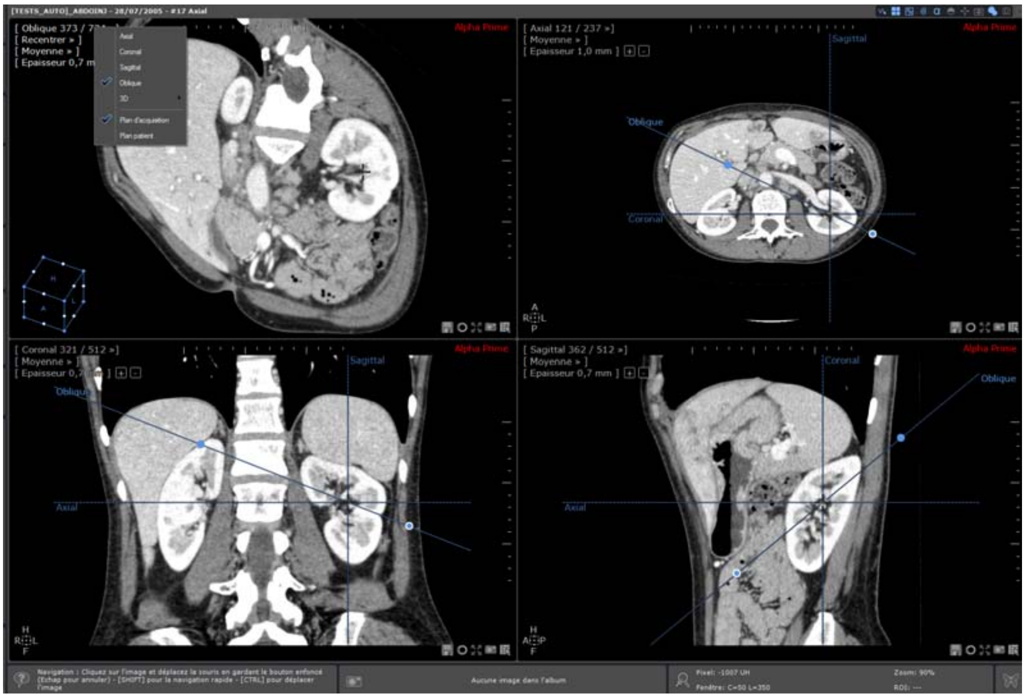


- Use the ‘White’ handle  to manipulate the ‘Simple-oblique’ view (other 2D views refresh orthogonally to the view as soon as it is manipulated)
- Use the ‘Blue’ handle  to manipulate the ‘Double-oblique’ view (other views maintain their current orientation)

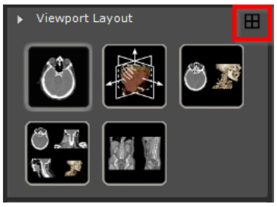
6.3 Coordinate system selection for improved volume visualization

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.

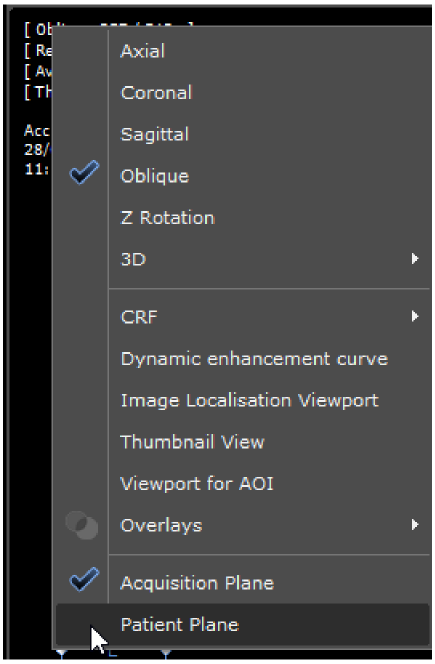


In order to reset the initial layout (windowing, MPR Basis, frame size…) you can use this button :



In the Viewport orientation menu, the following coordinate systems are available:

- **Acquisition Plane** or **Patient Plane**



- 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 shape) 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.

6.4 Create a Path

Example of use: to locate a bronchial tumor in the airways or a colic tumor in relation to the anal margin or to measure the distance from a stenosis to a vascular bifurcation

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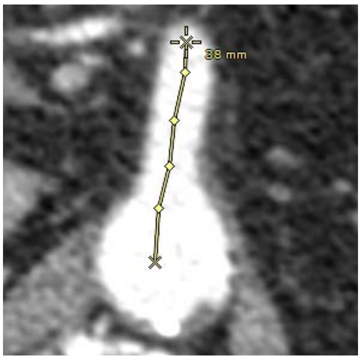
Quantification of the extent of stenosis is directly dependent upon the results of the calculation of the Centerline. Centerline alignment errors may cause stenosis calculation errors.

- Click on the ‘Create Path’ tool to open the Path Creation floating menu

- If it is not already done by default, click on to activate the ‘Path Creation’ drawing tool and trace a Path in any View by placing articulation points



To resume the creation of Path that has been interrupted:

- Click ✚, then
- Click on the Point you wish to continue on from
- Place more points as desired

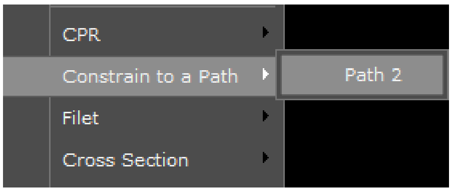
If a new Path Point is added while the Path Origin is selected, the newly created Path Point becomes the new Path Origin

---

Click on in the Display Options Toolbar to toggle display of the Path on/off

---

- Use to delete a Point or ✖ to delete the entire Path
- To lock the navigation of the "camera" to a Path, select 'Constrain to a Path' and the desired Path from the sub-menu



This will enable you to navigate in any plane of view along a Path of your choice

Some ROI creation engines automatically create Paths. These Paths are associated to the ROI created by their corresponding segmentation engine.

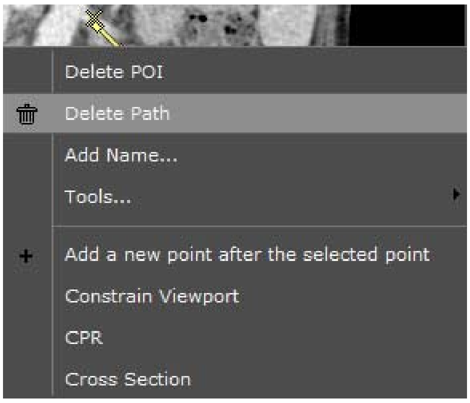
If you delete a ROI which is associated to a Path, the corresponding Path is also deleted

---

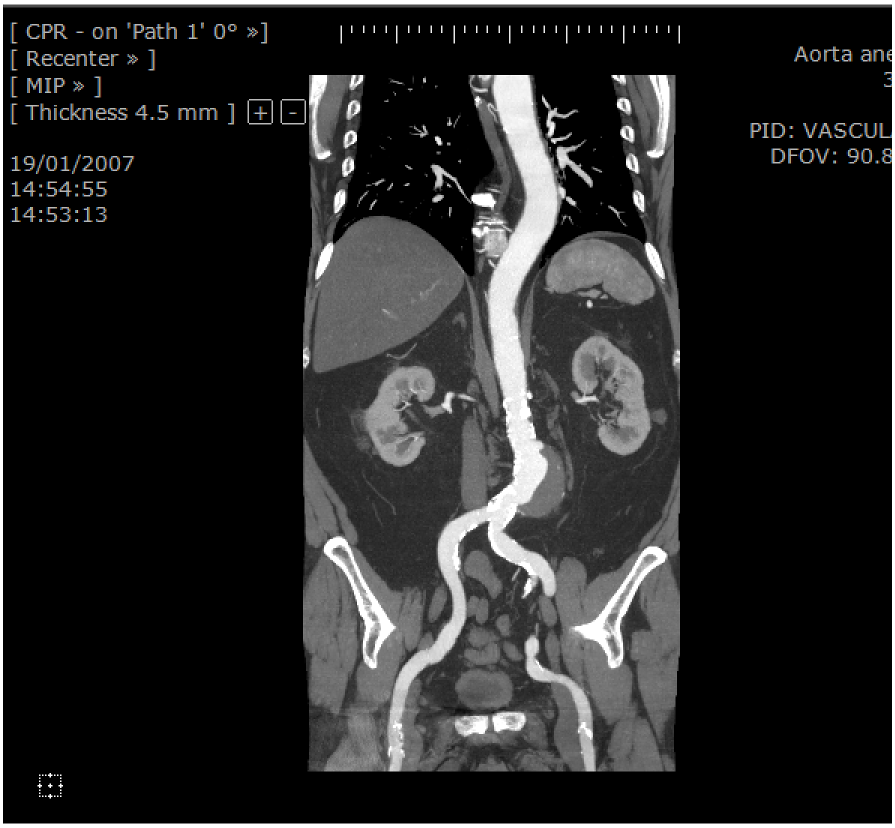
6.5 Curved Planar Reformatting (CPR) Mode

The CPR Mode function enables you to view entire vessels in one single 2D Plane of View. You need to create a Path before using the CPR function.

- Right-click on a Point to view the following menu

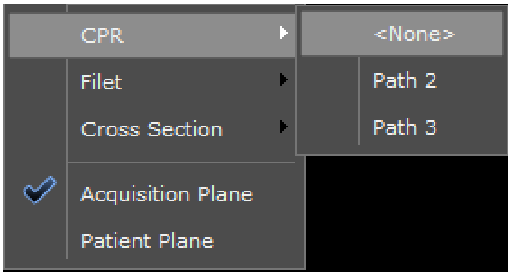


- Select ‘CPR’, then your desired Path in the resulting menu to launch curvilinear reconstruction of the anatomy surrounding your Path



The **orientation** of the CPR Viewport **auto adjusts to best-fit** the size and shape of the active Viewport

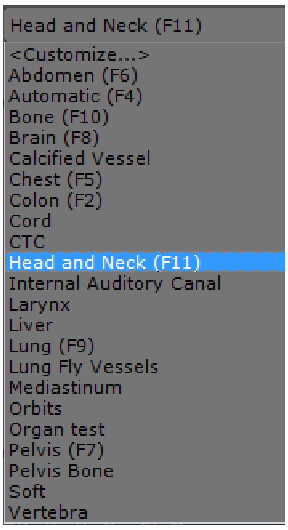
Select ‘None’ to return to the original orientation of the Viewport



7 MIP and MinIP Rendering

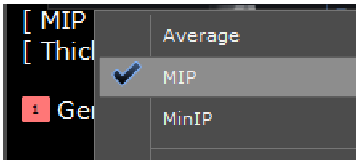
The MIP rendering tool can be used on PET studies with FDG [18F] fluoro-2-deoxyglucose and may be suitable for use with other oncological probes. Some adjustments may be required to optimize performance with other radiopharmaceutical products.

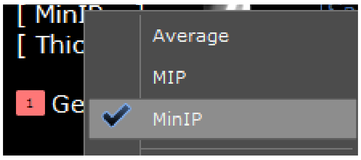
- Ensure you are in MPR Mode (MIP and MinIP cannot be accessed in Native Mode)
- Select the Windowing filter that is best adapted to your current diagnostic requirements



- Click on “Average” in the overlaid menu (top-left of the Image frame) to access the Intensity Rendering Menu

The three available Rendering modes are Average, MIP or MinIP:

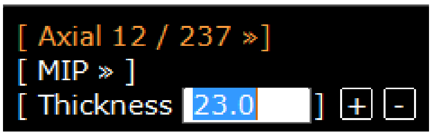




Axial, Coronal, Sagittal and Oblique images as well as Volume of Interest images can be rendered using Average, MIP, or MinIP modes; in Whole Volume images, only Average and MIP modes are available

---

- Increase the slice thickness to view the effect of MIP or MinIP modes, e.g. click on "Thickness" and enter a numeric value directly:



[Axial 12 / 237 »]
[MIP »]
[Thickness 23.0] + -

- or use ⊞ ⊟ to increment/decrement one unit at a time

' MIP' (Maximum Intensity Projection) mode: useful for Visualizing structures of high intensity such as bones or injected vessels

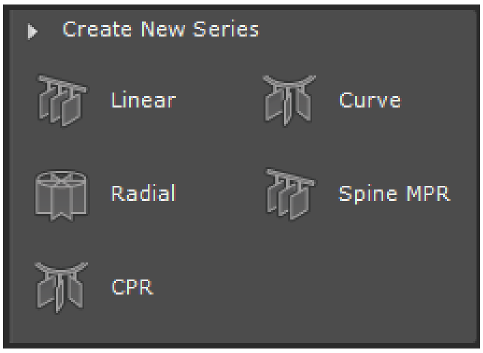
---

’MinIP' (Minimum Intensity Projection) mode: useful for Visualizing structures of low intensity such as airways in lungs or bile ducts.

8 SeriesCreator: Reformat and Create New Series

Reformatting planes only apply if the **MPR mode** is activated (i.e. the reformatting plane tools cannot be used in a Native viewport) and the selected series shows a coherent volume. By default, this functionality is included in the Standard and Advanced CT protocols.

- From the 'Create New Series' toolbox available in the Toolchest, select the appropriate reformating plane tool (rake) among those displayed according to the loaded series:

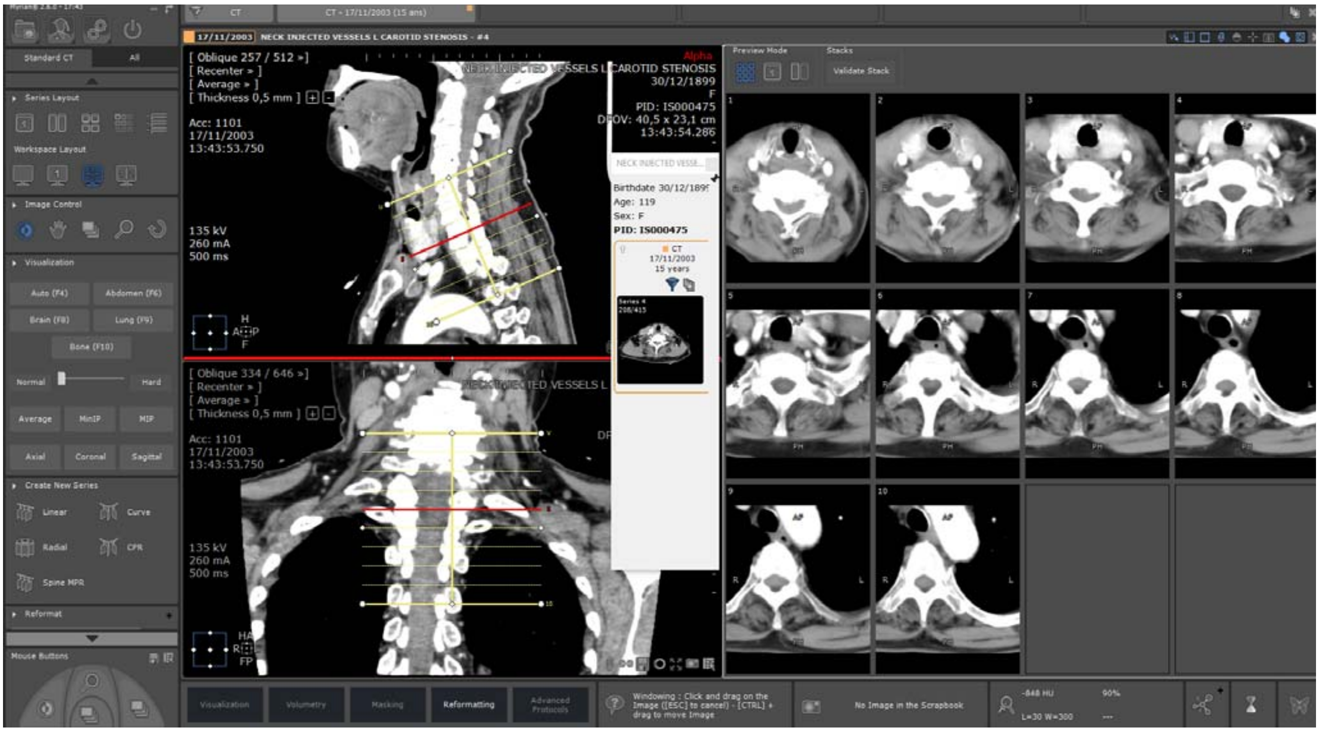


- Place the Reformatting Rake as desired on the image

The Reformatting Rake appears in 2 Planes of View. The position, orientation, spacing and size of Rake can be modified by hand.

Simultaneously, a preview window pops up in the right-part of the workspace displaying the generated images. The preview window reflects in real-time any changes performed on the rake.

By default, the generated images are displayed in the Preview area as thumbnails. However you can opt for full size or column preview mode clicking on the corresponding icon above the Preview Area.

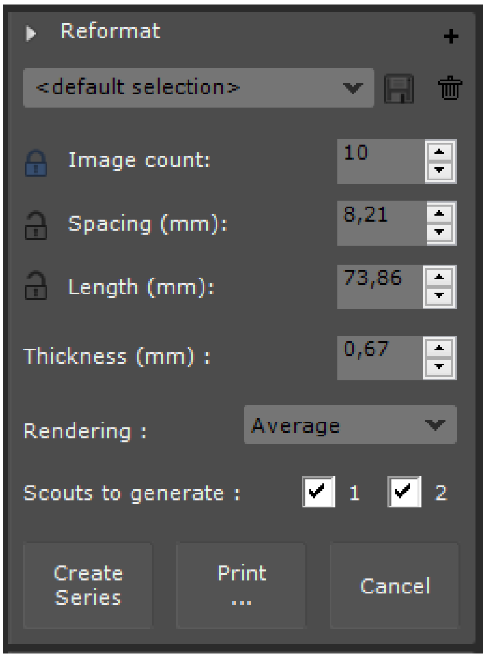


The ‘Full Size’ Preview allows you to see a close-up of the results of your Reformatting. All standard Image Control Tools (Panning, Windowing, Zoom, Navigation and Magnifying Glass) can be used on the preview images although zooming actually changes the size of the rake.

In Preview Mode, while mouse is over the image (Thumbnails, Full size or Column), it highlights in red the corresponding slice on the rake.

From the ‘Reformat’ toolbox, a number of parameters can be modified and tuned including additional ones:

- Total number of Images created,
- Spacing (between Images),
- Length,
- Thickness,
- Rendering (Average, MIP/MinIP)
- Number of Scout images created.



<default selection>

Image count: 10

Spacing (mm): 8,21

Length (mm): 73,86

Thickness (mm) : 0,67

Rendering : Average

Scouts to generate : ☑ 1 ☑ 2

User-defined rake settings can be saved for subsequent Series Creation by renaming and saving the newly-created rake profile (by default, <default selection>).

- Click on Create Series to create the new Series and visualize it automatically on the screen.

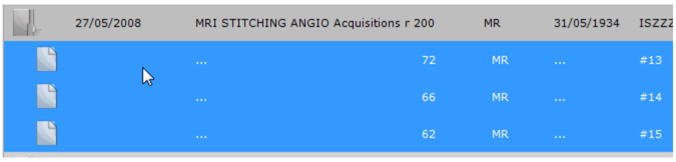
The new Series is automatically saved as a new DICOM series in the Local Study List and displayed on screen beside the active Series

- Click on Print ... to send the images to the PrintComposer. In that case, no new series is created.

9 Stitching (optional add-on): Combine multiple Series to produce a single image or volume

Method of use:

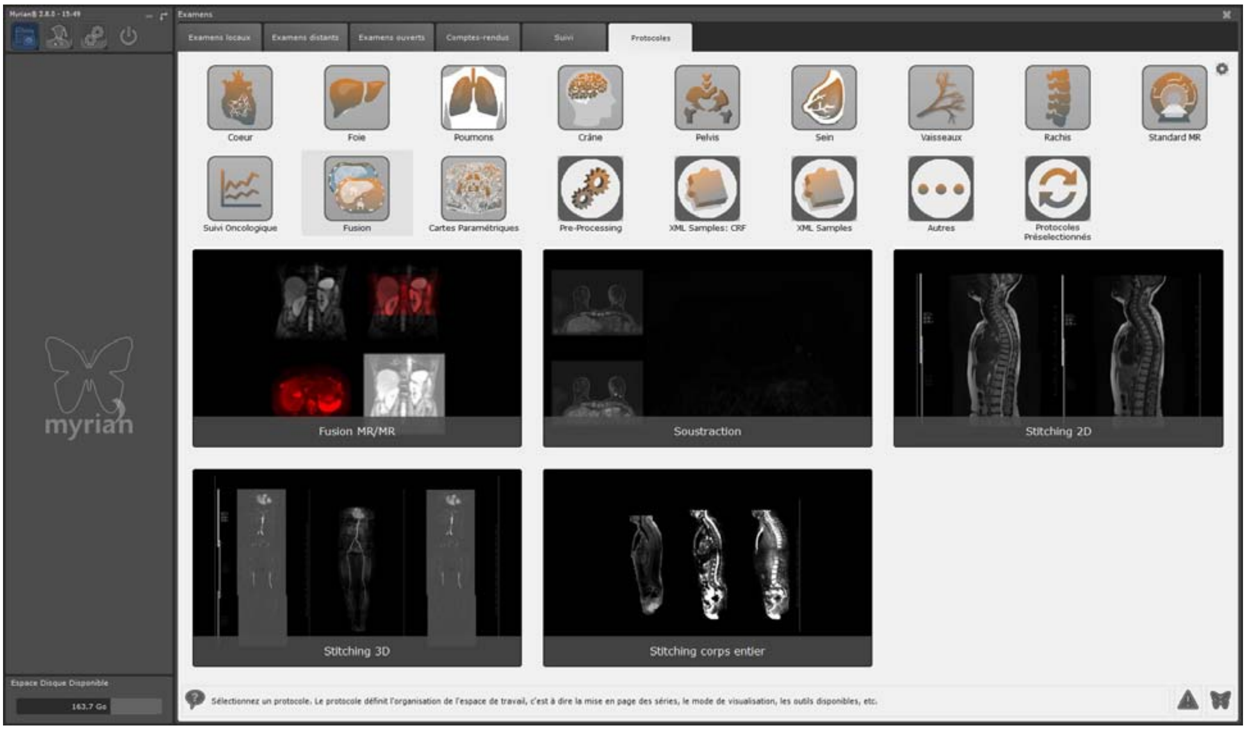
- Select the Series you wish to stitch together in the Study List



27/05/2008	MRI STITCHING ANGIO Acquisitions r 200		MR	31/05/1934	ISZZZ
	...	72	MR	...	#13
	...	66	MR	...	#14
	...	62	MR	...	#15

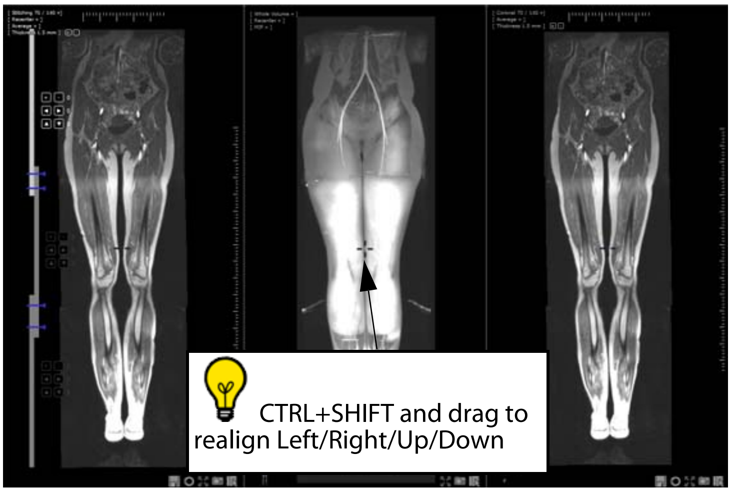
CTRL/Shift +click to make multiple choice in the list

- Click on the 'Open Series' button



Sélectionnez un protocole. Le protocole définit l'organisation de l'espace de travail, c'est à dire la mise en page des séries, le mode de visualisation, les outils disponibles, etc.

- Double-click on the Stitching Protocol of your choice
- Hold the 'CTRL+SHIFT' keys down and drag the mouse to realign the Series Left/Right or Up/Down (the mouse cursor then becomes a double-arrow cross) ✛



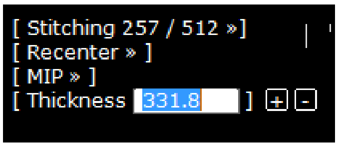
CTRL+SHIFT and drag to realign Left/Right/Up/Down

Click on ◄ ► ▲ ▼ at left of the Series to Move the Series Left/Right/Up/Down one unit at a time

---

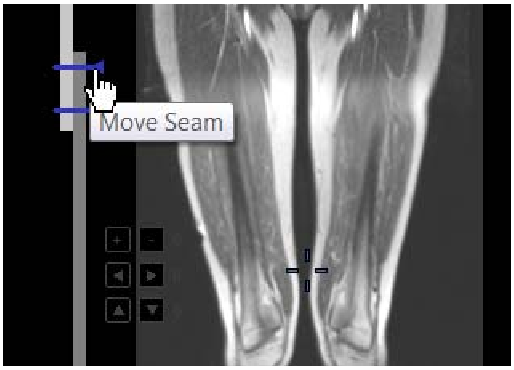
- Click on ⊞ ⊟ at left of each Series to navigate to and realign the Series Back/Forward one slice at a time

Activate MIP Mode and increase the slice thickness using the '+' and '-' in the Thickness Menu at top-left of the Stitching Viewport (or click on 'Thickness' and enter a value directly in the thickness value field) to improve visibility



[Stitching 257 / 512 »]
[Recenter »]
[MIP »]
[Thickness 331.8] ⊞ ⊟

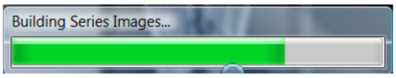
- Adjust the Overlap by dragging the blue-colored Stitching Seam at left Seam up or down



- Switch Viewport Layout in the Display Mode Toolbar to open a Volume of Interest Viewport to make fine adjustments to Series Alignment

- When 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 progress bar will appear to chart the progress of the Construction of the New Series



Building Series Images...

When the process is complete, the New Series will open alongside any other open Viewport in Native Mode (default setting) and will be automatically added to the Study.

10 Fusion

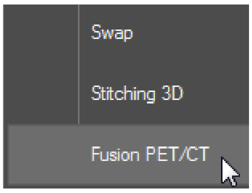
The “Fusion” option enables 2 Series to be superimposed and blended.

You can merge the following pairs of modalities:

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

To activate the Fusion tool:

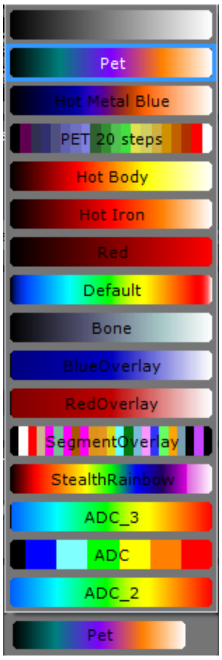
- Click on the title bar of one of the Series to be merged
- Drag and drop this Series onto the other Series
- Select "Fusion" from the drop-down menu



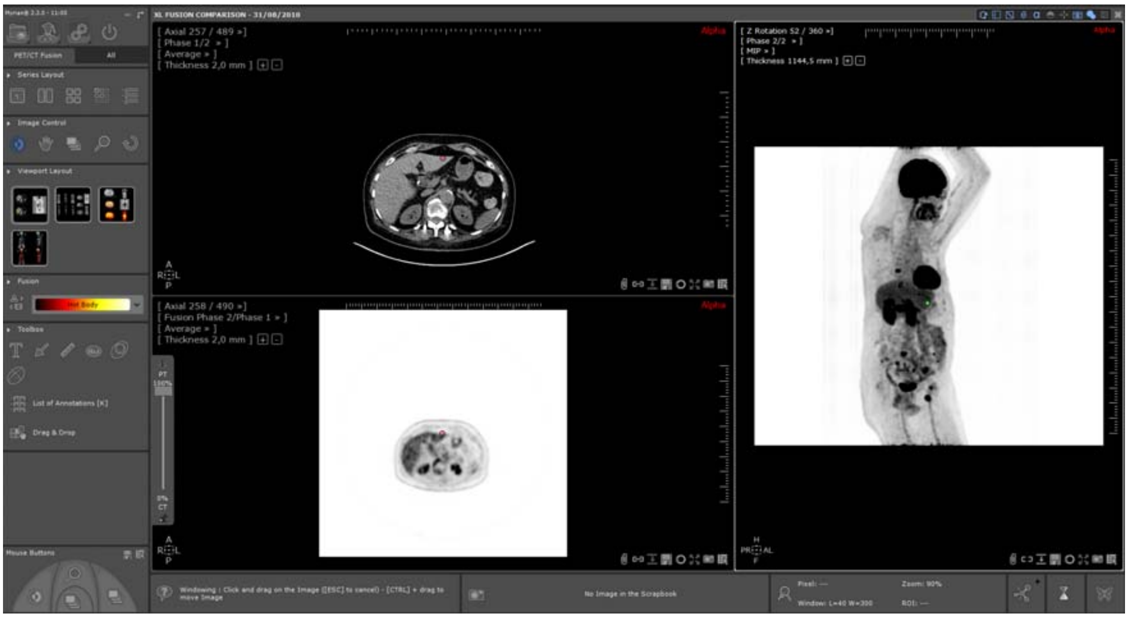
At the opening of the series in the PET/CT protocol, the Fusion View contains 2 Viewports:

- The Anatomical Series viewport (with each series corresponding to a phase) on the left part of the workspace which contains a grayscale Windowing 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 an auto-hide hover-over Color Lookup Table (CLUT) Slider at the bottom of the Viewport

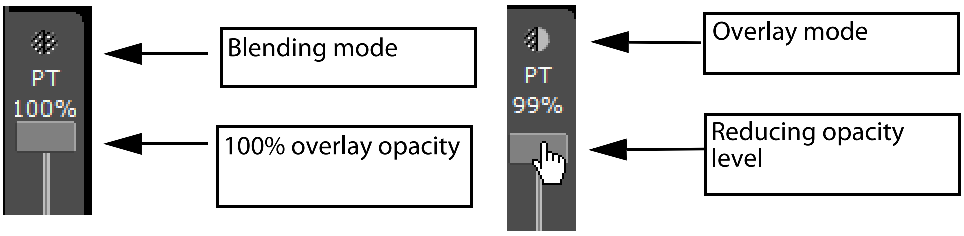
The Fusion Toolbar contains a Manual Alignment tool for the Series as well as various Color Look Up Table (CLUT) presets in a drop-down list.



You can Fuse Series in any plane of orientation

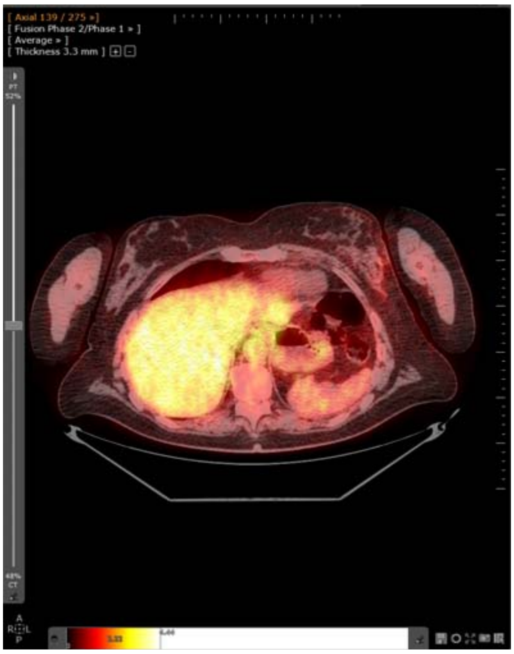


At opening, the overlay opacity is by default set at 100% in the fusion viewport (only the functional image is displayed, the CT image cannot be visualized at all). Additionally, the overlay series is initially displayed in inverted black & white (i.e. the CLUT is deactivated) and the fusion mode is automatically set to Blending mode.



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

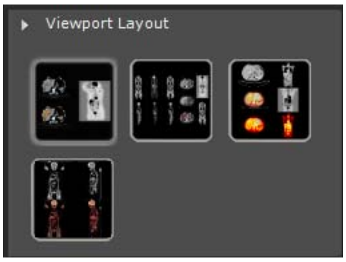
When you move down the transparency slider (under 100%), the blending mode automatically switches to Overlay mode, the CLUT is activated (the Black & White reverse mode is deactivated) and the Anatomical series appears.



CLUT presets can be customized freely using the CLUT slider (in Gray levels by default) which appears when you mouse-over the bottom of the Fusion Viewport.

- Click on the pin button to dock the CLUT slider.

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



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 computation performed according to the QIBA guidelines which required parameters are:

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

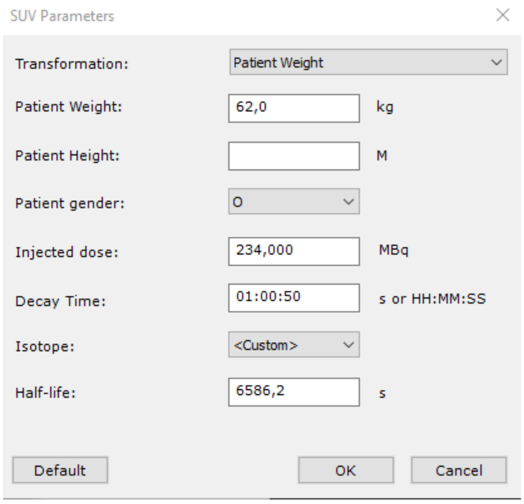
When selecting a Study to load in order to perform a SUV Calculation, you must be careful to select attenuation compensated and decay corrected PET Series with a valid acquisition start time according to the following prerequisites.
- Attenuation compensation: DICOM Corrected Image tag (0x0028, 0x0051) 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

The SUV Parameters window appears automatically at the Series load-up stage if any information is missing.

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

According to your calculation preferences, you can also choose from the corresponding drop-down menu, your preferred transformation method among the three available.

- Fill-in the missing information



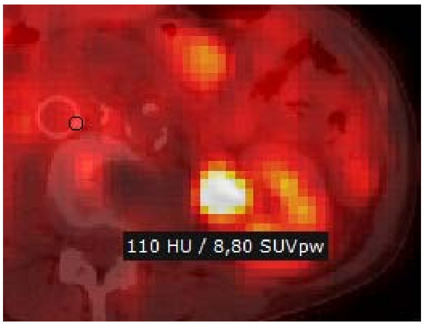
Transformation: Patient Weight
Patient Weight: 62,0 kg
Patient Height: M
Patient gender: O
Injected dose: 234,000 MBq
Decay Time: 01:00:50 s or HH:MM:SS
Isotope: <Custom>
Half-life: 6586,2 s

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

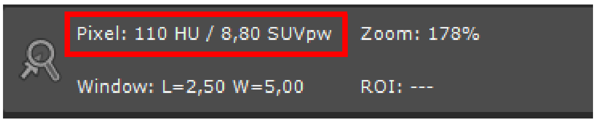
According to the selected transformation method, if all prerequisites are not fulfilled, the SUV computation cannot be performed.

SUV information can be displayed as follows:

- **Press <ALT>** while hovering the mouse pointer on the PET image to display the SUV value



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



Pixel: 110 HU / 8,80 SUVpw

Zoom: 178%

Window: L=2,50 W=5,00

ROI: ---

11 ‘QuickPatient’: loading other series and studies of the current patient

11.1 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 the appropriate default protocol.

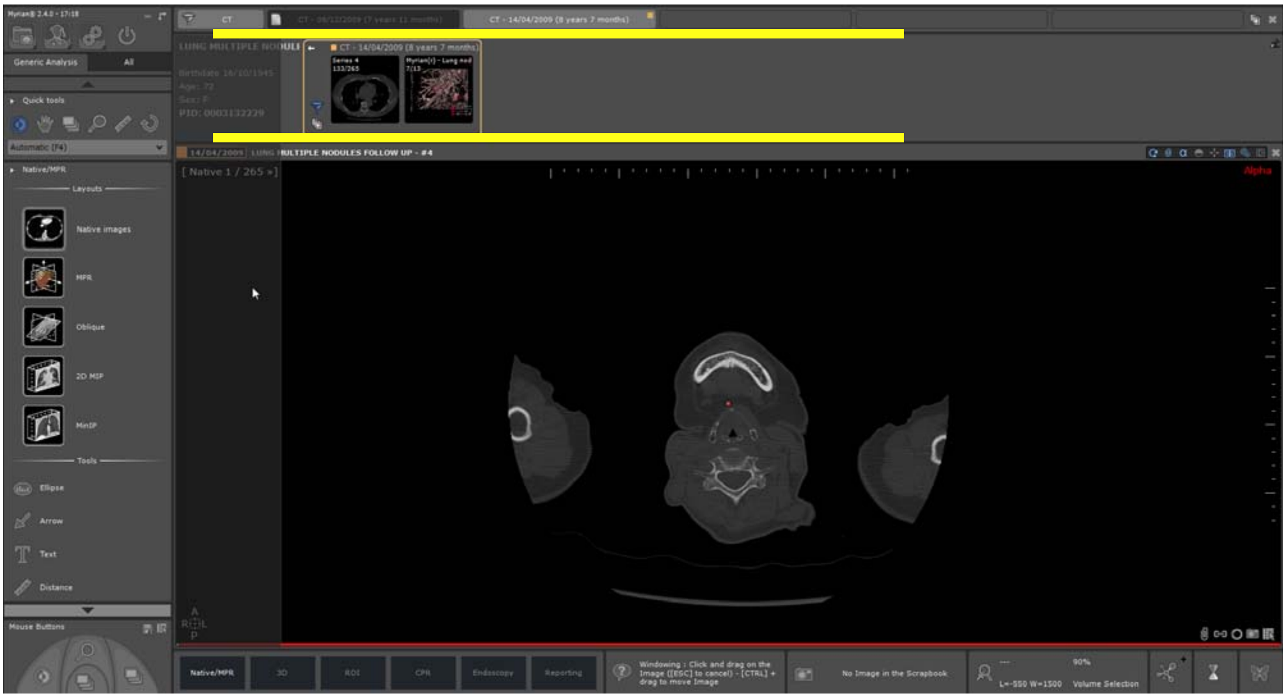
- With your series already open in the Workspace, click on in the Series Layout toolbar (or press the **’S’ keyboard** shortcut) to open the **QuickPatient window** and access the complete list of Series/Studies recognized as belonging to the current Patient (same Name, DOB, PID, gender, etc.) available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

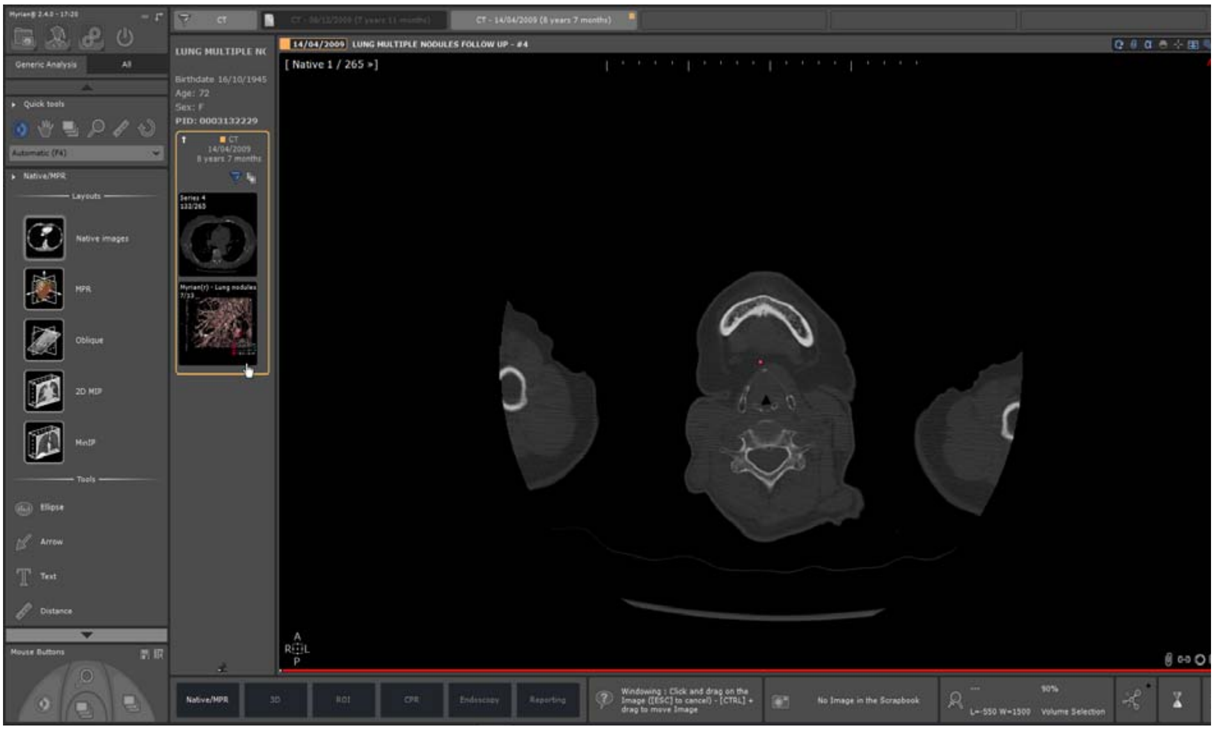
By default, the QuickPatient **opens docked horizontally at the top** of the workspace although it can be set **at the bottom or vertically on the left or on the right side of the workspace**, as preferred.

- 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.

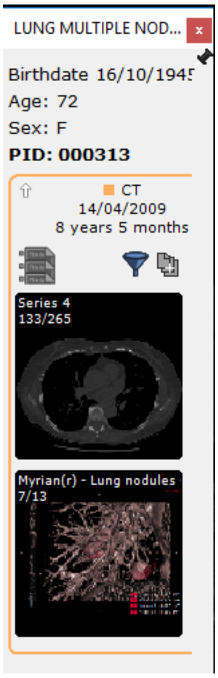
A phantom of the new position is visible depending on the cursor position.



- Drop it



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:



LUNG MULTIPLE NOD...

Birthdate 16/10/194!
Age: 72
Sex: F
PID: 000313

CT
14/04/2009
8 years 5 months

Series 4
133/265

Myrian(r) - Lung nodules
7/13

- 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

11.2 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. The Timeline displays one tab for every existing folder.

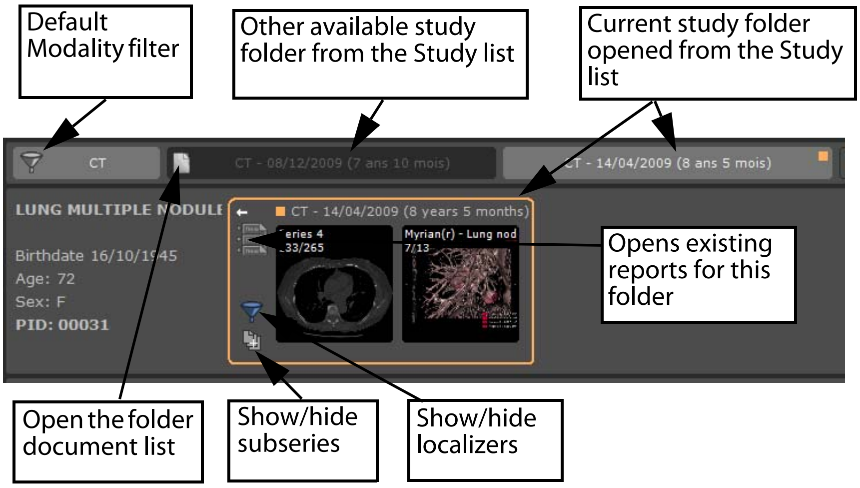
From the QuickPatient window, you have access to:

- 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 to which the open series in the workspace belongs to, is **highlighted in orange** in the Timeline and its content displayed by default.

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 orange**.



Birthdate 16/10/1945
Age: 72
Sex: F
PID: 00031

or

Birthdate 16/10/194
Age: 72
Sex: F
PID: 000313

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)

Description of the study in the timeline displayed in the tool type

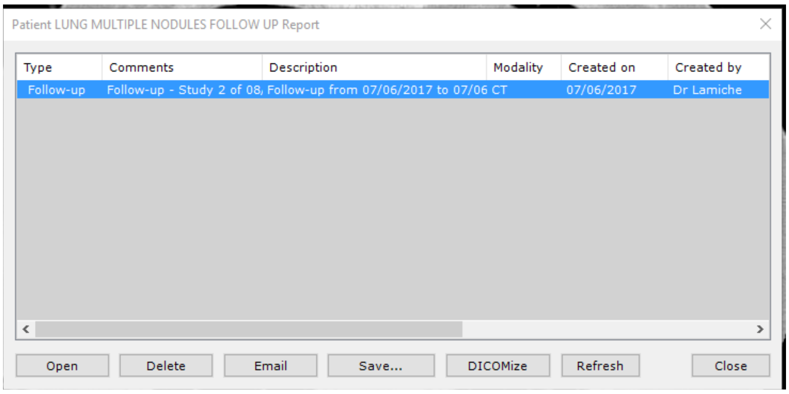
Current 4 view screening
Click to show studies for 01/01/2005

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.

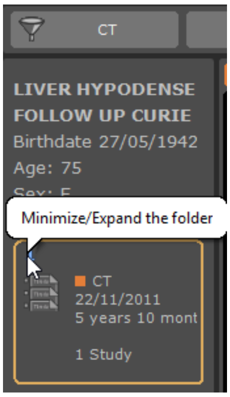

Patient LUNG MULTIPLE NODULES FOLLOW UP Report

Type	Comments	Description	Modality	Created on	Created by
Follow-up	Follow-up - Study 2 of 08, Follow-up from 07/06/2017 to 07/06		CT	07/06/2017	Dr Lamiche

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:

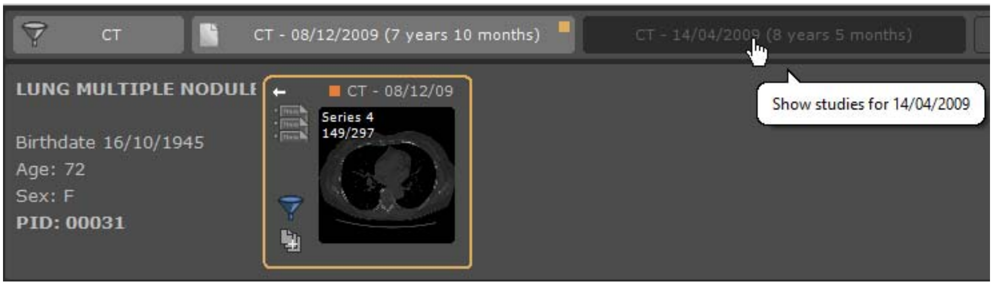
- Modality(ies) of the series included in the folder
- Folder date
- Folder age
- Number of studies belonging to this folder



- Double-click on the name of the study or click on the arrow to expand the folder and visualize its whole content or minimize it
- To load the whole study, click on the study name then drag and drop it in the workspace
- To load one single series from the study folder, select the desired series from the expanded folder then drag and drop it in the workspace

The **little orange square** shows the initially opened folder from the study list. By default, the contents of the other study folders available from the Timeline are hidden:

- To visualize its contents, click on the relevant 'Folder' tab as hereafter:



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 allows closing all the views simultaneously in the workspace.

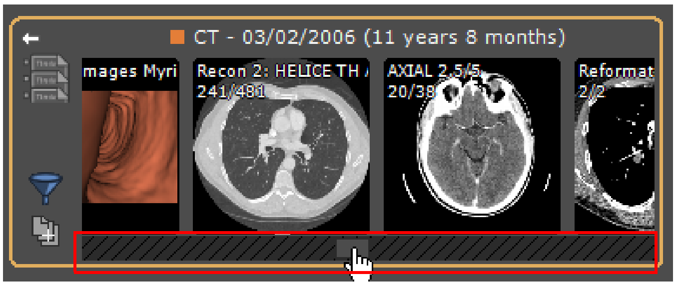
By default, you cannot select more than 10 folders in the Timeline.

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.

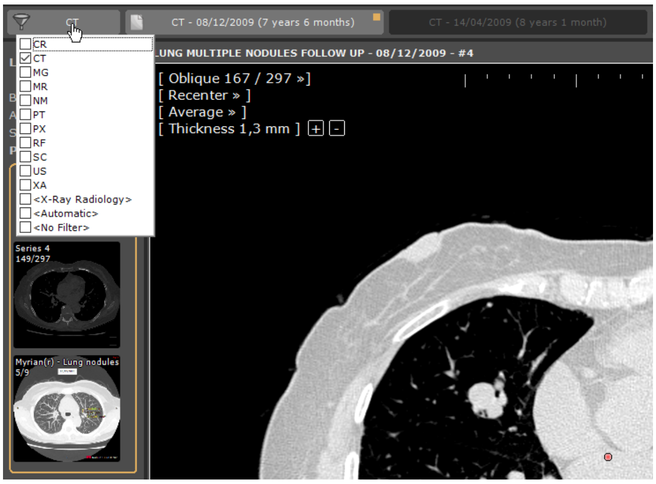
The rules to unselect a folder are the following:
- If the current folder is selected, the other one is unselected
- If the current folder is not selected, the older one is unselected.

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.



The 'Modality' button CT 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.



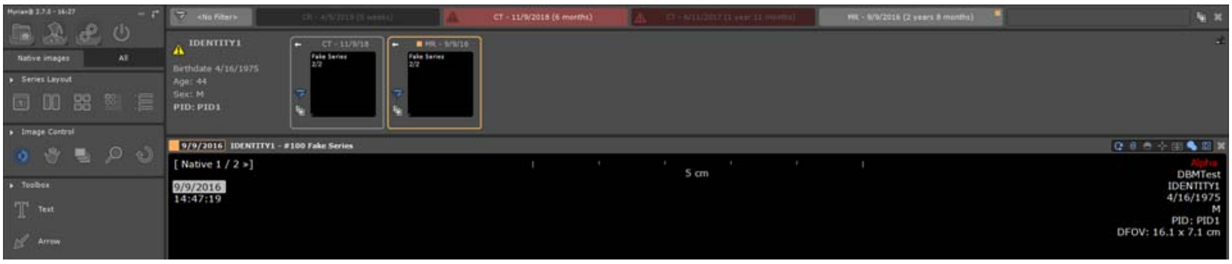
When clicking on this button, the usual modality list is displayed:

- 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).

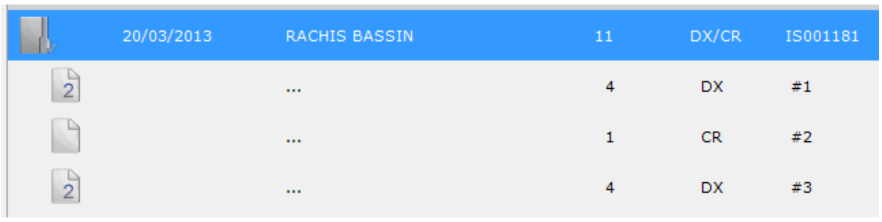
A new display mode allows showing all images of a CR Like study in the series preview.
CR Like studies belong to the modalities: CR, DR, DX, RF, XA, and MG.

When this mode is active, one thumbnail is created for every image in the study, instead of creating one thumbnail for every series or subseries.



IDENTITY1
Birthdate 4/16/1975
Age: 44
Sex: M
PID: PID1

DBMTest
IDENTITY1
4/16/1975
M
PID: PID1
DFOV: 16.1 x 7.1 cm



	20/03/2013	RACHIS BASSIN	11	DX/CR	IS001181
2		...	4	DX	#1
		...	1	CR	#2
2		...	4	DX	#3

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 Loading series/studies from the QuickPatient 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 11.3.2)
- CT and NM series included > NM/CT Fusion protocol (see Section 11.3.2)

Click once on a thumbnail to open the preview screen or **click and hold** to drag and drop

---

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.

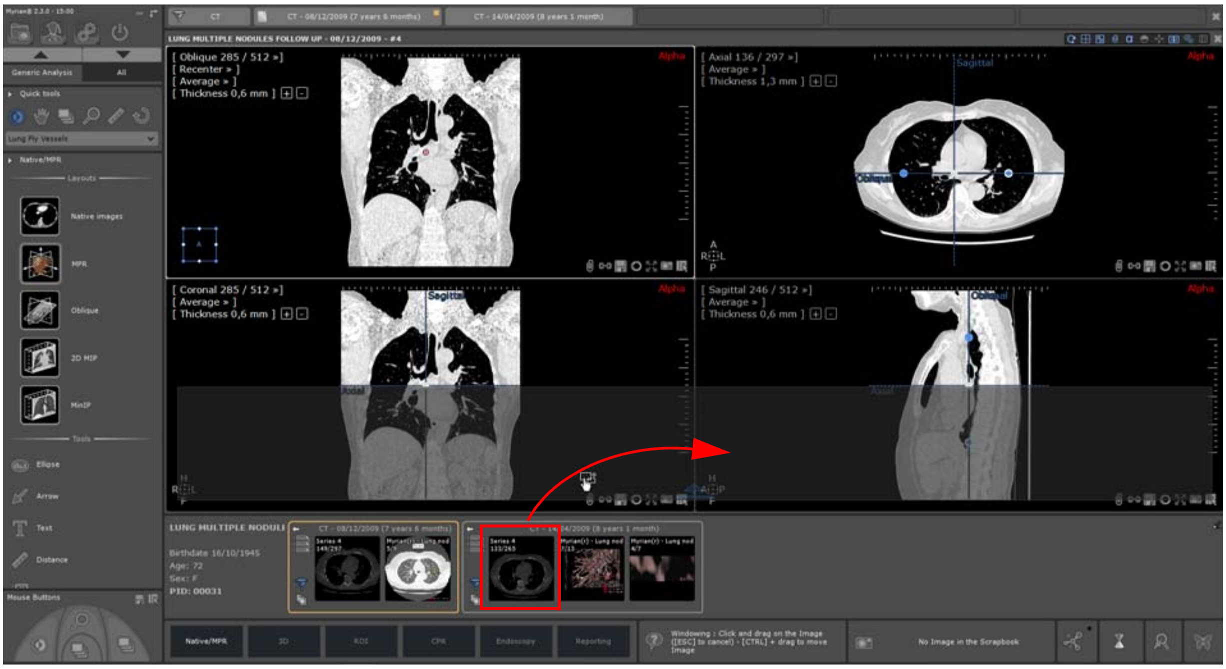
11.3.1 Drag and dropping one single series

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:

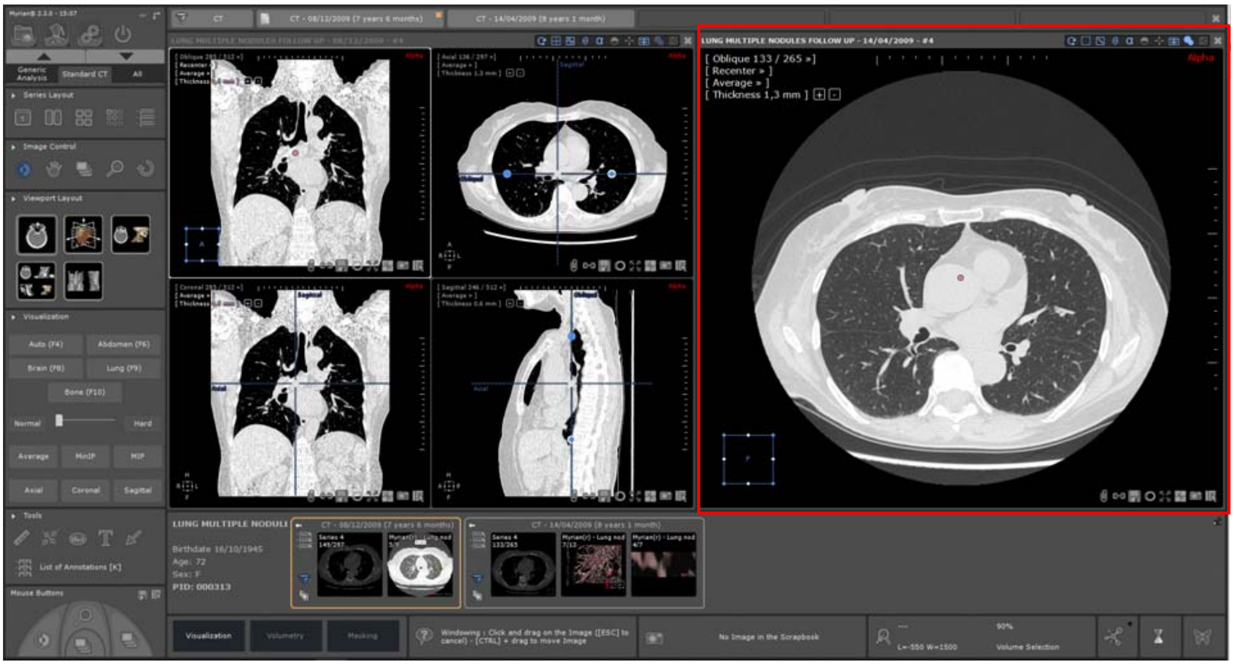
Dropping here,



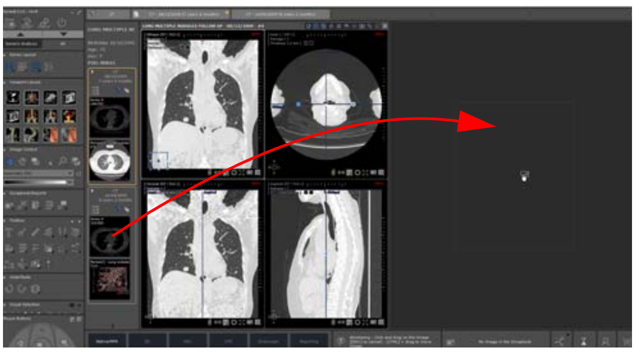
Results in the following:

While dropping here,

Results in the following:

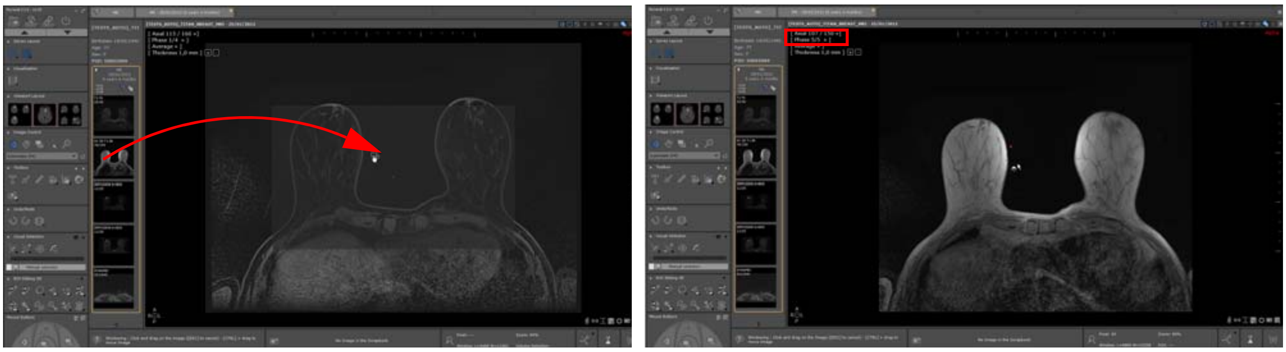


- **Above a free location**: the series is loaded in a single view at this location using a standard protocol corresponding to its modality.



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 added if needed, according to the current view layout mode.

- **Above a multiphase view**: the series is added inside the view when compatible (please refer to User Manual, in the section dedicated to the QuickPatient for detailed information)



The added series is automatically displayed in the workspace as if it was a regular phase initially loaded in the view and registered in the ’Phase’ menu as the last phase of the view.

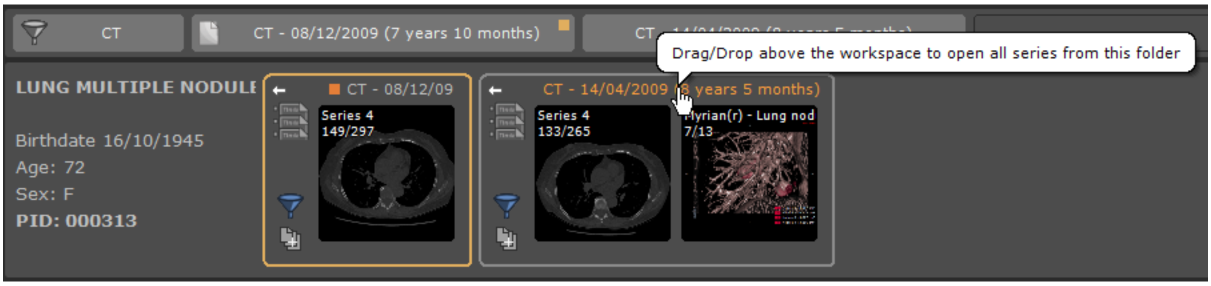
11.3.2 Drag and dropping multiple series

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.

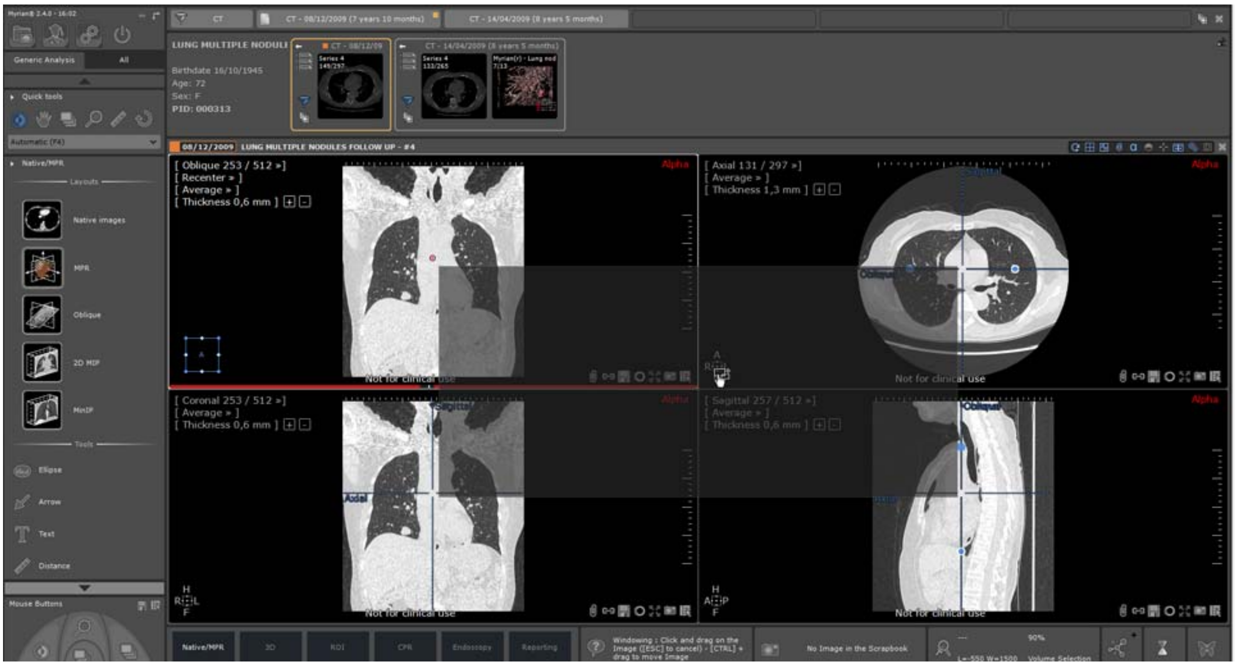
- Pass the mouse cursor over the folder name which highlights in orange then drag and drop it into the workspace.



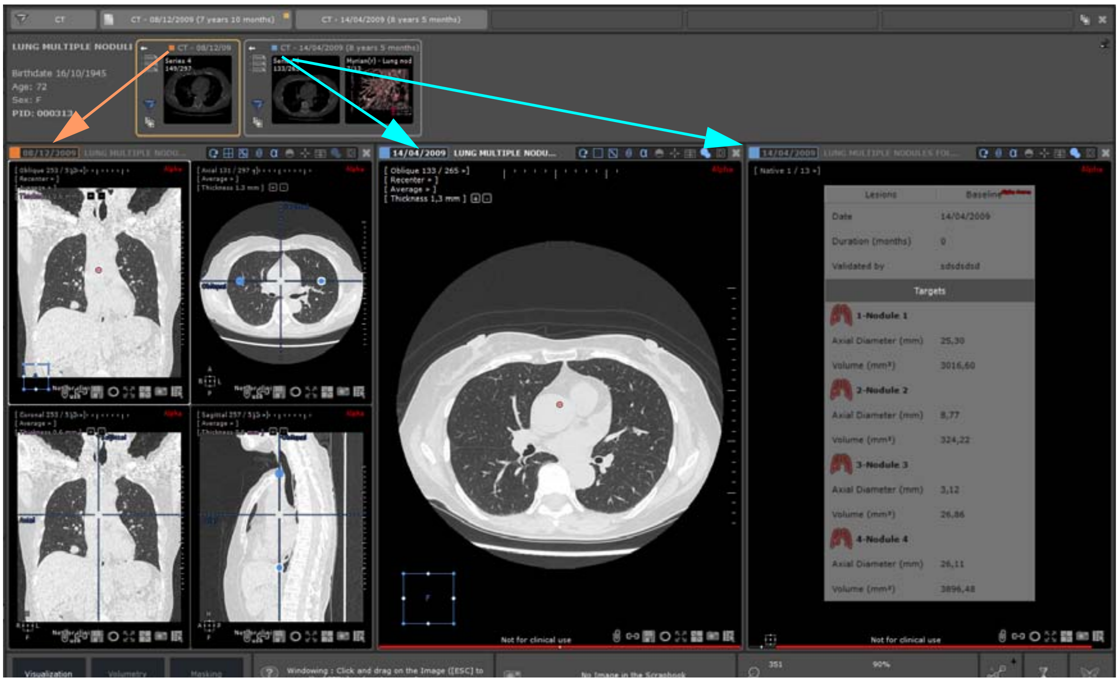
Drag/Drop above the workspace to open all series from this folder

- Drag it into the workspace over the existing view,

To each study folder is allocated a default color to help you distinguish series from one another folder.



- and drop it



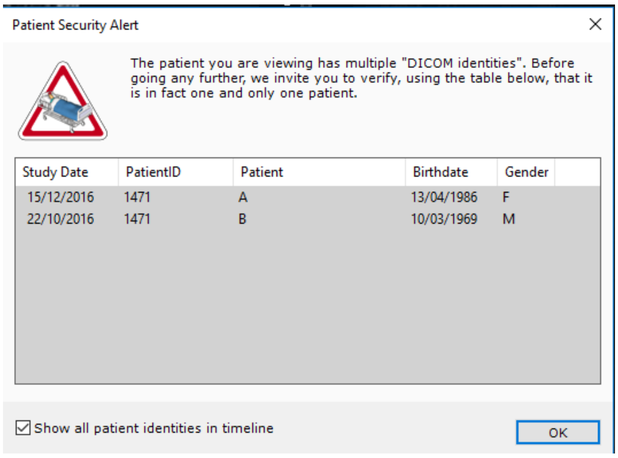
Otherwise, all the series are added on a free location, creating one or more if needed.

11.4 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.

XL-REGISTRATION
Birthdate 22/03/1948
Age: 69
Sex: M
PID: IS000556

A Patient Security Alert window pops up indicating the various identities found for the given patient.



Patient Security Alert

The patient you are viewing has multiple "DICOM identities". Before going any further, we invite you to verify, using the table below, that it is in fact one and only one patient.

Study Date	PatientID	Patient	Birthdate	Gender
15/12/2016	1471	A	13/04/1986	F
22/10/2016	1471	B	10/03/1969	M

☑ Show all patient identities in timeline

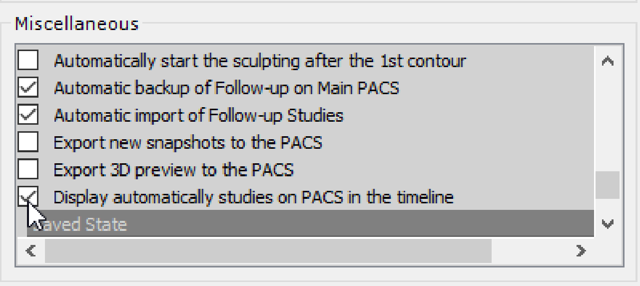
The study list displays the list of all the studies found for the corresponding patient ID including the patient details (name, gender, birth date) for each one.

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.

11.5 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.

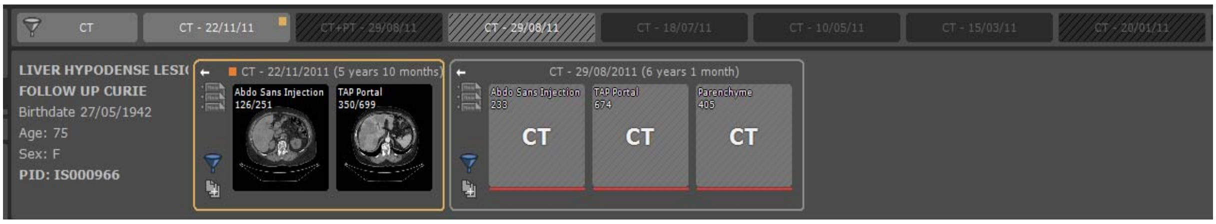


Miscellaneous

☐ Automatically start the sculpting after the 1st contour
☑ Automatic backup of Follow-up on Main PACS
☑ Automatic import of Follow-up Studies
☐ Export new snapshots to the PACS
☐ Export 3D preview to the PACS
☑ Display automatically studies on PACS in the timeline
aved State

If you don't want those available remote studies displayed in the workspace, you need to disable this option.

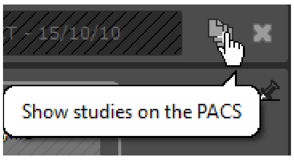
In the Timeline, studies that are **not yet in the local Study list** appear with a **hatched background**. When clicking on the title bar of such a study in the Timeline, the QuickPatient displays the corresponding series.



LIVER HYPODENSE LESI(
FOLLOW UP CURIE
Birthdate 27/05/1942
Age: 75
Sex: F
PID: IS000966

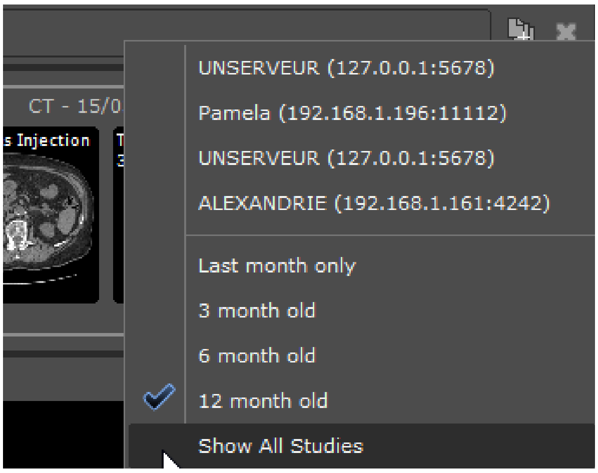
The remote series thumbnails are a simple hatched background with simply the modality displayed over it as those series are not local yet and so, image of the series cannot be displayed as real thumbnail.

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 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.



This menu can also be used to do a manual search on any of the available PACS.

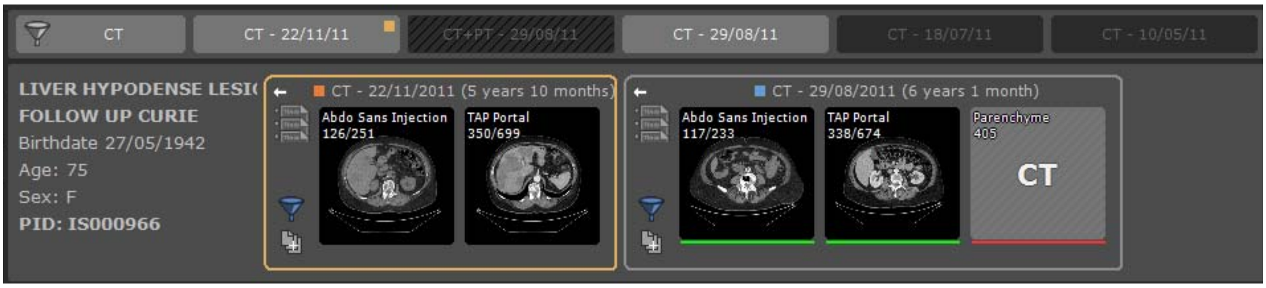
Only the Main PACS (if defined) is queried or the first PACS in the list (if any PACS is defined).

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:

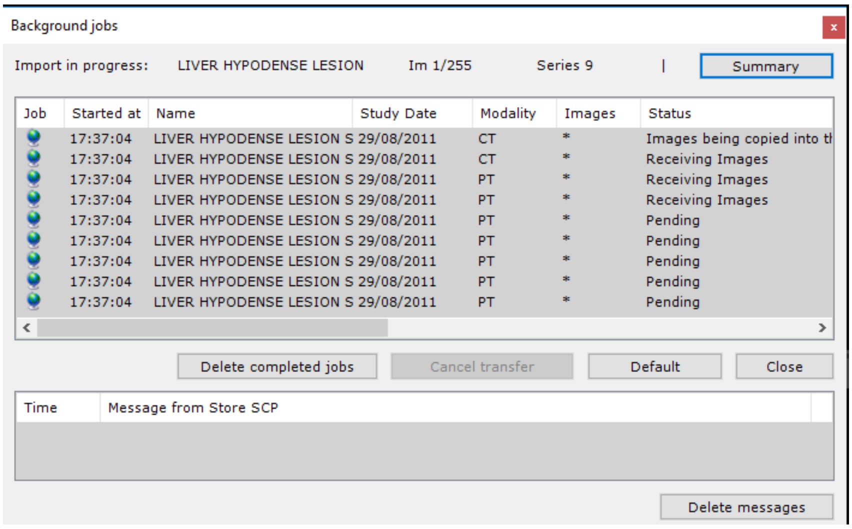
- A red progress bar for remote series that are not in the local study list
- Or a green progress bar for imported series.

Once the series is imported in the workspace, the real thumbnail representing the series can be visualized.



LIVER HYPODENSE LESI
FOLLOW UP CURIE
Birthdate 27/05/1942
Age: 75
Sex: F
PID: IS000966

You can also visualize the series download using the background jobs dialog . and inside the background job dialog, cancel any pending transfer.

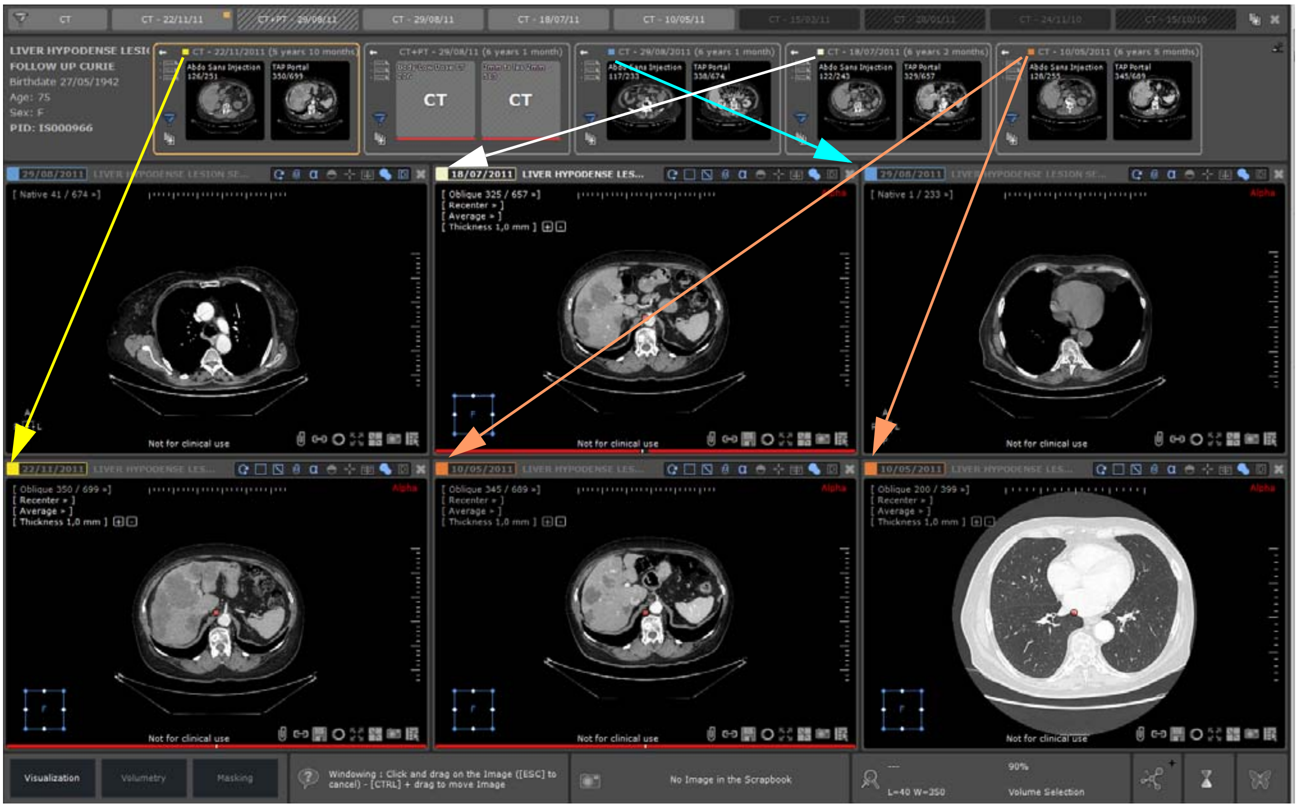


Background jobs

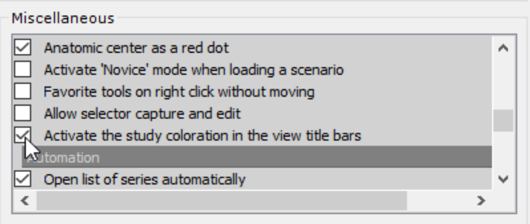
Import in progress: LIVER HYPODENSE LESION Im 1/255 Series 9

Job	Started at	Name	Study Date	Modality	Images	Status
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	CT	*	Images being copied into tl
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	CT	*	Receiving Images
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Receiving Images
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Receiving Images
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Pending
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Pending
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Pending
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Pending
●	17:37:04	LIVER HYPODENSE LESION S	29/08/2011	PT	*	Pending

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.



The coloration of the study date in the view title bar can be disabled from the Preferences>Display>Miscellaneous menu



Miscellaneous

- ☑ Anatomic center as a red dot
- ☐ Activate 'Novice' mode when loading a scenario
- ☐ Favorite tools on right click without moving
- ☐ Allow selector capture and edit
- ☑ Activate the study coloration in the view title bars

Automation

- ☑ Open list of series automatically

11.6 Show all images for CR Like studies in the Quick Patient

For every study visible in the Quick Patient, if the following conditions are fulfilled:
- all series in the study are CR Like
- the total image count in the study is less than 10 (value modifiable with a new QP setting)

Then the series preview for this study will show all images in the study. Otherwise it will show one thumbnail for every series/sub-series.

12 Measurement Annotation Tools

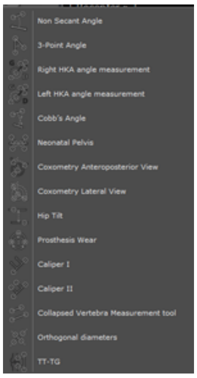
Distance Measurement

- Use to draw a straight Line.
- Select the Line by clicking on it to modify its position and use the handles on either end to adjust its length.

Complex AOI (Optional Add-ons)

- Use the AOI tools in the Toolbox to calculate complex angle measurements such as:
  - Cardiothoracic ratio (CTR)
  - Non Secant Angle
  - 3-Point Angle,
  - Right HKA Angle Measurement (only available for RF, CR and DX modalities)
  - Left HKA Angle Measurement (only available for RF, CR and DX modalities)
  - Cobb's Angle
  - Neonatal Pelvis
  - Coxometry, Anteroposterior View
  - Coxometry, Lateral View
  - Hip Tilt
  - Biometric Angles of both Right and Left Knees
  - Prosthesis Wear
  - Caliper I (One shot)
  - Caliper II (Step by Step)
  - Collapsed Vertebra
  - Orthogonal Diameters
  - Pelvic Incidence
  - Hip dysplasia
  - TT-TG

Furthermore, a set of Assisted Orthopaedic Tools enables the calculation of Prosthetic Angle measurements of both right and left knees



Click on the icon (top-right of the Main Workspace) to toggle display of Angles on/off)

Density

The density value of any pixel being hovered over by the Mouse is displayed at all times in the Mouse-Over tab at bottom-right of the Main Workspace

Pixel: -907 HU
Window: L=-600 W=1600
Zoom: 90%
ROI: ---

Alternatively, you can hold the ALT key down to force display of Pixel Density to appear beside the Pointer

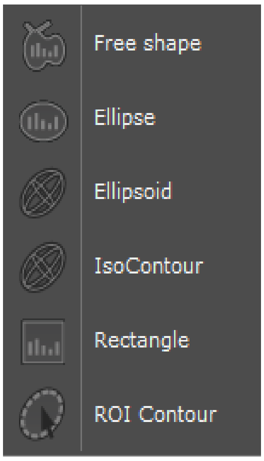
96 HU

Quantification Tools

- Measure Surface and Density of any area using Shapes/Outlines .

Choices are:

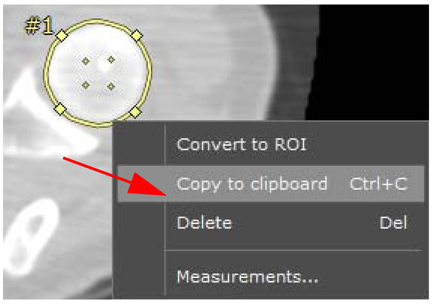
  - Free shape
  - Rectangle
  - Ellipse
  - Ellipsoid
  - IsoContour
  - Threshold
  - ROI Contour



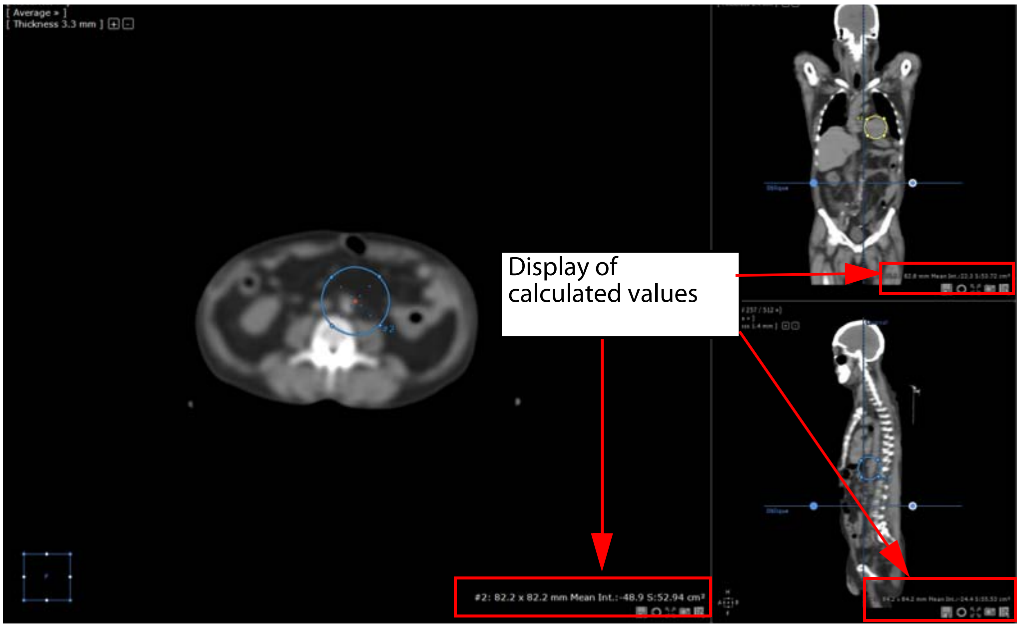
Once you have created a measure in one series, you have the possibility to duplicate it in a different viewport of the same image or in another image of the same series as many times as you wish.

Method of use of the Copy/Paste quantification shape tool:

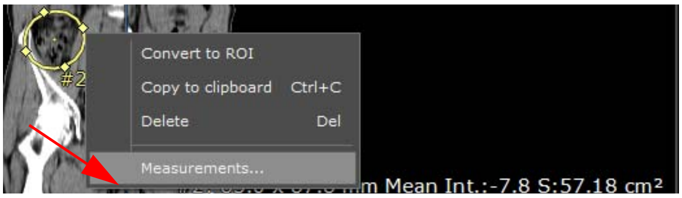
- First copy the annotation to the clipboard:
  - Select the annotation and press CTRL + C or right-click on the annotation and select 'Copy to Clipboard' from the context menu.



- 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.



- 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.



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

---

Pixel Calibration

- Use the Calibration tool to manually **scale images that have not yet been calibrated** (if the Series has already been calibrated, access to this Tool is denied)

Arrow and Text Annotations

You can add Arrow or Text annotations freely

At any time, you may consult the List of Annotations pressing

Note :
- For all AOIs, when you hold down the SHIFT key, the line draws that trace perfectly horizontal or vertical way.
- When two AOI intersect, a measurement angle is automatically displayed

All the Measurements and Annotations described above are automatically saved

Click on the Annotations button in the Display Option at top-right of the views to display/hide all annotations on the Images which could obstruct your vision of the images. To display/hide annotations on one selected viewport, click on located in the concerned viewport (the annotation display is activated by default on all viewports).

13 Regions of Interest (ROI)

Volume Measurements can be obtained instantly (in cm^3) on any tissue or structure captured using CT or MRI modalities.

- Activate the Region of Interest (ROI) Coloring function

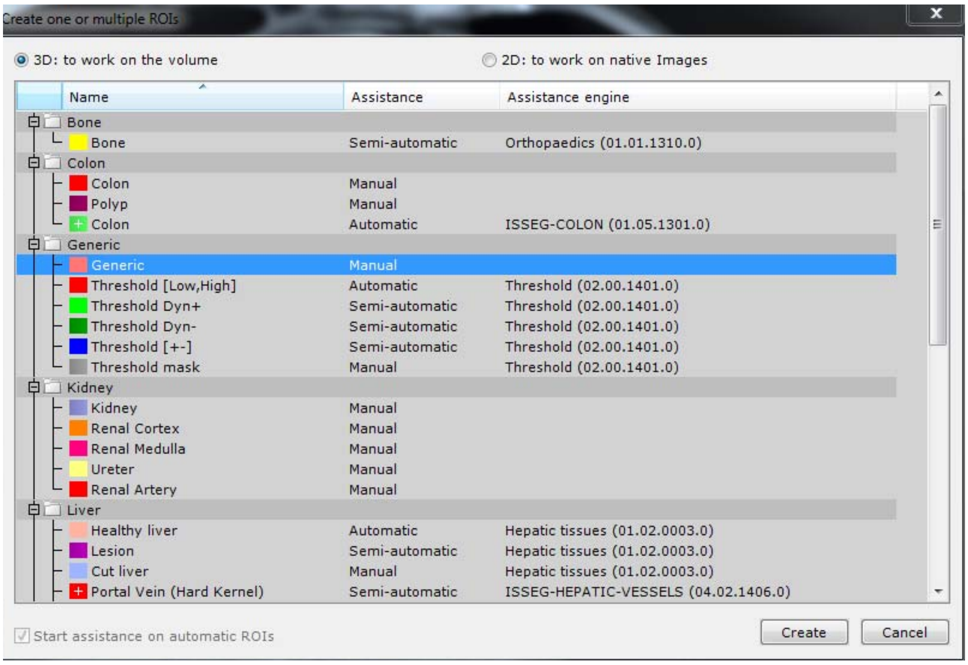
If the colors do not appear, check that ROI coloring has been activated

---

Check that the MPR feature is activated

- Click on the '+' in the Regions of Interest tab

The list of available ROI segmentation engines appears



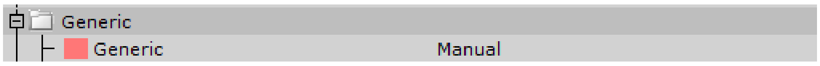
Create one or multiple ROIs

● 3D: to work on the volume ○ 2D: to work on native Images

Name	Assistance	Assistance engine
Bone		
Bone	Semi-automatic	Orthopaedics (01.01.1310.0)
Colon		
Colon	Manual	
Polyp	Manual	
Colon	Automatic	ISSEG-COLON (01.05.1301.0)
Generic		
Generic	Manual	
Threshold [Low,High]	Automatic	Threshold (02.00.1401.0)
Threshold Dyn+	Semi-automatic	Threshold (02.00.1401.0)
Threshold Dyn-	Semi-automatic	Threshold (02.00.1401.0)
Threshold [+-]	Semi-automatic	Threshold (02.00.1401.0)
Threshold mask	Manual	Threshold (02.00.1401.0)
Kidney		
Kidney	Manual	
Renal Cortex	Manual	
Renal Medulla	Manual	
Ureter	Manual	
Renal Artery	Manual	
Liver		
Healthy liver	Automatic	Hepatic tissues (01.02.0003.0)
Lesion	Semi-automatic	Hepatic tissues (01.02.0003.0)
Cut liver	Manual	Hepatic tissues (01.02.0003.0)
Portal Vein (Hard Kernel)	Semi-automatic	ISSEG-HEPATIC-VESSELS (04.02.1406.0)

☑ Start assistance on automatic ROIs

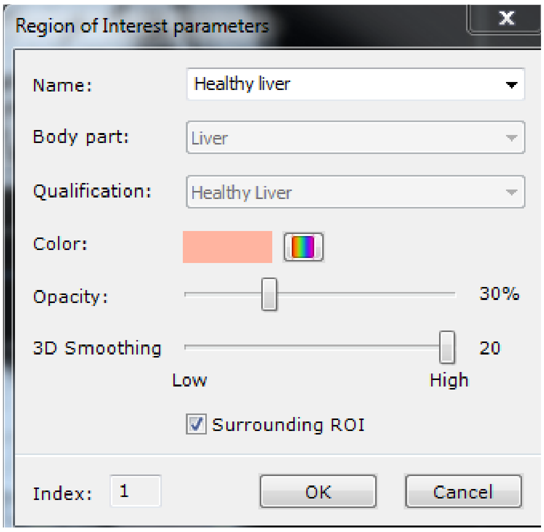
- Select "Generic ROI"



- Click on Create

- 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.
- Right-click on "Generic" in the Regions of Interest tab

- Select “Parameters” and modify the Name, Body Part, Color, etc. as desired



Region of Interest parameters

Name: Healthy liver

Body part: Liver

Qualification: Healthy Liver

Color:

Opacity: 30%

3D Smoothing 20 (Low – High)

☑ Surrounding ROI

Index: 1

Repeat these steps to create other ROIs

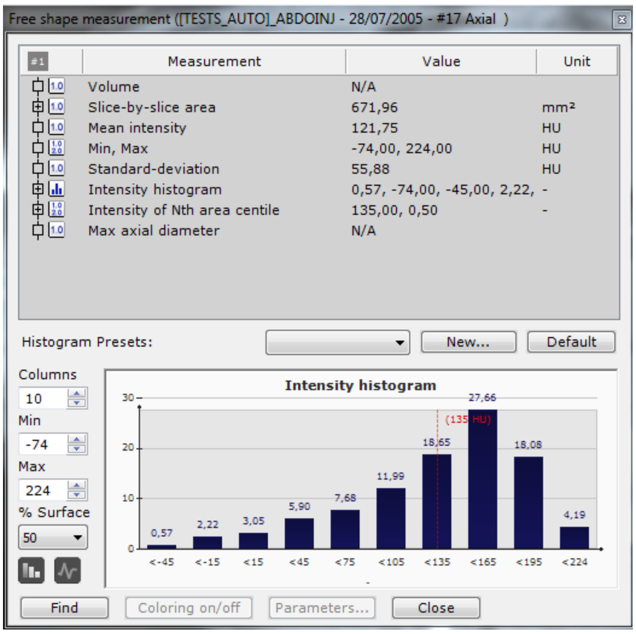
- Click on then to draw the outlines of a volume.

You can draw outlines in any plane of view (Axial, Coronal, and Sagittal)

Be sure to start and finish on the outermost slices (superior and inferior, proximal or distal) of the volume you wish to “Extrude”. You should trace selection outlines only on slices where the shape changes noticeably, for example on 1 slice out of 4.

- When you have drawn a sufficient number of outlines, click on . The colored shape then appears in all planes of view including the 3D frame.
- Double-click on of the ‘Transparent’ ROI Regions of Interest 3D <Transparent> in the ROI list to toggle on/off the display of all **pixels which are not included** in the other ROIs For all other ROIs (e.g. 1 Generic), click on to toggle on or off the display of ROI pixels and color
- Click on 1 to display/hide only the color of the ROI
- To display advanced measurements for a given ROI, right-click on its name in the list (see above) and select “Measurements”

A list of advanced measurements then appears, including Volume, Density, Area, Inertia Axis, Density Histogram, Standard Deviation, etc.



Free shape measurement ([TESTS_AUTO]_ABDOINJ - 28/07/2005 - #17 Axial)

Measurement	Value	Unit
Volume	N/A	
Slice-by-slice area	671,96	mm²
Mean intensity	121,75	HU
Min, Max	-74,00, 224,00	HU
Standard-deviation	55,88	HU
Intensity histogram	0,57, -74,00, -45,00, 2,22,	-
Intensity of Nth area centile	135,00, 0,50	-
Max axial diameter	N/A	

Histogram Presets:

Columns 10

Min -74

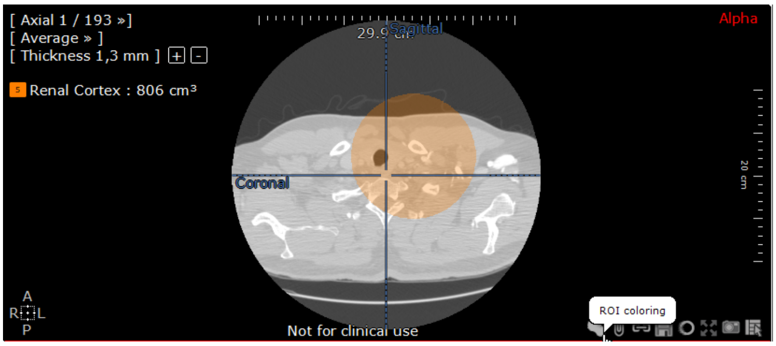
Max 224

% Surface 50

- Right-click on the Density Histogram box to customize column parameters or to copy them to the clipboard

13.1 toggle the ROI overlay independently in separate viewports in Myrian

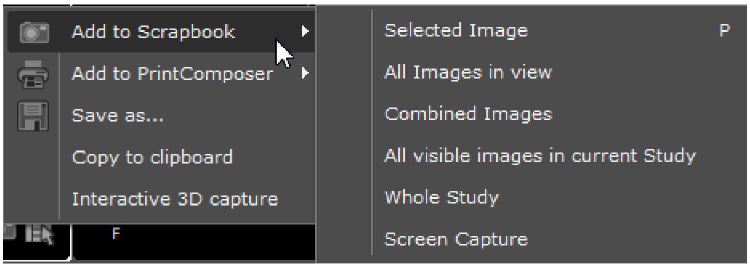
You can manage the coloration of the ROI overlay independently in separate viewports, so it can also be used on an active viewport.



14 Placing Key Images in the Scrapbook or PrintComposer

14.1 Capture Images

The Capture Image function at the bottom-right of all viewports opens a menu from which you can:



- Export individual or combined screenshots of the Workspace to the Scrapbook or PrintComposer
- Save image in various formats with a customizable selection of parameters
- Capture a View to the Clipboard
- Capture the current Workspace layout and settings to a Protocol

Both the Scrapbook and PrintComposer enable you to capture any Annotations or Viewing Settings such as Text, Pointers, Measurements, or Zooming, Windowing, Panning, etc. Such Images can subsequently be used for Patient Reports, Medical Staff Meetings, Case Reviews, Conferences, Presentations, emails, etc.

You can capture a full 3D rotation of the Whole Volume, Volume Rendering and Volume of Interest Viewports by right-clicking on the capture icon in the corresponding Viewport.

By default, this feature automatically exports 20 images, each at 18 degrees of rotation from the next.

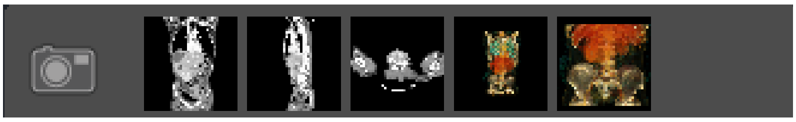
- Choose whether to capture your image to the Scrapbook or PrintComposer

In the corresponding submenu choose whether to capture:

- The Selected Image (shortcut: press the letter ‘P’)
- All images in view (as individual images)
- All images in view (as a combined image)
- All visible Images for Current Study
- The Whole Study
- An RGB screen capture of the entire image zone (active screen)

To include the colored zones (ROI) with your image(s), hold the ‘CTRL’ key down while you click on your choice in the "Add to..." menu

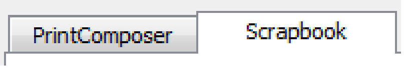
The content of the Image Scrapbook is automatically displayed as thumbnails in the tab at bottom-center of the screen.



- To open the Scrapbook and visualize its contents, click on the Printcomposer/Scrapbook button

14.2 Selection of multiple images in the Scrapbook

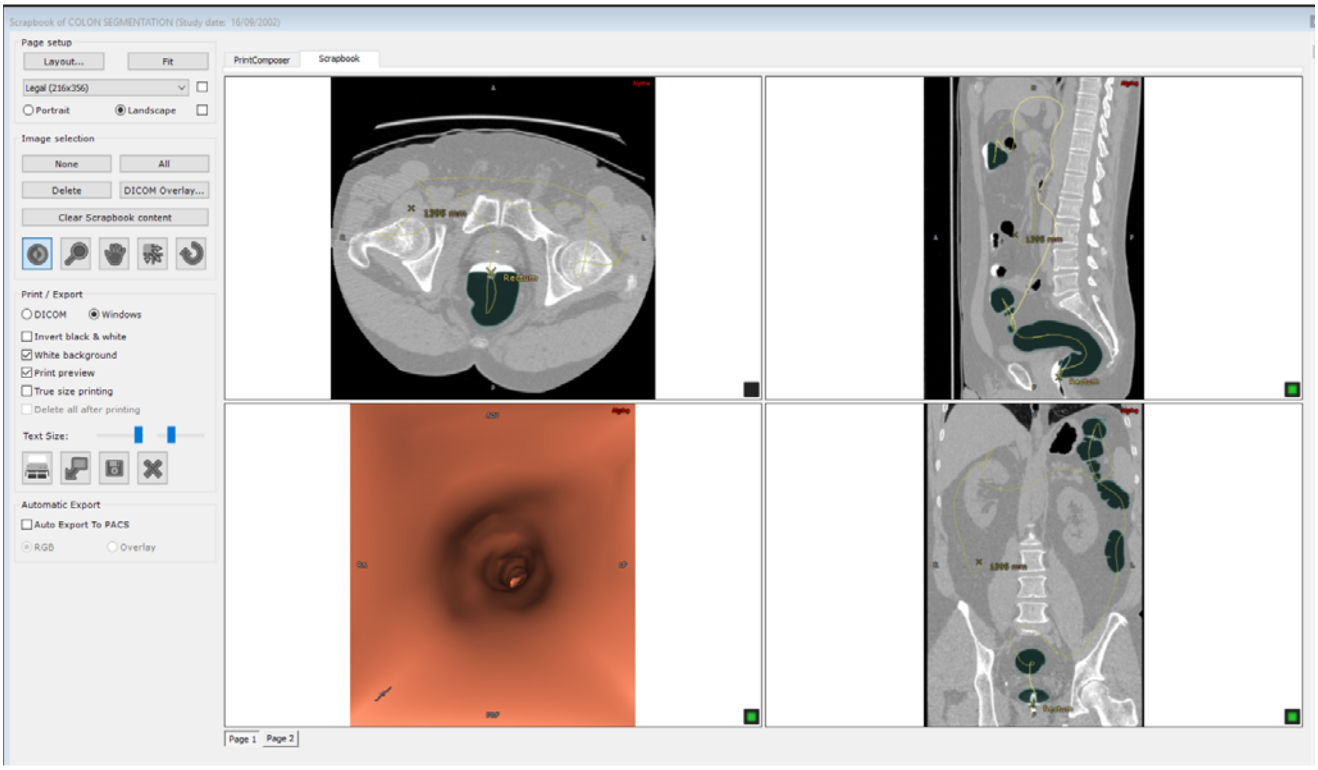
You can select or deselect each image added to the Scrapbook or PrintComposer from the dedicated tab



- To select an image, click anywhere on the image. The square at the bottom right of the image turns from black to green.
- To deselect an image, click anywhere on the selected image.

You can also select all images at once by clicking on All in the "Image Selection" area of the Scrapbook/PrintComposer tabs.

- To deselect all images at once, click on None at left in the "Image Selection" area.


Scrapbook of COLON SEGMENTATION (Study date: 16/09/2002)

Legal (216x356)

○ Portrait ● Landscape

● Windows

☐ Invert black & white
☑ White background
☑ Print preview
☐ True size printing
☐ Delete all after printing

☐ Auto Export To PACS

To select a range of images, you must:

- Click on the first image you wish to select (the image becomes active and is outlined with a grey 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.

It is possible to open one scrapbook for two studies.

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 43 cm 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

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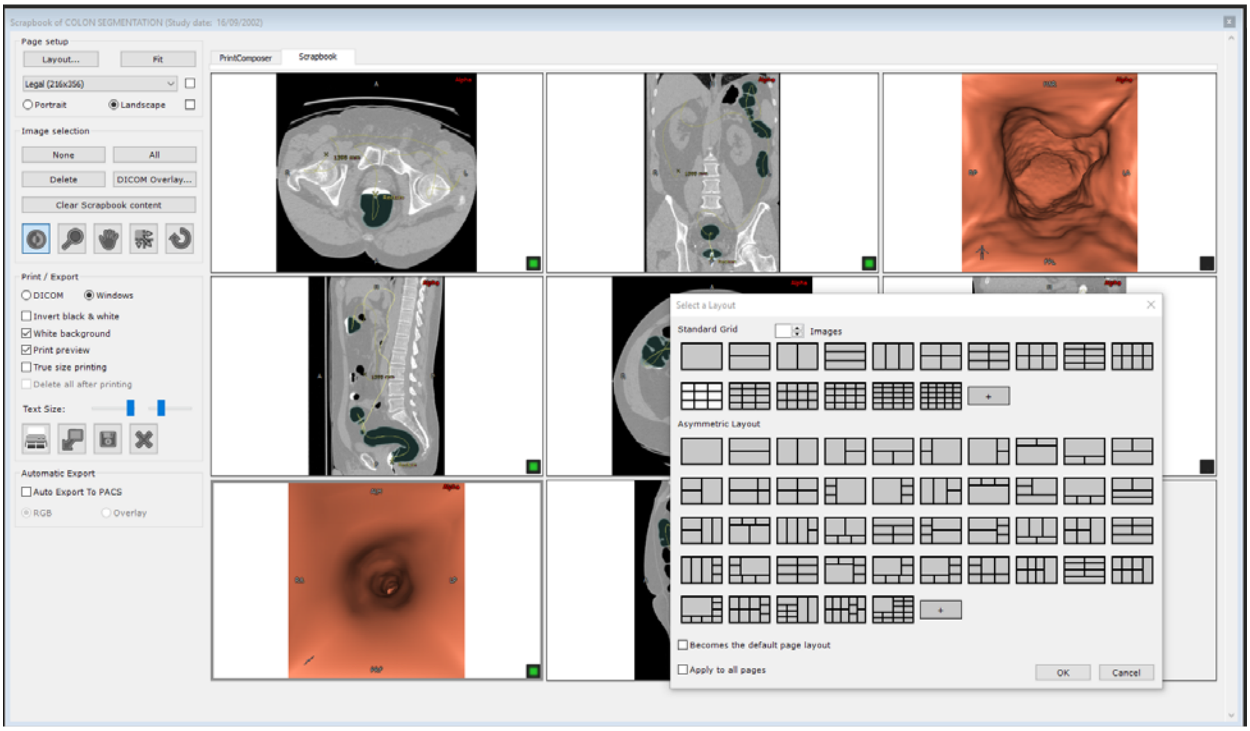
14.3 Print images

Selecting a predefined layout

In both the Scrapbook and PrintComposer tabs, you can select your print layout clicking on Layout... 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.**



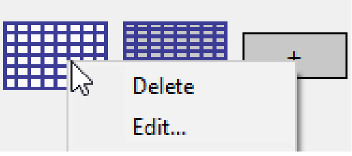
Legal (216x356)
○ Portrait ● Landscape
○ DICOM ● Windows
☐ Invert black & white
☑ White background
☑ Print preview
☐ True size printing
☐ Delete all after printing
☐ Auto Export To PACS
● RGB ○ Overlay
☐ Becomes the default page layout
☐ Apply to all pages

Layouts are ordered by image count.

Asymmetric layouts are supported both for Windows and DICOM printing

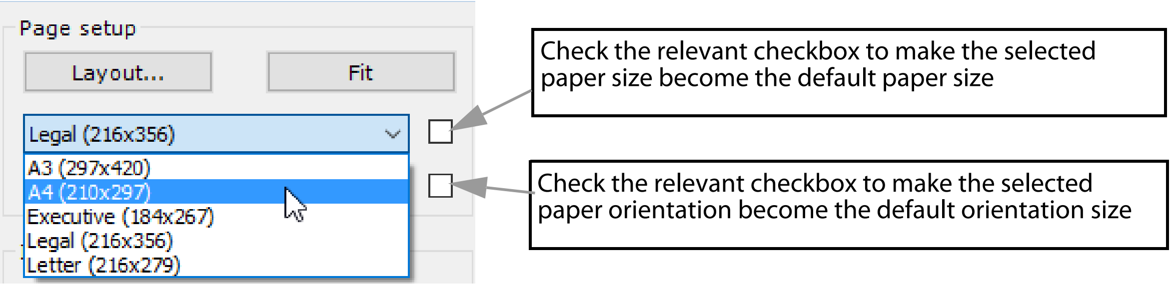
Predefined layouts can combine factory and user-defined layouts. They can be distinguished by their color (black gridlines for factory layouts against blue gridlines for user-defined ones).

When right-clicking on the newly defined layout, the following menu pops up:



An existing grid can only be edited.

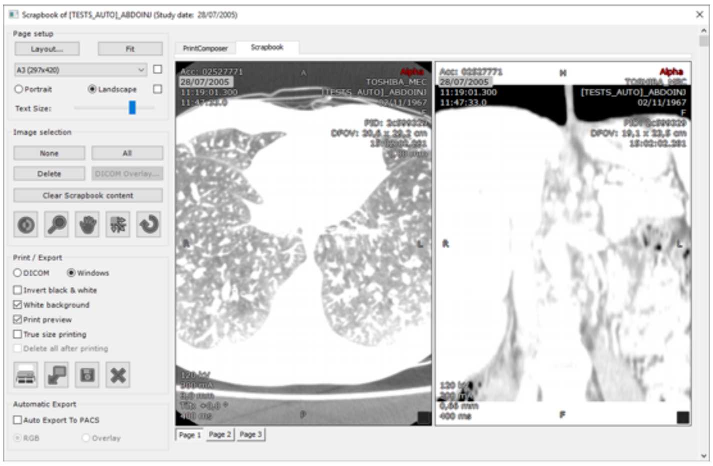
The paper size drop down menu enables you to select the page format of your choice



Check the relevant checkbox to make the selected paper size become the default paper size

Check the relevant checkbox to make the selected paper orientation become the default orientation size

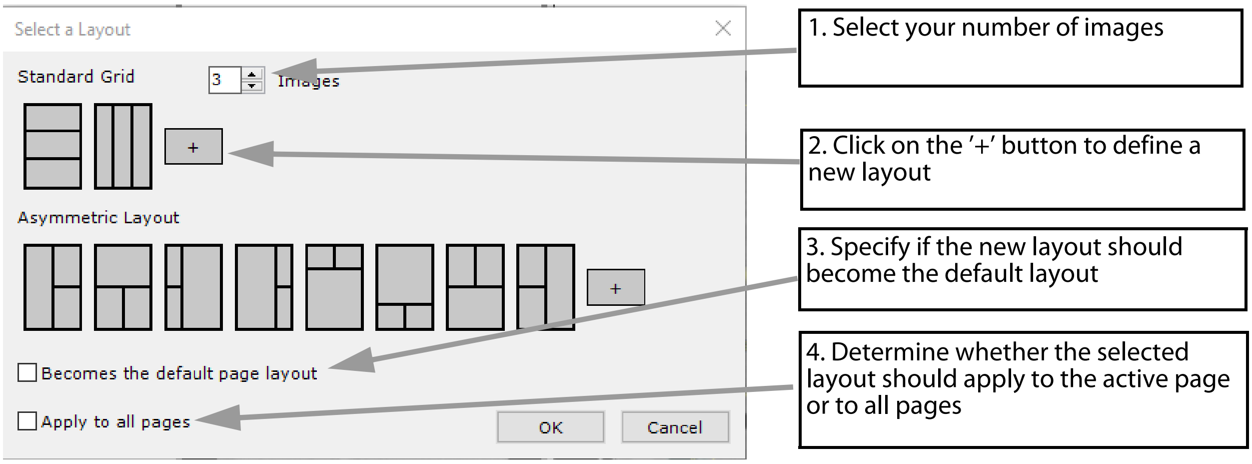
A Landscape/Portrait option is also available for you to select preferred paper orientation. Predefined layouts will then match the selected orientation.
Page orientation and Text size are now "per page". To force page orientation or text size to all pages, keep the CTRL key pressed while setting page orientation or text size.



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.



1. Select your number of images

2. Click on the '+' button to define a new layout

3. Specify if the new layout should become the default layout

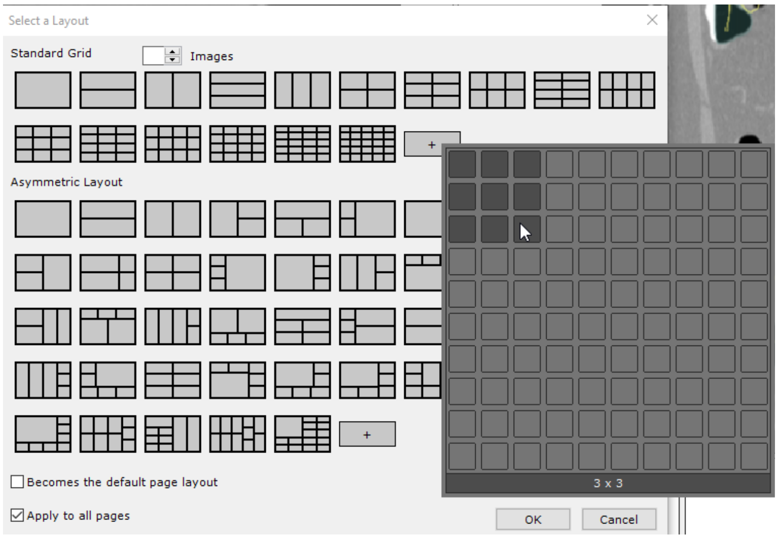
4. Determine whether the selected layout should apply to the active page or to all pages

- To choose a given layout, select the corresponding icon then click on the OK button, or double click on the preferred layout icon.
- To apply the selected layout to all the pages of the Scrapbook/PrintComposer, check the 'Apply to all pages' checkbox
- To create and add a new layout, click on the "+" button in the corresponding grid layout section.

By default, whether you have checked the 'Apply to all pages' checkbox or not, the last choice is preserved whatever the exam you open

Creating new Layouts

Clicking on the "+" button in the **standard grid layout section** opens the following grid selector.



☐ Becomes the default page layout

☑ Apply to all pages

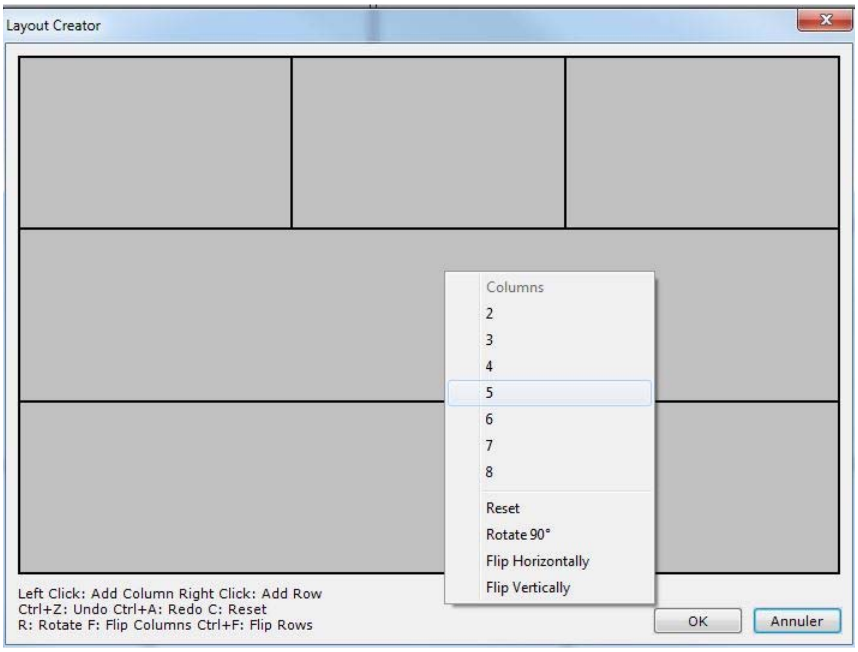
If you create a grid that already exists, the existing layout is automatically selected. No new layout is then created.

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
- Divide an existing cell in one or more columns
- Divide an existing cell in one or more rows
- Rotate the layout
- Flip the layout horizontally or vertically



Left Click: Add Column Right Click: Add Row
Ctrl+Z: Undo Ctrl+A: Redo C: Reset
R: Rotate F: Flip Columns Ctrl+F: Flip Rows

All these features can be activated using left and right mouse buttons or keyboard shortcuts.

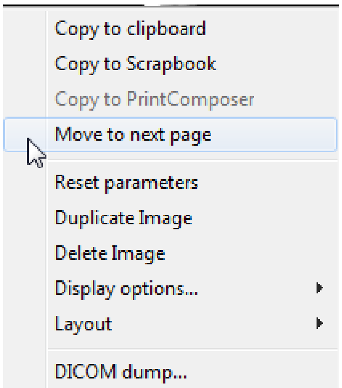
The newly defined layout is automatically added to the preexisting (standard or asymmetric) layout list and preserved upon closing Myrian® and whatever study is open.

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.

New page Layout

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.

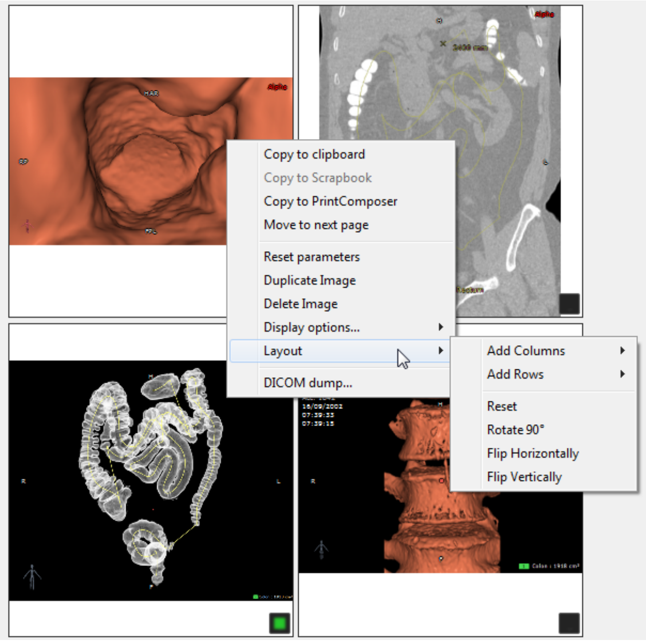


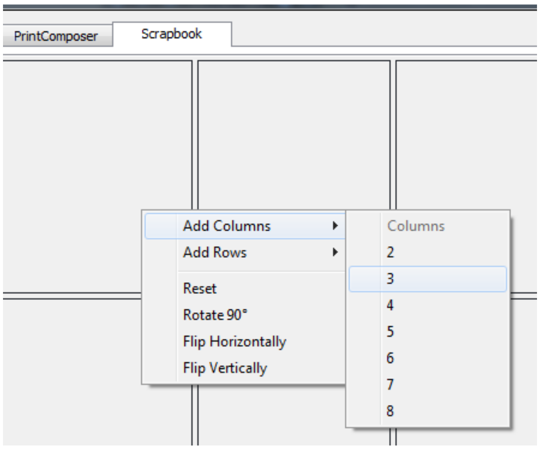
You can among other, move images across pages either to previous page (only if you are not on the first page) or to next page.

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 this menu, you can add columns or rows to 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.

DICOM information

- Click on the 'DICOM overlay...' button to edit the DICOM information displayed on images

---

In the Display Option Command Button Toolbar at top-right of the Workspace:

- Click on to toggle display of overlaid DICOM information on/off, or

- Right-click on to modify display settings of overlaid DICOM information

---

Automatic Export

- Tick the 'Auto Export to PACS' checkbox to **automatically export all the images contained in the Scrapbook** whenever a Study is closed. The entire Study's scrapbook content will be automatically exported in the form of a DICOM Series to your system's Main PACS (by default) or to the first available PACS listed in the Preferences>DICOM tab.

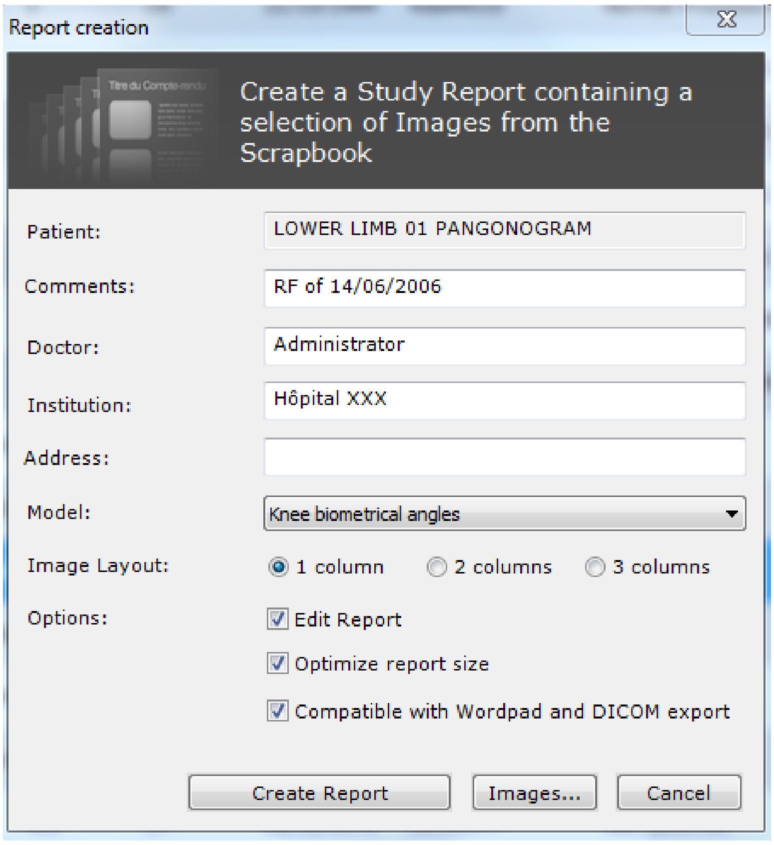
At any subsequent opening or closing of the Study, only those images which have been added to the Scrapbook since the last Automatic Export will be exported.

---

15 ReportCreator: create an illustrated Report

- Click on in the Scrapbook/Reports tab

The Report Creation window appears:



Report creation

Create a Study Report containing a selection of Images from the Scrapbook

Patient: LOWER LIMB 01 PANGONOGRAM

Comments: RF of 14/06/2006

Doctor: Administrator

Institution: Hôpital XXX

Address:

Model: Knee biometrical angles

Image Layout: ● 1 column ○ 2 columns ○ 3 columns

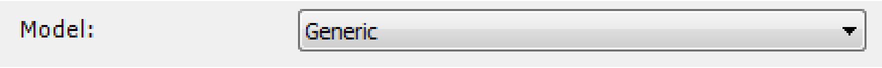
Options:
☑ Edit Report
☑ Optimize report size
☑ Compatible with Wordpad and DICOM export

1 In this screen, type-in:

- Your name
- Your Institution and address

2 Select the format

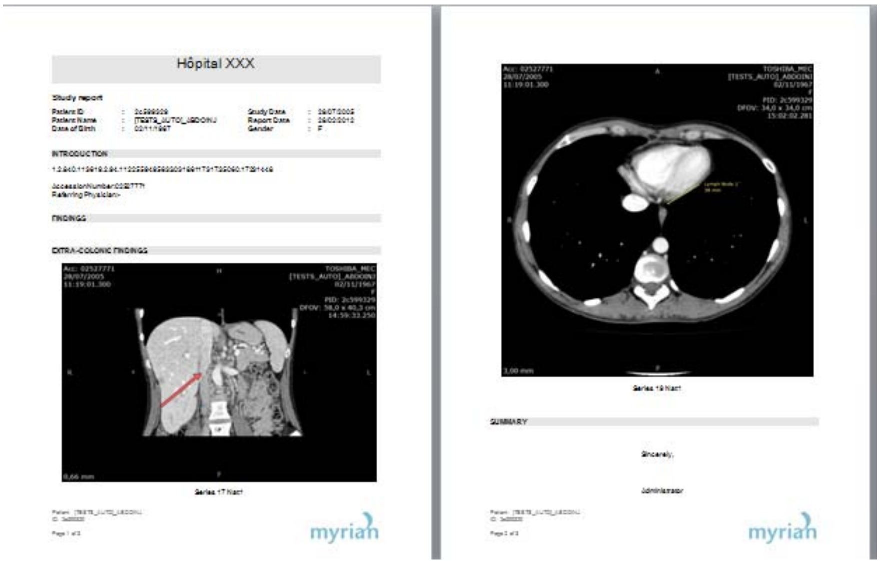
Be sure to select the appropriate template (Model)



Model: Generic

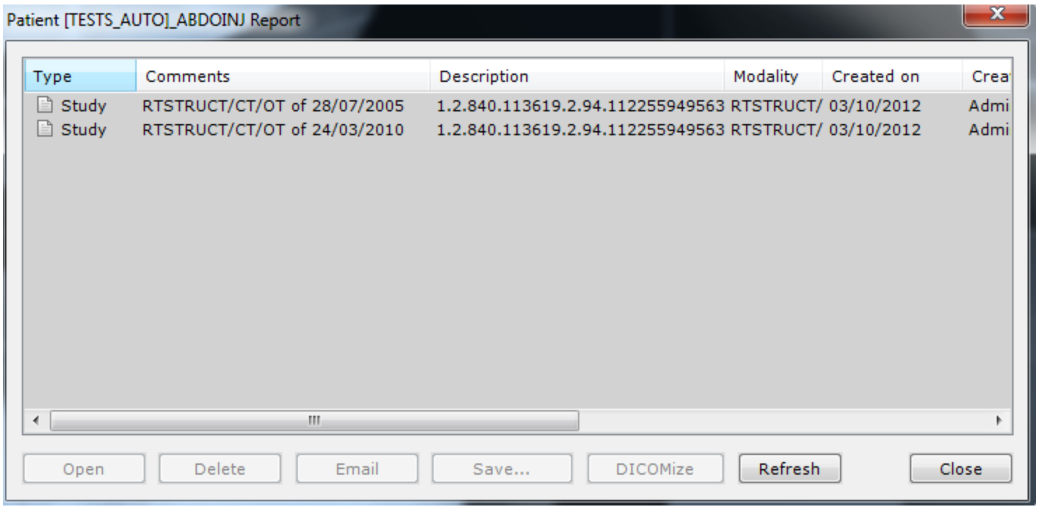
- Click on Create Report to generate the Report.

It will then launch in your default word processor



The Key Images that have been placed in the Scrapbook are automatically added to the Report and all ROI Volumes you have measured are displayed in a table. You can add any extra comments or remarks in the corresponding fields.

- Save the Report and Exit
- Click on to open the Reports List (see below)



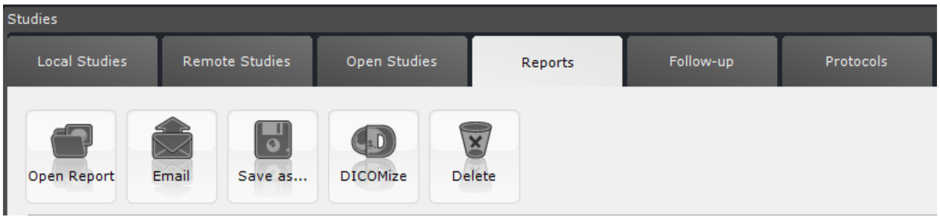
Patient [TESTS_AUTO]_ABDOINJ Report

Type	Comments	Description	Modality	Created on	Crea
Study	RTSTRUCT/CT/OT of 28/07/2005	1.2.840.113619.2.94.112255949563	RTSTRUCT/	03/10/2012	Admi
Study	RTSTRUCT/CT/OT of 24/03/2010	1.2.840.113619.2.94.112255949563	RTSTRUCT/	03/10/2012	Admi

The Report files are not deleted when their corresponding studies are removed.

You should keep a record of these documents elsewhere, e.g. CD, DVD or USB memory stick

You can DiCO Mize Reports by selecting a Report in the Reports tab and clicking on the “DICOMize” button in the toolbar at top.



DICOMized Reports are automatically added to the Local

List in the corresponding Studies

You can send a DICOMized Report to the PACS

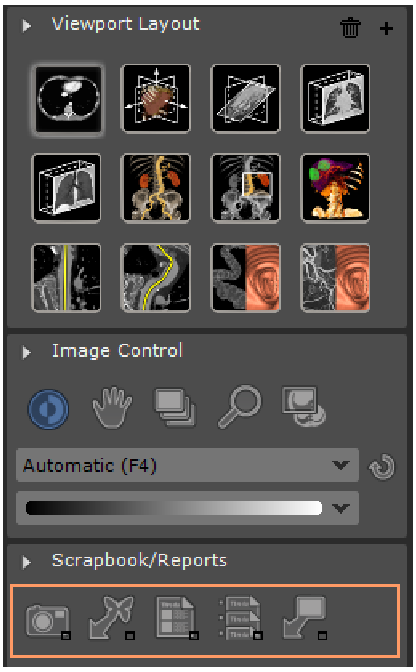
15.1 PDF ReportCreator

Generates interactive 3D PDF Reports. 3D Images are converted and embedded as 3D Objects which can be viewed and manipulated within a standard PDF.

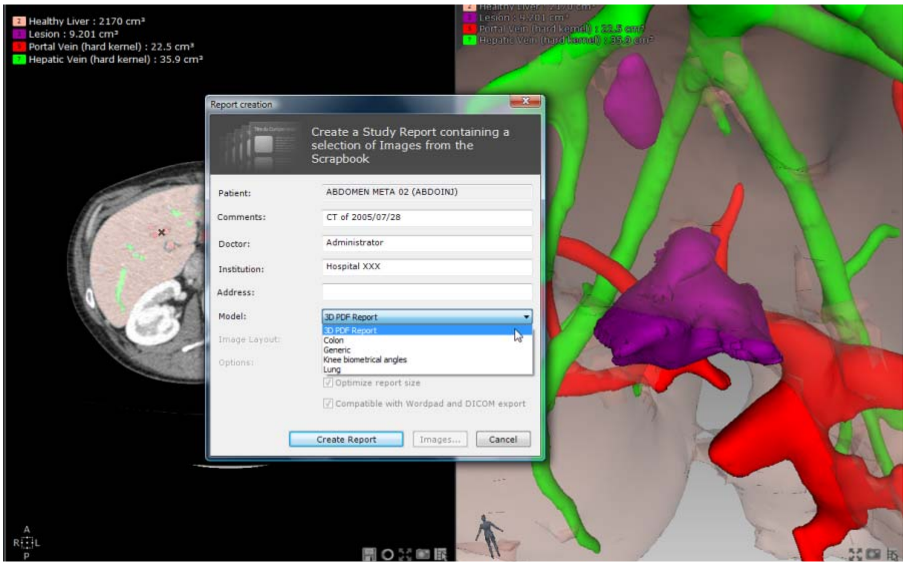
Typical use can be to illustrate various Liver Resection scenarios.

All Measurement Data is exported with the 3D View.

- Set any compatible View to 3D Mode
- Click on 'Create Report' button in the Scrapbook/Reports Toolbar



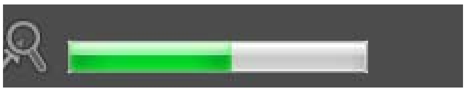
- Click on Create Report to launch Report Creation

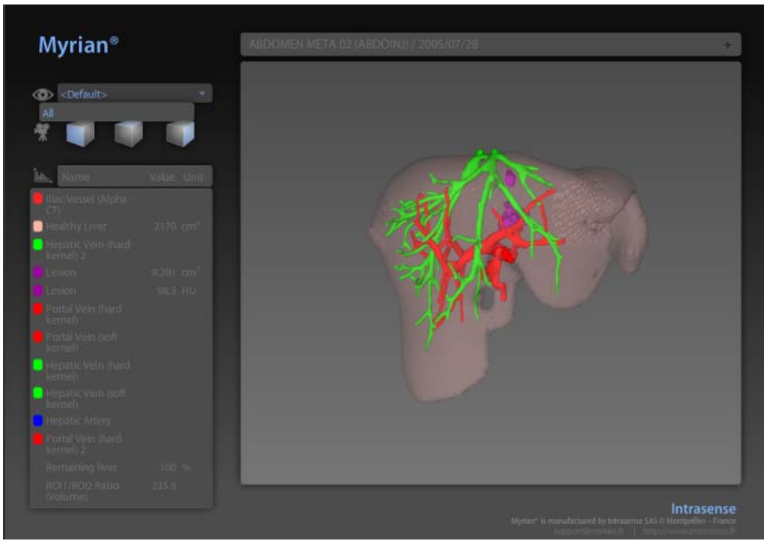

2 Healthy Liver : 2170 cm³
3 Lesion : 9.201 cm³
5 Portal Vein (hard kernel) : 22.5 cm³
7 Hepatic Vein (hard kernel) : 35.9 cm³

Report creation

Create a Study Report containing a selection of Images from the Scrapbook

Patient: ABDOMEN META 02 (ABDOINJ)
Comments: CT of 2005/07/28
Doctor: Administrator
Institution: Hospital XXX
Address:
Model: 3D PDF Report
Image Layout:
Options:
☑ Optimize report size
☑ Compatible with Wordpad and DICOM export

Report Creation status is charted by the Image Processing Progress Bar in the "Information Toolbar" at bottom-right of the Myrian® Workspace 


ABDOMEN META 02 (ABDOINJ) / 2005/07/28

Name	Value	Unit
🟥 Iliac Vessel (Alpha CT)		
🟧 Healthy Liver	2170	cm³
🟩 Hepatic Vein (hard kernel) 2		
🟪 Lesion	9.201	cm³
🟪 Lesion	98.3	HU
🟥 Portal Vein (hard kernel)		
🟥 Portal Vein (soft kernel)		
🟩 Hepatic Vein (hard kernel)		
🟩 Hepatic Vein (soft kernel)		
🟦 Hepatic Artery		
🟥 Portal Vein (hard kernel) 2		
Remaining liver	100	%
ROI1/ROI2 Ratio (Volume)	235.8	

Patient ID appears at the top of the Report


ABDOMEN META 02 (ABDOINJ) / 2005/07/28

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

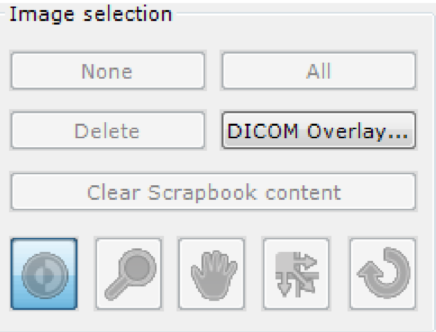
Name	Value	Unit
🟦 Hepatic Artery		
🟧 Healthy Liver	1070	cm^3
🟥 Portal Vein		
🟩 Hepatic Vein		
🟪 Lesion	0.423	cm^3
🟪 Lesion	49.5	HU

To generate 3D PDF Reports, Myrian® 3D Navigator and 3D Graphics Card compatibility are not required.

Adobe Reader 7 or above is recommended to view 3D PDF Reports

16 Printing and Exporting

- Use the ‘Image Selection’ an ‘Print/Export’ tools to adjust settings before printing or exporting
- Use the buttons at top of the Image Selection area to:
  - Select All/None of the key image captures
  - Delete any of the ‘checked’ images
  - Clear the entire content of the Scrapbook or PrintComposer pages
  - Configure the display of DICOM Overlays present on the original images



- Use the Image Adjustment buttons at the bottom of the Image Selection area to adjust the Windowing the Zoom or the Panning parameters of any of the Key Images

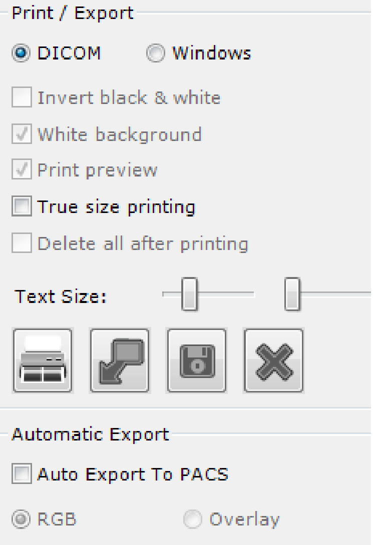
---

Click on to restore Factory Default settings

- Click on the ’Move Image’ button and drag any of the thumbnails to the desired position in the grid to change the order of the Key Images

16.1 Printing

- Print images directly from both the Scrapbook or the PrintComposer tabs
- Print to DICOM printers or standard Windows-compatible printers
  - Use the Print/Export area at bottom-left of the Scrapbook and PrintComposer tabs to set your Printing and exporting preferences



Print / Export

● DICOM ○ Windows

☐ Invert black & white

☑ White background

☑ Print preview

☐ True size printing

☐ Delete all after printing

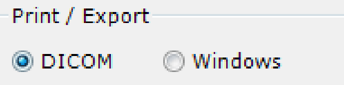
Text Size:

Automatic Export

☐ Auto Export To PACS

● RGB ○ Overlay

- Select your desired media at the top of the Print/Export section



Print / Export

● DICOM ○ Windows

The thumbnail layout at right adjusts automatically to display the layout of the selected media and selected paper or film size

---

1 Click on the print button at bottom-right

2 Modify your printer parameters in the resulting Print settings page

3 Click OK .at the bottom-right to launch printing

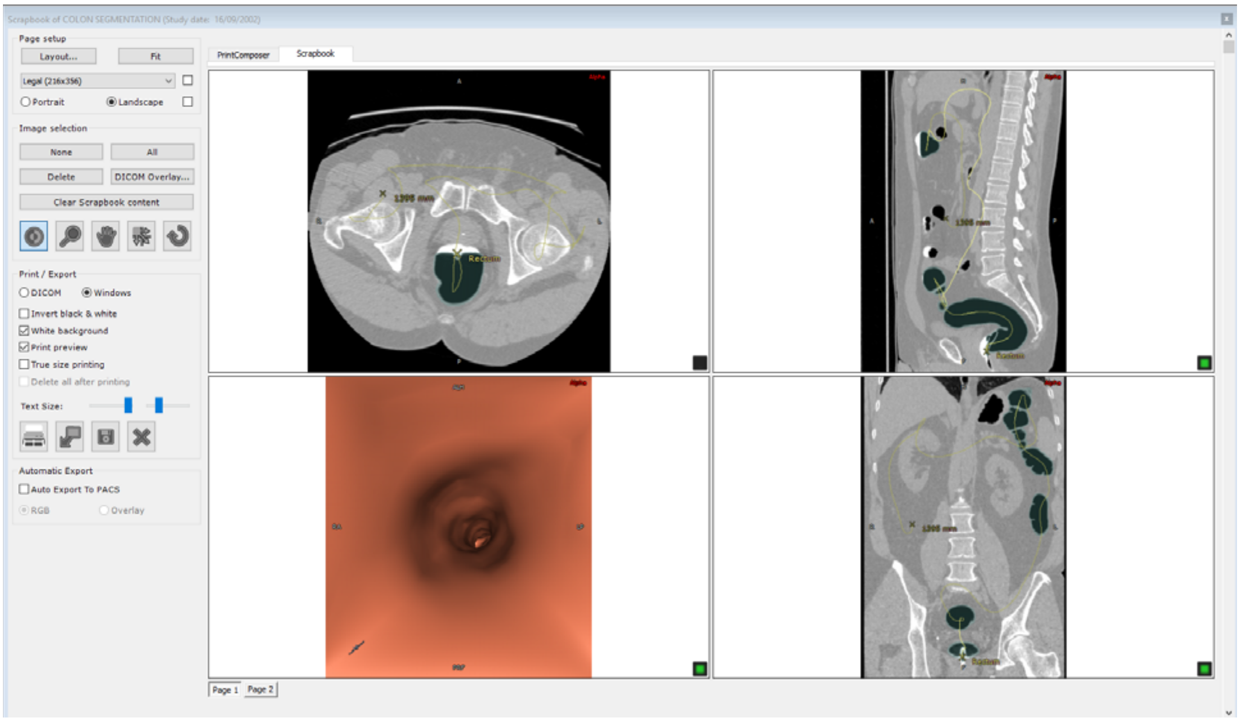
You can modify the size of the font of all the annotations/overlaid DICOM information on the image by adjusting each respective "Text size" slider Text Size: at bottom-left of the Scrapbook/PrintComposer window. Hover the mouse pointer over the cursor to display tooltips.

You can use the large cross-shaped button at the bottom-right of the Print/export area to exit the Scrapbook and PrintComposer tabs

---

16.2 Export to JPEG (email, postings, presentations, etc.)

1 Open the **Image Scrapbook** via the button at bottom-centre of the Workspace



Scrapbook of COLON SEGMENTATION (Study date: 16/09/2002)

Page setup
Legal (216x356)
○ Portrait ● Landscape

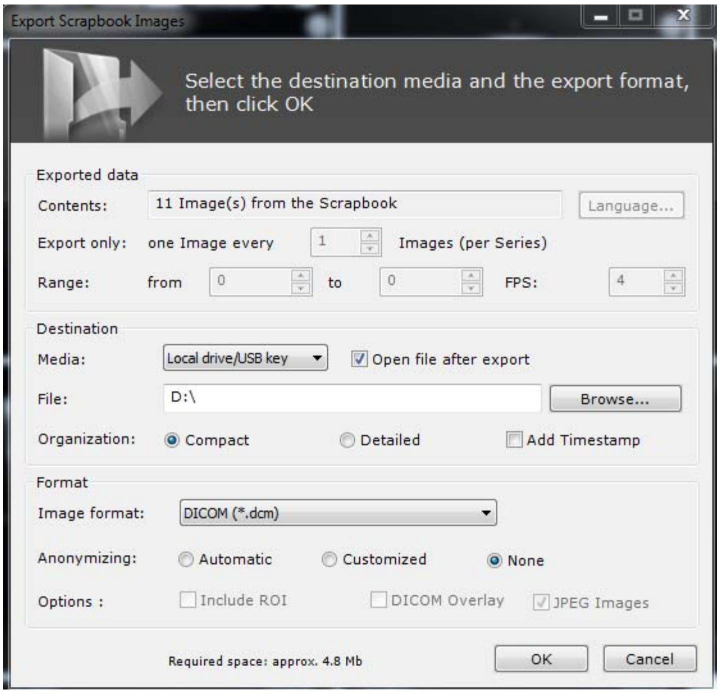
Print / Export
○ DICOM ● Windows
☐ Invert black & white
☑ White background
☑ Print preview
☐ True size printing
☐ Delete all after printing

Automatic Export
☐ Auto Export To PACS
● RGB ○ Overlay

2 Press Fit at right of the Page Setup field (top-left of the Scrapbook) to apply the best fit display for all the images contained in current module or select preferred layout clicking on the 'Layout..' button.

3 Click on the 'Export' button to launch export process.

4 Select/Modify the Destination Media and Export Format in the resulting window



Export Scrapbook Images

Select the destination media and the export format, then click OK

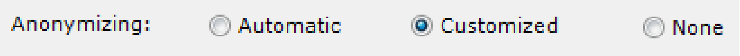
Exported data
Contents: 11 Image(s) from the Scrapbook
Export only: one Image every 1 Images (per Series)
Range: from 0 to 0 FPS: 4

Destination
Media: Local drive/USB key ☑ Open file after export
File: D:\
Organization: ● Compact ○ Detailed ☐ Add Timestamp

Format
Image format: DICOM (*.dcm)
Anonymizing: ○ Automatic ○ Customized ● None
Options : ☐ Include ROI ☐ DICOM Overlay ☑ JPEG Images

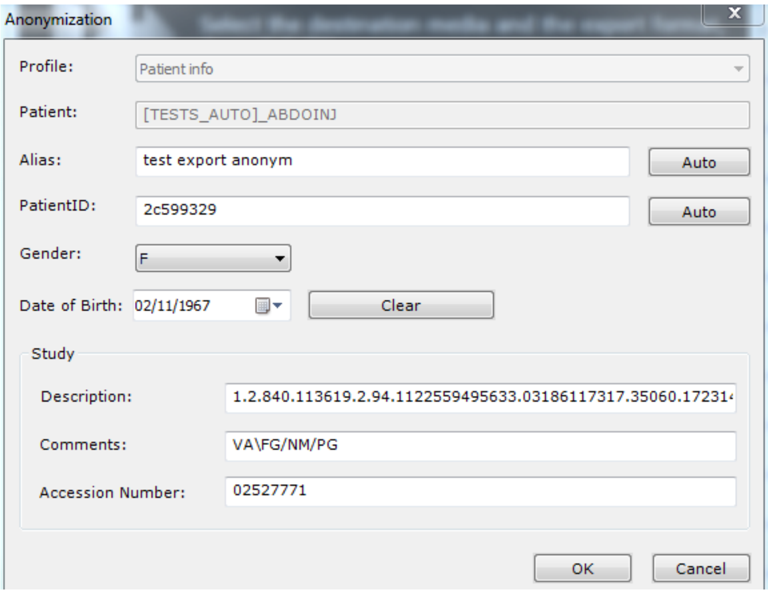
Required space: approx. 4.8 Mb

5 Select desired level of Anonymizing



Anonymizing: ○ Automatic ● Customized ○ None

6 Enter the Alias of your choice


Anonymization

Profile: Patient info

Patient: [TESTS_AUTO]_ABDOINJ

Alias: test export anonym

PatientID: 2c599329

Gender: F

Date of Birth: 02/11/1967

Study

Description: 1.2.840.113619.2.94.1122559495633.03186117317.35060.17231

Comments: VA\FG/NM/PG

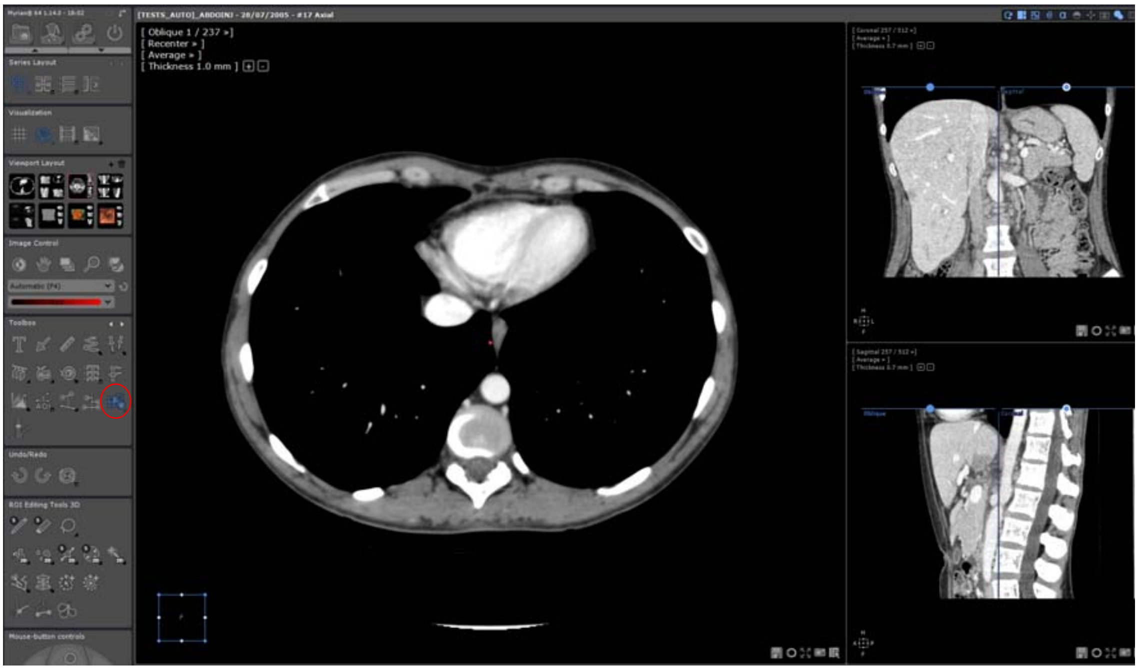
Accession Number: 02527771

Context: Clinical Research, Training, Education, etc.

If you activate the **'Auto Export to PACS'** function in the Scrapbook Screen, when a Study is closed, **all the images contained in the Scrapbook** are automatically exported as a DICOM Series to the Main PACS or to the first available PACS listed in the Preferences>DICOM tab. At any subsequent opening/closing of the Study, only new images which have been added since the last batch export will be exported.

16.3 Export to a third-party application

If you are running simultaneously Myrian® and 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 in the Toolbox

You now have two options available to click on:

- Either you can choose to **drag & drop one viewport** only (either 2D or 3D).

Or

- You 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 which accept dropping image files, 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:

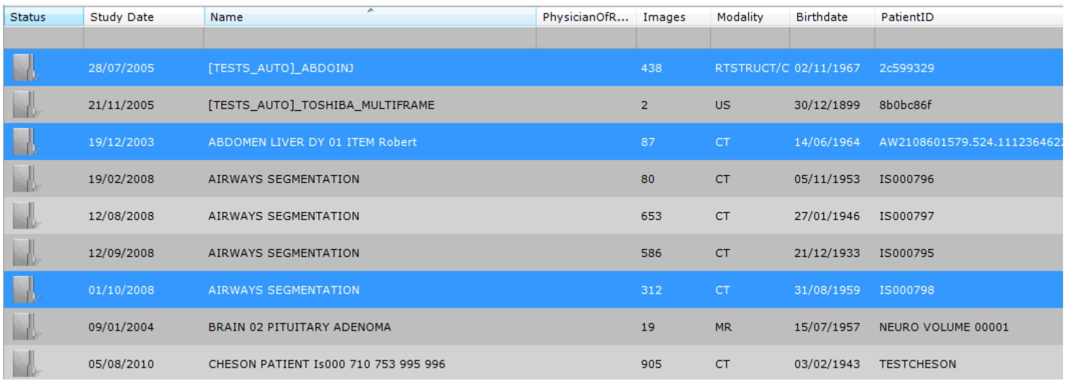
- Drop a viewport: Filename = patientName-se number-se desc-orientation-elevation-yymmdd-hhmmss.jpg (no elevation for 3D viewport)
- Drop a view: Filename = patientName-se number-se desc-yymmdd-hhmmss.jpg

The default file format is JPEG (.jpg) but can be changed in the user preference settings.

16.4 Export to DICOM

1 Click on the Local Studies button

2 Select one or more Studies. [CTRL]/[SHIFT]+Click to select multiple choices

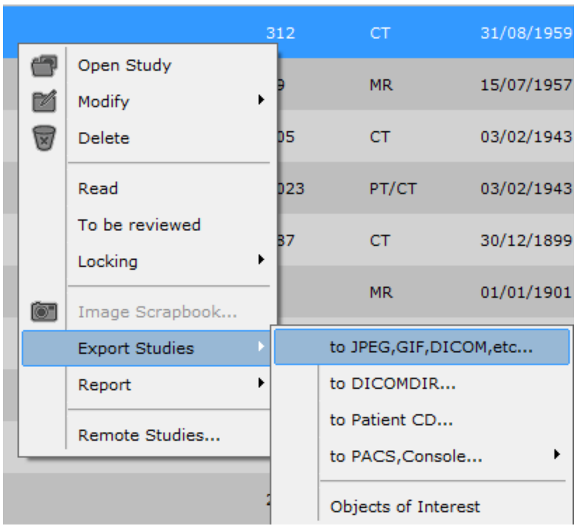


Status	Study Date	Name	PhysicianOfR...	Images	Modality	Birthdate	PatientID
	28/07/2005	[TESTS_AUTO]_ABDOINJ		438	RTSTRUCT/C	02/11/1967	2c599329
	21/11/2005	[TESTS_AUTO]_TOSHIBA_MULTIFRAME		2	US	30/12/1899	8b0bc86f
	19/12/2003	ABDOMEN LIVER DY 01 ITEM Robert		87	CT	14/06/1964	AW2108601579.524.111236462
	19/02/2008	AIRWAYS SEGMENTATION		80	CT	05/11/1953	IS000796
	12/08/2008	AIRWAYS SEGMENTATION		653	CT	27/01/1946	IS000797
	12/09/2008	AIRWAYS SEGMENTATION		586	CT	21/12/1933	IS000795
	01/10/2008	AIRWAYS SEGMENTATION		312	CT	31/08/1959	IS000798
	09/01/2004	BRAIN 02 PITUITARY ADENOMA		19	MR	15/07/1957	NEURO VOLUME 00001
	05/08/2010	CHESON PATIENT Is000 710 753 995 996		905	CT	03/02/1943	TESTCHESON

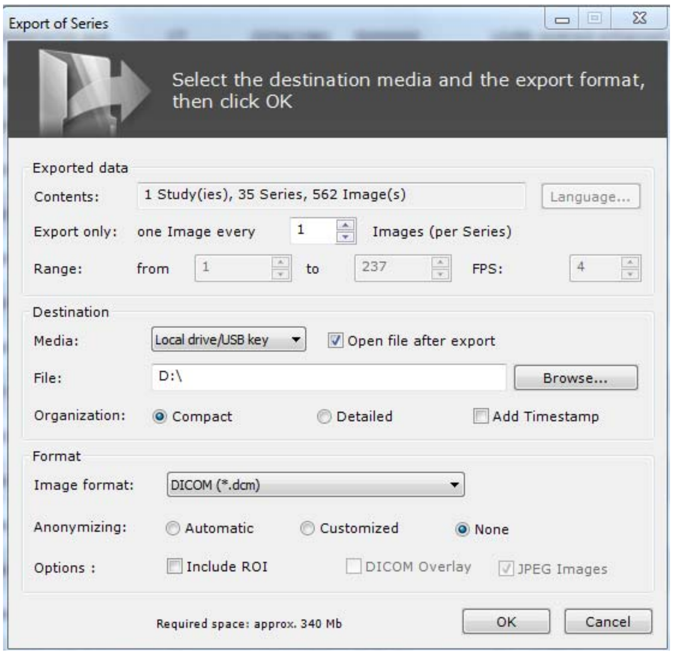
3 Right-click on a Study

4 Select "Export Studies"

5 Select your format from the submenu: JPEG, GIF, DICOM, etc.



The following screen appears:



Select the destination media and the export format, then click OK

Exported data

Contents: 1 Study(ies), 35 Series, 562 Image(s)

Export only: one Image every 1 Images (per Series)

Range: from 1 to 237 FPS: 4

Destination

Media: Local drive/USB key ☑ Open file after export

File: D:\

Organization: ● Compact ○ Detailed ☐ Add Timestamp

Format

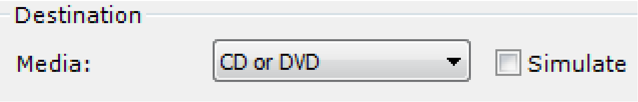
Image format: DICOM (*.dcm)

Anonymizing: ○ Automatic ○ Customized ● None

Options : ☐ Include ROI ☐ DICOM Overlay ☑ JPEG Images

Required space: approx. 340 Mb

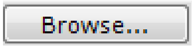
6 Choose the Export **Destination**



Destination

Media: CD or DVD ☐ Simulate

then



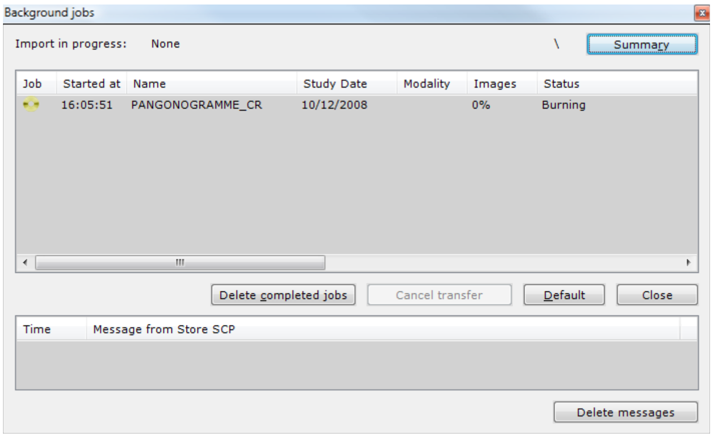
7 Create a CD/DVD by selecting CD or DVD in the ‘Media’ menu

The CD/DVD writing process is a background task. The Export screen disappears as soon as the Export command is launched.

Click on Myrian® Butterfly icon at the bottom-right of the screen to view the progress status of the Patient CD writing process

---

Tick the ‘Simulate’ checkbox to simulate the disc writing process to check that all parameters are correctly configured


Background jobs

Import in progress: None

Job	Started at	Name	Study Date	Modality	Images	Status
	16:05:51	PANGONOGRAMME_CR	10/12/2008		0%	Burning

Time	Message from Store SCP

“DICOM (*.dcm)” should appear in the **Format** box

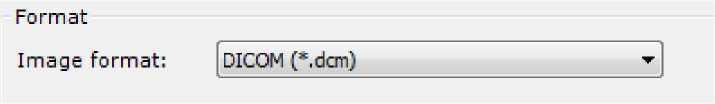
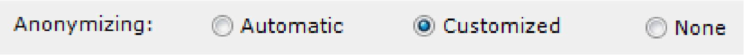
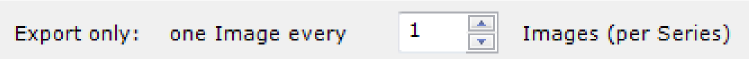

Format

Image format: DICOM (*.dcm)

8 Choose level of **Anonymizing**


Anonymizing: ○ Automatic ● Customized ○ None

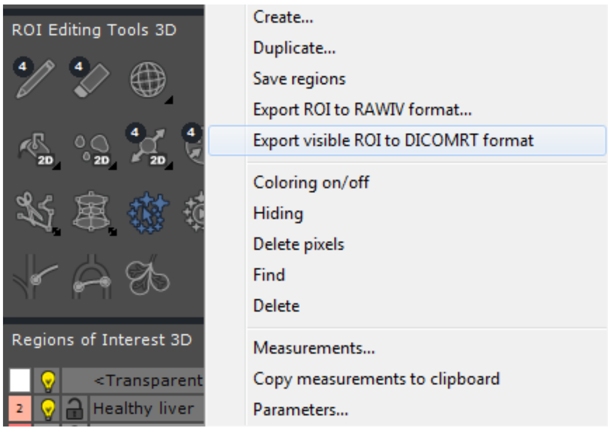
9 Use the Spacing section to Export **1 image out of 2, 3, etc**


Export only: one Image every 1 Images (per Series)

If the ‘Auto Export to PACS’ checkbox in the Scrapbook Window is ticked, whenever a Study is closed, **all the images contained in the Scrapbook** are automatically exported as a DICOM Series to your Main PACS.

16.5 Export to DICOM RT

You can export any visible ROI 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

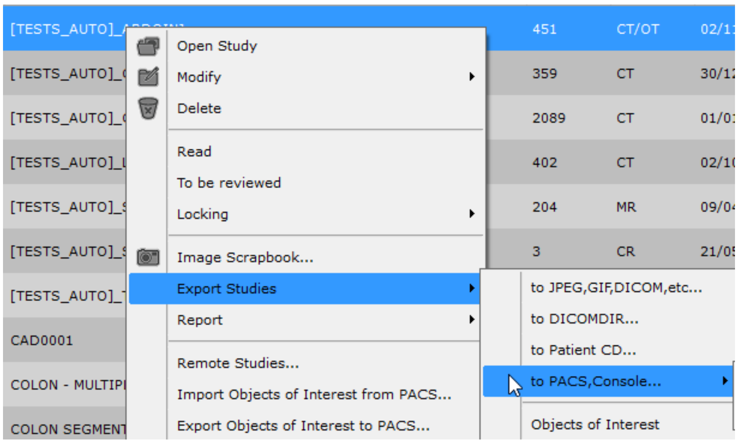


The “Visibility Level” of the ROI you wish to export must be set to any number greater than ‘0’ to be able to be exported. This is achieved by right-clicking on the light bulb icon at left of the listed ROI and selecting the desired visibility level from the resulting slider

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

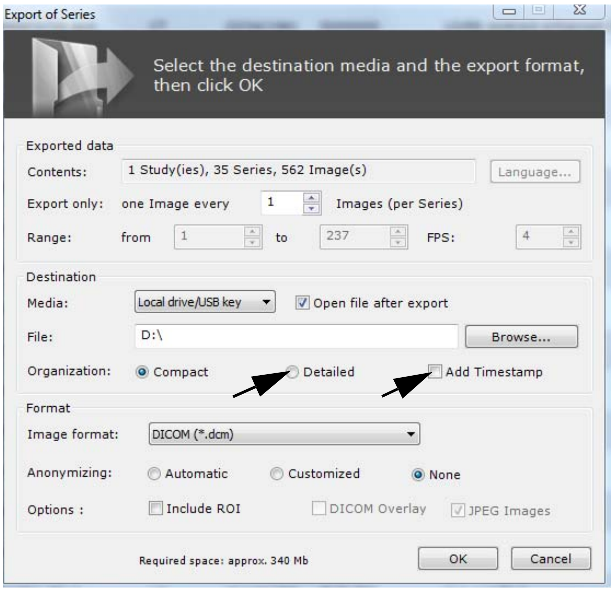
---

The new Series can be exported to a PACS, external drive, etc. via the right-click menu on the corresponding Series



16.6 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.**



Exported data
Contents: 1 Study(ies), 35 Series, 562 Image(s)
Export only: one Image every 1 Images (per Series)
Range: from 1 to 237 FPS: 4

Destination
Media: Local drive/USB key ☑ Open file after export
File: D:\
Organization: ● Compact ○ Detailed ☐ Add Timestamp

Format
Image format: DICOM (*.dcm)
Anonymizing: ○ Automatic ○ Customized ● None
Options : ☐ Include ROI ☐ DICOM Overlay ☑ JPEG Images

Required space: approx. 340 Mb

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

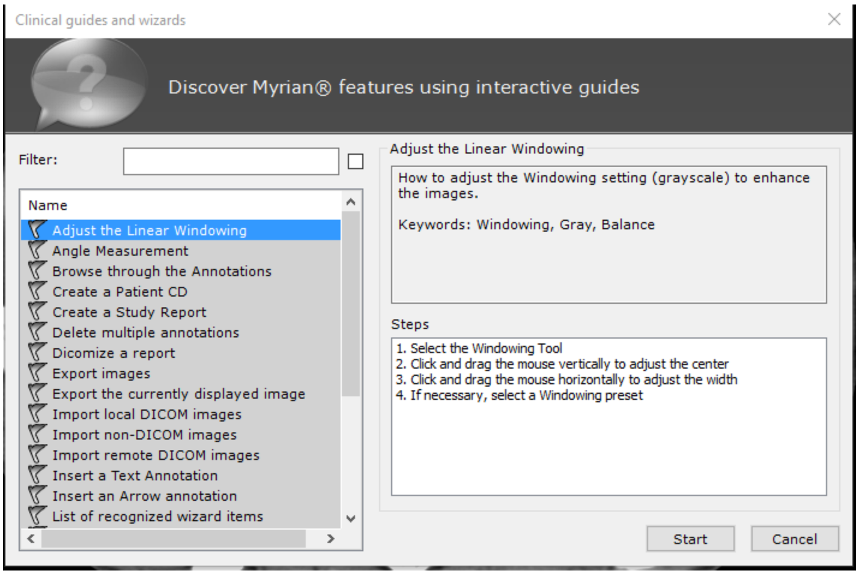
You can choose to add exportation date in the export folder name by ticking the box **Add Timestamp.**

Please note that flying over Compact, Detailed and Add Timestamp will automatically display the information specific to that item.

---

17 Interactive guides and tutorials

- Click on at the bottom-left of the screen to open a list of Clinical Guides and Wizards
- Click on the tutorial of your choice in the **left-hand column**



- Adjust the Linear Windowing
- Angle Measurement
- Browse through the Annotations
- Create a Patient CD
- Create a Study Report
- Delete multiple annotations
- Dicomize a report
- Export images
- Export the currently displayed image
- Import local DICOM images
- Import non-DICOM images
- Import remote DICOM images
- Insert a Text Annotation
- Insert an Arrow annotation
- List of recognized wizard items

Adjust the Linear Windowing

How to adjust the Windowing setting (grayscale) to enhance the images.

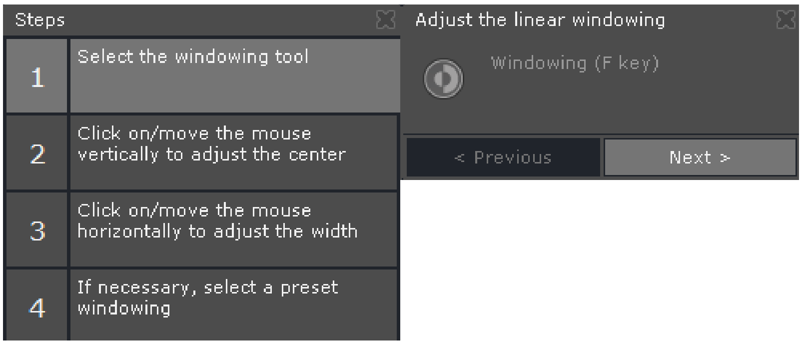
Keywords: Windowing, Gray, Balance

Steps

1. Select the Windowing Tool
2. Click and drag the mouse vertically to adjust the center
3. Click and drag the mouse horizontally to adjust the width
4. If necessary, select a Windowing preset

- Click on Start

The corresponding Step-By-Step guide will then appear:



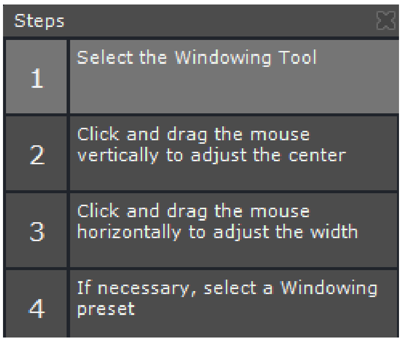
1 Select the windowing tool

2 Click on/move the mouse vertically to adjust the center

3 Click on/move the mouse horizontally to adjust the width

4 If necessary, select a preset windowing

- Follow each step (displayed on the left)



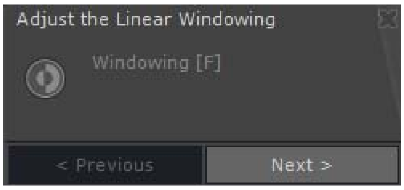
1 Select the Windowing Tool

2 Click and drag the mouse vertically to adjust the center

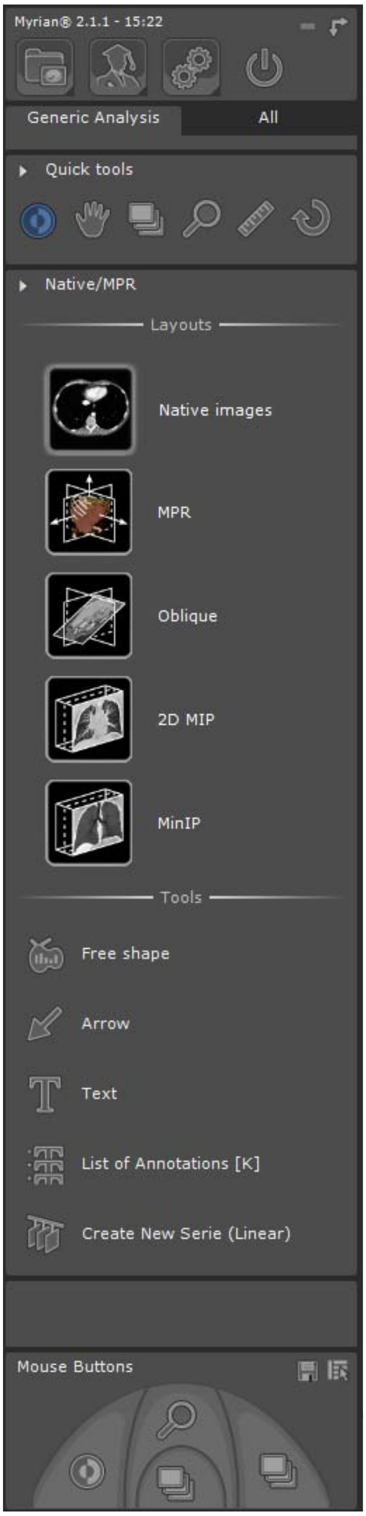
3 Click and drag the mouse horizontally to adjust the width

4 If necessary, select a Windowing preset

A tooltip on the right gives further explanation to the step



Each corresponding tool icon in the application itself will start to **flash** until you have moved on to the next step



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