Version 4.98

June 2025

TELEMIS-MEDICAL

Reference Manual

TERMS AND CONDITIONS

Notice

The following Terms and Conditions are an abstract of the Customer Software License and Maintenance Agreement signed between TELEMIS and the Client (as specified in the Agreement referred hereto). By using the Software, the Users are fully bound with the entire Customer Software License and Maintenance Agreement. Key points of this entire Agreement have been selected hereunder. For more information about the Customer Software License and Maintenance Agreement, a full version is made available for the Users at the Client site. "This Agreement" in the text hereunder referred to the entire Customer Software License and Maintenance Agreement.

Undertakings of the Client

Under this Agreement the Client undertakes:

(a) not to copy (other than for normal System operation and as specified in the Agreement), reproduce, reconfigure, decompile, disassemble, decrypt, translate, adapt, vary or modify the Software and the accompanying documentation nor to communicate the same to any third party;

(b) not to re-install the Software as a whole or a part of it (Software Module(s)) with a back-up copy. This could be the case, for example (but is not limited to this example) if for whatever reason, the Software as a whole or a part of it (Software Module(s)), has been erased from the System(s). This also could be the case if the System (where the Software Module is running on) has been accidentally destroyed. In such situations, (but is not limited to those ones) this re-installation of the erased or destroyed Software or the part of It, must absolutely be done by TELEMIS Engineers or TELEMIS authorized technicians.

(c) to maintain accurate and up-to-date records of the number and Location of all copies of the Software;

(d) to supervise and control Use of the Software in accordance with the terms of this Agreement. This shall include daily back-up precautions relating to the Use of the Software and to the data that are transferred with the Software.

This shall also include the managing of the Identification Key referred in this Agreement (incorporated in an identification medium) in accordance with typical professional practices and in respect of the legal obligation on privacy and confidentiality of medical data of the Country, for which TELEMIS cannot bear any liability. Each owner of an Identification Key is directly responsible for the Use of his/her Identification Key and for the Use of the Software associated with his/her Identification Key. In case of loss of his/her Identification Key, he shall immediately take contact with TELEMIS.

(e) to reproduce and include the copyright notice of TELEMIS on all and any copies, whether in whole or in part, in any form, including partial copies of modifications of the Software made herein;

(f) not to provide or otherwise make available the Software in whole or in part (including but not limited to program listings, object and source program listings, object code and source code), in any form to any person other than the Client's employees without prior written consent from TELEMIS;

(g) within fourteen (14) days after the date of termination or discontinuance of this Agreement for whatever reason (other than with respect to Maintenance only), to return or destroy (as TELEMIS shall instruct) the Software and all copies, in whole and in part, in any form including partial copies of modifications of the Software received from TELEMIS or made in connection with this Agreement and all documentation relating thereto and to furnish TELEMIS with a certificate, certifying that the same has been done, unless the Client has obtained the TELEMIS' prior written authorization to retain one copy for archive purposes only.

Patents, trademarks, copyright and intellectual property rights

(a) The Client acknowledges that any and all of the trade marks, trade names, copyrights, patents and other intellectual property rights used or embodied in or in connection with the Software or its Maintenance shall be and remain the sole property of TELEMIS or such other party as may be identified therein or thereon.

TELEMIS warrants and represents that it has acquired the necessary rights and authorizations to license the Software to the Client and that, to the best of Its knowledge, nothing in the Software nor in the trade marks or trade names is infringing upon any third party intellectual property rights.

(b) In the event that new inventions, designs or processes evolve in performance of or as a result of this Agreement, the Client acknowledges the same shall be the property of TELEMIS unless otherwise agreed in writing by TELEMIS.

(c) The Client shall indemnify Telemis fully against all liabilities, costs and expenses resulting from any infringement of third party intellectual property rights or privacy rights as a result of the Client's inappropriate Use of the Software.

Indemnity

The Client undertakes that TELEMIS or the Owner shall be given prompt notice of any claim, claim of infringements of patents, trade marks, industrial designs, copyrights or other property rights affecting the Software that is made against the Client. Or the Owner shall have the right to defend any such claims and make settlements thereof at its own discretion and the Client shall give such assistance as TELEMIS or the Owner may reasonably require to settle or oppose any such claims.

Confidential Information

(a) All information, data, drawings, specifications, documentation, software listings, source or object code which TELEMIS may have imparted and may from time to time impart to the Client relating to the Software or Maintenance thereof is proprietary and confidential. The Client hereby agrees that it shall Use the same solely in accordance with the provisions of this Agreement and that it shall not at any time during or after expiry or termination of this Agreement (in whole or with respect to Maintenance only), disclose the same, whether directly or indirectly, to any third party without TELEMIS prior written consent.

(b) The Client further agrees that it shall not itself or through any subsidiary, agent or third party modify, vary, enhance, copy, sell, lease, license, sub-license or otherwise deal with the Software or any part or parts or variations, modifications, copies, releases, versions or enhancements thereof or any supporting software or have any software or other program written or developed for it based on any confidential information supplied to it by TELEMIS.

Severability

In the event that any of the terms, conditions or provisions contained in this Agreement shall be determined invalid, unlawful or unenforceable to any extent, such term, condition or provision shall be severed from the remaining terms, conditions and provisions which shall continue to be valid to the fullest extent permitted by law.

Law

The parties hereby agree that the Agreement concluded between them and constituted on these Terms and Conditions shall be construed in accordance with Laws applicable in Belgium.

In the event of a dispute arising out or in connection with this Agreement and which cannot be settled in an amicable way, it will be submitted to the Courts of Brussels, Belgium.

Precautions regarding interpretation

Please note that the accuracy of calculations relating to distances, volumes and other physical properties conducted by the Telemis work station is dependent on the accuracy of the information supplied in the DICOM input images. It is the responsibility of the operator to ensure that these DICOM input images are correctly formatted and to adhere to all warnings displayed by the software during operation with regard to potential problems with the information supplied in these DICOM images.

Please note that in some cases, while there may be problems or inconsistencies in the DICOM information, Telemis will not be able to detect this, and erroneous images will be displayed as an unavoidable consequence, unless the user can properly ensure the accuracy of all the input data in advance. The types of problem that may be encountered with regard to errors in the DICOM information include in particular: inaccuracy in displaying of dimensions, orientation references or the calibration of pixel values. It is an important responsibility of the operator to ensure that the correct visualisation is achieved and that a complete review of the data has been carried out before any diagnosis or interpretive conclusion has been formulated in regard to the data set in question. The limits (such as those relating to spatial and potentially temporal resolution, pixel size and cutting width) of the initial input data persist through the processing of the data by Telemis. These restrictions must be taken into consideration when the equipment is used to view images. All the results must be validated by qualified doctors trained in the subject.

Telemis products provide tools and protocols that make it possible to quantify the measurements and distances relating to the structures on the screens or images acquired on CT or on RM and that are based on anatomic dimensions scanned or captured at the moment that the images are acquired from the patient and on the basis of settings defined by the acquisition tool. The convenience of these measures for a particular purpose, whatever it may be, in particular for monitoring or studying the progression of an illness, or classification by size or planning of a device to be implanted in the patient, depends on a number of factors including, but not limited to, the precision of the initial entry, the degree to which the images entered still reflect the anatomy of the patient and the manner in which the deployment of the actual device may change the anatomy to which it is introduced. Telemis reiterates that its products do not necessarily meet these aims. All of these activities should be cross-referenced with analyses based on other techniques so the doctor or doctors involved have an overall understanding of the patient and the procedure envisaged.

Intended Use and Purpose

Telemis-Medical is a Medical Image Management software package of the type PACS (Picture Archiving Communication System) designed to perform required functions for the import, storage, archive, distribution, review, analysis of digital medical images in DICOM and other formats.

Intended users of *Telemis-Medical* are divided into two distinct user profiles:

1. Healthcare professionals : This includes radiologists, anatomical pathologists, physicians, and medical technicians. These users possess medical education and use the software for its intended medical purposes, such as diagnosis, image review, and analysis.
2. Laypersons : This includes medical secretaries and assistants. Because they do not possess formal medical education in a relevant field, they are considered laypersons. Their use of the system is strictly restricted to administrative workflows. They are not intended, nor permitted, to use the diagnostic or clinical features of *Telemis-Medical*.

The prerequisites for using the device are basic computer usage. Training is provided by Telemis Application Engineers during installation phase or upon installation of each software major release. Training can also be provided directly by other trained users.

It is suitable for all patients and conditions.

Intended Patient population

Telemis-Medical is suitable for all patients and conditions.
No patients were involved during the entire analysis.
The device does not contact the patient, nor does it control any life sustaining devices.
There is no interaction with the human body whatsoever.

Indications and contraindications

Telemis-Medical allows healthcare institutions to manage their medical digital imaging and assists them in the move towards a filmless environment. *Telemis-Medical* line provides modular and scalable PACS solutions that will integrate into any existing healthcare information system software such as RIS, HIS and EPR.

Telemis-Medical product line includes a broad range of integrated clinical solutions for areas such as for orthopedics, cardiology, dermatology, breast imaging, oncology, radiotherapy, nuclear medicine, operating rooms, anatomopathology - in short, all hospital departments that manage medical images - meeting the unique requirements and specialized needs of today’s physicians.
The list is not exhaustive.

There are neither contraindications nor restrictions to the use of *Telemis-Medical*.

Hardware requirements, security, installation and maintenance

Hardware requirements are discussed and validated with the IT department upfront in the installation of *Telemis-Medical*. The requirements for new versions are discussed before upgrades.

Security requirements are discussed and validated with the IT department upfront in the installation of *Telemis-Medical*. *Telemis-Medical* employs a set of security measures to protect against unauthorized access and ensure safe operation, including User Authentication and Identity Management, Role-Based Access Control (RBAC), Data Encryption and Cryptography, Traceability and Auditing, Advanced Protection for Sensitive Data.

Installation is carried out by Telemis team, to ensure correctness and safety. Installation is validated by a delivery slip.

Regarding safety, the software itself, while running, doesn’t need periodic or preventive maintenance, nor periodic calibration. Nevertheless, preventive maintenance tools are integrated to validate the smooth operation.

Clinical benefits of *Telemis-Medical*

- Easier interpretation and comparison of studies
- Faster and more accurate diagnosis for patients
- Immediate access from any location to comprehensive images and reports
- Enhanced patient safety through process automation
- Facilitation of timely remote peer consultation
- Fewer patient exam delays
- Improved patient/physician satisfaction

Performance and Accuracy

Performance of *Telemis-Medical* is defined through image display and measurement tools. All tools are validated prior to release via Metrology testing against a reference database of standard DICOM images with known reference measures.

Acceptable level of precision have be defined by our CMO:

- Distance 1,5%
- Angle 1°
- Surface 3,5%
- Hounsfield density 2%
- SDNR 10%
- ROI 2% (mean)
- SUV 4%
- Volume 4,5%

Residual risks

Risk control measures are taken throughout development, testing, release, installation processes. It is a continuous iterative process throughout the entire lifecycle of *Telemis-Medical*. The severity of harm and the probability of occurrence of residual risks is deemed acceptable when weighed against the clinical benefits.

As also stated in the license agreement, all results, protocols, measurements made using *Telemis-Medical* must always be validated at the end by qualified and trained doctors and will be cross-analyzed based on other techniques so that the concerned physician(s) have a comprehensive understanding of the patient's health.

Incident Reporting

If a serious incident occurs in relation to *Telemis-Medical*, such as incoherent measurements or display, you must report it to the manufacturer and to the National Competent Authority of the country where you reside. List of national authorities can be found at at:

https://health.ec.europa.eu/medical-devices-sector/new-regulations/contacts_en

TABLE OF CONTENTS

1. THE BROWSER

The Browser of the *TM-Reception* is the main window of the application. Snapshots of the browser are given in Figure 1 to Figure 3 next page.

Through the browser, you can display a list of all the patients that you have studies realized and a list of all the studies and series for each patient. For each series (or *multimedia document*), the browser displays information about the document and a "preview" image.

The browser is divided into several areas:

- The top area is a toolbar that contains the buttons giving quick access to some important functions.
- The search area (described in section 1.4 page) proposes all the tools needed to search for a patient or a study.
- The lists display three levels of information (see section 1.3 page):
- the patients level contains a list of the patients and some details about their studies;
- the studies level contains a list of all the studies available for the selected patients and specific details about each study (the series constituting the study).
- the series level contains a list of all the series available for the selected studies, specific details about each series and a preview image for the series.
- The information area contains a line of text describing what the Telemis program is currently doing, the current selection and a progress bar showing the advance of the task.

The user can customize the list's display and the search tools via the use of the option panel described in section 1.15 page .

Sections 1.1 and 1.2 explain how to start and connect the *TM-Reception* application with the server.

Section 1.3 describes the content of the different lists and associated details and the management of the lists: select patient, select studies ….

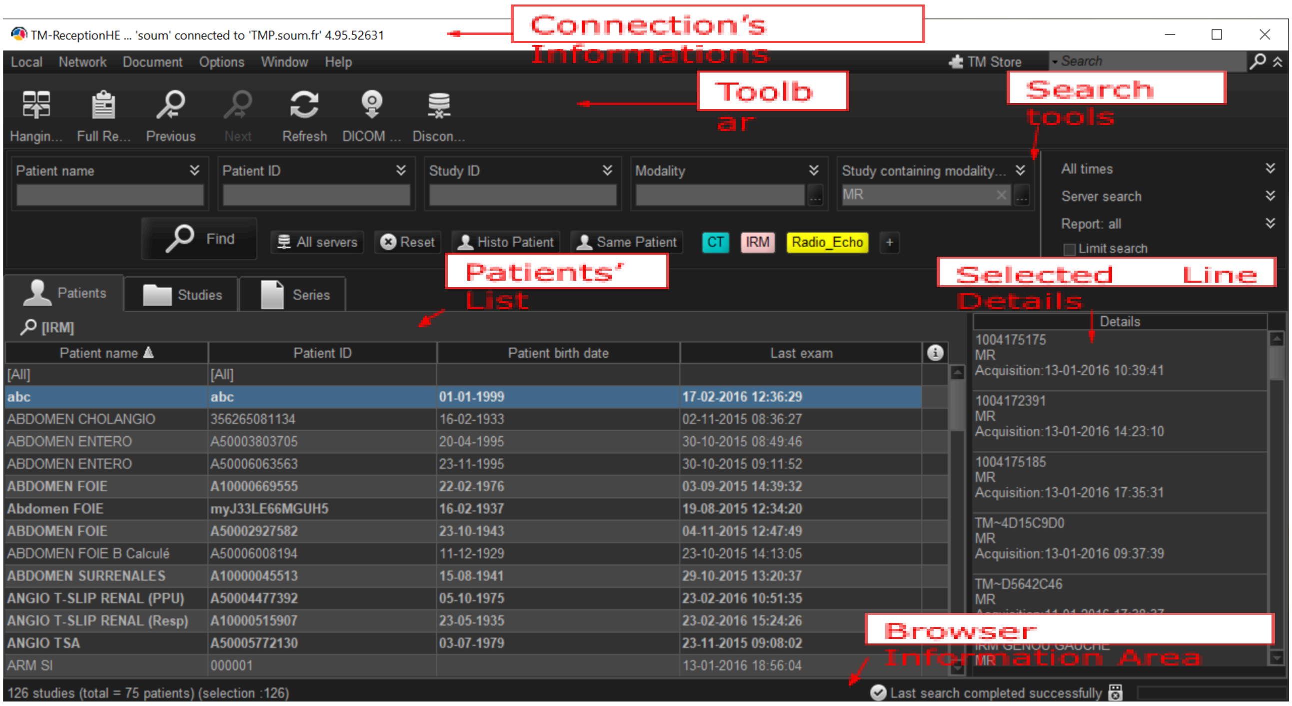
Section 1.4 shows everything about searching the server or the local database for specific patients or studies.

Section 1.5 focuses on opening, saving, deleting … studies.

Section 1.5.17 groups the other commands of the *TM-Reception* Browser: refresh lists, connect to another server… and section 0 groups the commands for the management of the viewers.

Sections 1.10 to 1.12 explain how to create documents and to build a CD-Rom with the content of studies.

Section 1.13 explains how to query and retrieve images from an external DICOM archive.



[IRM]

Patient name	Patient ID	Patient birth date	Last exam
[All]	[All]		
abc	abc	01-01-1999	17-02-2016 12:36:29
ABDOMEN CHOLANGIO	356265081134	16-02-1933	02-11-2015 08:36:27
ABDOMEN ENTERO	A50003803705	20-04-1995	30-10-2015 08:49:46
ABDOMEN ENTERO	A50006063563	23-11-1995	30-10-2015 09:11:52
ABDOMEN FOIE	A10000669555	22-02-1976	03-09-2015 14:39:32
Abdomen FOIE	myJ33LE66MGUH5	16-02-1937	19-08-2015 12:34:20
ABDOMEN FOIE	A50002927582	23-10-1943	04-11-2015 12:47:49
ABDOMEN FOIE B Calculé	A50006008194	11-12-1929	23-10-2015 14:13:05
ABDOMEN SURRENALES	A10000045513	15-08-1941	29-10-2015 13:20:37
ANGIO T-SLIP RENAL (PPU)	A50004477392	05-10-1975	23-02-2016 10:51:35
ANGIO T-SLIP RENAL (Resp)	A10000515907	23-05-1935	23-02-2016 15:24:26
ANGIO TSA	A50005772130	03-07-1979	23-11-2015 09:08:02
ARM SI	000001		13-01-2016 18:56:04

Details

1004175175
MR
Acquisition:13-01-2016 10:39:41

1004172391
MR
Acquisition:13-01-2016 14:23:10

1004175185
MR
Acquisition:13-01-2016 17:35:31

TM~4D15C9D0
MR
Acquisition:13-01-2016 09:37:39

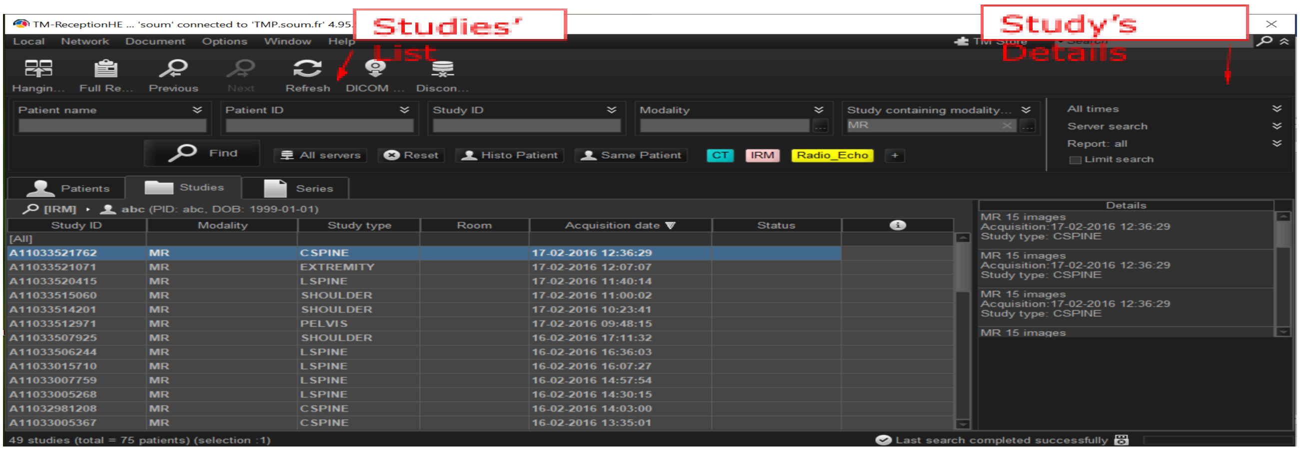
TM~D5642C46
MR

IRM GENOU GAUCHE
MR

126 studies (total = 75 patients) (selection :126)

Last search completed successfully

Figure 1 - TM-Reception browser, 'All patients'



[IRM] ▸ abc (PID: abc, DOB: 1999-01-01)

Study ID	Modality	Study type	Room	Acquisition date	Status
[All]					
A11033521762	MR	CSPINE		17-02-2016 12:36:29	
A11033521071	MR	EXTREMITY		17-02-2016 12:07:07	
A11033520415	MR	LSPINE		17-02-2016 11:40:14	
A11033515060	MR	SHOULDER		17-02-2016 11:00:02	
A11033514201	MR	SHOULDER		17-02-2016 10:23:41	
A11033512971	MR	PELVIS		17-02-2016 09:48:15	
A11033507925	MR	SHOULDER		16-02-2016 17:11:32	
A11033506244	MR	LSPINE		16-02-2016 16:36:03	
A11033015710	MR	LSPINE		16-02-2016 16:07:27	
A11033007759	MR	LSPINE		16-02-2016 14:57:54	
A11033005268	MR	LSPINE		16-02-2016 14:30:15	
A11032981208	MR	CSPINE		16-02-2016 14:03:00	
A11033005367	MR	CSPINE		16-02-2016 13:35:01	

Details

MR 15 images
Acquisition:17-02-2016 12:36:29
Study type: CSPINE

MR 15 images
Acquisition:17-02-2016 12:36:29
Study type: CSPINE

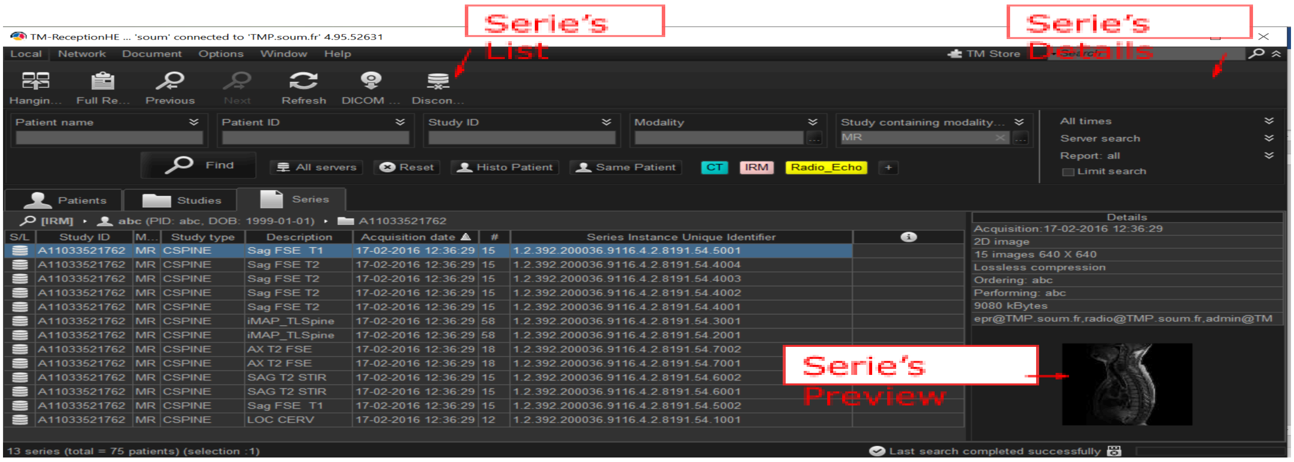
MR 15 images
Acquisition:17-02-2016 12:36:29
Study type: CSPINE

MR 15 images

49 studies (total = 75 patients) (selection :1)

Last search completed successfully

Figure 2 - TM-Reception browser, 'Studies'



[IRM] ▸ abc (PID: abc, DOB: 1999-01-01) ▸ A11033521762

S/L	Study ID	M...	Study type	Description	Acquisition date	#	Series Instance Unique Identifier
	A11033521762	MR	CSPINE	Sag FSE T1	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.5001
	A11033521762	MR	CSPINE	Sag FSE T2	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.4004
	A11033521762	MR	CSPINE	Sag FSE T2	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.4003
	A11033521762	MR	CSPINE	Sag FSE T2	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.4002
	A11033521762	MR	CSPINE	Sag FSE T2	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.4001
	A11033521762	MR	CSPINE	iMAP_TLSpine	17-02-2016 12:36:29	58	1.2.392.200036.9116.4.2.8191.54.3001
	A11033521762	MR	CSPINE	iMAP_TLSpine	17-02-2016 12:36:29	58	1.2.392.200036.9116.4.2.8191.54.2001
	A11033521762	MR	CSPINE	AX T2 FSE	17-02-2016 12:36:29	18	1.2.392.200036.9116.4.2.8191.54.7002
	A11033521762	MR	CSPINE	AX T2 FSE	17-02-2016 12:36:29	18	1.2.392.200036.9116.4.2.8191.54.7001
	A11033521762	MR	CSPINE	SAG T2 STIR	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.6002
	A11033521762	MR	CSPINE	SAG T2 STIR	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.6001
	A11033521762	MR	CSPINE	Sag FSE T1	17-02-2016 12:36:29	15	1.2.392.200036.9116.4.2.8191.54.5002
	A11033521762	MR	CSPINE	LOC CERV	17-02-2016 12:36:29	12	1.2.392.200036.9116.4.2.8191.54.1001

Details

Acquisition:17-02-2016 12:36:29
2D image
15 images 640 X 640
Lossless compression
Ordering: abc
Performing: abc
9080 kBytes
epr@TMP.soum.fr,radio@TMP.soum.fr,admin@TM

13 series (total = 75 patients) (selection :1)

Last search completed successfully

Figure 3 - TM-Reception browser, 'Series'

1.1. Start/Close the application

√ To start the *TM-Reception*, double-click on the *TM-Reception* icon (see Figure 4) on your desktop.

The *TM-Reception* browser appears on your screen after a few seconds.

Figure 4 - TM-Reception icon

√ To close the *TM-Reception*, Select [*Local*] □ [*Exit*] (click on the menu called *Local* and select the *Exit* line of the menu).

Or, click on the cross located at the top right of the browser.

1.2. Connection

1.1.1. Local/Network documents

The *TM-Reception* application is the interface between the user and the documents. It acts as a document manager, more or less the same way that your file manager (or file explorer) acts on your files.

Documents contain the results of studies. These documents are physically located on the server, which means on the network. They are not necessarily physically located on the computer you are presently using.

The advantage of this technique is that you can access your documents from any computer where the *TM-Reception* software is installed once you are connected to the server. Your documents follow you.

Passing through the network for every access can be rather slow (even if the downloading is optimized with the Telemis software). That is the reason why each time you access a document, it is in fact temporarily saved on your computer in a special directory called the 'cache directory' (see section 1.8.5 page for more details). This directory is only for temporary storage and is periodically cleaned. Anyway, the existence of this directory means that when a Telemis program works with a document, the local presence of this document guarantees an efficient work. Another advantage appears if you want to visualize a document that you have already visualised recently: the access is instantaneous because it is already on your computer.

If you definitely want to keep a document on your computer, you can save (see section 1.5.8 page) it on one of your disks. This copy of the original document is now permanently resident on your computer. This means that the disk space management becomes now your responsibility but that the access to this document is immediate, whether you are connected or not.

When the application starts, only local documents are available. Connect to the network (see section 1.2.2) and give your login, password to have access to the network resources.

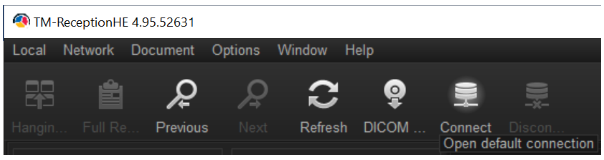
After you have accessed once to all the documents you need, you may close the connection.

1.1.2. Connect

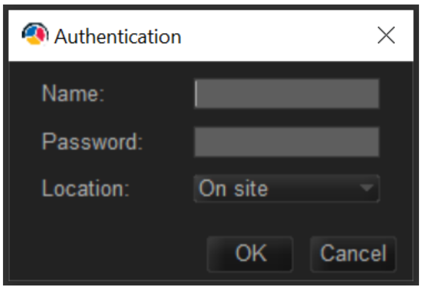
This command connects the *TM-Reception* software to the registered Telemis Server (*TM-Server*), i.e. the default server for this *TM-Reception*.

To trigger the command:

- √ Select [*Network*] □ [*Open default connection*] (click on the menu called *Network* and select the *Open default connection* line of the menu)
- √ Or, click on the "Connect" icon located on the toolbar of the browser.
- √ Or, Perform any search (see section 1.4 page).



The connection process is a negotiation between your software and the *TM-Server*. The program prompts to enter your login and password (Figure 5). If the authentication succeeds, the connection with the server is operational and you have access to the information available to you on the server.



Location: On site

Figure 5 - Login and password

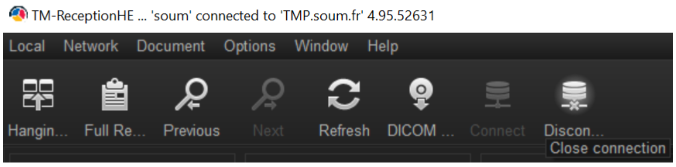
If your computer doesn't connect to the network via a permanent physical connection, the Telemis software won't automatically start your physical connection. If for example you connect to the network via a modem or a VPN, you must manually start this connection to enable the *TM-Reception* to connect.

1.1.3. Disconnect

This command disconnects the *TM-Reception* software from the *TM-Server*.

To trigger the command:

- √ Click on the icon located on the toolbar of the browser



- √ Or, select [*Network*] □ [*Close connection*].

Once disconnected, you can only access the local files.

If your computer connects to the network via a modem or VPN, you should manually close the connection after disconnecting the *TM-Reception*.

1.1.4. Automatic upgrade

For each connection to the server, the *TM-Reception(HE)* and *TM-Home* will automatically compare their version number to the last version number available at the server.

If these numbers differ, the automatic upgrade of the *TM-Reception(HE)* or *TM-Home* to the new version will take place. You have nothing to do, except wait a few seconds and restart your application to automatically benefit from the latest version of the software[1].

1.3. The lists

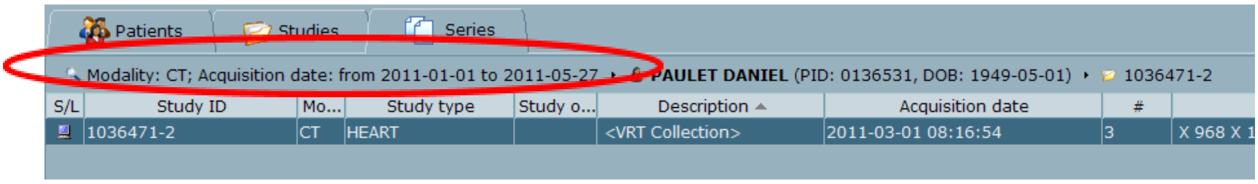
The browser list area displays three levels of information. This section focuses on the description of the content of the lists and on the management of the lists (sort, select, switch …).

At start-up, the browser presents a list of the patients that have studies available for you on the *TM-Server*.

If you select one or several patients, you can switch to a view presenting all the studies available to these patients.

1.1.5. List heading

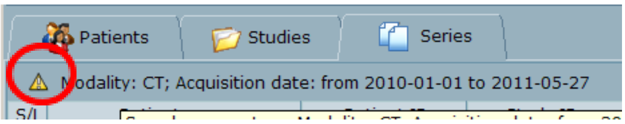
The parameters used to perform the search are always displayed next to the selection. Even if the user changes the content of the search fields, the original search fields value that led to the result are always visible.



Modality: CT; Acquisition date: from 2011-01-01 to 2011-05-27 ▸ **PAULET DANIEL** (PID: 0136531, DOB: 1949-05-01) ▸ 1036471-2

S/L	Study ID	Mo...	Study type	Study o...	Description ▲	Acquisition date	#	
	1036471-2	CT	HEART		<VRT Collection>	2011-03-01 08:16:54	3	X 968 X 1

If the search results have been limited (the TMRHE only shows the more recent elements if too much results available on the server), a warning icon is displayed instead of the search icon:



⚠ Modality: CT; Acquisition date: from 2010-01-01 to 2011-05-27

If the size of the window is too small to display completely the search parameters, they are replaced by "…". Move the mouse on this text line to show the complete information.

1.1.6. Basic operations

Each time the mouse passes on a cell of the list, a small text box appears, a "tool tip", giving you a complete text description of the information that wouldn't fit into the available column width or giving the textual meaning of a logo.

---

[1] This option is only available if your hospital has subscribed to the upgrade maintenance package.

1.1.6.1. Sort columns

In either list,

√ If you want to sort alphabetically a column, click on the header of the column.

√ If you want to sort reverse-alphabetically a column, click on the header of the column while pressing the 'Shift' key.

√ If you want to set a second sort criterion on a second column, click on the header of the second column while pressing the 'Ctrl' key (combine with 'Shift' for a reverse sort).

1.1.6.2. Resize columns

√ Click on the line separating two column headers, drag the mouse left or right and release the button to resize the left column.

√ It is possible to change the width of the details area (the panel at the right of the lists) by clicking on the thick dotted line between the list and the details, dragging this line left or right and releasing the mouse button.

1.1.6.3. Select lines

√ *To select one line* in any of the lists, click with the left button of the mouse on the line.

Once a line is selected, you can select the previous or next one by pressing the 'cursor up' and 'cursor down' keys.

There are two ways to perform *multiple selections*:

√ Hold the "Shift" key pressed and click with the left button of the mouse to add to the selection this line and all the lines that are between this one and the previously selected one.

√ Hold the control ('Ctrl') key pressed and click on a line with the left button of the mouse to add this line to the selection.

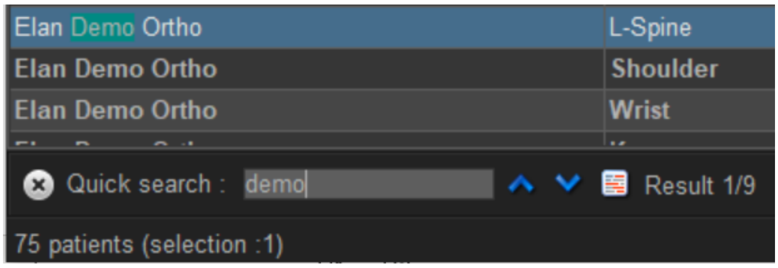
1.1.6.4. Quick search

To perform a quick search on the content of one of the cells of the shown list,

√ Press the 'Ctrl' and 'F' keys. The quick search line appears at the bottom of the lists.

Figure 6a - Quick search

Type in the text box a few characters.



Elan Demo Ortho	L-Spine
Elan Demo Ortho	Shoulder
Elan Demo Ortho	Wrist

Quick search : demo

Result 1/9

75 patients (selection :1)

Figure 7b - Quick search

The first occurrence of the searched text is highlighted in green and the cursor goes to this line. Press the up ▲ and down ▼ arrows to move the cursor to the previous / next occurrence.

Press the ☰ button to highlight in yellow all the occurrences of the text.

Press the red cross ✖ to close the quick search panel.

1.1.6.5. Copy / Paste information from the lists

Right click on any cell of one of the lists, select [*Copy*] □ [*Copy cell*] to copy the content of this cell to the clipboard. You can paste it in any other application.

Right click on any cell of one of the the lists, select [*Copy*] □ [*Copy table*] to copy the content of the whole list to the clipboard.

Select some lines of a list and select [*Copy*] □ [*Copy selection*] to copy the content of your selection to the clipboard.

1.1.7. “Patients” list

1.1.7.1. Content

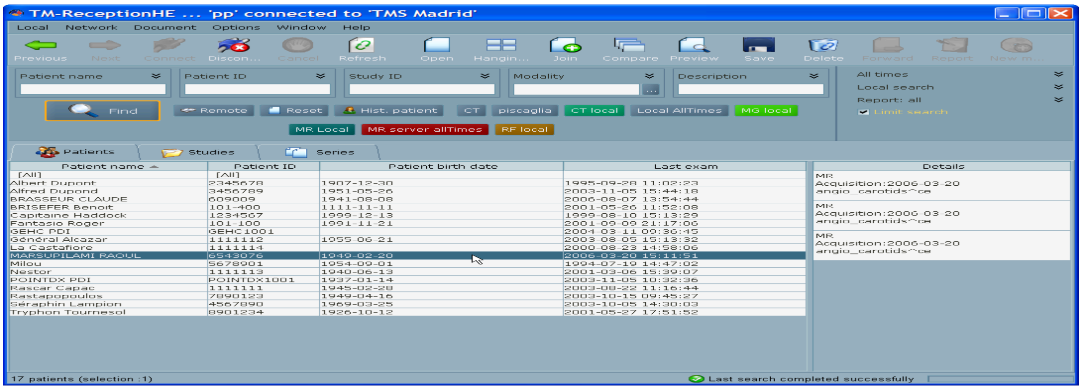
The ‘Patients’ list shown on Figure 8 typically presents four columns: the patient name, the patient hospital identification number, the patient birth date and the date of the last examination done on this patient.

A patient line is displayed in bold faced characters if there are unread studies for this patient.

If you click on one line of the list, the ‘details’ box on the right of the browser shows a few details about the studies available for this patient. There is one cell for each study, each cell containing typically the modality, the acquisition date, the body part … All the information displayed in the cells and the content of the details are customizable and the list of values displayable is shown in section 1.3.5.1.1 page .

There are two special patients:

- “All”: selecting this patient is the same as selecting all the patients of the list;
- “No Name”: this patient name is used when the document has no patient name information associated;



Patient name	Patient ID	Patient birth date	Last exam
[All]	[All]		
Albert Dupont	2345678	1907-12-30	1995-09-28 11:02:23
Alfred Dupond	3456789	1951-05-26	2003-11-05 15:44:18
BRASSEUR CLAUDE	609009	1941-08-08	2006-08-07 13:54:44
BRISEFER Benoit	101-400	1111-11-11	2001-05-26 11:52:08
Capitaine Haddock	1234567	1999-12-13	1999-08-10 15:13:29
Fantasio Roger	101-100	1991-11-21	2001-09-09 21:17:06
GEHC PDI	GEHC1001		2004-03-11 09:36:45
Général Alcazar	1111112	1955-06-21	2003-08-05 15:13:32
La Castafiore	1111114		2000-08-23 14:58:06
MARSUPILAMI RAOUL	6543076	1949-02-20	2006-03-20 15:11:51
Milou	5678901	1954-09-01	1994-07-19 14:47:02
Nestor	1111113	1940-06-13	2001-03-06 15:39:07
POINTDX PDI	POINTDX1001	1937-01-14	2003-11-05 10:32:36
Rascar Capac	1111111	1945-02-28	2003-08-22 11:16:44
Rastapopoulos	7890123	1949-04-16	2003-10-15 09:45:27
Séraphin Lampion	4567890	1969-03-25	2003-10-05 14:30:03
Tryphon Tournesol	8901234	1926-10-12	2001-05-27 17:51:52

Details

MR
Acquisition:2006-03-20
angio_carotids^ce

MR
Acquisition:2006-03-20
angio_carotids^ce

MR
Acquisition:2006-03-20
angio_carotids^ce

17 patients (selection :1)

Last search completed successfully

Figure 8 - 'All patients' list and details

The information line at the bottom of the browser shows the total number of patients returned by the last query and display in the list, and the number of selected patients.

1.1.7.2. Display patient/studies details

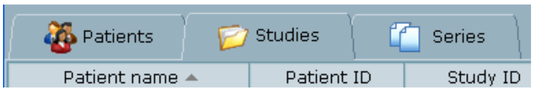
When you click on a line of the patients list, the details show a brief description of the list of studies available for this patient.

To switch to the 'Studies' list and view details about the studies of a selected Patient (from the Patient View), you can double-click on a line of the patients list.

If one or more patients are selected:

√ Press the 'Enter' or 'Cursor right' or 'Tab' keys to switch to the studies list for those patients

√ Click on the 'Studies' tab.



To switch to the 'Series' list for one of the study displayed in the details, double-click on this study in the details of the patient.

1.1.8. Studies list

1.1.8.1. Content

The list shown on Figure 2 page 7 presents two different faces according to the number of patients selected: one or more than one.

The 'Studies' list presents one line for each study.

If you click on one line of the list, the 'details' box on the right of the browser shows additional details about the selected study, i.e. about the different series constituting the selected study(ies). There is one cell for each series, each cell containing typically the modality, the number of images, the acquisition date and time, the body part … All the information displayed in the cells and the content of the details are customizable and the list of values displayable is shown in section 1.3.5.1.1 page 5.

The information line at the bottom of the browser shows the number of studies currently displayed in the list, the total number of patients returned by the last query and the number of studies selected.

1.1.8.1.1. One patient selected

If only one patient is selected, the patient information (name, hospital ID and birth date) is summarized on a line above the list itself. This leaves more place in the list for information about the studies.

Each column of the list presents information about the studies.

The column content, width and position are customizable (see section 1.16.1 page for instructions).

1.1.8.1.2. Several patients selected

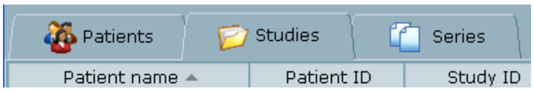
If several patients are selected, patient information is not a constant and must be displayed in the columns.

The content of the columns is different than in the 'one patient' case but the list of values displayable is the same.

1.1.8.2. Study selection

Once one or more studies are selected, to switch to the series list for those studies:

√ Click on the 'Series' tab



Or

√ Press the 'Cursor right', 'Tab' or 'Enter' keys.

To go back to the 'Patients' view:

√ Click on the 'Patients' tab

Or

√ Press the 'Cursor left' or the 'Backspace' key (the deletion key located above the 'Enter' key)

To open a study into the image viewer, either select some series in the series view, or see section 1.5 page .

1.1.8.3. Details

The details area is located on the bottom right of the browser.

When the browser displays a list of the studies for one patient or for several patients, the details area shows a summary of each series of the selected study.

The content of the details is customizable, and the list of values displayable is the same as the list showed in section 1.3.5.1.1 page .

Double-click on one line of the details to directly open a viewer on this series.

1.1.9. Series list

1.1.9.1. Content

This list shown on Figure 3 page presents two different faces according to the number of studies selected: one or more than one.

The 'Series' list presents one line for each series.

If you click on one line of the list, the 'details' box on the right of the browser shows additional details about the selected series, together with a small image proposing a first quick glance at the series.

The information line at the bottom of the browser shows the number of series currently displayed in the list, the total number of patients returned by the last query and the number of series selected.

1.1.9.1.1. One study selected

If only one study is selected, the study information (patient name, hospital ID and birth date, study identification (accession number)) is summarized on a line above the list itself. This leaves more place in the list for information about the series.

Each column of the list presents information about the series. The column content, width and position are customizable. See section 1.16.1 page for instructions.

The possible items are:

- **Creation date**: this is the date when the document has entered the *TM-Server*. This date will normally be quite similar to the study acquisition date, except if the hospital has a PACS or a modality that can re-send old studies to the Telemis system;
- **Element type**: the element type is currently "text" or "Set of 2D images";
- **Acquisition date**: the date when the acquisition machine realized the study of the patient;
- **Patient name**: the patient first and last names;
- **Patient ID**: the patient identification, internal to the hospital;
- Patient birth date;
- Patient sex;
- Other patient ID: a second identification for the patient, such as the national number.
- **Study ID**: the identification of the study internal to the hospital;
- **Ordering physician**: the doctor who requested the examination;
- **Performing physician**: the physician who will perform diagnostic tests: the radiologist who will make the diagnosis…;
- **Compression**: the kind of compression used for the study: lossless compression, multi-resolution lossless compression, lossy compression. See section 1.5.1 page for details about the compression schemes.
- **Modality**: the modality of the study: CT scan, CR (Conventional Radiography), XA (angiography), MR (magnetic resonance) …;
- **Study type**: a first field describing the study: typically "Thorax", "Foot", "Head" …;
- **Study orientation**: a second field describing the study: orientation, sub-description …;
- **Room**: room where the acquisition device is located, in order to distinguish between the 3 CT-scanners of the hospital;

- **Site**: site where the acquisition device is located. Especially useful for multi-sites installations;
- **Technician** operating the acquisition device;
- **Manufacturer Model:** acquisition device model name;
- **Images size**: this field gives the number of images and the size of each image. It will for example display "29 images 1024 X 1024" showing that the study is made up with 29 images, each image being 1024 points wide and 1024 points high.
- **Study size (kBytes)**: this field gives the size of the study is kBytes. This gives an idea of the transfer time between the server and your program. For example, on an ISDN modem line at 128 kbits/sec (for e.g. a Telemis-Home), 1000 kBytes will need more or less one minute to be totally transferred from the server to your computer. On the internal network of the hospital, only a few seconds will only be needed to transfer these 1000 kBytes.
- **Recipients**: the list of all the Telemis users who have access to this study;
- **S/L**: "Server/Local" document. This field is represented by a small logo:
- : the document is on the server and must be downloaded (transferred) by the *TM-Reception*;
- : the document is located on the server but there is a local copy in the temporary 'cache' directory (see section 1.8.5 page): the document has already been transferred by the *TM-Reception* and will open faster than a purely server located document;
- : the document is a purely local document, saved in your local database. There is a priori no copy of this document on the server.
- : the document has been stored on the server but is not available anymore, probably because the server has a limited storage space and the document is too old.
- : the document is not present on the main server, but is available on another server. It will be accessed as if it was on the main server; this server transparently requests the document for you to the remote server.
- : the document is not present anymore on the local disks of the server but an archived copy is still available, on a DVD jukebox for example. Its retrieval will be transparent for the user but slightly slower.
- **State**: the state of a document has currently two values: "read" or "unread"; A 'read' document has already been opened by you or somebody else using the same login.
- **Description**: this field contains additional description that couldn't fit in any other field;
- **Study Description**: the DICOM description applying to the whole study;
- **Series Description**: the DICOM description applying to the specific series;
- **Study Instance Unique Identifier**: the DICOM unique identifier for this study;
- **Series Instance Unique Identifier**: the DICOM unique identifier for this series;
- **Document internal ID**: this information will normally never be shown because it has no interest for the user;
- **Extended element type:** one item displaying the modality and the number of images, as for example "CT 175 images";
- **Report status:** no report done, report assigned to somebody ( ), report in progress ( ), report done ( ), report done with comments ( );
- **Report doctor:** the doctor that will do or has done the report;

- **Report date:** the date when the report status was last modified in Telemis;
- **Report comment:** a small text comment possibly encoded when setting the report to “Done”;
- **Report status summary:** report status and name of the reporter. The tool tip displays the comment and the report date.
- **Publication status:** is there a medium produced by the *TM-Publisher* for this document?
- ✉ : a green envelope means that a medium has been successfully produced for this document
- ✉ : a red envelope means that an error occurred when trying to produce a medium for this document
- No logo: no medium produced.
- **Label:** label associated with the series;
- **Pathology:** pathology code associated with the series.

1.1.9.1.2. Several studies selected

If several studies are selected, study information is not a constant and must be displayed in the columns. The content of the columns is different than in the ‘one study’ case but the list of values displayable is the same as the one showed in previous section.

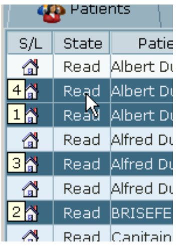
1.1.9.2. Series selection

The series selection follows the rules defined in section 1.3.1 page : use click, double-click, shift-click or ctrl-click to select one or several studies in the list. When the Ctrl key is pressed, the content of the details view (details and preview image) changes as the mouse moves along the different lines, easing the selection of multiple lines.

To open a series into the image viewer, see section 1.5 page .

If multiple series are selected, series will be opened or joined in the same order as they have been selected.

If the series are not selected in the top-to-bottom order, a number is displayed at the left of the line to show the index of this series in the selection.



S/L	State	Patie
	Read	Albert Du
4	Read	Albert Du
1	Read	Albert Du
	Read	Alfred Du
3	Read	Alfred Du
	Read	Alfred Du
2	Read	BRISEFE
	Read	Capitain

1.1.9.3. Details

The details area is located on the bottom right of the browser.

When the browser displays a list of the series for one study or for several studies, the details area shows for the selected series the details that are not available in the list.

The content of the details is customisable and the list of values displayable is the same as the list showed in section 1.3.5.1.1 page .

1.1.9.4. Image preview

The details area accompanying the ‘Studies’ list automatically shows a small image of the “main” image[2] of the series, to allow a very quick preview of the study.

1.4. Search tools

The best way to easily access one given patient or study is to directly search for it. The search tools box contains 5 input areas allowing you to type requests and several options to customise the search.

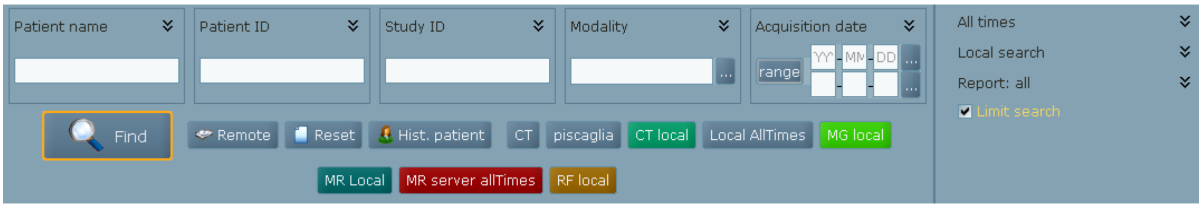


Figure 9 - Search tools

1.1.10. Search fields

The search tools allow to type up to 5 requests and to combine them to search for a precise study or patient.

√ For each field, click on the drop box (the ‘title’ (“Patient name”, “Patient ID” etc.) of each box, or the double vertical arrow) and select the kind of request that you want to set. The default value for the search fields can be personalized as shown in section 1.16.2.3 page .

√ According to the kind of request, one or two white text boxes appear below the field name. Type the text in these text boxes.

All the queries are case insensitive, i.e. searching for “DUPONT” has the same effect as searching for “Dupont”.

The propositions are the following.

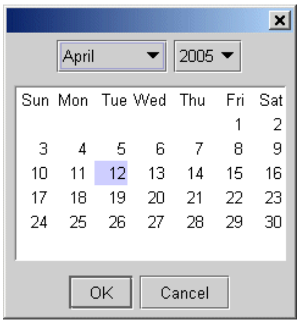
- **Patient name**: search for the name of the patient. Type in the text box the name of the patient that you are looking for, or a part of the name. You can use wildcards to specify that you have only typed a part of the name: use “*” to mean “any number of any characters” and “?” to mean “one character but I don't know which”. In the default configuration, the ending '*' is always added by the computer. For example, use “Dupo” to find “Dupont”, “Dupond”, “Dupol”, but use "*Dupo" to find "Redupont" … You can configure your search tools so that the *TM-Reception* will automatically use wildcards (see section 1.16.2.3 page). With this option set, typing “Winch” will find either “Winch Largo”, “Largo Winch”, “Winch”, “Winch L.” but the global search speed will be slower …
- **Patient ID**: search for the identification of the patient internal to the hospital. You can use wildcards. In the default configuration, no '*' is automatically added by the computer. Typing "12345" will not retrieve "123456". You must manually type the '*'.
- **Patient birth date**: search for the birth date of the patient.
- Select the kind of date search: before the white text box(es), the symbol “=” means search for a given date, [From] means search for all dates posterior to this date, [To] searches for

---

[2] The “main” image of a series is configurable for each modality on the Telemis image acquisition side. The main image can be the first image, the middle image or the last image of the series.

all dates anterior to this date, and [Range] shows two white text lines, searching for dates since the first date (included) until the second date (excluded). Click on this button to change the value.

- For each date, the first box contains the year (4 digits), the second box contains the month (2 digits between '1' and '12') and the third box contains the day (2 digits starting at '1'). Month and day boxes may remain empty. For example, typing '2001' in the first box, '11' in the second and leaving the third empty will select all patients born in November 2001. If you just type "2001", patients born in 2001 will be selected. Using "01" instead of "2001", "63" instead of "1963" will also work. You may also click on the box '...' at the right of the 'day' box to choose a date from a small calendar, as show on Figure 10.



Sun	Mon	Tue	Wed	Thu	Fri	Sat
					1	2
3	4	5	6	7	8	9
10	11	12	13	14	15	16
17	18	19	20	21	22	23
24	25	26	27	28	29	30

Figure 10 - Search tools - date calendar

- **Patient sex**: click on the [...] button located at the right of the search field to select the patient sex to search for: Male, Female or Other/Unknown.
- **Other patient ID**: search on an additional patient identification, if provided by the hospital. The additional patient identification is typically the national number.
- **Acquisition date**: search for the date and time when the acquisition machine realised the study on the patient. This field follows exactly the same rules as the patient birth date.
- **Study ID**: search for the identification of the study internal to the hospital (also called the accession number). You can use wildcards. In the default configuration, no '*' is automatically added by the computer. Typing "12345" will not retrieve "123456". You must manually type the '*'.
- **Study description**: The study description as set by the modality. You can use wildcards.
- **Series description**: The series description as set by the modality. You can use wildcards.
- **Description**: Additional description of the studies. You can use wildcards.
- **Study type**: search for the type of study: typically "Thorax", "Foot", "Head" ... You can use wildcards.
- **Study orientation**: search for the study orientation or sub-body part. You can use wildcards.
- **Ord. Physician**: search for studies required by a specific ordering physician. You can use wildcards.
- **Perf. physician**: search for studies related to a specific performing physician. You can use wildcards.
- **Modality**: search for studies from a specific modality (CT scan, CR (Conventional Radiography), XA (angiography), MR (magnetic resonance) ...). You can use wildcards. In the default configuration, no '*' is automatically added by the computer. Typing "C" will not retrieve "CR". You must manually type the '*'. The modality text box also lets you the possibility to select one of the pre-typed modalities. Click on the arrow at the right of the modality text box and select an item in the list (ex: MR – Magnetic Resonance). Only the series of this modality will be returned.

- **Study containing modality(ies)**: search for studies having at least one series of a given modality. Example: type in 'PT' (or select PT – Positron emission tomography in the '…' button) to search for all the studies having at least one series 'PT'. Not only the 'PT' series will be returned but all the series of this study, including the 'CT' in case of PT-CT modality and all the series of other modalities belonging to this study (SR, SC etc.)
-
- **Room:** enter the name of the room where the study has been performed. This field has generally a meaning if the hospital possesses several devices of the same modality. There are then the CT-scanner located in "room 1" or in "room 2". The search field will automatically propose the list of rooms present in the database.
- **Site:** for multi-sites installation, this field allows searching for studies acquired on one given site. The search field will automatically propose the list of sites present in the database.
- **Technician:** if the acquisition device allows encoding the name of the physician using it, this field contains this name.
- **Manufacturer Model:** the technical model name of the acquisition device, as specified by the manufacturer.
- **Report doctor**: search for studies with a report done by or assigned to a doctor containing the given text in their name.
- **Report date**: search for studies with a report done on a specific date, before or after a specific date. Use the three text boxes as described in the acquisition date.
- **Report comment**: search for studies with a report comment containing the given text.
- **Document status**: specific document status can be defined, for example *TBARC* (to be archived), *NARCH* (not archived), *ARCHG* (archiving) or *ARCHD* (archived). This search criterion is dedicated to expert users.
- **Label**: click on the […] button located at the right of the search field to select one of the 'favorite' labels or press the [*Select …*] menu option to select other labels. You can also directly type the label names in the search text field.
- **Pathology**: Click on the 'Select pathology classification ' button to select the kind of classicifation to use. Click on the […] button to select on pathology in the classification tree.

Be careful that the use of wildcards (* and ?) slows down the search.

Tip: in most of the search fields, it's possible to request the server to return results corresponding to one value or another one, separating the values with the "\" character. Example: enter in the modality search field "CT\PT" to receive the list of all the modalities equaling PT or CT.

1.1.11. Single search field

The single search functionality allows executing a quick search on multiple criteria. It can be displayed on two different places depending on the platform used and the configuration parameters.

On windows, it appears in the menu bar as shown in Figure 11.a.

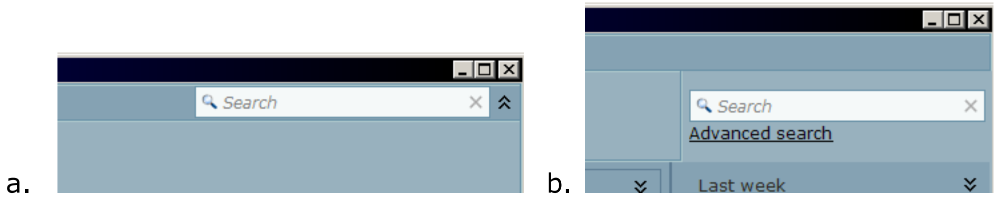


Figure 11 – Single search field

On Mac platform, it can appear either in the menu bar if visible or in the tool bar depending on your configuration (Figure 11.b).

By default the 5 "advanced" search parameters are hidden when the single search field is visible. They can be made visible (or hidden) by using the following buttons:

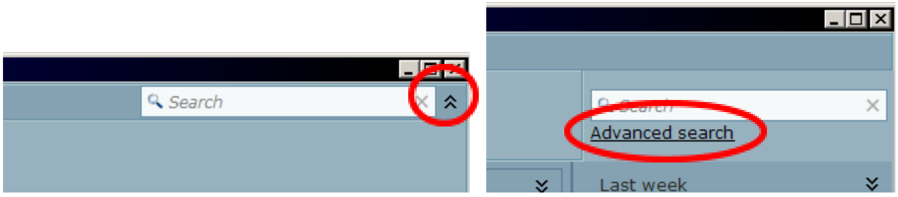


Figure 12 – Fold / unfold advanced search

When hidden only the search presets are displayed.

The "X" in the field can be used the clear the field content. It will not impact the search result list.

The single search is independent of the standard search functionality.

By clicking on the search icon, the list of search criteria on which the search will be executed can be selected, as shown in Figure 13.

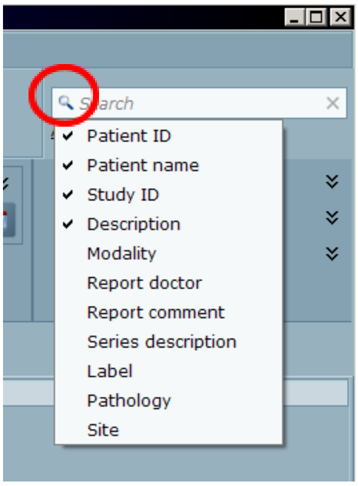


Figure 13 – Search config on-the-fly

Note: This list can be customized.

The search request will try to find all records for which any of the selected field contains the entered search value. The way the search value will be interpreted depends on the criteria in the same way as for the normal search. For example, searching on the description will do a search on "*search_value*" while searching on the patient name will do a search on "search_value*".

The quick search uses the following parameters that cannot be changed (see section 1.4.6 page for details):

- Time: All times
- Target: server
- Limit: default value (100)

1.1.12. Advanced Searching

To effectively start the search, you can either

√ press the 'Enter' key, or

√ click on the 'FIND' button on the bottom left of the search tools box.

The *TM-Reception* will then automatically query the *TM-Server* and display in the lists only the patients and studies matching the request.

If the browser displays all the patients, this list is simply updated.

If the browser displays some 'Studies', the list of studies only displays the studies corresponding to the request AND to the patients that are currently selected in the 'Patients' view.

If the browser displays some 'Series', the list of series only displays the series corresponding to the request AND to the patients / studies that are currently selected in the 'Patients' and 'Studies' view.

To display again the whole list, check on the 'RESET' button and then on 'SEARCH'.

1.1.13. Search on remote servers

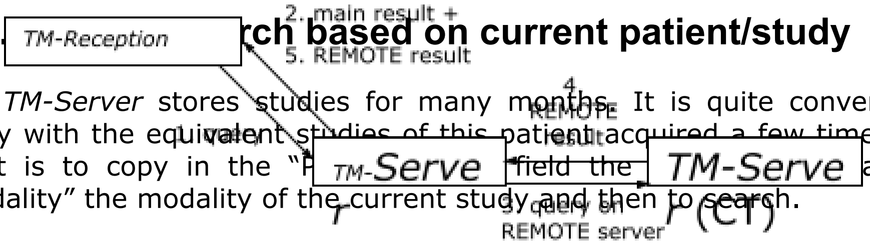
Depending on the configuration of the *Telemis-Medical* system in your hospital, there can be more than one server. There could be for example one server that holds all the CT-Scanner images (let's call it *CT-server*), including thin slices, while the main server only holds thick slices.

If you are connected to the main server looking for the studies of a certain patient, it could be interesting to complete this request, only returning the thick CT-scanner slices, with the thin slices coming from the CT-server.

In such a configuration, after searching on the main server with the 'FIND' button, the 'REMOTE' button located on the right of the 'FIND' button will change from grey colour to black.

√ Click on the 'REMOTE' button to complete the previous request on a server with the other servers of the hospital.

The list will show additional studies, marked as 'remote' (🖥), that you will open using exactly the same technique as if the study came from the main server.



1. rch based on current patient/study

The *TM-Server* stores studies for many months. It is quite convenient to compare this study with the equivalent studies of this patient acquired a few time ago. The first way to do it is to copy in the “P field the atient, to copy in the “Modality” the modality of the current study and then to search.

A more practical way to do this is to simply type "=" in the "Patient name" and "Modality" fields. Searching for "=" means to search for all the studies matching for this criterion the same value as the currently selected patient / study / series value for this field. Typing '=' in the 'Patient name' and 'Modality' fields retrieves all the studies of this patient and of the same modality.

1.1.15. Search options

You can decide the way the server will perform your search.

The default value for these options can be personalized as shown in section 1.16.2.3 page .

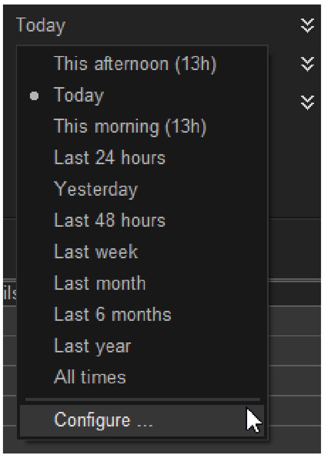
1.1.15.1. Search period

You can restrict the search to a certain time period.

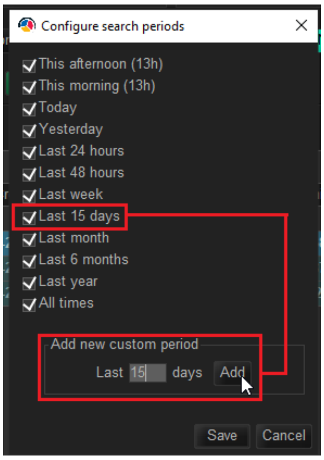
√ Click on the 'Search period' drop box located at the top right of the search tools box and select the appropriate search period.

The different possibilities are "This morning", "This afternoon", "Today", "Yesterday", "Last 24h", "Last 48h", "Last week", "Last month", "Last 6 months", "Last year" or "All times" and you may also create new ones for yourself :

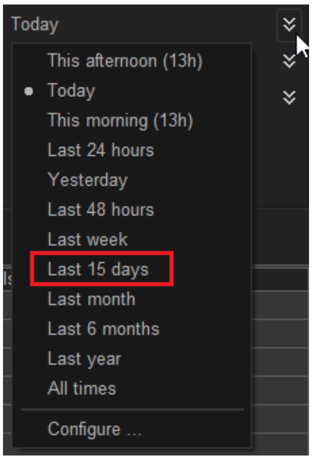
- Click on "configure" in the search period list.



- Choose the numbers of day and click on "add".



- The new period is now available in the list.



Be careful that this option takes the lead on the 'Acquisition date' field: if you ask for an acquisition date older than allowed by the search period, nothing will be returned. Always select an appropriate search period. Example: if today is November 28th, 2006 and if you search for a study having the acquisition date equal to November 2d, 2006, the search period must be at least "Last month". If you search for an acquisition date equal to October 2d, 2006, "Last 6 months" must be selected in the "Search period" field. In case of incoherency, the *TM-Reception* will prompt the user.

1.1.15.2. Search target

You can restrict the search to a certain location.

Some documents are purely local documents (local database, as will be explained in section 1.8.3 page). Most of the documents reside in the *TM-Server*.

√ Click on the 'Search target' drop box located at the bottom of the search tools box and select the appropriate search target.

The different possibilities are "Local documents only", "Server documents only", "Local + Server documents".

1.1.15.3. Report status

You can restrict the search to a certain report status.

√ Click on the 'Report status' drop box located at the bottom of the search tools box and select the appropriate report status.

You can retrieve documents regardless of their report status (select 'all'), only documents that haven't been reported yet by a doctor (select 'no report'), only documents assigned for reporting to a doctor but not reported yet (select 'assigned'), only document currently being reported by a doctor (select 'busy'), or only documents associated with a report (select 'done').

The report itself is not visible inside the *Telemis-Medical* system. Only the report status is available.

1.1.15.4. Number of documents

A search could potentially return a huge number of documents, for example if the search period = "All times" and no field contains text, you will potentially get all the documents of the server!

To prevent this problem, the option "Limit search" is automatically checked. This option limits the number of answers to a maximum of 300 documents. You can uncheck this option but have to keep in mind the potential number of answers that can result.

If this option has really limited the number of retrieved documents, the 'Limit search' text line color changes. Uncheck it to see the full result if you are interested into. Leave the mouse over this line to see the status of the limitation: either "Maximum number of documents retrieved = 800" or "The search result has been truncated to 800 documents".

This number 800 is a parameter. See section 1.16.2.3 to change its value.

1.1.15.5. Reset

√ To reset the search tools box, click on the RESET button.

This will restore the fields' selection, reset the content of the query text boxes and restore the default value of all the search options.

1.1.16. Navigate through history of searches

To fill the search tools with the parameters of the previous searches performed,

- press the "Previous search" button located at the left of the buttons toolbar of the browser, or
- select the [*Network*] [*Previous search*] menu, or
- press the "Alt" key together with the left cursor key

To fill the search tools with the parameters of the next searches performed, once you have navigated into the search history,

- press the "Next search" button located at the left of the buttons toolbar of the browser, or
- select the [*Network*] [*Next search*] menu, or
- press the "Alt" key together with the right cursor key

Once the correct parameters (search fields, search period, content of the text boxes etc.) are displayed in the search panel, press "Find" to perform again a previous search.

1.1.17. Search presets

Search presets are very useful to speed up the search process.

In place of typing "=" in the "Patient name", "CT" in "Modality" and "All times" in the "Search period" each time you want to search for all the CT studies of this patient, clicking on the "Patient CT" button is quite faster.

1.1.17.1. Using search presets

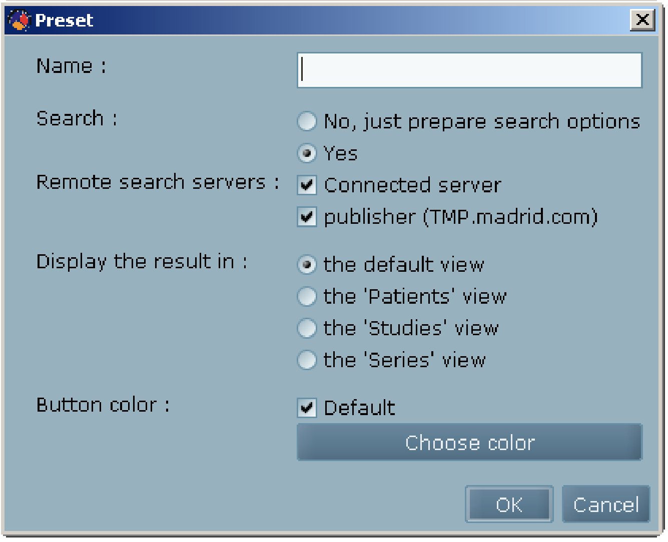
If search presets are defined on your *TM-Reception* software, just click on the search preset button to start the search. The search presets are the buttons containing *italic* text and located at the bottom right of the search tools ("Study", "Patient" and "Patient CT" on Figure 9 page).

1.1.17.2. Creating search presets

To create search presets:

- Enter in the search fields and options the appropriate value: search period, search target, "=" or a specific value in some text fields …
- Select [Options] [Search presets] [Create preset from current options] or press the '+' sign located at the end of the search presets list if the advanced search fields are visible.

- Type in the [Name] text field the name of the preset, as it will appear in the search tools, so make it intelligible with as few characters as possible.



Preset

Name :

Search : ○ No, just prepare search options ● Yes

Remote search servers : ☑ Connected server ☑ publisher (TMP.madrid.com)

Display the result in : ● the default view ○ the 'Patients' view ○ the 'Studies' view ○ the 'Series' view

Button color : ☑ Default

Figure 14 - Creating a search preset

- When the user clicks on the search preset button, the search fields and options are filled with the preset values. The next question lets you set the behaviour of the search preset: either the search will only start when the user will press the "FIND" button , or the search will take place automatically after the filling of the fields and options, or this search will even extend to some remote servers of the hospital, if any. The first option will use the preset to prepare the search and let the user change something before searching. The second option, probably the most often used, takes advantage of the search based on the current patient/study (see section1.4.5) to perform the search in one click.
- Next question let's you decide where the results will be displayed. Either use the default view, i.e. the one currently displayed, or force the browser to switch to the 'patients', 'studies' or 'series' view.
- Last option lets the user change the colour of the preset.
- Press [OK] to conclude the creation of the preset.

1.1.17.3. Deleting search presets

To delete a search presets, either:

- Select [*Options*] [*Search presets*] [*Delete preset …*].
- In the list that is displayed, select the preset to delete and press [OK].

Or

- Right-click on the preset to delete and choose [Delete] from the contextual menu.

1.1.17.4. Modifying a preset

To update a preset, enter in the search fields and options the appropriate value: search period, search target, "=" or a specific value in some text fields and either

- Select [*Options*] [*Search presets*] [*Modify preset with current options*].
- In the list that is displayed, select the preset to modify and press [OK].

Or

- Right-click on the preset to update and choose [*Modify preset with current options*] from the contextual menu.

1.1.17.5. Running a search preset at startup

If, each time that you start the TMR(HE), the first operation that you perform is executing a search preset, then your TMR(HE) can do it automatically for you.

√ Right-click on the given search preset and select [*Execute automatically at startup*] in the context menu.

Uncheck this option to stop executing this preset at startup.

1.5. Documents management

1.1.18. Open document

This section concerns the opening of a document. Under the same name *Open*, two aspects are grouped:

- The downloading of the document from the server to your computer if the document is on the network;
- The opening of the viewer associated with this document and the decompression and display of the images.

To open the studies selected (see section 1.3.4.2 page) in the “**Studies**” list or the series selected (see section 1.3.5.2 page) in the ‘Series’ list,

√ Press the *Enter* key (only in the ‘Series’ list) or

√ Select [Document] [Open document(s)], or

Open

√ Click on the 'Open’ icon.

To open one series displayed in the ‘Series’ list:

√ Double-click on the line of the ‘Series’ list that displays the series to open.

In the ‘Series’ list, only the series selected will open a viewer, in the same order as the selection order (see section 1.3.5.2 page). In the ‘Study’ list, all the series of the selected studies will be opened (this could represent 15 or more series with a Magnetic Resonance (MR) study for example).

To open one series displayed in the detailed view of the “Studies” list, double-click on the description of this series in the details.

These commands download the document(s) and open the appropriate viewer(s).

If you want to open several documents all together, you must select them in the ‘Studies’ or ‘Series’ list and click on the 'Open' icon or press the *Enter* key.

If you want to open only one series, you have three options: either select it in the series list and click on the ‘Open’ icon, or select it and press the *Enter* key, or double-click on the series in the series list.

The progress state is displayed in two “progress bars” and “Information lines” (see Figure 15):

- At the bottom right of the browser is located a first progress bar, that displays the download progress. At the left of this progress bar resides an information line that explains the current task of the *TM-Reception* (e.g. “Downloading elements …”)
- At the bottom right of the viewer is located a second progress bar, that displays the image decompression and display progress. The associated information line explains the current task of the viewer (e.g. “Decompression images …”)

Figure 15 - Progress bar and information line of the viewer

As long as the progress bars haven’t reached 100% and then becomes a light grey box, the computer works in the background (image transmission, decompression …). You can already perform every operation on the viewer and the images as soon as the first image is displayed. The computer will be a bit slower until the progress bar hasn’t reached 100%.

Depending on the way the document is created, the image format can be full image or multi-resolution image. Both formats lead to the same final image quality. They differ in the way the image is transmitted.

- The normal image format sends each image as one piece of data and then displays it. An example of an image sent on a slow network connection (modem …) is given in the following table. The table displays a time line and a snapshot of the viewer 2, 10 and 30 seconds after the ‘Open’ instruction. Only a part of the viewer is shown to make details visible in this manual.

‘Open’ instruction	‘Open’ + 2 sec	‘Open’ + 10 sec	‘Open’+ 30 sec
no image displayed	no image displayed	no image displayed	 Full quality image

Figure 16 - Classical transmission on a slow network (e.g. home connection)

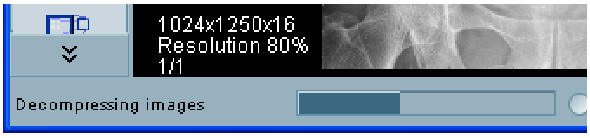
- The multi-resolution image format sends each image progressively. A low quality approximation of the image is sent first. This first quality is transmitted rapidly and displayed immediately. A document containing 20 images displays after a few seconds a first approximation of each image. Progressively, additional quality levels are transmitted, and refine the precision of the images displayed, up to the final full precision. The next table shows the same transmission as above but with the multi-resolution image format.

'Open' instruction	'Open'+ 2 sec	'Open'+ 10 sec	'Open'+ 30 sec
no image displayed	 Low precision image	 Medium precision image	 Full precision image

Figure 17 - Multi-resolution transmission on a slow network (e.g. home connection)

The Telemis multi-resolution image format enables the user to work with the images (zoom, contrast, brightness …) before the full quality is displayed. The working efficiency is increased by the reduction of the waiting time between the 'open' request and the moment when the work on the image can begin.

During the download of a multi-resolution image, the size of the image and the precision are displayed in the lower left corner of each image (see Figure 18). At each new resolution downloaded the image size (and precision) is doubled, up to the full size. The 'resolution XX%' indication disappears when the download is complete.



1024x1250x16
Resolution 80%
1/1

Decompressing images

Figure 18 – Multi-resolution reconstruction state

1.1.19. Join document

The generation of the documents depends on the generation rules that apply in the hospital. Usually, one document corresponds to one series of a study.

If you want to visualise all these images, you will need several viewers. To visualise several documents displayed in the 'Series' list, or all the series of a study displayed in the 'Study' list, in only one viewer, these documents are joined:

- √ Select the documents to join (see section 1.3.5.2 page to select series or 1.3.4.2 page to select a study).
- √ Chose [*Document*] [*Join document(s)*] or
- √ press the '+' key, or
- √ Click on the join icon in the toolbar of the browser.

The browser will load the selected documents, take all the images and display them in one Telemis Viewer.

The documents in the viewer will be sorted using the order in which you clicked on the series to select them (see section 1.3.5.2 page).

1.1.20. Basic comparison

To compare two equivalent series of two studies realised at different dates, show these series in the 'Series' list:

- select the patient (see section 1.3.3 page) and display the studies list;
- if needed, use the appropriate search preset to display the history of this patient (see section 1.4.8.1 page);
- select the two studies (see section 1.3.4.2 page) and display the series list;
- select the two series (see section 1.3.5.2 page).

To open one viewer for each series, displayed optimally on the screen and synchronised,

√ Choose [*Document*] [*Compare document(s)*] or

√ press the 'Alt' and 'C' keys, or

√ Click on the compare icon in the toolbar of the browser.

See section 2.9 page for a full description of the comparison mode.

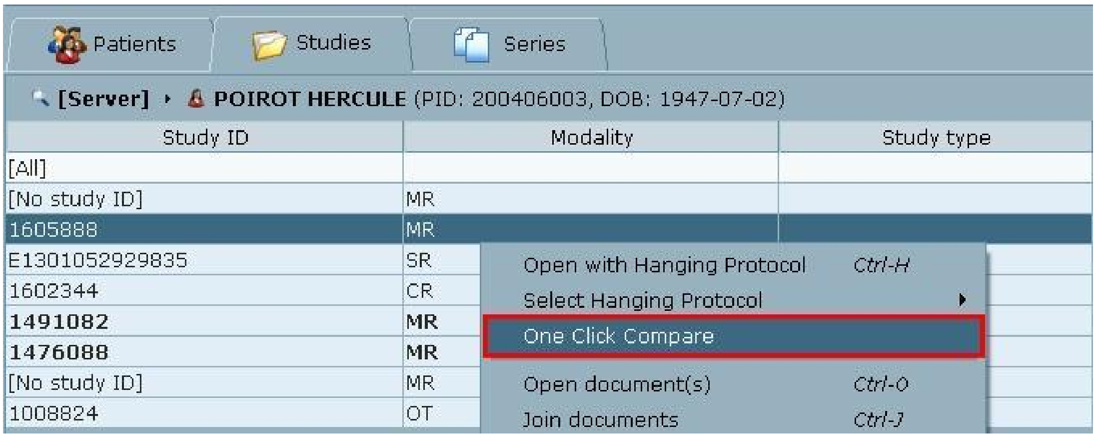
1.1.21. One-click comparison

The 'One click comparison' is a much more evolved comparison system: select one study, select 'One-Click compare' and let the system propose you, for each series, the most appropriate historical series to compare (or select the historical series to compare with).

1.1.21.1. Opening series directly in the 'One-click compare' mode

- select the patient (see section 1.3.3 page) and display the studies list and select a study;

√ Right-click on the study and select in the menu [*One Click Compare*], or



[Server] › **POIROT HERCULE** (PID: 200406003, DOB: 1947-07-02)

Study ID	Modality	Study type
[All]		
[No study ID]	MR	
1605888	MR	
E1301052929835	SR	
1602344	CR	
1491082	**MR**	
1476088	**MR**	
[No study ID]	MR	
1008824	OT	

Figure 19 - Start One-Click Comparison

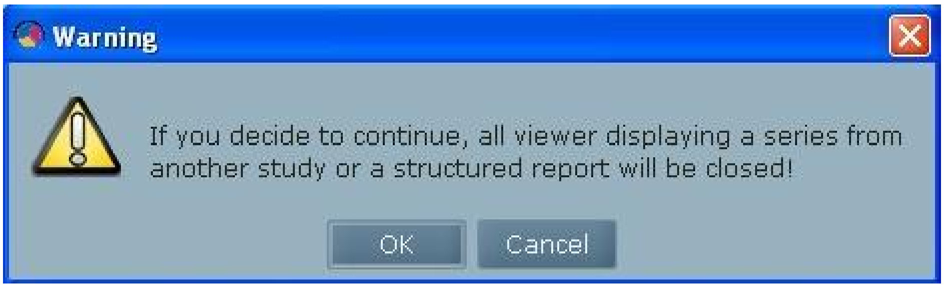
√ Select the menu [Document] [One click compare], or

√ In the toolbar, press the 'One click compare' button .

Attention: the One-Click Comparison is not applicable for non-DICOM data (video, structured report, etc).

The 'One-Click Comparison' mode could be automatically selected when opening a study with a 'hanging protocol' (see 1.5.7 page). Contact your system administrator for the configuration.

When starting a One-Click Comparison, all viewers not suitable for the comparison will be closed (after confirmation): viewers related to another study than the one clicked, or structured reports.



Warning

If you decide to continue, all viewer displaying a series from another study or a structured report will be closed!

1.1.21.2. Selection window

When the One Click Compare mode is enabled, the work space is divided into two sides: current study and historical studies. On the historical side, a Selection window is displayed to allow the user to choose the series/study to compare with (see Figure 20).

The One Click Compare can be used in two modes:

- Many current series from the same study to compare with one history series (single selection mode).
- One current series to compare with many history series (multi selection mode).

√ Press the "Switch to multi selection" / "Switch to single selection" button at the top left of the Selection window to switch mode.

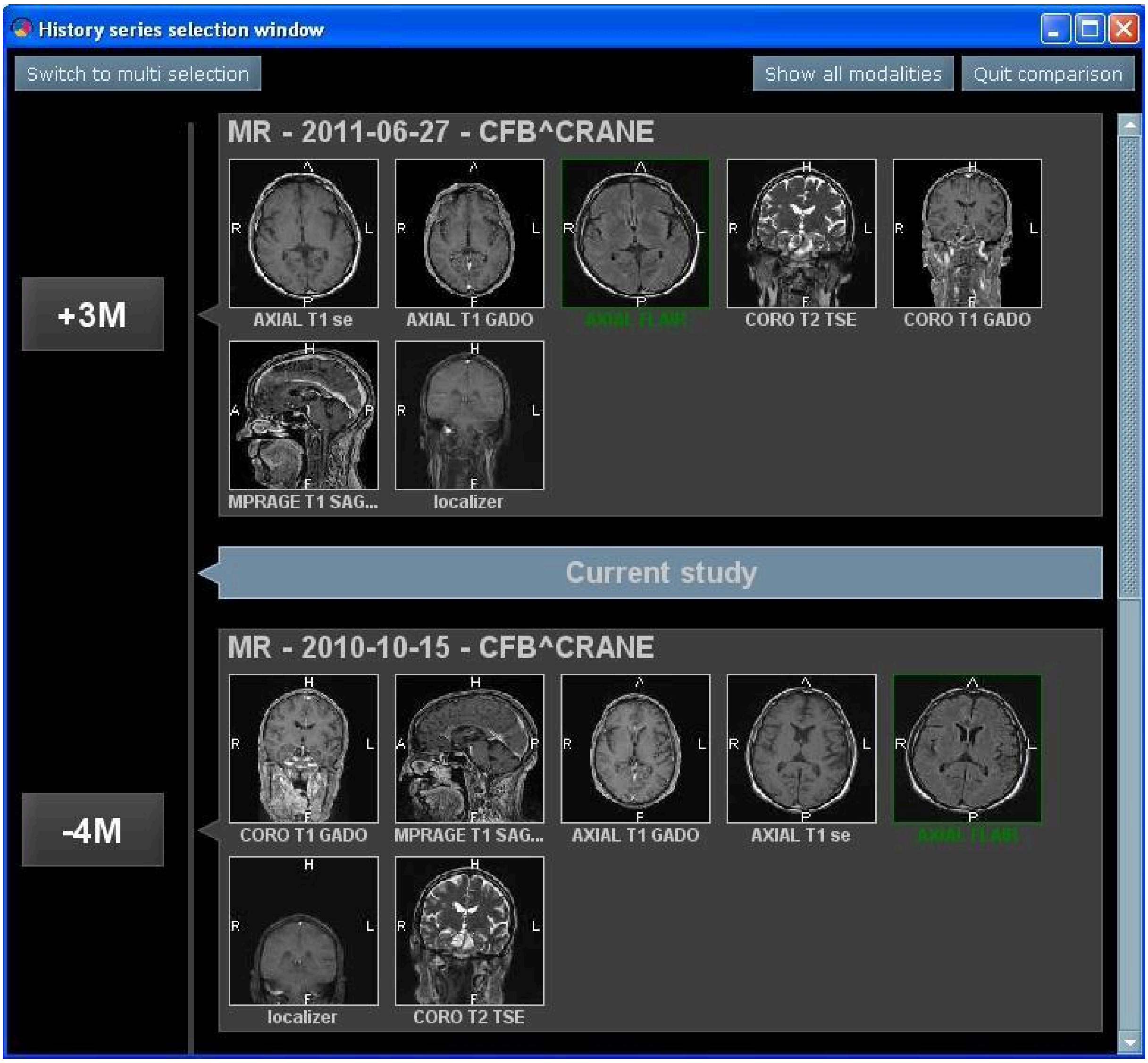
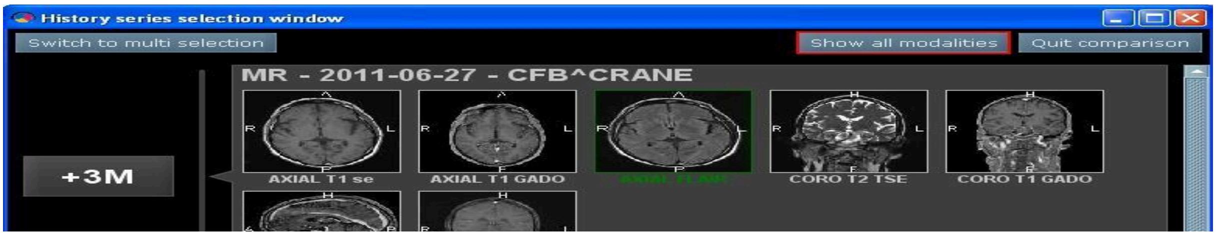
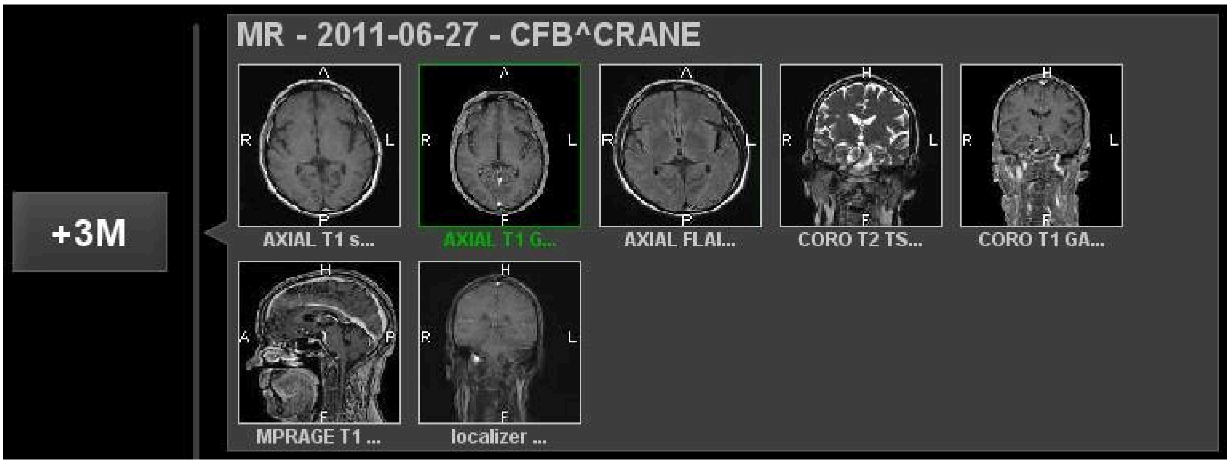


Figure 20 - Selection of the history (One-Click Compare)

By default, only studies containing series of the same modality than the current will be displayed. If the user wants to extend the search to all modalities, he can click on the “Show all modalities” button.



Each horizontal block represents a study with the list of its series.



Between the images and the age button ("+3M", "-4M"), is the time line, sorting the studies (newer on top, older at the bottom). One particular block, called "Current study", represents the position of the current study on this time line.

The age button of the selected study becomes blue.

Each series of the study is represented by a small image plus a short description text shown under the small image. Leave the mouse over the image to view more information about this series.

AXIAL T1 GADO
Number of slices : 61
Acquisition date : 2010-10-15

1.1.21.3. Single selection mode

This mode allows comparing one or many series from the same study with **one** history study. This is the default comparison mode.

1.1.21.3.1. Selection of the historical series

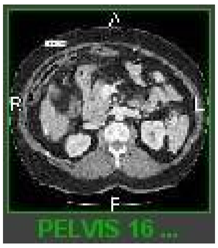
There are 2 ways to assign historical series to the current series:

- Automatically: select the historical study and let the TMRHE (try to) automatically select the most appropriate series. One click will launch the comparison for every opened current series.
- Manually: select an individual series to compare with your series. This operation must be done for each opened series.

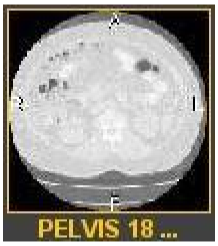
☐ **Automatic selection**

The system will try to automatically compute the best assignation for the historical series using the series description. It will display this information to the user using the border and the font color of the series preview image.

No matching: the system doesn’t consider this historical series as a potential match with the current series.



Perfect matching: the system considers this historical series as perfectly matching the current series.



Multiple matching: the system has found more than one perfect matching for the same history study thus it can’t choose itself what the good choice is.

If there is at least one *perfect matching* in a history study, automatic exam assignation is enabled (the study age button contains white text). If the user clicks on this button, the comparison will immediately start for every current series, selecting automatically the perfectly matching series of the selected historical study.

If a perfect match isn’t found for every opened series, the study age button is disabled (the text is black): there is no automatic selection possible.

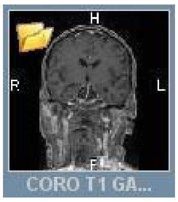
In the example show in Figure 20, both historical studies show a perfect match with the current one, enabling the automatic one-click comparison.

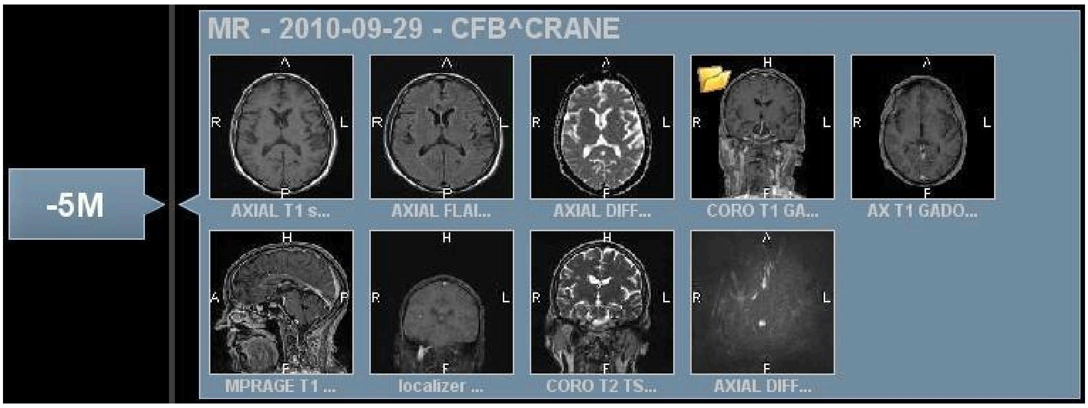
1.1.21.3.2. Manual selection

The user can manually assign a historical series to the current series, for example if there is no perfect matching detected or if there are multiple matching series. Simply click on the preview series image to assign this series to the current series.

As you can compare the current study only with one other study (we are in the single selection mode), if a series of a historical study is selected for another series of the current study, the historical study is de-facto selected for all the remaining viewers of the current study. The age button is shown in blue in this situation.

All the series of the selected historical study, already assigned to another viewer will be marked with a yellow sign at the top left of the preview series image.





You may not select manually a series from another study than the selected history study. If you do so, a message will be displayed to ask if you want to continue, closing all the previously assigned series.

You may not select a series already selected. If you do so, a message will be displayed to ask if you want to continue, closing the previous viewer.

1.1.21.4. Multi selection mode

The goal of this mode is to compare **one** series with several historical series. You can switch to the multi-selection mode:

√ By clicking on the "Switch to multi selection" / "Switch to single selection" button (on the top left corner of the selection window), or

√ By holding the 'Ctrl' key pressed when clicking on a preview series image to select the series.

In this mode, you must select one series in several studies. Once a series in selected, the other series of this study fade, as show in Figure 21).

To unselect a series, click on another series of the study.

Pressing the study selection button (the 'age' button) will select the best matching series, if the system has found one.

When you have selected all the desired series, press the 'Start comparison' button located at the bottom right of the Selection window.

Figure 21 - Multi-selection mode (one-click compare)

1.1.21.5. Switching to another historical study

Once the historical series have been assigned to the current series and the viewers are opened, there is an easy to quickly change the historical study.

√ Press the 'Image oldness' text ('-12M' in the example of Figure 22).

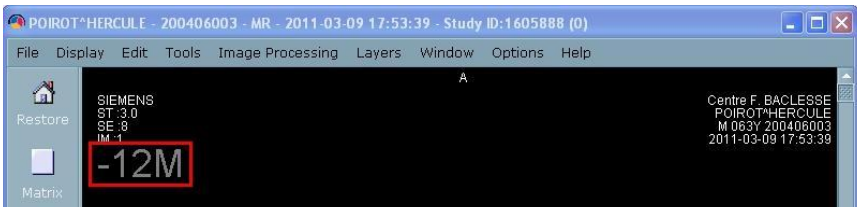


Figure 22 - One Click Compare: switch historical study

All the historical viewers will be closed and replaced by the Selection windows.

1.1.21.6. Quit the One-Click Comparison mode

To quit the One-Click Comparison mode,

√ Close all the opened viewers (see section 2.1 page for closing several viewers in one operation), or

√ In a viewer, uncheck the menu [Display] [One-Click Compare], or

√ Disable the One-Click Compare in the Selection Window, via the ‘Quit Comparison’ button shown at the top left of the window.

1.1.22. Fusion of two series in a viewer

1.1.22.1. Open the fusion

To perform a fusion between two series, ideally perfectly coregistrated, select both series in the browser and

Choose [*Document*] [*Fusion*], or

√ Press the fusion icon in the toolbar, if available

A viewer opens, containing both series (e.g. a CT and a PT acquired by a PET-CT scan) displayed one above the other (see Figure 23).

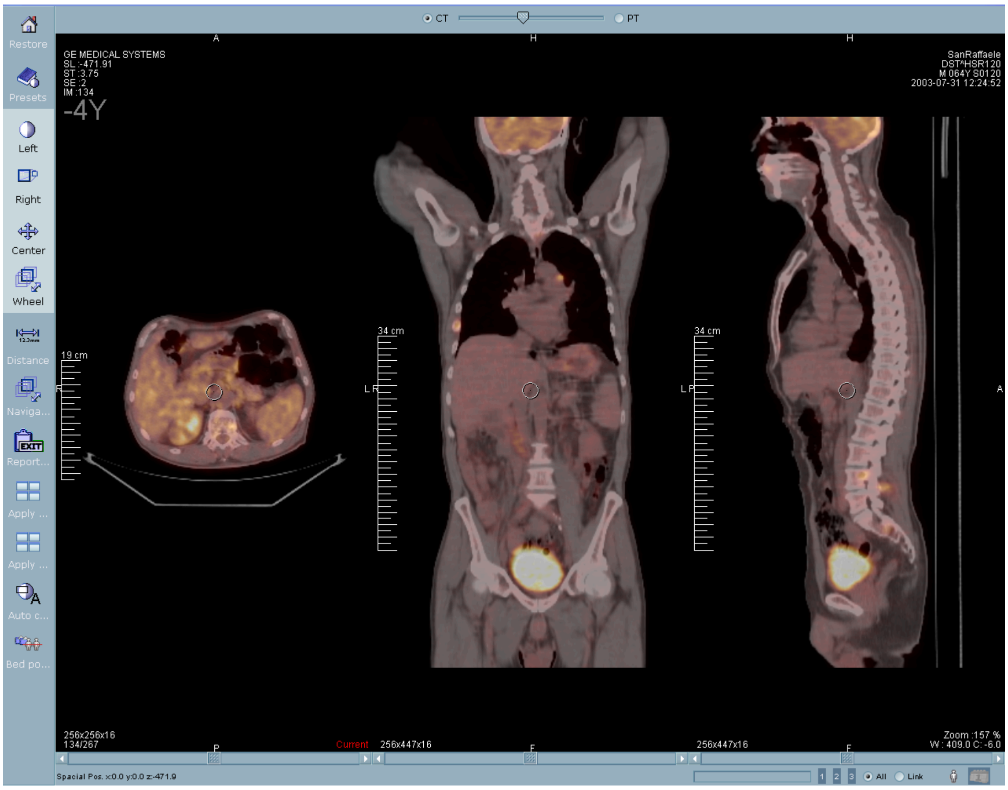


Figure 23 -Viewer containing 2 fusioned series

1.1.1.1. Basic fusion manipulation

Use the slider located at the top of the viewer (see Figure 24) to change the transparency and show more of the first or of the second series. You can also associate a keyboard shortcut with this action (see section 1.16.2.4 page). By default, actions to change the transparency to view the original, the middle or the fused series (CT, PT/CT or PT in this example) are associated with the keys ‘4’, ‘5’, ‘6’ of the numeric pad of the keyboard.

To change the contrast, brightness, Color Look-up Table etc. of one of both series, select it in this slider by clicking on the button located at the left or right of the slider ("CT" or "PT" in Figure 24).

Zoom and image position are common to both series.

Tools depending on the modality are only activated when this modality is selected (e.g.: the SUV value is only shown in the info bar of the viewer when the PT series is selected).

See the MPR section (section 2.17 page) for the management of the image thickness, MIP, MinIP, reconstructions etc.

1.1.1.2. Coregistration between both series

If the two series are not perfectly coregistered, the user has the possibility to manually align the series, panning the top series along the 3 axes (X, Y and Z axes). This feature is available in the 2D and in the MPR viewers.

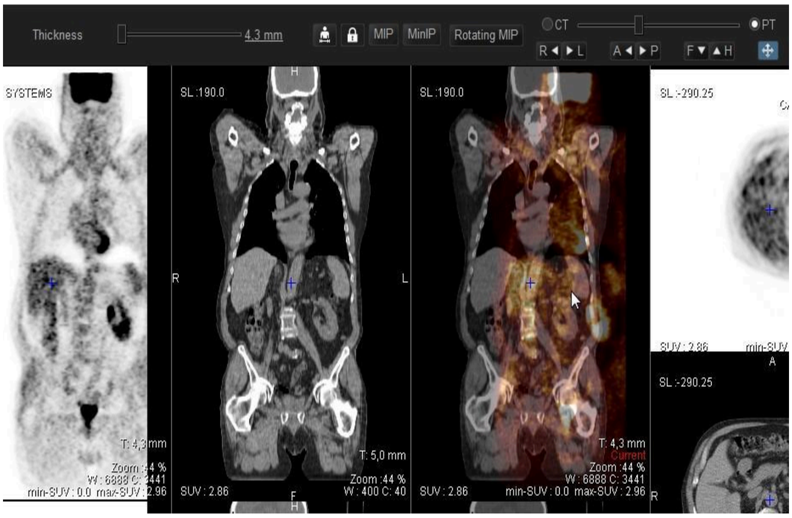
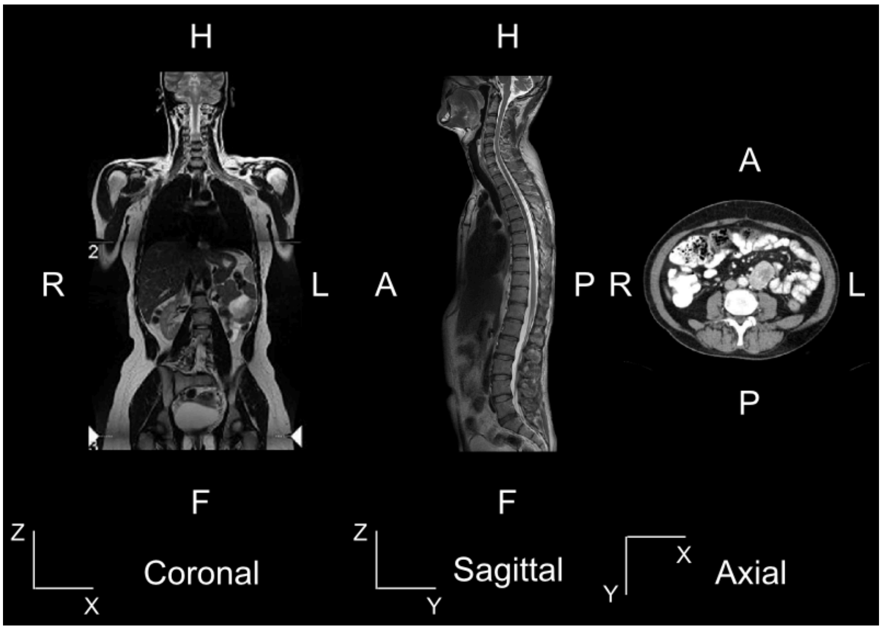


Figure 24 - PT and CT series need coregistration

A controller is present under the fusion slider, at the top right of the viewer. It offers 2 alignment modes:

- Pixel by pixel, using the R – L, A – P and F – H buttons. Simply click on those buttons to move the top image (typically the PT series) one pixel in the selected direction (resp. Right – Left, Antero – Posterior, Feet – Head directions). This is the more precise way to coregister the series.



- Using the mouse motion. Click on the 4-arrows button (✥) to activate this coregistration mode. Click (with the left mouse button) any point of the PT image and drag the mouse to move the PT relatively to the CT. Release the mouse button when finished. Click again on the 4-arrows button to leave this coregistration mode and return to the default tool.

1.1.2. Previewing

Some kinds of studies have many series (e.g. Magnetic Resonance). Choosing which series to open in this set is not always easy.

The previewer eases this task. To launch the Previewer,

√ select some series in the 'Series' list, or one study in the 'Studies' list (see section 1.3.5.2 page).

√ Choose [*Document*] [*Preview document(s)*] or

√ press the 'Alt' and 'P' keys, or

√ click on the Previewer icon in the toolbar of the browser.

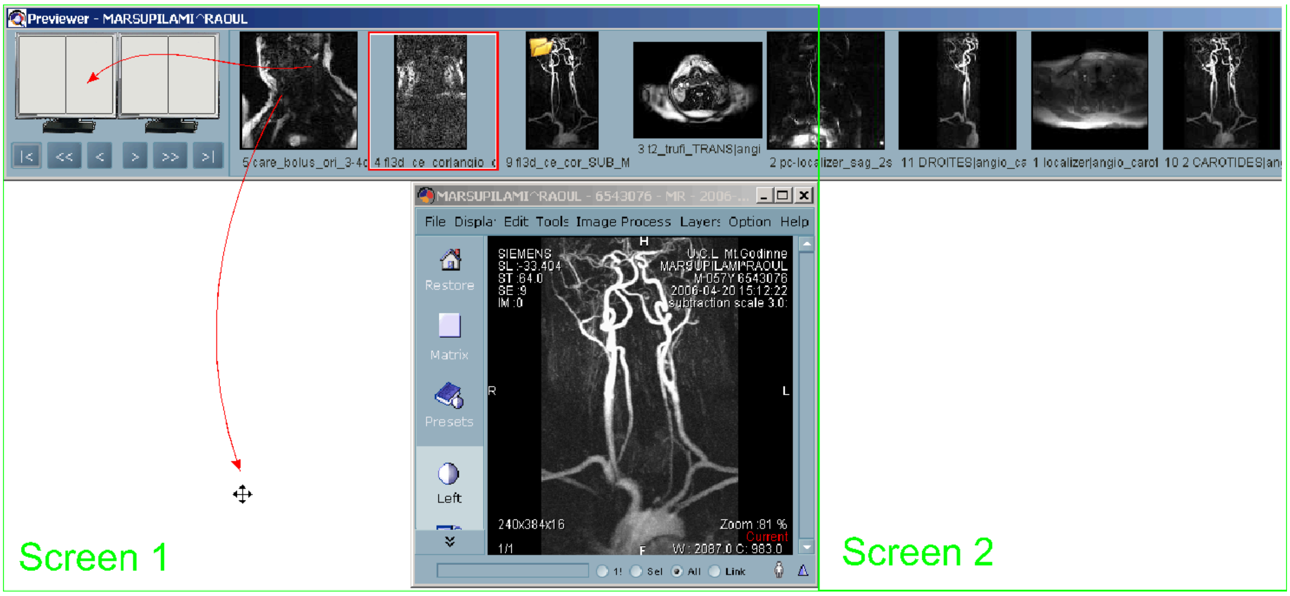


Figure 25 - the previewer

The leftist part of the previewer contains symbolic monitors, which represent your current system. Typically one or two monitors will be displayed. Those monitors contain separators which specify the viewers matrix, i.e. the number of viewers that will be displayed on each screen.

Under the monitors are 4 or 6 arrows that will be used to scroll along the previewer and display next/previous viewers.

The rightist part contains one preview icon per series. Drag & drop or double click those icons to open the corresponding viewers.

The **viewers position** will snap to a kind of grid, represented on the symbolic monitors.

Right-click on the symbolic monitors and select a new grid. For example, 3x2 will open 2 lines of 3 viewers on each screen.

To impose a different grid for the second monitor on a dual monitor environment, right-click on the second symbolic monitor and choose another division for this screen. Choose "As on screen #1" to have the same division on both monitors.

To **open a viewer**, you can either:

√ Double click on the text or icon of a series, or

√ Drag the icon to the localisation that the viewer must use on screen, or

√ Drag the icon to the localisation that the viewer must occupy, in the symbolic monitors, or

√ Right-click on the icon or text and select "Open" in the context menu.

At the top left of the icon appears the "opening" symbol when the viewer is opening. When it's completely opened, the "viewer opened" symbol replaces the opening symbol.

To **open a second viewer for the same series**, press “Ctrl” while dragging the icon to the symbolic monitors or to the screen. This will open a duplicate viewer, useful e.g. to show the scoot on both monitors.

Operations performed via the context menu apply either on the clicked series if no series are selected, or on the **selection**.

To select series, simply click on a series icon or text with the left mouse button.

To select or unselect all the series, choose the corresponding item in the context menu.

The other items of the **context menu** allow to

- Open a viewer directly in one of the MPR modes
- Open all the selected series in the comparison mode (see section 1.5.3 page)
- Open all the selected series, joined in one viewer (see section 1.5.2 page)
- Open the selected series using the hanging protocol (see section 1.5.7 page)
- Remove the selected series from the previewer
- Start the fusion between the two selected series (see section 1.5.4 page).
- Bring the viewer corresponding to the clicked series to the front. You may also press the 'ctrl' key while clicking on the series in the previewer to perform this operation.
- Close all the selected series
- Close all the series of the previewer
- Display the browser in the series panel, for the first selected series
- Hide or display the text bellow the icons, for each series.
- Decide if all the viewers related to series shown in the previewer must be closed when the previewer closes.

Right-click on the symbolic monitors to change the number of viewers that will be displayed on screen, as explained in section 2.4.5 page . Changing this number will re-organise the viewers on the screens.

To quit the previewer,

√ Press the 'exit' cross 🗗✕ at the top right of the previewer, or

√ In one of the viewers opened for a series present in this previewer, exit the study (press the 'Shift' and 'Backspace' keys, or select [*File*] [*Exit this study*]. (see section 2.1 page).

Several previewers may be opened simultaneously. Trying to open a previewer while another is still active will cause the *TM-Reception HE* to ask if it must re-use the existing previewer or open another one. This feature gives you the possibility to keep in memory the list of the important series if you are interrupted during the reporting, and to come back very easily to this job later on: just go back to the corresponding previewer. If you choose to "Always Re-use" the current previewer, the TMRHE will stop asking this question. Press the 'Shift' key while clicking the "Preview" button to show this question again.

The previewer offers the possibility to **scroll among the series of a study**, using the |<, <<, <, >, >> and >| buttons located under the symbolic monitors.

Let's start from the situation depicted in Figure 26: series 1, 2, 3 and 4 are displayed respectively on the first and second monitors.

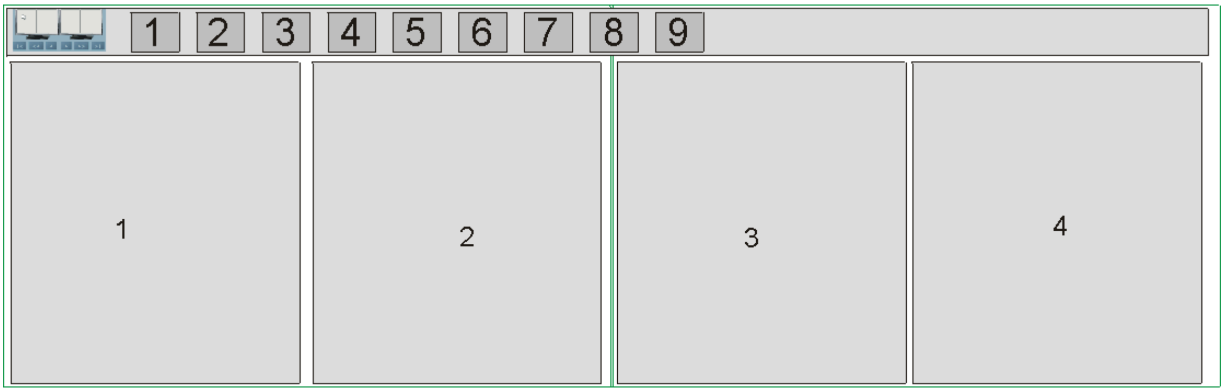


Figure 26 - Preview scroll screen(s)

Press the ">" button to scroll one screen to the right: series 3 & 4 will be moved on the first monitor and series 5 & 6 will be displayed on the first monitor

Press the ">>" button to scroll all screens to the right: series 5, 6, 7 & 8 will be displayed on the monitors.

Press the ">|" button to display the 4 last series (the number "4" comes from the fact that 2 monitors, displaying 2 series per monitor display a total of 4 series on the screens)

Buttons "|<", "<<", "<" have the same action but to the left side.

If several studies are previewed by the same previewer (e.g. the study realized today and the study realized one week ago), it may not be easy to distinguish to which study refers each opened viewer and preview image. To ease this operation and reduce the risk of confusing two studies, when several studies are previewed together in the same previewer, the previewer displays (see Figure 27):

- at the lower right corner of each image, a small colored geometrical form (triangle, cross, circle, square etc.). Each viewer has the same pattern drawn at the lower right corner.
- a list of colored tags in the previewer. Check or uncheck each tag to show / not show the corresponding study.

Remark: the stickers are configurable - figures, forms, coloured or not. We can set it for use numbers instead of stickers.

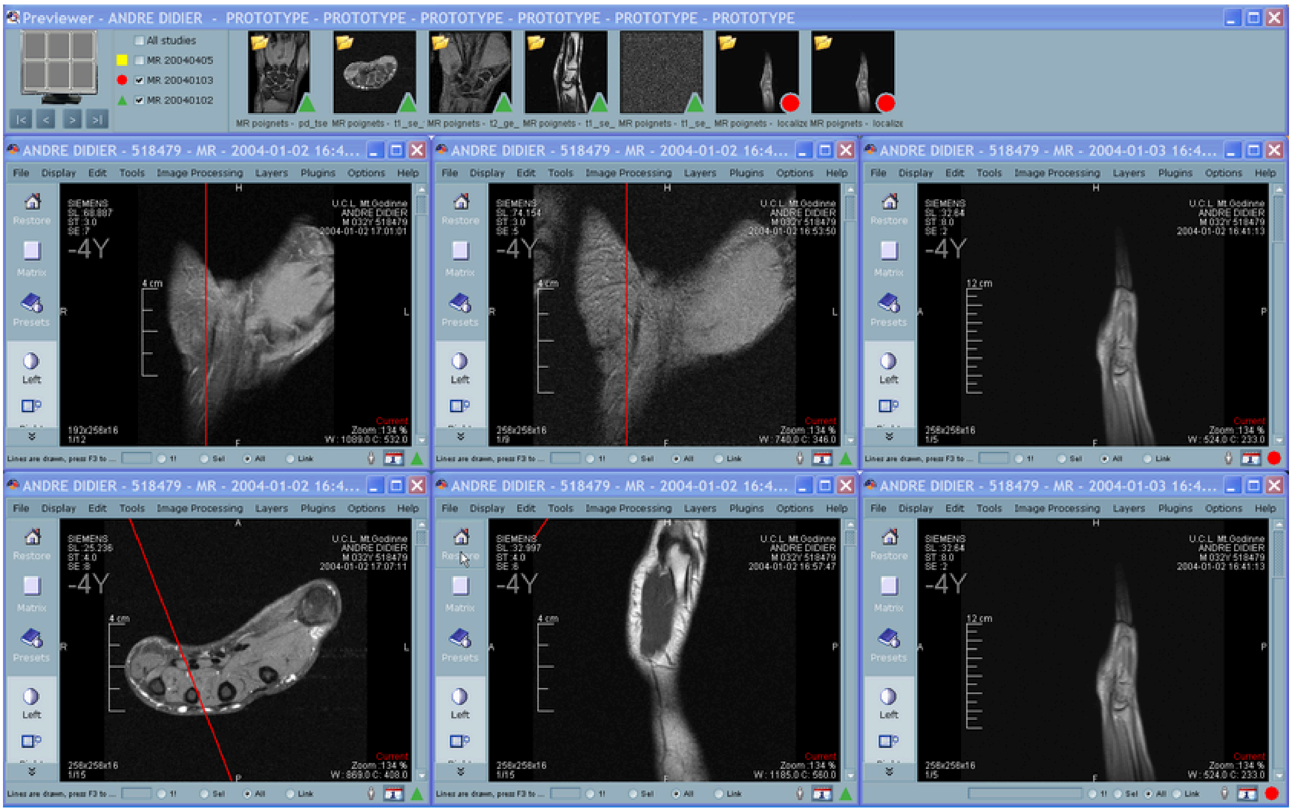


Figure 27 - Previewer showing several studies

The original size and position of the previewer, as well as the content of the description or the tool tips are completely configurable. Ask your IT manager for this configuration.

Once a previewer is opened, you can easily **add series from the browser to the previewer**:

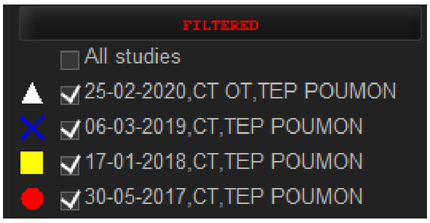
In the browser, select the series to add to the current previewer.

√ Right-click on one of the series in the browser, and select in the context menu [*Add documents to the previewer* …], or

√ Press the 'Alt', 'Ctrl' and 'P' keys.

In the Previewer, you can configure the variables of the history to be displayed and therefore restrict the modalities to be displayed for a given user.

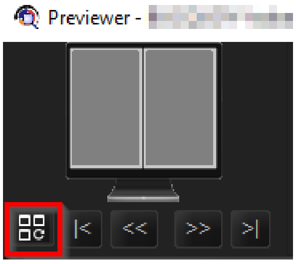
The label "Filtered" appears at the top of the history :



FILTERED
☐ All studies
△ ☑ 25-02-2020,CT OT,TEP POUMON
✕ ☑ 06-03-2019,CT,TEP POUMON
🟨 ☑ 17-01-2018,CT,TEP POUMON
● ☑ 30-05-2017,CT,TEP POUMON

To inactivate temporarily the filter, simply click on "FILTERED".

In the previewer you also recall your windows in one click, this lets you bring all open images back to the screen when they have gone to the background



When you minimise the previewer, the patient's images are minimised automatically at the same time, and re-open with the previewer when you select it again.

1.1.3. Hanging Protocols

Hanging protocols are configurations managing the opening of the previewer and of the viewers, the same way as the films were hanged up in the lightboxes.

To open a study with a hanging protocol automatically chosen by the TMRHE, select the study (or some series) in the Browser list and

√ select [*Documents*] [*Open with Hanging Protocol*], or

√ press the 'Ctrl' key together with the 'H' key, or

√ right click in the browser list on the series or study, and select in the context menu the [*Open with Hanging Protocol*] option, or

√ Press in the browser toolbar the 'Open with hanging protocol' button

To open a study with a manually selected hanging protocol, select the study (or some series) in the Browser list and

√ select [*Documents*] [*Select Hanging Protocol …*], or

√ right click in the browser list on the series or study, and select in the context menu the [*Select Hanging Protocol …*] option.

Hanging protocols allow to automatically:

- choose the series of the study that will be ignored,
- choose if the previewer must be opened or not,
- choose if some series must be automatically opened,
- choose the viewer matrix, as shown in the virtual monitors of the previewer (see section 1.5.4 page),
- define if the viewers must be referenced in all the perpendicular viewers (see section 2.5.8 page),
- choose if the viewers must be simply opened or placed in the comparison mode

- If additional series arrive for the study currently displayed in the hanging protocol, these series are automatically added into the previewer.
- etc.

There is no graphical user interface to configure the hanging protocol. Contact your local Telemis administrator to have a particular configuration.

1.1.4. Save series as local documents

These commands give you the ability to store a study or a series, using the Telemis Image format, on one of your disks (or removable disks: CD, floppy, Zip ...). A document that is locally saved becomes available even if the *TM-Reception* is not connected to the server.

To save study(s) or series in the **default 'local database'** directory (see section 1.8.3 page to change this (these) directory(ies)) :

√ Select the study(s) or series to save in the 'Studies' or 'Series' lists.

√ Click on [*Document*] [*Save document(s) in database*] or press the 'Ctrl' and 'S' keys.

The documents are automatically downloaded from the server, if necessary, and stored in the default database directory.

Unlike the 'Save in database' command, tied to the 'local database' directories, you can **save the document in any directory** with the following command.

√ Select the study(s) or series.

√ Click on [*Document*] [*Save document(s) as*].

√ In a directory in the file selector that opens, select the directory where the study(s) must be stored.

The format of the images on disk is specific to Telemis. In the directory that has been selected, a small file ending with ".header" is created. It contains the full header of the study. The images are stored in a big file ending with ".tme", in the sub-directory "em" (that is created if not found) of the directory containing the header.

All the documents that you have saved, either in the 'local database' or in a specific directory are local documents, available even if the *TM-Reception* is not connected to a *TM-Server*.

To display the local documents in the *TM-Reception*, set the list of the 'local directories', as explained in section 1.8.3 page and select in the "Search target" of the search tools the option "Local documents" or "Local + Server".

A local document is marked with the symbol 🏠 in the series list of the 'Series' view.

1.1.5. Delete

The delete command deletes the selected document(s).

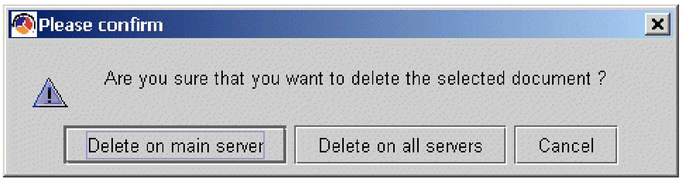
To trigger the command:

√ select [*Document*] [*Delete Document(s)*] or

√ click on the Delete icon, or

√ press the 'Ctrl' and 'D' keys.

If the document is local, it is really deleted from the disk. If the document is on the network, you loose the access to this document[3], on the current server or on all the servers, according to the answer to the confirmation dialog box (shown on Figure 28). Only administrative logins will really delete the documents on the server(s).



Are you sure that you want to delete the selected document ?

Figure 28 - Delete confirmation

Before *TM-Reception* executes the command, the user will be prompted to confirm the deletion.

This command is always available for local documents. Depending on the configuration of your *TM-Reception*, the delete permission is granted or not for the documents located on the server.[4]

1.1.6. Forward

If a document is addressed to you, you may decide to address it also to somebody else: you can forward it to him. Expressed with other words, you have the possibility to give somebody else the access permission to some documents.

You can only forward a document that is stored on the server. *TM-Reception* can't send a local document to another recipient (this is the goal of the Telemis Acquisition software).

To trigger the command, select a document in the 'Studies' or 'Series' lists and:

- √ select [*Documents*] [*Forward document(s) …*] and
- √ either directly select a recipient to directly send the document(s) to this recipient, or
- √ click on the [*Forward*] submenu.
- √ click on the Forward icon, or
- √ press the 'Ctrl' and 'F' keys.

A small window (see Figure 29) will appear with a text box containing the name of the documents that you have selected, and the 'Choose Receiver' button.

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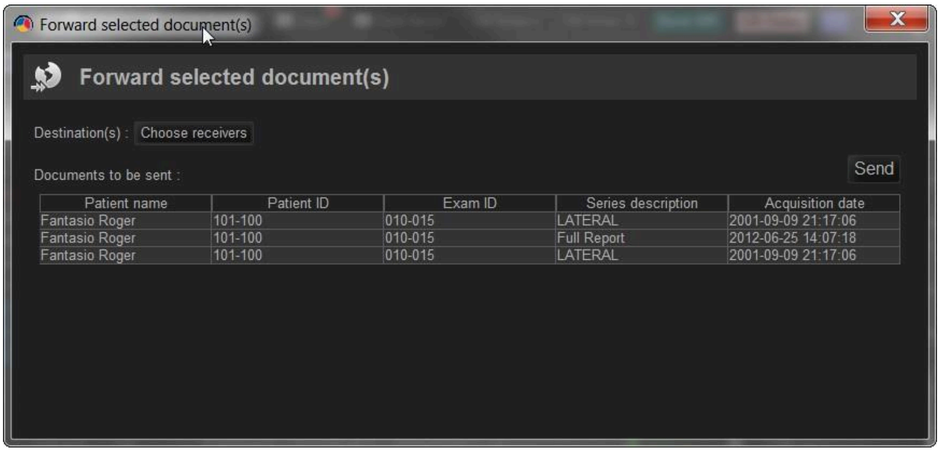
[3] When you delete a document that is stored on the server, you just remove your access to this document. The document will be physically deleted from the server when all the accesses to it are deleted or when an administrator deletes it.

[4] See your local Telemis Administrator for the *TM-Reception* permissions.



Documents to be sent :

Patient name	Patient ID	Exam ID	Series description	Acquisition date
Fantasio Roger	101-100	010-015	LATERAL	2001-09-09 21:17:06
Fantasio Roger	101-100	010-015	Full Report	2012-06-25 14:07:18
Fantasio Roger	101-100	010-015	LATERAL	2001-09-09 21:17:06

Figure 29 - forward window

Click on the 'Choose Receiver' button to open the User Access list (see Figure 30).

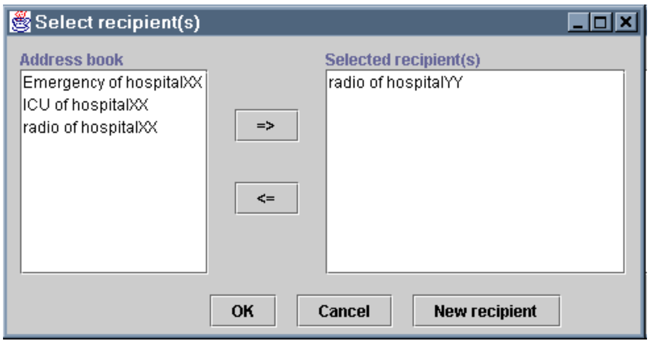


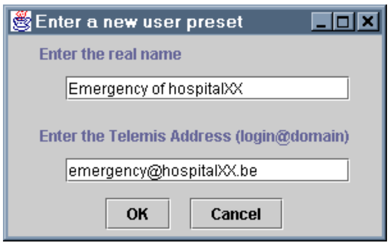
Figure 30 - User Access List

The list on the left contains all the registered users (*Address book*). The list on the right contains all the new recipients of the document that you are forwarding (*Selected recipient(s)*).

To add a user to the recipients list,

- √ click on his name to select the user in the left list (the *Address book* list) and then click on the '=>' button, or
- √ double click the user in the left list.

To create a new recipient user, whose address is not yet in the address book, click on the *New recipient* button. The window of Figure 31 will appear, in which you can enter the real name of the user (that is the name that will be displayed in the *Address book* and *Selected recipient(s)* lists) and its address. This new entry will be added to your address book. A Telemis address is '`login@unit.hospital.country`' (check with your colleagues or local IT manager to know their precise address).



Enter the real name: Emergency of hospitalXX

Enter the Telemis Address (login@domain): emergency@hospitalXX.be

Figure 31 - New Telemis user

To remove a user from the recipients list,

√ select the user in the recipients list and then click on the '<=' button, or

√ double click on the user in the recipients list.

When the list of receivers is filled, close the 'Select recipients' window with a click on *OK* and address the document(s) to the new recipients with a click on *Send* in the 'Forward selected document(s)' window.

Depending on the configuration of your Telemis Browser, the forward permission is granted or not.[5]

1.1.7. TM-community

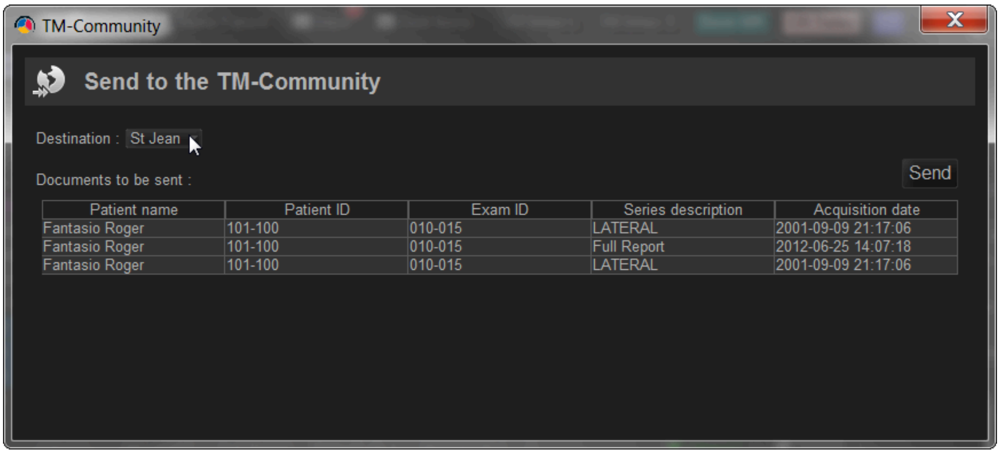
If your hospital is connected to other hospitals also equipped with the *Telemis-Medical* PACS, you can in a few clicks share studies with a colleague working in another hospital.

Select the series to share and

√ Select the menu [Document] [TM-Community], or

Click on the TM-Community button in the toolbar of the browser

In the TM-Community window that opens (see Figure 32), select the destination hospital and click on the '*Send'* button.



Destination : St Jean

Documents to be sent :

Patient name	Patient ID	Exam ID	Series description	Acquisition date
Fantasio Roger	101-100	010-015	LATERAL	2001-09-09 21:17:06
Fantasio Roger	101-100	010-015	Full Report	2012-06-25 14:07:18
Fantasio Roger	101-100	010-015	LATERAL	2001-09-09 21:17:06

Figure 32 - TM-community

---

[5] See your local Telemis Administrator for the browser permissions.

1.1.8. Only download

The "*download without viewing*" is a feature that may spare a lot of waiting time. Download a document that is on the server means transfer the document through the network to the local 'cache' directory (see section 1.8.5 page) of your *TM-Reception*.

If the connection to the server is rather slow (via a modem for example), the transfer may take some time. Imagine that you scan your patients/documents lists and select some interesting documents, but that you haven't currently enough time to visualise them, you can ask *TM-Reception* to download them. By this way, at the moment you will decide to view the documents, they are already on your computer and the opening of the viewer will be nearly immediate.

To only download the documents that you have selected:

√ select [*Documents*] [*Only download document(s)*].

You can automate this operation. You can choose to automatically download every new document. That means that at each refresh, if the *TM-Reception* detects that there are new documents for you, they will be automatically downloaded to your computer.

To automatically download the new documents,

√ check [*Network*] [*Auto download*].

You can further automate the operations if you combine with the *Auto refresh* option (see section 1.8.1 page). This option performs an automatic refresh of the lists. If the *Auto download* and *Auto Refresh* options are selected, the lists are updated every 3 minutes, and the new documents are automatically downloaded. This combination of options is very powerful if you are connected via a permanent line to the server: your documents are always cached locally each time you want to view them. On the opposite, don't check the *Auto refresh* if the connection is not permanent (modem ...), because the auto refresh re-opens the connection periodically.

1.1.9. Labeling some series

Labels may be used to set a "post-it" on some series ("I will show this series during the staff" or "for the teaching I give next week"), or to draw the attention of the clinicians and other radiologists on a series ("Attention we have found sth important").

Label can be public, restricted to a group of users, or private to a user.

All users see public labels. According to their privileges, users may search for labeled series, view private or group labels, set a label on a series and create a label.

1.1.9.1. Search for labelled series

In the search fields, simply select in the drop box the 'Label' field.

Type in the text box some letters of the label that you want to search for (the *TM-Reception* tries to automatically complete the label name).

Press 'Enter' or click on the 'Find' button to search for all the series having this label.

1.1.9.2. View labels

Labels may be private or public. Private labels are only visible for the user who sets the label. Public labels are visible for everybody.

Once a label is set on a series, it's visible as well in the browser at the bottom of the details and by the color changing of the line (see Figure 33.A), as at the bottom right of the viewer (see Figure 33.B). The text of the label is directly shown, and its description is shown as a tool tip when the mouse passes over the label name.

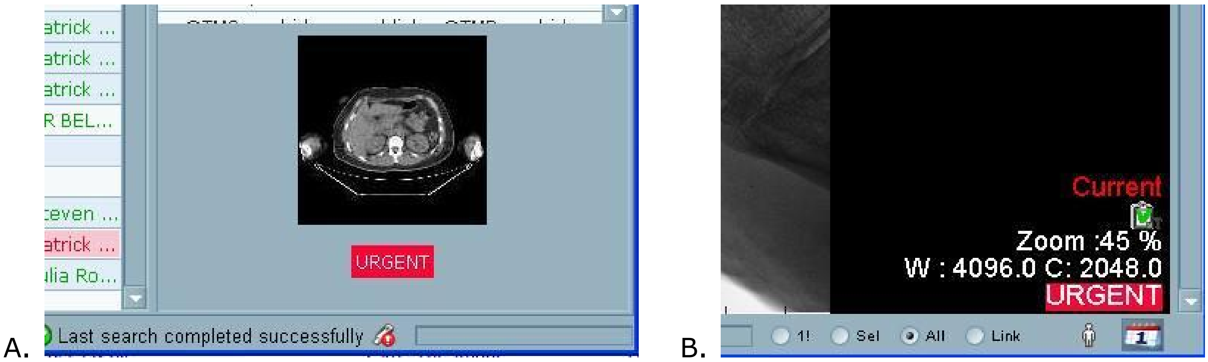


Figure 33 - labels

1.1.9.3. Set a label

For *TM-Reception HighEnd* users having the authorization to set a label,

Select the line(s) containing the series to label.

Right click and select [*Add label*].

The sub-menu shows some lines containing [*Add label XXXXX*] where XXXXX is the name of a favorite label. To set one of these labels, just click on this menu line, as shown in Figure 34.

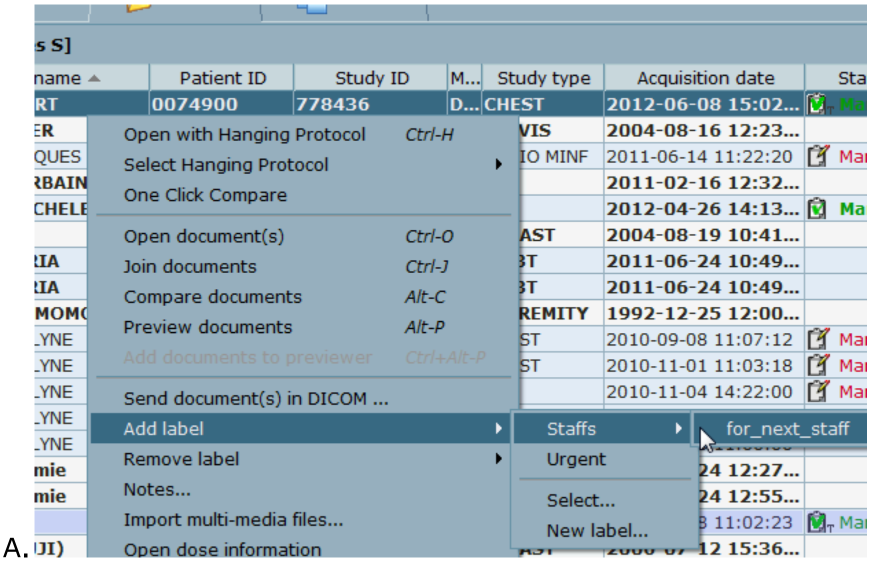


Figure 34 - add favorite label

For the non-favorite labels, select [*Add label*] and [*Select …*] in the sub-menu. The label selection dialog box opens. Labels are separated by category. Click on a label to select or unselect it. Press the 'OK' button when finished.

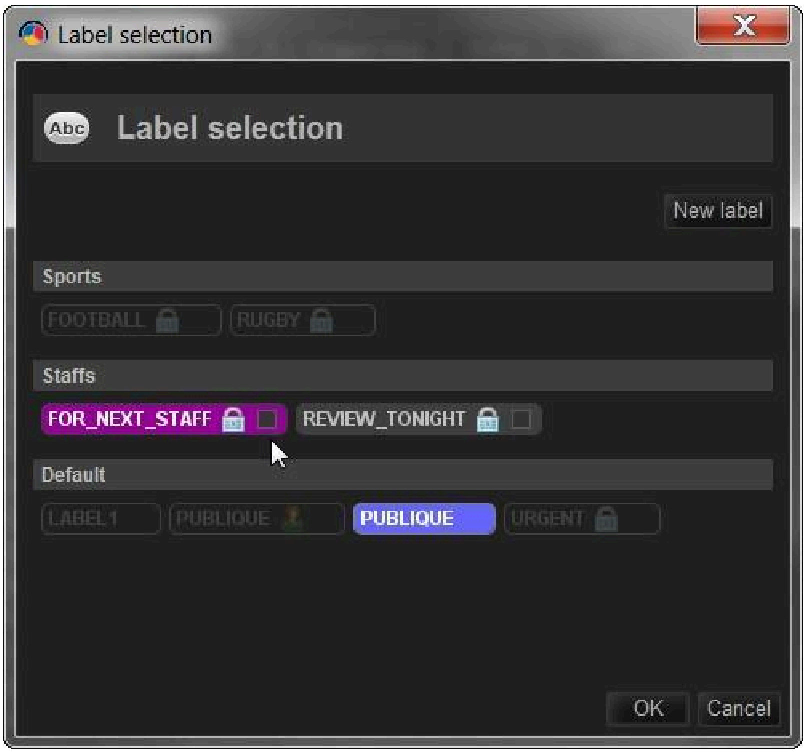


Figure 35 - Add label

Private labels are shown with a padlock (☐) if only visible for the owner of the label and with a person (👤) if visible by everyone.

1.1.9.4. Remove a label

Removing a label is exactly the same operation than setting a label, selecting [*Remove label*] instead of [*Add label*] in the context menu.

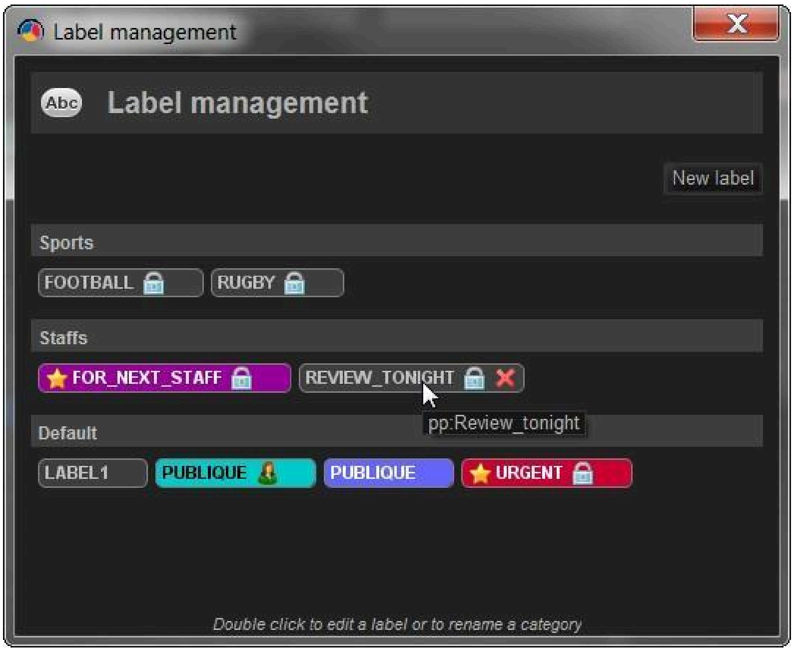
1.1.9.5. Manage labels

For *TM-Reception HighEnd* users having the authorization to create and delete labels,

Select the menu [*Options*] [*Label management*].

In the label management dialog box (see below), move the mouse over the label to modify or remove.

- √ Press the red cross appearing at the right of the label name to delete it.
- √ Double click on a label to modify it (see next section).
- √ Press the 'New label' button to create a new label (see next section).



Double click to edit a label or to rename a category

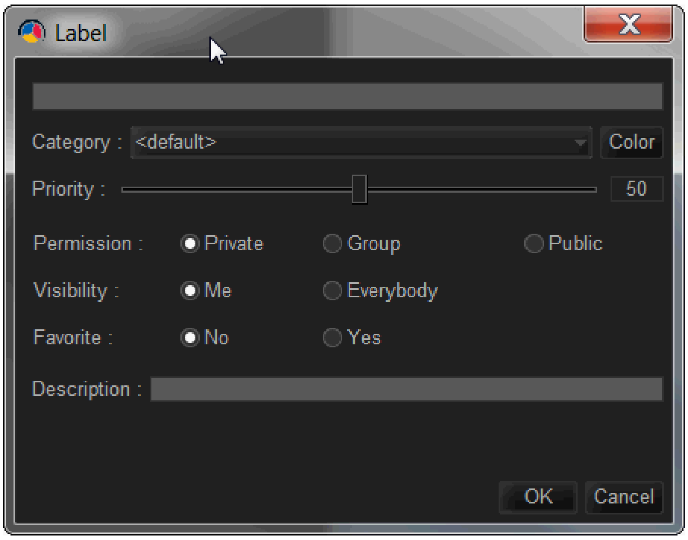
Figure 36 - Label management

A yellow star marks favourite labels.

1.1.9.6. Create labels

For *TM-Reception HighEnd* users having the authorization to create and delete labels,

Select the menu [*Options*] [*Label management*] and press the "New label" button, or press the "New label" button in the 'add a label' window (see Figure 35).



Category : <default>

Priority : 50

Permission : ● Private ○ Group ○ Public

Visibility : ● Me ○ Everybody

Favorite : ● No ○ Yes

Description :

Figure 37 - create a new label

The first line contains the name of the label that will appear in the browser and in the viewer, as explained here above.

A label might belong to a Label category ('Sports' and 'Staffs' for example). Select the category of your label or choose the last line 'Create a category' to create a new category name. Labels in the list are shown category by category. In this list, double-click on the category name to show or hide the labels contained in this category.

If desired, change the color of the label. This impacts the background color of the label name in the browser and viewer, and the background color of the line containing this series, study or patient in the browser.

The priority (a number between 0 and 100) is used when several labels are set on one series, or when several series of a study or a patient have different labels. The label with the higher priority gives its color to the line concerning the series, study or patient.

A label can be created as private (only the creator can add or remove this label), group label (only users sharing a specific role can add or remove this label) or public (everybody can add or remove it). Set or change the permission needed to associate this label with a series.

Choose if the label must be visible for all the users or only for its creator (or the role in case of 'Group' label).

A favorite label appears directly under the [*Add label*] or [*Remove label*] context menus. Other labels need the user to pass by the [*Select label*] sub-menu.

The description is shown when the mouse passes over the label.

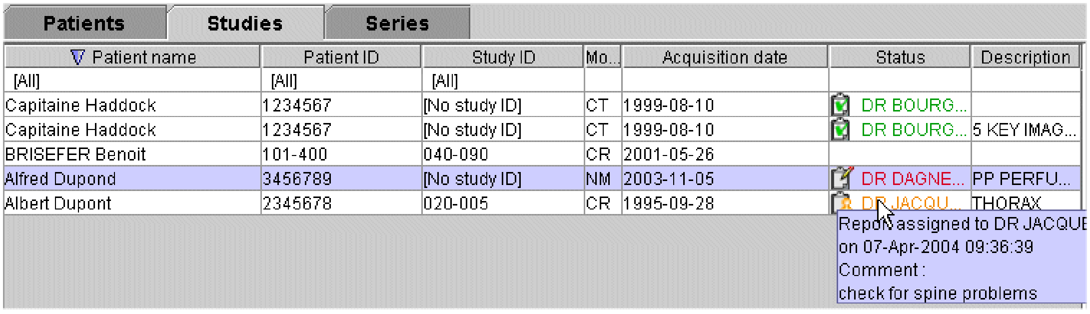
1.1.10. Report status

The status of a document shows if this series/study has (or not) a report associated, is currently being reported or is assigned to a doctor for reporting. Each status comes with a doctor name, event date and possibly a comment.

A report status is always applied to a study. It is impossible to declare one series not reported while the other series of a study have a report associated.

1.1.10.1. The status

Depending on the Telemis-Medical system configuration in your hospital, the browser will display the report status in the 'Studies' and possibly in the 'Series' list.



Patient name	Patient ID	Study ID	Mo...	Acquisition date	Status	Description
[All]	[All]	[All]				
Capitaine Haddock	1234567	[No study ID]	CT	1999-08-10	✓ DR BOURG...	
Capitaine Haddock	1234567	[No study ID]	CT	1999-08-10	✓ DR BOURG...	5 KEY IMAG...
BRISEFER Benoit	101-400	040-090	CR	2001-05-26		
Alfred Dupond	3456789	[No study ID]	NM	2003-11-05	✎ DR DAGNE...	PP PERFU...
Albert Dupont	2345678	020-005	CR	1995-09-28	👤 DR JACQU...	THORAX

Report assigned to DR JACQUE
on 07-Apr-2004 09:36:39
Comment :
check for spine problems

Figure 38 - Report status

When the mouse stays for more than one second on the status cell of a document, a text box appears as shown on Figure 38 giving the full doctor name, the event date and time and the comment if present.

- If no report has been done, nothing is shown in the status cell
- If the study has been assigned for reporting to a doctor, the cell shows an orange logo containing a person (👤) followed by the name of the doctor
- If the study is currently viewed by a doctor, the cell shows a red logo containing a pencil (✎), followed by the name of the doctor
- If the study has a report associated, the cell shows a green logo containing a 'V' (✓), followed by the name of the doctor.

1.1.10.2. Assign for reporting

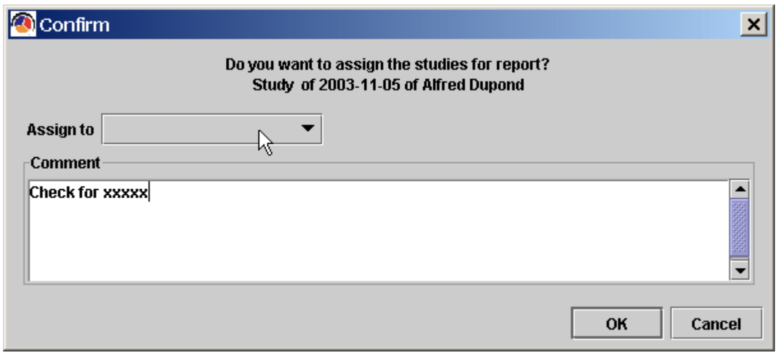
Only the *TM-Reception HE* version specifically configured for it may update the report status.

To assign one or several studies for reporting to a doctor,

√ Select either the study (studies) in the 'Studies' list, or some series in the 'Series' list;

√ Select [*Documents*] [*Assign for reporting …*]

Figure 39 shows the dialog box in which you must select a doctor to assign the study to via the list box on the right of the 'Assign to' text. You can enter a comment in the text area if needed. This comment can be considered as a kind of 'post-it' placed on the study to give a message to the person who will report this study.



Do you want to assign the studies for report?
Study of 2003-11-05 of Alfred Dupond

Assign to

Comment

Check for xxxxx

Figure 39 - Assign for reporting

Press 'OK' to assign or 'Cancel' to cancel this operation.

1.1.10.3. Start reporting / report in progress

Only the *TM-Reception HE* version specifically configured for it may update the report status.

The "Report in progress" status is an optional status. It is only useful if the possibility exists in the hospital that two doctors report accidentally the same study at the same time. If everybody's task is precisely defined, there is no risk. If a pool of radiologists report the first available study, the risk exists.

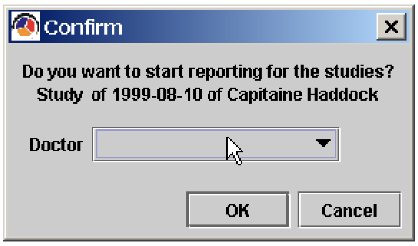
Depending on the *Telemis-Medical* system configuration and on the report permission of your Telemis login, opening a series belonging to a study not reported yet will open the dialog box shown in Figure 40. Select your name in the list if this is your first report since you started *TM-Reception HE*.

To force the status of a study to "Report in progress",

√ Select the study in the "Studies" list or one of its series in the "Series" list

√ Select [*Documents*] [*Start reporting…*]

Don't forget to select your name if you have just started *TM-Reception HE*.


Confirm

Do you want to start reporting for the studies?
Study of 1999-08-10 of Capitaine Haddock

Doctor

Figure 40 - start reporting

Press 'OK' to start reporting and setting the study status to "Report in progress", or 'Cancel' to simply have a look on the images.

1.1.10.4. Report done or aborted

Only the *TM-Reception HE* version specifically configured for it may update the report status.

You can close a study either because the report is finished, or because you must interrupt the report to start another urgent task.

To set the status of one or several studies to "**Report done**",

√ Select the study (studies) in the Browser list and select [*Documents*] [*Finished reporting…*], or

√ Select in the viewer of one of the series, [*File*] [*Report & exit …*], or

√ Press in the viewer toolbar the 'Report & Exit' icon, or

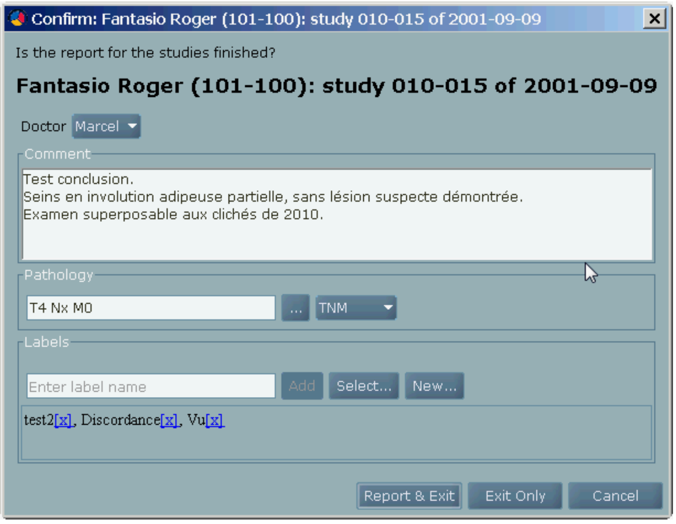
√ Press the CTRL and Backspace keys in the viewer.

The dialog box shown on Figure 41 looks like the 'Assign for reporting' dialog box. If you have already entered your name, it will be automatically selected in the 'Doctor' field.

If needed, type a comment in the text area. This comment can be used for retrieving this study later (see section 1.4.1 page , field "Report comment").

Select or change the report Doctor name and if needed add a pathology or a label.

Press 'Report & Exit' or the CTRL + backspace keys when finished.


Confirm: Fantasio Roger (101-100): study 010-015 of 2001-09-09

Is the report for the studies finished?

Fantasio Roger (101-100): study 010-015 of 2001-09-09

Doctor Marcel

Comment

Test conclusion.
Seins en involution adipeuse partielle, sans lésion suspecte démontrée.
Examen superposable aux clichés de 2010.

Pathology

T4 Nx M0 TNM

Labels

test2[x], Discordance[x], Vu[x]

Figure 41 - report finished

To **abort a report**, press 'Exit only' or simply close all the viewers of this study. The status will automatically change from "Report in progress" to "No report" (see section 2.1 page for more details about exiting the viewer).

If the configuration of the server allows this operation, you can reset the report status (i.e. set it back to 'No report') by selecting [*Document*] [*Reset report status*].

1.1.10.5. Encode the report while viewing the study

Only the *TM-Reception HE* version specifically configured may update the report status.

To open the report encoding window, or to set the current report encoding window to front:

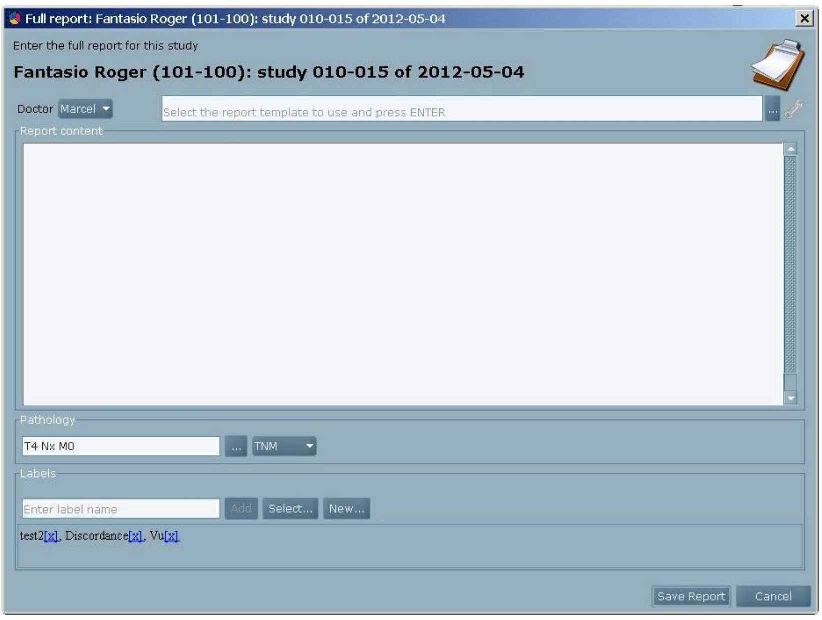
√ Select the study (studies) in the Browser list and select [*Documents*] [*Enter full report…*], or

√ Select in the viewer of one of the series, [*File*] [*Enter full report…*], or

√ Press in the viewer toolbar the 'Full report' icon

√ Or define a keyboard shortcut for the function (see section 1.16.2.4 page) and press the corresponding key in any viewer.

The 'Enter full report' dialog box shown in Figure 42 opens.



Full report: Fantasio Roger (101-100): study 010-015 of 2012-05-04

Enter the full report for this study

Fantasio Roger (101-100): study 010-015 of 2012-05-04

Doctor: Marcel

Select the report template to use and press ENTER

Report content

Pathology: T4 Nx M0 … TNM

Labels: Enter label name

test2[x], Discordance[x], Vu[x]

Figure 42 – 'Enter full report' dialog box

Type in the "Select the report template to use and press ENTER" selection box the first letters of a report template. If several templates match the typed characters, a drop-down list is shown. Continue to type characters to restrict the field of scope and press ENTER when only one template matches your input, or select an item in the list with the mouse of the up and down cursor.

You can also press the "…" button at the right of the "Select the report template to use and press ENTER" text to directly show a drop-down list of all the templates.

Press the key button ( ) to open the management panel for the report templates (see section 1.16.4 page).

Edit the text in the ‘report content’ text area to reflect the particularities of this study. Press the TAB key in the text area to switch to the template selection box.

You can work in any other viewer and come back to this report dialog as explained at the beginning of this section.

When the report text is terminated, press the ‘Save Report’ button to save it to the PACS and close all the viewers of this study. If configured in the Telemis Server, the report will be automatically exported to the RIS. An additional line will appear in the TMRHE with this report. The status of the study changes to “Report done”.

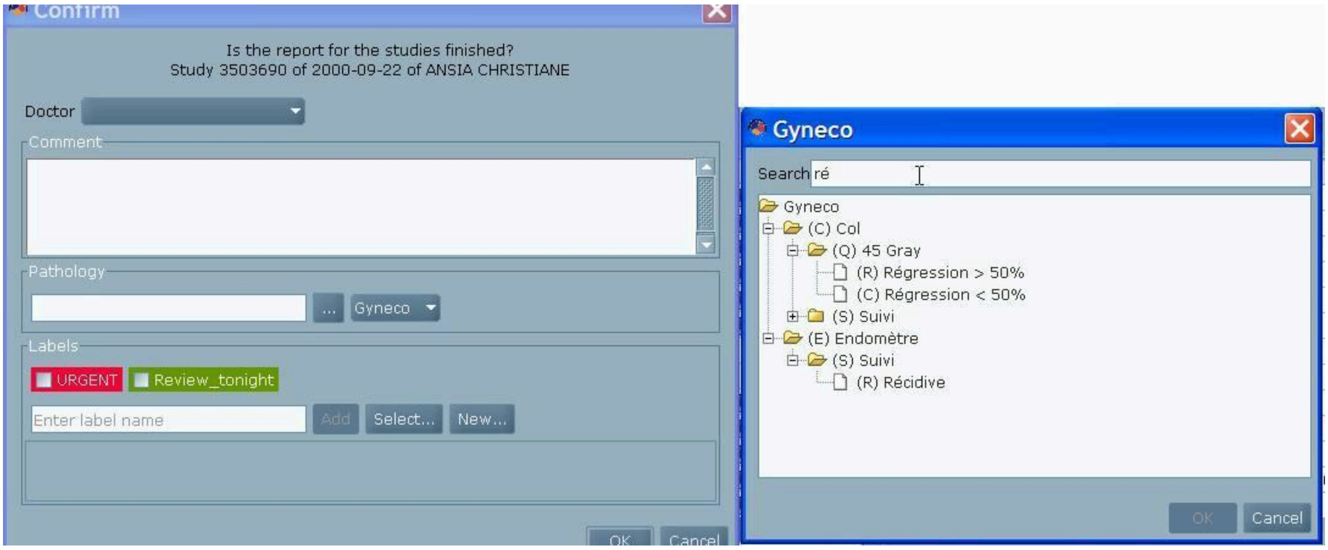
1.1.10.6. Pathology categories

If the pathology categories are activated in your PACS and if you have the permission to set a pathology you can, when setting the report status, set a pathology description to the study.

The 'pathology' is a code describing a pathology according to one classification (TNM, Bi-Rads, Gyneco etc.).

Press the '...' button to have access to the list or the tree representing the pathology classification. Select the item and options. Press OK to set the corresponding code.

The pathology code may be displayed in a separate column in the browser lists, and as an additional line in the description of a report status, as shown in paragraph 1.5.14.1 page .



Is the report for the studies finished?
Study 3503690 of 2000-09-22 of ANSIA CHRISTIANE

Search ré

Gyneco
(C) Col
(Q) 45 Gray
(R) Régression > 50%
(C) Régression < 50%
(S) Suivi
(E) Endomètre
(S) Suivi
(R) Récidive

Figure 43 – Pathologies

1.1.11. Discussion using notes and messages

1.1.11.1. Context

It can be useful to be able to ask advice to another radiologist about a study. When a clinician wants to ask advice to a radiologist, he must call him or send him an e-mail. The aim of the notes and messages is to discuss about the study directly from Telemis.

Two kinds of discussion are envisaged. The first one concerns general remarks about a study which are visible from anyone who can view these images (***notes***). The second one concerns messages exchanged between two or more specific users about a study (***messages***). A message can be used to ask advice to another doctor, and the advice can be replied to the initial message.

1.1.11.2. How to view and write notes/messages?

In the browser, in the last column of studies or series view, the 'Info' column shows the notifications about notes and messages, and allows to easily creating new notes and messages.

a. b.

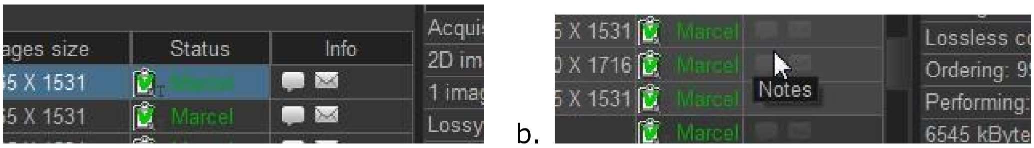


Figure 44 - Notes and messages notification (a. Notes and Messages available, b. No notes or messages for this study)

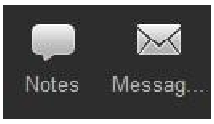
The little callout, if switched on (see Figure 44), signals that there is at least one note available for this study. The little envelope, if switched on, signals that there is at least one message for this study.

The last notes available for this study are shown at the bottom right of the browser.

The little callout and envelope are also shown in the bottom right of the viewers.

The notes or messages window will be accessible

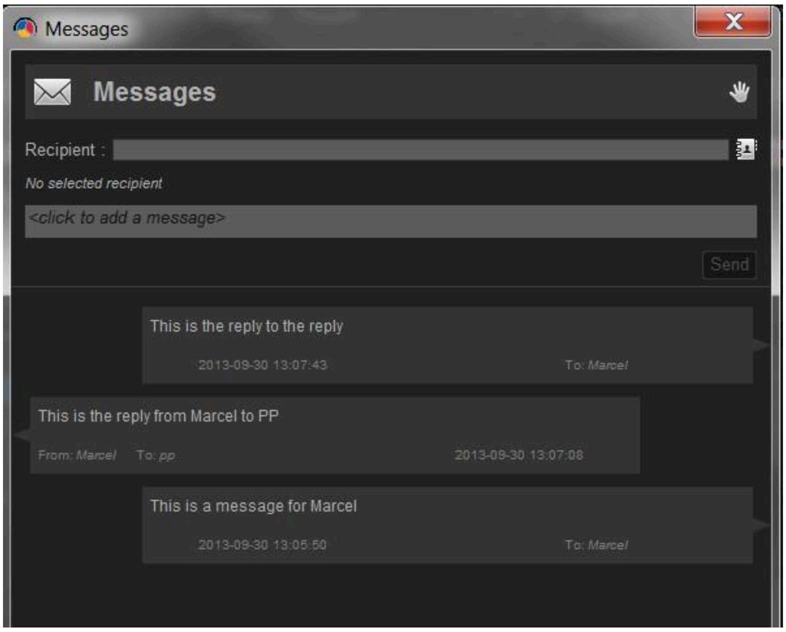
- By clicking on the little callout or envelope, in the browser or in the viewer (if present),
- From the contextual menu on a study in the browser (right-click on the line containing the study or series) and select the menu [*Notes ...*] or [*Messages ...*]
- In the browser menu [*Document*], select [*Notes ...*] or [*Messages ...*]
- In the viewer menu [*File*], select [*Notes ...*] or [*Messages ...*]
- In the viewer toolbar, double-click on the notes or messages button, if configured



- For notes, you can click in the 'Notes' part, at the bottom right of the browser.

The Notes window shows all the notes available for the current study and allows entering a new note.

The Messages window (see below) shows the full conversation and allows entering a new message or replying a message for a given recipient (or recipients)



This is the reply to the reply
2013-09-30 13:07:43 To: Marcel

This is the reply from Marcel to PP
From: Marcel To: pp 2013-09-30 13:07:08

This is a message for Marcel
2013-09-30 13:05:50 To: Marcel

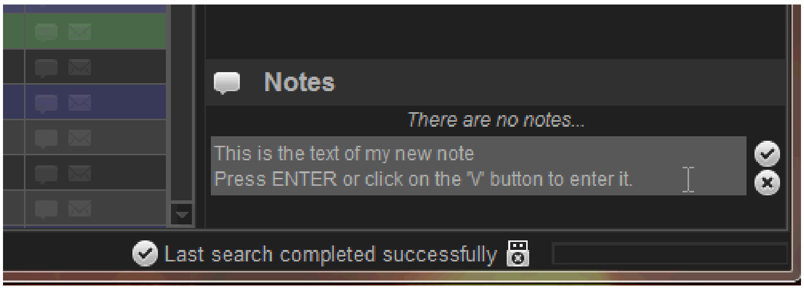
Figure 45 - Messages window

You can write a new note or a new message (if you have the permission to) from this window. He can also reply to another message.

Another quick way to add a note is to click in the Notes part at the bottom right of the viewer, in the text box containing "<click to add a note>".

Type the text and press the ENTER key to conclude this note (use the 'Alt' + 'ENTER' keys to insert a new line in the text). You can also click on the little at the right of the text to conclude it.

Click on the cross to cancel the note creation.

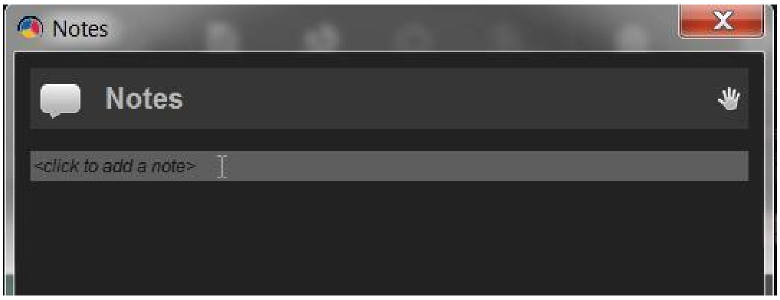


This is the text of my new note
Press ENTER or click on the 'V' button to enter it.

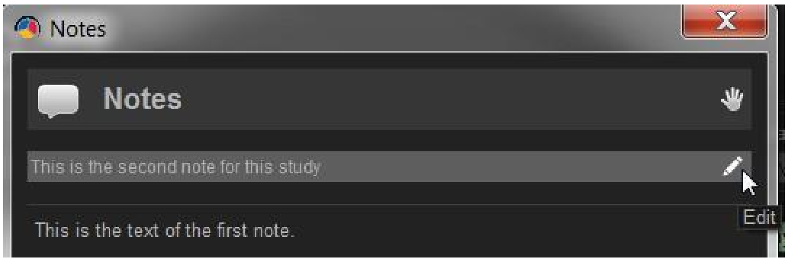
Figure 46 - Add a note directly in the browser

☐ New note

In the 'Notes' window, or in the 'Notes' part located at the bottom right of the browser, click in the "<Click to add a note>" text area to start typing your text.



To edit a text recently typed, move the mouse on the text area containing the note text. If the pencil shows at the right of the text area, you can simply click to edit the note.



This is the second note for this study

This is the text of the first note.

☐ New message

In the ‘Messages’ window, add and edit the text of the new message the same way as for a new note.

A message is a text and a (list of) recipient(s). Press the ‘Address book’ logo located at the right of the recipients text area to open the address book and chose one or several recipients. You can also directly type in the ‘recipient:’ text area the first letters of the recipient’s name: the TMRHE will automatically complete the name.

Figure 47 - New message address book

☐ Reply to a message

To reply to an existing message, open the ‘Messages’ window and either create a new message for a list of recipients, or simply press the ‘Reply’ arrow located in the message.

This is a message for Marcel
From: pp To: Marcel 2013-09-30 13:05:50

Figure 48 - Reply and Delete message

A notification will be sent (by e-mail) to the recipient of a message.

1.1.11.3. How to remove a note/message

In order to remove a note or a message, you must have the related permission. If it is the case, a small cross (see Figure 48) appears near the notes and the messages.

1.1.11.4. Export the notes and messages

Click on the little hand located at the top right of the notes and messages windows and drag & drop this hand onto a text-enabled application (Wordpad, Word etc.)

I've answer the last note.

1.1.11.5. How to search notes/messages?

Some search fields related to notes and messages searches have been added:

- Message author
- Message recipient
- Message status: 3 possible choices:
    - U (unread): all your messages that you haven't read yet
    - R (unread, read): all your messages, read or not
    - A (all): all your messages read or not, archived or not

And two new search presets have been added:

- Inbox: all unread and read messages for which you're a recipient
- Sent Items: all unread and read messages that you are the author of.

Figure 49 – Notes and messages related search presets

1.1.11.6. Messages status

☐ **Read/unread status**

When a doctor writes a message to one or multiple recipients, the message is considered as unread for all the recipients. When a recipient reads this message, the status of the message becomes “read” when the recipient closes the notes window.

1.1.12. Patient merge / update

Depending on your authorisation, it is possible to update patient information or to merge two patients together (same patient with two different spelling for example).

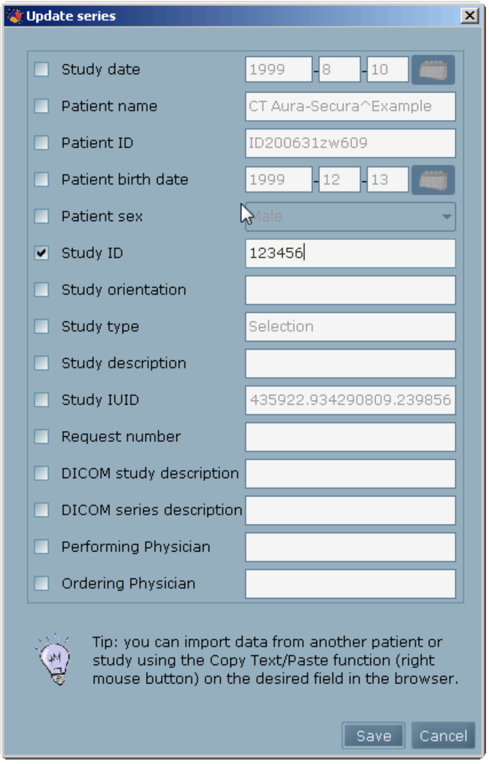
1.1.12.1. Series update

This method is typically used when, after a manipulation mistake on the acquisition device, a patient X performs the examination under the name Y (the name of the previous patient e.g.). The produced series must be transferred from patient Y to X.

√ Select the series to be transferred.

√ Select *[Documents] [Update series]*

The window shown on Figure 50 appears. The panel contains the data relative to the series: date, patient name, id, birth date, study ID (accession number), etc.



☐ Study date 1999 - 8 - 10
☐ Patient name CT Aura-Secura^Example
☐ Patient ID ID200631zw609
☐ Patient birth date 1999 - 12 - 13
☐ Patient sex Male
☑ Study ID 123456
☐ Study orientation
☐ Study type Selection
☐ Study description
☐ Study IUID 435922.934290809.239856
☐ Request number
☐ DICOM study description
☐ DICOM series description
☐ Performing Physician
☐ Ordering Physician

Tip: you can import data from another patient or study using the Copy Text/Paste function (right mouse button) on the desired field in the browser.

Figure 50 - Series update

To update a field, check the little box located at the beginning of the line and then edit the content of the text field(s).

Type in this field the new text or date value,

or go to the browser, select the text to copy, right-click on this cell, select 'Copy', go back to this dialog box, right click on the field to update and select 'Paste'.

√ When the values are corrected, press the "Save" button.

This will update the information associated to all the series selected in the first step of this procedure. All the fields having their little box checked will be updated on all the servers of the institution.

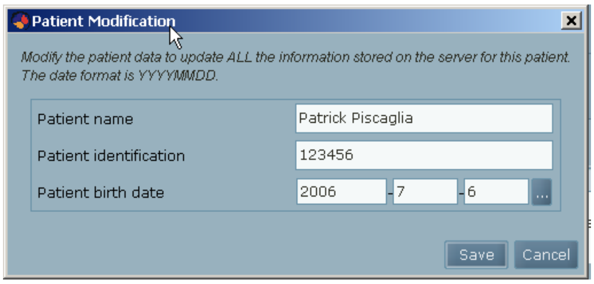
1.1.12.2. Patient Update

Updating a patient means permanently changing some information about a patient, e.g. the birth date. This update is applied to all the series of this patient currently on the servers, and to all the future series of this patient that will enter the system.

In the Browser, select ONE patient or one study or series of ONE patient.

√ Select *[Documents*] [*Update/Merge Patient...*]

The dialog box depicted on Figure 51 shows the information about the patient.



Modify the patient data to update ALL the information stored on the server for this patient.
The date format is YYYYMMDD.

Patient name: Patrick Piscaglia
Patient identification: 123456
Patient birth date: 2006 - 7 - 6

Figure 51 - Patient update

The patient birth date must be encoded in the format year (4 digits) month (2 digits) day (2 digits). Press the button [...] at the right of the date to open a calendar for selecting the date.".

Update the information and press 'Save' to update your local information and the information on all the servers of the hospital.

This will, according to the DICOM standard, transform ALL the patients having the original 'Patient identification'. Take care that this 'Patient identification' is unique!

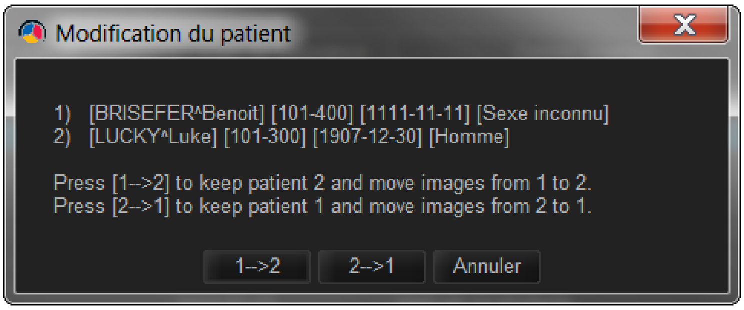
1.1.12.3. Patient Merge

This operation will permanently move the series of one patient to another patient, for all the series currently on the server and all the series to come. This method must be used to manage double entries, NOT to transfer SOME series (See the series update for this).

In the Browser, select TWO patients or studies or series of TWO different patients.

√ Select [*Documents*] [*Update/Merge Patient…*]

The dialog box depicted on Figure 52 shows the information about both patients.



1) [BRISEFER^Benoit] [101-400] [1111-11-11] [Sexe inconnu]
2) [LUCKY^Luke] [101-300] [1907-12-30] [Homme]

Press [1-->2] to keep patient 2 and move images from 1 to 2.
Press [2-->1] to keep patient 1 and move images from 2 to 1.

Figure 52 - Patient merge

Press the "1□2" button to remove patient 1 from the database and associate all the studies of this patient to patient 2.

Press the "2□1" button to remove patient 2 from the database and associate all the studies of this patient to patient 1.

These changes will take place in your local database and on all the servers of the hospital.

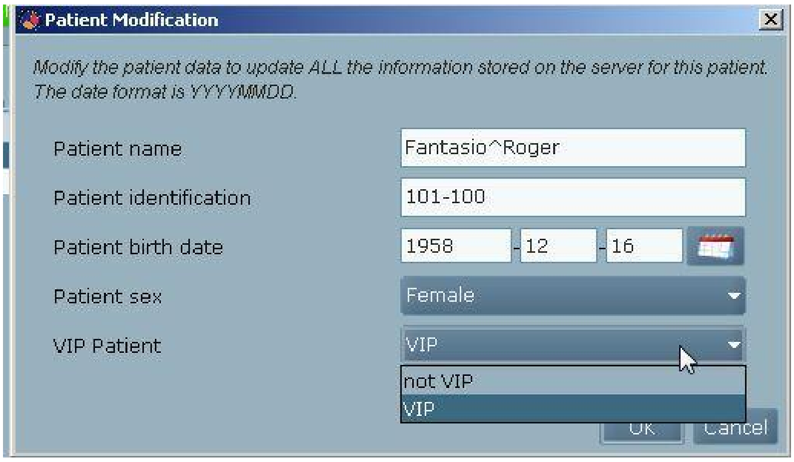
According to the DICOM standard, this will move ALL the data, present and future, on one patient to the other and delete the first patient. Don't use this to move some series accidentally performed under a bad patient identification! Take care that the 'Patient identification' is the unique identifier used to mix the patients. Don't create duplicates of this patient identification!

1.1.13. V.I.P. patients

When a patient is flagged as "V.I.P.", all accesses to these images can be logged and logs can be sent by email to a list of recipients. All data relative to VIP patients that are usually visible in the browser or viewer are replaced with stars ("******"), except patient name and identification number.

To manually change the status of a patient, authorized users have two possibilities once the patient is selected:

- √ Select [*Document*] [*Mark as VIP*] or [*Document*] [*Remove VIP status*], or
- √ Select [Document] [Update/Merge Patient] to show the patient update/merge dialog box shown in Figure 53 and change the VIP status.



Patient Modification

Modify the patient data to update ALL the information stored on the server for this patient.
The date format is YYYYMMDD.

Patient name: Fantasio^Roger
Patient identification: 101-100
Patient birth date: 1958 - 12 - 16
Patient sex: Female
VIP Patient: VIP

Figure 53 - Change VIP status

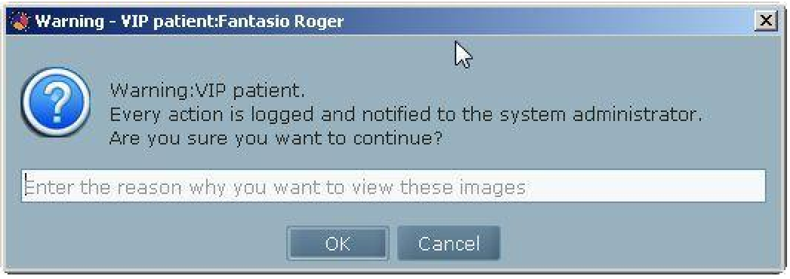
This VIP status of a patient may also be automatically updated is the modalities and/or the RIS generate the appropriate notification.

As soon as a patient is VIP, only his name and identification number are visible in the browser, as shown in Figure 54.

Patient name ▲	Patient ID	Patient birth date	Sex	Last exam
[All]	[All]			
Fantasio Roger	101-100	***	***	***

Figure 54 - VIP patient shown in the browser

Any attempt to open or view any information of a VIP patient will show the warning dialog of Figure 55 and send logs to the configured email addresses.



Warning - VIP patient:Fantasio Roger

Warning:VIP patient.
Every action is logged and notified to the system administrator.
Are you sure you want to continue?

Enter the reason why you want to view these images

Figure 55 - VIP patient: warning

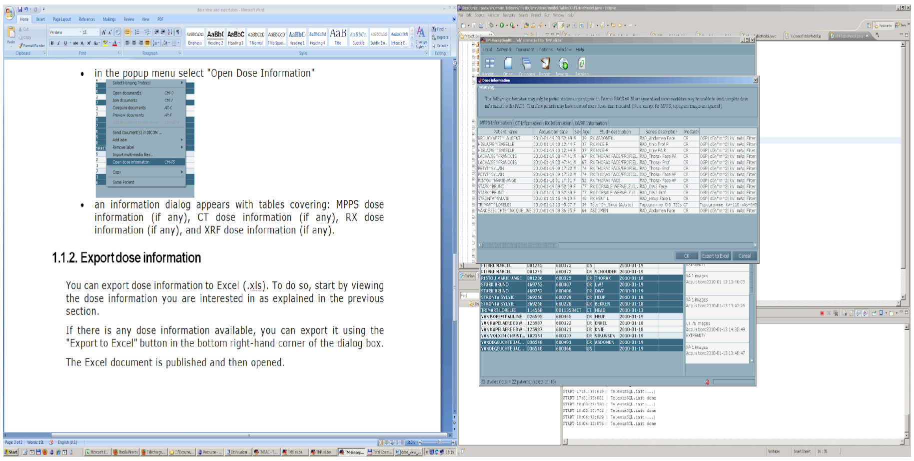
1.1.14. Dose management

1.1.14.1. View dose information

This section covers how to open and view dose information relating to the images/series/studies currently selected in the TMRHE search browser.

To open dose information, proceed as follows: select in the browser all the images/series/studies you are interested in knowing dose information. Right-click and in the pop-up menu select [*Open Dose Information*].

The information dialog (see Figure 56) appears with tables covering: MPPS dose information (if any), CT dose information (if any), RX dose information (if any), and XRF dose information (if any).



- in the popup menu select "Open Dose Information"
- an information dialog appears with tables covering: MPPS dose information (if any), CT dose information (if any), RX dose information (if any), and XRF dose information (if any).

1.1.2. Export dose information

You can export dose information to Excel (.xls). To do so, start by viewing the dose information you are interested in as explained in the previous section.

If there is any dose information available, you can export it using the "Export to Excel" button in the bottom right-hand corner of the dialog box.

The Excel document is published and then opened.

Figure 56 - Dose information window

1.1.14.2. Export dose information

You can export dose information to Excel (.xls). To do so, start by viewing the dose information you are interested in as explained in the previous section.

If there is any dose information available, you can export it using the "Export to Excel" button in the bottom right-hand corner of the dialog box. The Excel document is published and automatically opens.

1.2. Freeze / unfreeze the workspace

Typically, while you’re working on a complex study, having opened several viewers, selected images, zoomed etc, a colleague knocks on the door, asking urgently your advice for another patient. Either you find another computer, or you lose your work for showing the other patient’s series on your computer.

This situation will never happen again with the ‘Freeze’ and ‘Unfreeze’ functionality. In one click, close all your workspace. Open other viewers. An then in one click, restore your workspace to the state it was just before your colleague knocked on the door.

The Freeze Workspace option will save the state of the image viewers (2D and MPR), video viewers, Structured Report viewers, previewers, browser search and One-Click Comparison. Beware that the filmer and the drawing and measures won’t be saved (a warning message will remember you of this fact before really loosing them).

To freeze the workspace,

√ Press in the viewer or in the browser the button ‘Freeze’ (see section 2.15.5 page to know how to add a button in a toolbar), or

√ Select in the browser or in any viewer the menu [*Window*] [*Freeze workspace*]

To restore the saved workspace,

√ Press in the viewer or in the browser the button ‘Unfreeze’, or

√ Select in the browser or in any viewer the menu [*Window*] [*Unfreeze workspace*]

To reset or cancel a saved workspace,

√ Select in the browser or in any viewer the menu [*Window*] [*Reset workspace*].

1.3. Measure follow-up

The main goal of the Measure Follow Up is to compute and display the evolution of some selected lesions across the time. The evolution can be displayed individually for each lesion or globally. At each step, a report will be generated automatically.

Currently, no specific RECIST, CHESION, WHO or other protocol is defined. The user has the full control over the functionality.

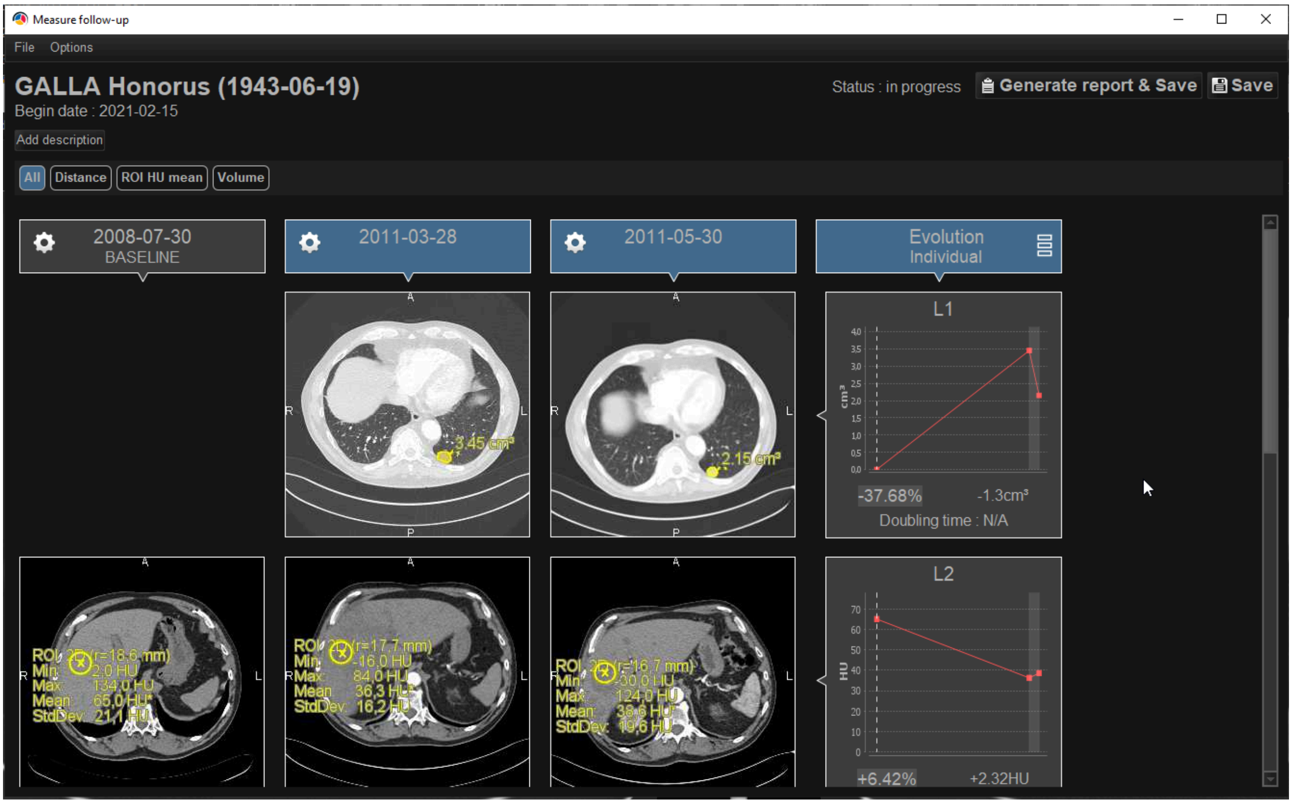


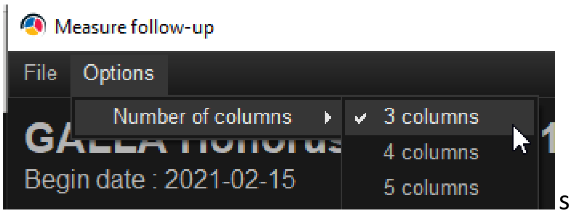
Figure 57 - Measure follow-up

Each column represents a study and each line a followed lesion. The last column is used to display evolution information.

1.3.1. Basics

- A patient can have several Measure Follow Ups but only one can be “In progress” and open at the same time.
- When a step is finished (a step can be considered as a study), the user needs to validate it and a full report will be automatically generated with all the available information.
- When a step (study) is validated, a lesion can always be added. When this occurs, all the reports will be re-generated.
- The NADIR (the best evolution from the beginning of the Follow Up) is automatically computed when a modification is done.
- You can have different type of measures in one measure follow-up. You can display all the measures or select the type that you want to see.

- You can select the numbers of columns.



1.3.2. Open an existing Measure Follow-up

There are various ways to open an existing Follow-up. From the browser:

√ Select menu [*Document*] [*Measure Follow Up*]

√ Click the browser toolbar icon “Measure Follow Up”

√ In the browser tables, click in the info column on the Measure Follow-up icon

√ Right click on a Patient/Study/Series and select [*Measure Follow Up*]

It can also be open from the viewer:

√ Select menu [*Display*] [*Measure Follow-up*]

√ Click in the viewer toolbar icon “Measure Follow Up”

1.3.3. Window management

The window displaying the Measure Follow-up is divided in two areas:

- The top of the window containing the global information about the follow-up (status, description, begin date, …) and the patient (name, birth date, …)
- The rest of the window is used to display the lesions contained in the Follow Up and the evolution.

The size of the window allows only to display simultaneously 3 columns for the lesions and one column for the evolution information.

If there are more than 3 studies in the Follow-up, the user can select which studies to display. By default, the baseline is always displayed as the first column. The two other columns display the two more recent studies.

To change the study displayed in a column, use the menu button available in the header of the concerned column “⚙”. The list of the available studies (represented by a date and a label) is displayed in the open menu:

Available studies :

2011-02-21 - BASELINE

2011-03-21

2011-04-29 - NADIR

2011-08-08

Note: The baseline can be only displayed in the first column.

1.3.4. Create a new Measure Follow-up

The creation of a new Measure Follow-up is automatically performed at the first lesion definition. If there is another Follow-up for the same patient, it must be closed (finished) before being able to create a new one.

1.3.5. Adding a new lesion

To add a lesion to a Measure Follow-up, first perform the measure (see section 2.5 page). Currently, only distance measures are supported.

To add the most recently drawn distance to the measure follow-up:

√ Select the menu [*Add measure to follow-up*], or

√ Press the 'Ctrl' 'M' keys, or

√ Click on the 'Add to measure follow-up' button of the viewer toolbar

To add a specific measure to the measure follow-up:

√ Right-click on the measure and select the menu [*Add measure to follow-up*], or

√ Click on the measure and press the 'Ctrl' 'M' keys, or

√ Click on the measure and on the 'Add to measure follow-up' button of the viewer toolbar

When the measure is added, the follow-up is automatically open (it always opens at its last position). The lesion is added to the corresponding column (i.e. to the corresponding study). It is placed at the end of the column. Remember that each line of the table represents one lesion: move this new measure up or down to let it corresponds to the correct lesion. A lesion cannot be added twice.

Name L1
Position 0
Type Target
Measure Volume (with mask)
Volume 5.17 cm³

Figure 58 - new lesion image and actions

The lesion thumbnail contains two different areas that appear only when the mouse passes over the image:

- The toolbox in the top right corner containing the actions available on the lesion.

🔍 Open a viewer for the series displaying the corresponding measure

⊖ Remove the lesion from the Follow Up (only available when the Measure Tracker is not yet validated)

⬆ Move the lesion on line up

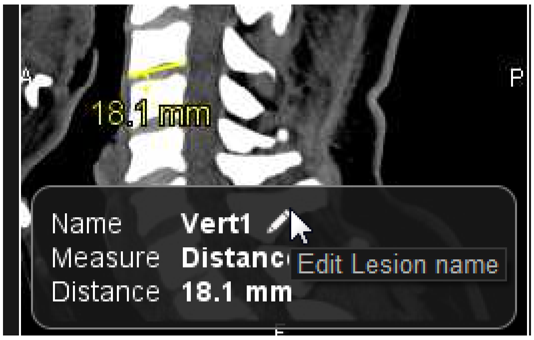
⬇ Move the lesion on line down

👁 Hide the lesion (only available when the study is validated (see infra))

- The information panel in the bottom containing the general information about the related lesion.

Note: Hidden lesions are stacked on the bottom of the Follow Up and are disabled.

The information panel displays information about the lesion such as its name, the type of measure, the value …



Name **Vert1**
Measure **Distanc**
Distance **18.1 mm**

The information panel allows editing the name of the lesion: place the mouse cursor over the name of the lesion. A pencil will appear. Double click on the name or click on the icon to set the field in edition mode.

Name L2

Modifying the name of a lesion, all the lesions located on the same line will be modified.

1.3.6. Study level actions

Each column in the follow-up represents a study. Some actions are available in the menu of the title of each column ⚙

✓ Validate the related study

✓✓ Validate all non validated studies

↦ Set the related study as base line

Validating a study means that all lesions have been added and that the report can be generated.

The baseline is by default the first study of the follow-up, but the user can change it, for example if an older study is imported into the PACS via a CD-Rom import. At this moment, all the reports will be re-generated.

1.3.7. Follow-up level actions

Some global actions are available for the Follow Up. The buttons located at the top right of the Measure follow-up windows allow to:

Save the current state of the follow-up

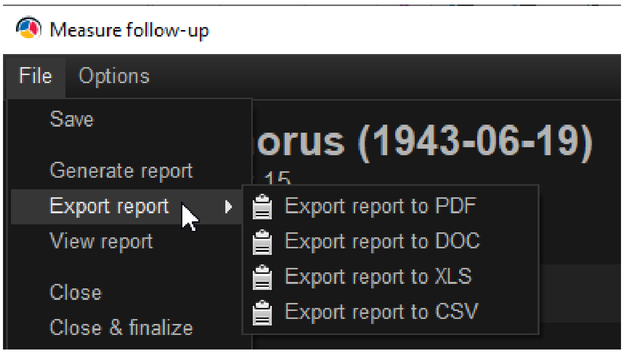
Generate report & Save

Press the "Add description" button located at the top left of the window to define a global description for this follow-up.

BUBOIS GILBERT (1959-02-22)
Begin date : 2013-08-12
Status : In progress

Figure 59 - follow-up level actions

You have more actions in the menu file at the top left of the window:



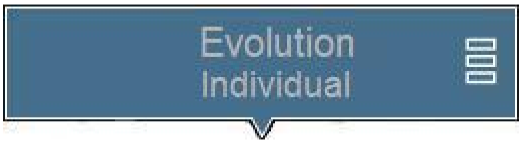
- finalize the follow-up by the menu File/Close & Finalize
- Generate report
- Export report in different formats
- View the report

1.3.8. Evolution Management

The evolution is displayed in the last column. There are two available evolution modes: individual graphs and global evolution graph.

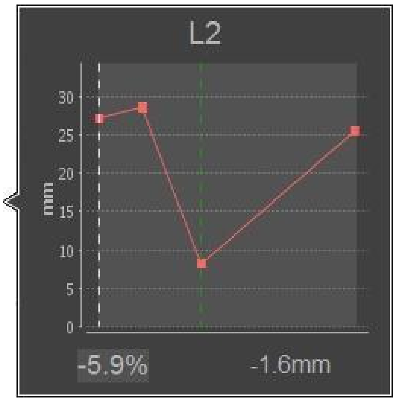
To switch between modes, click on the symbol on the right of the evolution column title: Σ & ☰

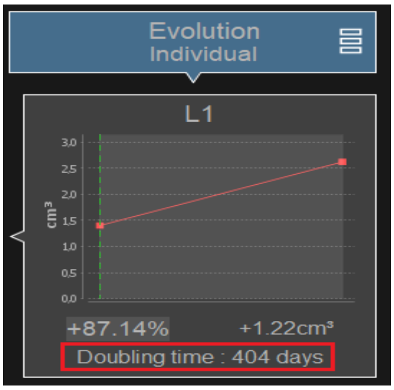
1.3.8.1. Individual evolution mode



In this mode, the evolution is computed individually for each lesion.

Each lesion (or line) will contain a specific evolution chart. In this chart, each lesion value will be added and a red line will define the evolution. The unit is the same than the measure (in this case, for the distance, it's in mm).





In this chart, we can see the evolution line in RED. There are also two vertical markers: a WHITE marker used to easily display the baseline and a GREEN marker used to easily display the NADIR. The evolution range is displayed with a LIGHT GRAY background (in this case the evolution covers the period from the baseline to the last study).

On the bottom, two others information are displayed. The relative (on the left) and the absolute in mm (on the right) evolution values computed according to the selected begin and end evolution period.

For the tool "lung nodule volume" this chart also shows the 'Doubling time' when you select two columns in 'Individual Evolution' mode (the value only appears in cases of an increase).

1.3.8.2. Global evolution mode

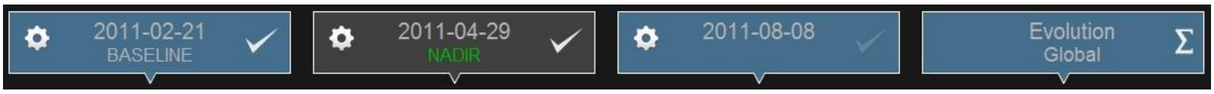
In this mode, the evolution is computed for the sum of the measures of each study (only non hidden lesions are taken into account). Only one chart is displayed in the evolution column

In this chart, we can see the evolution line in YELLOW. There are also two vertical markers: a WHITE marker used to easily display the baseline and a GREEN marker used to easily display the NADIR. The evolution range is displayed with a LIGHT BLUE background (in this case the evolution covers the period from the baseline to the last study).

On the top of the graph, the unit used is selectable. In this case the selected unit is **mm**. Simply click on "mm" or "%" to change the unit to use.

On the bottom, the relative (on the left) and the absolute in mm (on the right) evolution values computed according to the selected begin and end evolution period are displayed.

In the two modes (individual and global), the user needs to select the base and the target studies. The base study can be described as the beginning and the target study as the end of the evolution to compute. The selection is visible via the color of the column title. A blue title means that it is selected. The base is always the oldest selected study.



In this case, the baseline study 2011-02-21 is the base study and the target study is the 2011-08-08. To change the selection simply click on the column title to (un)select it.

1.3.9. Delete a Measure Follow-up

You can delete a measure follow-up if you have the permission to:

√ Right-click in the browser on a line containing the measure follow-up that you want to delete.

√ Select the menu [*Document*] [*Delete measure Follow-up*] and choose to delete one specific follow-up or all the follow-ups of this patient.

1.4. General browser commands

1.4.1. Refresh local/server lists

The *TM-Reception* browser presents a mixture of three "lists" in each view: it mixes the list of local patients/studies/series and the list of the patients/studies/series located on the server.

If new documents are available on the server, it doesn't immediately update all the *TM-Reception* users connected. One reason is that if you're working at home, you don't necessarily want to keep the connection opened all the time.

You can refresh each list either selectively or all together.

√ Select [*Local*] [*Refresh local list*] to refresh the local documents, i.e. to ask *TM-Reception* to scan all your "local directories" for documents.

√ Select [*Network*] [*Refresh server list*] or press the 'F5' key to refresh the server list, i.e. to ask the server an updated list of all the documents.

√ Click on the refresh icon Refresh to force a local and server refresh.

If the connection is closed, asking for a refresh re-opens it.

It is possible to automate this process and ask the *TM-Reception* to automatically ask the server an updated list every 3 minutes. Through this option the *TM-Reception* browser will always display a list up to date of the patients and documents available for the user currently connected.

√ To activate the auto-refresh function, select [*Network*] [*Auto refresh*].

If the auto refresh function is activated, the menu line is checked.

1.4.2. Cancel

Some actions need to be cancelled, as for example the download or opening of a study, or the reception of a very long list of headers if the "Limit number of documents" option has been inappropriately unchecked.

To cancel the current operation :

√ select [*Network*] [*Cancel network operations*] or

√ press the 'Esc' key (at the top left of the keyboard), or

√ click on the Cancel icon.

If for example you want to stop the download of a document, just click on the *Cancel* button and the download will stop after the end of the currently transmitted block of information (a block is either an image for studies with many small images or a part of an image for bigger images).

The cancel of the decompression and display of images into a viewer is also possible directly from the viewer, as shown in 2.11 page .

1.4.3. Change local directories

The browser displays two classes of documents: the documents stored on the server, and the *local* documents.

What is concerned by the *local* documents depends on your settings. Originally, the local files only include the files contained in the default save directory.

You can add as many directories as you want to the *local* directories.

√ Choose [*Local*] [*Change local directories list*].

A list of all the directories making up the *local* directory list is displayed in a small window, together with buttons to add and remove a directory to the list.

- To add a new directory to the list, click on the [*Add ...*] button. A file dialog opens, that lets you select a directory.
- To remove a directory from this list, click on the directory in the list to select it, and press [*Remove ...*].
- There is a special directory, the cache directory (see section 1.8.5). This directory is the directory called *header* and is sub-directory of the directory where your *TM-Reception* is installed. If you add this directory to your *local* directory, all the documents that are in your cache will be shown in the local files. Beware that this directory is only temporary and that the cache size is limited. At each cache cleaning, all or a part of these files are deleted.

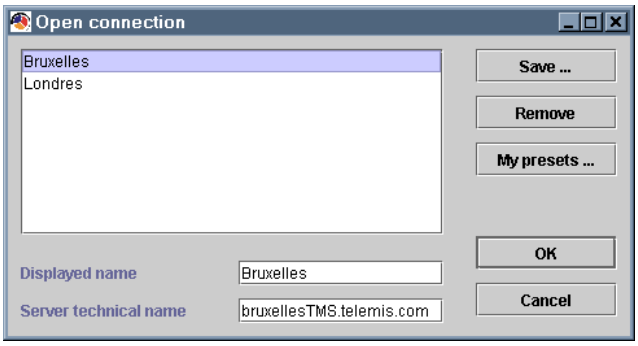
If files have been added to one of those directories by an external program,

√ Choose [*Local*] [*Rescan local directory list*] to rescan those directories and have access to the updated content.

1.4.4. Connect another server

The default connection connects the *TM-Reception* program to the closest *TM-Server* (TMS). In some cases, it is useful to connect to another TMS. Imagine that you work by hospital *A* and hospital *B*. A *TM-Reception* in hospital *B* will normally connect to TMS *B*. If you want to connect to the TMS of hospital *A*:

- √ Choose [*Network*] [*Connect …*]
- √ Select one of the servers shown in the sub-menu to directly connect to this server,
- √ Or select [*Open connection …*] to show the window of Figure 60 that prompts for the server that you want to connect.



Displayed name: Bruxelles
Server technical name: bruxellesTMS.telemis.com

Figure 60 - Open connection...

- √ Select a *TM-Server* from the list in the window. If you click on an element of the list, the *Server Displayed Name* and *Server Technical Name* text fields display the name showed in the list and the Telemis internal name of this server.
- √ Click on the *OK* button to connect to this server.
- √ You can manually enter values in the *Server Displayed Name* and *Server Technical Name* text fields, and click on *OK* to connect to this server.
- √ If you plan to regularly connect to this server, you can save its parameters. Click on the *Save* button to save this new server preset in your profile.
- √ To update the list with all the server presets that are present on your profile, click on the *My presets* button.
- √ To remove a preset from your profile, you click on the *Remove* button.
- √ Click on the *Cancel* button to exit the window without connecting.

1.4.5. The 'cache' directory

Most of the documents that you will access are probably stored somewhere on a *TM-Server* and accessed via the network. If you had to do all the operations on these remote documents, passing through the network for each operation, *TM-Reception* would be quite slow.

To solve this problem, each remote document that you access is downloaded first on your hard disk, in a temporary directory: the *Cache directory*. Every operation (decompression, visualisation ...) is then performed on this local temporary copy of the original document and is thus much faster.

This directory must be cleaned sometimes. The cache can be cleaned manually or automatically:

To *manually* empty this cache directory,

√ select [*Options*] [*Clear Cache*]

Be careful that once the cache is cleaned, every document that is stored on the server will have to be downloaded again before each operation. Cleaning the cache directory doesn't of course change anything to the original documents stored on the *TM-Server*s.

The cache is *automatically* checked each time you start the *TM-Reception*, and at a regular time interval. If the cache size is above the limit, the oldest files are automatically removed.

1.4.6. Change password

According to the security rules of the hospital, each user has or not the possibility to change his password :

√ Choose [*Options*] [*Change password …*].

The window depicted in Figure 61 appears.

Enter the login name that you want to change the password of, the old password and the new one. You must type the new password twice to be sure that you don't make any typing mistake.

The password is updated when you press 'Ok'.

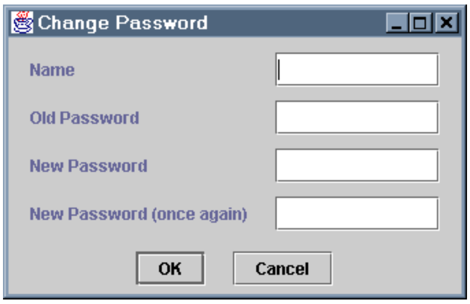


Figure 61 - Change password window

1.4.7. View log file

During some operations, or if errors occur, the *TM-Reception* writes textual information in a "log file".

√ To view the content of the log file, select [*Options*] [*View log file*]

1.4.8. View DICOM logs

Each time the TMRHE performs a DICOM Send or a DICOM Query/retrieve operation, it logs the date/time, the study description, the DICOM send destination and the transmission status (success or error).

Importation of CD via the TMR or TMRHE also report errors in this DICOM log.

The DICOM logs window automatically opens after a transmission or importation error.

√ To manually open this log window, select in the browser [*Options*] [View DICOM logs]

1.4.9. View shortcuts list

√ Select *[Help] [Shortcuts],*

To view the list of all the mouse and keyboard shortcuts, of the browser and the viewer, as shown in Appendix 10.1 page .

1.4.10. Visualise the user guide and reference manual

Select [*Help*] [*Quick user guide*],

To view the Acrobat Reader PDF version of the small user guide (about 20 pages A5 format).

Select [*Help*] [*Reference manual*],

To view the Acrobat Reader PDF version of this complete *TM-Reception HE* reference manual.

1.5. Management of the viewers

The browser gives several functions to work with the viewer: lay them out on the screen(s), close them all or hide the browser.

1.5.1. Arrange viewers

If you want to visualise simultaneously two series displayed in two separate viewers, the best way is to lay the viewers out on the screen(s), one next to the other, in order to view both of them together.

You can do this manually through resizing and moving the viewers. You can also do this automatically:

√ Select [*Windows*] [*Arrange all viewers*], or

√ Press the ’Ctrl’ and ‘F4’ keys together.

If you have one screen and want to arrange two viewers, they each will open on a half screen. If you have two screens, each will fully occupy one screen. Figure 62 shows some examples.

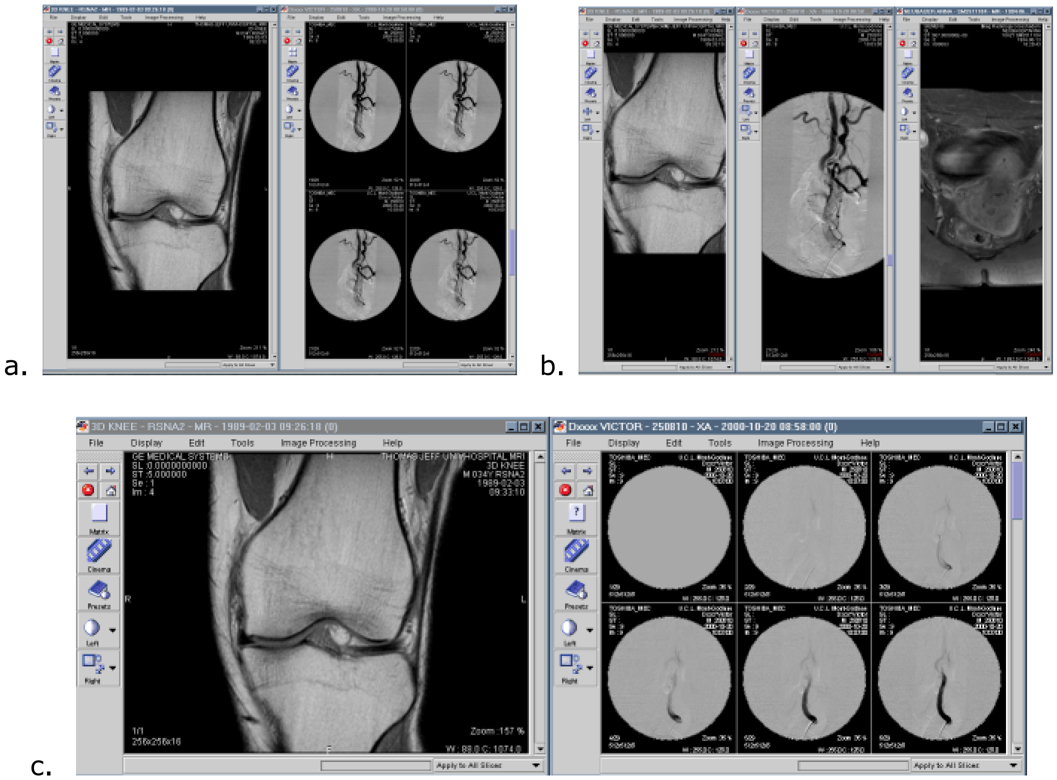


Figure 62 - Viewers automatic layout: a. 2 viewers on one screen,
b. 3 viewers on one screen, c. 2 viewers on two screens

Only the *TM-Reception HE* version manages multiple screens but all the versions can arrange viewers on one screen.

You can also trigger this command from the viewers, as shown in section 2.4.4 page .

From the Previewer, you can set this behaviour as the default layout of the viewers: check the "Auto-arrange" option in the previewer (see section 1.5.4 page for the Previewer).

To directly compare 2 series in 2 viewers, see section 1.5.3 page .

1.5.2. Close all viewers

To close all the viewers opened,

√ select [*Window*] [*Close all windows*].

1.5.3. Browser to front/back

When you work with Telemis viewers, you sometimes need functions, lists of the browser that is hidden by all the viewers opened. Bringing the browser back on top of the windows with one key should be convenient. Going then back to the viewers should also be eased. The F12 function key switches between browser and viewers.

√ Press the 'F12' function key from the browser or the viewers to send the Telemis browser to the back of the screen. Press again to send it to the front.

1.6. Creation of Telemis documents from local images

The *TM-Reception HE* is able to create a new document from local images, from many file formats (JPEG, GIF, AVI, MPEG, PDF, DICOM etc.). The user selects images, creates a first version of the document in the viewer and then sends this document to the *TM-Server*.

In the *TM-Reception* High-End browser,

√ Select [*Local*] [*Import multi-media files …*], or

√ Press the 'F1' key.

The importation window appears on the screen (see Figure 63).

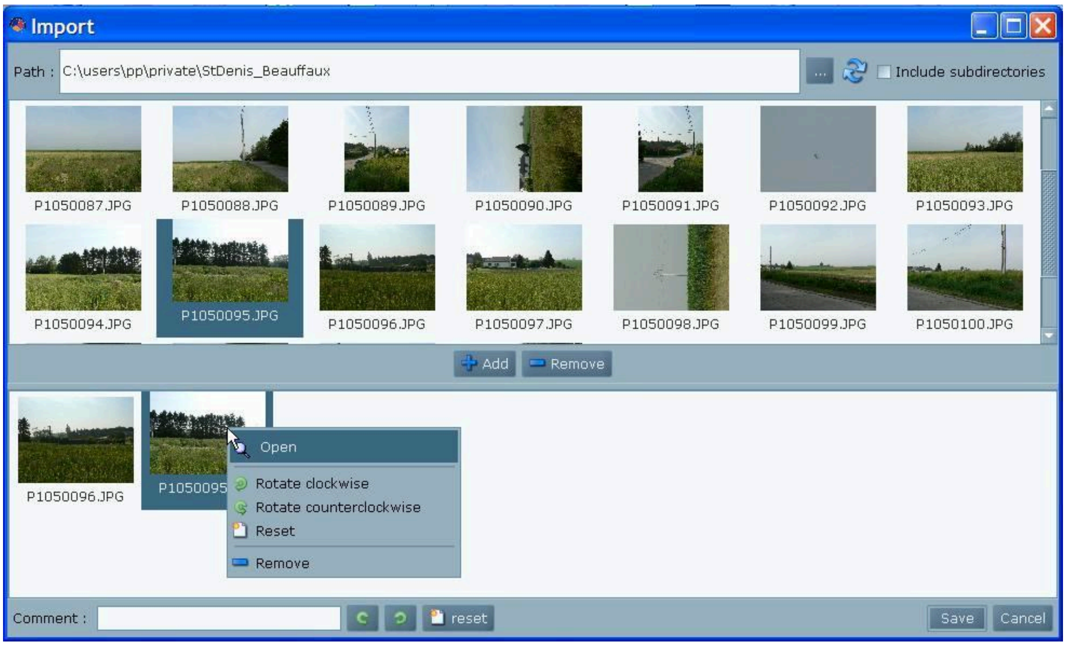


Figure 63 - Create new documents from images

To select a directory where to look for images, press the '…' button (at the top of the dialog box) and select a path. The program will propose to remember this path as the default path for importing images.

All the images of this directory are scanned. Select "include subdirectories" to include the 2 first levels of sub-directories. Use the slider at the right of the list to scroll among all the available images.

Press the ' Refresh' button to refresh the list if some additional files have been added, removed or modified in this directory.

To select one or several images on the top list, click on the images. Use the 'Ctrl' or 'Shift' keys while clicking to select several images.

Right click on an image and choose [*Open*] to open a viewer containing this image or all the selected images to preview these images.

Use the ' Add' button to transfer the selected images from the top to the bottom list, i.e. to mark them as 'to be imported'.

In the bottom panel, right click on any image and select [*Open*] to preview it in a viewer (still image viewer or video player, according to the content), [*Rotate clockwise*] or [*Rotate* *counterclockwise*] to rotate the image, [*Reset*] to reset the rotation. You can also press the ↺, ↻ or 🗋 icons to manage the image rotation.

Select one or several images in the bottom list and type a comment in the 'Comment:' text box. This comment will be associated with the image(s) and show at the top right of the viewers.

Press the '▭ Remove' button or right click on image(s) to remove the selected images from the import list.

To conclude the image importation, press the 'SAVE' button. Encode the patient and study information into the dialog box that opens, or press the 'Worklist' button to directly fetch this information into the worklist server.

You can bypass the first part of the importation if the images are selected in an external program. Select some images in e.g. the File Explorer (or the Finder on Mac). Drag them to the browser on a patient or a study.

The importation dialog opens, showing only the bottom list containing the selected images.

When pressing 'Save', the patient (and study) details are already filled according to the patient or study on which the images have been dropped.

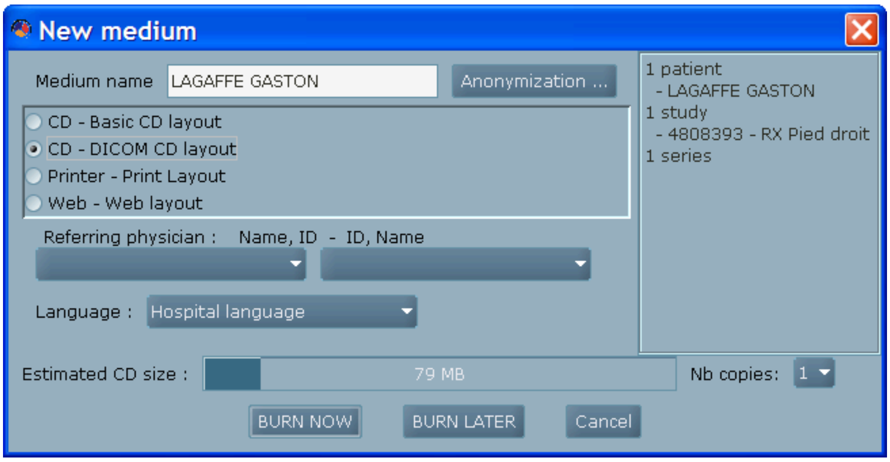
1.7. Requesting the *TM-Publisher* to produce a medium

The *TM-Reception HE* may be used to order the *TM-Publisher* to burn a CD, print series on paper etc. The *TM-Publisher* must be installed in the hospital and the *TM-Reception HE* must be configured properly.

Select some series, studies or patients in the browser. To open the TM-Publisher Controller interface show on Figure 64,

√ select [*Document*] [*Create a new medium via the TM-Publisher*], or

√ select the "New medium" tool in the browser toolbar



New medium

Medium name: LAGAFFE GASTON

○ CD - Basic CD layout
● CD - DICOM CD layout
○ Printer - Print Layout
○ Web - Web layout

Referring physician : Name, ID - ID, Name

Language : Hospital language

Estimated CD size : 79 MB

Nb copies: 1

1 patient
- LAGAFFE GASTON
1 study
- 4808393 - RX Pied droit
1 series

Figure 64 - new TM-Publisher medium

If the selected series concern only one patient, the name of this patient is used as CD name and typed in the text box at the top of the interface. Update this text if desired. If images come from several patients, the name of the first patient is used as CD name, but displayed in red in the interface to attract your attention.

The rightist part of the interface is a summary of the number of patients (and their name), the number of studies (and the study index if there is one study) and the number of series.

The top left part of the interface contains a list of (medium – layout) choices. In this example, four layouts are available to burn a CD and one layout to print on paper.

If available in the hospital, the referring physician name and ID can be selected. In the first combo box, the list is sorted according to the physician's name while it is sorted according to the physician's index in the second list.

The default language depends on the hospital. Other languages are available and may be selected via the 'Language' combo box.

The bottom right combo box lets you select the number of copies to be printed.

On the bottom of the dialog box, the size of the CD is estimated. The images won't fit on the CD if the box is filled in red. In this situation, either manually cancel and remove some series, or let the *TM-Reception HE* split the images on several CDs.

√ Press BURN NOW to send the medium creation and printing commands to the *TM-Publisher*.

Press BURN LATER to simply request the *TM-Publisher* to create the medium in its database. This medium will be printed later on when requested by a user.

If the CD size exceeds the CD capacity, the program will propose to cancel or automatically split the medium into several media. Press 'Split' in this dialog box to have the medium split, trying to keep if possible patients and studies on the same CD. A new dialog box informs you that the CD is split and in how many CDs. Press 'Go' to burn these CDs.

Your current *TM-Server* will forward this medium creation/printing order to the *TM-Publisher*, together with the series that would be present on the *TM-Server* but missing on the *TM-Publisher*.

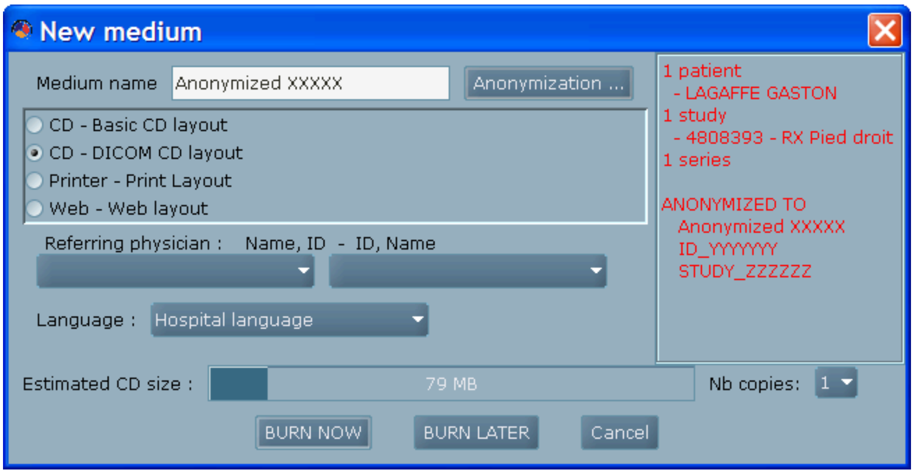
1.7.1. Production of an anonymized medium

Producing an anonymized medium, having the patient name, identification and study index changed, and all other patient information removed (military status, address etc.) is a very easy to perform operation via the [*Create a new medium*] interface.

Click on the [*Anonymization …*] button on the top of the *New Medium* dialog box shown in Figure 65.

Change the patient name, identification and study ID and press the [*Save*] button.

The *New Medium* interface now shows the old and new patient information, and the medium name is now the anonymized patient name. In this example, the medium will name the patient as ‘XXXXX’ etc.



Medium name: Anonymized XXXXX

○ CD - Basic CD layout
● CD - DICOM CD layout
○ Printer - Print Layout
○ Web - Web layout

Language : Hospital language

Estimated CD size : 79 MB

Nb copies: 1

1 patient
- LAGAFFE GASTON
1 study
- 4808393 - RX Pied droit
1 series

ANONYMIZED TO
Anonymized XXXXX
ID_YYYYYYY
STUDY_ZZZZZZ

Figure 65 - Create a new anonymized medium

1.8. Creation of a CD-ROM content on the local computer

The *TM-Reception HE* can generate manually the content of a CD-ROM containing the selected studies. This function produces the same CD content as the *TM-Publisher* does, except that the *TM-Publisher* does this operation and burns the CD and its label automatically.

The CD-ROM contains:

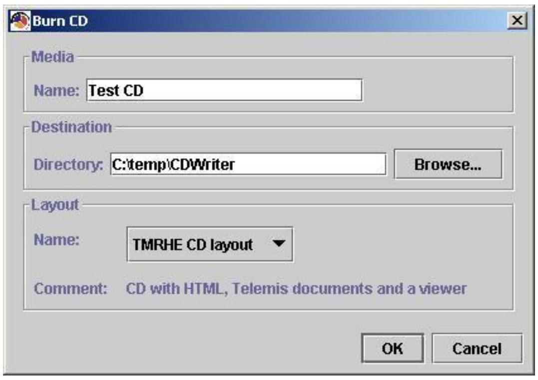
an HTML version of the images, available on any computer (even a slow computer) without any program to install.

- a *TM-Reception Lite* program (the standard *TM-Reception*, without the connectivity and with a subset of the functions) that runs from the CD (no installation required) and delivers a high quality viewer, for computers at least as fast as a Pentium III.

To generate the content of the CD-ROM, select some studies or patients in the browser,

√ Select [*Document*] [*Burn document(s) on CD …*]

The 'Burn CD' window appears on the screen (see Figure 66)



Name: Test CD

Directory: C:\temp\CDWriter

Name: TMRHE CD layout

Comment: CD with HTML, Telemis documents and a viewer

Figure 66 - Burn CD window

The media name is by default the patient name if only one patient is concerned with the studies. If several patients will be present, type in a media name in the first text box.

If needed, change the destination directory, where the files will be written. Pay attention that the content of the directory will be deleted before the generation of a new CD content.

If several layouts are available, select the appropriate one ("TMRHE CD Layout" is the default layout).

√ Press 'OK' to generate the content.

A progress bar explains the status of the content creation.

The directory contains a start-up file: index.html. It also contains files to allow automatic start-up of the CD on the Windows platforms.

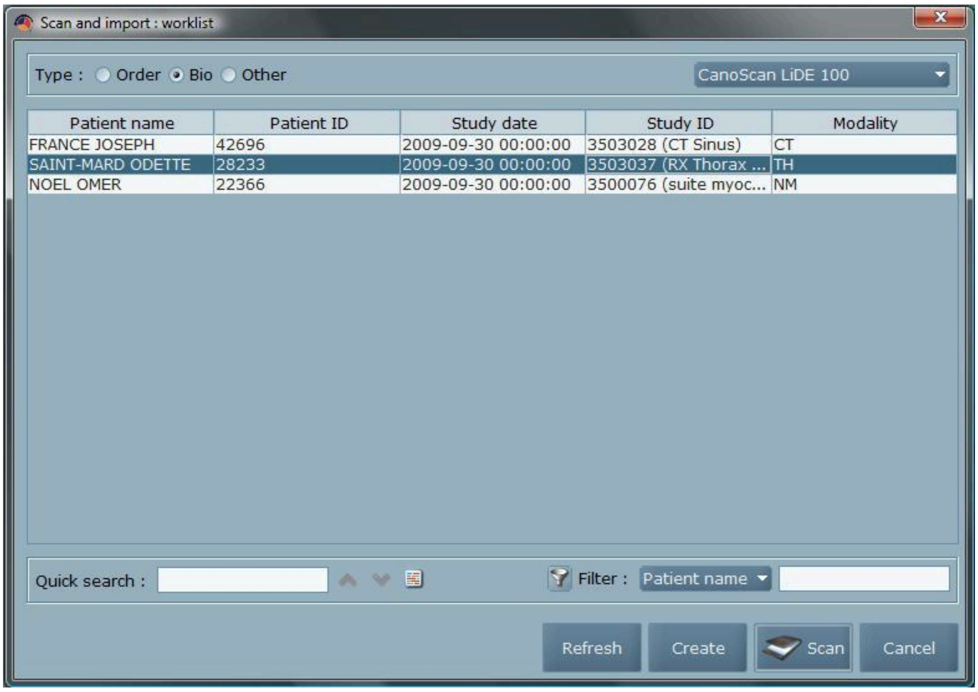
If your destination directory is a "direct CD" virtual drive, just eject the CD to let is being really burned. If your destination directory is a standard directory, you can burn the content of the directory onto a CD.

1.9. Scan and import external documents

Even in the film-less hospital, there remain many papers: external laboratory results, study orders etc. To scan those external documents and import them into the PACS:

√ Select [*Local*] [*Scan & Import*]

The main interface of this scan & import functionality opens, as shown in Figure 67.



Scan and import : worklist

Type : ○ Order ● Bio ○ Other   CanoScan LiDE 100

Patient name	Patient ID	Study date	Study ID	Modality
FRANCE JOSEPH	42696	2009-09-30 00:00:00	3503028 (CT Sinus)	CT
SAINT-MARD ODETTE	28233	2009-09-30 00:00:00	3503037 (RX Thorax ...	TH
NOEL OMER	22366	2009-09-30 00:00:00	3500076 (suite myoc...	NM

Quick search :   Filter : Patient name

Figure 67 - Scan & Import documents

Select the worklist corresponding with the document that you will scan. If the list contains many items, use the 'Quick Search' text area to highlight some of them, of the 'Filter' option to restrict the list. You can manually encode the patient information, corresponding date, description etc. by clicking the 'Create' button.

If several scanners are available on your computer, select the appropriate one in the drop box located at the top right of the interface.

To ease later searches, you can tag the document that will be created, by clicking on one of the pre-defined “type” tags (top left of the interface).

Press the [Scan & Go] button to start scanning the document that you have placed in your paper scanner.

From this moment, if you have correctly placed the paper in the scanner and if the scanner if correctly configured, the remaining of the job won’t require any more human action. Anyway, if you want to manage the remaining of the job, perform as follows.

A second dialog box appears to remind you to put the paper in the scanner, show a confirmation of the selected worklist and ask to press the [*Confirm*] button to go. If you don’t react, the scanning will automatically start after a few seconds.

When the scanning is done, a preview window shows the scanned document. You can zoom in the image, rotate the image. Press the [*Confirm*] button to send the document immediately. If you don’t react, the document will be automatically sent to the PACS after a few seconds.

1.10.Querying a DICOM server

To query a DICOM Server external to the Telemis system and retrieve some studies from this server, see section 3.1 page .

1.11.TM-Mobile

In some situations, you would like to take away some studies to report and continue working off-line later.

The TM-Mobile concept allows exporting from the *TM-Reception HE* (running on a computer) some series or studies plus potentially a viewer on a USB key or any external storage device.

Plug-it later on another computer and view the images with the in-board viewer. There is no need to install any software on this computer.

Please note that the TM-Mobile is not intended to be used on modern mobile devices such as mobile phones or tablets but only on computers.

If several mobile devices are attached to your computer, first select the one to use. Click [*Local*] [*TM-Mobile*] [*Select mobile device*]. See Figure 68.

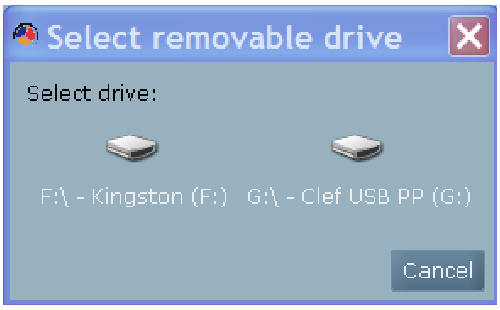


Figure 68 - Select mobile device

To export some series to this mobile device:

√ Select the series to export in the browser.

√ Press [*Local*] [*TM-Mobile*] [*Export to mobile device*].

The *TM-Reception HE* will copy the selected series to the removable drive. If no viewer is present on the drive, a 'mobile' *TM-Reception* will be copied on the drive.

Unplug the removable drive and plug it later on into another computer, at home, at friends etc. Double-click on the 'tmrhe.exe' program located in the root directory of the drive to start the on-board *TM-Mobile* viewer.

In the TM-Reception-HE, select [*Local*] [*TM-Mobile*] [*View mobile device info*] to view the repartition of the space consumed on the disk by the viewer and the images.

1.12. Customizing the browser

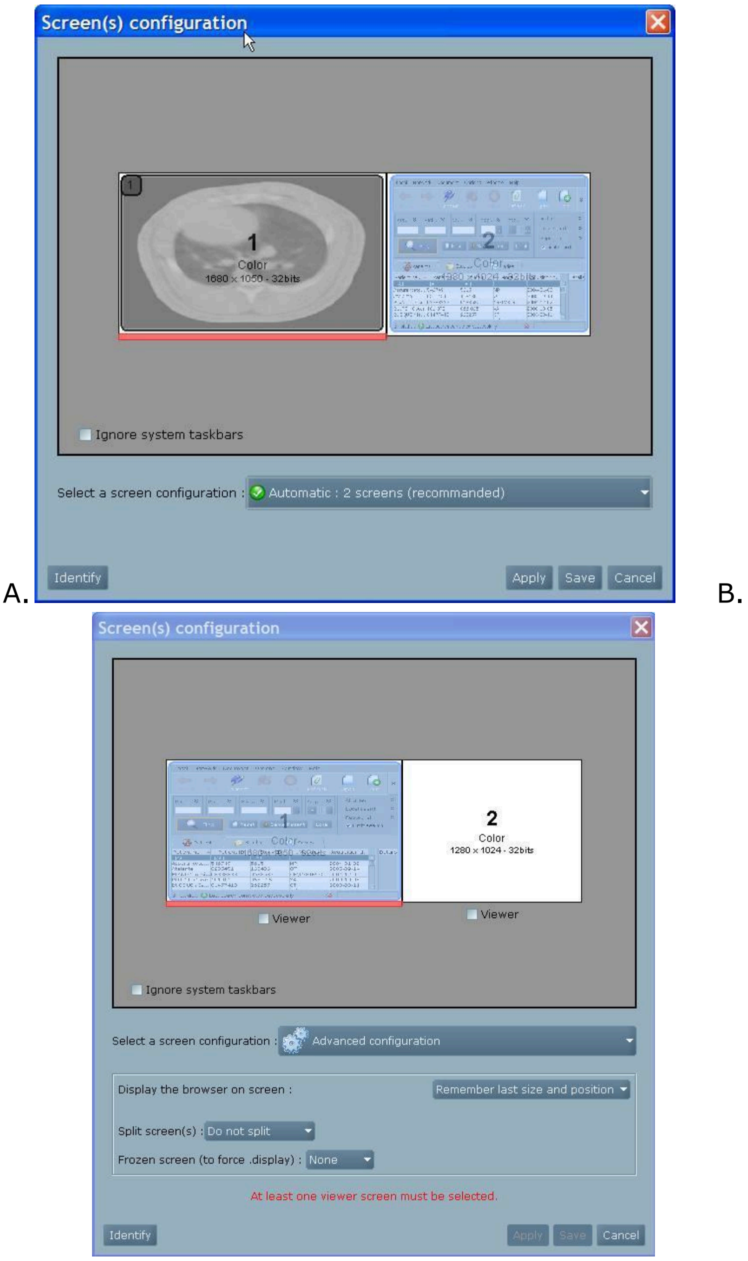
Many options allow the customisation of the *TM-Reception* program: automatic refresh, change language, default search options … This section describes these options.

As a general rule, all the options are changed via the options panel. The options are shown in black colour. Each option changed by the user becomes red.

1.12.1. Screens configuration

To change the screens configuration on a TM-Reception HighEnd,

√ Select [*Options*] [*Screen(s) configuration*] to open the screen configuration panel.



Select a screen configuration : Automatic : 2 screens (recommanded)

Select a screen configuration : Advanced configuration

Display the browser on screen : Remember last size and position

Split screen(s) : Do not split

Frozen screen (to force .display) : None

At least one viewer screen must be selected.

Figure 69 - Screen(s) configuration panel

The main box presents a schematic view of the screens current configuration: number of screens, size and number of colors. It shows the current location of the Telemis browser and the viewer(s).

Check "Ignore system taskbars" to let the browser and viewers ignore the taskbars when setting their position: they will appear behind or in front of the taskbars if these don't automatically hide. Current task bar position is represented in red.

To change the configuration, you can

√ Select in the drop box one of the recommended configurations or

√ Select 'Advanced configuration' to have access to customatisation as shown in Figure 69.B.

- Check the 'Viewer' boxes under each screen to let the *TM-Reception HighEnd* place or not viewers on this screen. All screens containing viewers must have the same size.

- Specify the browser position by choosing to simply remember the last size and position of the browser, or force it to use one of the screens at startup.
- Some graphic cards present two adjacent screens as one big virtual screen. Choose to split this big virtual screen to configure viewers independently.
- Frozen displays are screens where no viewer may be located, except if forced by a particular configuration (contact your local IT manager for more information)

Press "Identify" to show a "1" or "2" sign on each screen, clearly identifying which real screen corresponds to which screen as shown in the graphical interface.

Press "Apply" to apply this setting to the browser and viewers immediately, without leaving this interface.

Press "Save" to keep this new configuration, while saving the previous one as a backup.

1.12.2. Browser options

1.12.2.1. Customise browser toolbar

To customise the content of the browser toolbar, or the order of the buttons, you can either

√ Right-click at any place in the browser toolbar and select the [*Configure toolbar …*] option, or

√ Select the [*Options*] [*Configure toolbar …*] menu.

The dialog box shown in Figure 70 opens.

To **add a button** to the toolbar,

√ Click on one icon of the leftist list, called "available toolbar buttons" and press the "`Add ->`" button.

To **remove a button** from the toolbar,

√ Click in the rightist list, called "current toolbar buttons", on the icon of the button to remove. Press the "`<- Remove`" button.

To change the buttons order in the toolbar,

√ Click in the "current toolbar buttons" on the button to move and press the "Move up" or "Move down" buttons to move the button to the top or to the bottom of the toolbar.

Press "OK" to set the changes, or

Press "Cancel" to cancel the changes.

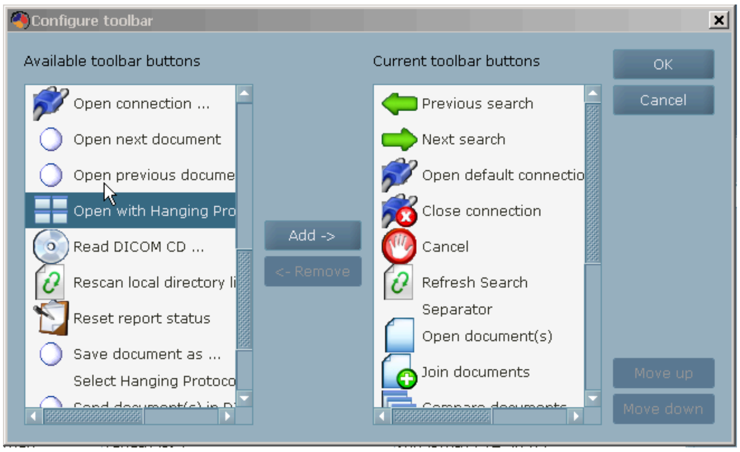


Figure 70 - Configure browser toolbar

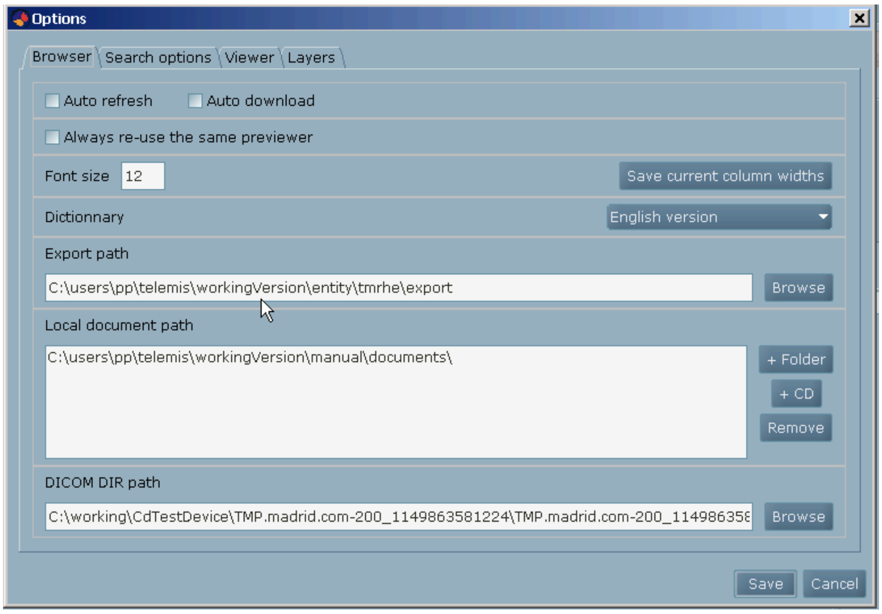
1.12.2.2. Browser general options

The main theme (look of the buttons, colors or the graphical interface etc.) may be changed via

√ the menu [*Options*] [*Theme*] and selecting one of the themes available.

To change the options of the *TM-Reception* browser via the options panel shown on Figure 71,

√ select [*Options*] [*Browser options …*].



☐ Auto refresh ☐ Auto download

☐ Always re-use the same previewer

Font size 12

Dictionnary English version

Export path C:\users\pp\telemis\workingVersion\entity\tmrhe\export

Local document path C:\users\pp\telemis\workingVersion\manual\documents\

DICOM DIR path C:\working\CdTestDevice\TMP.madrid.com-200_1149863581224\TMP.madrid.com-200_11498635

Figure 71 - TM-Reception Browser options

Change the options as explained in the following paragraphs.

√ Click on 'Save' to confirm the modification of the options, or on 'Cancel' to cancel the modification and come back to the previous values.

You can check or uncheck the **auto refresh** option to automatically refresh the content of the lists coming from the server (see section 1.8.1 page). This option is personal and will follow you on any *TM-Reception*. The option will take effect immediately.

You can check or uncheck the **auto download** option, to automatically download in the local temporary 'cache' directory every new study available on the server (see section 1.5.11 page). This option is personal and will follow you on any *TM-Reception*. The option will take effect immediately.

You can specify if you always want to **re-use an already opened previewer**, or be prompted "re-use same previewer / open a new previewer" each time you open a previewer while another one is currently opened.

You can change the **font size** used by the application. Default value is 12.

To save the 'Patients', 'Studies' or 'Series' columns width that you have manually changed (see section 1.3.2.2 page), press the '**Save current column widths**' button.

You can change the **language** used by the *TM-Reception*. The selection drop box called 'Dictionary' contains all the languages available on your computer. Simply select one from the list to change the language for the next time you will start this *TM-Reception*. Be careful that this option is NOT personal and will affect the *TM-Reception* itself: all the users that will connect to the program after the change will have to use the language that you have selected.

You can change the **export path**, i.e. where the *TM-Reception* Viewers will export JPEG, BMP … versions of the images (see section 2.8.2 page). This option is personal and will follow you on any *TM-Reception*. The option will take effect immediately.

- Edit the content of the 'Export path' text box, or
- Click on the 'Browse' button, select a directory in the file selector window and click on 'Save'.

You can change the **local document path**, i.e. all the directories scanned by the *TM-Reception* Browser for local documents, displayed as "🏠" studies in the studies list. Several directories can be added. Only the first one fill be used during the 'Save in my database' operations. This option is personal and will follow you on any *TM-Reception*.

- To add a hard disk or network directory, click on the '+ Folder' button, select a directory in the file selector window and click on 'Save' to add a directory to the list
- To add a CD reader, that can contain images in different predefined location, click on the '+ CD' button, select the path of the CD (ex: "E:") in the file selector window and click on 'Save' to add this CD reader.
- Click on a line of the local document path list and click on the 'Remove' button to remove the selected directory from the list.

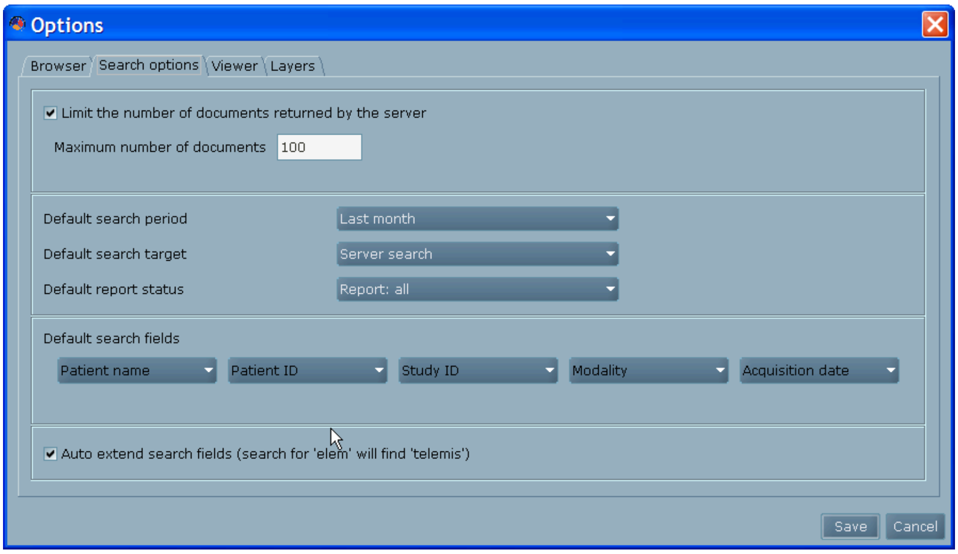
The **DICOM dir path** is the file path and name of the DICOMDIR file of a specific DICOMDIR structure. See section 3.6 for more details.

1.12.2.3. Search options

To change the options of the *TM-Reception* browser via the options panel shown on Figure 72,

√ select [*Options*] [*Browser options …*];

√ click on the 'Search options' tab located at the top of the options window.



☑ Limit the number of documents returned by the server

Maximum number of documents: 100

Default search period: Last month

Default search target: Server search

Default report status: Report: all

Default search fields: Patient name | Patient ID | Study ID | Modality | Acquisition date

☑ Auto extend search fields (search for 'elem' will find 'telemis')

Figure 72 – TM-Reception Search options

Change the options as explained in the following paragraphs.

√ Click on 'Save' to confirm the modification of the options, or on 'Cancel' to cancel the modifications and come back to the previous values.

All these options are personal and will follow you on any *TM-Reception*.

You can check or uncheck the **Limit number of documents** options (see section 1.4.6.4 page). If the option is checked, you can modify the maximum number of documents returned by a server search.

You can specify the default **search period** (see section 1.4.6.1 page). Click in the drop box at the right of the 'Default search period' text and select one of the proposed possibilities.

You can specify the default **search target** (see section 1.4.6.2 page). Click in the drop box at the right of the 'Default search target' text and select one of the proposed possibilities.

You can specify the default **report status** (see section 1.5.13 page). Click in the drop box at the right of the 'Default report status' text and select one of the proposed possibilities.

For each of the 5 search fields, you can specify a default **search field** (patient name, modality …) (see section 1.4.1 page). For each of the 5 fields, select one of the possibilities proposed by the corresponding drop box (including the first 'empty' possibility that will leave this field empty).

You can check or uncheck '**Auto extend search fields**' to let the Telemis Browser search for a field "containing the text" (option checked) or for a field "equalling the text" (option unchecked). You can always add the wildcards '*' and '?'. For example, if you check the option, typing 'upon' will find 'upon', 'Dupont', 'Mr Dupont'… If you uncheck this option, typing 'upon' will only find 'upon'. You will have to type '*upon*' to find 'Dupont', 'Mr. Dupont' …

Ask you IT manager to change the way the starting or ending "*" are automatically added or not to the search fields.

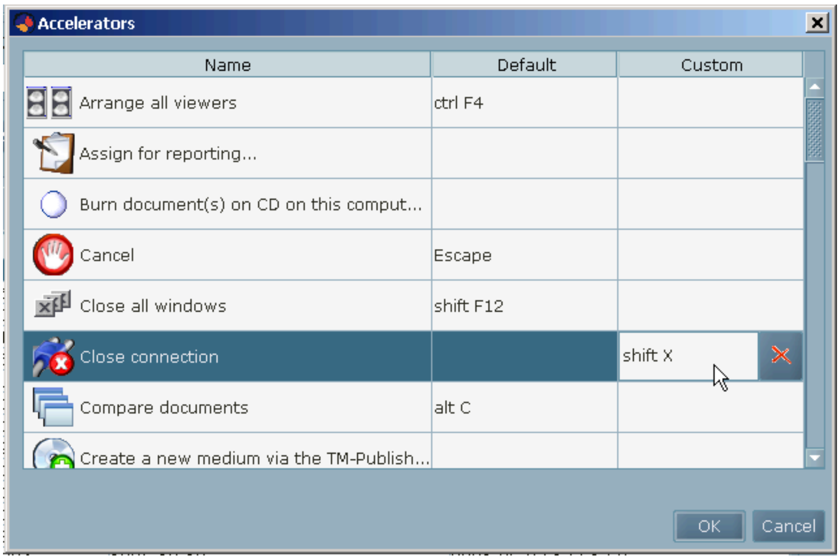
1.12.2.4. Customise keyboard shortcuts

Keyboard shortcuts (also called accelerators) may be completely configured.

√ Select the menu [*Options*] [*Modify keyboard shortcuts …*] to open the customization dialog box shown on Figure 73.

Press 'OK' to accept your modifications, or

Press 'Cancel' to cancel the modifications.



Name	Default	Custom
Arrange all viewers	ctrl F4	
Assign for reporting...		
Burn document(s) on CD on this comput...		
Cancel	Escape	
Close all windows	shift F12	
Close connection		shift X
Compare documents	alt C	
Create a new medium via the TM-Publish...		

Figure 73 - Customise keyboard shortcuts

The first column displays the action. The second column shows the default keyboard shortcut. The last column shows the shortcuts that you have personally assigned to some actions.

√ Click on a line to edit a shortcut for this action, or modify or remove it.

Press a key or a combination of keys (Ctrl + a key, Alt + a key, Shift + a key, Ctrl + Shift + a key etc.) to **assign this action to the key**. In this example, pressing Shift X will close the current connection with the server.

Press another key or combination of keys to **modify** the assignment.

Press the red cross at the right of the column to **remove** this assignment.

1.12.2.5. Browser columns

It's possible to change the width and the content of the columns of the 'Patients', 'Studies' or 'Series' views.

To change the columns content,

√ Right-click in the column header and select "Choose columns".

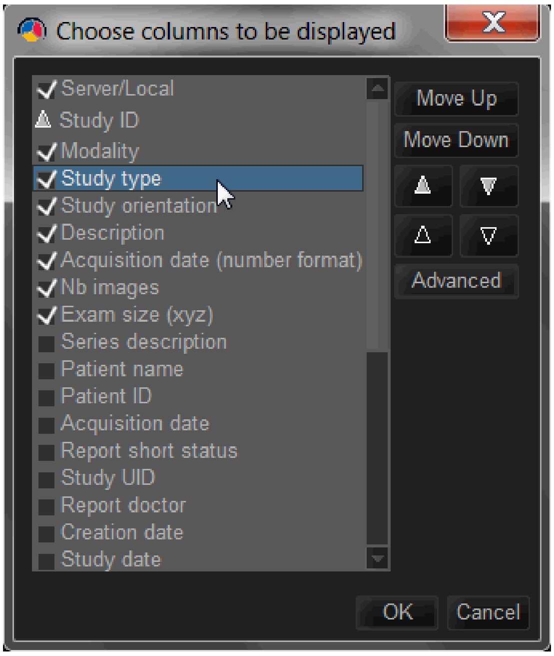
Check any field to show the column.

When a field is selected,

- press 'Move up' or 'Move down' to change the order of the columns.
- Press the plain up and down arrows (▲ ▼) to set the sort order (ascending / descending) for the main sort.
- Press the empty up and down arrows (△ ▽) to set the sort order for the secondary sort criterion.

Press 'Advanced' to show or hide the list of advanced fields (photometric interpretation, filter name etc.)

Do this for each of the 3 views (Patients, Studies, Series).



- ☑ Server/Local
- ▲ Study ID
- ☑ Modality
- ☑ Study type
- ☑ Study orientation
- ☑ Description
- ☑ Acquisition date (number format)
- ☑ Nb images
- ☑ Exam size (xyz)
- ☐ Series description
- ☐ Patient name
- ☐ Patient ID
- ☐ Acquisition date
- ☐ Report short status
- ☐ Study UID
- ☐ Report doctor
- ☐ Creation date
- ☐ Study date

Figure 74 - change browser columns content

To change the width of the columns, simply resize them.

To save the width of the columns,

√ Right-click in the column header and select "Save current columns width".

1.12.3. Connect with another *TM-Server*

You could regularly have to connect with another *TM-Server* than the default server of your hospital, for example if you work part time in two hospitals and sometimes want to access images from the other hospital.

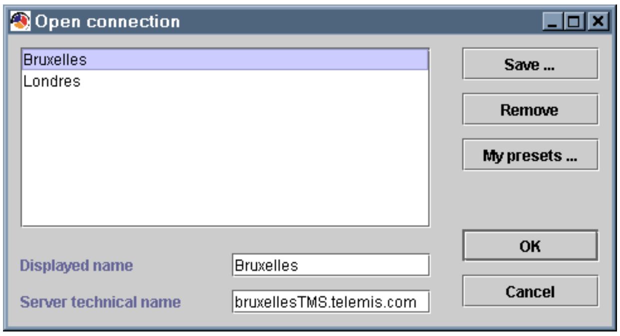
To accelerate the connection, you can create a preset for the other servers.

√ Select [*Network*] [*Open connection*].

√ In the "Displayed name" text box of the window displayed in Figure 75, enter the description of the server, i.e. the text that will be displayed in the list. For example, type the name of the second hospital.

√ In the "Server technical name" text box, enter the technical name of the server. Ask your local IT manager for this information. The classical way of setting Telemis technical names is "Name_of_the_server@hospital.country".

√ Click on the "Save …" button to save this new server preset. Your presets follow you on any *TM-Reception*.



Bruxelles
Londres

Displayed name: Bruxelles
Server technical name: bruxellesTMS.telemis.com

Figure 75 - Connection with another server

1.12.4. Management of the full report templates

1.12.4.1. Template list management

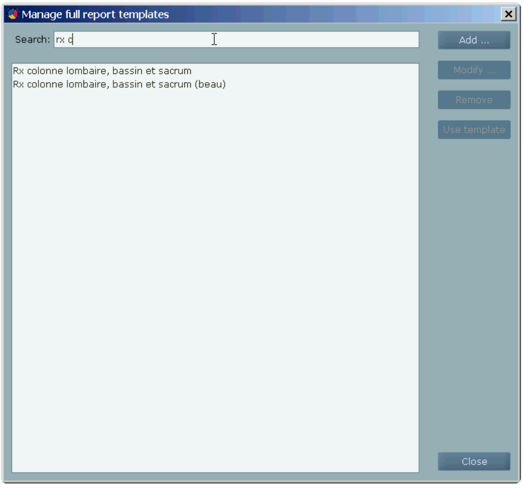
To open the full report template management dialog,

√ Select [Options] [Manage full report templates] in any viewer, or

√ In the 'full report' dialog box, press the "…" button to show the list of templates and select the last one called [Manage full report templates …], or

√ In the 'full report' dialog box, press the icon.

The 'Manage full report templates' dialog box opens, as shown in Figure 76. You can type some characters in the 'search' text field, to filter the list.



Search: rx c

Rx colonne lombaire, bassin et sacrum
Rx colonne lombaire, bassin et sacrum (beau)

Figure 76 - Manage full report templates

Press 'Add ...' to create a new template.

Select one template in the list and

press 'Modify ...' to modify the template;

press 'Remove' to delete it;

press 'Use template' to use it in the full report dialog and close this management box. This option is only available if called from the full report dialog box.

1.12.4.2. Add or Modify a template

When adding or modifying a template, you can always start working from another template. Use the 'Select the report template to clone and press ENTER' box to filter and select a template, as explained in section 1.5.14.5 page .

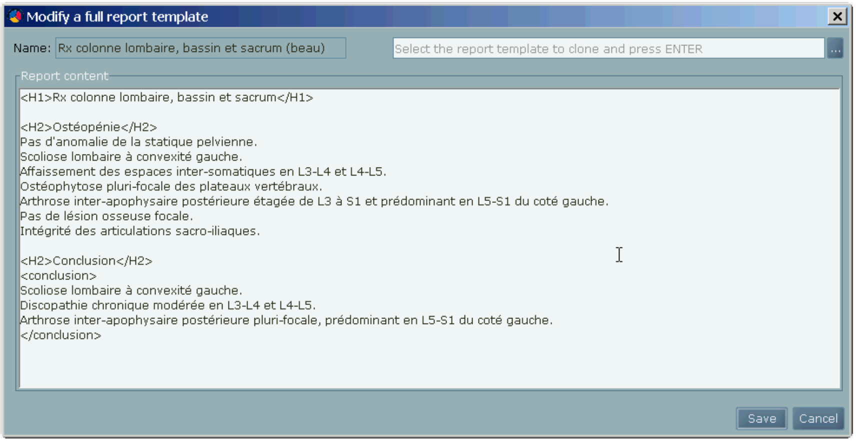
When adding a template, you must provide a valid and unique name.

Add or modify the text on the 'report content' section. You can use different keywords to create styling. Attention: ALWAYS use the closing tag after using the opening one.

- `<BLOCKQUOTE>` and `</BLOCKQUOTE>`: indent the text included in the block quotes.
- `<BR />`: insert a carriage return.
- `<EM>` and `</EM>`, or `<I>` and `</I>`: italic
- `<STRONG>` and `</STRONG>`, or `<B>` and `</B>`: bold
- `<U>` and `</U>`: underline
- `<H1>` and `</H1>`: main heading
- `<H2>` and `</H2>`: secondary heading.

You can also add a functional block:

- `<CONCLUSION>` and `</CONCLUSION>`: all the text included in this block (except starting or ending carriage return) will be automatically added in the report comment field, show in the TMR(HE) browser (see section 1.4.1 page , field "Report comment").



Name: Rx colonne lombaire, bassin et sacrum (beau)

```
<H1>Rx colonne lombaire, bassin et sacrum</H1>

<H2>Ostéopénie</H2>
Pas d'anomalie de la statique pelvienne.
Scoliose lombaire à convexité gauche.
Affaissement des espaces inter-somatiques en L3-L4 et L4-L5.
Ostéophytose pluri-focale des plateaux vertébraux.
Arthrose inter-apophysaire postérieure étagée de L3 à S1 et prédominant en L5-S1 du coté gauche.
Pas de lésion osseuse focale.
Intégrité des articulations sacro-iliaques.

<H2>Conclusion</H2>
<conclusion>
Scoliose lombaire à convexité gauche.
Discopathie chronique modérée en L3-L4 et L4-L5.
Arthrose inter-apophysaire postérieure pluri-focale, prédominant en L5-S1 du coté gauche.
</conclusion>
```

Figure 77 - Modify a report template

2. THE IMAGE VIEWER

An image viewer in a Telemis application is a window that displays a set of 2D images and proposes functions to modify them. Figure 78 presents a snapshot of a viewer opened for a CT scanner series.

The image viewer gives **basic tools** to work with the images: select images, change contrast and brightness, zoom, apply a color look-up table … Section 2.3 page details these commands.

The **format of the image viewer** is configurable through several commands explained in section 2.4 page : number of images displayed, information text displayed or not, maximization of the display, automatic optimization of the viewers position and size on screen...

The image viewer also delivers more **advanced tools** to draw lines, perpendicular lines, labels and to measure distance, angles or density on the images. All details in section 2.4.8 page .

Image processing tools rotate and flip the images, change the grey scale … See section 2.6 page for explanations.

The image viewer lets you **manage the studies**: open next or previous study, open new viewers, save, restore, refresh, print or export images ... You will find details about that in sections 2.6.8 and 2.11 pages and .

The viewers can be linked together to ease **comparison** between studies, as explained in 2.9 page .

The viewer is shipped with a Cine Viewer (section 2.12 page) that animates the images of the image viewer.

Finally, the customization options are discussed in section 2.13 page .

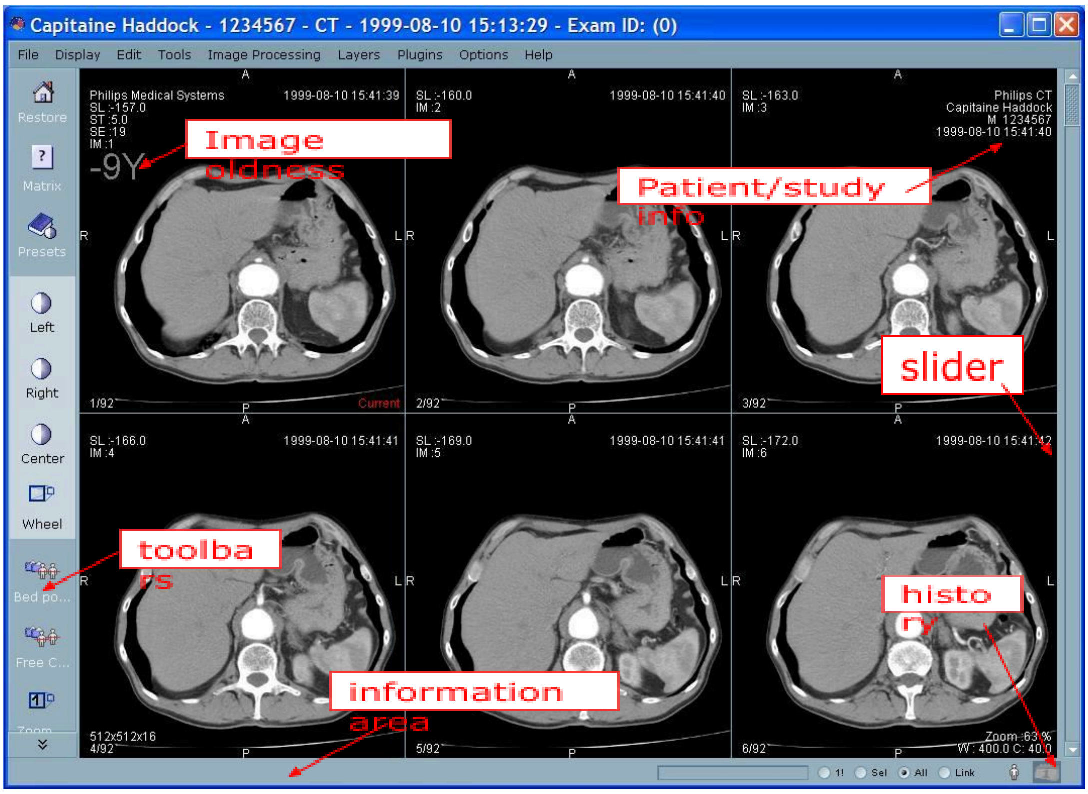


Figure 78 - Telemis Image Viewer

On the top left of each viewer is show the oldness of the images, if older than one week ("-9Y" means 9 years, "-11M" means 11 months and "-3W" means 3 weeks)

The top right of each viewer shows the patient and basic study information.

The bottom right calendar icon shows the history availability.

The bottom line is the information area.

2.1. Open/Close

There are several ways to **open** a Telemis Viewer for a study. From the *TM-Reception* Browser,

√ press the *Enter* key or

√ click on the Open icon, or

√ select [Document] [Open document(s)]

to open one or several series that are selected (see section 1.3.5.2 page) in the 'Series' list or to open all the series of a study selected in the 'Studies' list (see section 1.3.4.2 page).

To open one series that is not currently selected in the 'Series' list:

√ Double-click on the line of the 'Series' list that displays the study to open.

At the bottom right of the viewer is located a progress bar (see Figure 78) that displays the image decompression and display progress. The associated information line explains the current task of the viewer (e.g. "Decompressing images …")

To **close** the current Image Viewer,

√ select [*File*] [*Exit*], or

√ click on the cross button at the top right of the window ( ), or

√ press the 'Backspace' key (the suppression key, just above the 'Enter' key).

To close all the Image Viewers related to the same study,

√ select [*File*] [*Exit this study*], or

√ press the 'Shift' and 'Backspace' keys.

To close all the opened Image Viewers,

√ select [*File*] [*Close all windows*], or

√ press the 'Shift' and 'F12' keys.

To **conclude the report** of a study and close all the Image Viewers related to series of this study,

√ Select [*File*] [*Report & exit …*], or

√ Press in the viewer toolbar the 'Report & Exit' icon.

2.1.1. Warning if several patients shown

When several viewers are opened, showing series from different patients, a specific logo appears at the bottom right of the viewers, warning the user about the fact.

This will help prevent confusion between the viewer of a patient and another old viewer, remained opened.

2.2. The toolbars

The toolbar is the area **embedded** in each viewer, at the left of the images and that contains the tool buttons, as shown in Figure 78 or hereunder.

The toolbar can also be separated from the viewers: only one **single toolbar** is shown per screen, saving space if several viewers are opened. The single toolbar automatically appears on each screen containing at least one viewer, and automatically disappears when the last viewer of the screen is closed.

The toolbar contains:

- the restore original display parameters button,
- the display matrix button,
- the contrast/brightness presets button,
- the tool associated with the left mouse button,
- the tool associated with the right mouse button,
- the tool activated when pressing the mouse wheel (center button)
- the tool activated when rolling the mouse wheel

The detailed description of these tools will be given in the next sections.

√ You can display or hide the embedded toolbar via the [*Display*] [*Display toolbars …*] menu item or by pressing 'K7' key. The single toolbar will always be shown (if activated).

√

See section 2.15.5 page to customize the content of the main toolbar.

Some tools may be associated to the left or right mouse button: click on the "Left" or "Right" white button and select a tool in the list that drops down. The different possibilities are magnifier, zoom, mover, contrast, navigator and the selector. They will be detailed in section 2.3 page .

If you leave the mouse cursor for more than one second on a button, a small text window will appear that gives a short description of the tool associated with this button.

2.3. Tools

The tools delivered with the *TM-Reception* Viewer allow navigating through the images, changing the contrast/brightness, zooming, moving, magnifying …

Section 2.3.1 defines to which images the tools apply and section 2.3.2 describes how to select images.

Sections 2.3.3 to 2.3.10 explain the navigation, brightness & contrast, zoom, mover, magnifier and color look-up table tools.

When a tool is selected, the "Left" and "Right" white toolbar buttons show the icon corresponding to the tool associated with the left/right mouse button. If the tool is available via a menu, the check box on the left of the menu line is checked when this tool is selected.

2.3.1. Tools application domain

Most of the tools act on one or several images of the study, according to the 'tools application domain' selected. The four application domains available are:

- **Current slice** (abbreviated "1!"): apply the tool only to the last clicked image (the 'Current image' is marked with a little red 'Current' text on the bottom right of the image).

- **Selection** (abbreviated "Sel"): apply the tool only to the images that are selected. See next section for image selection.
- **All slices** (abbreviated "All"): apply the tool to all the images of the study.
- **Linked viewers** (abbreviated "Link"): apply the tool to all the images of the study and to all the images of the linked viewers. See section 2.8.5 page to link viewers.

To select the tools application domain:

√ click on the large drop down button located at the bottom right of the viewer and select one item in the list, or

√ select [*Edit*] [*Tools Application Domain …*] and select the desired sub-item, or

√ press the "t" key to toggle between the tools application domains.

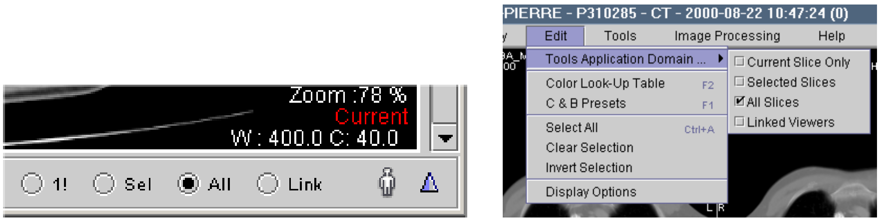


Figure 79 - Tools application domain selection

2.3.2. Image selection

To apply a tool on a specific subset of the images of a viewer, the images must be selected.

To select an image, you must first choose the “Selection” tool:

√ Select the “Selection” tool in the “Left” or “Right” drop boxes of the toolbar , or

√ press the “S” key to associate the selection tool with the left button or the “Shift” and “S” keys to associate the selection tools with the right button.

Once the selection tool is activated,

√ click on the images with the left or right mouse button to select them (left or right button depending on the association with the left or right mouse button (“S” or “Shift” “S” shortcuts keys)

To unselect an image, click again on the image: the selection is an on/off feature.

Another way to select images is to click images while the “Shift” or “Ctrl” keys are pressed.

√ Hold the “Ctrl” key and click on images to select / unselect individual images.

√ Hold the “Shift” key and click on an image to select all the images between this image and the “current” image (the last image that received the focus)

√ To select all the images in one click, select [*Edit*] [*Select All*] or press the “Ctrl” and “A” keys.

√ To select all the images between the first selected image of the study and the last image of the study to be selected, choose [*Edit*] [*Select between extremities*].

√ To unselect all the images, select [*Edit*] [*Clear selection*].

The last menu operation on selection is [*Edit*] [*Invert selection*]. This operation selects all the images currently unselected and unselects all the images currently selected. This is useful to select all the images of a study but a few ones. Select these few images and invert the selection. For example, if a study is made up with a scoot image and 100 other images, selecting the 100 images summarizes in selecting the scoot image and inverting the selection: this is much easier than selecting manually the 100 images!

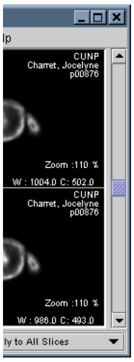
The images that are selected are marked with a little red 'Selected' on the bottom right on the image and with red text annotations instead of white texts.

The Image Viewer info line displays the number of images selected.

2.3.3. Navigation

If a series contains 100 images but that only 6 images are displayed at the same time in the viewer, the navigation tools will help moving along the study and displaying the requested images. Navigation in the study is possible via the keyboard (cursor, home, end, page up or page down) or via the mouse (the slider of the viewer (see Figure 80) or the navigation tool).

- To **move to the first image** of the study, press the 'Home' key (represented by the arrow "□" on some keyboards)
- To move one line up,
- press the 'cursor up' key (often marked by the "↑" symbol), or
- click the arrow at the top of the slider (see Figure 80).
- To move one page up,
- press the 'Page Up' key (sometimes marked by the "⇑" symbol), or
- click in the slider between the upper arrow and the central blue box (see Figure 80).
- To move image after image,
- Select the "Navigation" tool in the "Left" or "Right" drop boxes of the toolbar, or press the "N" key to associate the navigation tool with the left button or the "Shift" and "N" keys to associate the navigation tool with the right button.
- Click on one image, keep the mouse button pressed and drag the mouse up to move image after image towards the first image, or drag the mouse down to move image after image towards the last image. Once you release the button, the neighboring images are updated.
- Press 'Ctrl' while you move the mouse to increase the navigation speed, with a light reduction of the displayed quality during the navigation (the quality once the mouse button is released remains unchanged)
- The second possibility to move image after image is to click on the central blue box of the slider (see Figure 80) and to drag the mouse up or down.
- To move one page down,
- press the 'Page Down' key (sometimes marked by the "⇓" symbol), or
- click in the slider between the lower arrow and the central blue box (see Figure 80).
- To move one line down,
- press the 'cursor down' key (often marked by the "↓" symbol), or
- click the arrow at the bottom of the slider (see Figure 80).
- To **move to the last image** of the study, press the 'End' key



One line up

One page up

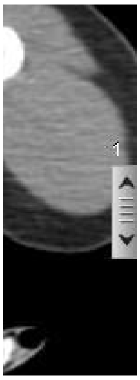
Move the slider to move image after image

One page down

One line down

Figure 80 - Navigation slider

- To scroll all images upward or downward, move the mouse to the rightist part of the image. The scrolling tool appears. Click on this tool and hold the mouse button pressed. Move the tool upward or downward. The number indicated above the tool indicates the speed: "1" means slowest speed: all images are showed. Higher numbers (ex: 5) mean that the viewer will show one image each 5 (in this example) images. The speed is much higher but it'



2.3.4. Contrast and brightness

A grey-scale image is composed of numerous grey level values. It is sometimes too dark or too light. Sometimes, the image contains thousands of grey level values, much more than the human eye can catch. You need to focus on an interesting window in the grey levels.

If you imagine the pixel intensity of an image as a long sequence of grey levels (the horizontal axis of the 4 images of Figure 81), you are in fact interested in a window on this sequence. A darker displayed image is an image for which you see a grey level window that is centered higher in the image values: all the image values below the "a" value are represented in black, all the image values above the "b" value are represented in white and all the values between "a" and "b" are expanded or contracted into 256 grey scale levels displayed on the screen. This situation is represented in first image of Figure 81. The second image described the same situation for a lightened image.

A more contrasted image is an image for which the grey level display window is narrower (see the third image of Figure 81) : the display window enhances the small window of the image that is kept. The small number of image values contained between "a" and "b" are expanded to 256 grey levels. On the opposite, a poorly contrasted image contacts a wider values range ("a" to "b") into these 256 grey levels, as shown on the fourth image of Figure 81.

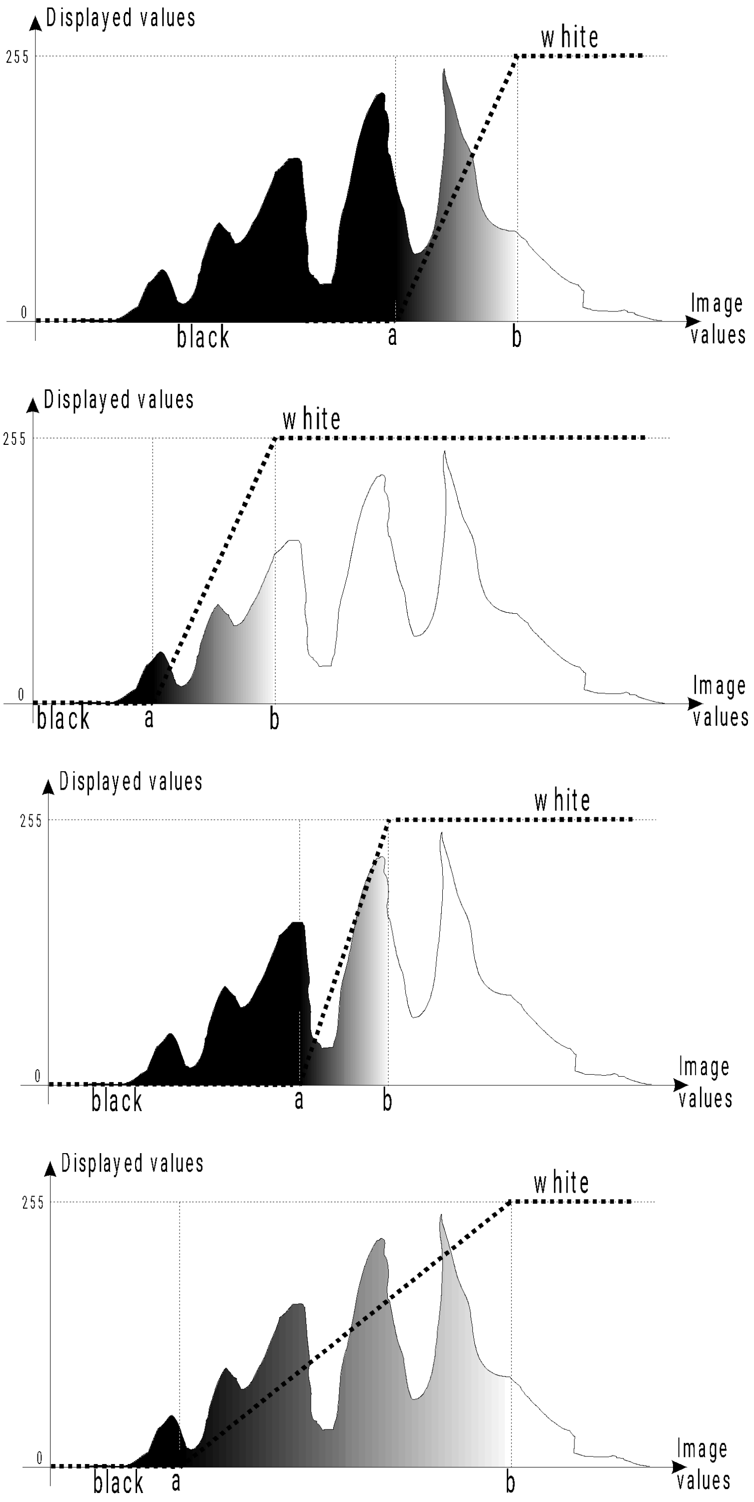
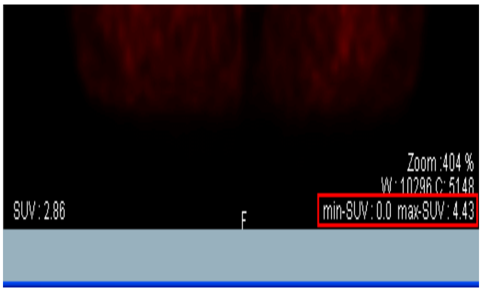


Figure 81 – Lighter – darker – more contrasted – less contrasted image

The centre of the grey level display window represents the brightness of the displayed image. Its width represents the contrast of the displayed image.

The bottom right information displayed on the images shows the width and center values for this image ("W:" and "C:" values).

For PT-scan images shown in the MPR viewer, this value is also displayed using the SUV scale, showing the SUV value corresponding to the lower point and the SUV value corresponding to the upper point of the 'Image values' – 'Displayed values' curve.



2.3.4.1. Manual changing

To *manually* change this display window on-line,

1) Select the contrast/brightness tool:

√ Select the "Contrast" tool in the "Left" or "Right" drop boxes of the toolbar, or press the "C" key to associate the contrast tool with the left button or the "Shift" and "C" keys to associate the contrast tool with the right button.

2) Apply the tool on the images:

√ to change the **brightness** (the centre of the window) : click somewhere in the image. Keep the button pressed and move the mouse upward to darken the image, downward to lighten the image.

√ to change the **contrast** (the width of the window) : click somewhere in the image. Keep the button pressed and move the mouse to the left to increase the contrast, and to the right to decrease the contrast.

You can move the mouse outside the image. The only thing that matters is the image clicked when you first pressed the button. The contrast and brightness change until you release the button of the mouse.

The changes will propagate to other images according to the tools application domain.

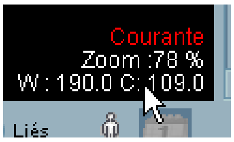
2.3.4.2. Presets

You can also use *presets* to change these values. You can access your C&B presets either via the context menu or via the dialog box.

The context menu is an easy way to access your presets for the contrast and brightness changing.

√ Click on the Contrast & Brightness context menu button in the toolbar of the viewer.

√ or double-click on the windowing values at the bottom right of the images.



The context menu drops down with your presets. Click on any of them to apply this Contrast & Brightness to your image(s) (see Figure 82).

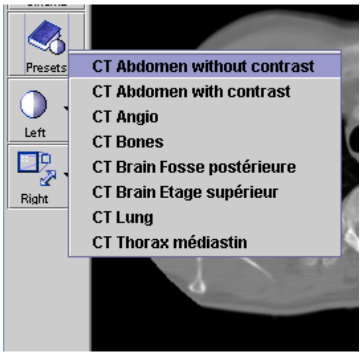
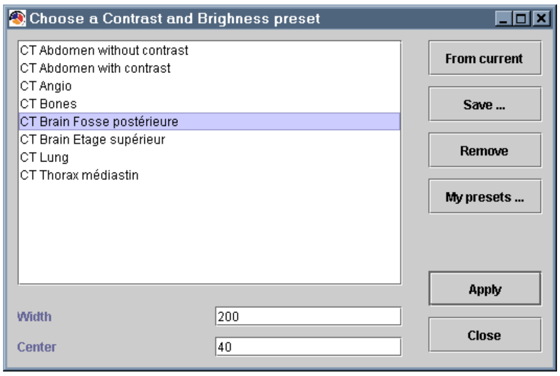


Figure 82 - Context menu for Contrast and Brightness

The second possibility that offers more options is the following.

√ Click on the F1 function key or select [*Edit*] [*C & B presets*].

A window (see Figure 83) appears that gives the possibility to apply a preset for a couple of values brightness – contrast to the tools application domain of the viewer.



Width 200
Center 40

Figure 83 - Brightness and contrast presets

√ You can select a preset from the list in the window. If you click on an element of the list, the Width and Centre text fields display the width and centre values of this preset.

√ Click on the *Apply* button to apply this brightness and contrast to the images concerned by the tools application domain.

√ You can manually enter values in the *Width* and *Centre* text fields, and click on *Apply* to apply these values.

√ If you have manually reached an optimum contrast and brightness in the viewer, you can automatically get the numerical values of the width and centre into this window if you click on the *From Current* button. The values of the current slice are displayed in the Width and Centre text boxes.

√ If a couple of values are of importance to you, you can save it. Click on the *Save* button to save it under the name that you will give. This new preset is saved on your profile and will follow you on any *TM-Reception*.

√ To update the list with all the presets that are present on your profile, click on the *My presets* button.

√ You can remove a preset from your profile if you click on the *Remove* button.

√ Click on the *Close* button to exit the Contrast and Brightness window.

All the Contrast & Brightness changing apply on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

2.3.4.3. Automatic contrast & brightness for each image

The Automatic Contrast and Brightness adaptation of the image is done with one click. This feature will try to automatically find the best contrast and brightness values to apply on the image. This feature works best with Conventional Radiography (CR) images. Applied on a series of image, each image will be optimized independently.

√ Select the [*Image Processing*] [*Auto-Contrast*] menu item, or

√ press the 'A' key.

2.3.4.4. Automatic SUV-based contrast & brightness

When the viewers show a PT-scan series, the [Image Processing] [Auto contrast SUV] menu is activated.

Select this menu to automatically tune the windowing (contrast & brightness) of the series, in order to show in black all the points having a SUV value under a minimum threshold (typically 0) and in white all the points having a SUV value above a maximum threshold (typically SUV = 5), using a linear scale for all the points in-between.

See section 2.15.1.2 page to learn how to change those thresholds.

2.3.4.5. Automatic contrast & brightness for the whole series

Optimizing each image separately is optimum in 2D viewers, but could be problematic in MPR visualization, or in any situation where all the images must have the same windowing (i.e. contrast & brightness).

To perform the automatic contrast & brightness with a global optimization for the whole series,

√ Select the [*Image Processing*] [*Auto contrast on the whole series*].

2.3.4.6. Automatic contrast & brightness on a region

In some situations, the same image must be analyzed with 2 windowings, or the default contrast is not accurate enough for the part of the image of interest.

Optimizing the contrast on a given area of the image helps solving those situations.

√ Select the [*Image Processing*] [*Auto contrast on area*] menu item.

Draw a rectangle: click on one corner of the area of interest, move the mouse and click a second time to specify the position of the opposite corner (see Figure 84.a and Figure 84.c). The image windowing will enhance this area (see result on Figure 84.b and Figure 84.d resp.) and propagate the new windowing (contrast & brightness) to all the images belonging to the Tools Application Domain (see section 2.3.1 page).

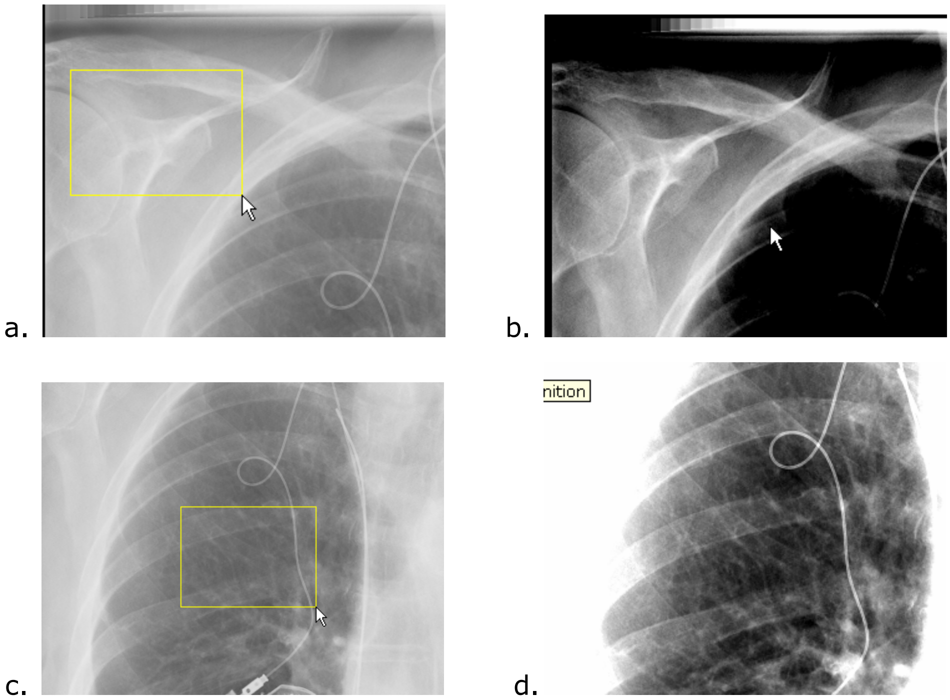


Figure 84 - Auto contrast on area (action a. and c., results b. and d.)

2.3.5. Zoom

This tool zooms in or zooms out the image(s).

√ Select the "Zoom" tool in the "Left" or "Right" drop boxes of the toolbar, or press the "Z" key to associate the zoom tool with the left button or the "Shift" and "Z" keys to associate the zoom tool with the right button.

√ Click in an image and keep the mouse button pressed. The point clicked will stay glued at its place (it is the centre of the zoom). Move upward to zoom out and downward to zoom in. Release the button when you have finished zooming.

This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

2.3.6. Symmetrical zoom

This tool zooms in or zooms out the image(s), reporting the modification symmetrically to the other images. This tool is especially useful with mammography images.

√ Select *[Image processing] [Symmetrical zoom]*, or press the "Sym Zoom" button.

√ Click in an image and keep the mouse button pressed. The point clicked will stay glued at its place (it will be the centre of the zoom). Move upward to zoom out and downward to zoom in. Release the button when you have finished zooming.

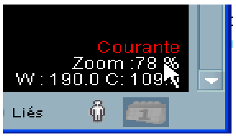
This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain) symmetrically.

2.3.7. Zoom 100%

This tool sets the images zoom to 100%, one pixel of the image being one pixel on screen.

√ Press the “Zoom 100%” button, or press the “/” key on the numeric pad, or select *[Display] [Zoom 100%]* to trigger the "zoom 100%" tool.

√ You can also double-click on the zoom factor shown at the bottom right of the pictures.



This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

2.3.8. Mover

The mover tool moves the zoomed image in its display area.

√ Select the “Mover” tool in the “Left” or “Right” drop boxes of the toolbar, or press the “V” key to associate the mover tool with the left button or the “Shift” and “V” keys to associate the mover tool with the right button.

√ Click in an image and keep the mouse button pressed. Move the mouse to move the image inside its display area. Release the button when you have finished moving the image.

This function has no effect if the image is displayed with a 1:1 zoom. It occupies all the available display space. It has only effect if the zoom ratio is greater than 1:1.

This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

2.3.9. Magnifier

The magnifier magnifies the part of the image that you are on.

√ Select the “Magnifier” tool in the “Left” or “Right” drop boxes of the toolbar, or press the “M” key to associate the magnifier tool with the left button or the “Shift” and “M” keys to associate the magnifier tool with the right button.

Figure 85 shows the result if you press the button of the mouse around the centre of the image: a square moves with the mouse, which enlarges two times the content of the image that is under its centre.

If you click once, the magnifier appears at the place of the click and remains visible.

If you click and keep the button pressed, the magnifier follows the mouse until you release the button.

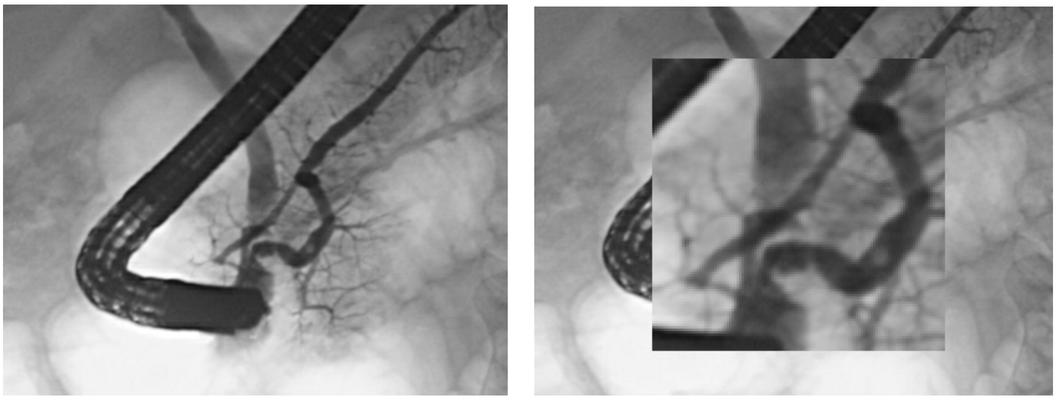


Figure 85 - Left: Normal image, Right: Magnified image

2.3.10. Context menu

On the right mouse button is available the 'context menu' tool.

√ Select the "Context menu" tool in the "Right" drop boxes of the toolbar.

Press the rightist mouse button anywhere in the viewer to drop the context menu.

This menu contains all the actions available in the "Left" mouse button of the toolbar, plus all additional actions that have been configured.

To configure additional actions on the context menu,

√ Select [*Options*] [*Configure context menu …*].

Choose in the left panel the tools to add to your context menu, select actions in the rightist panel and press the [Move up] and [Move down] to re-organize them.

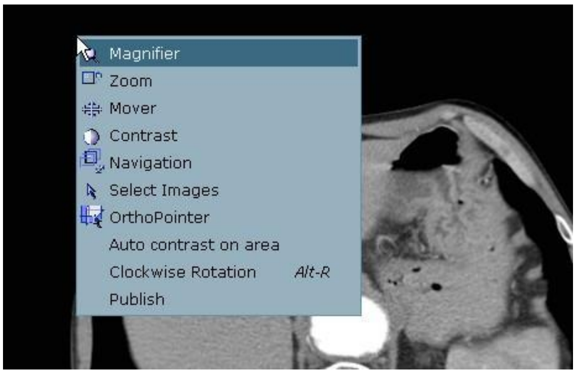


Figure 86 - context menu

2.3.11. Color Look-Up Table

An image is made up with points, technically called pixels (for PICture ELement). For an image where each pixel is coded with 8 bits, each pixel intensity is between 0 and 255. You can apply any transformation between those values and the values that are displayed on the screen.

The simplest transform is no transform: the image is displayed as it is. This is the normal display mode of the program.

The transform can apply the original grey scale on any grey or color scale: this is the Color Look-Up Table (*CLUT*) transform.

√ When you select [*Edit*] [*Color Look-Up Table*] or press the F2 function key, the Color Look-Up Table window appears (see Figure 87). You can select one color look-up table from the list and click on the *Apply* button or double click in the list to apply the changes to the tools application domain of the viewer.

If you have some personal presets, you can refresh the list with the *My Presets* button.

This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

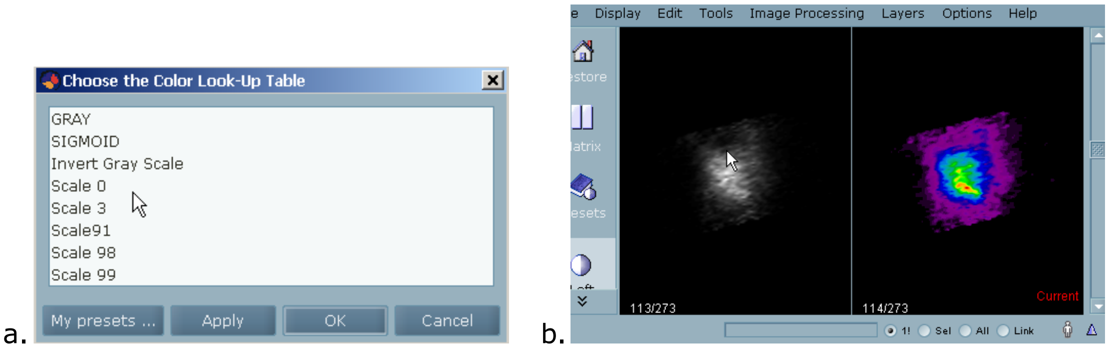


Figure 87 – a. Color Look-Up Table window b. Classical image display on the left, display with a color look-up table on the right.

SIGMOID color look-up table is typically used with mammography images, while scale XX color look-up tables are classically used in nuclear medicine.

2.4. Display control

This section describes the methods to control what the viewer displays: the number of images displayed in one time in the viewer, the additional text on the screen, the size of the viewer, hide/show the toolbars ...

2.4.1. Display matrix

The image matrix is the number of images displayed in the viewer. If the viewer displays 6 images: 3 in the horizontal direction and 2 in the vertical direction, we will say that the display matrix is *3 x 2*.

√ You can control the display matrix with the matrix button of the control panel. Click on the matrix button to drop a list of display matrix presets:

- the first button selects a matrix displaying one image at a time;
- the second displays two images one above the other;
- the third displays two images side by side;
- the fourth displays two lines of two images;
- the fifth displays three lines of three images;

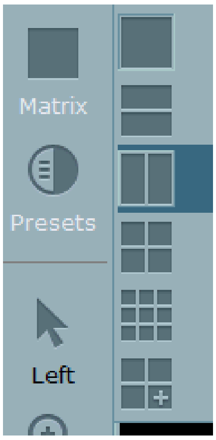
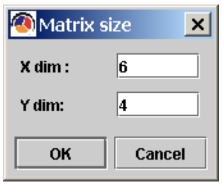


Figure 88 - Image matrix toolbar

√ The last button has the same effect than the [*Display*] [*Display matrix*] menu: a custom control of the display matrix. A small dialog box (see Figure 89) lets you enter the number of *X* (horizontal direction, i.e. number of columns) images and the number of *Y* (vertical direction, i.e. number of lines) images displayed by the viewer. In this example, the viewer will display 4 lines of 6 images.



X dim : 6

Y dim: 4

Figure 89 - Image matrix dialog box

√ When a viewer is the active window, the '+' key increments the number of images displayed in each direction and the '-' key decrements this number of images. For example, if the viewer displays 3 lines of 2 images, a press on the '+' key displays 4 lines of 3 images.

2.4.2. Text on screen

You can add text information on the images. This text summarizes some important information:

- Upper-left:
- The acquisition device;
- DICOM information: the acquisition sequence, the image index inside the sequence ...
- Upper-right:
- Information about the patient : name, birth date;
- Information about the acquisition : acquisition place, date ...
- Lower-left:
- The index of the image vs. the total number of images in the study;
- The size of the image: X (number of horizontal pixels) x Y (number of vertical pixels) x Z (number of bits per pixel);
- Lower-right:
- Information about the display : zoom, width and centre of the brightness & contrast window;
- A red ‘Selected’ tag if the image is selected and/or a red ‘Current’ tag if the image is the current image.

You can choose to switch this display on or off (for example if numerous small images are displayed in the viewer) either

√ by selecting [*Display*] [*Text on Screen*], or

√ by pressing the ‘F3’ function key.

This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

It is possible to modify the content of the text displayed in the corners. See section 2.15.2 page for more information.

2.4.3. Display size and position

To **change the size** of the viewer,

√ Move the mouse to the external border of the viewer: the mouse cursor becomes a double arrow. Keep the mouse clicked while moving it until the appropriate window size, and release the mouse button.

The size of the viewer and the images will then be automatically adjusted and the images will be zoomed to fit into this new window size.

To **maximize** the space taken by the viewer **on the screen**,

√ click on the maximize button in the upper-right of the window, or

√ double-click on the title bar of the viewer, or

√ press the 'F10' function key.

To **maximize** the space taken by the window on **all the available screens** (if you have several screens connected to your computer),

√ press the 'F11' function key.

This maximization displays a viewer for this study on each screen connected to the computer. It then maximizes the size of the viewers and the number of images displayed to a compromise between the number of images and their size. This last function is only available in the *TM-Reception HE* version of the software.

To **change the position** of a viewer that doesn't occupy the whole screen size, you can

√ click on the title line of the viewer and drag it (i.e. move the mouse while keeping the button pressed) to the desired position.

In a *TM-Reception HE* program, the multiple screen management delivers additional functions to move the viewer:

√ press the '1' key to send a viewer to the first screen;

√ press the '2' key to send a viewer to the second screen (if available);

√ press the '3' key to send a viewer to the third screen (if available);

√ press the '4' key to send a viewer to the fourth screen (if available);

To **exchange the position and size** of two of the currently opened viewers,

√ Select [*Display*] [*Exchange position with another viewer*] or press the 'Ctrl' key together with 'F5' in the first viewer.

√ Click on any point of the second viewer.

Both viewers will instantly exchange size and position.

2.4.4. Arrange viewers on screen

To visualize simultaneously two series displayed in two separate viewers, you can lay the viewers out on the screen(s), one next to the other, in order to view both of them together.

You can do this manually through resizing and moving the viewers. You can also do this automatically:

√ Select [*Display*] [*Arrange all viewers*], or

√ Press the 'Ctrl' and 'F4' keys together.

If you have one screen and want to arrange two viewers, they will open each on a half screen. If you have two screens, they each will fully occupy one screen. Figure 62 page shows some examples.

2.4.5. Change the number of viewers per screen

To change the number of viewers displayed on each screen,

√ In the previewer, a right click on the Screen icon gives you options to change the display of the viewers:

Figure 90 - Number of viewers per screen

2.4.6. Display selected only

You can choose to visualize in the Telemis Image Viewer only the images that you have selected (see section 2.3.2 page for the selection of images).

To perform the operation,

√ click on [*Display*] [*Selected only*] or

√ press the 'F8' function key.

If this option is selected, the line is checked on the menu.

Click the menu line or press *F8* again to uncheck the option and display all the images.

This option will be particularly useful to print the viewer (see section 2.8.3 page).

2.4.7. Full screen display

The full screen mode removes the viewer title, toolbars, menus, slider and info line. The viewer uses the full screen size.

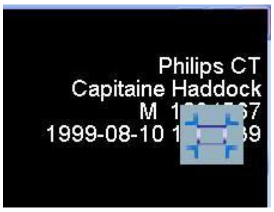
You can activate the full screen automatically via configuration (contact you IT manager).

To activate this configuration manually, either

√ Click on [Display] [View full screen] or

√ Press the 'Shift' and 'F11' keys.

To de-activate this mode,



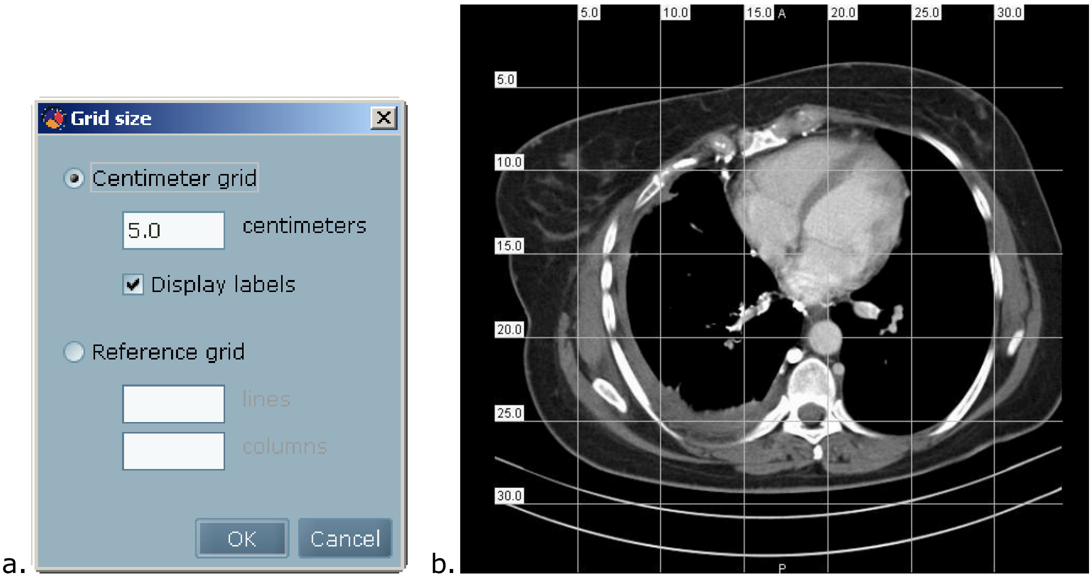
- √ Click the 'Full screen' icon at the top right of the viewer, or
- √ Press the 'Shift' and 'F11' keys

2.4.8. Reference grid

To ease the localization of pathologies on images or to better handle surface or distance comparison, you can activate the reference grid on images.

- √ Select [*Display*] [*Reference grid*]

To activate or de-activate the display of those grids. When activating the grid, the 'grid size' control shown in Figure 91.a. It allows chosing the grid size as a number of cm, to show or not the label (the number of cm) on each grid, or to specify a grid containing a certain number of lines and columns.



Grid size

● Centimeter grid

5.0 centimeters

☑ Display labels

○ Reference grid

lines

columns

OK Cancel

Figure 91 - reference grid

- √ Select [*Display*] [*Edit reference grid preferences*] to show the control and update the grid when it is displayed.

2.4.9. Exchange images position

Some series represent a volume, where the position of images is defined by the spatial coordinates (most CT, MR series for example). Other series are composed of independent images that could be swapped, such as the face and profil images of a CR study.

To swap two images, move the mouse to the top left corner of the first image. When the small hand appears (see Figure 92), click and drag the image to the position where it must be moved.

Drag to another position, or drag to an external application

Figure 92 - Swap images inside a viewer

2.4.10. User display presets

For some kinds of studies, you also have to perform each time the same operations before starting to really watch the images: zoom, change the display matrix, change the contrast, apply a color look-up table (CLUT) etc. You can easily save these operations as a macro, called a 'user display preset', and recall them later to perform all those operations in one click.

The user display presets save the following operations: Contrast / Brightness, Zoom factor, Matrix, Show/hide text on viewer, apply a CLUT, apply filtering, the tools application domain etc.

2.4.10.1. Save a user display preset

Open a viewer, performs all the needed operations.

√ Select [*Display*] [*Save display preset*], or

√ Click on the 'Save display preset' button

and type in the dialog box the name of the preset.

2.4.10.2. Apply a user display preset

In a viewer,

√

√ Select [*Display*] [*Apply display preset*], or

√ Click on the 'Apply display preset' button

and select the preset in the list.

2.4.10.3. Manage the user display presets

In a viewer,

√ Select [*Display*] [*Apply display preset*] or click on the button, and select the last line of the list: [*Manage*].

Select a preset in the dialog box and press 'Rename' or 'Remove'.

'Close' the dialog when finished.

Figure 93 - Manage user display presets

2.5. Drawing and measure tools

Section 2.5.2 details the drawing tools: hands free drawing, line, infinite line, perpendicular line, infinite line, rectangle, text label...label…

Section 2.5.2.12 deals with measurement tools: distance, angle, angle between two lines, Hounsfield density, measurement calibration...calibration…

Section 2.5.3.17 talks about complex tools: Gonometry, Coxometry, TAGT, Telos distance…

Section 2.5.5 will explain the management of the drawings and measures: select an item, clear the selection, delete the selected items, delete all items and burn the objects into the images.

2.5.1. Accuracy of the measures

During the Software Validation Process that takes place at each release of a new version of the *Telemis-Medical* software, each feature that includes metrology is completely verified, based on specific medical images provided by Belgian hospitals.

Those images are generated by introducing objects with pre-known dimension values into medical devices (CT-Scanner, RX, etc.). Those values are then measured using the *Telemis-Medical* software as validation.

Measured values might not always be exactly the same as the original value. Reasons are acquisition device error margin or pixel size error margin. Therefore, measured values and margin are checked together with medical doctors.

We will describe the precision of each measure, together with the acceptable precision limits, based of the acquisition device error margin and the pixel size error margin.

2.5.2. Drawing

2.5.2.1. Hands free continuous drawing

The hands free continuous drawing tool allows the user to draw on the images, for example to highlight a region of the image.

√ Select the hands free continuous drawing tool in the menu with [*Tools*] [*Draw continuous*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the ‘ESC’ key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ To draw on the image, click with the left button and move the mouse while keeping the button pressed. A yellow drawing follows the mouse pointer until the button is released.

When you release the mouse button, a dialog box asks if the contour must be closed or not. Some measures (e.g. surface measure) only work on closed contours.

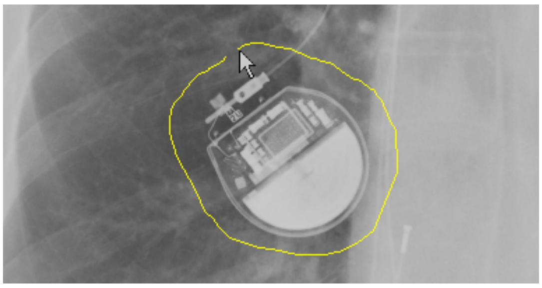


Figure 94 - hands free continuous drawing

2.5.2.2. Hands free polygon drawing

The hands free polygon drawing tool allows the user to draw on the images, for example to highlight a region of the image, by specifying points that the program joins with lines.

√ Select the hands free polygon drawing tool in the menu with [*Tools*] [*Draw* polygon].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ To draw on the image, click with the left button. Release the button and move the mouse. Click with the left button to mark a point that is joined by a straight line to the previous point.

Double-click to conclude the object: a dialog box asks if the contour must be closed or not. Some measures (e.g. surface measure) only work on closed contours.

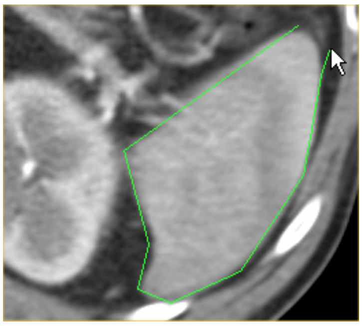


Figure 95 - hands free polygon drawing

2.5.2.3. Line

To draw a new line on an image of the viewer,

√ select [*Tools*] [*Line*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at the point where you want the line to begin. Release the button and move the mouse: the end of the line will follow your mouse pointer. Click again to conclude the line.

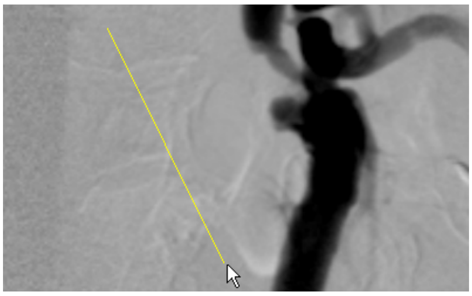


Figure 96 - New line drawing

The next click on the left button will start a new line, until the right button of the mouse is pressed.

2.5.2.4. Infinite line

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at one of the two points which will define the infinite line. Release the button and move the mouse: the infinite line will be drawn related to your mouse pointer as second point. Click again to conclude the line.

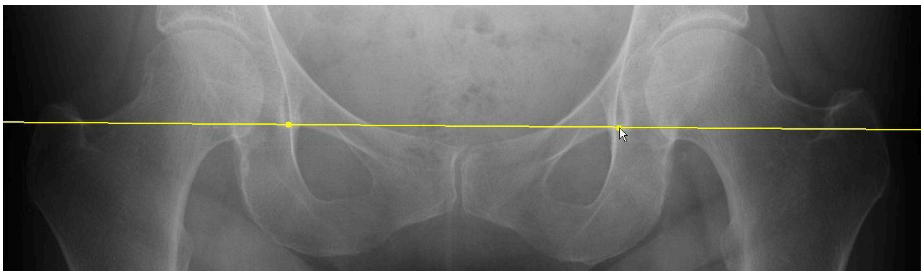


Figure 97 - New infinite line drawing

The next click on the left button will start a new infinite line, until the right button of the mouse is pressed

2.5.2.5. Segment

A segment is a line containing a sign marking its center.

√ select [*Tools*] [*Segment*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at the point where you want the segment to begin. Release the button and move the mouse: the end of the segment will follow your mouse pointer. Click again to conclude the segment.

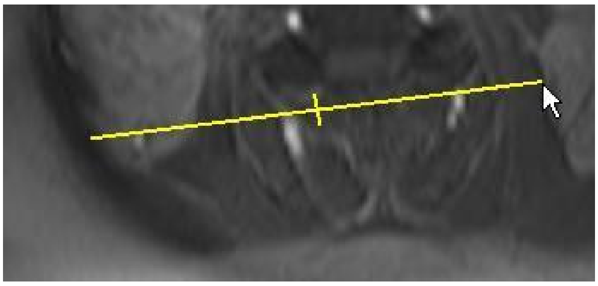


Figure 98 - New segment drawing

The next click on the left button will start a new segment, until the right button of the mouse is pressed.

2.5.2.6. Perpendicular line

This tool draws a line perpendicular to an existing line.

√ Select [*Tools*] [*Perpendicular line*]

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Move the mouse. When the mouse pointer is closed to a "selectable" line, this line becomes thick.

√ Chose the line that must be the 'original line', as shown on Figure 99.a: click with the left button when this line is "selectable" (with small circles at the extremities) at the point that must be the first extremity of the perpendicular line.

√

√ Move the mouse. The horizontal position of the mouse is the horizontal place of the second extremity of the line while its vertical place is set in order to draw the line perpendicular to the original one.

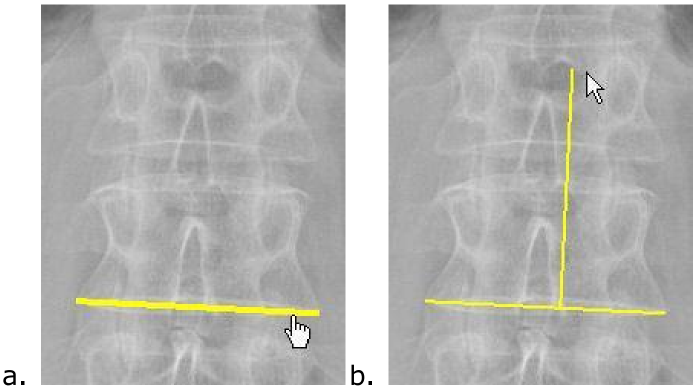


Figure 99 - Draw perpendicular line. a) Original line is chosen, b) Draw perpendicular line

2.5.2.7. Rectangle

To draw a new rectangle on an image of the viewer,

√ select [*Tools*] [*Rectangle*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the ‘ESC’ key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at the point that must be a corner of the rectangle. Release the button and move the mouse: the rectangle will follow your mouse pointer. Click again to conclude the drawing.

The next click on the left button will start a new rectangle, until the right button of the mouse is pressed.

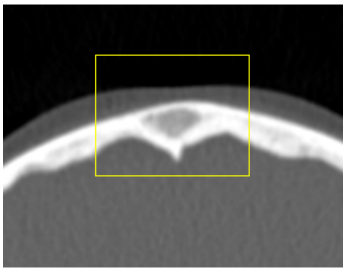


Figure 100 - New rectangle drawing

2.5.2.8. Circle

To draw a new rectangle on an image of the viewer,

√ select [*Tools*] [*Circle*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the ‘ESC’ key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at the point that must be the center of the circle. Release the button and move the mouse: the circle will follow your mouse pointer which will define the radius of the circle. Click again to conclude the drawing.

The next click on the left button will start a new circle, until the right button of the mouse is pressed.

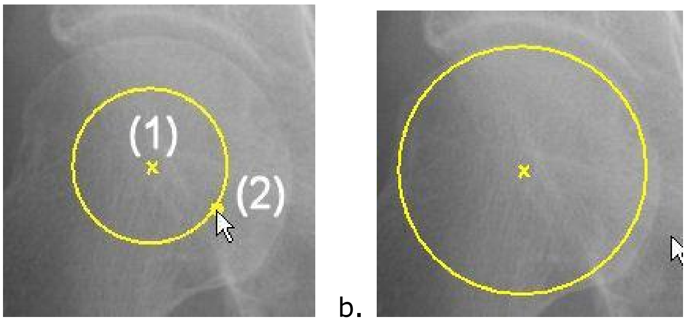


Figure 101 - New circle drawing. a) Define center point b) Determine the radius point

Right-click on the circle and select [*Display/Undisplay diameter*] to show or hide the diameter of the circle.

2.5.2.9. Ellipse

To draw a new ellipse on an image of the viewer,

√ select [*Tools*] [*Ellipse*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at the point that must be the center of the ellipse. Then, click to define one of the axis (horizontal or vertical axis). Release the button and move the mouse: the ellipse will follow your mouse pointer. Click again to determine the other axis and conclude the drawing.

The next click on the left button will start a new ellipse, until the right button of the mouse is pressed.

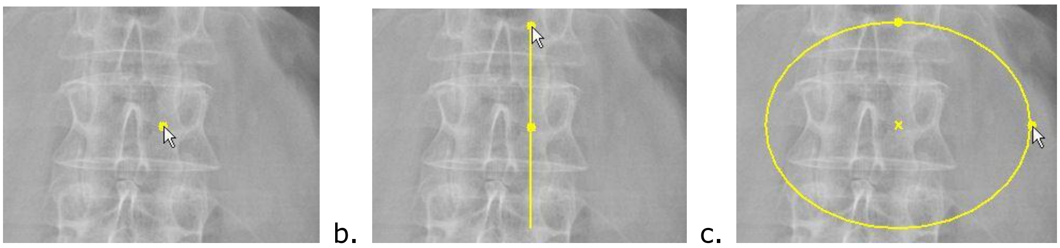


Figure 102 - New ellipse drawing. a) Define center point b) Define one of the axis c) Define the other axis

2.5.2.10. Right angle

To draw a new right angle on an image of the viewer,

√ select [*Tools*] [*Right angle*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click with the left button of the mouse, in an image at the point that must be the center of the right angle.

The next click on the left button will start a new right angle, until the right button of the mouse is pressed.

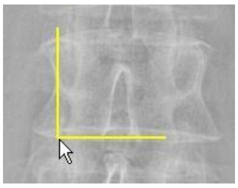
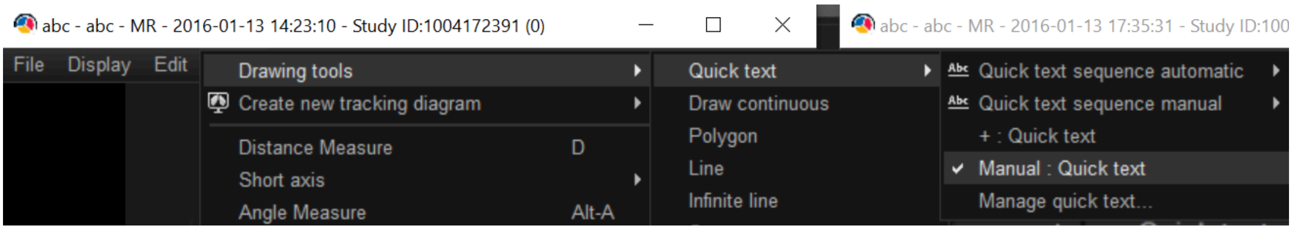


Figure 103 -Right angle drawing

2.5.2.11. Text in the image

This tool allows the adding of a text to a measure, drawing … as shown on Figure 104.a

√ select [*Tools*] [*Text*]



or

√ press the 'Text' button in the toolbar

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ Click on the point of the image that must be pointed by the arrow, as shown on Figure 104.a (1)

√ The window depicted in Figure 104.b opens. Type in the text that must be displayed in the label on the image and press 'Enter'. The window closes and the text appears on the image at the extremity of the yellow arrow.

√ The end of the arrow follows the mouse motion and will be set by a left click: (2) in Figure 104.a.

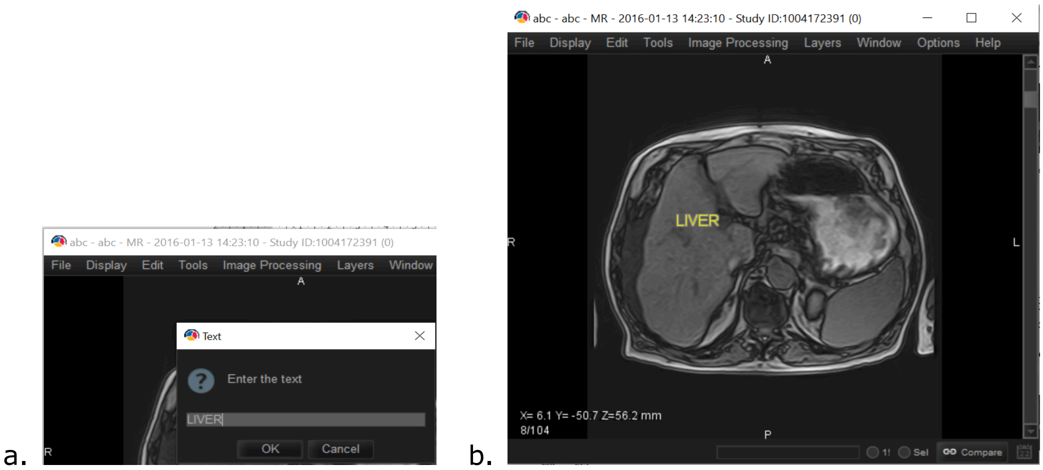


Figure 104 - Text. a) Enter the text in the window b) Text on the image

2.5.2.12. Pointer in the image

This tool allows the adding of a pointer into the image, as shown on Figure 105.

√ select [*Tools*] [*Pointer*], or

√ press the 'Pointer' button in the toolbar.

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

√ Click on the point of the image that must be pointed by the arrow, as shown on Figure 105, point (1).

- √ The end of the arrow follows the mouse cursor and will be set by a left click: (2) in Figure 105.

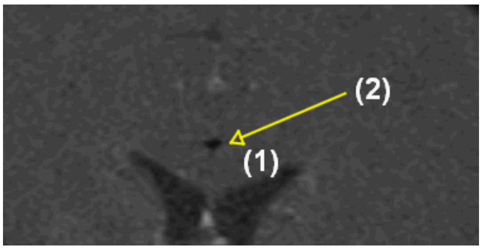


Figure 105 - Pointer

2.5.2.13. Quick texts

The tool called 'quick texts' allows the user to easily put a series of digits or characters in the image. These quick labels can easily be referenced in the report.

This tool is handled with the left and right buttons of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

2.5.2.13.1. *Quick texts with manual text increment*

This version of the tool is the easiest way to mark some organs with the same code on different images (see "tracking diagrams" here under).

- √ select [*Tools*] [*Quick text*] [*Quick text sequence manual*] and choose the kind of sequence ("ABC" for a sequence of letters, "123" for a sequence of numbers, "+" for simple "+" marks or "manual" to systematically choose the text to show), or
- √ press the 'Quick text' button in the toolbar.

To draw the first label on the image, click with the left button of the mouse on the point of the image that must be marked, as shown on Figure 106 point (1).

Continue to left-click to write the same text at different locations.

Right-click to switch to the next item in the sequence: A □ B □ C, or 1 □ 2 □ 3 etc.

To change a posteriori the text drawn, either double click on the label, or right click on the label and select [*Modify the label*].

The counter is reset when all viewers are closed or when the type of sequence is changed.

The texts drawn are saved the same way as the other measures are saved.

2.5.2.13.2. *Quick texts with automatic text increment*

This version of the tool is the easiest way to mark and count lesions in an image. Simply click to draw for example '1', '2', '3', ...

- √ select [*Tools*] [*Quick text*] [*Quick text sequence automatic*] and choose the kind of sequence ("ABC" for a sequence of letters, "123" for a sequence of numbers, "+" for simple "+" marks or manual to systematically choose the text to show), or
- √ press the 'Quick text' button in the toolbar.

- √ To draw the first label on the image, click on the point of the image that must be marked, as shown on Figure 106 point (1). Left or right click have the same behaviour for the first label.
- √ For next labels,
  - √ Left-click to increment the counter and draw the label (ex: point (2) in Figure 106: left-click to draw "2" in the image, or point (4): left click to draw "3")
  - √ Right-click to draw the same label as the previous click did, without changing the value of the counter (point (3): right click to draw "2" again)

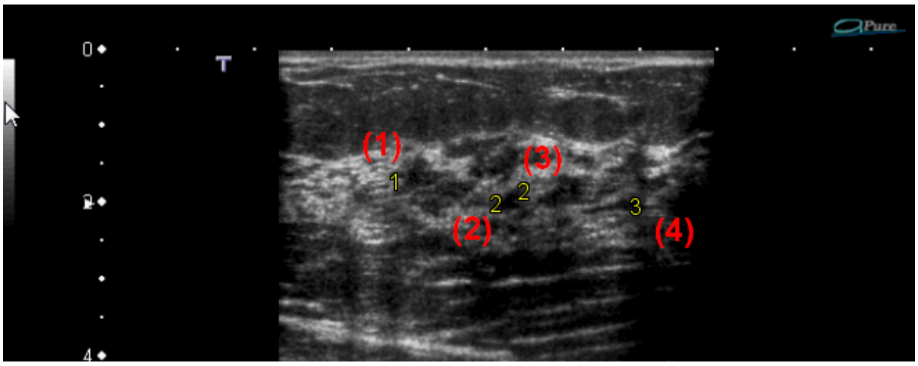


Figure 106 - Quick texts

To change a posteriori the text drawn, either double click on the label, or right click on the label and select [*Modify the label*].

The counter is reset when all viewers are closed or when the type of sequence is changed.

The texts drawn are saved the same way as the other measures are saved.

2.5.2.14. Tracking diagrams

Tracking diagrams are typically used in conjunction with the quick texts. To select a template diagram, open it and save it as an additional series in the current study:

- √ select [*Tools*] [*Quick text*] [*Create new tracking diagram*] and choose one template.

Both viewers are now opened side by side.

Simply use the quick labels to mark one point in the tracking diagram and the same point, with the same label, in the images of the patient.

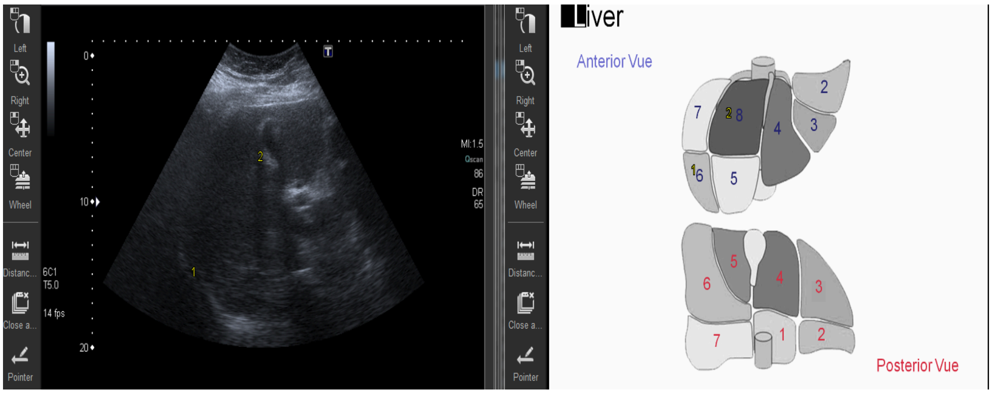


Figure 107 - tracking diagrams

2.5.3. Measures

2.5.3.1. Distance

This tool computes the distance between two points of an image[6]. A distance is a line with a length measure associated. If the scale information is available in the original DICOM file sent by the acquisition device to Telemis, or if you have calibrated the measurement tools (see section 2.5.3.9), the measure distance is computed in millimeters. If not, it is computed in pixels.

Computing the distance is similar to drawing a line:

√ select [*Tools*] [*Distance Measure*], or

√ select the "Distance" tool if available in the toolbars, or

√ press the "Alt" and "D" keys to associate the distance tool with the left button.

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ Click with the button of the mouse in an image at the point where the distance measure must begin: (1) on Figure 108.

√ Release the button and move the mouse: the end of the line will follow the mouse pointer and the distance is displayed together with the line. Click again to position the second extremity of the measure: (2) on Figure 108.

√ The measure will automatically be placed on the image.

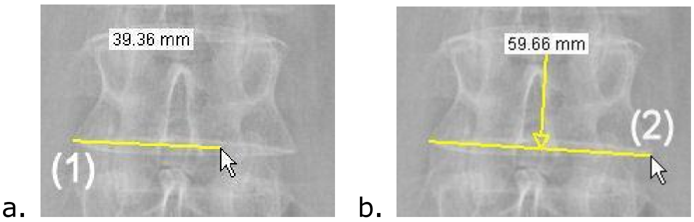


Figure 108 - Distance measure – a) Place the first point b) Define the second point

2.5.3.2. Angle

To compute an angle in an image[7],

√ select [*Tools*] [*Angle Measure*], or

√ select the "Angle" tool if available in one or the toolbars, or

√ press the "Alt" and "A" keys to associate the angle tool with the left button.

---

[6] The tool precision verification tests have given the following results, on a rectangular object:

Length Real value = 40.0 mm Measured value = 39.9 mm Acceptable limits = [39.4 – 40.6 mm]
Width Real value = 30.0 mm Measured value = 29.6 mm Acceptable limits = [29.4 – 30.6 mm]

[7] The tool precision verification tests have given the following result:

Angle Real value = 53.1° Measured value = 53.8° Acceptable limits = [52.1° – 54.1°]

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ Click with the button of the mouse, in an image at the point where the top of the angle will be (Point #1. in Figure 109).

√ Release the button and move the mouse: the end of the line will follow the mouse pointer. Click again (Point #2. in Figure 109) to state the first line of the angle. A line will be drawn between the point #1 (the 'top' of the angle) and your mouse.

√ The angle measure is drawn around the line and evolves as the mouse moves. Click a third time (Point #3. in Figure 109) to conclude the angle drawing.

√ The angle is automatically computed and placed on the image: inside the angle to compute the small angle (e.g. 40°) and outside the angle to compute the big value of the angle (320°), as shown in Figure 109.B.

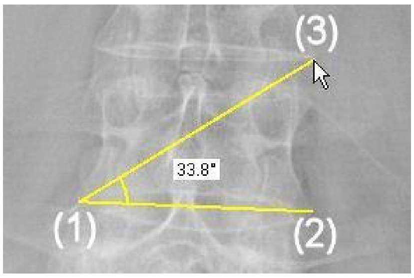


Figure 109 – Angle measure

2.5.3.3. Angle between two lines

The previous method to measure angles supposes that the centre of the angle is accessible. In some situations (for example the angle between two bones as shown in Figure 110.b, it is easier to measure the angle between the two lines[8] passing in the centre of the bones.

First draw the two lines.

√ Then select [*Tools*] [*Angle between two lines*]

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Move the mouse. The line closest to the mouse pointer is "selectable": When the mouse pointer is close to a "selectable" line, this line becomes thick.

√ Chose the line that must be the 'original line', as shown on Figure 110.a: click with the left button when this line is "selectable".

√ Select the second line (the second click on Figure 110.b). The measure is then computed and automatically displayed on the image.

---

[8] The tool precision verification tests have given the following result:

Angle Real value = 53.1° Measured value = 53.9° Acceptable limits = [52.1° – 54.1°]

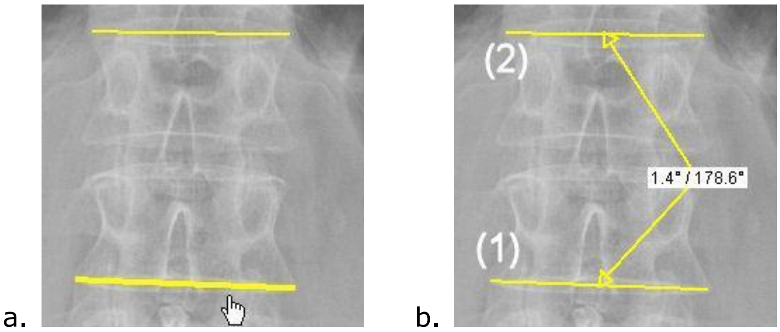


Figure 110 - Angle between two lines. a) Select the first original line b) Second line and position of result

The next click on the left button will start a new measure, until the right button of the mouse is pressed.

2.5.3.4. Cobb angle

The measure of the Cobb angle is often used with pathologies such as scoliosis. It consists in measuring the angle between 2 vertebras. This measure is possible by combining other tools (draw lines and compute angle between 2 lines). Using the Cobb Angle tool eases this operation.

√ Select the [*Tools*] [*Cobb angle*] tool,

√ Or click on the 'Cobb angle' button in the toolbar

- Click to mark the two extremities of the first line (points 1. and 2. of Figure 111),
- Click to mark the two extremities of the second line (points 3. and 4. of Figure 111). The measure is then computed and automatically displayed on the image.

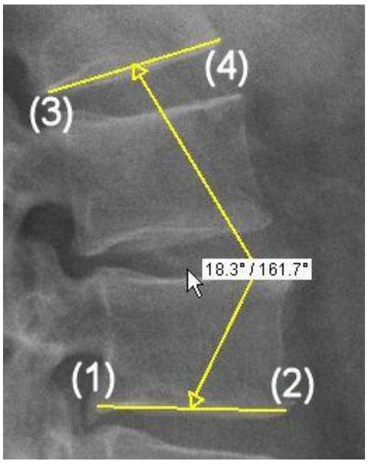


Figure 111 - Cobb angle

2.5.3.5. Cobb angle between slices

The measure of the Cobb angle is often used with pathologies such as scoliosis. It consists in measuring the angle between 2 vertebras. This measure is possible by combining other tools (draw lines and compute angle between 2 lines). Using the Cobb Angle tool eases this operation. In this case, the two lines can be drawn on different slices.

√ Select [*Tools*] [*Cobb angle between slices*].

- Click to mark the two extremities of the first line (points 1. and 2. of Figure 111) in a first slice, Click to mark the two extremities of the second line (points 3. and 4. of Figure 111) in another slice. The measure is then computed and automatically displayed on the image

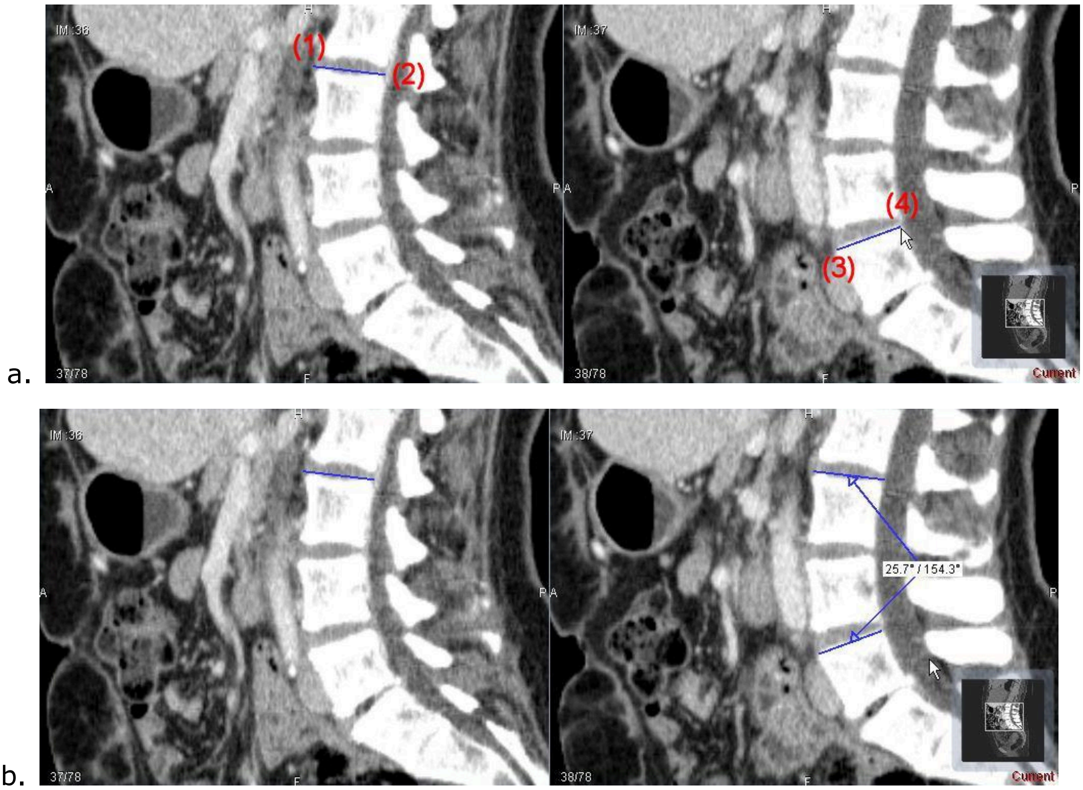


Figure 112 - Cobb angle between slices - a) Draw the 2 lines on different slices b) Cobb angle automatically displayed

2.5.3.6. Ratio between two distances

To compute the ratio between two distances

√ Select *[Tools]* *[Ratio between two distances]*.

As shown on Figure 113,

Draw the two distances measures in the image. When the second distance is concluded, the ratio is automatically computed and displayed in the image.

This measure displayed represents $Ratio = \frac{\text{Distance1}}{\text{Distance2}}$

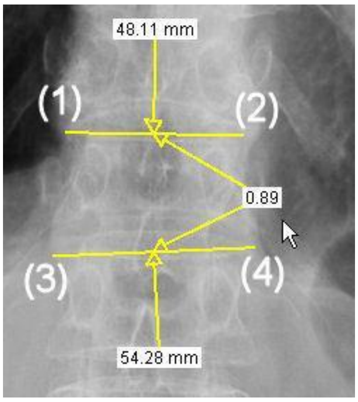


Figure 113 - Ratio between two distances

Ratio can be inverted in order to measure the following ratio:

$$Ratio = \frac{\text{Distance2}}{\text{Distance1}}$$

To compute this ratio, right-click on the preceding ratio, and in the contextual menu, select “Invert ratio” (Figure 114)

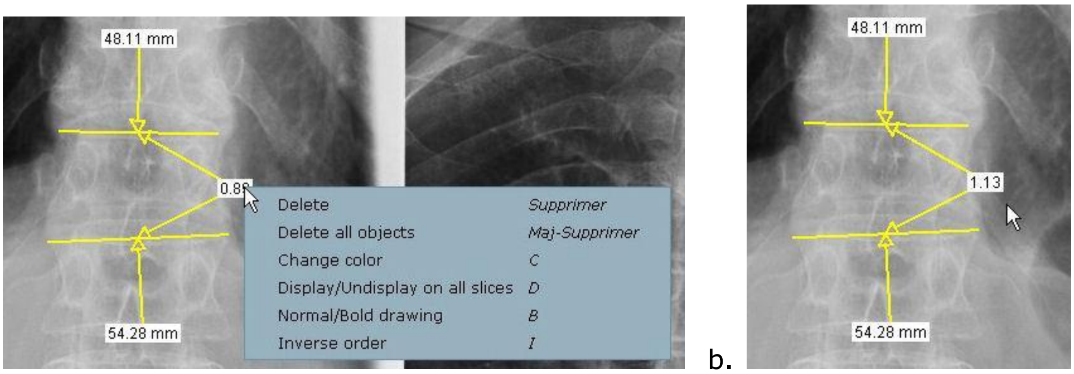


Figure 114 - Inversion of the ratio - a) Select option in the contextual menu b) Ratio inverted

2.5.3.7. Height measure

To compute the height difference[9] between two points of an image,

√ Select [*Tools*] [*Height Measure*]

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the ‘ESC’ key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ Click with the button of the mouse, in an image at the first point (Point #1. in Figure 115).

√ Release the button and move the mouse: the measurement tool will follow the mouse pointer and the height difference between the first point and the current one is displayed together with the lines. Click again to position the second point of the measure: (2) on Figure 115. The measure is automatically placed on the image.

√

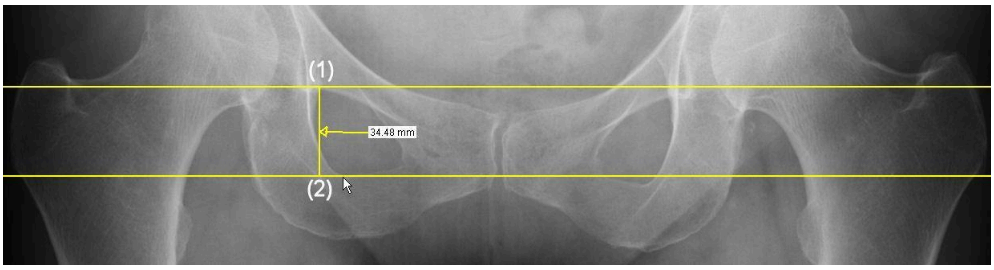


Figure 115 - Height difference measurement

---

[9] The tool precision verification tests have given the following results, on a rectangular object:

Height Real value = 100.0 mm Measured value = 99.9 mm Acceptable limits = [99.4 – 100.6 mm]

2.5.3.8. Hounsfield density

The Hounsfield density measures apply to CT scanner images. A Hounsfield Unit (HU) is an x-ray attenuation (density) measurement used to describe voxel values in CT scanning. In a 12-bit CT image, the voxel values will range from -1024 to +3071 HU. For example, water is defined as 0 HU, air as -1024 HU, fat as -100 to -20 HU, soft tissue as +20 to +80 HU, and bone as > +500 HU

√ select [*Tools*] [*Hounsfield density*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ Click on any point of the image to mark the beginning of the measure.

Move the mouse. A small text box follows the mouse pointer and contains the Hounsfield density measure for the point under the mouse (see Figure 116.a).

√ To set the measure for a point, click on this point. Move the mouse until the position of the extremity of the yellow line (that is the place where the text will be draw) suits you and click again to conclude the measure.

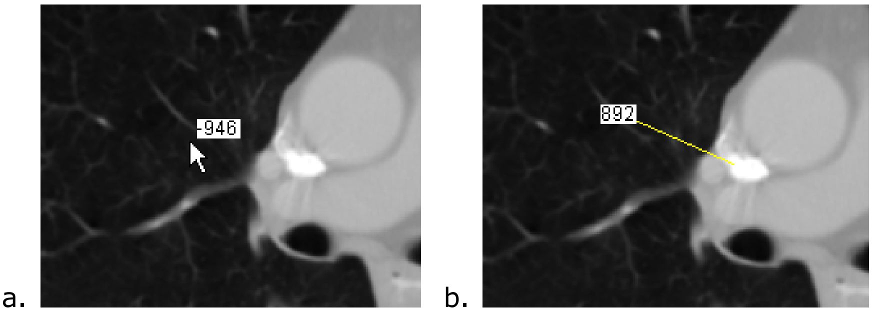


Figure 116 - Hounsfield density measure. a) During mouse motion b) Final result

2.5.3.9. Region of Interest (ROI)

CT scanner images are best diagnosed if some measures are provided on a region: the minimum, maximum and average value of the region of the image[10].

On each ROI drawn, right-click and select [*Add measure to follow up*] to add this measure to a measure follow-up (see section 1.7 page).

---

[10] The tool precision verification tests have given the following results, on the central region of the sample image and on the air:

	Real value	Measured value	Acceptable limit
Minimum	100	111	90
Maximum	150	139	160
Black air	-1000	-1006	[-980 - -1020]

2.5.3.9.1. *Circle ROI*

To compute a circular ROI,

√ select [*Tools*] [*ROI*] [Circle *ROI*], or

√ click on the 'Circle ROI' button in the toolbar

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

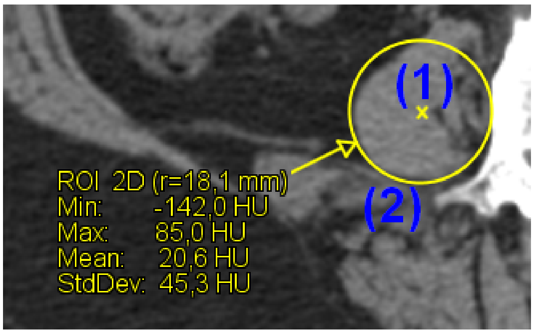
Click a first time to mark the centre of the region (Point #1. in Figure 117).

Move the mouse. The size of the circle follows the pointer. Click a second time to mark the size of the region (Point #2. in Figure 117).

The 2D ROI values are finally computed and automatically displayed on the image.

The values and units are computed according to the kind of image:

- for CT images: Hounsfield Units (HU)
- for PT images: SUV



ROI 2D (r=18,1 mm)
Min: -142,0 HU
Max: 85,0 HU
Mean: 20,6 HU
StdDev: 45,3 HU

Figure 117 – Circular region of Interest

2.5.3.9.2. *Rectangle ROI*

To compute a rectangle ROI,

√ select [*Tools*] [*ROI*] [Rectangle *ROI*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click to mark the rectangular region (Figure 118) : a first time to define a corner of the rectangle, and a second time to determine the opposite corner.

The ROI values are finally computed and automatically displayed on the image.

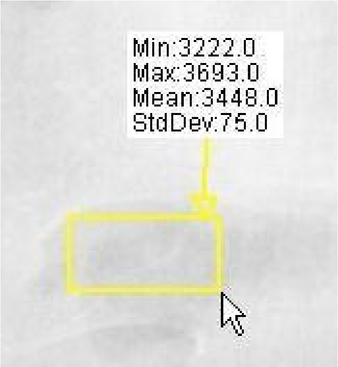


Figure 118 - Rectangle region of interest

The units of the measure depend on the modality of the images (example: PT scan : SUV ROI, CT scan: Hounsfield Units ROI, ...)

2.5.3.9.3. Polygonal ROI

To compute a polygonal ROI,

√ select [*Tools*] [*ROI*] [Polygonal *ROI*].

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

Click to mark the polygonal region (Figure 119) : click to define the contour points, and double-click to close the polygon.

The ROI values are finally computed and automatically displayed on the image.

Figure 119 - Polygonal region of interest

The units of the measure depend on the modality of the images (example: PT scan : SUV ROI, CT scan: Hounsfield Units ROI, ...)

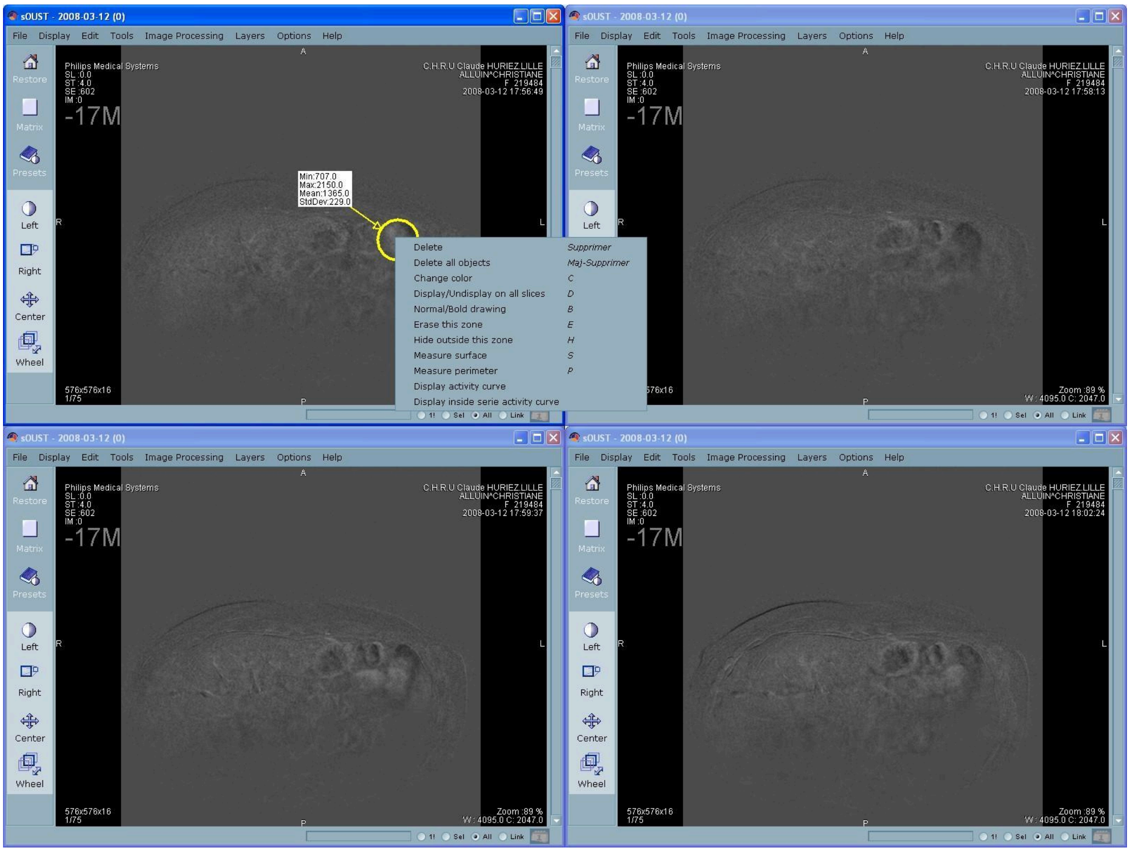
2.5.3.10. Activity curve

With several studies, plotting the evolution of some values gives a good idea of the evolution of a parameter, as for example in magnetic resonance studies between a reference series and some series taken along the time.

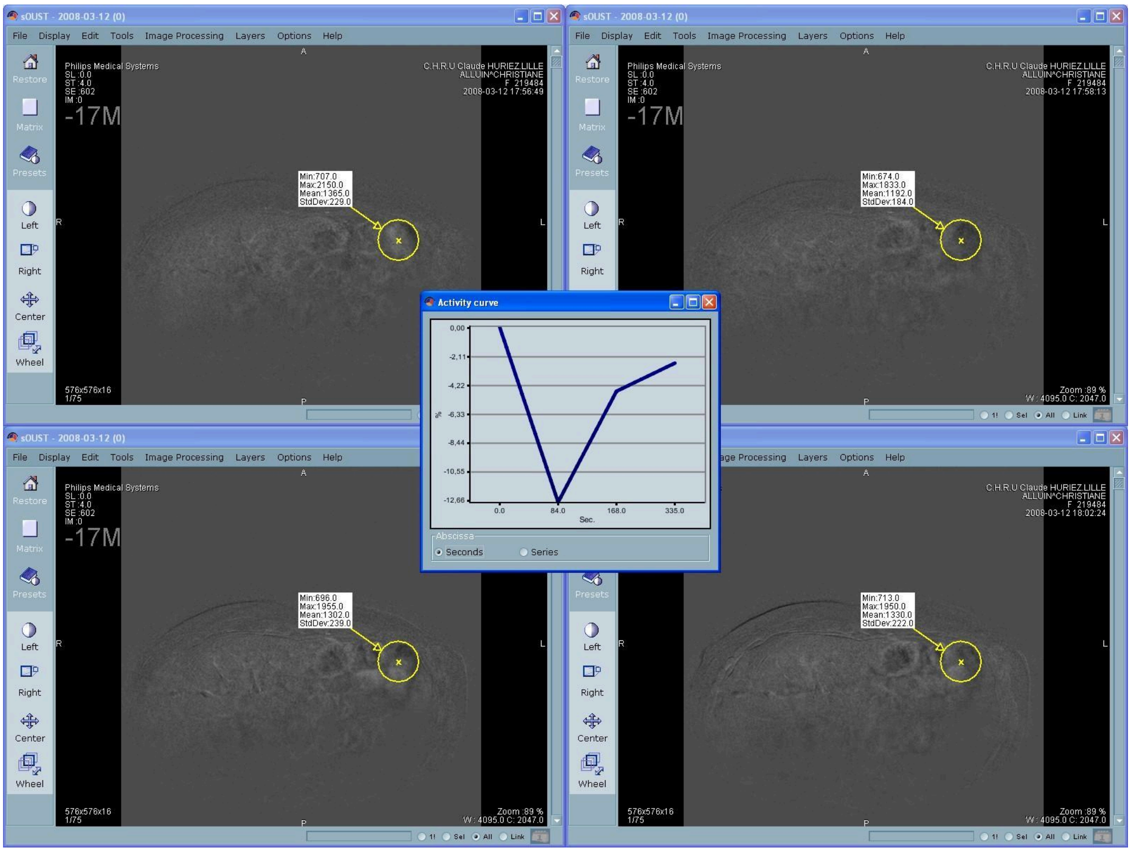
In a *TM-Reception HE*, open all the viewers containing the reference series and the other series.

In one of the viewers, draw a Region of Interest on a slice (see section 2.5.3.9) and right-click on it to display the contextual menu. Select "Display activity curve" in this menu.

The *TM-Reception HE* will use all the viewers opened for series of the same study, sort them by acquisition date and plot the evolution of the RoI value as a percentage of the reference image (see Figure 120) related to the time. It is possible to display the serie number instead of the time in abscissa in clicking on the button "Serie" below the graph. The RoI is drawn on all opened viewers, but can be modified only on the slice where it was initially drawn.



a.



b.

Figure 120 - Activity curve – a) Select "Display activity curve" in the contextual menu of the ROI. b) Activity curve graph

2.5.3.11. Inside serie activity curve

In a same study, plotting the evolution of some values gives a good idea of the evolution of a parameter, as for example in magnetic resonance studies between a reference slice and the other slices of the serie taken along the time.

In a *TM-Reception HE*, open the interesting serie. In one of the slices, draw a Region of Interest on a slice (see section 2.5.3.9) and right-click on it to display the contextual menu. Select "Display inside serie activity curve" in this menu.

The *TM-Reception HE* will use all the slices of the serie, sort them by acquisition date and plot the evolution of the RoI value as a percentage of the reference image (see Figure 121) related to the time. It is possible to display the serie number instead of the time in abscissa in clicking on the button "Serie" below the graph. The RoI is drawn on all slices, but can be modified only on the slice where it was initially drawn.

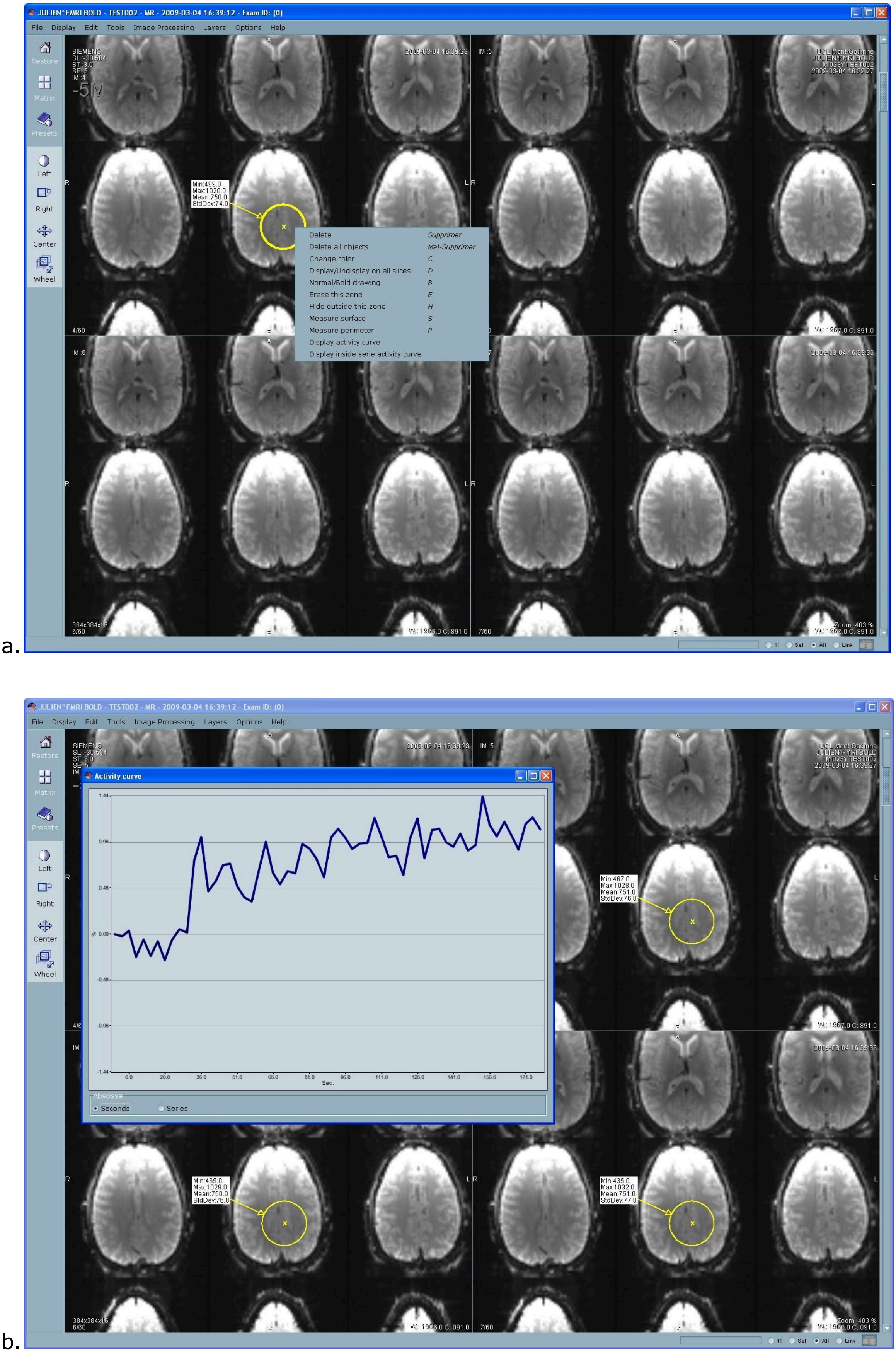


Figure 121 - Activity curve intra serie – a) Select "Activity curve intra serie" in the contextual menu of the ROI. b) Activity curve graph

2.5.3.12. Perimeter measurement

This tool measures the perimeter of an object defined by a contour[11], i.e. a rectangle, a circle, an ellipse, a continuous or polygon hand free drawing.

The object must first be defined by one of these tools. The perimeter measure can also be obtained for a circle, a rectangle or a polygonal ROI.

When the object is defined, right-click on it to display the contextual menu, and select "Perimeter measure" (see Figure 122.a).

The perimeter measure is automatically displayed on the image (see Figure 122.b and Figure 122.c).

To undisplay the measure, right-click again on the object to display the contextual menu, and select "Measure perimeter" (see Figure 122.a).

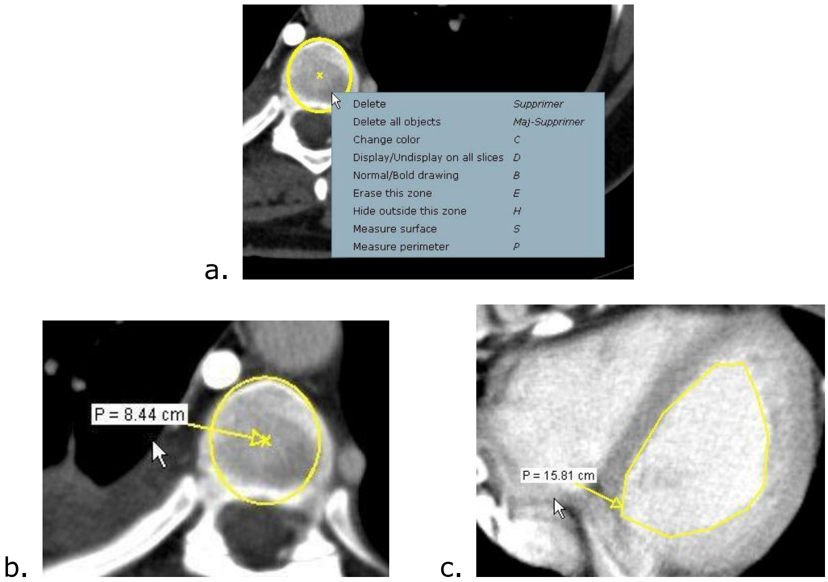


Figure 122 - Perimeter measure – a) Select "Measure perimeter" in the contextual menu of the area. b) Perimeter measure of an ellipse. c) Perimeter measure of a polygon

2.5.3.13. Surface measurement

This tool measures the area of a surface defined by a closed contour[12], i.e. a rectangle, a circle, an ellipse, a continuous or polygon hand free drawing.

The surface must first be defined by one of these tools. The surface measure can also be obtained for a circle, a rectangle or a polygonal ROI.

When the area is defined, right-click on it to display the contextual menu, and select "Measure surface" (see Figure 123.a).

The surface measure is automatically displayed on the image (see Figure 123.b and Figure 123.c).

---

[11] The tool precision verification tests have given the following results, on a rectangular object:

Perimeter Real value = cm Measured value = cm Acceptable limits = [–cm]

[12] The tool precision verification tests have given the following results, on a rectangular object:

Surface Real value = 12.0 cm² Measured value = 11.72 cm² Acceptable limits = [11.58 – 12.42 cm²]

To undisplay the measure, right-click again on the area to display the contextual menu, and select “Measure surface” (see Figure 123.a).

√

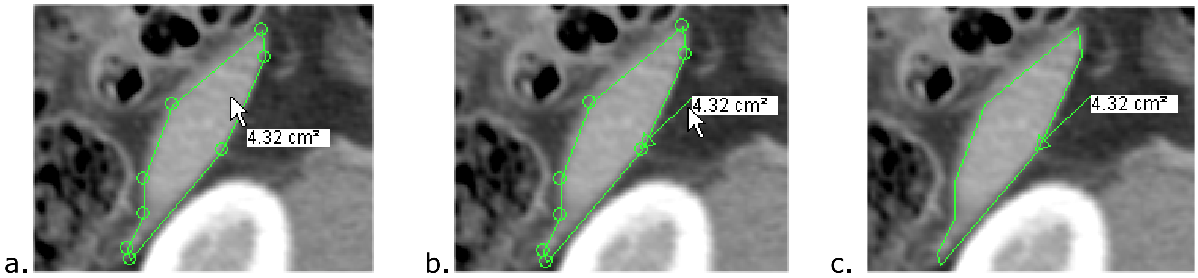


Figure 123 - Surface measure – a) Select “Measure surface” in the contextual menu of the area. b) Surface measure of a circle. c) Surface measure of a polygon

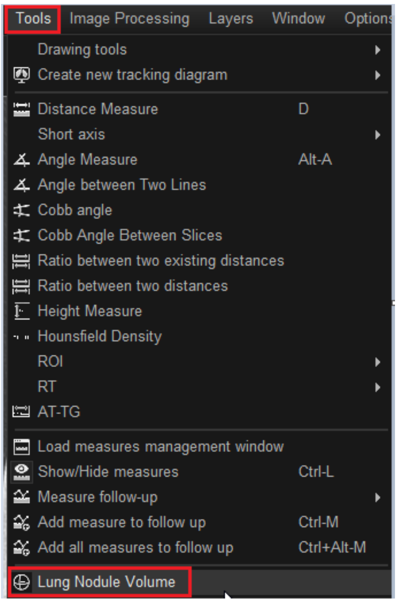
2.5.3.14. Volume of pulmonary nodules

Telemis has perfected a tool for calculating the volume of pulmonary nodules. The aim of this tool is to be able to track more easily the changes in such nodules over time. The results will be useful in the follow-up tool. The tool functions with a single click which enables the algorithm to calculate automatically the nodule’s limits, thus allowing the calculation to be reproducible regardless of which user is involved. It is impossible to modify the volume of the nodule.

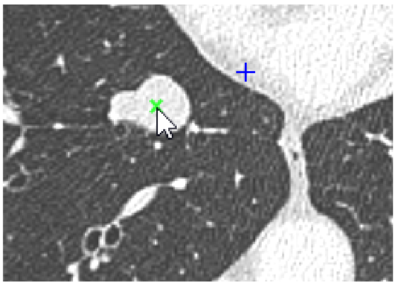
The following notions should be understood when using the nodule volume calculation tool:

- Users remain responsible for measuring and they must validate the result visually.
- The tool is only validated for use with pulmonary nodules.
- The tool has not been validated for necrotic nodules.
- The tool must be used on parenchymal type volumes.
- Follow-up must always be carried out with the same type of windowing (parenchymal windowing).
- The tool is only usable in **MPR mode on the volumes**.
- Ideally, selecting the nodule should be done in the axial plane by clicking on the centre of the nodule on the slice where the nodule is at its widest.
- The tool may be activated and deactivated. Therefore, the user must request Telemis or the on-site PACS manager to activate the tool.

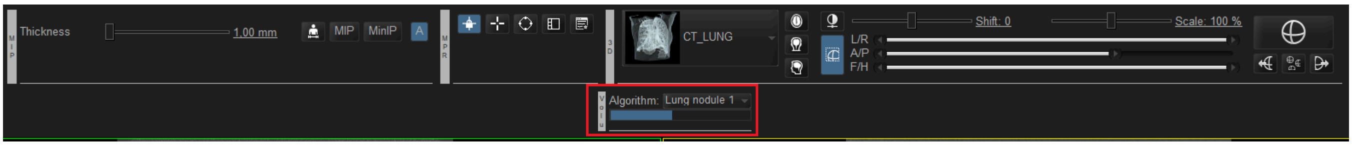
- Opening a series (parenchymal volume) in MPR.
- Select the tool - beware, you need to reactivate the tool for each nodule. You may also add it to the tool bar.



- Select an axial slice where the nodule is at its widest.
- Click on the centre of the nodule. You may zoom into the image to help.

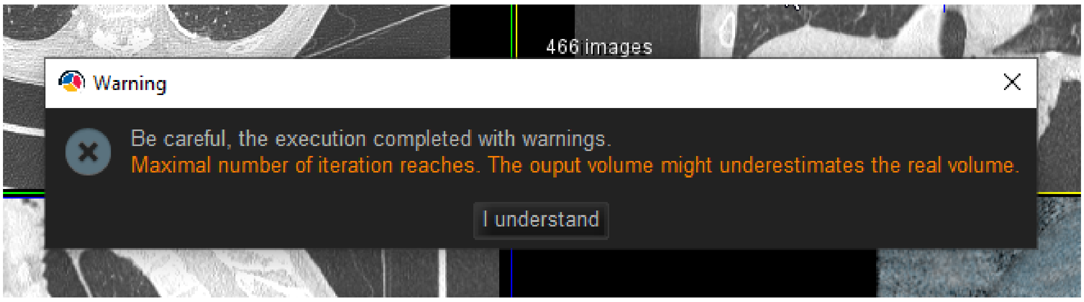


- The tool carries out the calculation and you can follow its progress on the loading bar.



Algorithm: Lung nodule 1

- If it’s a large volume and the number of iterations of the algorithm is reached, the result may be underestimated. In this case, the following message appears to alert you.



Be careful, the execution completed with warnings.
Maximal number of iteration reaches. The ouput volume might underestimates the real volume.

- The TMRHE will indicate the nodule’s measurements, if you use a multiplanar viewer the orthopointer tool will be positioned on 3 planes of the nodule being calculated and will appear in yellow in the VRT (if also selected).

2.5.3.15. Calibration

If the Telemis elements have been acquired from a DICOM study, calibration is most of the time included in the element. This means that the conversion between a number of pixels (point of an image) and a number of millimeters is stored in the Telemis element. This information makes it possible to compute distance measures in the Telemis Image Viewer.

If the elements don’t come from a DICOM study, or if the DICOM doesn’t contain the calibration information, or if the user wants to manually tune the default calibration, the Telemis Image Viewer proposes the calibration tool.

To calibrate[13] the Image Viewer (or some images independently) via a known distance, you have to know the real distance between two points of the image. The calibration looks **like a distance measure** between those points but lets you enter the real value corresponding to the measured one.

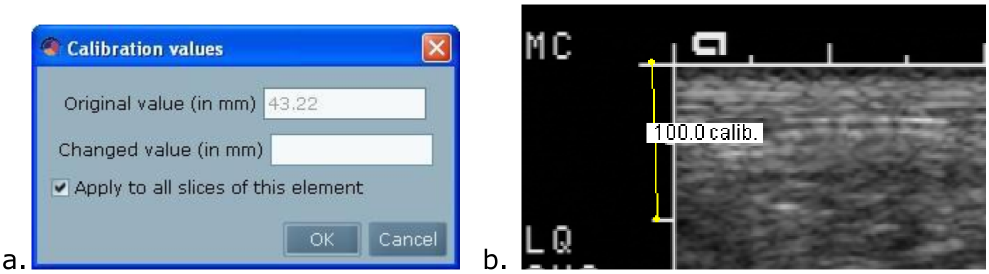
√ Select [*Tools*] [*Calibration measure*]

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the ‘ESC’ key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

√ Click with the left button of the mouse, in an image on the first point of the calibration measure. Release the button and move the mouse: the end of the calibration line will follow the mouse pointer. Click again to conclude the measure.

The distance, measured with the actual calibration parameters, is displayed on the line.


Calibration values

Original value (in mm) 43.22

Changed value (in mm)

☑ Apply to all slices of this element

Figure 124 – calibration tool a) Calibration values window b) Calibration on an ultrasound study

A small window appears (see Figure 124.a) to prompt for a modification of the calibration. The actual measure is displayed in the first text box. Change the value of the second text box to modify the calibration. Change the text of the third box if the new unit is not millimeters.

Check ‘Apply to all slices of this element’ to apply this new calibration parameter to all the images of this viewer. Uncheck to apply to only the current image.

Click on ‘OK’ to transform all the previous and future measures of this image (or of all the images of this Viewer) according to the new calibration.

---

[13] The tool precision verification tests have given the following result, on a rectangle (Width = 29.35 mm recalibrated to 50.0 mm, original height = 39.3 mm):

Height Real value = 66.95 mm Measured value = 67 mm Acceptable limits = [66 – 68 mm]

It is possible to modify the calibration in double-clicking on the calibration value. The window in Figure 124.a appears and the value can be changed.

It is also possible to perform a **manual calibration**:

√ Select [*Tools*] [*Edit calibration param …*]

The small window presented in Figure 124.a lets you manually change the calibration parameters.

If the calibration is performed with a ball, a circle calibration tool can be used in order to adjust the diameter measure (See Figure 125). In this case,

√ select [*Tools*] [Circle *calibration measure*]

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

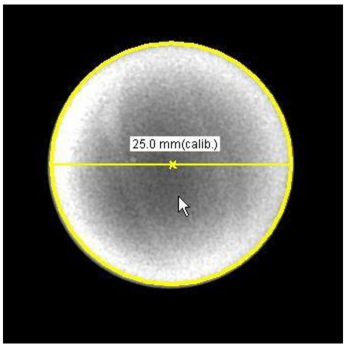


Figure 125 - Circle calibration

2.5.3.16. Display in real size

This option is only available in the *TM-Reception HE* version.

For e.g. orthopedic applications, it is important to display the images on screen respecting the real size: one mm on screen must correspond to one real mm.

√ Select [*Display*] [*Display in real size*]

Click on any image of the Viewer to automatically zoom the image up to the real size: one displayed mm corresponds to one millimeter on the patient.

The first time that this function is used, the real size tool must be **calibrated**. The ruler shown on Figure 126 appears on screen. If you change the display monitor connected to your *TM-Reception HE*, you MUST recalibrate the tool via

√ Select [*Display*] [*Recalibrate real size*]

Measure on your screen the size of the ruler, from point 1. to point 2. Enter this measure in mm in the text area under the drawn ruler and press 'OK'.

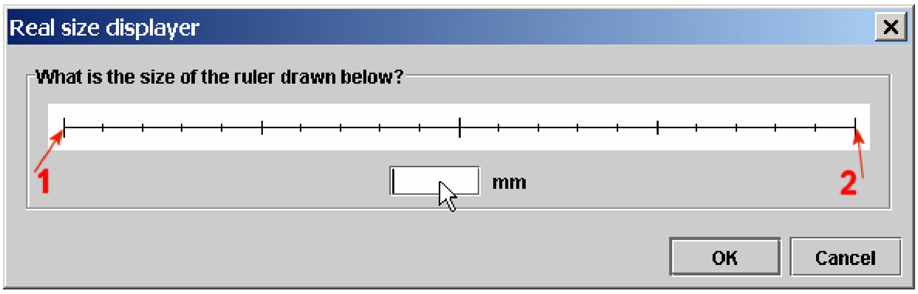


Figure 126 - ruler for real size display calibration

2.5.3.17. Short axis

This tool is only available in the *TM-Reception HE* version.

This tool measures the bigger diameter of a lesion perpendicular to the biggest diameter of the same lesion. This tool is used a.o. in the RECIST protocol to measure nodal lesions (only the value of the short axis is used in this case).

√ Select [*Tools*] [*Short axis*] [*Short axis*]

Via the first and second clicks, determine the longest diameter of the region to measure (see Figure 127 points 1. and 2.)

The third and fourth clicks will set the longest diameter perpendicular to the first drawn line (see Figure 127 points 3. and 4.)

The tools computes the length of the first line ("Long"), of the perpendicular line ("Short") and the product of both lengths.

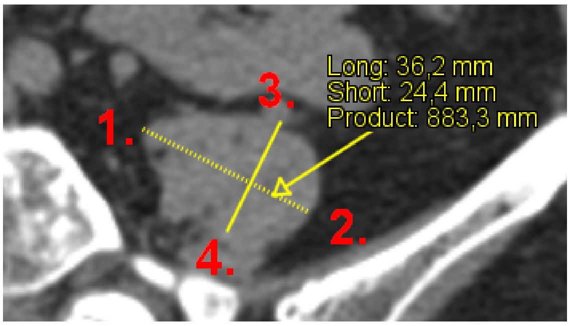


Figure 127 - Short axis tool

√ Select [*Tools*] [*Short axis*] [*Short axis mode*] and select one of the proposed modes to set the measure that will be followed-up in the measure follow-up, if the result of the measure is added to a follow-up (see section 1.7 page): "Long" measure, "Short" measure, "Product" of both measures.

2.5.4. Complex tools

Some more complex tools are available: gonometry, coxometry, TAGT, Telos distance...

These tools are a combination of several simple drawings and measures, but the number of clicks needed is reduced related to the total number of clicks needed to draw all the objects separately.

2.5.4.1. Gonometry

To measure a gonometry,

√ Select [*Tools*] [*Complex measures*] [*Gonometry*]

The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 128).

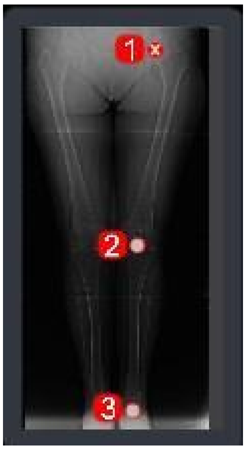


Figure 128 - Help image for gonometry measure

- √ Gonometry is drawn on the basis of three reference points as shown on Figure 129. Click a first time to mark the centre of the femoral head. Then click to place the center of the knee, and finally click to place the ankle segment.

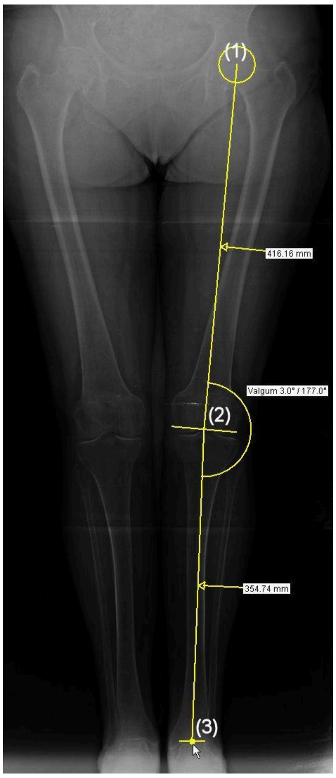


Figure 129 - Gonometry measure

The complete drawing is automatically established on the basis of these three points. Three measures are displayed: the angle between the femoral axis and the tibia axis, and the length of these axes. Other segments are created: the knee axis and the ankle axis, and a circle is displayed around the femoral head (to help positioning of the femoral head center).

2.5.4.2. Coxometry

To measure the hip coxometry,

- √ Select [*Tools*] [*Complex measures*] [*Hip coxometry*]
- √ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 130).

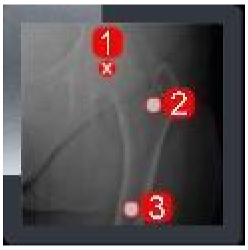
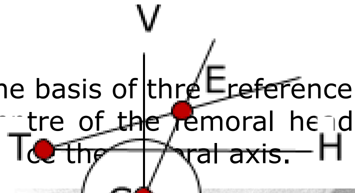


Figure 130 - Help image for coxometry measure

Schema below shows all needed reference points to compute the interesting angles of the coxometry. They can be formulated as angles VCE, HTE and angle formed by the femoral neck axis and the femoral axis.



Coxometry is drawn on the basis of three reference points as shown on Figure 131. Click a first time to mark the centre of the femoral head. Then click to mark the femoral neck axis, and finally click to place the femoral axis.

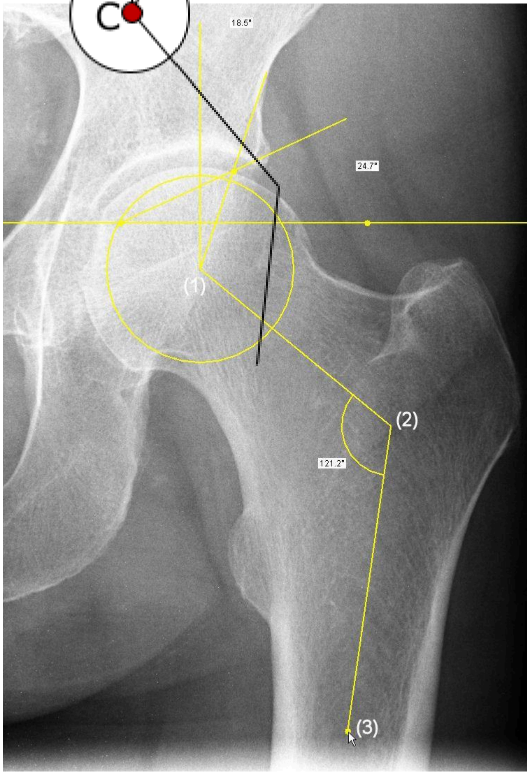


Figure 131 - Coxometry measure

The complete drawing is automatically established on the basis of these three points. The points T, H and E (see schema above) are estimated in order to compute the interesting angles. Some segments are created: segment between points T and E, segment between the femoral head center and point E, the femoral neck axis and the femoral axis, and a circle is displayed around the femoral head (to help positioning of the femoral head center). The vertical line from the femoral head center and the horizontal line from the point T are also automatically drawn. Three angle measures are thus displayed: the angle between the femoral axis and the tibia axis, and the length of these axis.

2.5.4.3. Coxometry false-profile

To mesaure the angle of the coxometry false-profile,

- √ Select [*Tools*] [*Complex measures*] [*Coxometry false-profile*]
- √ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 132).

Figure 132 - Help image for coxometry false-profile

Drawing coxometry on the false-profile view is performed by clicking on two points (see Figure 133): the femoral head center and the other point needed to define the angle formed by these two points and the vertical line drawn from the femoral head center.

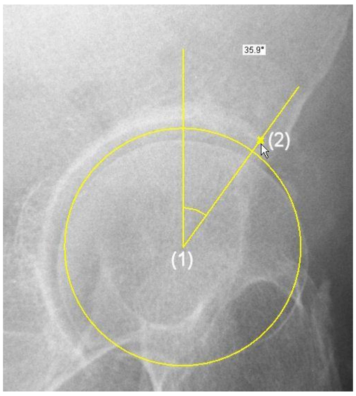


Figure 133 - Coxometry false-profile measure

The circle around the femoral head and the interesting angle are automatically computed and displayed.

2.5.4.4. TAGT

To measure TAGT,

- √ Select [*Tools*] [*Complex measures*] [*TAGT*]
- √ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 134).

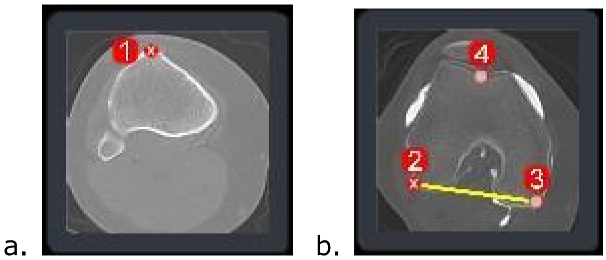


Figure 134 - Help image for TAGT

TAGT is drawn on the basis of one reference point on a first slice and a reference line and another point on a second slice as shown on Figure 135. Click a first time to mark the reference point on the first slice (see Figure 135.a.). Then click to define the reference line on the second slice (see Figure 135.b.), and finally click to place the last point on the same slice as the line (see Figure 135.c).

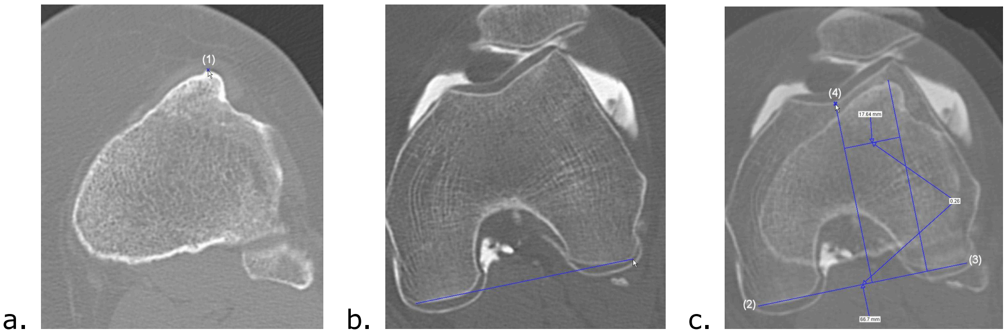


Figure 135 - TAGT measure: a. Point on a first slice b. Reference line and second point on the second slice c. Measures

The TAGT measure is automatically computed and three values are displayed (see Figure 135.c.): the distance of the reference line, the TAGT distance and the ratio between them.

At the top of the viewer, you will find a slider. Drag the slider cursor to the left or right to show the first image (Figure 135.a), the second image (Figure 135.b and c) or any mix between them.

2.5.4.5. Telos distance

To measure the Telos distance,

- √ Select [*Tools*] [*Complex measures*] [*Telos distance*]
- √ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 136).

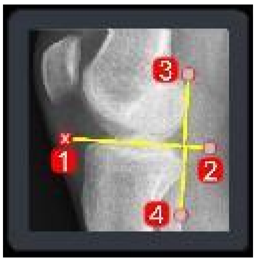


Figure 136 - Help image for Telos distance

Telos distance measure is drawn on the basis of four reference points as shown on Figure 137. Click on these points in the order explained on this figure. This will form a line with the two first points, and two perpendicular lines will be drawn from the other points related to the line.

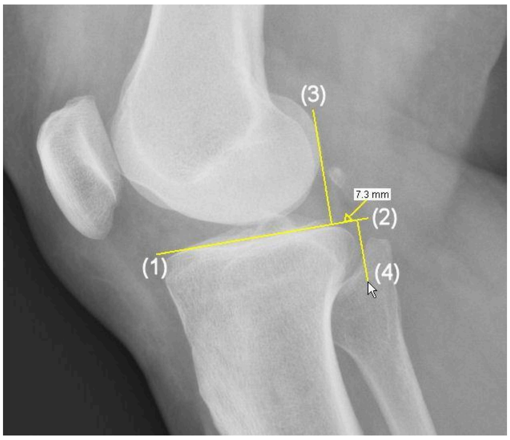


Figure 137 - Telos distance measure

The distance between the two perpendicular lines is automatically computed and displayed.

2.5.4.6. Transischial line

To measure the transischial line distances,

√ Select [*Tools*] [*Complex measures*] [*Transischial line*]

√ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 138).

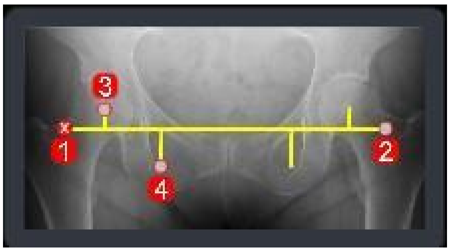


Figure 138 - Help image for transischial line measure

Transischial line distances are drawn on the basis of four reference points as shown on Figure 139. Click on these points in the order explained on this figure. This will form a line with the two first points, and two perpendicular lines will be drawn from the other points related to the line. Symmetric perpendicular lines are then estimated and drawn on the other side of the base line.

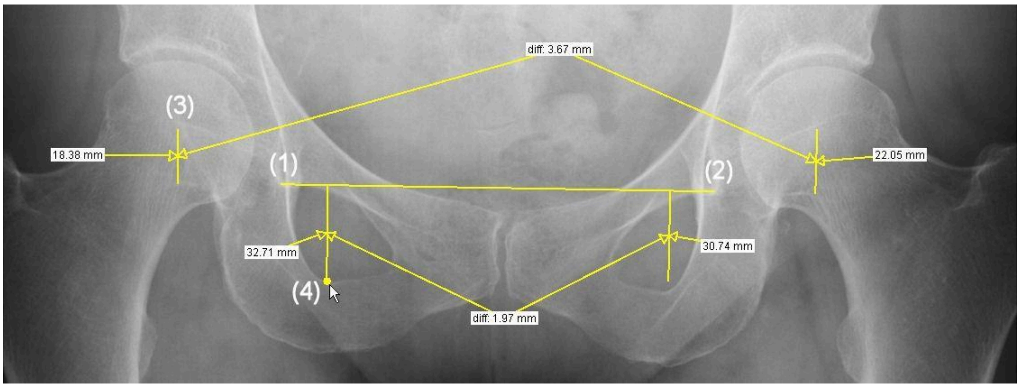


Figure 139 - Transischial line measure

Four distances are automatically computed and displayed, as well as the difference between corresponding distances (the two distances above the base line, and the two others) as shown on Figure 139.

2.5.4.7. Hilgenreiner line

To measure the Hilgenreiner line distances,

√ Select [*Tools*] [*Complex measures*] [*Hilgenreiner line*]

The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 140).

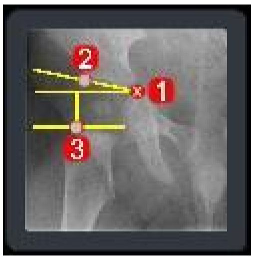


Figure 140 - Help image for Hilgenreiner line measure

Hilgenreiner line distances are drawn on the basis of three reference points as shown on Figure 141. Click on these points in the order explained on this figure. This will form a horizontal line from the first point, which constitutes an angle with the second point. Another horizontal line is drawn from the third point.

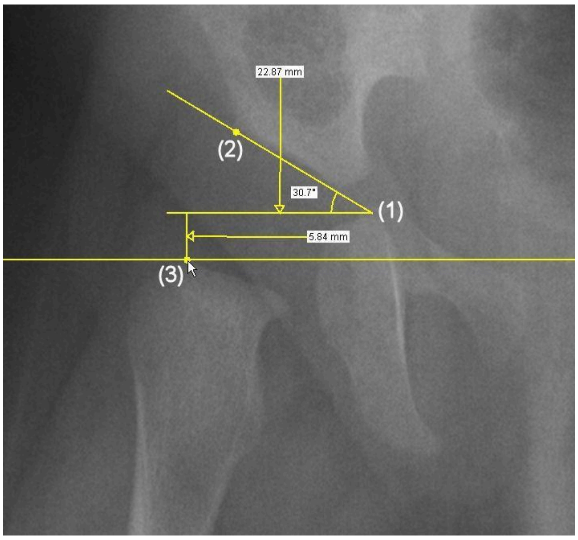


Figure 141 - Hilgenreiner line measure

Various measures are automatically computed and displayed (see Figure 141): the angle between the two first points and the corresponding horizontal line, the distance between the two horizontal lines and the horizontal distance between the first and the third point.

2.5.4.8. Hip congenital luxation

To draw hip congenital luxation lines,

- √ Select [*Tools*] [*Complex measures*] [*Hip congenital luxation*]
- √ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 142).

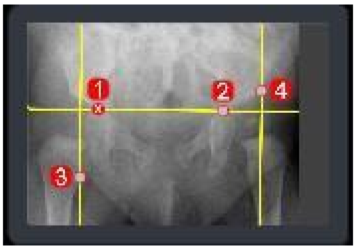


Figure 142 - Help image for hip congenital luxation draw

Hip congenital luxation lines are drawn on the basis of four reference points as shown on Figure 143. Click on these points in the order explained on this figure. This will form a line with the two first points, and two perpendicular lines will be drawn from the other points related to the line.

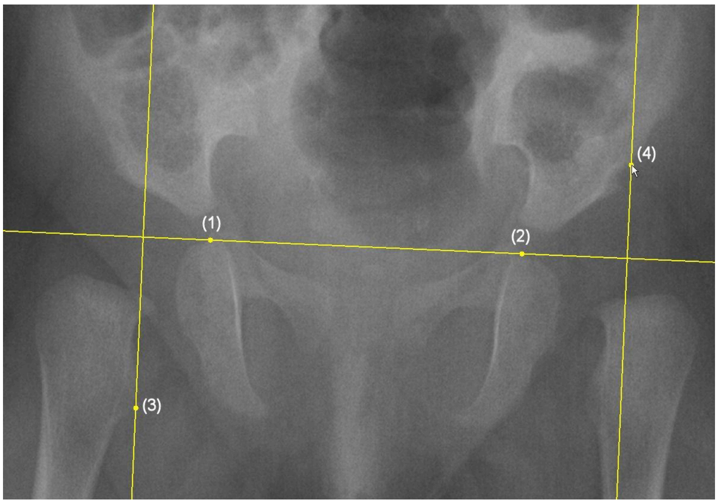


Figure 143 - Hip congenital luxation draw

2.5.4.9. Femoral head height

To measure the femoral head height related to the trochanter major,

- √ Select [*Tools*] [*Complex measures*] [*Femoral head height*]
- √ The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 153).

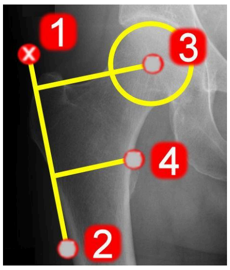


Figure 144 - Help image for femoral head height measure

Femoral head height lines are drawn on the basis of four reference points as shown on Figure 145. Click on these points in the order explained on this figure. This will form a line with the two first points, and two perpendicular lines will be drawn from the femoral head center and the trochanter major point related to the line.

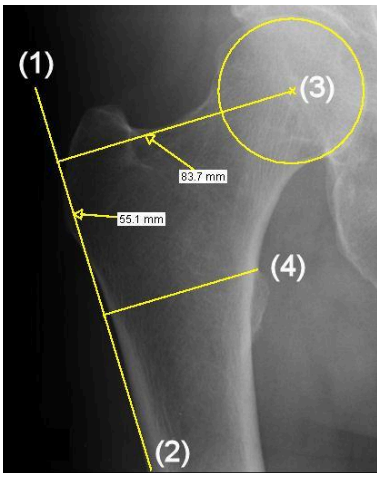


Figure 145 – Femoral head height draw

2.5.4.10. Foot angles

To measure the foot angles,

√ Select [*Tools*] [*Complex measures*] [*Foot Angles*]

The information line at the bottom of the viewer displays a short explanation on how to use this tool and a help image is displayed near the image to guide the drawing (see Figure 146).

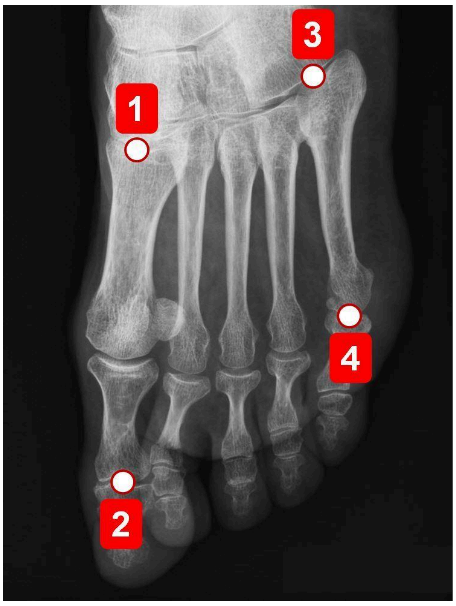


Figure 146 - Help image for foot angle measures

√ "Foot Angles" is drawn on the basis of four reference points as shown on Figure 146. Click a first time to mark the center of the articulation between the medial cuneiform and the first metatarsal. Next click to place the center of the articulation between the first distal phalange and the first proximal phalange, then click to place the center of the articulation between the cuboid and the fifth metatarsal. And finally click to mark the center of the articulation between fifth proximal phalange and the fifth metatarsal.

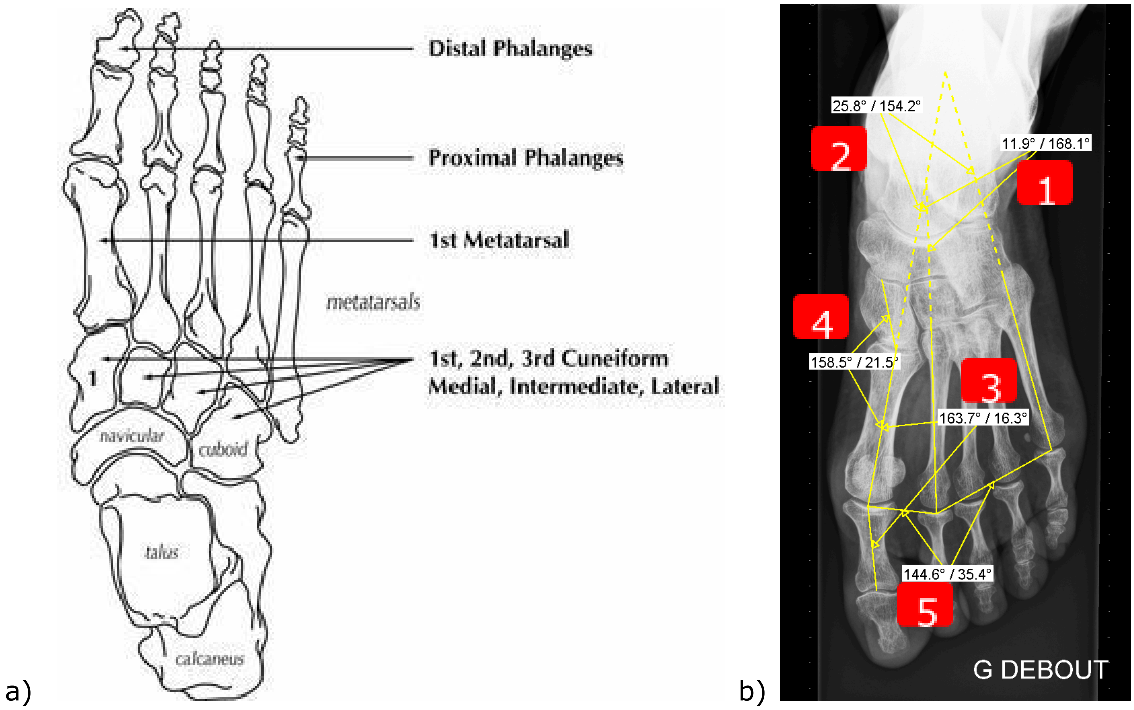


Figure 147 – a) Foot anatomy, b) Foot angle measures

The complete drawing is automatically established on the basis of these four points.

Four additional points are evaluated (see Figure 147.b):

- the center of the articulation between the second metatarsal and the intermediate cuneiform;
- the center of the articulation between the second metatarsal and the second proximal phalange;
- the center of the articulation between fifth proximal phalange and the fifth metatarsal;
- the center of the articulation between the navicular and the medial cuneiform.

All drawn axis and theirs extremities can be moved at any time with the mouse and all measures are automatically recomputed.

Five angle values are displayed (See Figure 147.b):

1. the angle between the first and the second metatarsals;
2. the angle between the first and the fifth metatarsals;
3. the angle between the first metatarsal and the first proximal phalanges;
4. the angle between the first metatarsal and the cuboid;
5. the angle on the second finger feet formed by the axes between the phalange articulations.

2.5.5. Cardiac measures and ultrasound regions

Most ultrasound DICOM images are split in several regions that have their own measurement units and 'pixel spacing', the conversion between a number of pixels and a number of millimeters.

When selecting a measurement tool in the viewer, only the regions compatible with this tool will allow performing the measure. These regions are bordered by a yellow rectangle and the type and format[14] of the region are displayed in the upper left corner.

It is not possible to perform a measure outside a compatible region. For example, distance measure may only be performed in regions having units expressed in mm in both directions, i.e. in regions of type 'tissue' and format '2D'.

Drawing tools (circle, rectangle, line, perpendicular line etc.) can be used anywhere in the images, regardless of the regions.

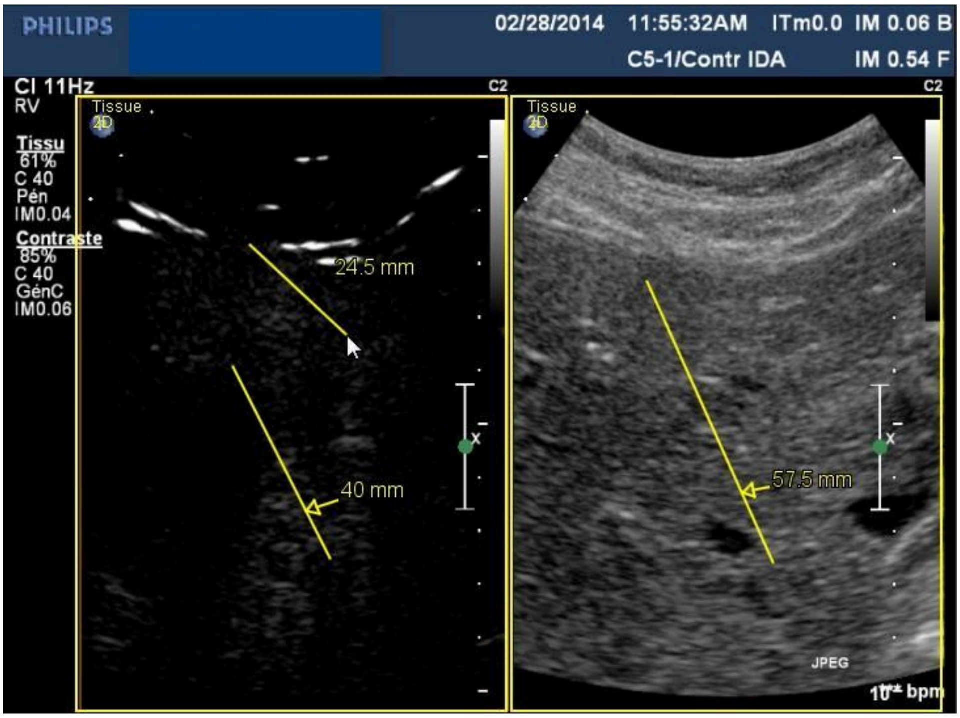


Figure 148 - Ultrasound region measures

Some measurements tools have been specifically developed to work on ultrasound cardiac images as explained here under.

2.5.5.1. Doppler – Velocity

This tool measures the velocity at a point located in a Doppler region.

√ Select the menu [*Tools*] [*Ultrasound measures*] [*Doppler – Velocity*]

The region must be of type 'Doppler' and format 'Spectral'.

The units provided in the metadata of the images are cm/sec along the vertical axis and seconds along the horizontal axis.

Simply click on a point of the region to mark the point to be measured. The measure value will not appear directly in the image but in the measures management window (to open it, see section 2.5.6.1 page . For example, select the menu [*Tools*] [*Load measures management window*]).

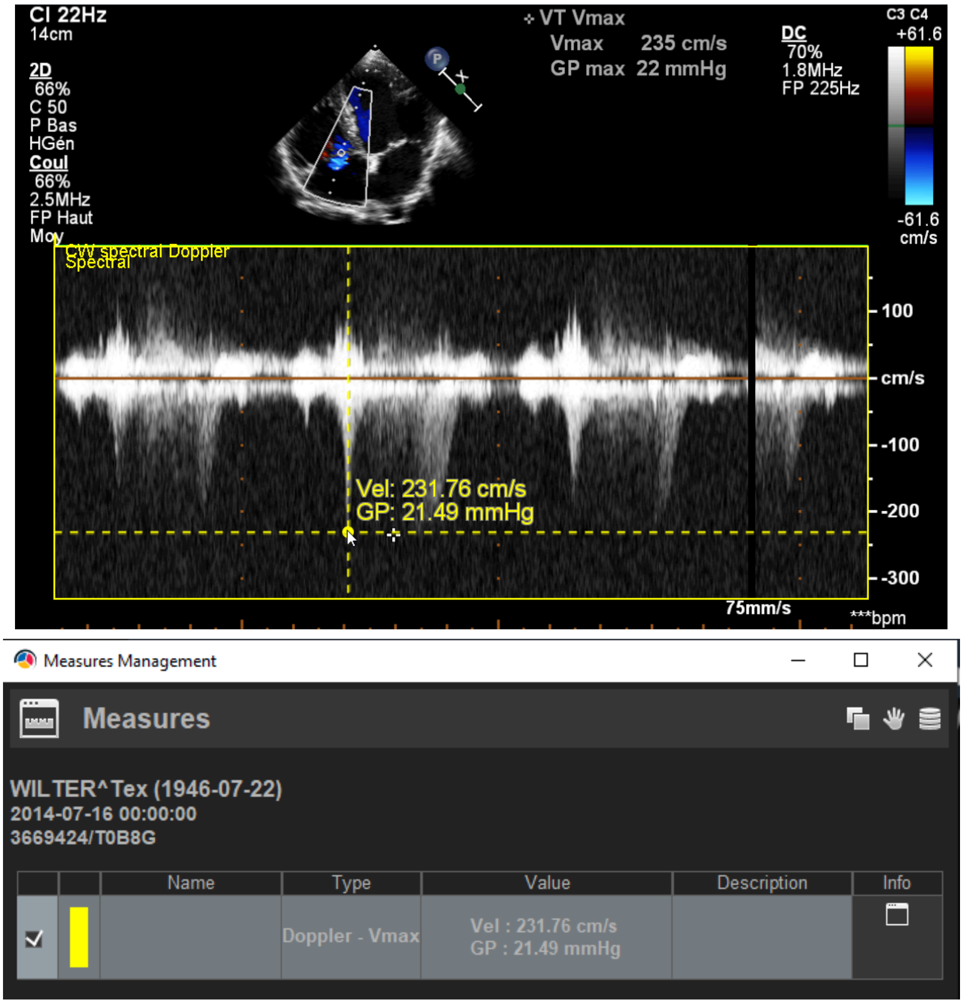
---

[14] Possible type values are: tissue, color flow, PW spectral Doppler, CW spectral Doppler and graphics.

Possible format values are: 2D, M Mode, spectral, wave and graphics.

The measured values are:

- The velocity: the vertical position in cm/sec.
- The Gradient of pressure, computed on base of the velocity using the simplified Bernoulli formula (4 V²), expressed in mmHg i.e. the pressure in mm of mercury.



WILTER^Tex (1946-07-22)
2014-07-16 00:00:00
3669424/T0B8G

		Name	Type	Value	Description	Info
☑	🟨		Doppler - Vmax	Vel : 231.76 cm/s GP : 21.49 mmHg		

Figure 149 - US Doppler - Velocity. a. draw measure. b. Measure value in the management window

2.5.5.2. M-Mode - Distance

This tool measures the distance between 2 points in an M-Mode region.

√ Select the menu [*Tools*] [*Ultrasound measures*] [*M-Mode – Distance*]

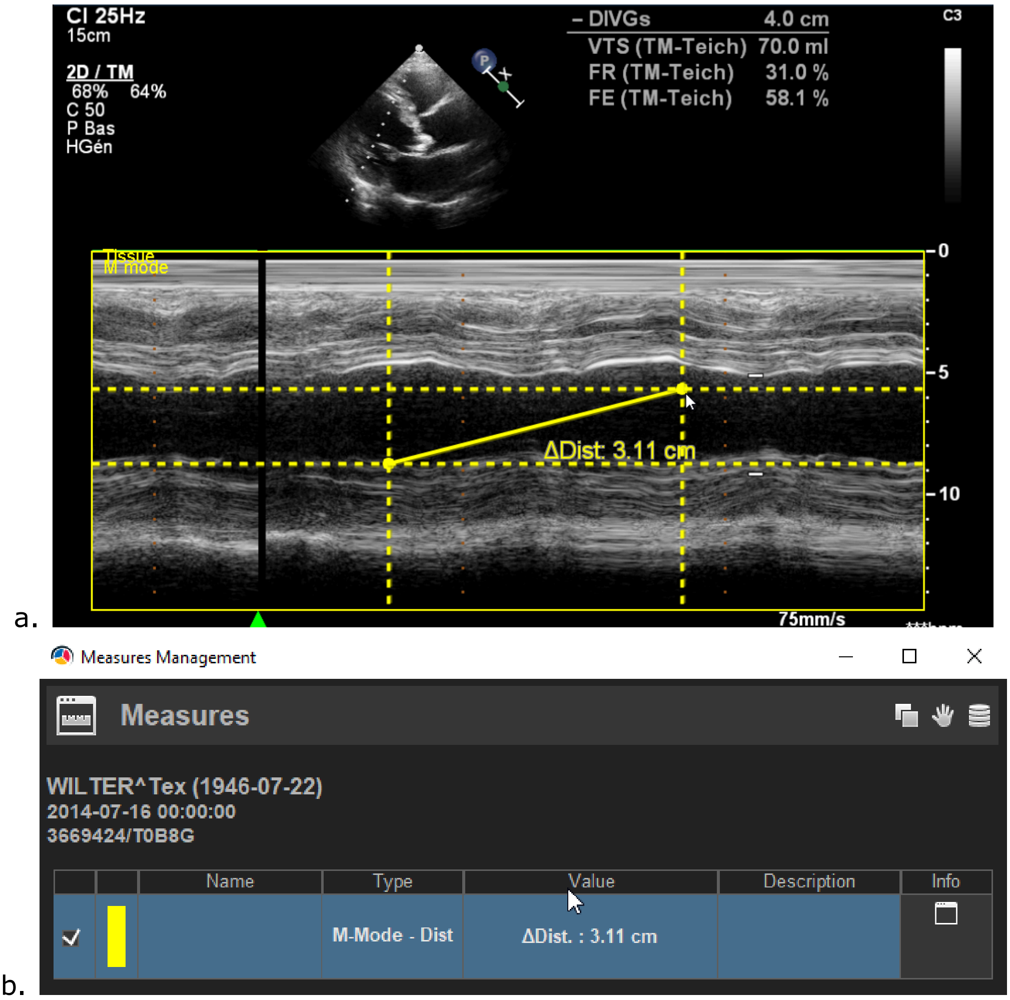
The region must be of type 'M-Mode' and format 'Tissue'.

The units provided in the metadata of the images are cm along the vertical axis and seconds along the horizontal axis.

Click on a point of the region to mark the first point to be measured and click a second time to mark the end point. The measure value will not appear directly in the image but in the measures management window (to open it, see section 2.5.6.1 page . For example, select the menu [*Tools*] [*Load measures management window*]).

The measured values are:

- The distance: the vertical distance expressed in cm.



WILTER^Tex (1946-07-22)
2014-07-16 00:00:00
3669424/T0B8G

		Name	Type	Value	Description	Info
☑	🟨		M-Mode - Dist	ΔDist. : 3.11 cm		

Figure 150 - US M-Mode distance. a. draw measure. b. Measure value in the management window

2.5.5.3. Doppler – Slope

This tool measures the slope between 2 points located in an M-Mode region.

√ Select the menu [*Tools*] [*Ultrasound measures*] [*Doppler – Slope*]

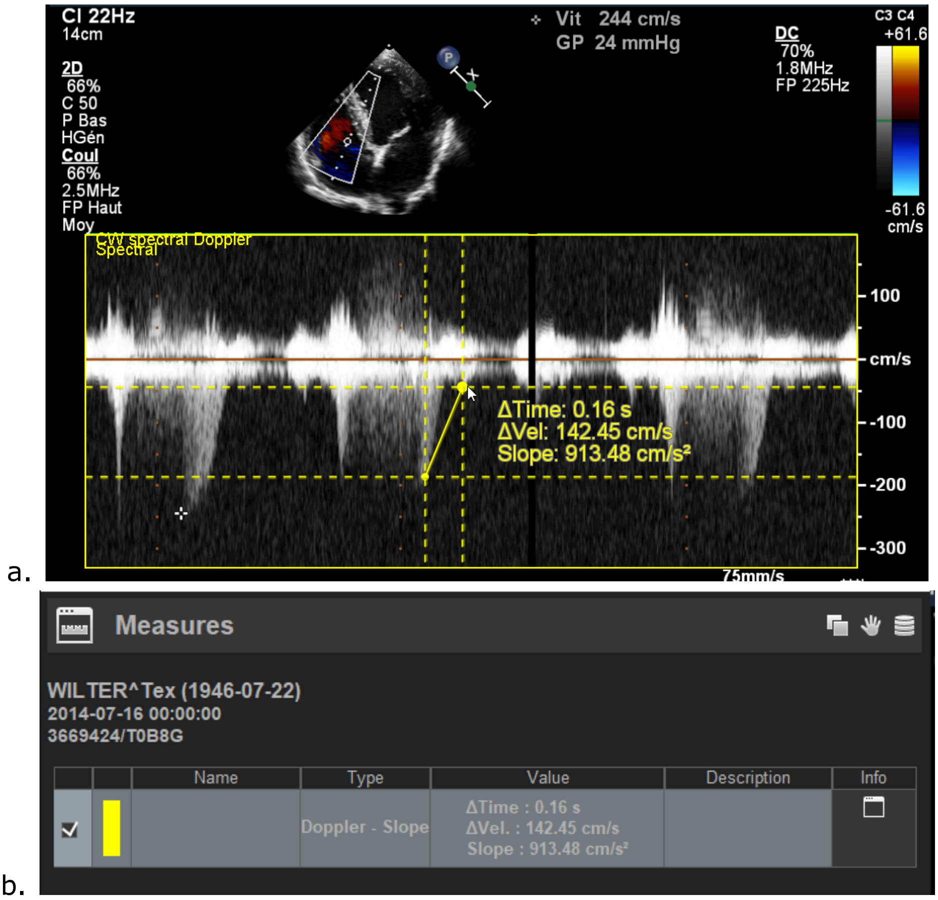
The region must be of type 'Doppler (PW or CW)' and format 'Spectral'.

The units provided in the metadata of the images are cm/sec along the vertical axis and seconds along the horizontal axis.

Click on a point of the region to mark the first point of the measure. Click on a second point to conclude it. The measure value will not appear directly in the image but in the measures management window (to open it, see section 2.5.6.1 page . For example, select the menu [*Tools*] [*Load measures management window*]).

The measured values are:

- The time: the horizontal time difference expressed in seconds.
- The delta velocity: the velocity difference expressed in cm/s.
- The slope: the distance / time ratio, in cm/sec².



WILTER^Tex (1946-07-22)
2014-07-16 00:00:00
3669424/T0B8G

		Name	Type	Value	Description	Info
☑	🟨		Doppler - Slope	ΔTime : 0.16 s ΔVel. : 142.45 cm/s Slope : 913.48 cm/s²		

Figure 151 - US Doppler - Slope. a. draw measure. b. Measure value in the management window

2.5.5.4. Doppler – Trace

This tool computes the maximum and average velocity during a heartbeat, the maximum and average gradient of pressure and the time/velocity integral.

√ Select the menu [*Tools*] [*Ultrasound measures*] [*Doppler – Trace*]

The region must be of type 'Doppler (PW or CW)' and format 'Spectral'.

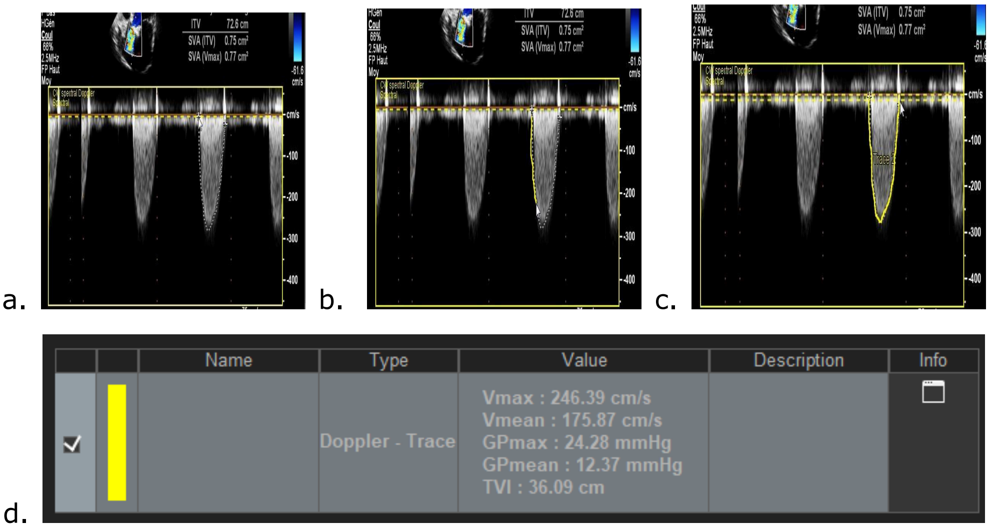
The units provided in the metadata of the images are cm/sec along the vertical axis and seconds along the horizontal axis.

Click a first time to locate the reference line from which the values will be evaluated (see Figure 152.a). Click on a point of the trace and, without releasing the button, follow the trace (see Figure 152.b). Release the mouse button when the whole trace has been drawn (see Figure 152.c).

The measure value will not appear directly in the image but in the measures management window (to open it, see section 2.5.6.1 page . For example, select the menu [*Tools*] [*Load measures management window*]).

The measured values are

- Vmax: the maximum velocity along the curve (cm / sec).
- Vmean: the mean velocity along the curve (cm / sec).
- GPmax: the gradient of pressure computed from the Vmax (mmHg).
- GPmean: the gradient of pressure computed from the Vmean (mmHg).
- ITV: time / velocity integral (cm)



		Name	Type	Value	Description	Info
☑	🟨		Doppler - Trace	Vmax : 246.39 cm/s Vmean : 175.87 cm/s GPmax : 24.28 mmHg GPmean : 12.37 mmHg TVI : 36.09 cm		

Figure 152 - US Doppler - Slope. a.,b.,c. draw measure. d. Measure value in the management window

2.5.6. Management of drawings/measures

Once graphical objects have been drawn, it is possible to move, resize/reshape or delete some objects, to delete all the objects or burn all the objects into the images. This section details these operations.

First of all, to manage an existing drawing or measure, no tool can be active. As a tool is active, only the labels of existing objects can be moved.
To deactivate the current tool, just click right button.

Let us explain the general mechanism of the objects. First of all, objects are interactive. Indeed, an object is highlighted when the mouse pointer is in its neighborhood (see Figure 153). It means that the object becomes "enabled", and can be manipulated.

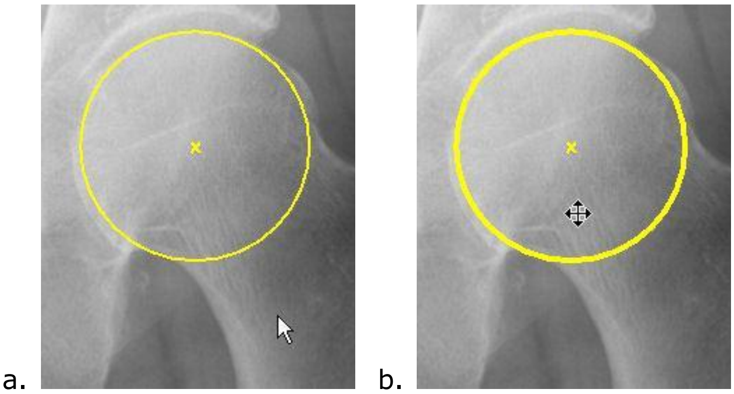


Figure 153 - Interactive objects: a. Disabled b. Enabled

Another property of the objects is the contextual menu associated at each object. It is displayed by right-clicking on an object (when it is enabled). This menu suggests actions related to the current object. For example, the menu associated to the circle proposes to measure its surface with option "Measure surface" as shown on Figure 154. This possibility is not present in the contextual menu of the line. On the other hand, the actions "Delete" or "Change color" are valid for all objects.

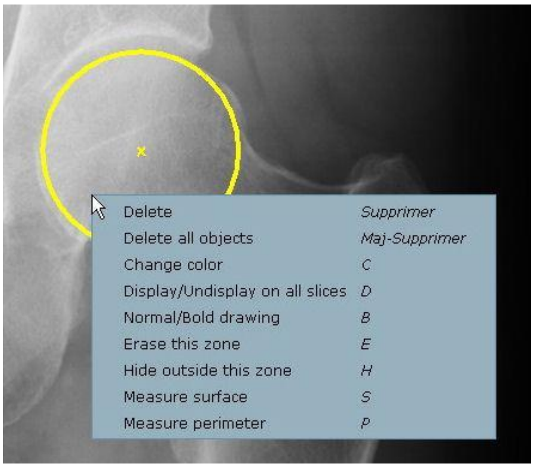
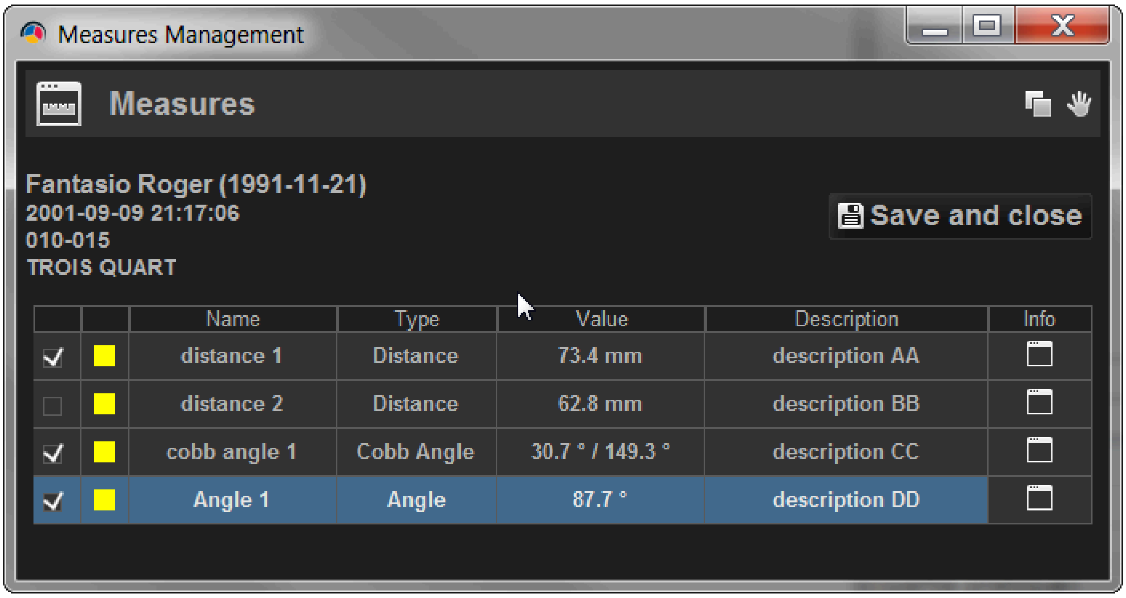


Figure 154 - Contextual menu of the circle

2.5.6.1. Measures management window: save, export and more

The main goal of this Measures management window is to save or export measures, and set a label and a description for each measure.



Fantasio Roger (1991-11-21)
2001-09-09 21:17:06
010-015
TROIS QUART

		Name	Type	Value	Description	Info
☑	🟨	distance 1	Distance	73.4 mm	description AA	
☐	🟨	distance 2	Distance	62.8 mm	description BB	
☑	🟨	cobb angle 1	Cobb Angle	30.7 ° / 149.3 °	description CC	
☑	🟨	Angle 1	Angle	87.7 °	description DD	

Figure 155 - Measures management window

Not all measures are manageable by this window. The only available measures are:

- Distance
- Angle and cob angle
- ROI (circle, rectangle and polygon ROI)

2.5.6.1.1. *Open the measures management window*

To open the measures management window, either:

√ In the browser lists, click on the 'Measures Management' icon in the 'info column' in the 'studies' or 'series' view.

√ In the toolbar of any viewer, click on the 'Load measures management window' icon.

Load m...

√ In the viewer, select the [*Tools*] [*Load measures management window*] menu

2.5.6.1.2. Basics

The measures displayed in the measure management window concern all the measures done on a study.

You can modify the name and the description of each measure.

You can remove one or several measure(s).

You can save all the displayed measures on the server.

The displayed measures can be exported locally.

The measures management can open the viewer containing the associated image, with the measure drawn on it.

Measures underlined are unsaved measures.

Check or uncheck the first column to show or hide each measure.

2.5.6.1.3. Edit the name and description of a measure

Double click on the name or description of a measure to modify the content.

Press the enter key or click anywhere else to exit the edition mode.

If the Measure Follow-up logo is present in the 'Info' column, this measure is a member of a measure follow-up and it will be impossible to delete it.

2.5.6.1.4. Show the measure in the image

To open a viewer showing the image associated with the measure and the measure drawn on it,

√ Double-click on the type or on the value of the measure.

If the MPR logo is present in the column 'Info', the measure must be shown in a MPR viewer.

2.5.6.1.5. Export or Save the measures

According to your configuration, the measures drawn are always or never automatically saved to the server, or the TMRHE will prompt the user to save measures when the measure management window is opened.

To save manually to the server all the measures shown in the measures management window and close this window,

√ Press the 'Save and close' button

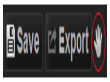
Save and close

All measures saved to the server will be automatically shown on any appropriate viewer opened by any user.

To export all the measures shown in the measures management window to a local file, either in the AIM v3 format or in text format:

√ Press the 'Export' button

√ Click on the hand button to drag & drop the measure on a text-enabled program (Wordpad, Word, etc.)



√ Click on the 'Copy to the clipboard' button located at the top right of the window to copy all the measures into the clipboard.

2.5.6.1.6. Show or hide the measures in the viewer

To show or hide all the measures in the current viewer,

√ Press the 'Show/Hide measures ' button, or

√ In the viewer, select the [*Display*] [*Show/Hide measures*] menu

√ Use the keyboard shortcut associated to this action (by default 'Ctrl' 'L')

2.5.6.2. Delete object

To delete graphical object,

choose [*Delete*] in the contextual menu of the object. To delete all the graphical objects of the tools application domain,

√ choose [*Delete all objects*] in the contextual menu of one of the objects

2.5.6.3. Move objects

To move an object,

place the mouse near the object to be moved in order to highlight this object. Click with the left mouse button, keep the button pressed and move the mouse: the object follows the mouse motion. Release the button to set the new object position.

2.5.6.4. Reshape objects

To change the shape of objects by moving individual constitutive points of the objects,

click on an extremity of an object, keep the button pressed and move the mouse: this point follows the mouse motion. Release the button to set the new point position.

Updating a point constituting a measure automatically updates the measure.

- **Line**: click on one of the extremities of the line. Drag the mouse to move the point and release the button when the good location is reached. This extremity of the line is moved.
- **Rectangle**: click on one of the corners of the rectangle. Drag the mouse to move the point and release the button when the good location is reached. This corner is moved and the rectangle is reshaped.
- **Circle**: click on the circle rim. Drag the mouse to move the point and release the button when the good location is reached. The radius of the circle is adapted and the circle is reshaped.
- **Ellipse**: click on one of the axis points of the ellipse. Drag the mouse to move the point and release the button when the good location is reached. This axis point is moved and the ellipse is reshaped.

- **Right angle**: click on one of the two extremities of the right angle. Drag the mouse to move the point and release the button when the good location is reached. This extremity is moved and the right angle is reshaped.
- **Label**: click on one of the extremities of the line. Drag the mouse to move the point and release the button when the good location is reached. This extremity of the line is moved, whether it was the extremity carrying the arrow or the extremity carrying the text.
- **Distance**: click on one of the extremities of the line, or on the arrow pointing from the text to the line (on the text side). Drag the mouse to move the point and release the button when the good location is reached. This extremity of the line is moved and the measure is updated, or the place where the measure is drawn is changed.
- **Angle**: click on one of the three points constituting the angle. Drag the mouse to move the point and release the button when the good location is reached. The angle is reshaped and the measure updated.
- **Angle between two lines, Ratio between distances**: Only the point where the text is displayed is movable. To change the measure, reshapes the lines.
- **Height**: click on one of the two points constituting the measure. Drag the mouse to move the point and release the button when the good location is reached. The horizontal and the vertical lines concerned by this measure are moved and the measure is updated.
- **Hounsfield density**: click on one of the extremities of the arrow. Drag the mouse to move the point and release the button when the good location is reached. This extremity of the line is moved.
- **Circle ROI**: The Region of Interest is characterized by two "points": the centre of the circle and any point of the contour. Click on one of those points. Drag the mouse to move the point and release the button when the good location is reached. The circle is reshaped and the measure is updated.
- **Rectangle ROI**: click on one of the corners of the rectangle. Drag the mouse to move the point and release the button when the good location is reached. The rectangle is reshaped and the measure is updated.
- **Polygonal ROI**: click on one of the points of the polygon. Drag the mouse to move the point and release the button when the good location is reached. The polygon is reshaped and the measure is updated.
- **Polygon hand free drawings** points' motion allows changing the shape of the contour.
- **Continuous hand free drawings** are in fact made up with points drawn at regular time interval during the building of the contour. They can be updated the same way as polygons.

2.5.6.5. Modify contours

There is another possibility to alter the shape of a contour than updating point after point. The 'Modify polygon' tool replaces a part of the contour by a new drawing.

√ choose [*Modify polygon*] in the contextual menu of the polygon to be modified (see Figure 156.b). In order to modify the contour drawn on Figure 156.a to remove the left part of the contour and obtain the new contour drawn on Figure 156.d,

√ Draw the new part of the contour, starting from point 1. to point 2. of Figure 156.c. Click on point 1., release the button, click on all the intermediate points (2.) and double-click on point 3. to conclude the new part of the contour.

√ Specify the part of the original contour that must disappear to be replaced by this new part: click on any point of the part of the contour to be deleted (e.g. in Figure 156.c, click on point 4.).

The new contour is now made up with the new part in place of the old one.

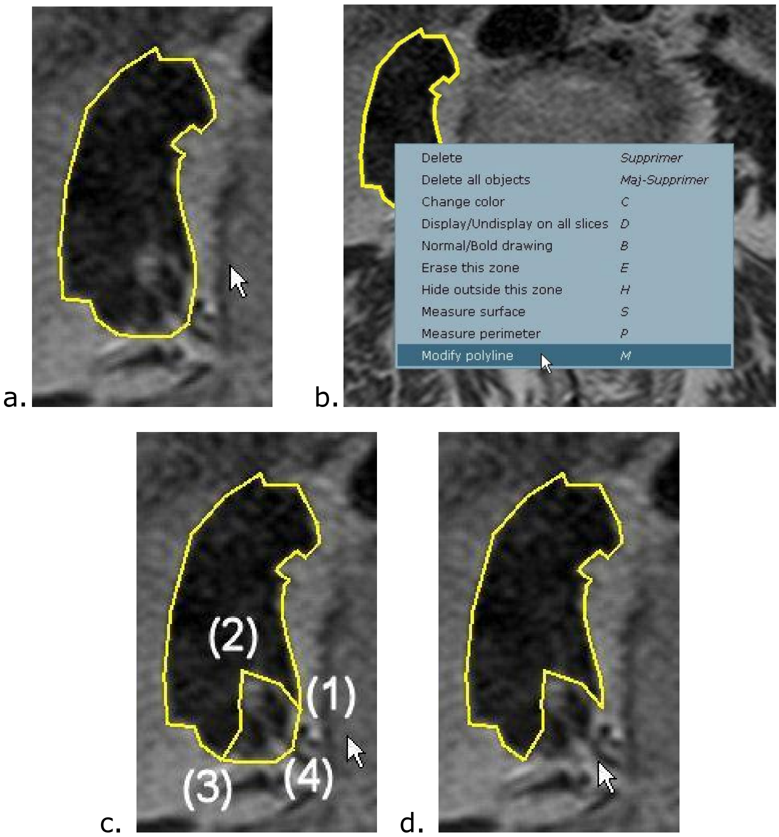


Figure 156 - Modify contours

This tool is handled with the left button of the mouse and will remain associated with it until the right mouse button is clicked or the 'ESC' key is pressed.

The information line at the bottom of the viewer displays a short explanation on how to use this tool.

2.5.6.6. Burn objects into study

This option is only available in the *TM-Reception HE* version.

The graphical objects are not sent with the DICOM image exportation or saved in the local database. To keep the objects in these situations, burn them into the images.

√ Select [*Tools*] [*Burn objects in the study*] to burn the objects into the images.

The graphical objects are then permanently associated with the images and can not be removed anymore.

This feature is useful to associate measures to images exported or sent in the DICOM format (see sections 3.2 and 3.3 page) or to a local copy of a study saved in the local database (see section 2.8 page).

2.5.6.7. Change objects color

To change the color of an object or of all the selected objects,

Select [*Change color*] in the contextual menu of the concerned object.The color chooser shown in Figure 157 is displayed. The preview area shows the effect of the new color on text and surfaces (in this example, the new color is the blue) and compares it to the old color (in this example, the green).

To select a new color, simply click on one of the collared square, or use the one of the two other available color models: HSB and RGB.

When the new color is chosen, press 'OK'.

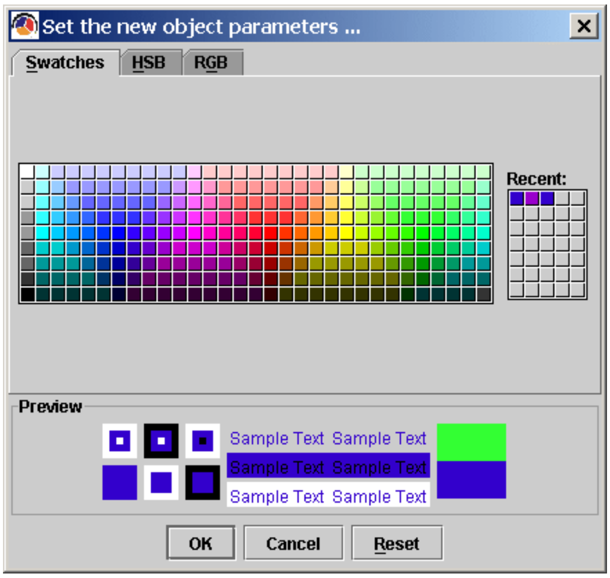


Figure 157 - Change objects color

2.5.6.8. Display an object on all the slices of the Viewer

In some situation, a reference line drawn on a specific image should be reported on the other images to visualize the evolution of a region in regard to this reference line.

To display an object on **all the slices** of the viewer,

select [*Display/undisplay on all slices*] in the contextual menu of the object.

To display an object **only on the original slice**, simply select [*Display/undisplay on all slices*] in the contextual menu of the object. The copies will be removed from the other images. This will only work if you click on the original object, drawn in the original image.

2.5.6.9. Bold drawing

Sometimes, it is useful to draw an object in bold, in order to make it more attractive.

To make an object in bold,

- √ select [*Normal/Bold drawing*] in the contextual menu of the object.
- √ To display the object with a normal width, select the same action once again.

2.5.6.10. Erase a zone

Some parts of the image sometimes should be erased, for example in order to make it anonymous or to correct a wrong annotation.

This tool is in fact one of the closed shape (rectangle, circle, ellipse, polygon, continuous polygon...), which its inside is filled in black.

To erase a zone of the image, begin to draw the zone to be erased and

- √ select [*Erase this zone*] in the contextual menu of the zone.
- √ To display original object, select the same action once again.

2.5.6.11. Hide outside a zone

In some situation, it is useful to display only a part of the image. This is possible for all closed shapes (rectangle, circle, ellipse, polygon, continuous polygon...).

To hide outside a zone, draw the zone and

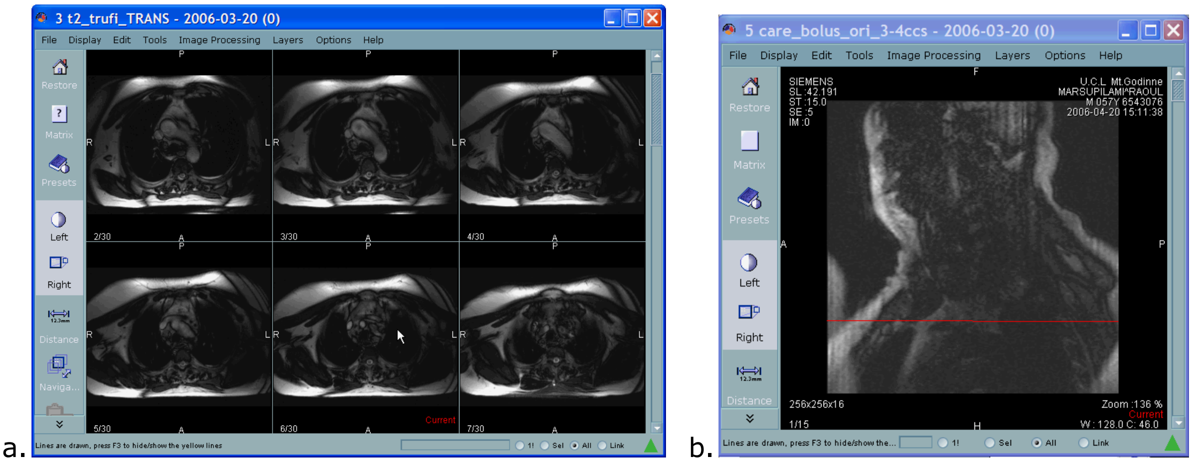
- √ select [*Hide outside this zone*] in the contextual menu of the zone.
- √ The part of the image outside this zone is filled in black. To display the original image with the zone drawn, select the same action once again.

2.5.7. Draw reference lines

In many situations, two series are related to each other: the first in taken in a perpendicular direction can be used to visualize the position of the images of the second series. One example is a scout and the CT-scanner series.

To help positioning the images of a first series via a scout or another image, open both series into two separate viewers and

- √ Select [*Display*] [*Draw references lines on scout*] in the viewer showing the scout, or
- √ select the "Draw reference lines on scout" tool if available in the toolbars (main toolbar or CT toolbar) of the viewer showing the scout.



Lines are drawn, press F3 to hide/show the yellow lines

Lines are drawn, press F3 to hide/show the...

Figure 158 - Draw reference lines on scout: a. complete series, b. scout

Figure 158.a shows the first series. Figure 158.b shows another series used as a scout for the first series.

One yellow line is drawn on the scout for each image found in another viewer and having an intersection with the scout. The image of the other viewer that is 'Current' is shown on the scout as the red line. The information is updated in real time as the 'Current' image changes.

To remove the yellow lines and only keep the red line marking the position of the current image, in the scout viewer either

- √ press the 'F3' key, or
- √ uncheck [*Display*] [*Text on screen*].

Attention: this tool references an image in all the other viewers of the same study having an intersection with this image. If the study is composed by 2 sets of independent series, the tool may not decide if the series match or not. It could draw a reference line on an inappropriate image (ex: MR lungs study with one sub-set concerning the inspiration and the other the expiration).

2.5.8. Reference this image in all perpendicular views

There is another way to reference images. Instead of using one series as the 'scoot' for all the others, ask all the series to reference, if possible, the current image of the current series.

√ Check the [*Display*] [*Reference this image in all views*] menu in the series (viewer) that must be referenced everywhere.

Every other viewer will, if possible, draw a red line at its intersection with the current image of the current viewer, as shown in Figure 159: the second viewer is referenced in the first and fourth viewers, showing a perpendicular image. The third viewer, showing images taken in the same orientation as the second one, doesn't draw any red line.

The hanging protocols (see section 1.5.7 page) can force this referencing to be automatic.

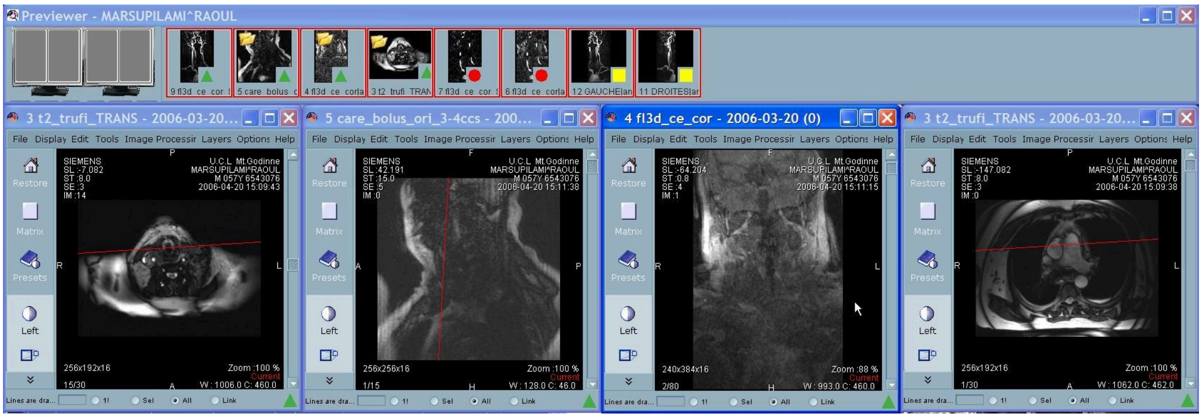


Figure 159 - Reference this image in all views

2.6. Image Processing

2.6.1. Rotation

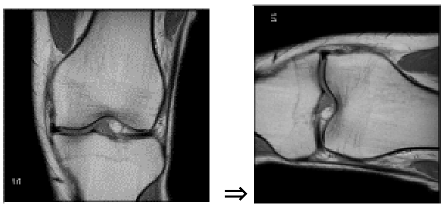
This tool rotates the images belonging to the tools application domain (see section 2.3.1 page).

To rotate the images clockwise,

√ select [*Image Processing*] [*Clockwise rotation*], or

√ press the 'Alt' and 'R' keys.

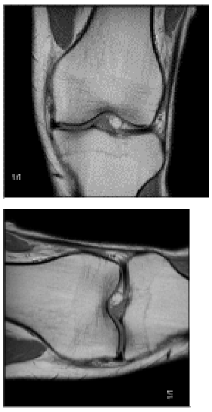
√



To rotate the images anti-clockwise,

√ select [*Image Processing*] [*Anti-clockwise rotation*], or

√ press the 'Alt', 'Shift' and 'R' keys together.



⇒

2.6.2. Flip

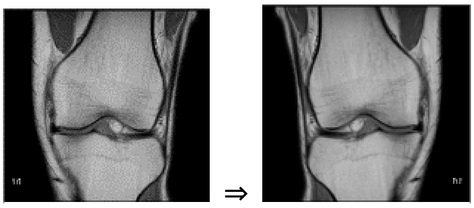
This tool flips the images belonging to the tools application domain (see section 2.3.1 page).

To flip the images horizontally,

√ select [*Image Processing*] [*Horizontal Flip*], or

√ press the 'Alt' and 'H' keys.

√

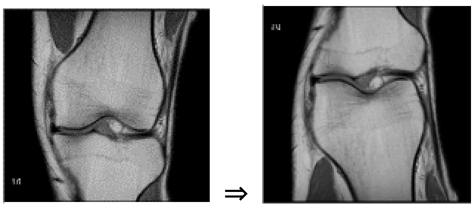


To rotate the images clockwise,

√ select [*Image Processing*] [*Vertical Flip*], or

√ press the 'Alt' and 'V' keys.

√



2.6.3. Invert image stack

This tool inverts the image stack, i.e. reverses the order in which the images are displayed in the viewer: the first image becomes the last etc. (goes from Figure 160.a to Figure 160.b).

To invert the images stack,

√ Select [*Image Processing*] [*Invert image stack*]

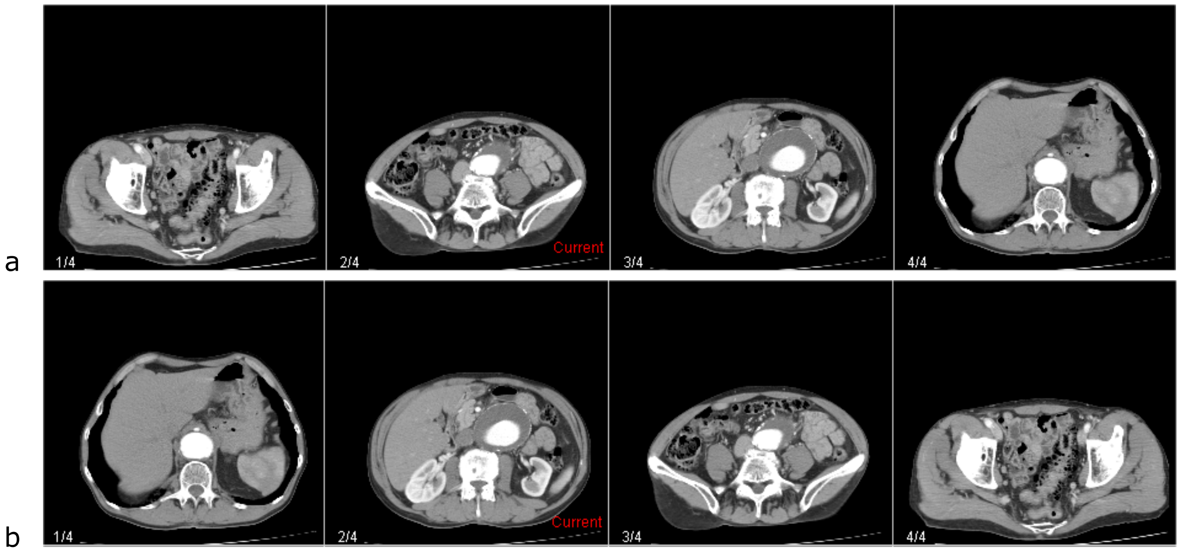
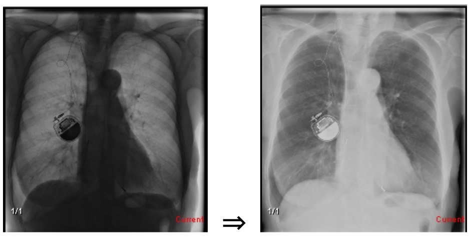


Figure 160 - Invert image stack: a. Original, b. inverted

2.6.4. Grey scale inversion

This tool inverts all the grayscale levels of the image. Every light area becomes dark, every dark area becomes light.

To invert the grey levels of the images belonging to the tools application domain (see section 2.3.1 page) of the study,



√ choose [*Image Processing*] [*Invert grey scale*], or

√ press the 'i' key.

2.6.5. Conversion to grey scale

To convert a colored image into a grayscale version,

√ select [*Image Processing*] [*Convert to grey scale*].

This function applies on the tools application domain of the viewer (see section 2.3.1 page for the description of the tools application domain).

2.6.6. Slice thickness/spacing modification

To reconstruct a series with another slice thickness or spacing,

√ select *[Image Processing] [Make a MIP on the study]*.

Enter the thickness of each slice (in mm), the gap between each slice (in mm), i.e. the space between the centre of two consecutive slices, and the reconstruction method: MPR (average value) or MIP (maximum value).

A new series will be built and shown in another viewer.

2.6.7. Image filtering

To apply a particular filtering on the images,

√ Select [*Image Processing*] [*Filtering*].

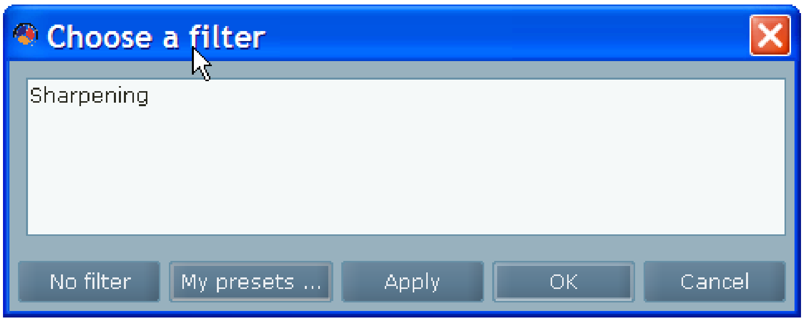


Figure 161 - Choose a filter

Select one of the filters shown in the list and press [Apply] to apply it directly to the images.

Select [No Filter] to show the original image.

Select [OK] to apply the selected filter and close this dialog box.

Sharpening filters enhance the contours in the images, as show in Figure 162.

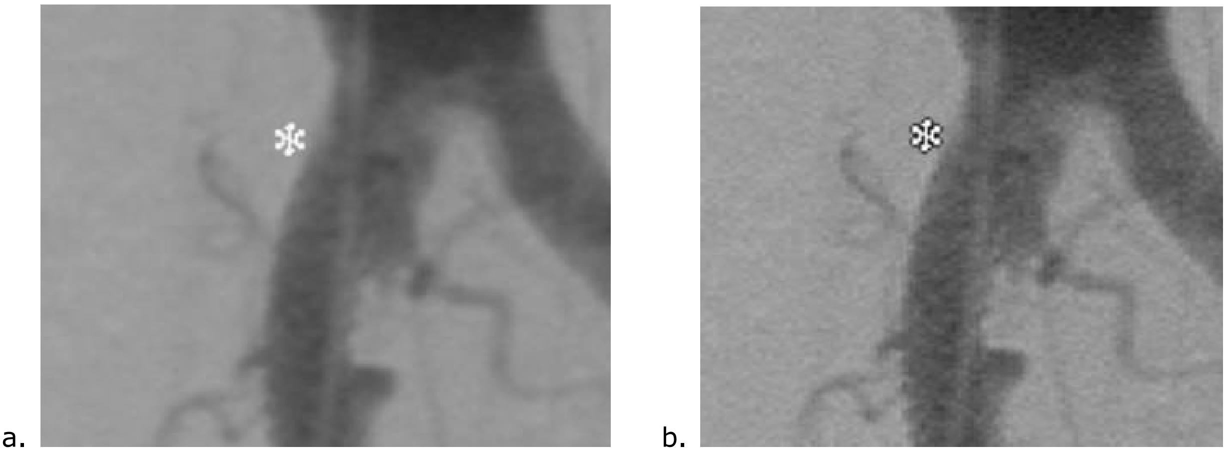


Figure 162 - a. original image b. sharpened image

Every filtered image is marked in the viewer by an 'attention' symbol to clearly specify that the image is post-processed.

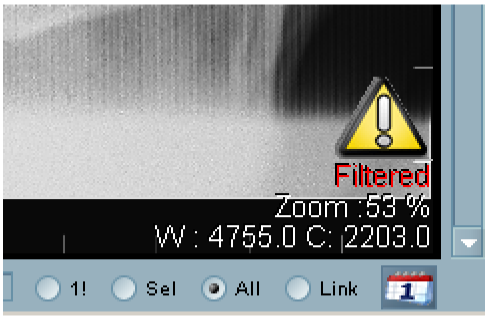


Figure 163 - "Image filtered" notification

2.6.8. Stitching tool.

This tool is only available in the TM-Reception HE.

The aim of the stitching tool is to stitch RX images together, for instance for measures on full spine images. The resulting image will be integrated as an additional series in the PACS.

The original images must displayed in a single viewer of the TM-Reception HE. (If necessary, join the images to display them all in one viewer, as explained in section 1.5.2 page).

Adjust the contrast of the individual images. Select the images you want to stitch. If no image is selected, all images will be taken into account.

√ To send those images to the "stitching" tool, select [*Image Processing*] [*Stitching tool*].

The window shown in Figure 164 opens.

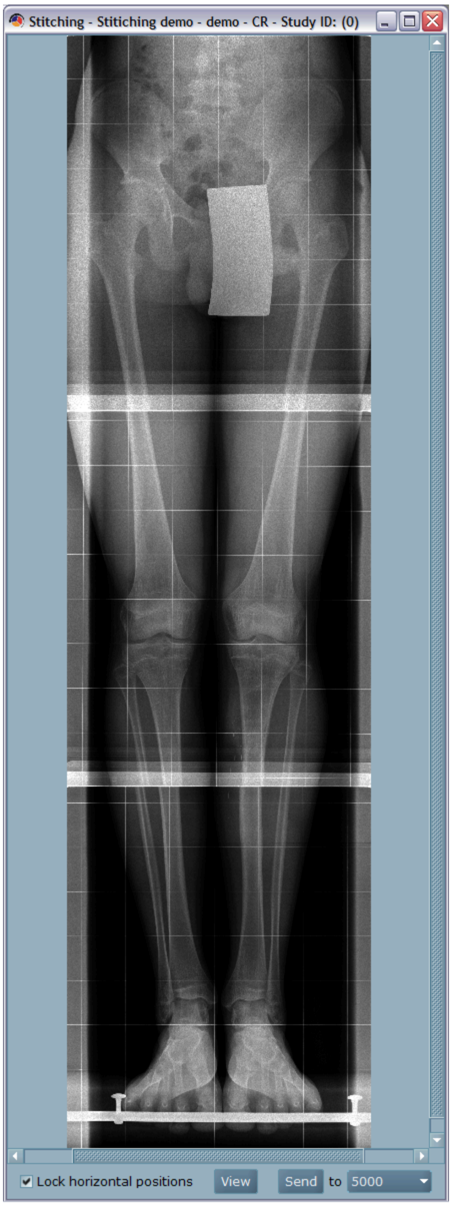


Figure 164 - Stitching tool

2.6.8.1. Adjust image positions

To adjust image positions on the vertical axis, just click the images and drag them upwards or downwards.

To adjust image positions on the horizontal axis, first unlock the horizontal positions, using the checkbox underneath the images. Then click the images and drag them as wanted.

2.6.8.2. Zoom in / out

To zoom in or out, please use the mouse wheel. You can then adjust the view by using the right and bottom scrollbars.

2.6.8.3. Result

To take a look at the resulting image, click the "View" button underneath the images. A new viewer opens with the resulting image.

√ To send the resulting image to the PACS, select a destination and use the "Send" button.

2.7. Interactivity between users

This functionality allows sharing the same viewer with another user (radiologist, clinician) in the same hospital or in another site. No more need to physically move to your collegue's office. All you need is to call your collegue on the telephone and watch your screen!

2.7.1. Notify the server that you are available.

Only users having explicitely set themselves as 'available' will be callable other persons to share viewers and give advices about a study.

You can set your 'availability' status in the TMRHE browser, using the menu *[Network] [Set available for interactivity]* as shown in Figure 165.

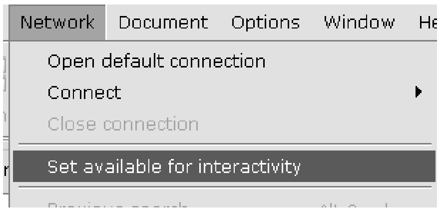


Figure 165 –Set you as available for interactivity

When you specify that you are available, you may enter a small text that the other users will see next to your name in the 'available users list'. Typically, users will type a phone number in this text field (see Figure 166).

Fill in contact informations (Phone number, Mobile,...)

Dr House 066666

Figure 166 – Fill contact information to be easily reachable

2.7.2. Start an interactive session

When using a TMRHE viewer, you can share it with another Telemis user (who has set himself as available for interactivity sessions), i.e. send a copy of the viewer to the other user's screen.

√ Select *[Window]* *[share this viewer]* (see Figure 167.a)

Share this viewer with :

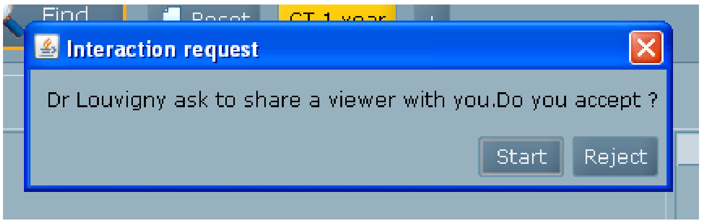
☑ demo (02/485.12.13)

☐ Dr Louvigny (1245)

Figure 167 – Share your viewer with one of the available doctors

The TMRHE presents a list of the users set as available for interactivity, together with the small text (typically their phone number), as shown in Figure 167.b. Select the user that you want to contact. He will

After you select the user, this one receives a message to accept or refuse the session (see Figure 168). If he accepts to start an interactive session, the on-line refreshed content of your viewer is showed on his screen.



Dr Louvigny ask to share a viewer with you.Do you accept ?

Figure 168 – A doctor can ask you to share a viewer with him

All actions that you perform on the viewer are automatically shown on your partner's copy (contrast, measures, zoom …). Your mouse position is also visible on the other viewer, letting you "point" on a specific location. If your partner moves his mouse on his copy of the viewer, you will see the location of his mouse on your viewer, to let him also "point" on a location.

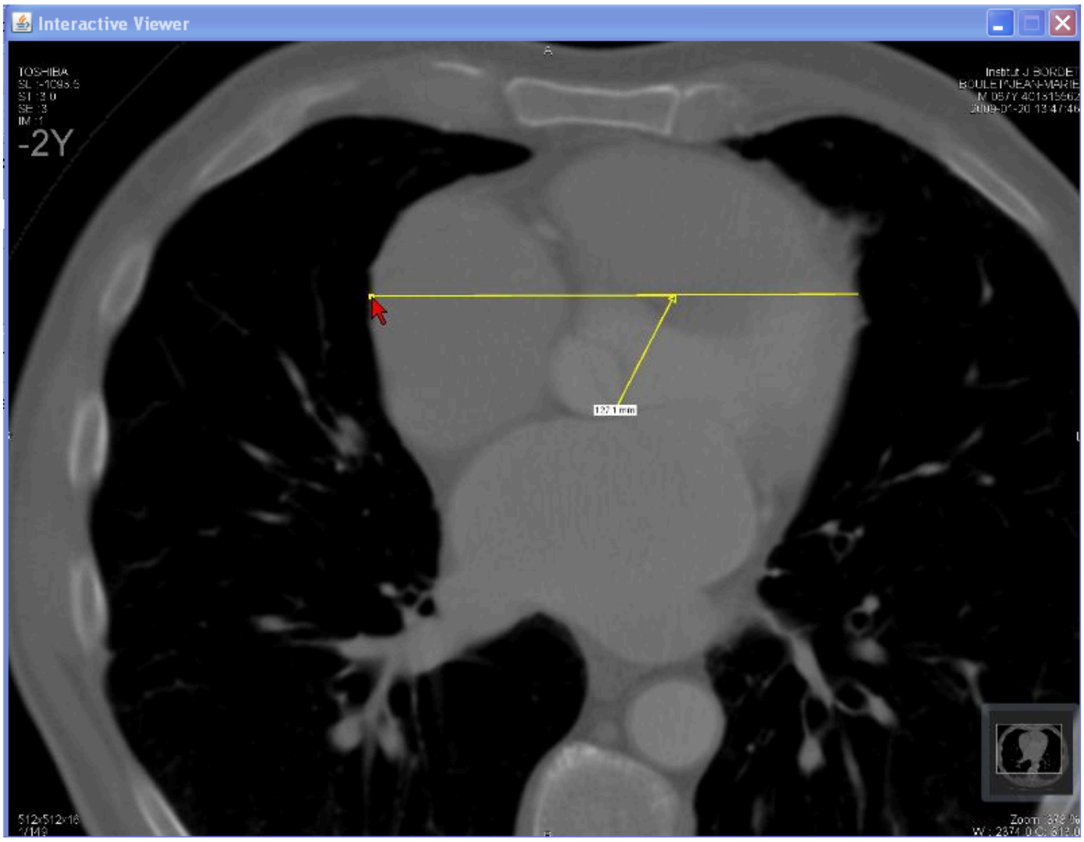


Figure 169 – The other doctor's mouse pointer is visible remotely

Closing the viewer or his copy stops the interactive session.

You can share simultaneously several viewers with your partner, and reciproquely if you are also "available for interactivity".

Uncheck the 'set available for interactivity' option in the browser to automatically stop all interactive sessions and prevent any other user to try to contact you.

2.8. Study management

2.8.1. Save on local PC

These commands give you the ability to store one or several series or studies, using the Telemis Image format, on one of your disks (or removable disks: CD, floppy, Zip ...). A document that is locally saved becomes available even if the *TM-Reception* is not connected to the server.

To save the document displayed in this viewer in the **default 'local database'** directory (see section 1.8.3 page to change this (these) directory(ies)) :

√ Click on [*File*] [*Save on local PC*] or

√ press the 'Ctrl' and 'S' keys.

A dialog box asks if you want to save the images with or without your modifications. To save the images with the contrast, brightness, zoom … used for the original display, click on 'No'. To save the images with the current contrast, brightness, zoom …, click on 'Yes'. To cancel the save operation, click on 'Cancel'.

The drawing and measurements are not saved with the images, except if they are burned into, as explained in section 2.5.6.6 page .

The information line at the bottom of the viewer shows the evolution of the saving: "Saving document" and then "Document correctly saved".

To **choose the directory** where the viewer will store this document,

√ click on [*File*] [*Save as*].

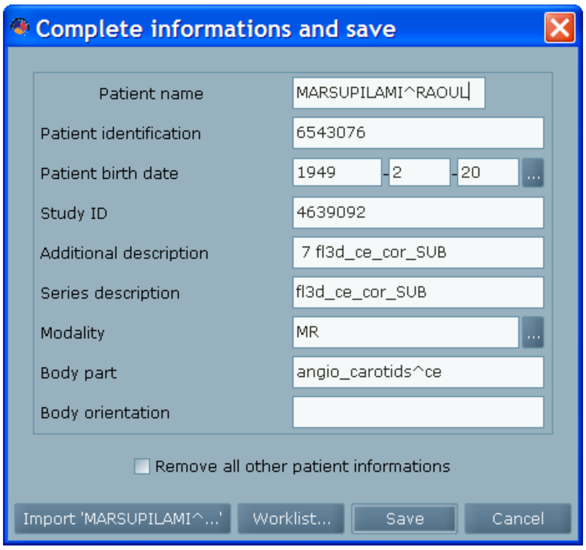
A file dialog box lets you enter the directory where the document must be saved. This directory will contain the header of the document (a small file ending with ".header"). The images are stored in a bigger file ending with ".tme" and located in the "em" sub-directory of the selected directory. This "em" directory is created automatically if it doesn't exist yet.

The remaining of the operations are similar to the "Save on local PC" command.

If the content of the viewer doesn't have enough information about the study, the window depicted in Figure 170 appears to prompt for more information. This will mainly happen if the viewer displays the result of a join between several studies (see 1.5.2 page).

This window allows the user to enter the patient name, patient hospital internal identification, patient birth date, study identification, modality, the body part concerned by the viewer, the body orientation (this field may also contain sub-body part information), and finally an additional description that can contain any text that wouldn't fit in another field.

Click on 'Save' to save the document or on 'Cancel' to cancel the operation.



Patient name	MARSUPILAMI^RAOUL
Patient identification	6543076
Patient birth date	1949 -2 -20
Study ID	4639092
Additional description	7 fl3d_ce_cor_SUB
Series description	fl3d_ce_cor_SUB
Modality	MR
Body part	angio_carotids^ce
Body orientation	

☐ Remove all other patient informations

Figure 170 - Completion of information before save

To create a **summary of the study**, containing only the most relevant images,

√ Select the most relevant images

√ Chose [*Edit*] [*Delete unselected images*]. All the unselected images are removed from the viewer.

√ Save this new document in the database.

This newly created document is a modified COPY of the original document. The original document is NEVER modified.

√ If this viewer contains a joined document with several patients or studies, or needs additional information to **provide a complete description** on this future document, edit the document information as explained in section 2.8.7 before saving.

2.8.2. Export to other image formats

The selected images can be exported as BMP and JPEG image files.

On the *TM-Reception HE* version, the AVI video exportation and the specific DICOM medical images file format are also available.

See section 2.3.2 page for the selection of slices in a Telemis viewer.

To launch the exportation dialog box:

√ select [*File*] [*Export as*], or

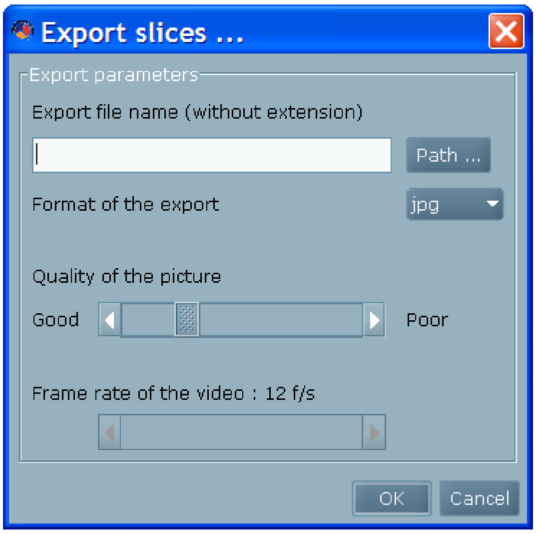
√ press the 'E' key.

The exportation functionality only exports **selected images**. If no image is selected, a first dialog box asks if the exportation must apply to all the images of the viewer. Click on 'OK' to export all the images or 'Cancel' to cancel the exportation.

A second dialog box asks if the **overlays** must be exported with the images. Overlays are all the drawings and measurements but also the text displayed on the four corners of the images (patient name, zoom level, size of the image …). Click on 'Yes' to export the image with the overlays, on 'No' for the image without the overlays. Only the displayed overlays are exported: if you wish to export the measures but not the text of the corners, hide this text (via 'F3' or [*Display*] [*Text on screen*] as explained in section 2.4.2 page).

The file dialog box of Figure 171 lets you choose the **path and file name** of the saved images. Click on the 'Path' button to select the directory where the images must be written. The program will append to the name that you type in the *Export file name* text box the index of the image and the extension '.bmp', '.jpg' ... depending on the chosen **format**. Click on the drop box containing 'bmp' to choose between the available image formats.

For example, if you have chosen the BMP file format, typed "image" in the *export file name* text box and selected 3 images in the viewer, the file names will be "image000.bmp", "image001.bmp" and "image002.bmp".



Export file name (without extension)

Format of the export: jpg

Quality of the picture

Frame rate of the video : 12 f/s

Figure 171 - image exportation

The format Jpg (JPEG) is different from the other formats on the quality point of view. The other formats always give an image that is exactly the same as the original one. Jpeg introduces some losses in the quality of the images but achieves much better compression ratios (i.e. the generated file is much smaller). The slider at the bottom of the dialog box enables you to choose the **quality of the JPEG** exportation: from good (large files) to poor quality (very small files).

For video exports, set the frame rate of the video, in number of frames displayed per second. This means that if the series contains 100 frames, 25 frames per second will create a 4 seconds video sequence.

2.8.3. Export to other applications

You can directly export some images to any other "image-enabled" or “file-enabled” application, such as any drawing program, PowerPoint, Word, any email program (Outlook etc.), any file system (USB memory stick etc.), …

Move the mouse to the top left corner of any image. A small hand appears (see Figure 172). Press the mouse button and drag this hand into any other opened application to automatically paste the image into this application.

Figure 172 - Drag an image to an external application

You may also copy the last clicked ("current") image to the clip board, to later paste it in another graphical application (drawing program, power point, word etc.)

√ Choose [File] [Copy image to clipboard], or

√ Press the "Ctrl" and "C" keys

2.8.4. Print

These commands allow you to print the content of the viewer or the whole series to any printer connected to your computer. This option will work with any printer recognized by Windows, Macintosh OS, Linux …but not to a specific DICOM printer.

2.8.4.1. Print the viewer

The print function sends to the printer the content currently displayed in the viewer, including the drawings, measurements, contrasts, zooms, number of images displayed …

Format the images and the viewer exactly as it must be printed:

- Select the images to display (see section 2.3.2 page) and possibly display only the selected images (see section 2.4.5 page).
- Chose a display matrix (see section 2.4.1 page).
- Chose a zoom, contrast, brightness … for each image (see section 2.3 page).
- Display or not the text on screen (see section 2.4.2 page).
- Perform drawings and measurements (2.4.8 page).

√ Select [*File*] [*Print on paper*] or press the 'Ctrl' and 'P' keys to send the images displayed to the printer.

To preview the result before it is sent to the printer:

√ select [*File*] [*Print on paper: preview*].

2.8.4.2. Print the whole series

This command sends to the printer all the images of the viewer, currently displayed or not, including drawings, measurements, contrasts, zooms, number of images displayed per page …

The program prints as many pages as necessary to print all the images of the viewer, with the same number of images per page as the number of images displayed in the viewer. If the viewer displays 3 lines of 2 images for a study containing 100 images then 17 pages will be printed, each page containing 3 lines of 2 images.

To print the full viewer,

√ select [*File*] [*Print all on paper*].

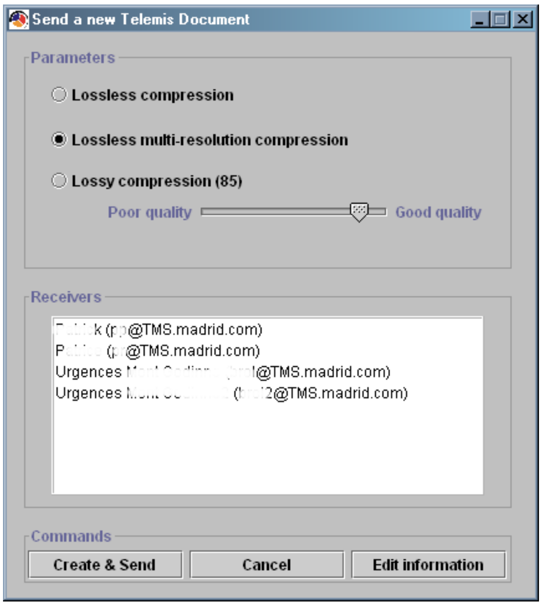
2.8.5. Send the document to the server

This command gives you the ability to create a new document from the current one and to make it available on the server for other users. An example is to allow the radiologist to create a "summary" document with the 40 relevant images of a 300 images CT scanner study, lay them out correctly and generate a document available on the server for the clinicians.

Open a document in a viewer. Change contrast, brightness, zoom …

√ Select the most relevant images

- √ Choose [*Edit*] [*Delete unselected images*]. All the unselected images are removed from the viewer.
- √ Select [*File*] [*Send the document*].
- √ Select the parameters in the dialog box that opens (see Figure 173)



○ Lossless compression
● Lossless multi-resolution compression
○ Lossy compression (85)

[redacted]k ([redacted]@TMS.madrid.com)
P[redacted] ([redacted]@TMS.madrid.com)
Urgences [redacted]l@TMS.madrid.com)
Urgences [redacted] ([redacted]2@TMS.madrid.com)

Figure 173 - Send a new document - creation parameters

Select the compression method:

- Lossless compression gives a perfect image but takes more place on the server and more time to transfer.
- Lossless multi-resolution gives also a perfect image, takes more or less the same place on the server as the lossless compression but transfers more efficiently (see section 1.5.1 page for a complete description).
- Lossy compression goes from a nearly perfect image nearly comparable to lossless compression (the slider around "Good quality" (about 85%) gives no visible default) to a rougher image that transfers very fast and takes very few place on the server.

Lossless multi-resolution and Lossy compression (around 85%) give the best results.

Select the receivers:

Click on a receiver name while holding the "Ctrl" key pressed to add / remove this receiver from the list. According to your configuration, one line could define a group of several recipients.

If this viewer contains a joined document with several patients or studies, or needs additional information to **provide a complete description** on this future document,

- √ click on the "Edit information" button (bottom right of the dialog box) (see section 2.8.7 for more details).

To conclude, click on the « Create & Send » button to compress the images and send them to the server, or on « Cancel » to abort.

ATTENTION: This method works with any kind of document (images, video, PDF etc.) but, as it sends information directly to the server, there is no notification to Electronic Patient Record or other third party software. You should preferably use the "Publishing images" functionality, as explained in the next section.

2.8.6. Publishing images

This method publishes images to the Telemis Acquisition machine, making the images follow exactly the same way as if they came from the modality. It is more flexible, allows Electronic Patient Record (E.P.R.) or other third party software to be notified, but only works with images. It doesn't work with movies, PDF or other documents.

The interest is to create e.g. a new series with key images at the destination of the clinicians or of the E.P.R., including measures etc.

In an opened viewer, select the images to be sent. If no images are selected, all the images of the viewer will be sent.

√ Select *[Files]* *[Publish]*.

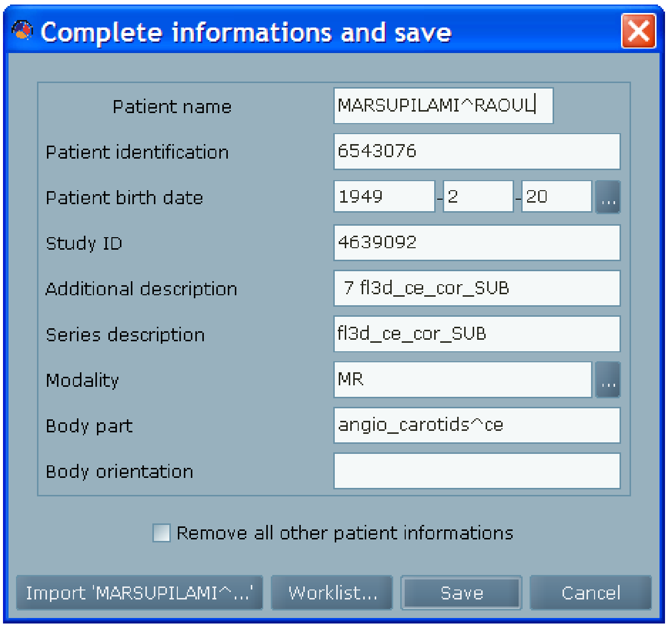
Enter a description to overwrite the current description, or leave it blank to keep it.

If measures or drawing are present on some of the selected images, the program will ask what to do with those layers, as shown in section 2.10.4 page (drop them, burn them into the images etc.).

2.8.7. Edit document information

Before saving a document on the server or in the local database, the information must sometimes be completed, for example if the viewer contains a joined document with several patients or studies, or simply needs additional information to **provide a complete description**.

√ Select [*File*] [*Edit information*] to open the dialog box depicted in Figure 174.



Patient name: MARSUPILAMI^RAOUL
Patient identification: 6543076
Patient birth date: 1949 - 2 - 20
Study ID: 4639092
Additional description: 7 fl3d_ce_cor_SUB
Series description: fl3d_ce_cor_SUB
Modality: MR
Body part: angio_carotids^ce
Body orientation:

☐ Remove all other patient informations

Figure 174 - Edit document information

Update the fields and press “Save” or ‘Cancel”.

The birth date must be entered in the yyyy mm dd format, i.e. 4 digits for the year, 2 for the month and 2 for the day. Example: July 7th, 1948 is written “1948 06 07”. You can also press the "..." button at the right of the date field to use a calendar to enter the date.

Check the [*Remove all other patient information*] to remove the patient address, military status, spouse name etc. from the header of the images. This flag is especially useful to anonymize a study.

If a line is selected in the browser, the [*Import 'name of the patient…'*] button appears at the bottom left of this dialog box. Press the button to import this patient information into the patient fields.

If a worklist server is configured in the hospital, it is possible to use the [*Worklist* …] button to query the worklist server and retrieve information for all the fields.

2.8.8. Selection for printing or building a summary: the filmer

▌This tool is only available in the *TM-Reception HE*.

The aim of this selection is to compose, from a set of series, a medical images summary for the clinicians or general practitioners. This summary will be integrated either as an additional series in the PACS, or printed on paper or on a radiological film.

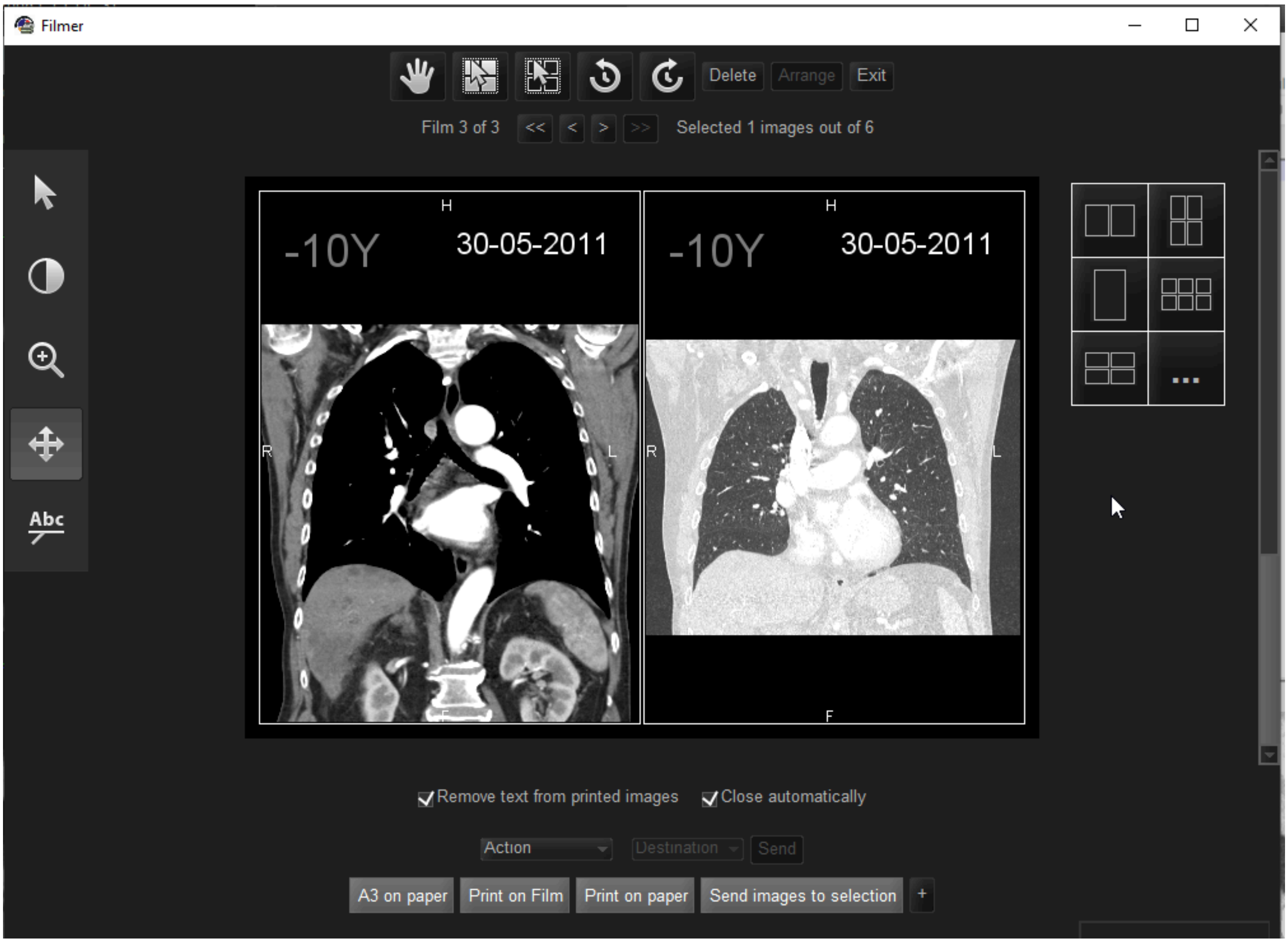
One or several series are displayed in one or several viewers of the *TM-Reception HE*. Some of the images should be saved as "key images". Lay those images out as they must be stored, with appropriate zoom, contrast, measures etc. Select the images to be marked as "key images" (see section 2.3.2 page for the image selection). To send those images to the "filming" tool,

√ Press the spacebar, or

√ Select [*File*] [*Filmer*]

To add new images to the filmer, you can also drag and drop them. To do so, go to the top left corner of the image inside the viewer. A small white hand appears. Click it and drag it to the desired location inside the filmer.

Acquisition date and age of the image: the acquisition date and the age of the image at the time of filming are now displayed. The age appears top left and the acquisition date top right for each image added to the filmer.

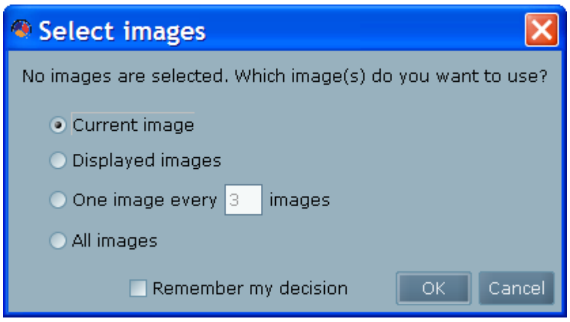


☑ Remove text from printed images ☑ Close automatically

Figure 175 - Filmer

This filmer is active until it's closed. Closing viewers doesn't affect the filmer. Select key images in different viewers and insert them into the filmer. If no image is selected when pressing the spacebar, the dialog box (shown on Figure 176) appears. You may choose to send to the filmer either only the current image (marked with a red 'current' at the bottom right of the image), all the images currently displayed in the viewer, one image every X images among all the images of this viewer, or all the images of the viewer. Check "Remember my decision" to have always the same action performed if no image is selected (always the current one e.g.).

To display this dialog box again, select the [*File*] menu and, while pressing the 'Shift' key, select [*Filmer*].



No images are selected. Which image(s) do you want to use?

● Current image
○ Displayed images
○ One image every 3 images
○ All images

☐ Remember my decision

Figure 176 - Filmer selection method

2.8.8.1. Navigate in the filmer

If the number of images selected is too important to fit on one page with the current layout, the filmer automatically creates new pages. The top section of the filmer shows e.g. "Film 2 of 5" if it displays the second page out of the 5 pages needed to contain all the images with this layout.

To scroll one page forward, press the '>' button (at the top of the filmer), press the 'Page down' key or move down the scroll bar (at the right of the filmer).

To scroll one page backward, press the '<' button (at the top of the filmer), press the 'Page up' key or move up the scroll bar (at the right of the filmer).

To go to the last page, press the '>>' button.

To go to the first page, press the '<<' button.

2.8.8.2. Update the filmer

In the filmer, you have the possibility to delete or move the images.

√ Click on an image to select or unselect it (a selected image has a red border). Right click on any image and click on [*Select all*] or [*Unselect all*] to select or unselect all the images of this filmer. You can also press the [*Select all*] (▦) or [*Unselect all*] (▦) buttons.

√ To delete one or several selected images, click on the 'Delete' button (at the top right of the filmer), or click on [*Delete*] in the context menu shown after a right-click on an image. Select several images and click on [*Delete selected*] or [*Delete unselected*] in the context menu to delete all the images selected, or all the images un-selected.

To move one or several selected images from one place to another:

- If the destination is on the same page, simply drag and drop an image to it's new location. If there already was an image at the new location, the two images will be switched.
- If the destination is on another page, right click on the image and click on “Cut”. Go to the appropriate page, right click on the new location and click on “Paste”.
- If you click on the “Arrange” button, all empty locations will be removed. You can also right click on an image and click “Arrange”.

2.8.8.3. Adjust images

You can adjust the images inside the filmer. Using the left panel, you can adjust contrast and brightness, zoom, pan and add text labels, just like in the viewer. You can also rotate the selected images clockwise and counterclockwise, by clicking on the buttons located above the images.

By default, the active tool is the “selection” tool.

Tools act on the selected images: to apply the same zoom for example on each image of the filmer, press the [*Select all*] (▦) button, select the zoom tool if not already done (🔍) and zoom any image: all the images will behave accordingly.

2.8.8.4. Change layout

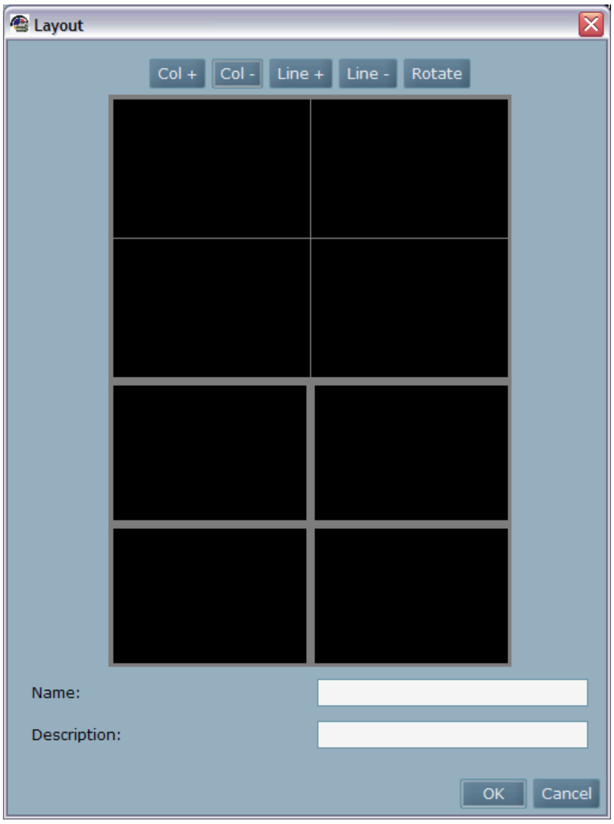
To change the layout of the locations on the page and the paper orientation, select one of the predefined layouts in the combo box located at the top left of the filmer.

To create a new layout preset, select the last item of the combo box, called "Manage …". The dialog box showed on Figure 177 appears.

Figure 177 - Manage filmer layouts

Select one preset and press 'Remove' to delete this preset, 'Set as default' to use it as the default preset, or 'Properties …' to update it.

To create a new layout, press 'Add …'. At the bottom of the dialog box, type a name (displayed in the combo box) and a description.



You must now define the grid of boxes which will constitute your layout. At the top of the dialog box, you can add or remove lines and columns. You can also rotate the layout to switch from portrait to landscape mode.

You can now define larger boxes in your layout, based on the displayed boxes. To do so, please click on the top left corner of the new box and drag the mouse down to the lower right corner of this same new box. Final boxes are separated by thick gray stripes.

2.8.8.5. Print on film

To send the result to a film DICOM printer,

- select the printer in the combo box at the bottom left of the filmer or select 'Manage …' to create a new preset;
- click on "Print on film" at the bottom left of the filmer.

- If you select the "Anonymize images" checkbox, no text will be displayed in the corners of the printed images.

Printing the filmer will automatically close it if the [*Close automatically*] option is checked, on the top right corner of the filmer.

2.8.8.6. Print on paper

To send the result to a classical printer (laser printer, inkjet …),

- Click on "Print on paper" at the bottom right of the filmer.
- If you select the "Anonymize images" checkbox, no text will be displayed in the corners of the printed images.

Printing the filmer will automatically close it if the [*Close automatically*] option is checked, on the top right corner of the filmer.

2.8.8.7. Send in DICOM

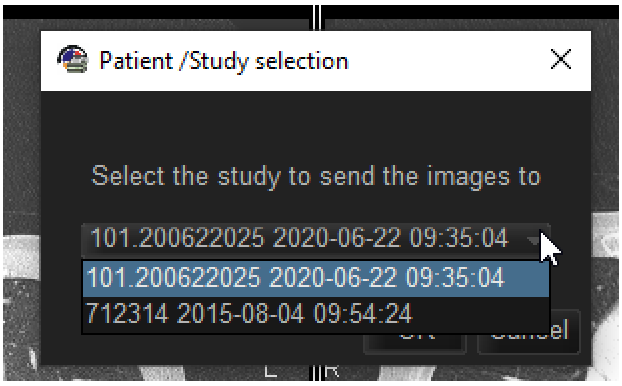
To send the result to the PACS or any other DICOM destination,

- select the DICOM destination in the combo box at the bottom of the filmer;
- you can choose to send the images which are inside the films, or the resulting films as large images, or both the images and the resulting films;
- click on the 'Send' button at the bottom of the filmer.

Sending the content of the filmer will automatically close it if the [*Close automatically*] option is checked, on the top right corner of the filmer.

Pay attention to one limitation of the filmer: it produces snapshots on the images currently displayed when you send them to the filmer via the spacebar. This means that images are not the original 16 bits/pixel ones but 8 bits/pixels snapshots. The full diagnostic quality is lost for images generated via the filmer.

- Choice of the summary sheet study: when sending to the PACS a filmer containing images from several exams, a window opens enabling selecting the exam in which you wish to send the summary sheet. The most recent exam is displayed at the top of the list.



Patient /Study selection

Select the study to send the images to

101.200622025 2020-06-22 09:35:04

101.200622025 2020-06-22 09:35:04

712314 2015-08-04 09:54:24

2.9. Comparisons

The comparison between two series (of the same study or not) is a classical operation in medicine: two series of the same patient but separated by a few days for example.

There are three methods to compare series:

- If the TMRHE is able to match the anatomical structures of both series (bones and/or soft tissues of CT scanner images), both series are aligned corresponding to those anatomical structures, even if the scope of the series is different or the position of the patient is not the same on the table.
- if the patient bed position of both series is comparable (i.e. if the patient hasn't changed position between both acquisitions), the computer will automatically link the corresponding images.
- If the patient bed position is not comparable (i.e. studies taken at different dates and/or patient position in the modality has changed), the equivalence between two images must be set by the user and then the computer will link the images using this information.

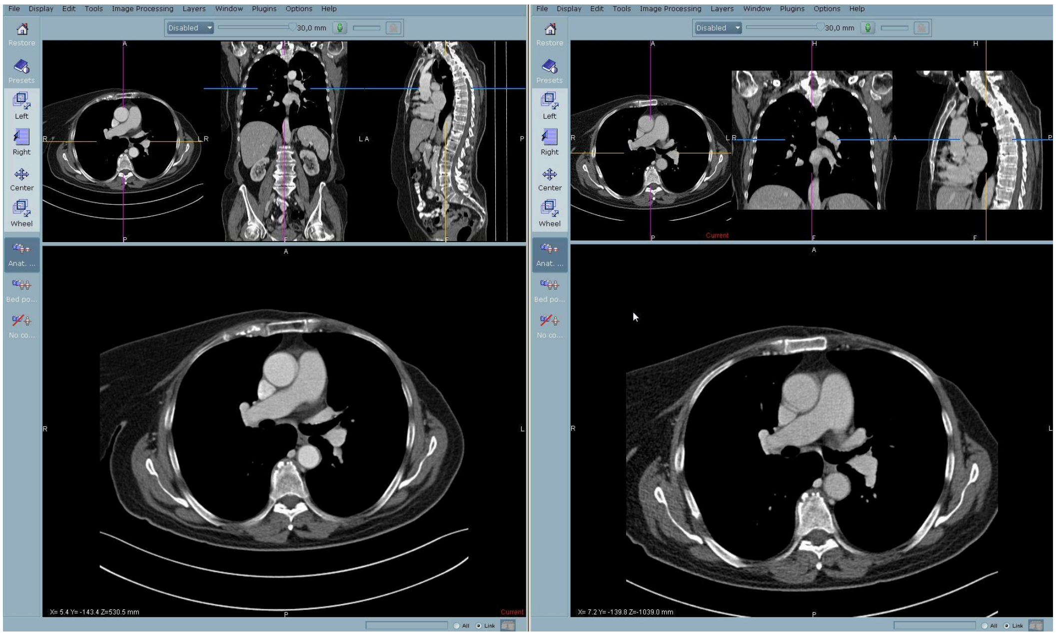


Figure 178 - anatomical comparison

2.9.1. Start/Stop comparison

This section will show you how to open the basic comparison between 2 viewers. See section 1.5.4 page for the more elaborated 'One-Click Comparison' mode.

If none of the series is already opened, the comparison can be started from the Browser, as explained in section 1.5.3 page . The program always tries then to start the comparison in the 'Bed position comparison mode'.

To start the comparison between several series those are currently opened in an Image Viewer,

√ Choose [*Display*] [*Anatomical comparison*], or

√ click on the 'Anatomical comparison' button available in the toolbar

If the TMRHE doesn't succeed in automatically finding the anatomical structures, it will try the bed or free comparison modes.

To **start the comparison** between two series those are currently opened in an Image Viewer and to force the **bed positions compare mode**,

√ Choose [*Display*] [*Bed position comparison mode*], or

√ click on the ‘Bed position comparison mode’ button available in the CT toolbar

To **start the comparison** between two series those are currently opened in an Image Viewer and with **different bed positions**,

Choose the first reference image in one of the two viewers by making it ‘current’ (simply click on the image to let a ‘current’ text appear at the bottom right of the image)

Navigate in the second viewer to find the corresponding image (see section 2.3.3 page) and make it ‘current’ in this second viewer.

√ Choose [*Display*] [*Free comparison mode*], or

√ click on the ‘Free comparison mode’ button available in the CT toolbar

To **stop the comparison** between two viewers,

√ Choose [*Display*] [*No comparison mode*], or

√ click on the ‘No comparison mode’ button available in the CT toolbar

You can add or remove a viewer from the set of compared viewers simply by changing the "Tools application domain" (see section 2.3.1 page): select "link" to add the viewer to the comparison, select "1!", "Sel" or "All" to remove it from the comparison.

2.9.2. The comparison

The comparison resizes the viewers to best fit on the number of available display monitors. The size and position of the viewers may change. On a *TM-Reception HE* using two screens, if the viewers were split over the two screens, the number of viewers may change to optimize the display.

Once the comparison is started, all the operations done in one of the compared viewers will be sent to the other viewers:

- change the display matrix,
- navigate in the studies (moving to the 10th image in one viewer locates the other viewers on the corresponding image)
- change contrast, brightness, zoom …

For example, a zoom in a particular image in the first viewer will zoom identically the corresponding image of the second viewer.

Images are synchronized using the image position information. Comparing one series having 5 mm between slices with a series having 1 mm between slices will keep the images synchronized: the image shown from the 1 mm series is the one closest to the currently displayed 5 mm image & vice-versa.

2.9.3. Change the offset between viewers

If you have opened the comparison with an erroneous correspondence between the images, you have to change this correspondence. You can either use any of the 3 following methods to synchronize the viewers, i.e. move the image in only one of the viewers:

√ Press the ‘Alt’ key while navigating in one series (via the mouse wheel, mouse button or the slider): when the ‘Alt’ key is pressed, only the current viewer will be impacted by the navigation: this is the easier way to synchronize 2 viewers.

√ In one of the viewers, move the mouse towards the right of the image. The scrolling tool appears (see section 2.3.3 page) together with two special green arrows, allowing the user to scroll only this series in both directions without exiting the comparison mode.

Change only this slice location while staying in comparison mode

√ Stop the comparison, mark one image of each viewer as ‘current’ and start again the comparison using the ‘Free comparison mode’.

2.9.4. Link Contrast & Brightness

Two series realized at a few days interval will not necessarily need the same optimal contrast and brightness parameters. Neither two series acquired on a different modality or with different acquisition parameters. Comparing them via the linked viewer for the zoom, displacement and navigation in the viewer should not share the contrast and brightness between the viewers, but let each viewer keep its optimal contrast and brightness settings.

To share everything except the contrast and brightness,

√ uncheck [*Display*] [*Link C&B*].

This line is checked by default, sharing contrast and brightness. Uncheck it to stop sharing them.

2.9.5. Link zoom

Sometimes it can be useful to compare two series displayed with a different zoom factor.

√ Uncheck [*Display*] [*Link Zoom*].

2.9.6. Compare the same series with different Contrast & Brightness

To compare one series on two different Contrast & Brightness presets (e.g. a CT Scanner series on the ‘Abdomen with contrast’ and ‘Abdomen without contrast’ presets),

Open the series in a viewer,

√ select [*Display*] [*New viewer with independent CB*], to open a second viewer with the same images,

select another contrast & brightness (via the presets or using the tools)

Compare the two viewers in the ‘Bed position comparison mode’.

2.9.7. Comparing series with different slice spacing

If some of the series compared have a different slice spacing (number of mm between 2 images), the viewer matrix automatically switches to 1x1 to only show one image per viewer in order to guarantie that only the corresponding images will be shown.

2.9.8. Shared cursor between 2D viewers

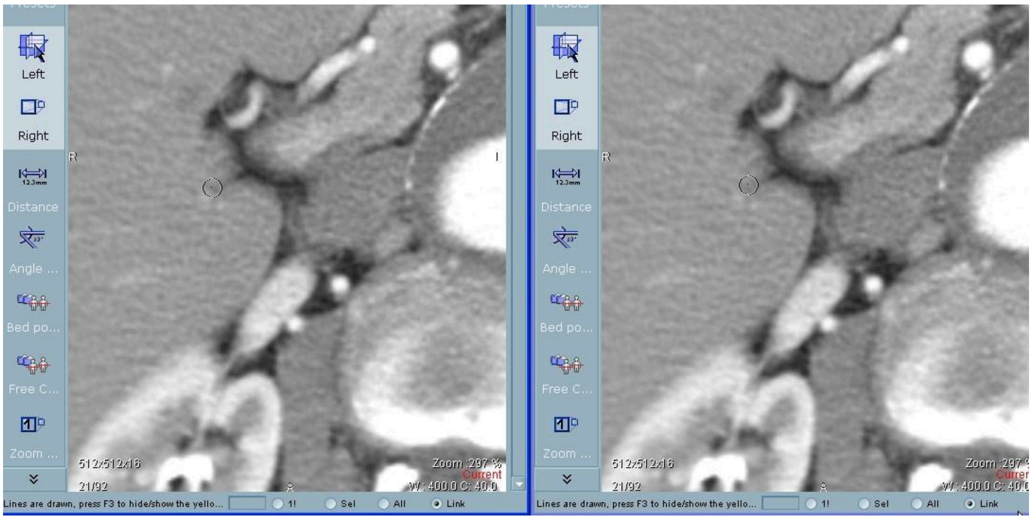
When comparing two 2D viewers, navigation, zoom, contrast etc. are shared operations that are reflected on the other shared viewers when performed on one particular viewer.

The comparison could be developed one step further if it was possible to navigate inside an image and see the pointer move at the corresponding location on the corresponding image of the other viewer(s). This is the role of the

√ Select the "Ortho Pointer" tool in the "Left" or "Right" drop boxes of the toolbar to associate the comparison tool with the left button or right button.

Set all the viewers to compare in the appropriate comparison mode ([*Display*] [*…. Comparison mode*] or press the [*Link*] button at the bottom right of the viewers, as explained in previous sections).

Click on a point in one of the image: a circle appears, with the corresponding circle in the other images, as shown in Figure 179.



Lines are drawn, press F3 to hide/show the yello...

Figure 179 - Shared cursor between 2D viewers

If the coordinates in both images do not perfectly match, the circles don't point to precisely the same body part in the images. To set an offset in an image in order to correctly synchronize the shared pointer,

- unlink one viewer (select the [All] button at the bottom right of the viewer),
- click in the image on the point that really corresponds to the circle drawn in the other image(s),
- link this viewer again (select the [Link] button again)

2.9.9. Compare with history

If the user, diagnosing a study of the day, desires to compare it with an older similar study, he must go back into the browser, perform the "Patient History" search, select a comparable study, select the corresponding series, open it and start the comparison.

Since version 3.9, a new functionality eases this operation.

√ In the viewer, press [*Display*] [*Compare with history*], or

√ Click on the 'Compare with history' button of the toolbar, or

√ press the 'H' key.

After a few seconds, the TMR(HE) presents the search result, as shown in Figure 180.

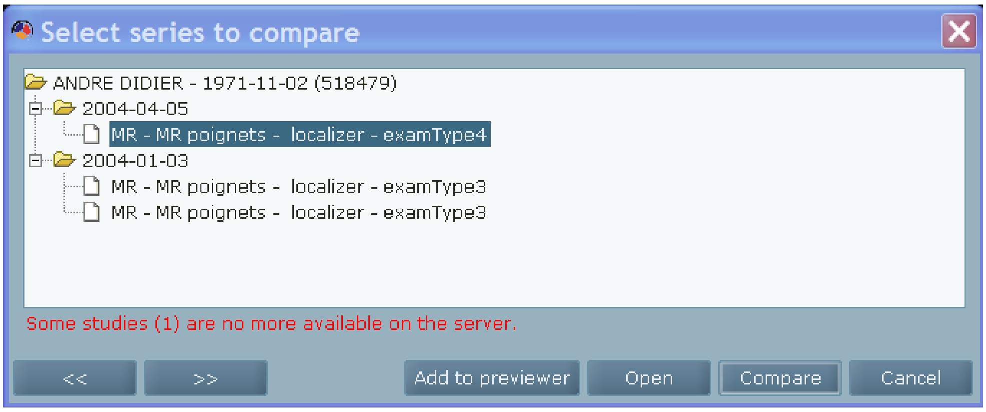
This window shows a tree, with one branch for each study corresponding to the current viewer (same patient, modality and study type).

Select one or several series in the list, in the same or in different studies, and press

√ Either [Add to previewer] to add the selected series to the currently opened previewer (option only available if a previewer is opened)

√ Or [Open] to open the selected series side by side with the current viewer, or

√ Or [Compare] to open them in the comparison mode.



Select series to compare

ANDRE DIDIER - 1971-11-02 (518479)
  2004-04-05
    MR - MR poignets - localizer - examType4
  2004-01-03
    MR - MR poignets - localizer - examType3
    MR - MR poignets - localizer - examType3

Some studies (1) are no more available on the server.

Figure 180 - Compare with history

According to your configuration, two additional buttons may appear in the lower left corner.

√ Press the [<<] button to narrow the search, i.e. make it more restrictive.

√ Press the [>>] button to extend the search, i.e. make it less restrictive (e.g. show all the studies of the patient with the same modality, or show all the studies of this patient).

If several servers are configured in the hospital, the default behavior is to search on all the servers. If for any reason some of the remote servers did not answer, a red error message warns the user.

The content of the dialog box and the search criteria for the different levels are configurable. Contact your local IT manager for more details.

2.9.10. Automatically search for history

According to the configuration of your *TM-Reception HE*, each viewer opened may display at the bottom right an icon (see Figure 181) if there is a history available on the server for this study.

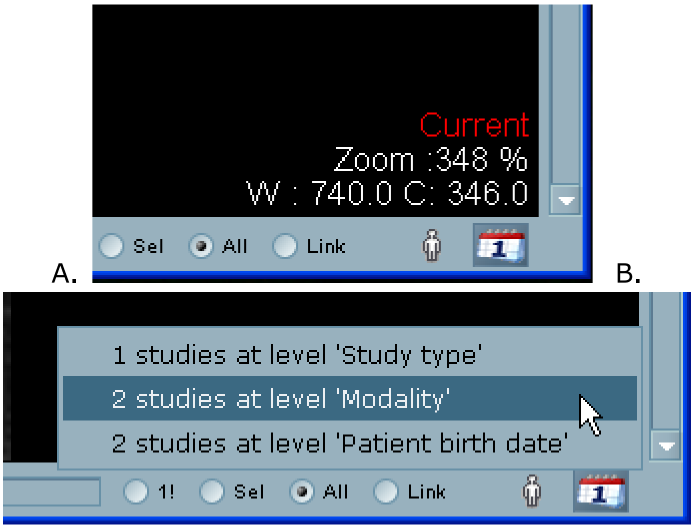


Figure 181 - Automatic search for history. A. history is available B. direct access to a search level.

The TM-Reception HE searches at different levels (typically studies with the same patient, modality and study type, studies with the same patient and modality, and all the studies of this patient. Your local IT manager can modify this configuration.). Right click on the auto-search calendar logo to have a direct access to the studies list at a particular level.

It's possible to configure the *TM-Reception HE* to automatically, for some given kinds of modalities, add the historical series to the previewer.

2.9.11. Automatic comparison with historical series

According to the configuration of your TM-Reception HE, opening a study with a hanging protocol will use the "automatic comparision with historical series" mode.

This feature provides a mode where a study can be compared with other studies. The screen is divied in two parts, either horizontally, vertically or monitor per monitor. On part of the screen contains the series of the current study while the other part contains the series of a previous study.

When a series is opened from the previewer, the corresponding series of the previous study is opened in the corresponding position in the other part of the screen.

When a series is moved, the corresponding series is moved on the other part of the screen.

If a series does not have a corresponding series in the previous study, its corresponding location on the screen is left empty.

The previous study is always selected as default. To select another study among the history of the patient, use either:

- √ The [Display] [Select history to compare] menu of the viewer, or
- √ Click in the image on the image age (e.g. "-12 M").

This comparison mode quits when the the previewer is closed.

2.10.Layers

2.10.1. DICOM layers

Many medical images come with additional information, encoded in the DICOM header as Curves (graphical objects stored as a set of coordinates, using ‘vectorial’ encoding) or Overlays (a kind of second image, superimposed on the original image and containing points) layers: graphs, additional textual information, curves, regions of interest etc.

Depending on your configuration (see section 2.10.3), the viewer will never show this information, will prompt the user to display it or will always display it.

If you have chosen to never see the layers, or refused to see them when prompted, it is possible to initialize them at any moment. In the Viewer,

√ Select [*Layers*] [*Initialize curves*] and/or

√ Select [*Layers*] [*Initialize overlays*].

These lines are enabled only if curves or overlays are present in the images.

2.10.2. Manage layers

The DICOM layers, as well as all the drawings and measurements done in the viewer, are stored in layers. To copy, hide, delete those layers, use the Layers Manager.

√ Select [*Layers*] [*Layers Manager*] in the viewer to display the window shown on Figure 182.

There is originally one layer which name is “Layer 0”.

√ To rename a layer, click on the cell containing its name and type the new name.

√ To create a new layer, click on the “New” button.

√ To duplicate an existing layer and all the objects that it contains, click on the layer with the right button of the mouse and select “Copy”.

√ To delete a layer and all the objects that it contains, click on the layer with the right button of the mouse and select “Delete”.

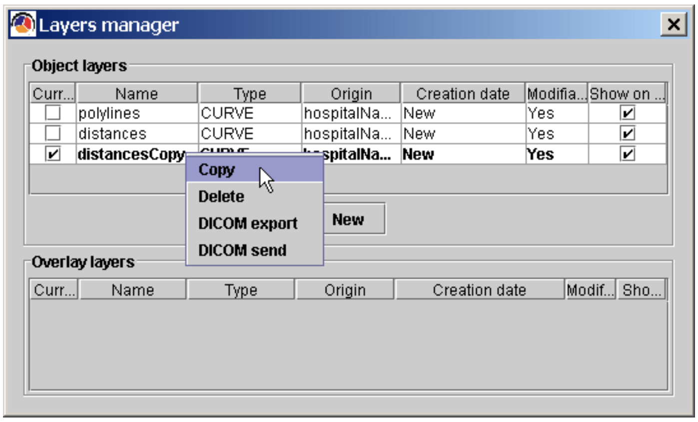
√ To display or hide the objects contained in a layer, check or uncheck the “Show on images” cell (the last one) of this layer. The current layer is always displayed.

√ To specify which layer is the current one, check the “Current” cell (the first one) of the layer.

√ To export a layer in a DICOM file or send it using the DICOM protocol, click on the layer with the right button of the mouse and select “DICOM export” or “DICOM send”. All the images of the viewer are sent or exported in the DICOM format, with their layers.

The drawings and measurements drawn on images are always stored in the current layer.

In version 3.72, the layers originally contained in a DICOM image will follow the image if this image is exported or save in the DICOM format. New layers can be added to the images via the DICOM export function. But it remains impossible to store in the Telemis format new layers, i.e. to save layers drawn in a viewer and retrieve them later.



Object layers

Curr...	Name	Type	Origin	Creation date	Modifia...	Show on ...
☐	polylines	CURVE	hospitalNa...	New	Yes	☑
☐	distances	CURVE	hospitalNa...	New	Yes	☑
☑	**distancesCopy**	**CURVE**	**hospitalNa...**	**New**	**Yes**	☑

Overlay layers

Curr...	Name	Type	Origin	Creation date	Modif...	Sho...

Figure 182 - Layers manager

2.10.3. Configure layers

To configure the opening of the DICOM layers,

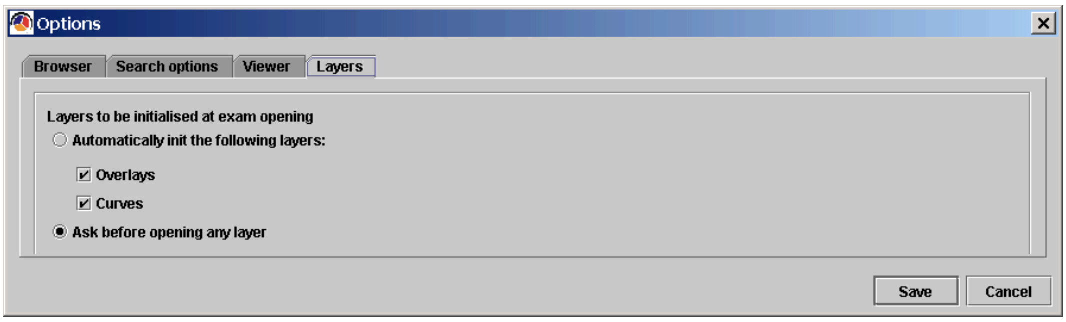
√ Select [*Options*] [*Browser options*] in the Browser, or select [*Options*] [*Viewer options*] in the Viewer;

√ Choose the "Layers" tab in the options window to view the content of Figure 183.

To always see the layers associated with the images, check "Automatically init the following layers", "Overlays" and "Curves".

To have the computer prompt to open or not the layers, check "Ask before opening any layer"

To never see the layers, check "Automatically init the following layers" and uncheck "Overlays" and "Curves".



Layers to be initialised at exam opening

○ Automatically init the following layers:

☑ Overlays

☑ Curves

● Ask before opening any layer

Figure 183 - Layers configuration

2.10.4. Layers exportation

When saving or sending in DICOM images containing measures or drawing done by the user in the viewer, the *TM-Reception HE* will propose to

- Save the images without including the measures
- Automatically burn these objects on the images (see section 2.5.6.6 page)
- Include them into the images as DICOM curves. Remark that in the actual implementation of the DICOM standard, the texts and arrows will not be saved.

2.11. General commands

2.11.1. Cancel

The progress bar located at the bottom right of the viewer shows the progress state of the decompression of the images of the study.

To cancel the opening of this study, you can do this from the browser as explained in section 1.8.2 page .

To cancel the operation from the viewer, click on the cancel button located in the toolbar of the viewer to stop the download, decompression and display of the images for this viewer. This operation doesn't close the viewer.

2.11.2. New viewer

To open a second viewer for the study displayed in the current viewer,

√ select [*Display*] [*New viewer*], or

√ press the 'F9' key.

The new viewer shows the same display matrix, zoom, contrast … as the original viewer.

A second viewer can be useful in several situations, for example if a document actually contains two studies. If the acquisition machine has generated one document with the 'T1' and 'T2' MRI sequences, opening a second viewer allows to view the T1 images (for examples images 1 to 100 of the document) in the first and the T2 images (for example images 101 to 200 of the document) in the second viewer. These two viewers can then be linked (see section 2.8.5 page) to easily compare the T1 and T2 sequences.

2.11.3. Refresh

If, for any reason, the display of the viewer is slightly disturbed, you can refresh it:

√ select [*Display*] [*Refresh the view*] or

√ press the *F5* function key

2.11.4. Restore

You can restore the images of the tools application domain (see section 2.3.1 page) to their original contrast, brightness, zoom, ... settings. This operation 'undo' all your previous operations on these images.

To perform the restore,

√ select [*File*] [*Restore*] or

√ click on the restore button of the viewer toolbar.

2.11.5. Browser to front/back

When you work with Telemis viewers, you sometimes need functions or lists of the browser that is hidden by all the viewers opened. Bringing the browser back on top of the windows with one key should be convenient. Going then back to the viewers should also be eased. The F12 function key switches between browser and viewers.

√ Press the ‘F12’ function key from the browser or the viewers to send the Telemis browser to the back of the screen. Press again to send it to the front.

2.11.6. Open a previewer

Select *[Display]* *[Open a new previewer]* or press the ‘F4’ key,

to display the previewer (see section 1.5.4 page) for all the documents currently selected in the browser, i.e. to call the same command as if you came back to the browser and requested the previewer to open.

Select [*Display*] [*Show current previewer*] or press the ‘Alt’ and ‘P’ keys, if there is a previewer currently opened, but hidden by one of the viewers, to show it. If there is no previewer currently opened, this function is not available.

2.11.7. Show next/preview study or patient

√ From the viewer, to close all the currently opened viewers and switch to the next or previous patient or study:Press the CTRL and "+" keys (on the numeric pad) to switch to the next study shown in the browser list

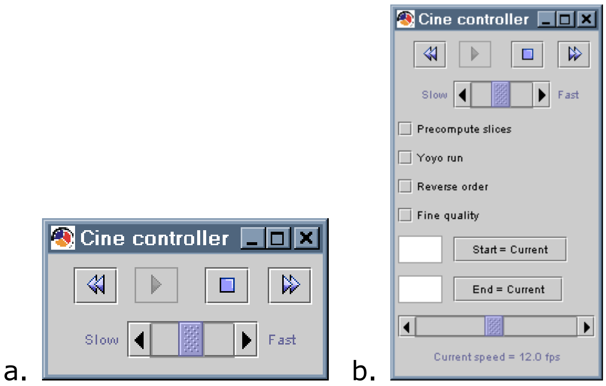
√ Press the CTRL and "-" keys (on the numeric pad) to switch to the previous study shown in the browser list

√ Press the CTRL and SHIFT and "+" keys (on the numeric pad) to switch to the first series of the next patient shown in the browser list

√ Press the CTRL and SHIFT and "-" key (on the numeric pad) to switch to the first series of the previous patient shown in the browser list

2.12. Cine Viewer

The Telemis Cine Viewer is an animation tool for the Telemis viewer. The Cine Viewer plays a sequence with all the images contained in the element. They are displayed as a movie animation, giving a *live* view of the 3D or temporal images.



a. b.

☐ Precompute slices
☐ Yoyo run
☐ Reverse order
☐ Fine quality

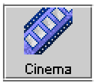
Current speed = 12.0 fps

Figure 184 - The Cine Viewer Controller window. a) TM-Reception b) TM-Reception HE

2.12.1. Activation

To activate a Cine Viewer,

- √ select [*Display*] [*Cine viewer*] from a Telemis Image Viewer, or
- √ press the 'Alt' and 'C' keys, or
- √ Click on the 'Cinema' button in the toolbar.



The cine viewer controller window displayed Figure 184 appears.

The whole animation will take place in one image of the Telemis Image Viewer: the current one (see section 2.3.2 page for selecting an image). If you try to start the animation without a current image, the animation will take place in the first image of the viewer.

For the best view, you should preferably use a small display matrix.

To close the Cine Viewer,

- √ click on the cross at the upper-right of the Cine Viewer window (✕).

2.12.2. Play/Stop

To *play* the Cine Viewer,

- √ click on the *Play* button ▷.

The Cine Viewer will display all the images one after the other until the last one. When the last image has been displayed, the animation automatically restarts, playing cyclically all the images. When the Cine Viewer controller opens, the animation starts automatically.

To *stop* the Cine Viewer,

- √ click on the *Stop* button ▣.

The Cine Viewer stops the display on the image currently displayed.

2.12.3. Speed control

You can control the speed of the animation.

The speed slider (see Figure 185) shows the speed of the display between *Slow* (to the left) and *Fast* (to the right). Move the slider to the left to slow down the display, to the right to speed it up.

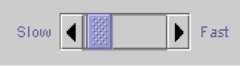


Figure 185 - Cine Viewer speed slider

The line located at the bottom of the Cine Viewer controller shows the current speed of the animation, in number of images displayed per second.

2.12.4. Display options

You can act on several display parameters:

- √ Check 'precompute slices' to increase the display speed (but also the memory consumption of the Cine Viewer).

√ Check 'Yoyo run' to change the display order. If this option is unchecked, the Cine Viewer plays from the first to the last image, then again the first to the last. If this option is checked, the Cine Viewer plays from the first to the last, then backward from the last to the first, then forward again from the first to the last …

√ Check 'Reverse order' to change the display order from "first to last image" to "last to first image".

√ Check 'Fine Quality' to display higher quality images during the animation. Keep in mind that this option increases significantly the memory consumption of the Viewer.

The display limits can be modified. The display limits are the first and last image of the series to be displayed. All the images in between will be displayed by the Cine Viewer.

√ To set the index of the first image to display, use the slider located at the bottom of the controller or the Rewind/Forward buttons to move the displayed image to the one that you want to be the first. Click on the 'Start = Current' button.

√ To set the index of the last image to display, use the slider or the Rewind/Forward buttons to move the displayed image to the one that you want to be the last. Click on the 'End = Current' button.

√ When the Cine Viewer starts, it plays the animation at a configurable frame rate.

2.13.Dynamic cardiac viewer

This viewer is only available in the *TM-Reception HE*.

Cardiac US, XA and MRI modalities produce multiple dynamic sequences of images[15]. We typically find one sequence per heartbeat.

The aim of the dynamic cardiac viewer is to offer synchronized viewing of those sequences.

In the browser, select the study to open in the cardiac viewer. Once the cardiac viewer is configured correctly, select [*Document*] [*Open with Hanging Protocol*].

The dynamic viewer appears. Dynamic sequences automatically start playing. Static images are displayed without playing.

---

[15] Technically, following SOP Class UID are taken into account by the Dynamic cardiac viewer:

- MR Image Storage (1.2.840.10008.5.1.4.1.1.4)
- Ultrasound Multi-frame Image Storage (1.2.840.10008.5.1.4.1.1.3.1)
- Ultrasound Image Storage (1.2.840.10008.5.1.4.1.1.6.1)
- X-Ray Angiographic Image Storage (1.2.840.10008.5.1.4.1.1.12.1)
- Multi-frame True Color Secondary Capture Image Storage (1.2.840.10008.5.1.4.1.1.7.4) with RecommendedDisplayFrameRate (0008,2144)

Figure 186 - cardiac viewer

Classic controls of a 2D viewer are available, like contrast, zoom, measurement tools, filmer, etc.

The upper toolbar allows controlling the dynamic display:

Play / Pause

Frame rate adjustment

Display of the active sequence / all sequences

2.13.1. Play / Pause

To Play / Pause the displayed sequences, use the Play / Pause button located in the upper toolbar.

2.13.2. Frame rate adjustment

To change the frame rate, use the slider located in the upper toolbar. All sequences are synchronized and may be displayed at different frame rates. The frame rate of each sequence is displayed in the lower left corner of the sequence.

2.13.3. Manual navigation

To navigate manually through a static sequence or through a paused dynamic sequence, use the mouse wheel on this sequence.

2.13.4. Sequence selection

To display a single sequence on the screen, use the icon located in the upper toolbar or double-click on the desired sequence. To go to the next / previous sequence, use the scrollbar on the right or the [*Page up*] / [*Page down*] keys. To go back to displaying all sequences, use the icon located in the upper toolbar or double-click on the sequence.

2.14. Specific Nuclear medicine fusion viewer

> This viewer is only available in the TM-Reception HE

2.14.1. Activation of the fusion

To activate a specific nuclear medicine fusion viewer, check with your Telemis contact that you have an appropriate configuration, then select the PT and CT series and

√ select [*Document*] [*Fusion*] from a Telemis Browser, or

√ Press the fusion icon in the Browser toolbar, if available

The TMRHE will classically open and fusion the PT and CT series but using in a layout that shows the axial, coronal and sagittal views for the CT, PT and the fusion. See Figure 187.

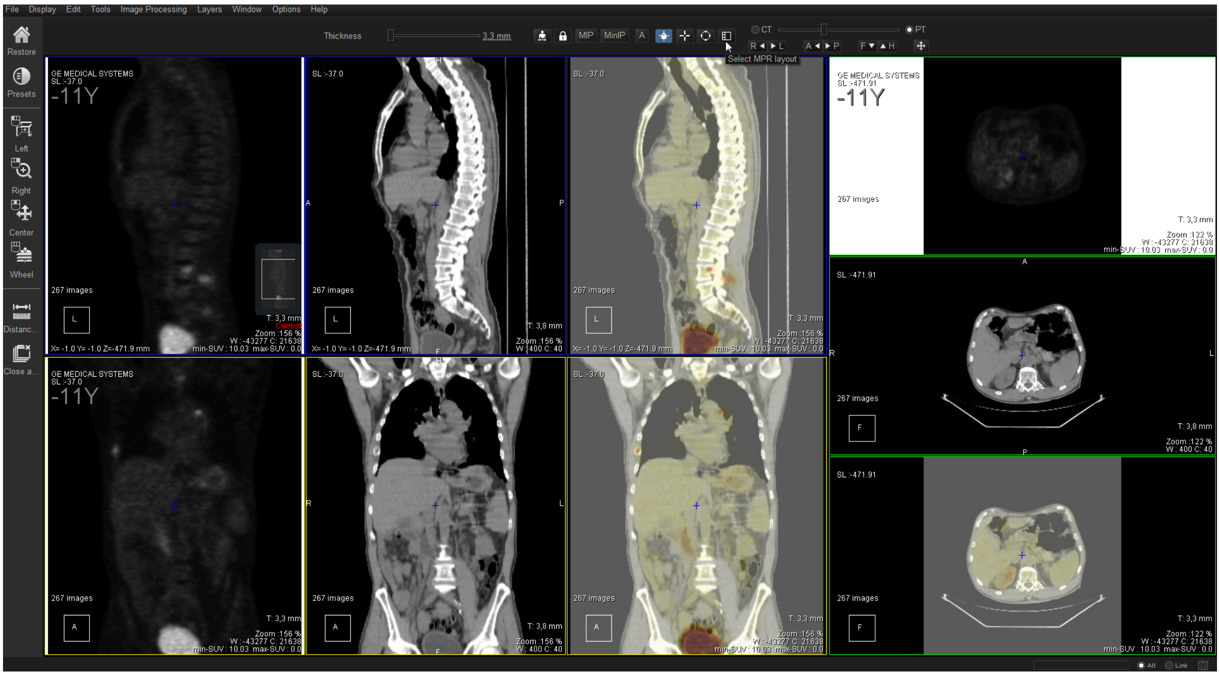


Figure 187 - nuclear medicine viewer mode

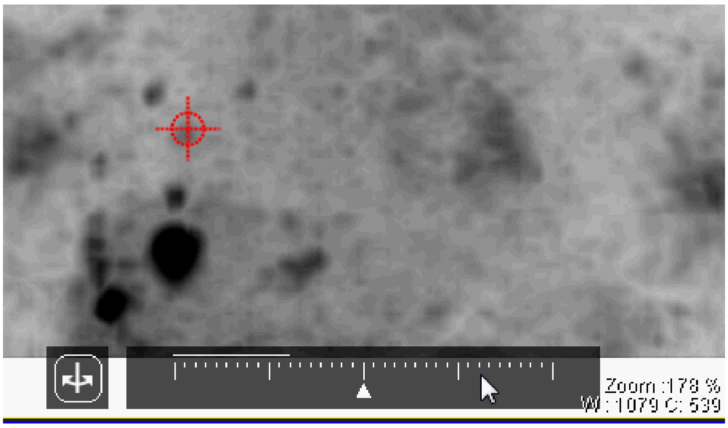
2.14.2. Rotating full MIP

You can switch from this layout to another one allowing the 'Full MIP' functionality:

√ In the tools available on top of the images, select the 'Select MPR Layout' tool.

Choose a layout containing a 'Full MIP', for example "3 axial + full MIP"

Move the mouse on the bottom of the MIP image to show the full MIP controller.



The horizontal bar on top of the controller is the progress of the background full MIP computation. When the computation is finished, the Play / Pause buttons appear on the left and right of the controller (see Figure 188)

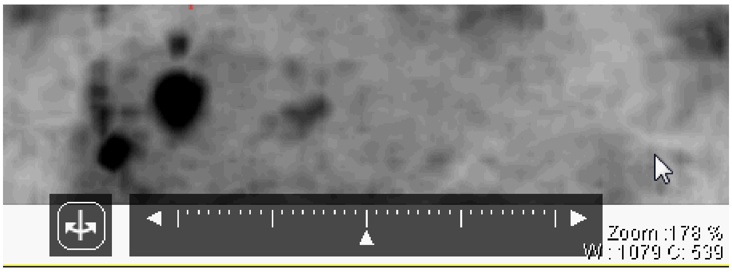


Figure 188 - MPR full MIP controller

With the mouse located in the controller, you can

- Use the mouse wheel to navigate along the full MIP reconstruction.
- Move the arrow located under the bar to navigate into the reconstruction.
- Click at any place in the progress bar to navigate to this position.
- Press the left or right Play ☐ button to animate the full MIP in each direction. The Play button is then transformed into a Pause button. Press it to pause. Pressing the 'point' key also starts / stops the animation.
  - Select the rotation tool located at the left of the progress bar. Click at any place in the image and drag the mouse left or right to rotate the MIP left or right.
- Double-click on the image to maximize it or to go back to its original size.

To locate precisely in the Axial, Coronal or Sagittal views the 'hot' point seen in the MIP, you must triangulate in 2 steps, in the view 'Mednuc + full MIP':

In the first view, locate the cursor on the hot spot as shown in Figure 189 point 1. In the second view, move horizontally the cursor to match the hot point position as shown in Figure 189 point 2.

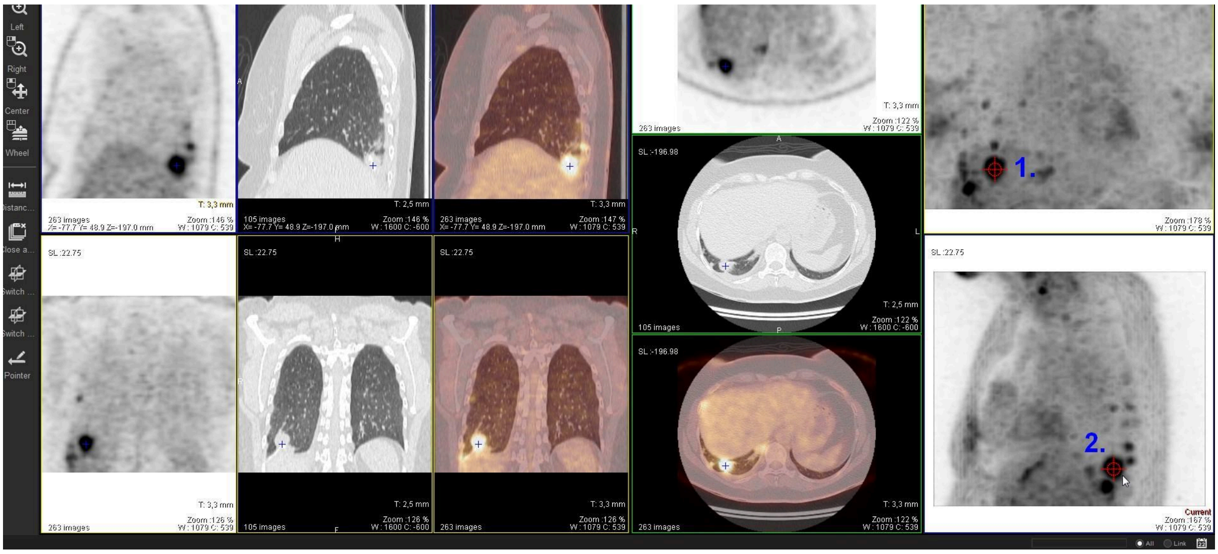


Figure 189 - Full MIP - Triangulate on the hot point

2.15.Customizing the viewer

2.15.1. General options

You can customize the way the viewers look via the option panel. To open the viewer options panel,

√ select [*Options*] [*Browser options*] in the browser and then select the “Viewer” tab in the options window, or

√ select [*Options*] [*Viewer options*] in any viewer.

2.15.1.1. Windowing (contrast & brightness) options

The contrast and brightness settings can be changed automatically, as explained in section 2.3.4.3 page . Two parameters manage the limits used to set the display window.

As shown in Figure 190, the automatic contrast sets the width and centre of the display window (see Figure 81 page) to set the window borders on the first and last point of the histogram of the image.

You can configure the automatic contrast to not take into account the x first °/oo of the surface of the histogram for the upper and lower limits, to reduce the sensitivity of this function to the noise inherent in the images.

Enter the lower and upper limits (values between 0 and 999) in the viewer options panel.

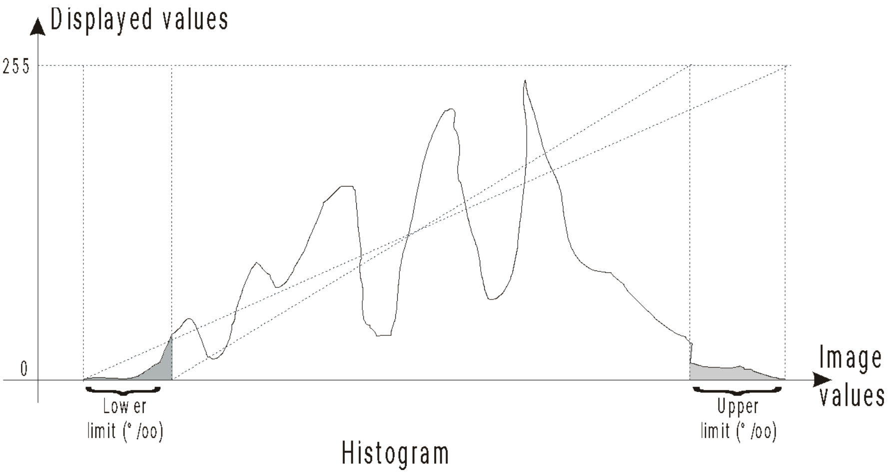


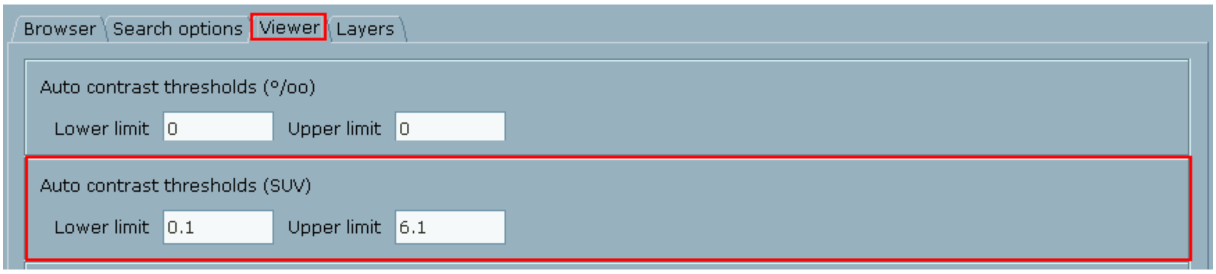
Figure 190 - Automatic contrast upper and lower limits

2.15.1.2. SUV-windowing options

The image viewer, used to display PT-scan images, offers an automatic windowing, based on the SUV values (See section XX).

This option sets to zero (black) the displayed value of all pixels having a SUV value under the minimum value, sets to 255 (white) the displayed value of all pixels having a SUV value above the maximum, and uses a linear scale for all the pixels in-between.

In the viewer options panel, adjust the 'auto-contrast SUV thresholds'.



Auto contrast thresholds (°/oo)

Lower limit 0 Upper limit 0

Auto contrast thresholds (SUV)

Lower limit 0.1 Upper limit 6.1

2.15.1.3. Confirm viewer closing

Each time you close a viewer, a window prompts for a confirmation. To suppress this window, uncheck the "*Confirm the closing of a viewer*" check box.

2.15.1.4. Automatically draw a reference line for the current image on the other series

Activate or de-activate the automatic drawing of the reference lines, as explained in section 2.5.8 page .

2.15.1.5. Interpolation

Activate or de-activate the interpolation on images when the zoom is superior to 100%. The default value is 'activated'. It should only be de-activated on Mammography-dedicated *TMReception-HE*.

You can also activate or de-activate the interpolation via the

√ [*Display*] [*Interpolate images*].

2.15.1.6. Display texts in toolbar

Display or not the text under each icon in the toolbars. Removing this text saves space in the toolbar and allows more tools to be shown.

2.15.1.7. Cine Viewer options

When the Cine Viewer starts, it plays the animation at a configurable frame rate.

Change the value in "Animation rate (images/sec)" to specify the number of images per second that must be displayed.

2.15.1.8. Default MPR layout

Select the default layout used when opening the MPR viewer.

2.15.1.9. Cursor shape

The cursor shape for the 3D pointer is configurable.

Select the appropriate shape in the "3D cursor shape" drop box. The available shapes are a circle, an arrow or a cross.

2.15.1.10. Default tools for the mouse buttons

Check / uncheck mouse button management. The default value is to manage the left and right buttons, the rolling of the wheel and pressing the wheel (called 'central button').

This option panel associates default tools to each activated button when a viewer opens. Different default values can be set for 2D and 3D (MPR) viewers.

The available tools are: contrast, magnifier, zoom, mover, navigation, selection or orthogonal pointer.

2.15.1.11. Display the CLUT scale

√ Select [*Display*] [*CLUT*]

To show or hide a Color (or grayscale) look-up vertical bar, at the left of the images.

2.15.1.12. Use Saturation contrast & brightness

This option is specially usefull for Nuclear medicine.

√ Select [*Display*] [*Use saturation C&B*] to force the starting point of the 'image value' – 'displayed value' to be glued to the '0 – 0' position, i.e. forcing point A. of Figure 81 page to stay at the '0' – '0' position.

2.15.1.13. Use Min-max contrast & brightness

This option is specially usefull for Nuclear medicine.

√ Select [*Display*] [*Use Min-max C&B*] to show the values at the bottom right of the images expressed as minimum percentage and maximum percentage of the image values, instead of showing absolute values.

2.15.2. Dependent display parameters

It is possible to configure the Telemis Image Viewer to open differently, according to the kind of images contained in the study.

It is for example possible to ask *TM-Reception* to open angiography studies directly with a 1x1 display matrix and directly animated. It is also possible to ask *TM-Reception* to open PET SCAN studies directly within the orthogonal 3D viewer.

√ Select [*Options*] [*Edit display layout*] in the Viewer.

Editing these parameters is only available with the *TM-Reception HE* software. Contact your local IT manager or Telemis s.a. for a proper configuration of these dependent parameters.

2.15.3. Compression

You can customize the decompression of the images via the viewer options panel.

2.15.3.1. Uncompress only the displayed images

When a viewer opens for a document containing many images, it must decompress and prepare for the display each image. These operations take a bit of time and slow down the rest of the computer. Two behaviors are possible:

- the viewer decompresses all the images in the background. The progress bar at the bottom right of the viewer shows the progress of this decompression. After a few seconds (during which the computer looks a bit slower) all the images are decompressed for the whole lifetime of the viewer.
- the viewer decompresses only the images to be displayed. This means that the period of slowness of the computer is much shorter but this also means that if you request the display of an image not currently displayed, this image must be decompressed at this moment, introducing a small delay. This strategy uses less memory than the first one if only a few images of the study are to be displayed. The memory consumption is equivalent if all the images are displayed.

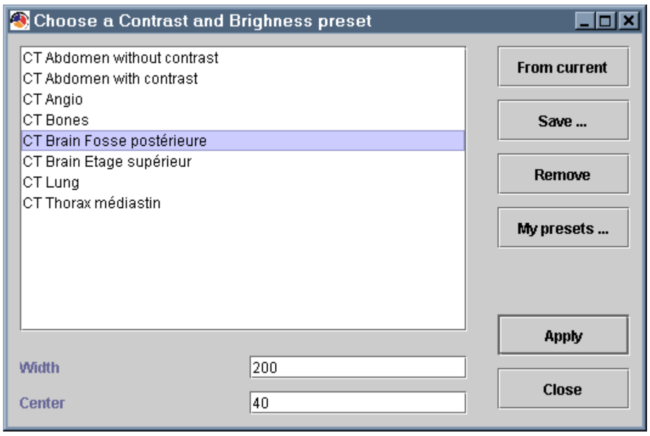
Check or uncheck the "*Uncompress only the images displayed*" in the viewer options panel according to the behavior that best suits you.

2.15.4. Presets

Several features of the *TM-Reception* program use presets: contrast and brightness, Color Look-Up Tables …This section explains how to create these presets.

2.15.4.1. Contrast & Brightness

In a Telemis Viewer, open the contrast and brightness window: select [*Edit*] [*C&B presets*] or press the *F1* function key.



CT Abdomen without contrast
CT Abdomen with contrast
CT Angio
CT Bones
CT Brain Fosse postérieure
CT Brain Etage supérieur
CT Lung
CT Thorax médiastin

Width 200
Center 40

Figure 191 - Brightness and contrast presets

To create a new preset, values must be fed in the "Width" and "Centre" text boxes:

√ you can manually enter values in the *Width* and *Centre* text fields, or

√ if you have manually reached an optimum contrast and brightness in the viewer, you can automatically get the numerical values of the width and centre into this window if you click on the *From Current* button. The values of the current slice are displayed in the Width and Centre text boxes.

To save this contrast and brightness setting as a preset, that will become available in the preset icon Presets of the toolbar,

√ click on *Save* to save it under the name that you will give.

This new preset is saved on your profile and will follow you on any *TM-Reception* program.

√ You can remove a preset from your profile if you click on the *Remove* button.

√ Click on the *Close* button to exit the Contrast and Brightness window.

2.15.4.2. CLUT

In this version of the *TM-Reception* program, it is not possible to create automatically a color look-up table preset.

Contact your local IT manager or Telemis s.a. to create a new CLUT preset.

2.15.5. Customize the toolbars

See section 2.1.1 page to hide or display the toolbar embedded in the viewer.

This section explains how to set the type of toolbar and define its content.

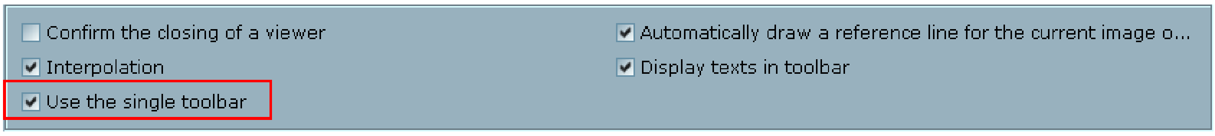
2.15.5.1. Choose between embedded or single toolbar

To activate the single toolbar bar or use the embedded toolbar,

√ Select in the viewer the menu [*Options*] [*Viewer options*], or

√ Select in the browser the menu [*Options*] [*Browser options*] and switch to the *Viewer* panel.

Select the "Use the single toolbar" option to activate the single toolbar, unselect it to activate the embedded toolbars.



☐ Confirm the closing of a viewer

☑ Interpolation

☑ Use the single toolbar

☑ Automatically draw a reference line for the current image o...

☑ Display texts in toolbar

You can also click in the toolbar with the right mouse button and select or unselect [*Use single toolbar bar*].

This change will only be taken into account when all the viewers are closed.

√ Determine the position of the single toolbar

To determine where the single toolbar will show on each screen,

√ Select in the viewer the menu [*Options*] [*Viewer options*], or

√ Select in the browser the menu [*Options*] [*Browser options*] and switch to the *Viewer* panel.

Check the check box named "*Use the single toolbar*" if not already done.

Select in the "Single toolbar disposition" box the option most suitable for you (see Figure 195):

- *All on the left*: Display the single toolbar on the left of each screen
- *All on the right*: Display the single toolbar on the right of each screen
- *All on the extremities*: Display the single toolbar on the extremity of the screens

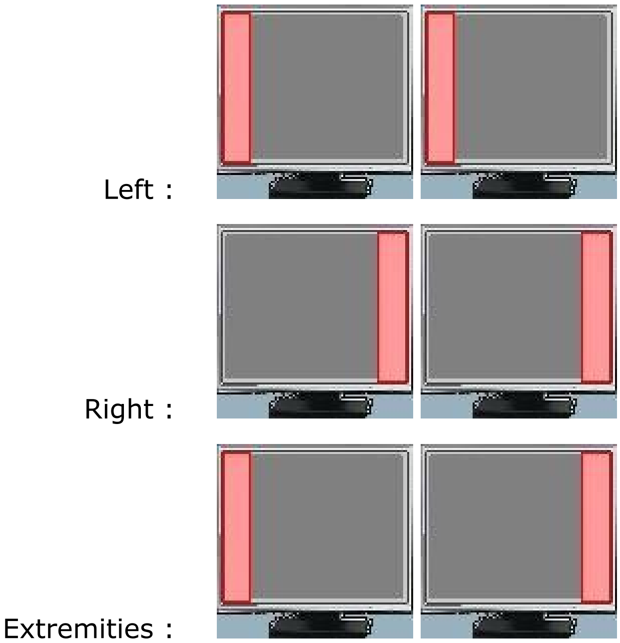


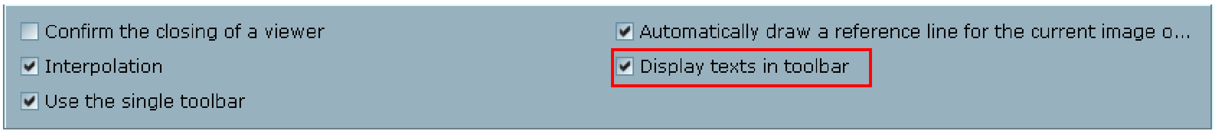
Figure 192 - single toolbars position

2.15.5.2. Show the text below icons in the toolbars

To show or hide the text below the icons of the toolbars,

√ Select in the viewer the menu [*Options*] [*Viewer options*], or

√ Select in the browser the menu [*Options*] [*Browser options*] and switch to the *Viewer* panel.



☐ Confirm the closing of a viewer
☑ Interpolation
☑ Use the single toolbar
☑ Automatically draw a reference line for the current image o...
☑ Display texts in toolbar

√ You can also click in the toolbar with the right mouse button and select or unselect [*Display text below the buttons]*.

This change will only be taken into account when all the viewers are closed.

2.15.5.3. Number of columns in the single toolbar

This option is only available for the single toolbar.

√ Click in the toolbar with the right mouse button, select [*Change the number of columns]* and select the desired number.

This change will only be taken into account when all the viewers are closed.

2.15.5.4. Configure the content of the toolbars

To configure the content of the toolbars, i.e. the list of tools directly available, in the Viewer,

√ Click in the toolbar with the right mouse button and select [*Configure toolbar …*].

The dialog box show in Figure 193 appears.

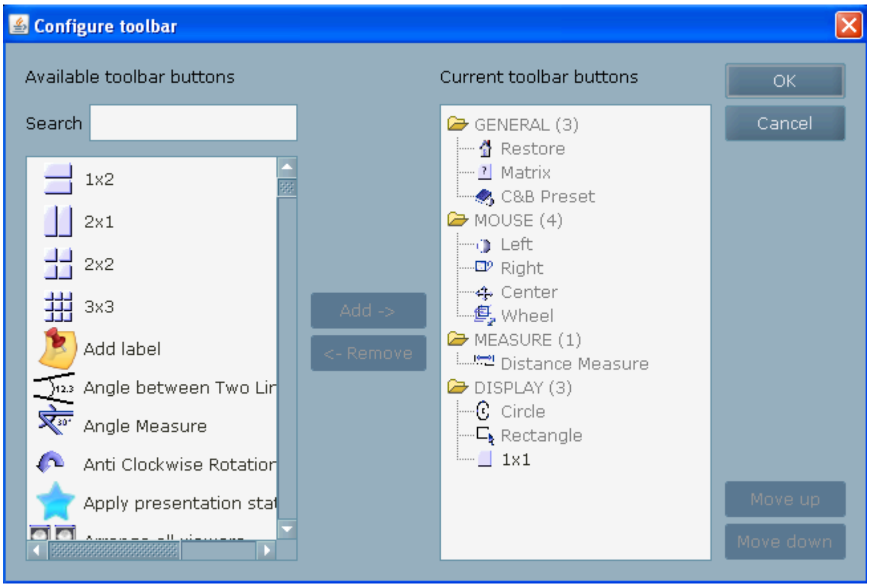


Figure 193 - Configure main toolbar

The rightist panel presents the content of the toolbar. Some tools present in this 'current toolbar buttons' are not configurable (grey colored), either because these are basic tools, or because they have been defined by your system administrator. You can only configure the bottom of the toolbar.

The panel on the left contains all the available.

Toolbars are organized in categories.

√ To create a new category, right click in the 'current toolbar buttons' list and select [*Add a new category*].

A dialog box will prompt you for entering the name of the category (see Figure 194).

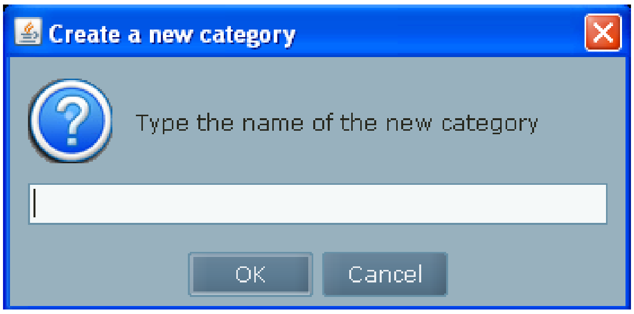


Figure 194 - create a new toolbar category

√ To add a tool to the main toolbar, select it in the left panel and press the "Add " button, or double-click on the tool in the left panel.

√ To remove a tool or a separator from the main toolbar, select it in the rightist panel and press the " Remove" button.

To arrange the selected tools, you can select a tool in the "Current toolbar buttons" panel, and press the buttons "Move up" or "Move down" to change their displayed position.

2.15.6. Others

The content of the title bar of each viewer is customizable. Contact your local IT manager for more details.

2.16.Integration with external image processing programs

The *TM-Reception HE* can be configured to integrate with external tools, such as orthopedic or 3D reconstruction programs.

Contact your IT manager to check for the availability of an extension for a specific program.

Once configured, images selected in the viewer are sent to the external program when selecting it in the [*Extension*] menu (only available if extensions are configured).

Such plug-ins are also available from the browser. They act on the selected series.

This program will perform some processing with the images and will return the result as a new viewer in the *TM-Reception HE*.

Exact interactions with the external program (deliver all images / only the selected images, include measures, image format etc.) depend on the integration configuration for this program.

Examples of integrated programs are Voxar, Orthoview and many post-processing programs developed locally at the hospitals.

2.17.M.P.R. Viewer

The MPR (Multi-Planar Reconstruction) image viewer is only available in the *TM-Reception HE* application. It is a window that displays a set of 2D images in a 3D MPR layout.

The orthogonal viewer possesses many functions of the classical Image Viewer, plus some 3D specific functions.

The **opening** of the MPR Viewer, its **description** and the list of the functions that are common with the Image Viewer are described in sections 2.17.1 to 2.17.3.

The MPR viewer shows images using different viewing modes. A summary is presented in section 2.17.4. Details will be available in sections 2.17.5 to 2.17.8.

The third dimension requires new methods to navigate into the study. Section 2.17.5.1 details this aspect.

3D image processing tools compute new views of the study using maximum computations or limiting the display area or displaying the study with different viewing angles. See section 2.17.5.2.2.

Finally, section 2.17.9 describes the options available in the orthogonal viewer to optimize the display or the measures.

2.17.1. Open/Close

Opening a viewer starts identically whether the viewer is classical or MPR.

The viewer associated with a series opens if the series is selected in the browser and either you press the 'Enter' key or you click on the 'Open' icon or you choose [*Document*] [*Open documents…*]. See section 1.5.1 page for more details.

In some situations, the MPR Viewer will directly start when you open the document. This will happen for *PET SCAN images* for example, or for other kinds of studies, depending on the 'Dependent display parameters' as explained in section 2.15.2 page .

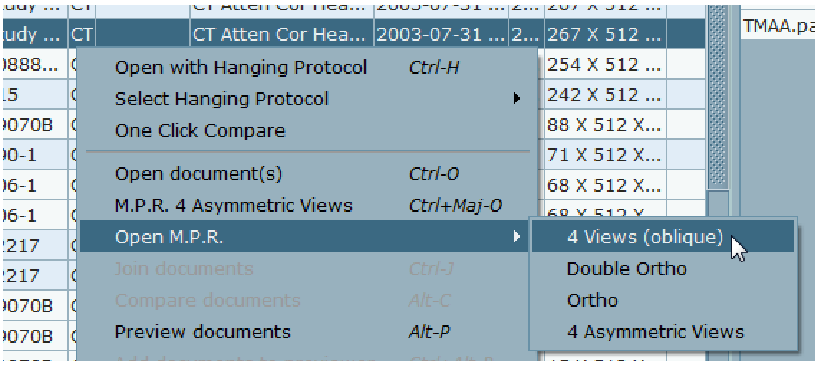
√ To force the opening of the MPR viewer using the default MPR layout,

- select the series in the browser and select the [*Document*] [*Open M.P.R. xxxx*] menu, or
- right-click on the line in the browser to show the context menu and select the [*Open M.P.R. xxxx*] menu item, or
- press the 'ctrl' , 'Shift' and 'o' keys together

where 'xxxx' is one of the M.P.R. layouts. See section 2.17.10.2 page to learn how to change the default M.P.R. layout.

√ To force the opening of the MPR viewer using a particular MPR layout,

- select the series in the browser, select the [*Document*] [*Open M.P.R.*] menu and select one of the MPR layouts, or
- right-click on the line in the browser to show the context menu, select the [*Open M.P.R.*] menu item and select one of the MPR layouts



To **close** the M.P.R. Image Viewer,

√ select [*File*] [*Exit*], or

√ click on the cross button at the top right of the window ( ), or

√ press the 'Backspace' key (the suppression key, just above the 'Enter' key).

2.17.2. Axial/Coronal/Sagittal

This section explains the basics of the multi-planar reconstructions, for the readers not experienced with this concept.

A representation of the Telemis MPR Image Viewer for a radiological study of the abdomen (CT scanner study) is given in Figure 195.

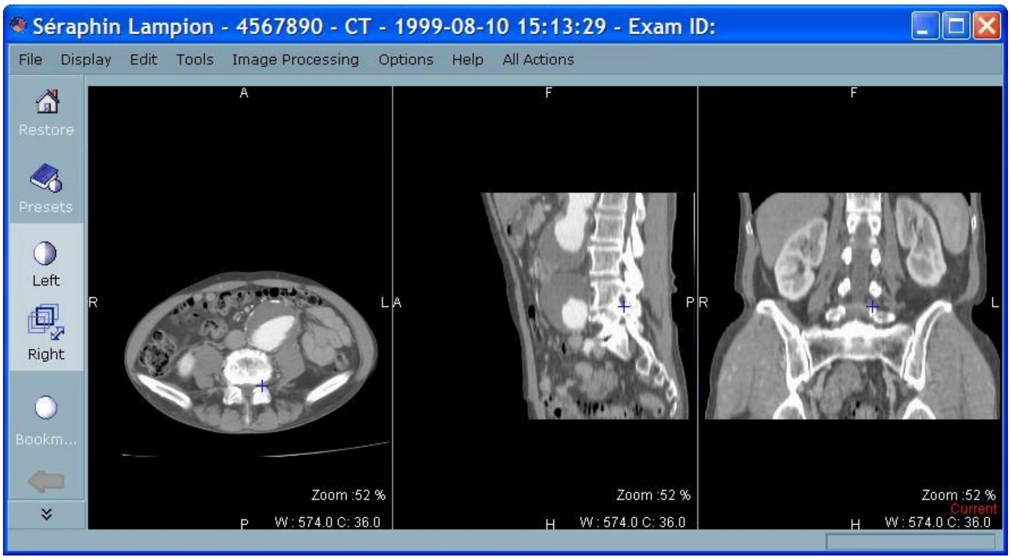


Figure 195 - Orthogonal Viewer for a CT study

The viewer shows three orthogonal views: the Axial, the Coronal and the Sagittal views. On Figure 196 the yellow plane is the axial plane (corresponding to coordinates X and Y), the red plane is the coronal plane (corresponding to the coordinates X and Z) and the blue plane is the sagittal one (Y and Z).

The Telemis MPR viewer receives a set of axial slices of the body and reconstructs the coronal and sagittal views on the fly.

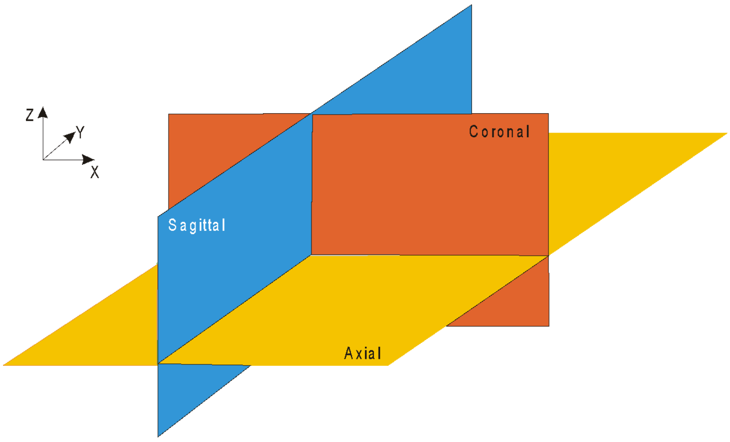


Figure 196 - 3D views: axial, coronal and sagittal

The 3D pointer drawn in the three viewers (a circle, an arrow or a cross, depending on your configuration) is the intersection of the three planes, or in other words is the coordinate used to generate the three views.

2.17.3. Tools common with the Image Viewer

Most of the classical tools of the Telemis Image Viewer are available in the Telemis MPR Image Viewer. Here follows a list of the tools.

- Display/Hide toolbars (see section 2.1.1 page);
- Text on screen (see section 2.4.2 page);
- Resize, Maximization and Screen positioning (see section 2.4.3 page);
- Comparison with the history of the patient (see section 2.9.9 page);

- Color and Brightness changing (see section 2.3.4 page). Manual changing with the mouse and automatic changing with presets are both available;
- Magnifier, zoom, mover (see sections 2.3.4.5 to 2.3.9 page);
- Color Look-Up Tables – CLUT (see section 2.3.10 page);
- Print (see section 2.8.4 page) and image exportation (see section 2.8.2 and 2.8.3 pages to).
- Filming (see section 2.8.8 page) is available through the [*File*] menu, the context menu or the space bar.

2.17.4. The different MPR layouts

The MPR viewer allows viewing series in different layouts.

Figure 197 shows an example of the some available layouts. They will be explained in the next sections.

We will describe in details the first layout, the Double Orthogonal layout in section 2.17.5. Following sections will describe the differences between a layout and the Double Orthogonal one.

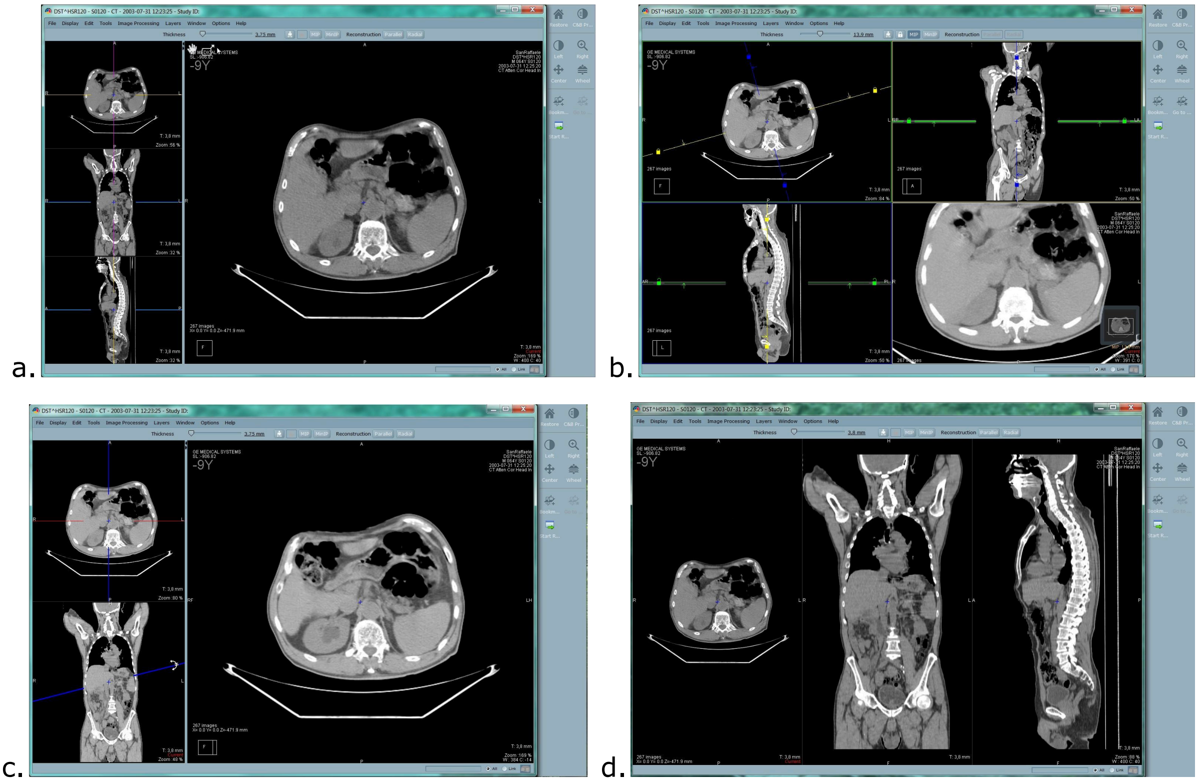

a. b. c. d.

Figure 197 - MPR layouts: a. 4 asymmetric views, b. 4 oblique viewers, c. Double orthogonal, d.Orthogonal, c.

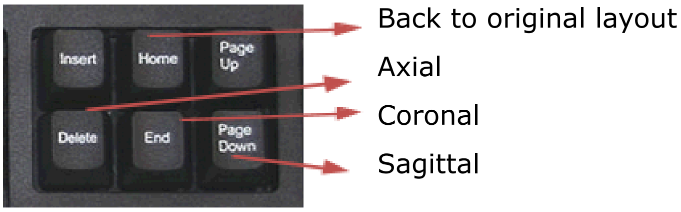
2.17.4.1. Open new MPR layouts

To open a new viewer with another MPR layout,

√ Select *[Display]* *[New MPR layout]* and select one of the available layouts

Some layouts show only one image orientation (axial, coronal, sagittal), some layouts contain 2 orientations, some add a MIP (see 2.14.2 page) view, some are more complex (see here under).

You can associate keyboard shortcuts to any of these actions (see section 1.16.2.4 page for associating keyboard shortcuts). Some are defined by default, such as Ctrl + Delete (Axial view), Ctrl + End (Coronal), Ctrl + Page down (Sagittal), Ctrl + Home (back to the original layout).



2.17.4.2. Switch between MPR layouts

To switch between MPR layouts without opening a new viewer,

√ Click on the button "Select MPR layout" located at the top right of the viewer. Select one of the layouts.

You can associate keyboard shortcuts to any of these actions (see section 1.16.2.4 page) for associating keyboard shortcuts). Some are defined by defaut, such as Delete (Axial view), End (Coronal), Page down (Sagittal), Home (back to the original layout).

You can also maximize one view by double-clicking or pressing the key 'F11' at any place in this view. Double-click or press 'F11' again to go back to the original layout.

2.17.5. Double Orthogonal viewing layout

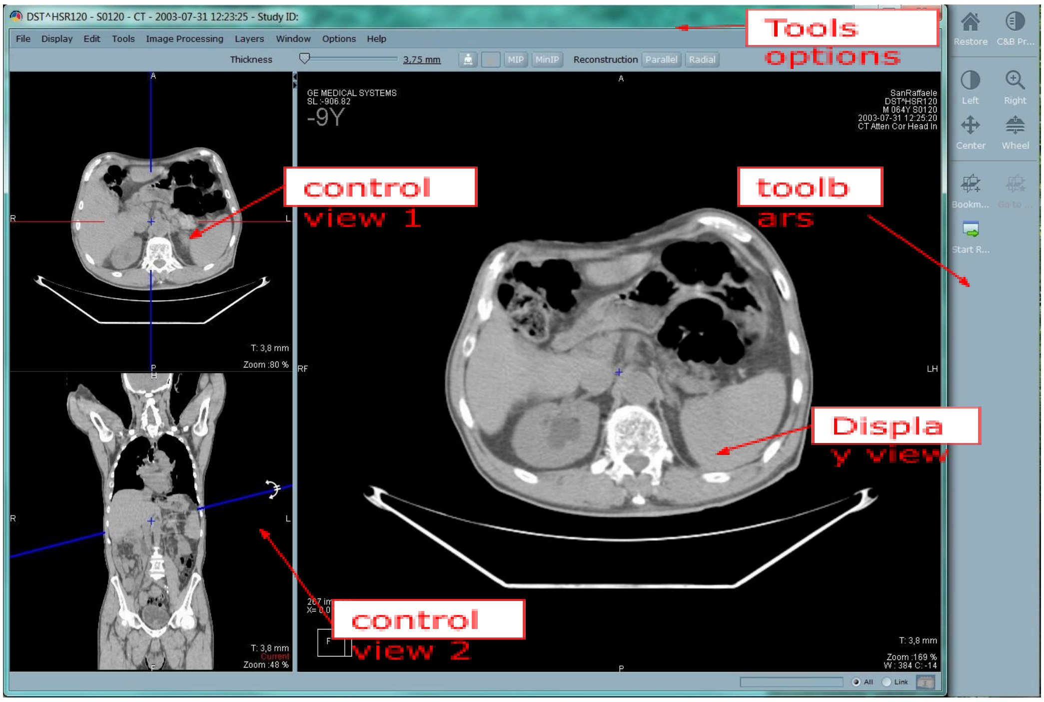


Figure 198 - Double Orthogonal MPR viewing layout

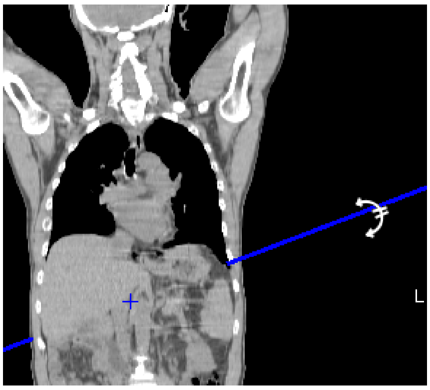
The screen is divided into several sections:

- The toolbars, with most of their tools common with the 2D image viewer

- The tools options bar, showing options of different tools, modifiable on-line during image manipulation
- The 2 control views, used to determine the intersection of the display plane with the 2 axial and coronal/sagittal planes
- The display view, showing the intersection of the display plane with both control images.

2.17.5.1. Image navigation

In this double orthogonal viewing layout, both control view will always remain perpendicular to the intersecting plane and are then subject to change in localization and orientation. Control view #1 and the display view are always perpendicular to control view #2.

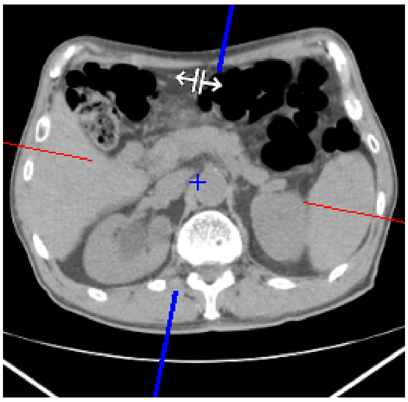


√ To change the **orientation of the intersection** of the plane with one of both control images, place the mouse near the extremity of the blue intersection line (the mouse cursor becomes a curved double arrow),

Click with the left mouse button and drag the mouse to change the orientation of this intersection.

The displayed view refreshes on-line.

√ Place the mouse near the center of the line (marked with a '+'), the mouse cursor becomes a fourfold arrow. Click with the leftist mouse button and drag the mouse to move the center of this intersection.



√ Place the mouse on the first half of the line. The cursor becomes a double arrow. Click with the left mouse button to move this plane parallel to itself.

The intersection orientation and center of the display plane with the axial control view may be changed the same way.

The blue line represents the intersection of the display view with both control views, while the red line represents the intersection of the control image #2 within the axial control image #1.

√

In the displayed view, you can change the intersection point with the control views by dragging the blue '+' marking this intersection point. Control views will be updated.

√ If the 'Orthogonal Pointer' is the tool associated with the leftist mouse button, click on any point of any view to change the position of this intersection point.

√ If the 'Navigation' is the tool associated with the leftist mouse button, click on any point of any view and drag the mouse up or down to navigate along slices parallel to this plane.

Three **presets** are available **to set a starting intersection**, giving an axial, coronal or sagittal displayed view.

√ If not selected yet, select for the rightist mouse button the context menu. Press the rightist mouse button in any of the 3 views to show a context menu.

√ Select in the context menu the [*MPR*] item and choose [*Axial*], [*Coronal*] or [*Sagittal*] in the sub-menu to set one of these presets.

At some point during the navigation, the user can set a '**Bookmark'**, to remember this particular location.

√ Press the 'bookmark' icon to mark the current intersection (location and orientation).

Continue navigating into the series.

√ Press the 'Go to bookmark' icon to display the intersection and orientation corresponding to the previously encoded bookmark.

2.17.5.2. Image display parameters

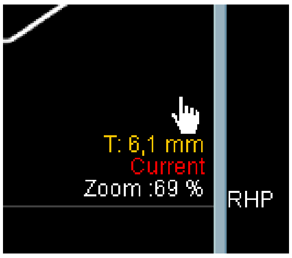
The way the image is constructed in the display view is managed by the options of the "tools option bar", located at the top of the viewer.

2.17.5.2.1. Average, Maximum or Minimum Intensity Projection

You can show in each viewer an image built using a bigger thickness than the original slide thickness. Several kinds of reconstructions are available.

By default, the thickening method computes the average of the pixel values.

The Intensity Projection is by default computed in the 'Current' view, i.e. the last view of the layout that has been clicked, the view containing at the bottom right the text 'Current'.



Press the 'whole body' button ( ) to compute the Intensity Projection on the whole body.

You can select precisely the Intensity Projection thickness by clicking on the thickness value (the orange "T: 6,1 mm" located at the bottom right of each Max/Min IP enabled image) and dragging the mouse up or down. Once activated, a click on the value will come back to the slice thickness (and deactivate MIP or MinIP option – see below).

You can also use the 'thickness' slider located at the left of the tools option bar, or click on the value displayed at the right of this slider to type a precise value. This will have an effect on the working view. The working view is different depending on the chosen MPR layout. For example in a 4 views asymmetric, it is the main view. In a 4 views (oblique), it is the current view.

√ Press the 'whole body' button to compute the Intensity Projection on the whole body.

√ Press the 'MIP' button to enable the **Maximum Intensity Projection** image construction instead of the average method.

√ Press the 'MinIP' button to enable the **Minimum Intensity Projection** image construction instead of the average method.

√ To apply the same Intensity Projection on all the views of the layout in one click, press the button 'Apply MIP values to all views', or press Alt + 'M'

Clicking again on one of these buttons to deactivate the MIP or MinIP.

Both control views show in addition to the blue intersection line, 2 green lines representing the thickness of this reconstruction.

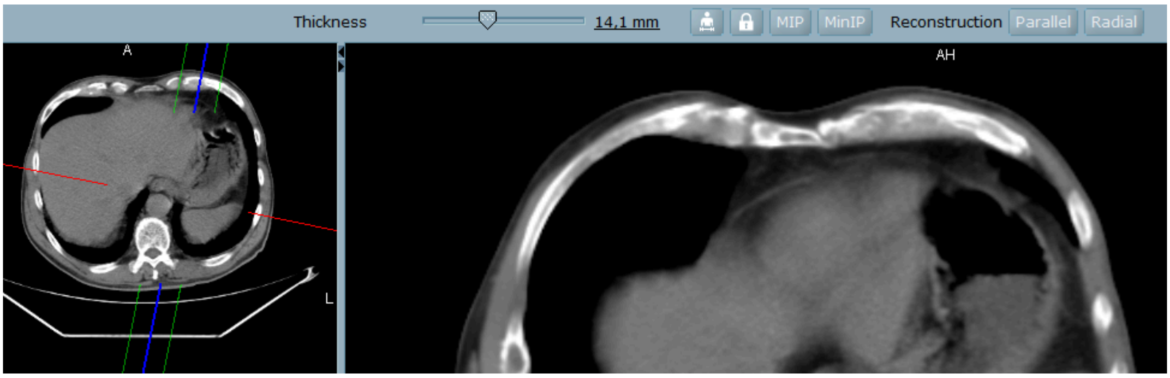


Figure 199 - MPR MIP reconstruction

If your computer is fast enough, you can press the button "Immediate MIP computation" located in the middle of the tools option bar. The MIP reconstructions will be performed in live during the navigation instead of navigating through normal images and only computing the MIP when the navigation ends.

2.17.5.2.2. Show / Hide the axis

By default, the axes are always shown in the different views of the MPR layouts.

√ You can hide or show the axes by clicking on the "Hide/Show axes" button located at the top right of the viewer, on press Ctrl + 'A'

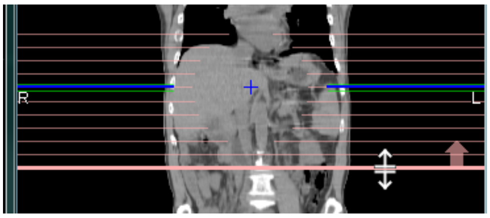
2.17.5.3. Series reconstruction

2.17.5.3.1. Parallel reconstruction

To start building a new series along a particular oblique plane, creating a set of parallel slices,

√ Press the 'Parallel' button located in the tools option bar.

Additional controls appear in this option bar as shown in Figure 200, to let you change the gap between each reconstructed image (use the 'Gap' slider or click on the value) and to change the global scope of the reconstruction (use the 'Scope' slider or click on the scope value). The number of images that will be reconstructed is shown at the right of the 'Gap' control.



You can also change the reconstruction scope using the mouse and the control views.

Move the mouse along one of the extremities of the reconstruction comb. The cursor becomes a double arrow. Drag the mouse to change the position of this extremity.

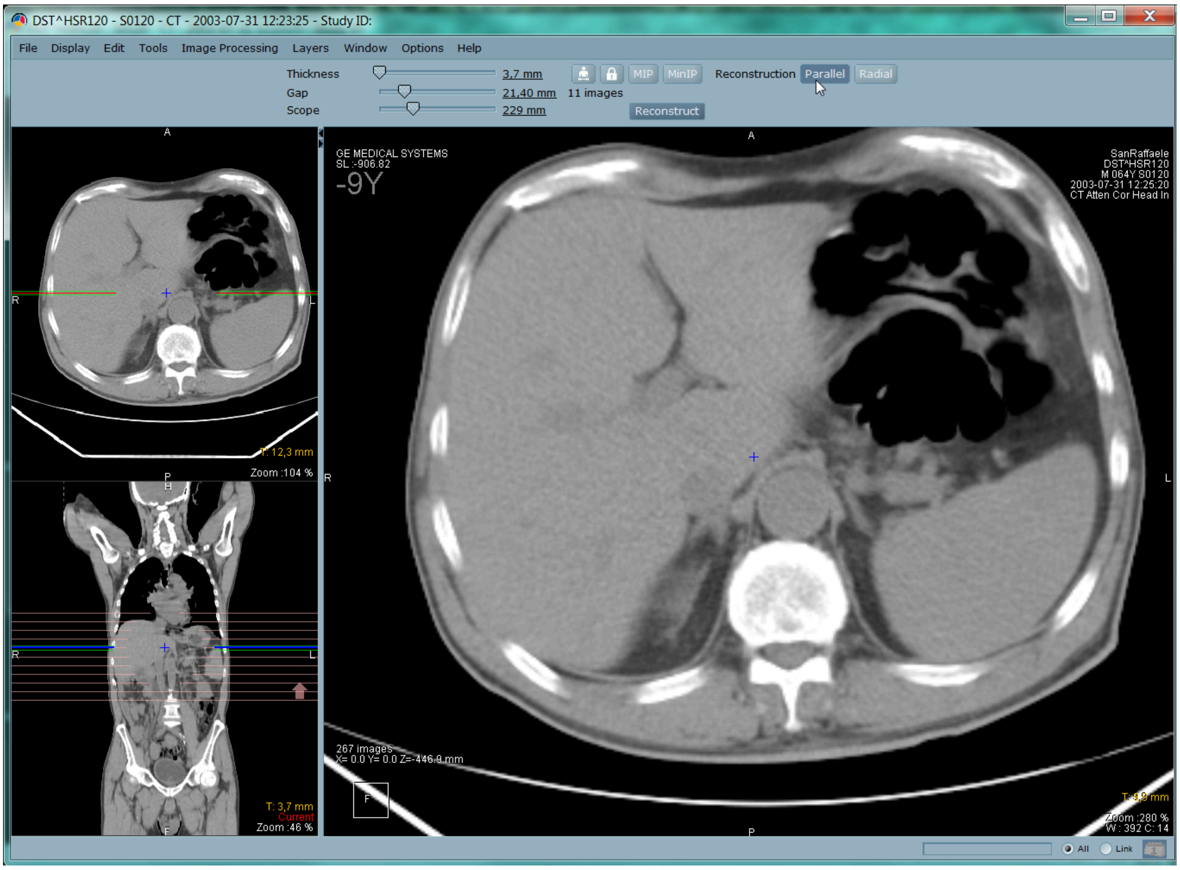
Move the mouse around the white line of the reconstruction comb and drag it to displace it. In the same way, the reconstruction comb can be rotated by placing the mouse on one the extremities of the white line and dragging it (mouse cursor will change to indicate a rotation). Please note that the reconstruction comb is always perpendicular to view that has been used to initialize the reconstruction. As a consequence, the rotation of the comb is also only possible in this view but the view itself can be rotated in the other views. Except for that, the reconstruction comb is independent of the visualization views.

Double-click on the 'reconstruction order' arrow ( ) to determine the reconstruction order: the arrow starts from the first reconstructed image to the last.

Finally, you can preview every reconstructed image in the display view (the big one) by clicking on any tooth of the comb: click on the pink line to let the display view show the reconstruction located at this position.

You can combine reconstructions and image thickness (MIP etc.) by changing the thickness in the reconstruction view.

√



DST^HSR120 - S0120 - CT - 2003-07-31 12:23:25 - Study ID:

Thickness 3,7 mm

Gap 21,40 mm 11 images

Scope 229 mm

Reconstruction Parallel

Figure 200 - MPR reconstruction parallel slices

√ Press the [Reconstruct] button to generate a new series that will be shown in a new viewer.

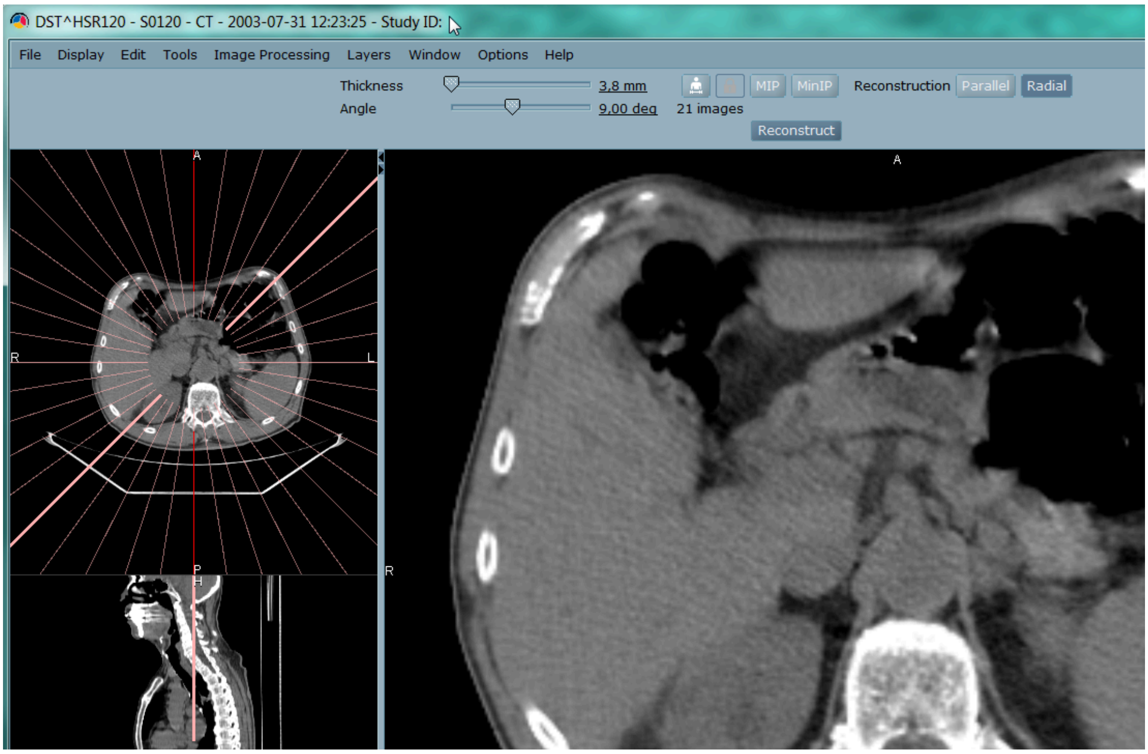
2.17.5.3.2. *Radial construction*

To start building a new series along a rotating plane, creating a new set of slices,

√ Press the 'Radial' button located in the tools option bar.

√

The "reconstruction MPR" option bar appears at the top of the viewer, as shown in Figure 201, and the control views show the reconstruction range.



DST^HSR120 - S0120 - CT - 2003-07-31 12:23:25 - Study ID:

Thickness 3.8 mm

Angle 9.00 deg

21 images

Figure 201 - MPR reconstruction radial slices

Use the 'Angle' slider or click on the angle value ('9.00 deg' in this example) to change the angle used to reconstruct. The pink lines are updated in the control views and the angle is changed in the option bar.

The number of images that will be created, depending on the scope and the gap, is displayed in this option bar.

Combine with the MIP options to change the thickness and reconstruction method of the slices.

Reconstructions will always occur in planes perpendicular to the displayed image. The center of the reconstruction will always be the 3D Pointer.

You can click on any of the radial pink line of the control view to show the corresponding reconstructed image in the display view.

√ Press the [Reconstruct] button to generate a new series that will be shown in a new viewer.

2.17.6. Orthogonal viewing layout

Figure 202 – Orthogonal MPR viewing layout

This is the simpliest MPR viewing layout.

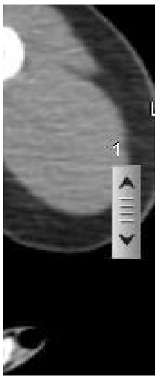
There are no specific control views but 3 views, one axial, one coronal and one sagittal.

2.17.6.1. Navigation

To navigate through the series,

Either drag the blue '+' marking the intersection between the 3 planes, or

- √ Select the 'Orthogonal Pointer' in the 'Left' mouse button, click on any point of any view to change the position of this intersection point. You can drag the mouse to move in live inside the series
- √ If the 'Navigation' is the tool associated with the leftist mouse button, click on any point of any view and drag the mouse up or down to navigate along slices parallel to this plane.
- √ To scroll all images upward or downward, move the mouse to the rightist part of the image. The scrolling tool appears. Click on this tool and hold the mouse button pressed. Move the tool upward or downward. The number indicated above the tool indicates the speed: "1" means slowest speed: all images are showed. Higher numbers (ex: 5) mean that the viewer will show one image each 5 (in this example) images. The speed is much higher but it'



2.17.6.2. Series reconstruction

Series reconstruction works nearly as for the Double Orthogonal viewing layout.

To select the plane along which the reconstruction must be done, click on one of the 3 views. A red 'Current' appears at the bottom right of the viewer.

Reconstruct a new series as explained in section 2.17.5.2.2 page .

2.17.7. Four asymmetric views viewing layout

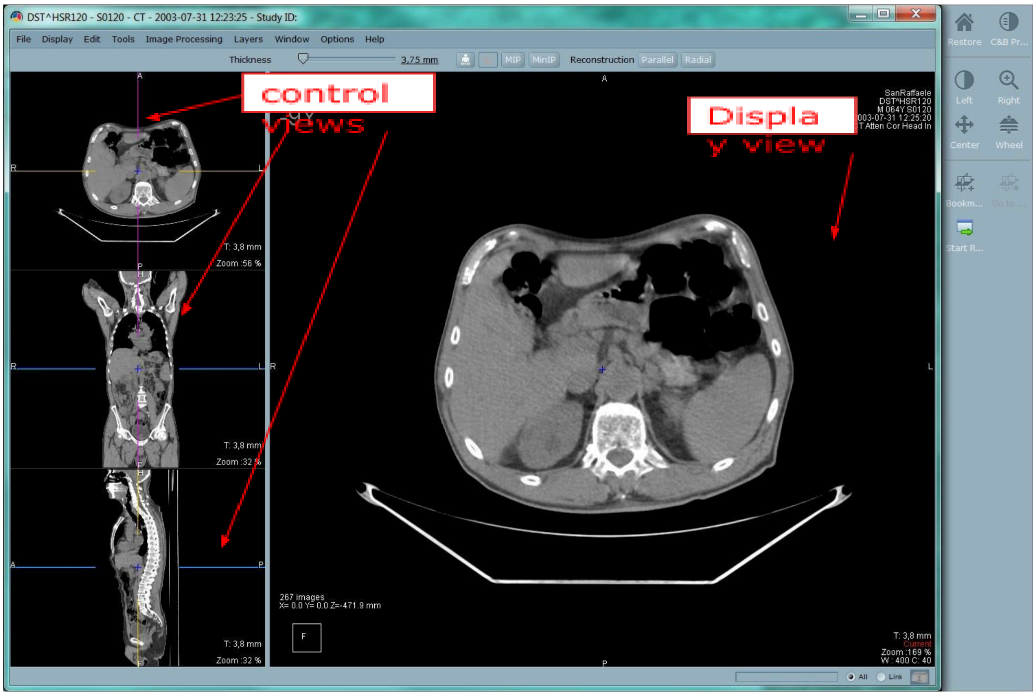


Figure 203 - MPR 4 asymmetric views viewing layout

This viewing layout contains 3 control views and one display view.

2.17.7.1. Image navigation

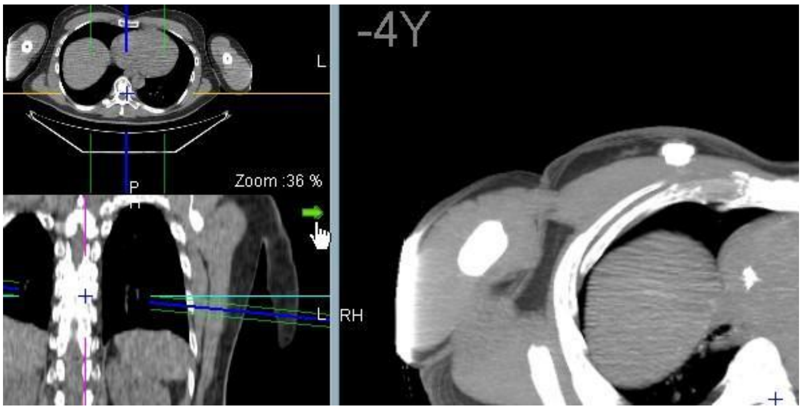
It is possible to change the center and orientation of the intersecting plane using the blue lines drawn in the 3 control views, as explained for the Double Orthogonal viewing layout in section 2.17.5.1. The image located on this intersecting plane in shown in the display view. The blue lines always mark the intersection of the display view into the different control views.

Additional lines are drawn on the control views, to show the mutual intersection of those control views.

- The first (axial) control view is surrounded with a cyan rectangle. The cyan line present on the 2 others control views mark their intersection with the axial view.
- The second control view is surrounded with an orange rectangle. Orange lines in the two other views mark their intersection.
- The third control view is surrounded with a pink rectangle. Pink lines in the two other views mark their intersection.

OrthoPointer, Navigation and Bookmark tools work as explained in section 2.17.5.1.

√ To reset the displayed view to one of the Axial, Coronal or Sagittal view, move the mouse to the top right of a control view and click on the green arrow that appears.



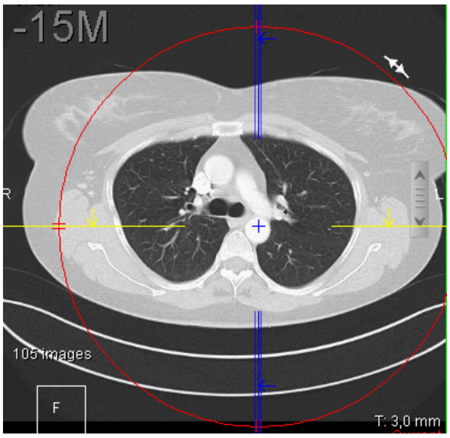
It’s also possible to rotate the images around any point.

√ Place the MPR pointer at the point that must be the center of the rotation.

√ Select the tool “Enable/Disable rotation” located at the top right of the MPR viewer, or press Ctrl + ‘R’.

√ Move the mouse in one view until a red circle appears centered on the MPR pointer and the cursor becomes a double arrow.

√ Press the mouse button and rotate the image.



2.17.7.2. Image display parameters

Maximum, Minimum and Average Intensity Projections work as explained in section 2.17.5.2.

2.17.7.3. Series reconstruction

Export MPR Parallel tool works as explained in section 2.17.5.2.2.

2.17.8. Triple oblique viewing layout

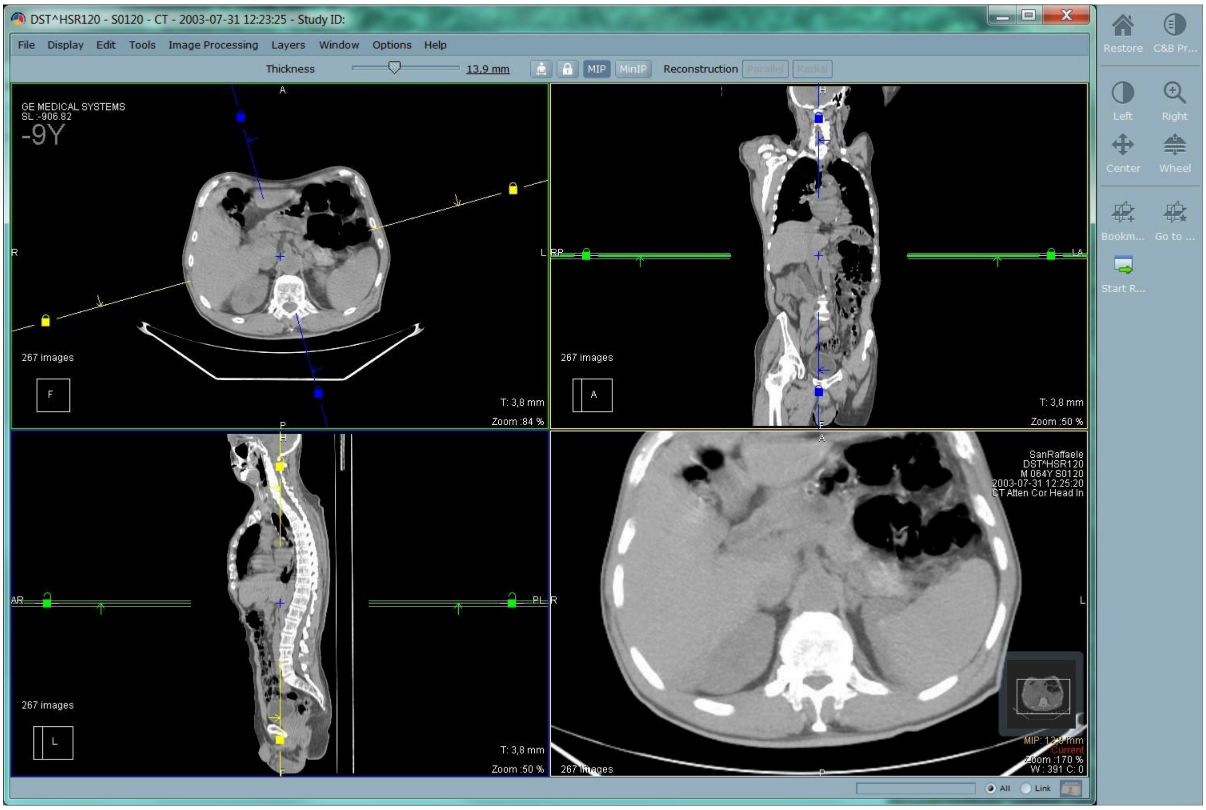


Figure 204 - MPR 4 oblique viewing layout

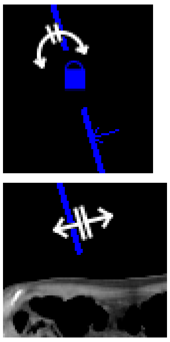
This viewing layout shows 3 main images plus the reconstruction object.

In this layout, each axis can move regardless of the other axis. You can lock or unlock the angle between the planes. This mode provides the most freedom for view adjustment.

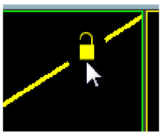
2.17.8.1. Image navigation

In this viewing layout, as in most MPR layouts, each view is surrounded by a colored rectangle. The other views show an intersection line, having the same color as the intersecting view (in this example, the blue line shown on both top views (shown in Figure 204) represent the intersection with the top left view, surrounded by a blue rectangle.

You can rotate or move each intersection axis as shown in section 2.17.5.1 page).



By default, the angle between the planes is locked. Rotating the blue plane in the top left view also rotates the yellow one. You can unlock both axes by clicking on the padlock located on the axis intersections.Click on the padlock located at the top of the viewer, or press Shift + ‘A’, to lock or unlock the angle between the planes.



OrthoPointer, Navigation and Bookmark tools work as explained in section 2.17.5.1.

2.17.8.2. Image display parameters

Maximum, Minimum and Average Intensity Projections work as explained in section 2.17.5.2.

2.17.8.3. Series reconstruction

Export MPR Parallel tool works as explained in section 2.17.5.2.2.

The reconstructed images are always shown in the bottom right view.

2.17.9. Tools common to all layouts

2.17.9.1. SUV measure

SUV (Standardized Uptake Values) intensity measures[16] are typical to nuclear medicine. The SUV tool is automatically activated when the MPR viewer shows PT images.

The SUV measure will only be available if the modality has been validated for the SUV measures. Contact your PACS manager if the SUV measure is not available for your PT scanner.

To compute the measure, simply move the Ortho pointer. The SUV value is shown at the bottom left of the image.

The result of the measure in the 20 mm diameter circle is displayed in the information line located at the bottom of the viewer.

The SUV measures the intensity of the pixels in the small circle, weighted by the injected dose, the rest/injection time and the weight of the patient. See section 2.17.10.4 for the definition of the parameters and the measure.

---

[16] The tool precision verification tests have given the following results:

Real value

Measured value

Acceptable limits

Urinary bladder

19.1

19.1

[18.9 – 19.3]

Liver

22.68

22.68

[22.48 – 22.88]

Three intensity measures are proposed:

- the maximum value inside the circle,
- the average value in the circle,
- the average value among the nine maximum values in the circle.

√ Choose the SUV type from either the [*Tools*] [*SUV Type …*] menu or by right clicking on the SUV value and select [*SUV Type …*]. Select [Maximum of the region], [Average of the region] or [Average of 9 maximums of the region].

√ You can associate the SUV tool with the left or right button of the mouse.

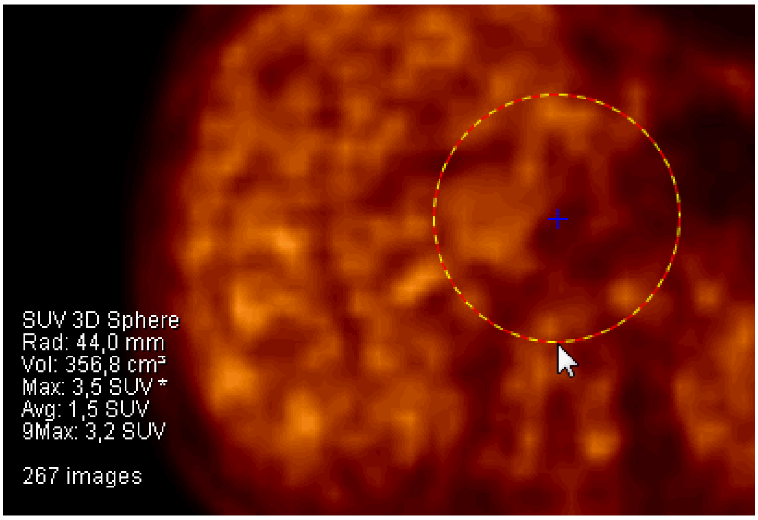
or

√ You can also select the 3d Pointer that will also show the SUV but not the circle.

On the lower left corner of the image, the SUV values are indicated: 2D or 3D, radius of the sphere, volume in cm³, the maximum, the average and the average of the 9 maximum values in the sphere).

√ Click on the circle and drag the mouse to change the circle's radius.

√ Right-click on the text to add the measure to the Measure Follow-up (see section 1.7 page) or to the Measure Manager (2.5.6.1 page).



SUV 3D Sphere
Rad: 44,0 mm
Vol: 356,8 cm³
Max: 3,5 SUV *
Avg: 1,5 SUV
9Max: 3,2 SUV

267 images

SUV measures are computed only if the needed data is available in the images (patient weight, radiopharmaceutical data, image must be 'attenuation corrected' …)

Note : Be careful with the values displayed in the lower left corner of the viewer. These values are related to the SUV pointer and the Ortho pointer. If you measure a ROI on a PT series, be careful to don't mix the values of the ROI (linked using an arrow to the ROI) and the value of the Orhto/SUV pointer (displayed on the lower left corner)!

2.17.9.2. Layout tools

For the double orthogonal and 4 asymmetrical views layouts, there is a "main" image and there are control images.

To change the orientation of the main image, move the mouse into one of the control images and press the little green arrow located at the top right of the image. This will select this orientation as the orientation of the main image.

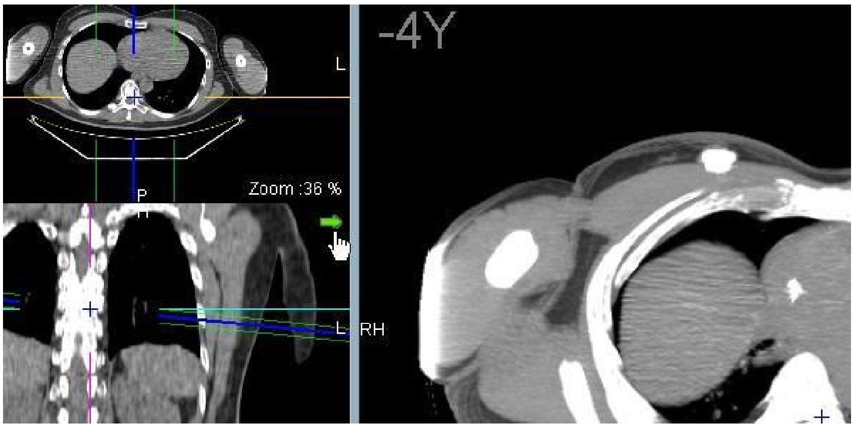


Figure 205 - change displayed image in MPR

For all views, to let one image occupy the full viewer size, move the mouse at the top left of the image and press the "Maximize the slice" button (☐).

To return the image to its original size, press again the button (☐).

Figure 206 - enlarge MPR current image

2.17.10. Options

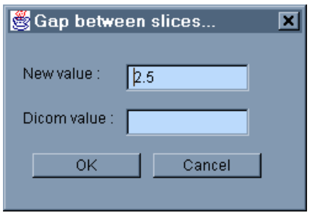
2.17.10.1. Cubic voxels

The correct 3D positioning of the images requires some DICOM fields to be filled in the images[17]. If those fields are not correct or empty, the *Z* positioning of the images is not correct. You can manually modify these values:

- √ select [*Image Processing*] [*Cubic Voxels*] in the menus of the Orthogonal Viewer.
- √ In the window that will appear, fill in the '*New value*' text box with the spacing in millimeters along the *Z* axis (vertical) between each image (see Figure 207). This value will allow the viewer to correctly position the images along the third axis. The DICOM value is given for reference.

---

[17] The 'GapBetweenSlices' field contains the number of millimeters between each image. If this field is not correctly filled, Telemis Orthogonal Image Viewer tries to use the 'SliceLocalization' DICOM parameter to find the *Z* localisation of each image.



New value : 2.5

Dicom value :

Figure 207 - Gap Between Slices

The schematic explanation of the meaning of the 'Gap between slices' value is given in Figure 208.

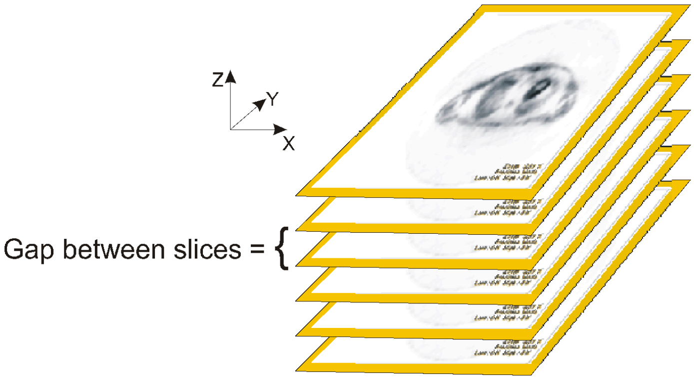


Figure 208 - Gap between slices : schema

To revert to the original values for the 'gap between slices',

- √ select [*Image Processing*] [*auto Cubic Voxels*] in the menus of the Orthogonal Viewer.

2.17.10.2. Invert image stack

Some acquisition machine will sometimes produce images in the reverse order: from feet to head instead of from head to feet. The orthogonal viewer relies on the images order to display them and will then also display the patient feet over the head.

- √ To invert the images order, select [*Image Processing*] [*Invert image stack*].

2.17.10.3. Changing the default MPR layout

Open the viewer options:

- √ From the browser, select [*Options*] [*Browser options*] and press the [Viewer] tab
- √ From the viewer, select [*Options*] [*Viewer options*]

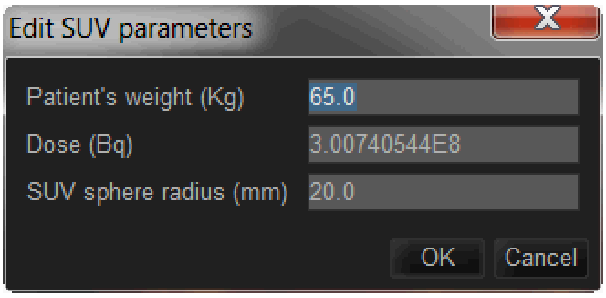
Select the default MPR layout desired in the "Default M.P.R. Layout" combo box. Select "Classic" for the MPR layout as available up to version 3.90 (best for NM et PT studies), or one of the "Double Ortho", "Ortho", "4 asymmetric views", "Double oblique" layouts.

2.17.10.4. SUV parameters

The activity concentrations provided by the PET scanner are transformed into standardized concentration values called SUVs (Standardized Uptake Values). The SUVs are normalized activity concentrations values for the dose applied and the body volume. As these uptake values can be affected by other parameters, the measured uptake value was corrected, if necessary, by dividing with a calibration factor. The SUV calculated is a non-dimensional parameter which characterizes the distribution of a substance. In the case of even distribution of this substance over the entire body, the SUV=1; accumulation in certain regions, that exceeds the mean concentration leads to SUVs greater than 1.

√ To edit the SUV parameters, select [*Tools*] [*Edit SUV parameters*].

The window depicted in Figure 209 allows you to modify these parameters.



Patient's weight (Kg) 65.0
Dose (Bq) 3.00740544E8
SUV sphere radius (mm) 20.0

Figure 209 - SUV parameters

The last value is the size of the circle used to measure the SUV value. This size is expressed in mm.

2.18. Video viewer

Since version 4.10, TMR and TMRHE contain an imbedded video player.

Opening a video is as simple as opening another series, as explained in section 1.5.1 page .

2.18.1. The video player

The video player is depicted on Figure 210.

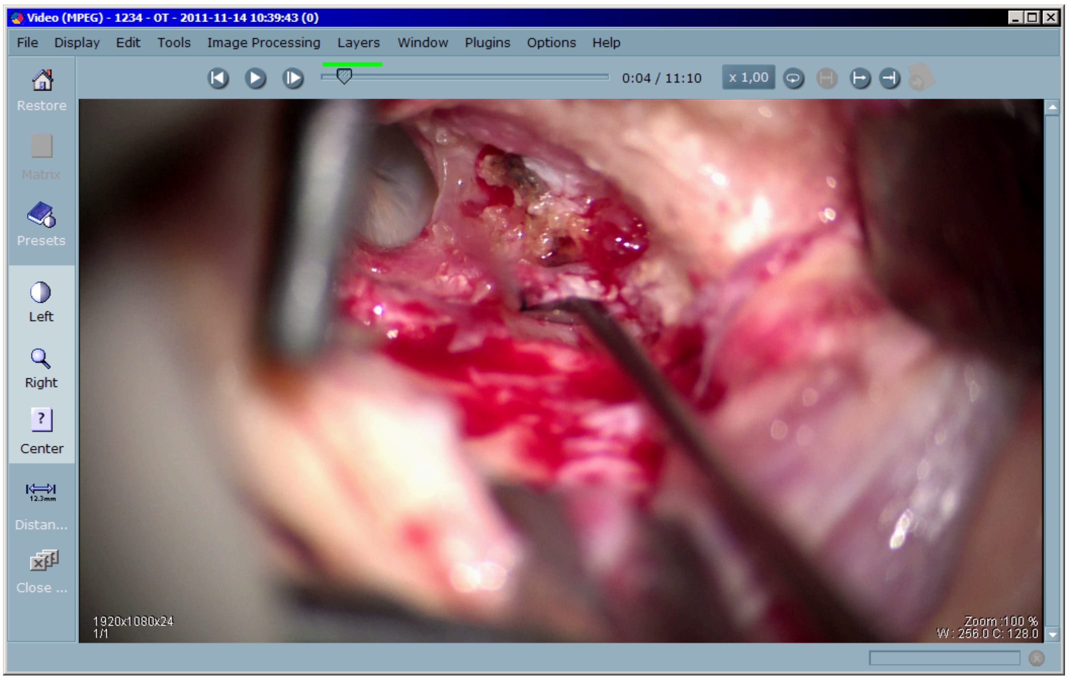


Figure 210 - video player

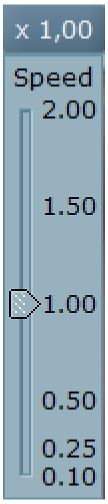
The following table presents the different commands available for controlling the video player:

▶	Play	Play the video
⏸	Pause	Pause the video
⏮	Restart	Go to the beginning of the video
⏭	Next	Go to next image
🔁	Loop mode	When the video reaches the end, it restarts automatically
↔	Subsequence mode	Play only the current subsequence (see the sub-sequence section)
↦	Subsequence start	Set start of subsequence (see the sub-sequence section)
⇥	Subsequence end	Set end of subsequence (see the sub-sequence section)
📄	Export	Export the subsequence to the PACS (see the sub-sequence section)

The player progression is displayed in the slider as shown below:

Note: the green bar represents the progress of the video download and is hidden when the download is completed.

The playing speed can be controlled using the button next to the slider indicating the current speed factor:



Note: the speed at which the video can be played depends on the computer power. For example, all computers cannot play a HD movie at twice the speed.

Some of the tools available in other viewers are also present in the video player such as measures, lines, texts, … In the same way, the filmer and drag and drop functionality are supported. This allows easy exportations of video still images that can be annotated with text and graphics.

2.18.2. Working with subsequences

Subsequences allow you to select time limited sequences of interest. This allows to

Only play the subsequence using the subsequence mode button

Export only the subsequence and import it to the PACS

To define a subsequence, play the video or move the slider to the start position and press the subsequence start button:

Then play the video or move the slider until the desired end and press the subsequence end button:

Note: the start and end of subsequence can be changed later by using the same buttons again.

Once a subsequence is defined, a white bar under the slider is displayed as shown in the following picture:

To play only the subsequence, press the subsequence mode button:

Finally, you can export the subsequence to the PACS as a bundle by using the "Export selection" button:

The exported subsequence is then imported as a new document in the PACS.

3. DICOM COMMANDS

The *TM-Reception HE* contains some commands that manage the DICOM format:

- direct query/retrieve a PACS, a modality or a DICOM workstation;
- use the “DICOM Send” protocol to directly send images to a workstation;
- export images in DICOM to create and save on disk DICOM files for some images;
- DICOM directory structure (“DICOM_DIR”) viewer.

The DICOM functions are not available on every *TM-Reception HE*. Contact your local IT manager if you need these functions on your program and can’t find them.

3.1. Query/Retrieve

To launch the Query/Retrieve functionality,

√ select [*Network*] [*Query/Retrieve*] in the menus of the Browser.

The window depicted in Figure 211 appears. The five fields on the bottom on the window contain the values of the DICOM Query/Retrieve transaction. The first field describes your machine. You will query the ‘Database’ (the three following fields) and send the result of the query to the ‘Destination’ (the last field). This *TM-Reception HE* and the destination must be known by the database: the AE_TITLEs must be sufficient for the database to completely know the sender of the request (your TMR-HE) and to which entity the results must be sent.

You can for example query a PACS and send the results to the *TM-Auto-Acquisition* program that will automatically create a Telemis document with the resulting images and send this document to the *TM-Server*.

√ Select a preset from the list in the window. If you click on an element of the list, the IP, port and AE Titles text fields display the values for this preset.

√ Click on the *Send* button to use these DICOM Query/Retrieve parameters.

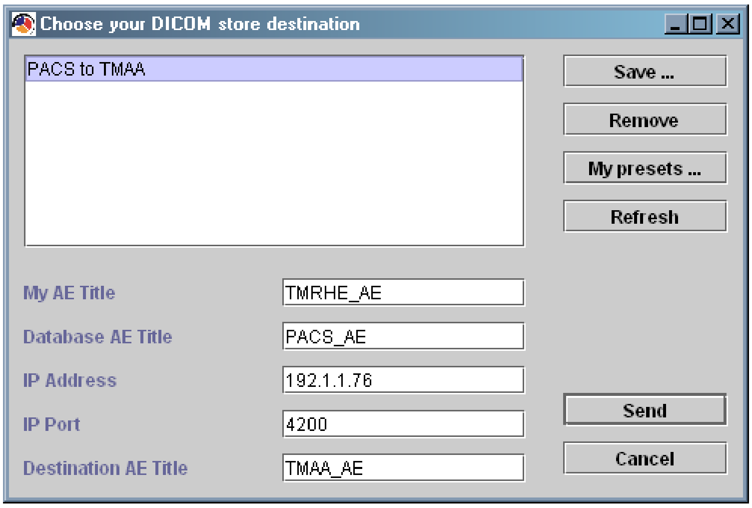
√ You can manually enter values in the text fields, and click on *Send* to use these values.

√ If a set of values is of importance to you, you can save it. Click on the *Save* button to save it under the name that you will give. This new preset is saved on your profile.

√ To update the list with all the presets that are present in your profile, click on the *My presets* button.

√ To remove a preset from your profile, click on the line containing the preset in the list and then on the *Remove* button.

√ Click on the *Cancel* button to exit the window without query/retrieving any DICOM entity.



PACS to TMAA

My AE Title: TMRHE_AE
Database AE Title: PACS_AE
IP Address: 192.1.1.76
IP Port: 4200
Destination AE Title: TMAA_AE

Figure 211 - Chose the DICOM store destination

If no preset is available in the list, contact your local IT manager for a proper configuration of the addresses and AE Titles.

After pressing the 'Send' button, the query/retrieve window appears, as in Figure 212.

√ Fill one or more fields in the search criteria box: patient name, patient ID, accession number (i.e. the DICOM synonym for 'examination identification number'), acquisition date and modality. If there is a series, study or patient selected in the browser before launching the Query/Retrieve, the "patient ID", "accession number", "date" and "modality" fields are automatically filled, if available.

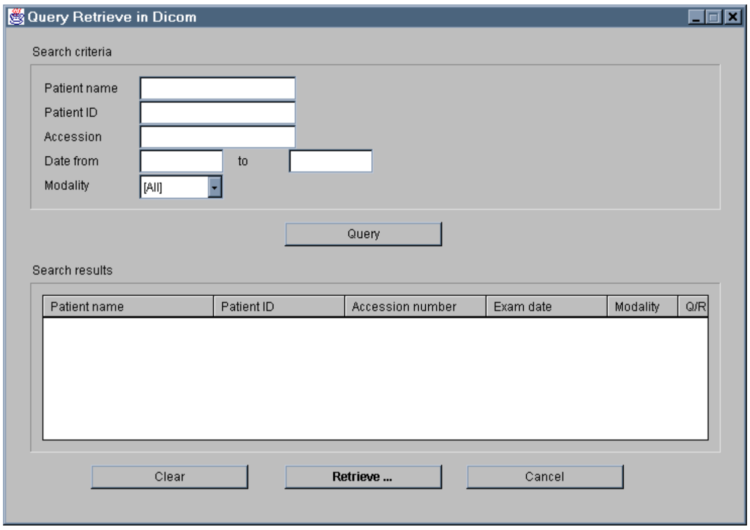
√ Click on the *Query* button to query the 'database' for these studies.

The list of studies matching this query is displayed in the table. Click on any column header to sort the table according to this column.

Click on the *Clear* button to clear the search fields and possibly start a new search.

√ Click on the line displaying a study to select it. Click on the *Retrieve* button to send this study to the 'destination' DICOM entity.

Click on the *Cancel* button to close this window and cancel this Query/Retrieve operation.



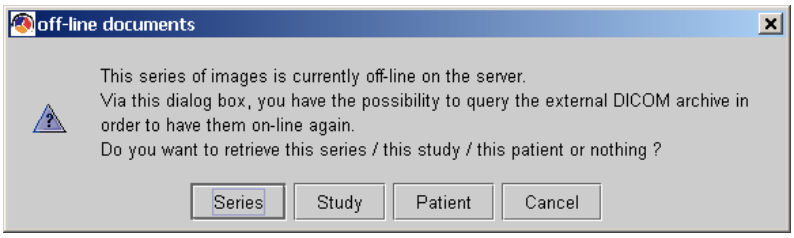
Modality: [All]

Patient name	Patient ID	Accession number	Exam date	Modality	Q/R

Figure 212 - DICOM Query/Retrieve window

3.1.1. External DICOM archive

If your hospital is equipped with an external DICOM archive, the Telemis Server will be configured to propose you to automatically retrieve images if not available anymore on the Telemis Server. Images will be retrieved for the patient, the study, or one series, as show on Figure 213 an will be on-line again a few minutes after the retrieval.



This series of images is currently off-line on the server.
Via this dialog box, you have the possibility to query the external DICOM archive in order to have them on-line again.
Do you want to retrieve this series / this study / this patient or nothing ?

Figure 213 - retrieval of off-line documents via an external DICOM archive

3.2. DICOM export

3.2.1. In the Viewer

From the Image Viewer of a *TM-Reception HE*, you can export images in the JPEG and other bitmap formats but also as DICOM files.

The method is exactly the same as a bitmap exportation from a viewer.

Open a viewer for a study, as explained in section 1.5.1 page .

Follow the exportation procedure exactly as explained in section 2.8.2 page but select *DICOM* instead of *BMP* in the 'format of the export' drop box of the exportation window.

Keep in mind that the drawings and measures will only be partially exported. If you answer 'Yes' to the question "Export the overlay drawn on the examination ?", the overlays except the ones with texts (for example measures) will be added to the DICOM images as DICOM curves.

To include all the overlays in the exported images, you must burn them into the images as described in section 2.5.6.6 page .

3.2.2. In the Browser

To export a set of Telemis Documents using the DICOM format, into a specified directory, it is not necessary to open systematically a viewer and perform the DICOM exportation as explained in section 3.2.1.

In the Browser, select a set of documents (see sections 1.3.4.2 and 1.3.5.2 pages and for the selection of studies and series).

√ Select *[Document] [Export document(s) in DICOM …]*

Chose the path where the DICOM files will be created and press 'Save'.

For each document selected, the *TM-Reception HE* will if needed download it from the *TM-Server*, and then create one DICOM file for each image of the document, using the default display options for this kind of study. The information line at the bottom of the viewer displays the progress of the exportation (example: "Exporting documents in DICOM 5/15 (downloading document)" if, for the 5th document among the 15 documents selected, the *TM-Reception HE* downloads the document from the *TM-Server*).

To export only some images, change the display parameters … before exporting, chose to export via the Viewe

3.3. DICOM send

To send some images in the DICOM format to a workstation, it is possible to export some images as DICOM files in a directory, then share it with the workstation or send those DICOM files to the workstation via any communication channel (ftp protocol, Email, file copy …) and finally to open these files on the workstation.

The use of the "DICOM send" protocol is much easier: the *TM-Reception HE* will directly use the *DICOM send* protocol to communicate with the workstation and will send the selected images in one click. No more files to write on disk, no more files to copy.

3.3.1. In the Viewer

To send in DICOM some selected images of a series, perform this operation from the viewer.

Open a viewer for a series, as explained in section 1.5.1 page .

Select some images as explained in section 2.3.2 page if you don't want to send all the images of the study.

√ Select [*File*] [*Send in DICOM*] to open the DICOM send controller window shown in Figure 214.

The four fields on the bottom on the window contain the values of the *DICOM Send* transaction. The first field describes your machine. The images will be sent to the 'Destination' machine (the last three fields).

√ Click on an element of the list to select a preset: the IP and AE Titles text fields display the values of this preset.

√ Click on the *Send* button to use this *DICOM Send* parameters.

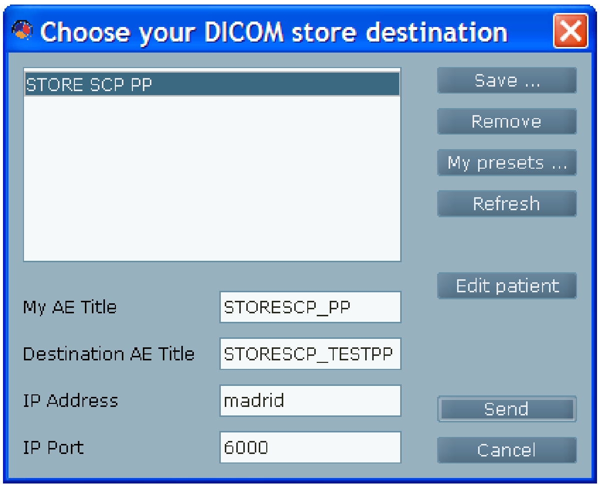
√ You can manually enter values in the text fields, and click on *Send* to use these values.

√ If a set of values is of importance to you, you can save it. Click on the *Save* button to save it under the name that you will give. This new preset is saved on your profile.

√ To update the list with all the presets that are present on your profile, click on the *My presets* button.

√ You can remove a preset from your profile if you click on the line containing the preset in the list and then on the *Remove* button.

Click on the *Cancel* button to exit the window and cancel the *DICOM Send* operation.



STORE SCP PP

My AE Title: STORESCP_PP

Destination AE Title: STORESCP_TESTPP

IP Address: madrid

IP Port: 6000

Figure 214 - DICOM Send window

3.3.2. In the Browser

To send in DICOM all the images of a set of Telemis Documents, it is not necessary to open systematically a viewer and perform the DICOM send as explained in section 3.3.1.

In the Browser, select a set of documents (see sections 1.3.4.2 and 1.3.5.2 pages and for the selection of documents).

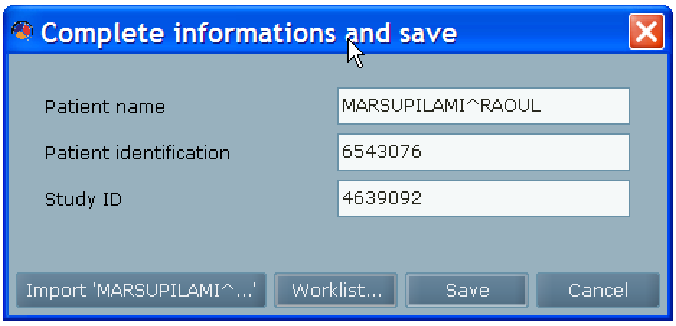
√ Select [Document] [Send document(s) in DICOM …]

The DICOM send window depicted in Figure 214 opens. Follow the instructions given in section 3.3.1 to perform the DICOM send, create a destination preset …

3.3.3. Update the patient and study information

If called from the browser, an additional feature is available before the DICOM Send: the 'Edit patient' functionality.

Press the [Edit Patient] button located in the middle right of the dialog box.



Patient name: MARSUPILAMI^RAOUL

Patient identification: 6543076

Study ID: 4639092

Figure 215 - Edit patient information before a DICOM Send

Update the patient name, patient identification and study identification manually, or press the [Worklist] button if available in your hospital (contact you local IT manager if you desire this functionality).

Press [Save] or [Cancel] to save this modification or cancel it.

This functionality is very convenient to anonymize a patient before a transfer: change its name and id by the given coded name and id, and DICOM Send then to the destination.

3.3.4. Logs

Each DICOM Send is logged, as explained in section 1.8.8 page .

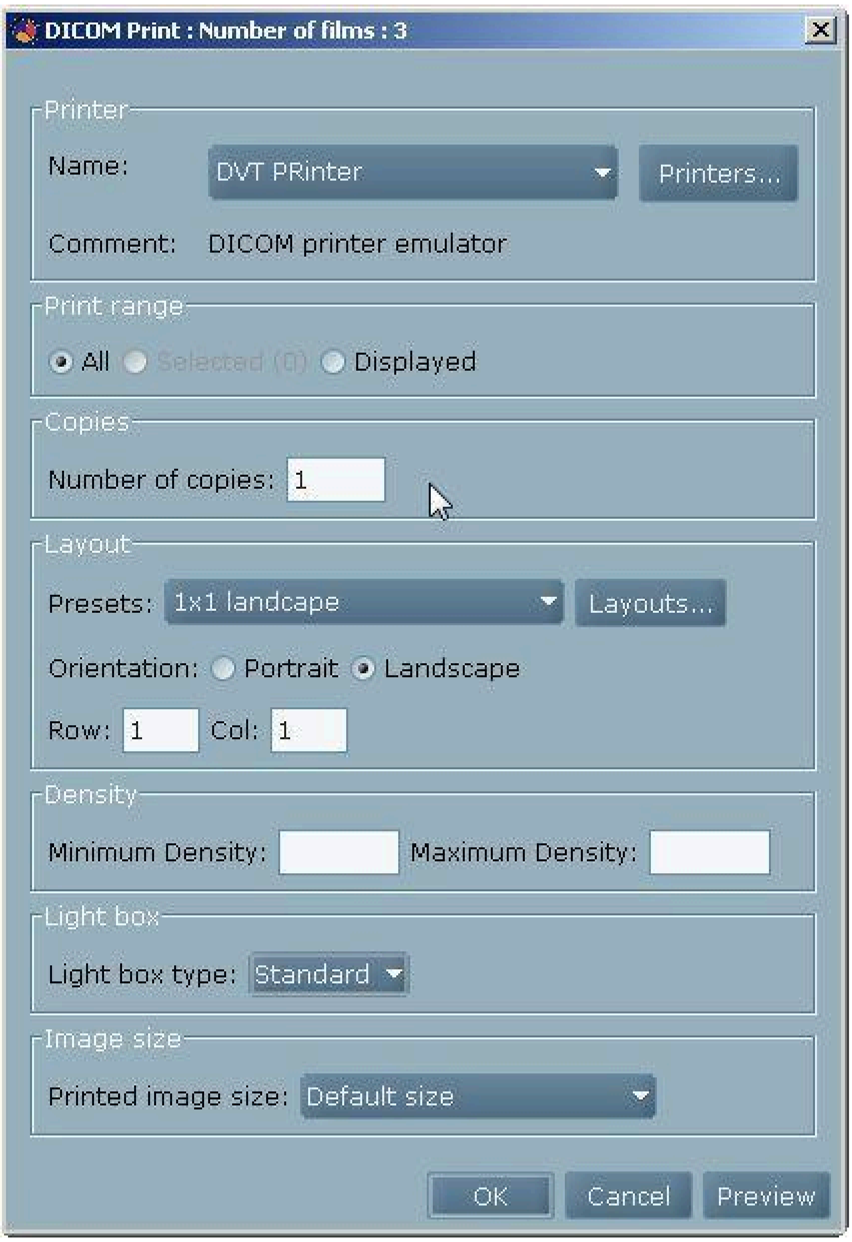
3.4. DICOM Print on film

3.4.1. Print

To print images on a DICOM printer, using the "DICOM Print" protocol, open a viewer with the images to be printed and

√ Select [*File*] [*Print on film …*].

The main 'DICOM printer' window appears (see Figure 216).



DICOM Print : Number of films : 3

Printer

Name: DVT PRinter

Comment: DICOM printer emulator

Print range

● All ○ Selected (0) ○ Displayed

Copies

Number of copies: 1

Layout

Presets: 1x1 landcape

Orientation: ○ Portrait ● Landscape

Row: 1 Col: 1

Density

Minimum Density: Maximum Density:

Light box

Light box type: Standard

Image size

Printed image size: Default size

Figure 216 - DICOM print

In the 'Printer' box, select the destination printer.

Select the 'Print range':

- All the images of the viewer
- The selected images (this button is disabled if there is no selection)
- Only the images displayed

Select the number of copies to be printed.

Select the layout:

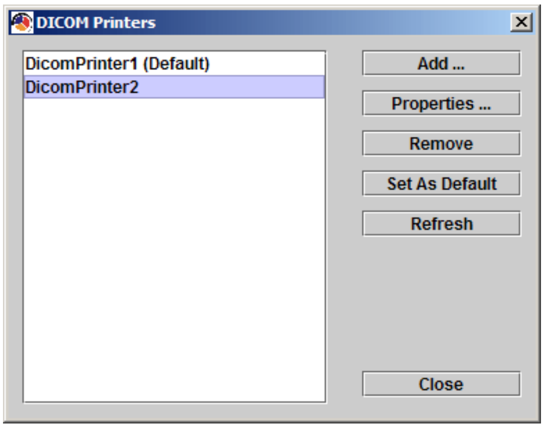
- page orientation: portrait (vertical page) or landscape (horizontal page)
- Number of rows and columns.

Select the print density, the light box type and the image size (either the default size or force the real size (force to the maximum resolution of the printer)).

Press ‘OK’ to start printing. A progress bar will display the printing progress.

3.4.2. Configuration

To change the parameters of a DICOM printer, or to parameterize new one, press the ‘Printers …’ button. The printer management window appears (see Figure 217).



DicomPrinter1 (Default)
DicomPrinter2

Figure 217 - DICOM printer management window

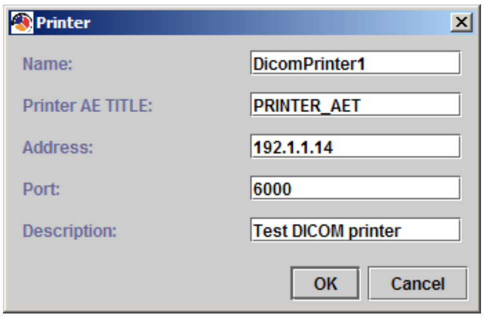
Select a printer.

Press ‘Remove’ to remove the printer.

Press ‘Set as default’ to set it as the default printer

Press on ‘Properties …’ to change the properties of this printer. The DICOM printer configuration window appears (see Figure 218).

Press on ‘Add …’ to create a new printer. The DICOM printer configuration window appears (see Figure 218).



Name: DicomPrinter1
Printer AE TITLE: PRINTER_AET
Address: 192.1.1.14
Port: 6000
Description: Test DICOM printer

Figure 218 - DICOM printer configuration window

The name is the text string that appears in the list of printer of the DICOM print window.

The AE_TITLE (a ‘DICOM’ name for the printer), the IP address and the Port are parameters of the printer and must be given by the manufacturer of your local IT manager.

The description is the text string that appears below the printer name in the DICOM print window.

3.5. Display DICOM Image info

For the very advanced users, you can have complete information about the DICOM images. This option has no meaning for non-DICOM images.

To open the DICOM info window:

√ select [*Help*] [*Display DICOM info ...*].

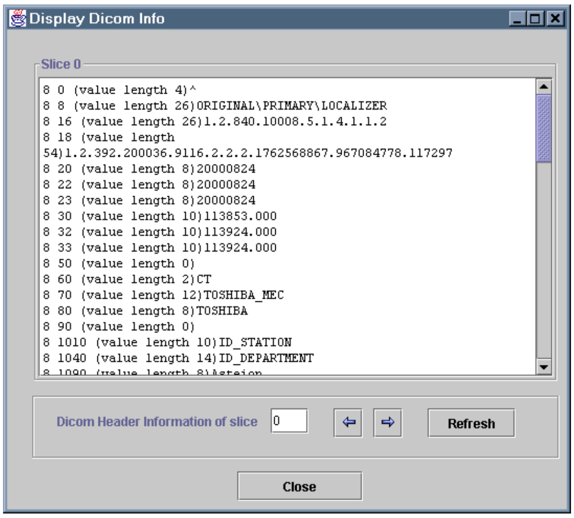
This window gives for each image of the study the complete information contained in the DICOM header.

Each line contains the DICOM group and subgroup, the length of the value contained in the field and the content of the field.

Click on the arrows to display the DICOM information for the next or previous images.

Enter a number in the text box and click on the *Refresh* button to go directly to a specific image.

Click on the *Close* button to close the window.



```
8 0 (value length 4)^
8 8 (value length 26)ORIGINAL\PRIMARY\LOCALIZER
8 16 (value length 26)1.2.840.10008.5.1.4.1.1.2
8 18 (value length
54)1.2.392.200036.9116.2.2.2.1762568867.967084778.117297
8 20 (value length 8)20000824
8 22 (value length 8)20000824
8 23 (value length 8)20000824
8 30 (value length 10)113853.000
8 32 (value length 10)113924.000
8 33 (value length 10)113924.000
8 50 (value length 0)
8 60 (value length 2)CT
8 70 (value length 12)TOSHIBA_MEC
8 80 (value length 8)TOSHIBA
8 90 (value length 0)
8 1010 (value length 10)ID_STATION
8 1040 (value length 14)ID_DEPARTMENT
8 1090 (value length 8)Asteion
```

Dicom Header Information of slice: 0

Figure 219 - DICOM information panel

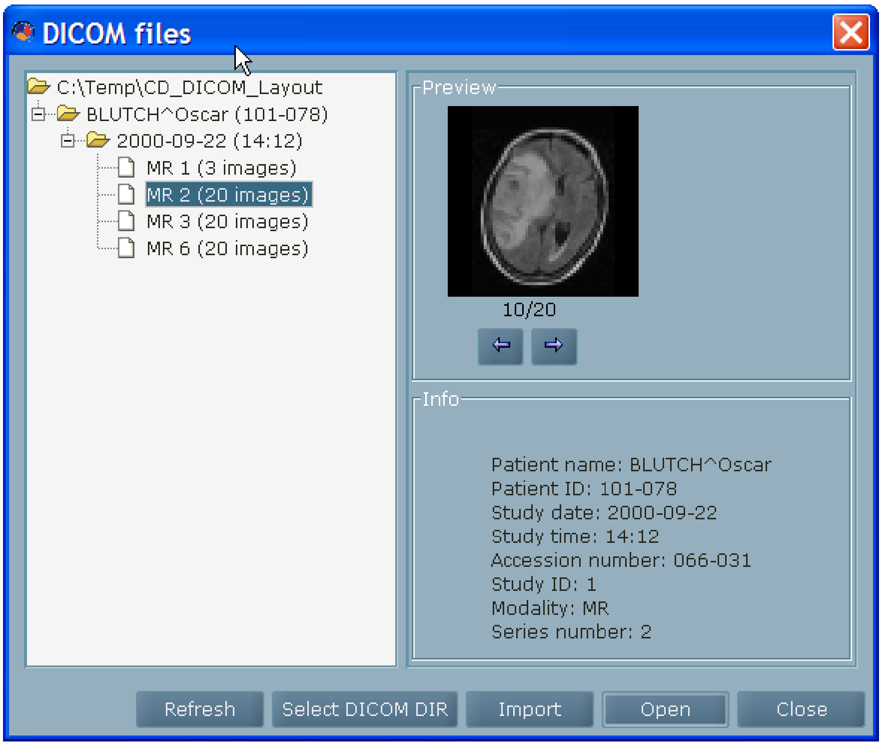
3.6. Display the content of a DICOM DIR

When receiving a CD containing DICOM images described by a DICOM DIR, the *TM-Reception HE* will help selecting the right images to visualize.

√ Select [*Local*] [*Import DICOM CD / Files …*]

The first time this function is used, *TM-Reception HE* prompts for the directory where the “DICOM-DIR” file is located. Select your CD Drive and answer ‘Yes’ to the “Do you want to keep this location as the default DICOM DIR path” question.

In the “Images” tree of Figure 220, select the information desired.



C:\Temp\CD_DICOM_Layout
BLUTCH^Oscar (101-078)
2000-09-22 (14:12)
MR 1 (3 images)
MR 2 (20 images)
MR 3 (20 images)
MR 6 (20 images)

Patient name: BLUTCH^Oscar
Patient ID: 101-078
Study date: 2000-09-22
Study time: 14:12
Accession number: 066-031
Study ID: 1
Modality: MR
Series number: 2

Figure 220 - DICOMDIR importation

For each series selected in the "Images" tree, the "Preview" and "Info" panels show the images (in low quality) and some information about this series.

- In the Preview panel, click on the arrows to show the different (low quality) images of the series.
- In the Info panel, the patient name, study date, time and ID and the modality are shown.

√ Click on the "Refresh" button to refresh the list if the DICOM DIR changes (if you insert another CD for example)

√ Click on the "Select DICOM DIR" button to select a DICOM DIR located at a different place.

√ Click on the "Import" button to import the images into your PACS. In the dialog box that opens, type in the patient name, patient id and study identification, or click on the "Worklist" button if configured (this will depend on your hospital configuration) to access this information through a worklist. Press the "Save" button to send those images, with this new identification, to your PACS.

√ Click on the "Open" button to open a Telemis Viewer for this series. The appropriate viewer (still image or video) will open.

√ Click on the "Cancel" button to cancel this DICOM DIR browsing.

4. ADDON 4.60 TO 4.70

4.1. What's new in 4.70: 4D viewer

4.1.1. Description of the 4D viewer

The 4D viewer lets you navigate in space and/or navigate in the fourth acquisition dimension, which could be:

- time
- diffusion factor
- echo time
- any other parameter defined in the DICOM H. of the images

4.1.2. User instructions

4.1.2.1. Step 1: Image preparation

For the 4D functions to be used, all 4D images must open in only one viewer in 3D/MPR mode in native view.

Ideally, all 4D acquisition images should be in one series by default to facilitate the use of the 4D viewer.

If you have the slightest doubt, contact your Site Manager directly, or contact Telemis Support via the menus: Help => My Telemis Helpdesk.

4.1.2.2. Step 2: Display

4.1.2.2.1. Automatic mode:

- All 4D image series are located in a single line in the browser
- configuration of a display mode which opens these images in 3D/MPR native view
- 4D mode is activated automatically

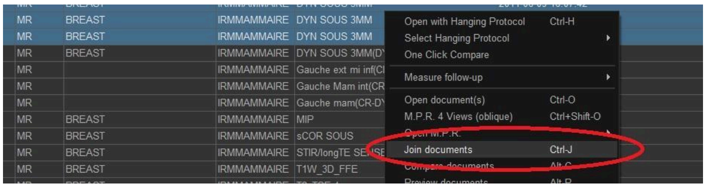
4.1.2.2.2. Semi-automatic mode:

- The 4D image series are independent in the browser
- configuration of a Hanging Protocol which attaches the 4D images
- configuration of a display mode which opens these images in 3D/MPR native view
- 4D mode is activated automatically

4.1.2.2.3. Manual mode:

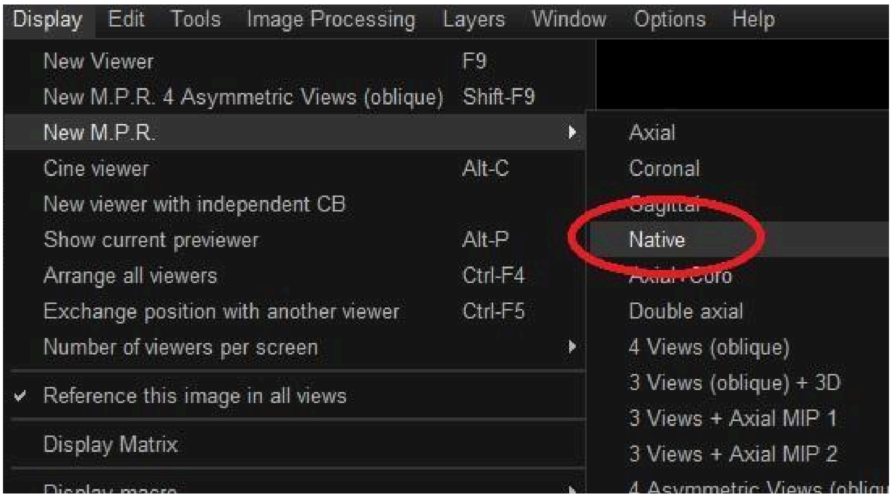
- The 4D image series are independent in the browser
- you must select dynamic/diffusion/multi-echo series manually

- attach the series
    - click the attach button on the TMRHE
    - or right-click => attach documents
    - or ctrl-J



MR	BREAST	IRMMAMMAIRE	DYN SOUS 3MM
MR	BREAST	IRMMAMMAIRE	DYN SOUS 3MM
MR	BREAST	IRMMAMMAIRE	DYN SOUS 3MM(D
MR		IRMMAMMAIRE	Gauche ext mi inf(C
MR		IRMMAMMAIRE	Gauche Mam int(CR
MR		IRMMAMMAIRE	Gauche mam(CR-D
MR	BREAST	IRMMAMMAIRE	MIP
MR	BREAST	IRMMAMMAIRE	sCOR SOUS
MR	BREAST	IRMMAMMAIRE	STIR/longTE SE
MR	BREAST	IRMMAMMAIRE	T1W_3D_FFE

- if configuration of a display mode which opens these images in 3D/MPR native view
    - 4D mode is activated automatically
- if a dedicated display mode not configured
    - you must click:
        - Display
        - New M.P.R.
        - Native
    - 4D mode will then be enabled



4.1.2.3. Step 3: Navigation

4.1.2.3.1. 2D navigation

Once 4D mode has been enabled, you can navigate in 2D space using your usual tools (wheel, mouse click, scroll bar on the right).

1.3.1.2. 4D navigation

To navigate in 4D, you can:

use the left/right arrows on your keyboard

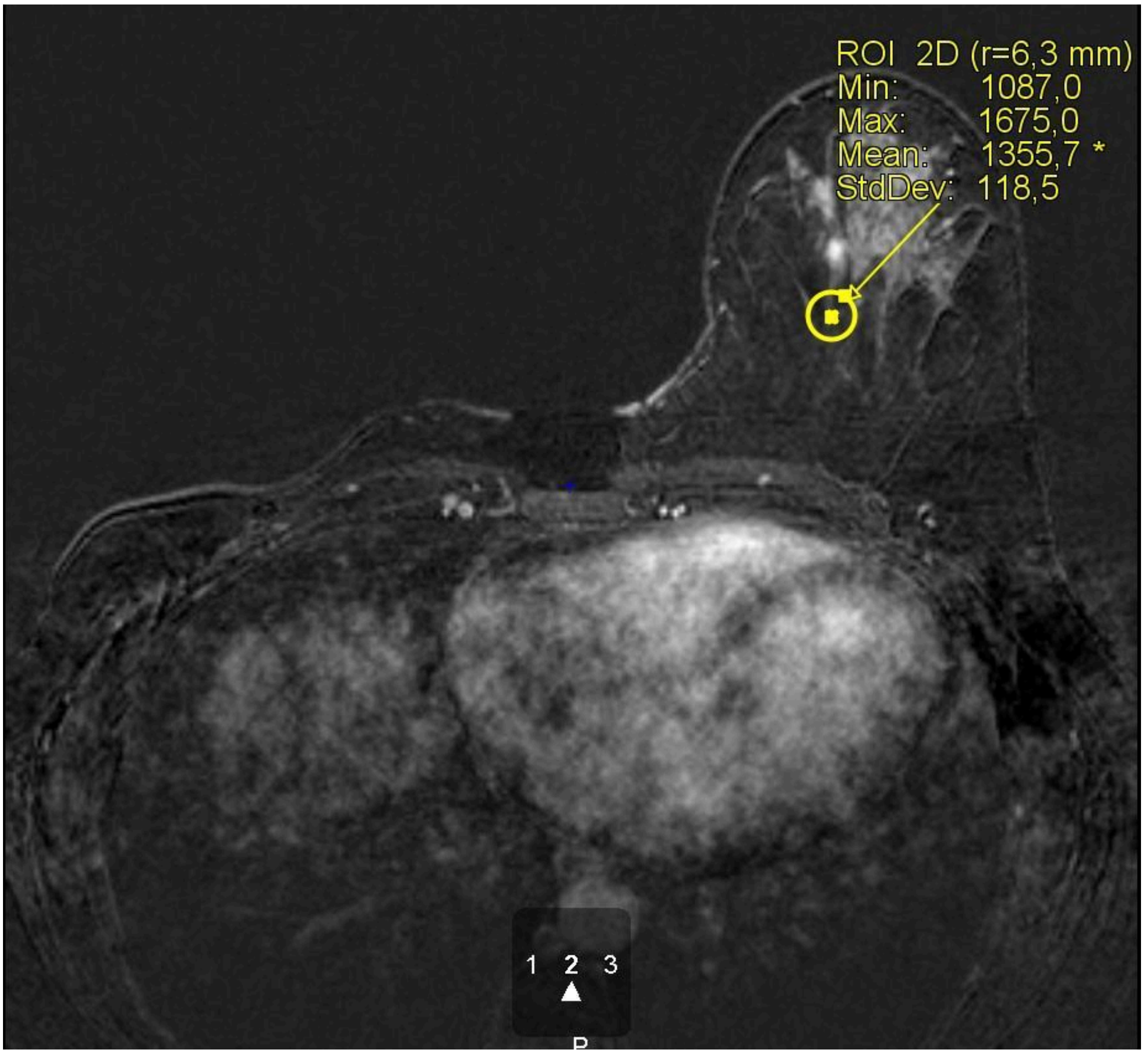
if scrolling is performed by clicking the mouse:

- press and hold the mouse button
- move the mouse from left to right

4.1.2.3.2. 4D navigation

To navigate in 4D, you can:

- use the left/right arrows on your keyboard
- if scrolling is performed by clicking the mouse:
    - press and hold the mouse button
    - move the mouse from left to right

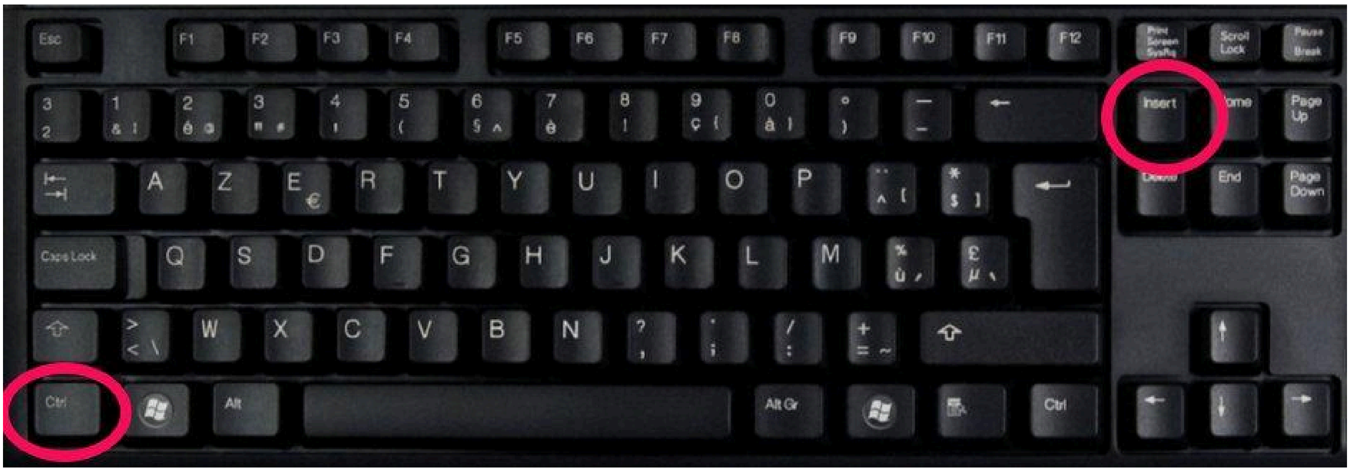


4.1.3. Applications

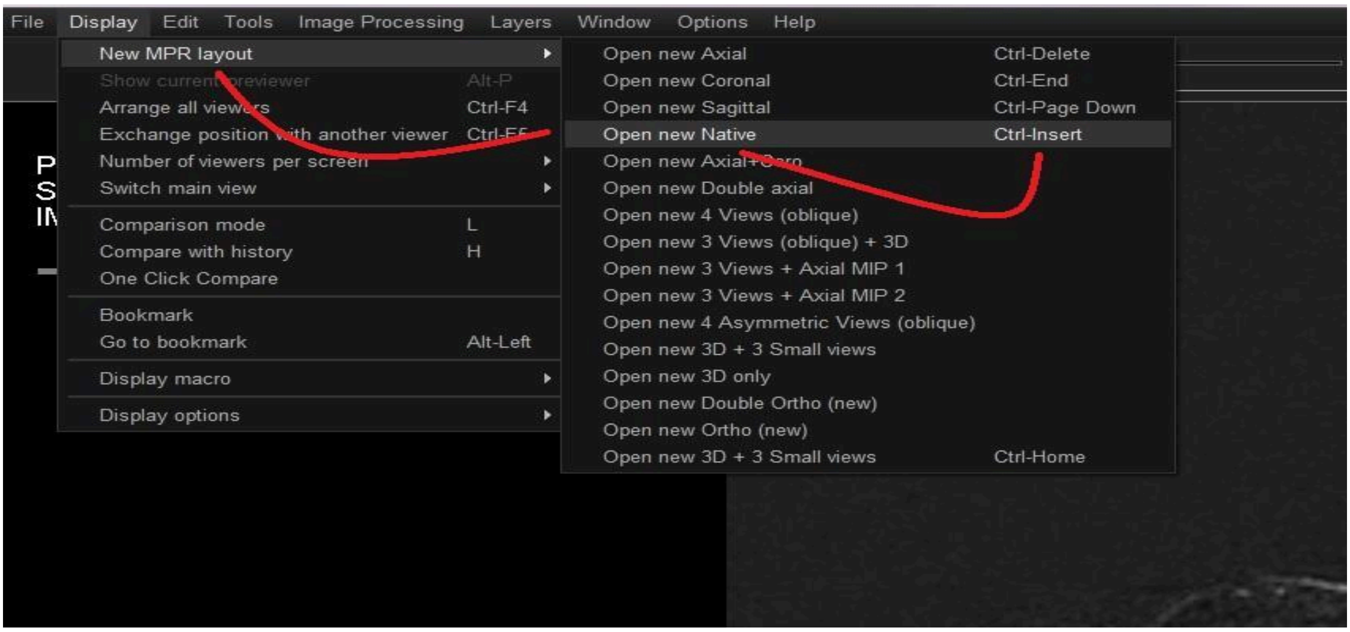
4.1.3.1. Comparison

If you wish to compare one of the dynamics (or other type of 4D image) with other series of the exam, you can isolate it via the following actions:

- ctrl + insert



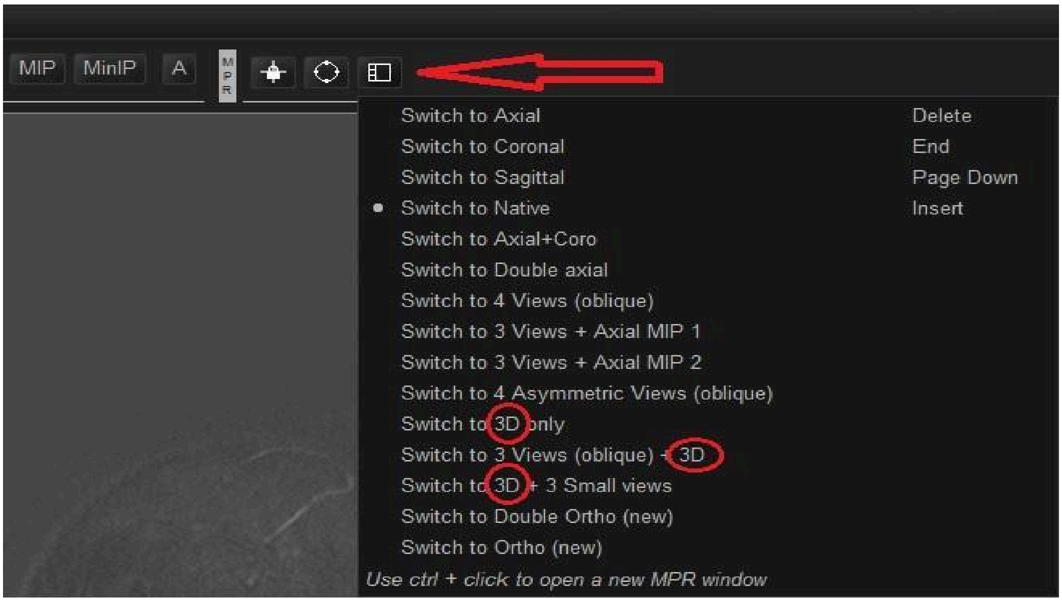
- or via the New MPR layout menu => Native View



4.1.3.2. 4D + 3D/VRT

The 4D functions can be combined with the 3D/VRT views.

To do this, simply open the images concerned in "4D view", and then select a "3D" view of the MPR module.



When your block of 4D data is loaded into the 3D/VRT module, you can switch from one dynamic (or other type of 4D image) to the other (refer to the point on 4D Navigation).

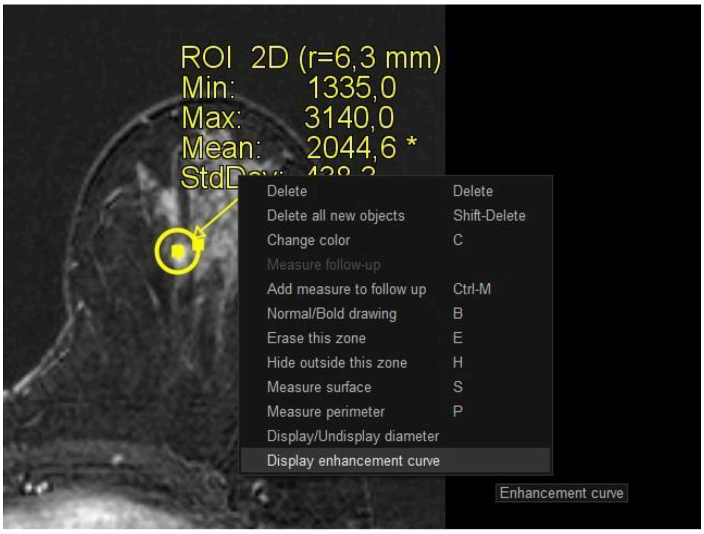
4.1.3.3. Dynamic image processing

4.1.3.3.1. Display enhancement curves

The 4D viewer is particularly well suited to analysing enhancement curves.

Once the images are open, you can:

- trace an ROI
- right-click your ROI
- Select "Display enhancement curve"



In the new window, you can display the enhancement curves as a function of the percentage enhancement between phases:

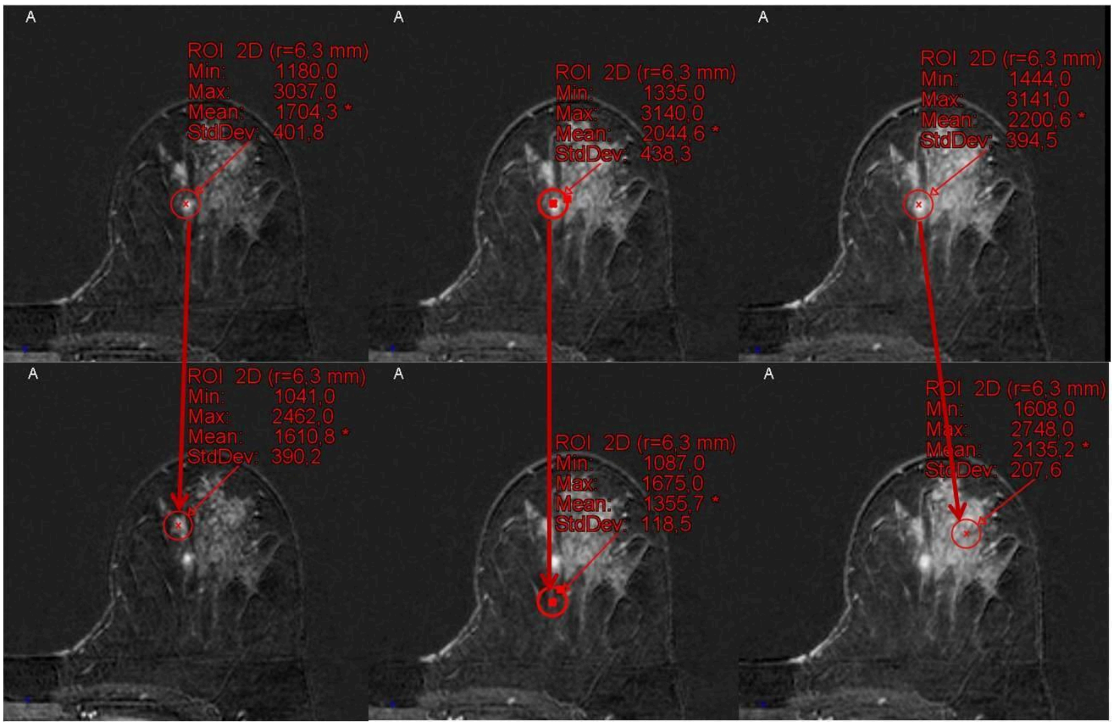
or as a function of the mean value of each ROI on each phase:

Y-Axis
○ %
● Means

4.1.3.3.2. *Correcting the ROI position*

It is possible that the ROIs drawn are no longer correctly positioned on one of the phases (e.g., if the patient has moved).

Now you can correct them manually by left-clicking the ROI position phase by phase.



4.2. What's new in 4.70: Volume measurement

4.2.1. Description of volume calculation

The automatic volume computation system is based on the following four rules:

neighbour-to-neighbour growth by threshold

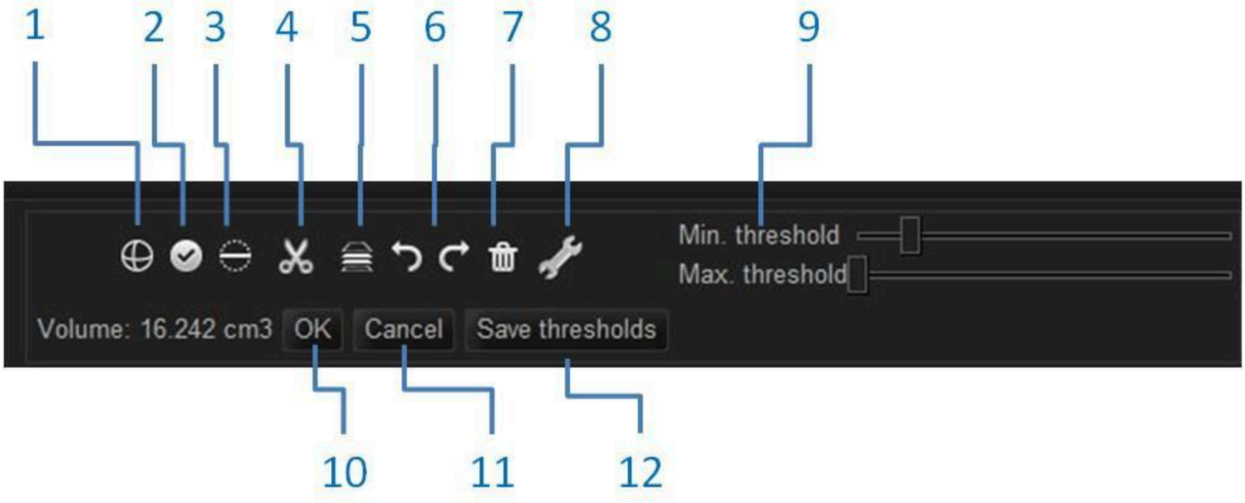
circular delineation of the volume to be computed

manual exclusion of all sections greater or less than a referenced section

a more targeted exclusion via section-by-section zone selection

4.2.2. User instructions

4.2.2.1. Summary of functions



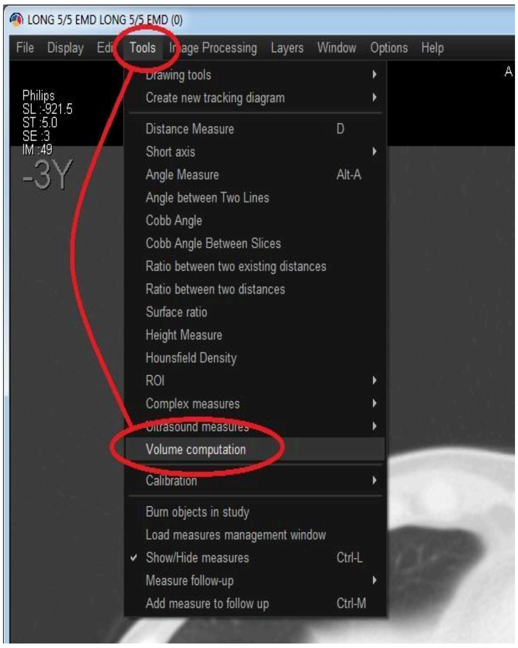
1. Computing a new volume
2. Volume computation without circular delineation
3. Show circular delineation
4. Contour tool for zone to be excluded
5. Tool to exclude sets of sections
6. Undo last operation
7. Delete volume
8. Advanced tools
9. Adjusting the detection threshold
10. Volume confirmation

11. Undo
12. Save the detection threshold settings
13. Change the unit of measurement
14. Transparency adjustment

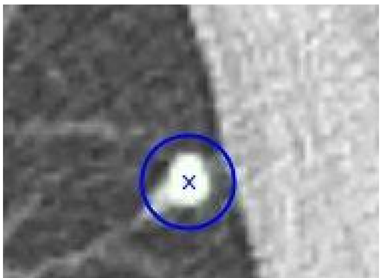
4.2.2.2. Step 1: Lesion selection

You can access the automatic volume computation tool via the following menu: Tool => Volume computation

You can also add the button for this menu to the tool bar via the usual procedure.



After selecting the tool, you can:



- click on one end of the lesion
- hold down the mouse button and draw a line through the lesion from one side to the other
- include the whole lesion inside the circle
- when the circle has been drawn, you can enlarge it manually by left-clicking

4.2.2.3. Step 2: Excluding a set of sections

When voxels of similar density or contrast are selected, the system might be too sensitive and might include a set of voxels located above or below the lesion.

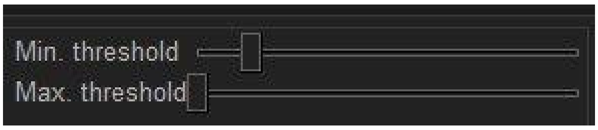
To exclude all those sections with one click, simply place the mouse at the height of the first section located outside the lesion and click the button: ≡

According to the position of the section with respect to the median volume section, all sections above and below will be excluded.

You can cancel a step at any time by clicking this icon ↶

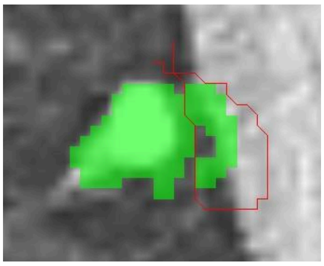
4.2.2.4. Step 3: Adjusting the detection threshold

You can refine detection by adjusting the minimum and maximum thresholds using the cursors provided for this purpose:



You can save the detection thresholds at any time by clicking this menu


Volume: 16.242 cm3



4.2.2.5. Step 4: Excluding a section zone

To refine the volume measure, you can exclude certain zones section by section:

- Click this tool: ✂
- surround the area to be deleted.

This operation must be performed section by section.

You can finalise your measurement at any time by clicking OK.

4.2.2.6. Advanced parameter

Click 🔧 for access to an advanced menu which will let you:

- change the units of the computer volume (cm³ or mm³)
- adjust the transparency of the selected voxels

4.3. What's new in 4.70: Measure follow-up

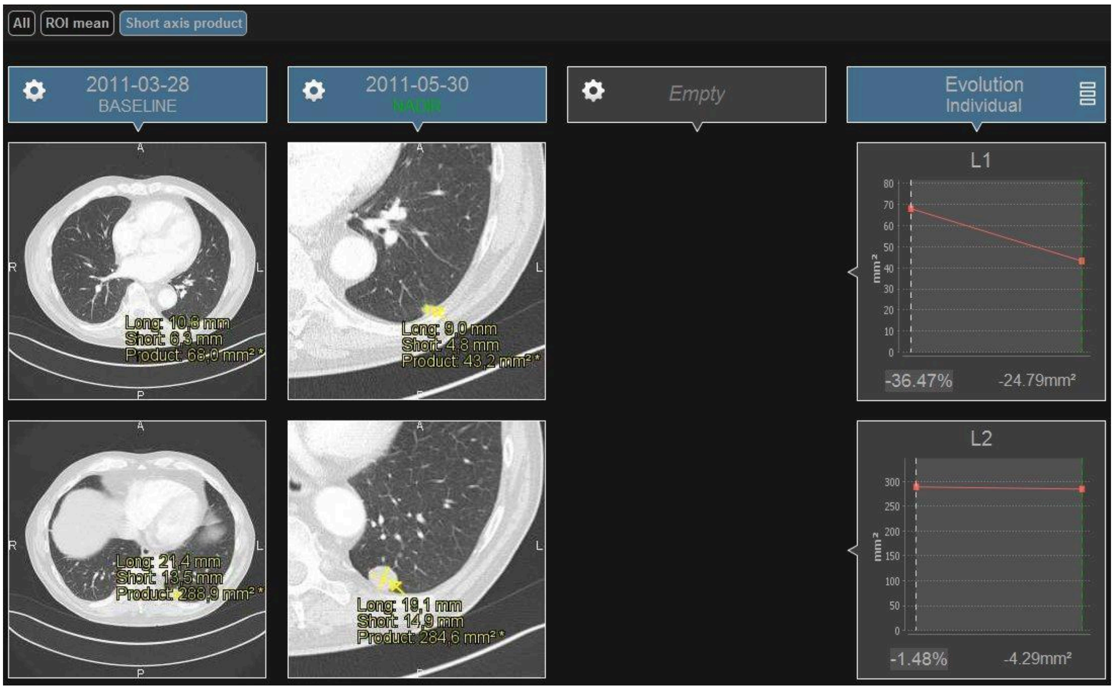
4.3.1. Description of measure follow-up

Measure follow-up is a feature that lets you measure lesions and monitor their evolution over time.

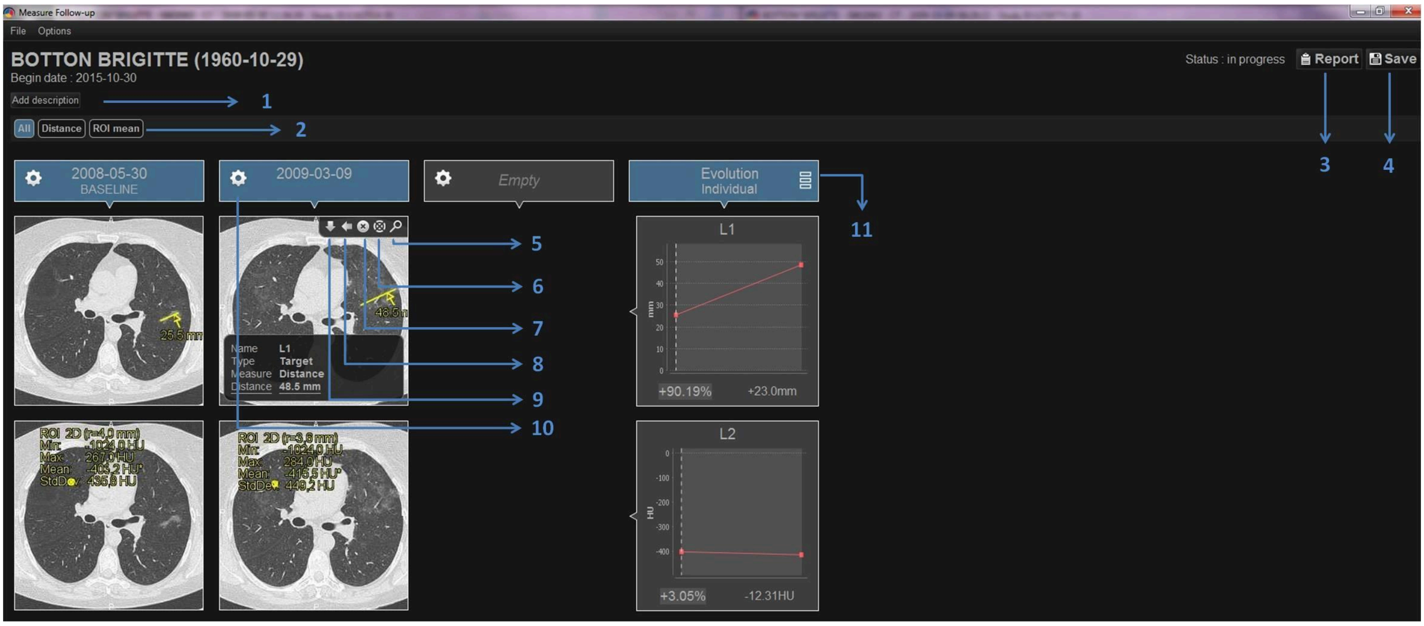
An unlimited number of measures or annotations can be added (see point Annotations concerned by measure follow-up) in the same exam.

Once the first measure has been added to the follow-up, a window opens with an image of the measurement taken and its value.

Once the day's study is complete and all measures have been added to the follow-up, a window of the following type appears:



4.3.2. User instructions



4.3.2.1. Measure follow-up window option

1. Add description
2. Grouping by type of tool

if you integrate different types of measure in your follow-up, this is the menu that will give you a view of the follow-up according to tool type

3. Generate report
4. Save the follow-up in progress

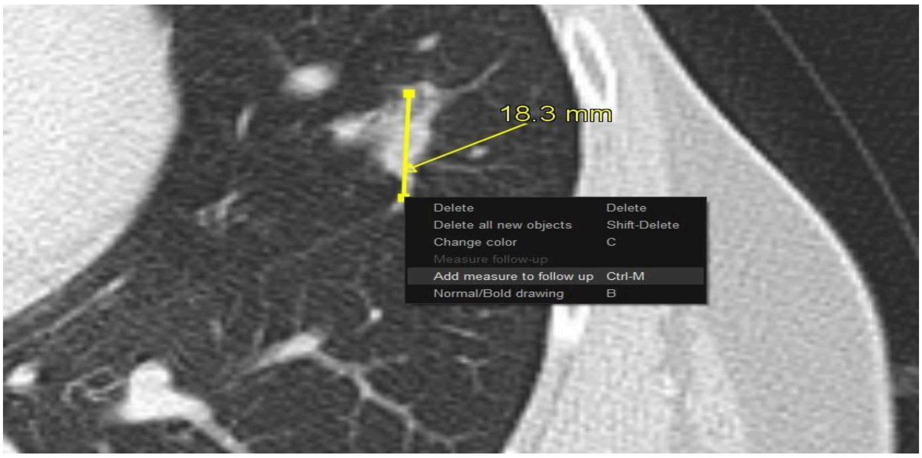
5. Open the study on the measure
6. Erase measure
7. Define a lesion as target or non-target
8. Group two studies in the measure follow-up
9. Manual displacement of a measure to ensure a match
10. Study date management parameter
11. Switching from evolution view by lesion to global patient evolution view

4.3.2.2. Step 1: take one or more measurements

4.3.2.3. Step 2: add the measurement(s) to the follow-up

To integrate a measure in the follow-up protocol:

- you can use the keyboard shortcut Ctrl-M
- or right-click the measure and select the line "Add measure to follow up"



4.3.2.4. Step 3 (optional): add descriptions and mark certain measurements as non-targets

Please see point 1 Measure follow-up window option for more details.

4.3.2.5. Step 4 (optional): generate a report

Please see point 1 Measure follow-up window option for more details.

4.3.2.6. Step 5: Click Save in the upper right-hand corner of the follow-up window

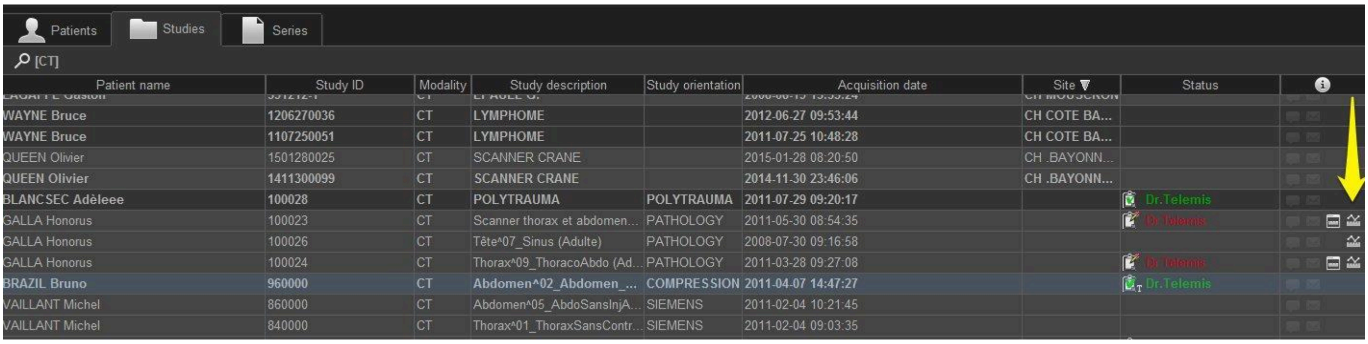
Please see point 1 Measure follow-up window option for more details.

4.3.3. Applications

4.3.3.1. Measure follow-up and one-click comparison

To find the relevant information more quickly in the context of a comparative study, we suggest you combine Measure follow-up with one-click comparison.

When a patient undergoing a study arrives for a second visit, you will find a follow-up notification in the "Info" column.



Patient name	Study ID	Modality	Study description	Study orientation	Acquisition date	Site	Status	i
WAYNE Bruce	1206270036	CT	LYMPHOME		2012-06-27 09:53:44	CH COTE BA...		
WAYNE Bruce	1107250051	CT	LYMPHOME		2011-07-25 10:48:28	CH COTE BA...		
QUEEN Olivier	1501280025	CT	SCANNER CRANE		2015-01-28 08:20:50	CH .BAYONN...		
QUEEN Olivier	1411300099	CT	SCANNER CRANE		2014-11-30 23:46:06	CH .BAYONN...		
BLANCSEC Adèleee	100028	CT	POLYTRAUMA	POLYTRAUMA	2011-07-29 09:20:17		Dr.Telemis	
GALLA Honorus	100023	CT	Scanner thorax et abdomen...	PATHOLOGY	2011-05-30 08:54:35		Dr.Telemis	
GALLA Honorus	100026	CT	Tête^07_Sinus (Adulte)	PATHOLOGY	2008-07-30 09:16:58			
GALLA Honorus	100024	CT	Thorax^09_ThoracoAbdo (Ad...	PATHOLOGY	2011-03-28 09:27:08		Dr.Telemis	
BRAZIL Bruno	960000	CT	Abdomen^02_Abdomen_...	COMPRESSION	2011-04-07 14:47:27		Dr.Telemis	
VAILLANT Michel	860000	CT	Abdomen^05_AbdoSansInjA...	SIEMENS	2011-02-04 10:21:45			
VAILLANT Michel	840000	CT	Thorax^01_ThoraxSansContr...	SIEMENS	2011-02-04 09:03:35			

1. Simply double-click the Measure follow-up icon to display the lesions measured previously.

2. Click the magnifier to show the image with the measure concerned.

Refer to point 3 Measure follow-up window option for additional details.

3. In your tool bar, click the "1CC" button once. The system then offers you the series of the day to select.

If you have no buttons in your bar, you can go to the Display menu and then select the "One Click Compare" menu.

4. Select the series to be compared, and the system will automatically align the two series.

In four clicks you will have your lesions in compare mode

5. If a correction is necessary, you can hold the <> key down to scroll through one of the two

6. Then measure the lesion on the study of the day.

7. Add it to measure follow-u and you will immediately see the evolution of the lesion

If you have other lesions to compare, you can go back to the measure follow-up window and select another measure.

4.3.3.2. Follow-up methodology

The Measure follow-up tool is intended to be flexible.

This means that it does not bind you to any particular follow-up methodology (e.g., RECIST 0, RECIST 1, PERCIST, etc.)

You may, however, impose one if you wish.

For example, if you are monitoring a patient using RECIST x, it will be up to you to integrate these criteria, i.e.:

- maximum number of target lesions
- maximum number of target lesions per organ
- type of measure
    - long axis

  - short axis
  - product of the two
- etc.

Then, using the target/non-target lesions function, you can incorporate other lesions which will be isolated for the purpose of generating the report and which you can still keep in the same Measure follow-up.

4.3.4. Description of measure follow-up features

4.3.4.1. Notification in the explorer

In the Info column of the explorer, a notification tells you that a follow-up is in progress for this patient.

This notification occurs at patient level, meaning that the next time you see this patient, it will tell you that a follow-up is in progress even before you open that day's study.

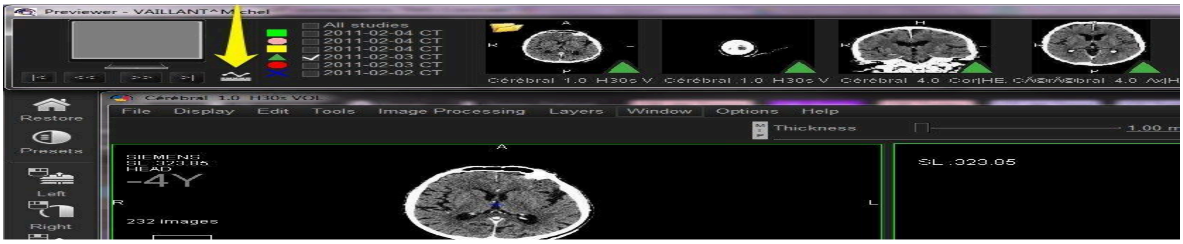
Double-click this icon to open the follow-up window, which gives the option to open the last study, for example.

4.3.4.2. Notification in the previewer

This icon is also shown in the previewer window.

This is designed for users who do not always work with the Telemis worklist.

Likewise, double-click this icon to open the follow-up window, which gives the option to open the last study, for example.



4.3.5. Annotations concerned by measure follow-up

Distance Measure	
Short axis/long axis measurement	*For this tool, you must specify which mode will be used for the follow-up (short axis, long axis, or the product of the two)* *How? Go to the Tools menu => Short and long axes => Short and long axis mode => select mode* 
ROI value (circle, rectangle, polygon)	*For this tool, you must specify which mode will be used for follow-up (Min, Max, Mean)* *How? Go to the Tools menu => ROI => ROI mode => select mode* 
Spherical SUV value Warning: for SUVs,you must - select the SUV tool by right-clicking - right-click in the lower left-hand corner and add the measure to the follow-up  	*For this tool, you must specify which mode will be used for the follow-up (the maximum, mean, or mean of the nine maximum values of the sphere)* *How? Go to the Tools menu => SUV3D => SUV Type => select mode* 
Angle (normal angle, right angle, Cobb Angle)	
Height Measure	
Ultrasound measures	
Hounsfield Density	

Line (segment, infinite, horizontal, vertical)	
Geometric shape (polygon, rectangle, circle or ellipse)	
Pointer, Text, Quick text	

4.4. What's new in 4.70: 3D/VRT

4.4.1. User instructions

4.4.1.1. Mouse operation

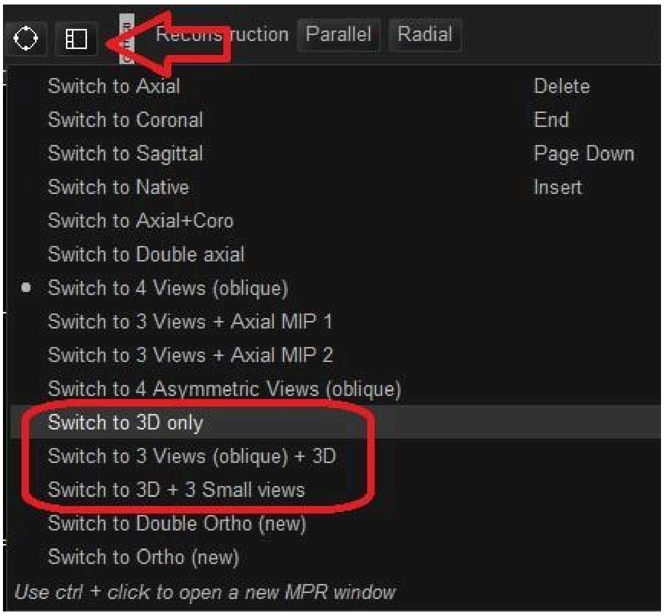
The mouse functions are set in the following way by default:

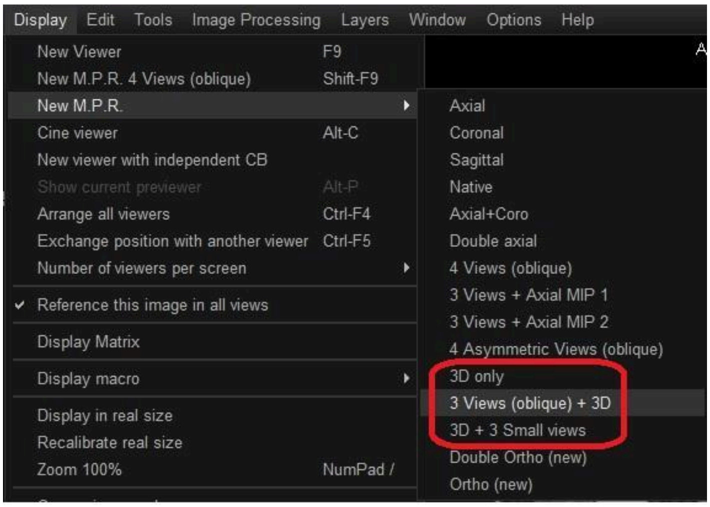
- left-click: rotate volume in space
- right-click: zoom
- Central button: move volume without rotation
- Wheel: disabled

4.4.1.2. Display

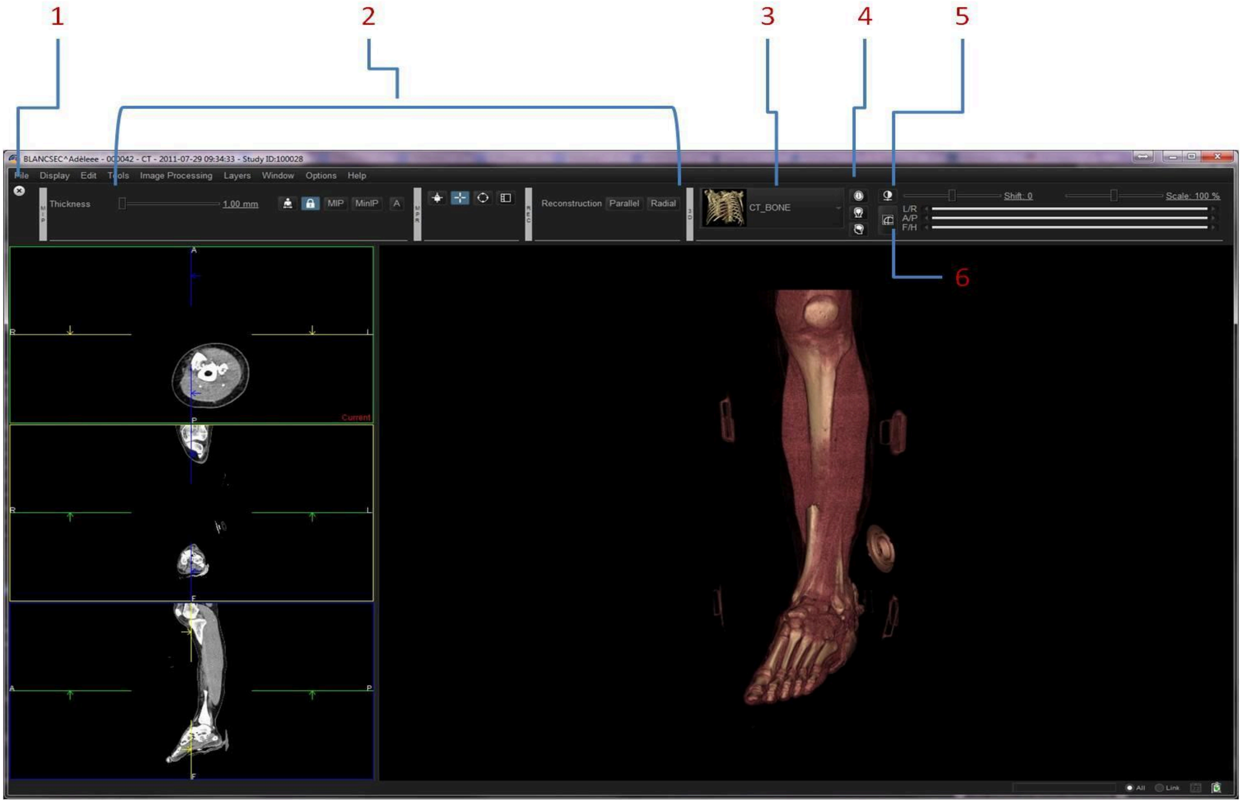
The 3D/VRT viewer applies the same principle as other MPR viewers and is therefore accessible via predefined layouts.

You will see the following entries in the menus.



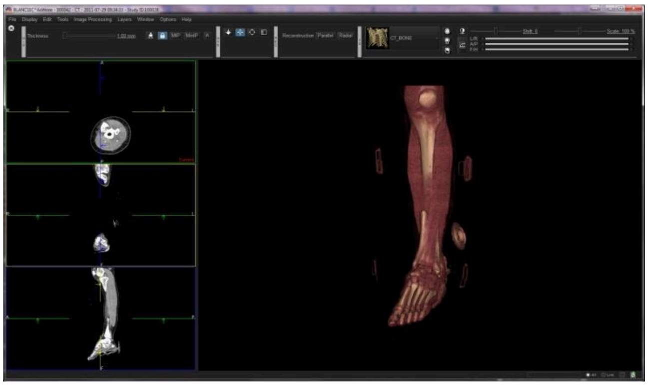
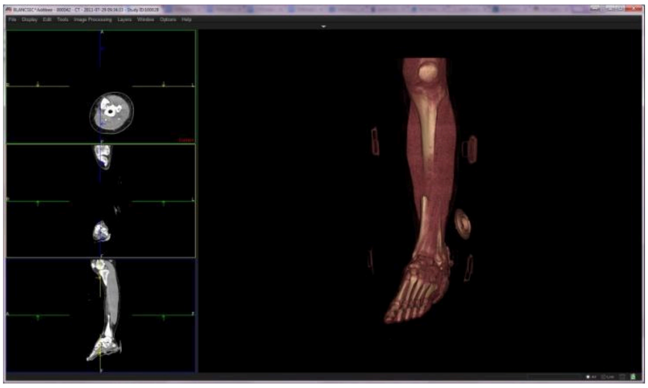


4.4.1.3. Operation of the 3D/VRT viewer

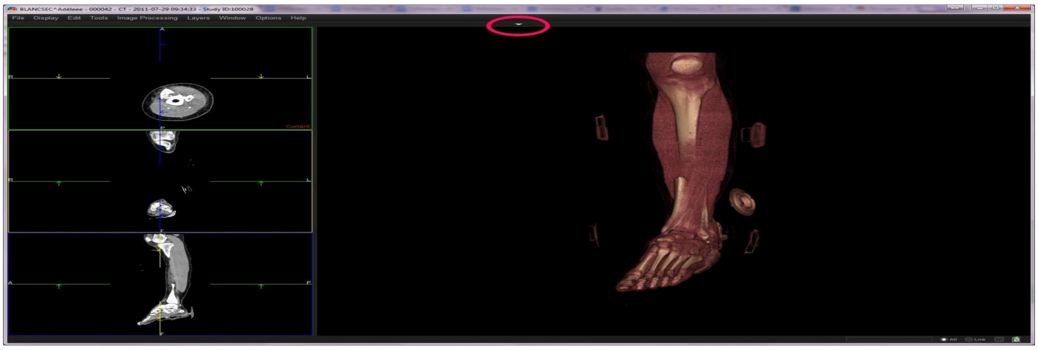


1. Hiding the 3D tool bar
2. MPR management tools
3. Colour code selection drop-down menu
4. Restoration of the VRT in an orthogonal plane
5. Modification of the LUT/colour contrast
6. Volume trimming

4.4.1.3.1. Hiding the 3D tool bar

BEFORE	AFTER
	

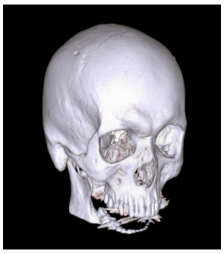
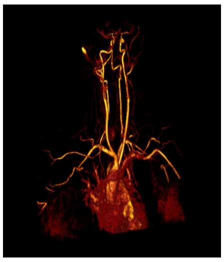
To show the 3D tool bar again, click the following button:

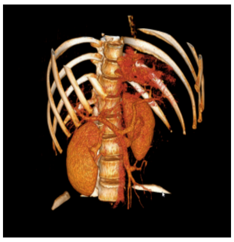
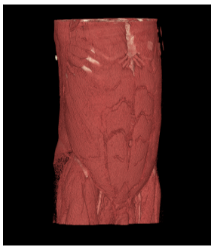


You can also hide parts of the tool bar by clicking one of the icons circled below:

4.4.1.3.2. *Colour codes*

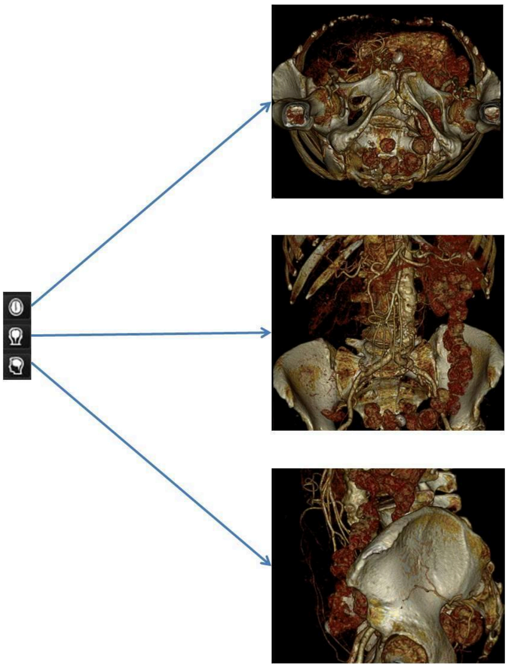
There are several colour codes configured by default:

CT Bone 1	
CT Bone 2	
CT Carotid	
CT De Lung	
CT Vascular	

CT CTA	
CT Muscle	
CT MIP	
MR MIP	

4.4.1.3.3. *Restoration of the VRT in an orthogonal plane*

You can restore the VRT view in a strict axial, coronal, or sagittal plane by clicking the dedicated icons:



4.4.1.3.4. Modification of the LUT/colour contrast

You can modify the colours or transparency of the VRT; this is similar to the way contrast is modified in native images.

The difference is that in VRT, you do not modify the contrast in grey scale, but rather you assign a specific colour or transparency to a Hounsfield density range.

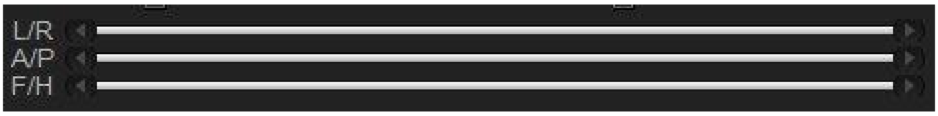
The two cursors are used to move and change the scale of the colour/transparency curve, thus modifying the zones that are displayed, for example, to adapt to a patient whose bones have offset Hounsfield densities.

You can also assign another colour to another range and assign a transparency level to a third range.

4.4.1.3.5. Volume trimming

You can trim certain areas of the volume.

This is the dedicated menu:



By moving the cursor:

- L, you trim the left-hand part of the volume
- R, you trim the right-hand part of the volume
- A, you trim the anterior (front) part of the volume
- P, you trim the posterior (rear) part of the volume
- F, you trim the lower part of the volume
- H, you trim the upper part of the volume

4.4.2. Applications

4.4.2.1. 3D/VRT + Display layout

You will be able to configure specific layouts based on the description of the series, for example, to automatically show a series in 3D/VRT mode with a specific colour code.

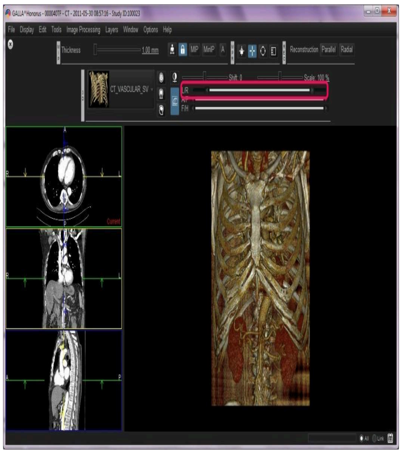
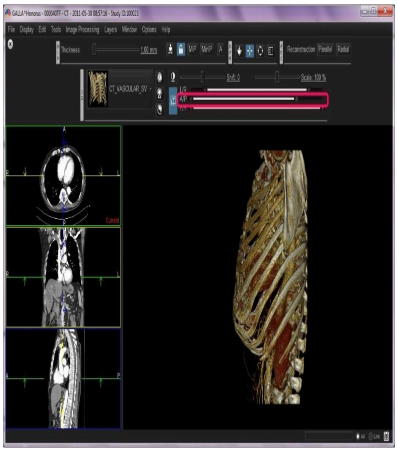
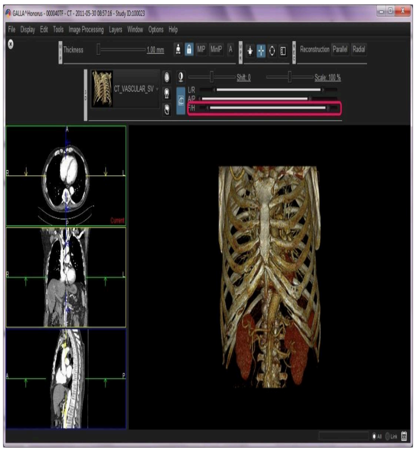
For example, automatically show the:

- CT Angio Thoracic volumes in 3D/VRT Vascular
- CT Angio Lower Limb volumes in 3D/VRT CT MIP
- Raw MR Angio carotid images in 3D/VRT MR MIP

4.4.2.2. Deleting the table

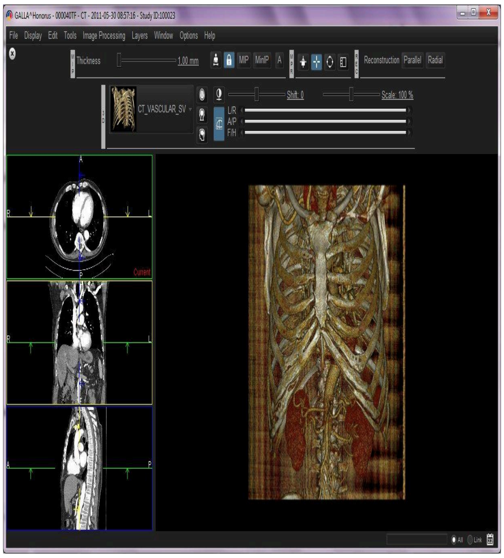
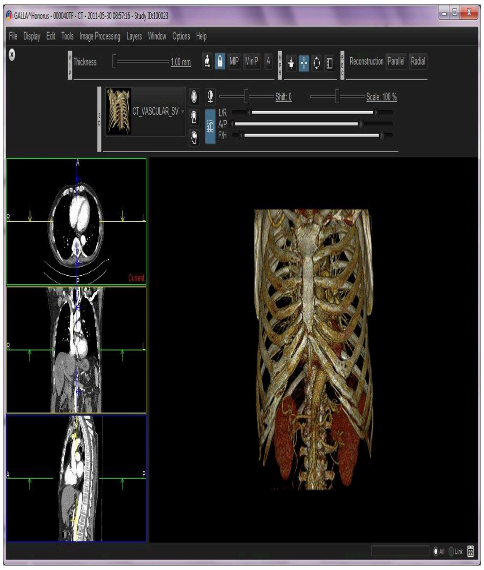
It is very easy to delete the CT table, for example, by combining the restoration functions in the orthogonal planes and volume trimming.

Let's start with an image like this one:

By clicking the coronal plane button and then using the R/L trimming functions, we obtain this:	Next, by clicking the sagittal plane button and then using the A/P trimming functions, we obtain this:	Next, by clicking the coronal plane button and then using the F/H trimming functions, we obtain this:
		

The end result is a volume with a clean shape, on which we will be able to work with greater precision.

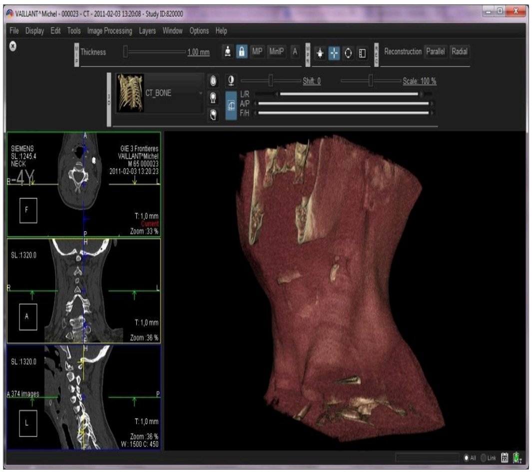
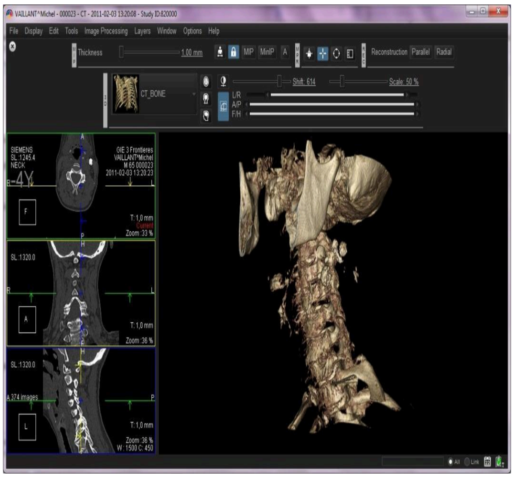
BEFORE	AFTER

4.4.2.3. Modifying the colour code

In cases of polytrauma, it is sometimes useful to rework the volume so that both the tissue appearance and the bony part of an anatomical area can be studied.

This is how to give very different appearances to the same volume by adjusting the colour codes and the settings in the associated menu.

BEFORE	AFTER
	

4.5. What's new in 4.70: Miscellaneous

4.5.1. TMRHE function

4.5.1.1. Double Click => Hanging Protocol

Since 70, we have created a new parameter to open studies in Hanging Protocol via a double click.

Contact your Site Manager for implementation.

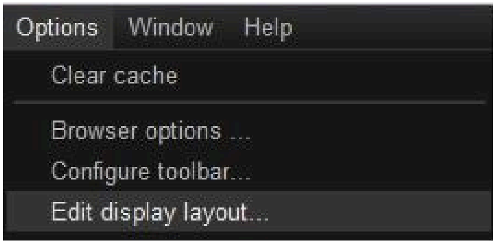
4.5.1.2. Modifying the menus

4.5.1.2.1. In the Telemis browser

Modifications to patient information, studies, or series are now located in a single sub-menu: Document => Patient/series modifications

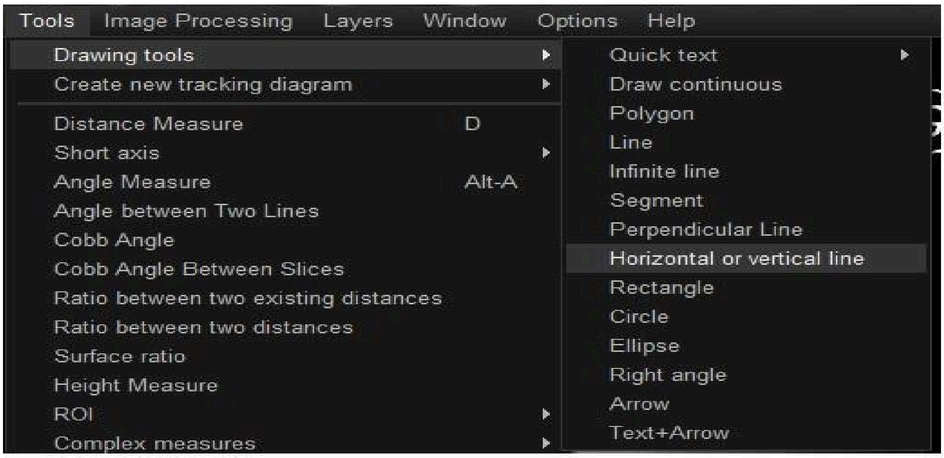
All menus concerning the status of the report in Telemis are now located in a single sub-menu: Document => reporting

You can access the display layouts directly from the browser via the menu: Option => Display layout



4.5.1.2.2. In the Telemis viewer

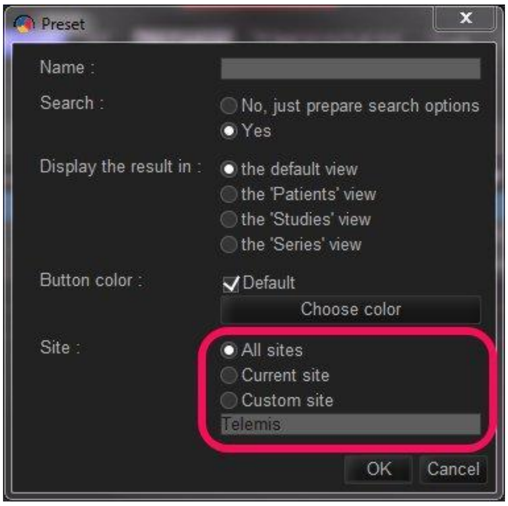
All of the drawing tools are located in a single sub-menu: Tools => Drawing tools


Tools
Image Processing
Layers
Window
Options
Help
Drawing tools
Create new tracking diagram
Distance Measure D
Short axis
Angle Measure Alt-A
Angle between Two Lines
Cobb Angle
Cobb Angle Between Slices
Ratio between two existing distances
Ratio between two distances
Surface ratio
Height Measure
ROI
Complex measures
Quick text
Draw continuous
Polygon
Line
Infinite line
Segment
Perpendicular Line
Horizontal or vertical line
Rectangle
Circle
Ellipse
Right angle
Arrow
Text+Arrow

4.5.1.2.3. In the search presets

When creating search buttons, you will see a new Site menu appear.

This menu lets you define whether the button you create will be available on all sites, the current site only, or another site.



Name :

Search : ○ No, just prepare search options ● Yes

Display the result in : ● the default view ○ the 'Patients' view ○ the 'Studies' view ○ the 'Series' view

Button color : ☑ Default

Site : ● All sites ○ Current site ○ Custom site

Telemis

4.5.1.3. Vertical - Horizontal Line

You will find the horizontal or vertical line tools in the menu: Drawing tools => horizontal or vertical line.

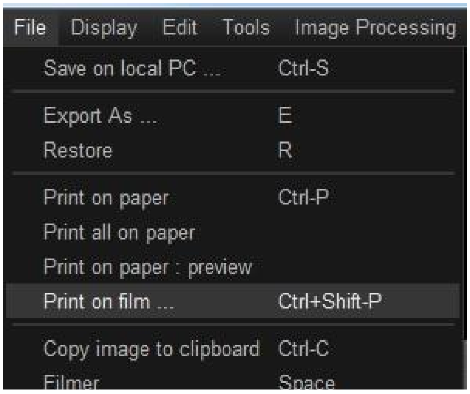
4.5.1.4. Actual size printing

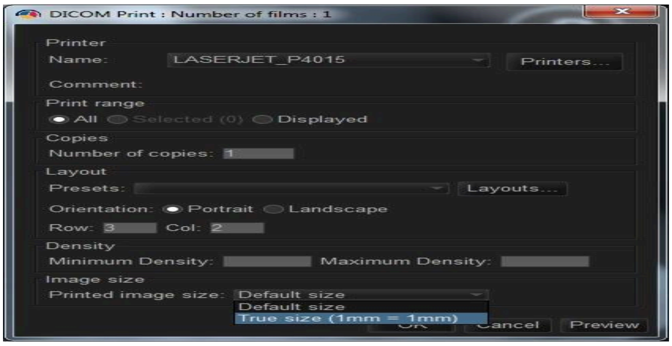
We have completely redeveloped the film printing part.

Ti enable actual size printing, please contact your Site Manager to enable the function and validate printing.

To print in actual size, you must:

- open the image to be printed
- go to the File menu
- select the "Print on film" menu
- Select "Print actual size".





DICOM Print : Number of films : 1

Printer

Name: LASERJET_P4015

Comment:

Print range

● All ○ Selected (0) ○ Displayed

Copies

Number of copies: 1

Layout

Presets:

Orientation: ● Portrait ○ Landscape

Row: 3 Col: 2

Density

Minimum Density: Maximum Density:

Image size

Printed image size: Default size

Default size

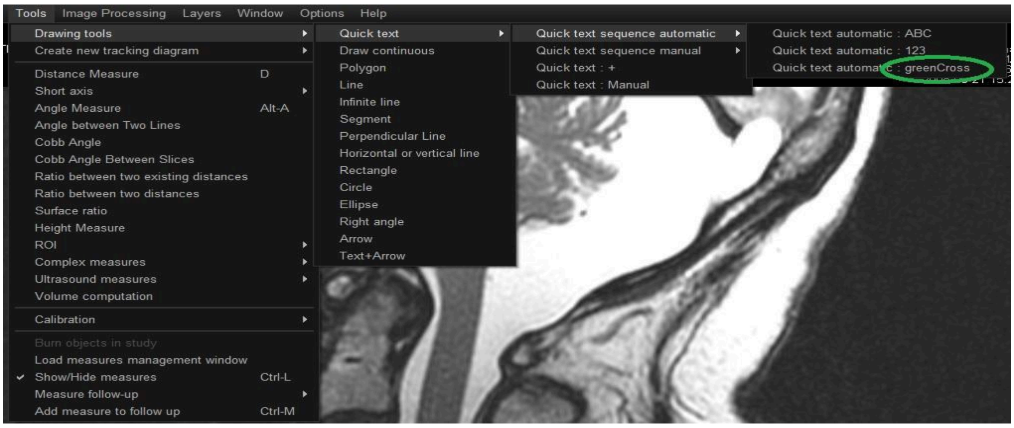
True size (1mm = 1mm)

4.5.1.5. Green cross

You can easily affix a green cross to images to make them key images and to draw attention to the important area.

To access the menu, go to:

- drawing tools
- Quick Text
- Quick Text automatic sequence
- Quick Text automatic: green cross

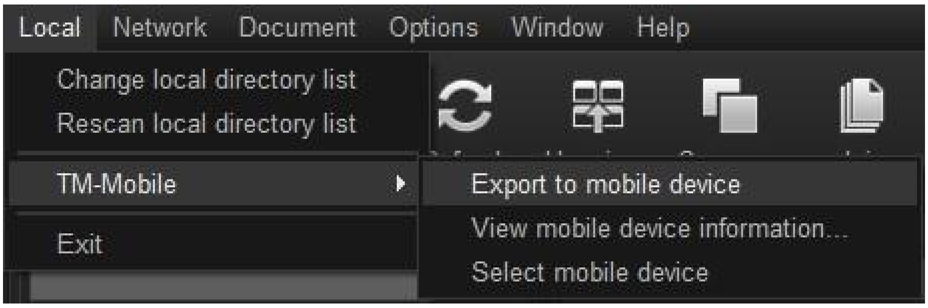


4.5.1.6. Anonymous TM-Mobile

You could already carry your PACS around in your pocket, with your selection of noteworthy cases.

Starting from version 70, you can anonymise the patients you export to the USB key.

4.5.1.6.1. Step 1: export to mobile device



4.5.1.6.2. Step 2: anonymise

Do you want to export these series to your mobile device ?

4.5.1.7. TMRHE improvements

4.5.1.7.1. Previewer

We have optimised the order of the acquisitions in the previewer.

4.5.1.7.2. Security

A user account will be blocked after too many incorrect attempts to log in.

4.5.1.7.3. Series update ergonomics

Option to update just one series of a particular study.

4.5.1.7.4. Ergonomics in comparison mode

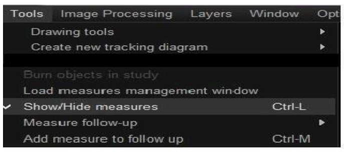
You can use a mouse + keyboard combination to temporarily decouple two series when you are in comparison mode.

To do this, click the

button while navigating with the mouse.

4.5.1.7.5. Measure display ergonomics

You can use the keyboard shortcut or the menu, Tools => Hide measures, to hide all the recorded measures.



4.5.2. TM Capture - Wound Management

The TM Capture's first big upgrade will provide:

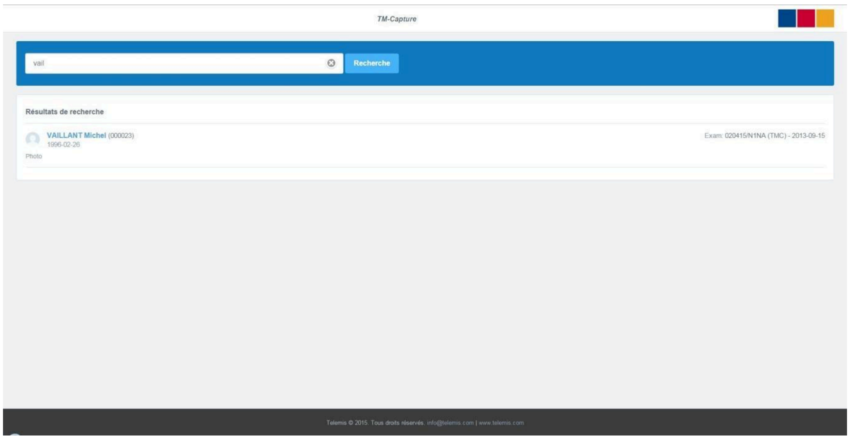
- a set of bug fixes
- the possibility of adding descriptions to images
- the possibility of a search using the patient login
- access to all available worklists

4.5.2.1. Applications

By using all the resources offered by the Telemis PACS, we have been able to set up a new wound management system.

An example procedure is shown below:

1. Image acquisition via the TM Capture
    a. Use of a worklist if available



vail

Résultats de recherche

VAILLANT Michel (000023)
1996-02-26
Photo

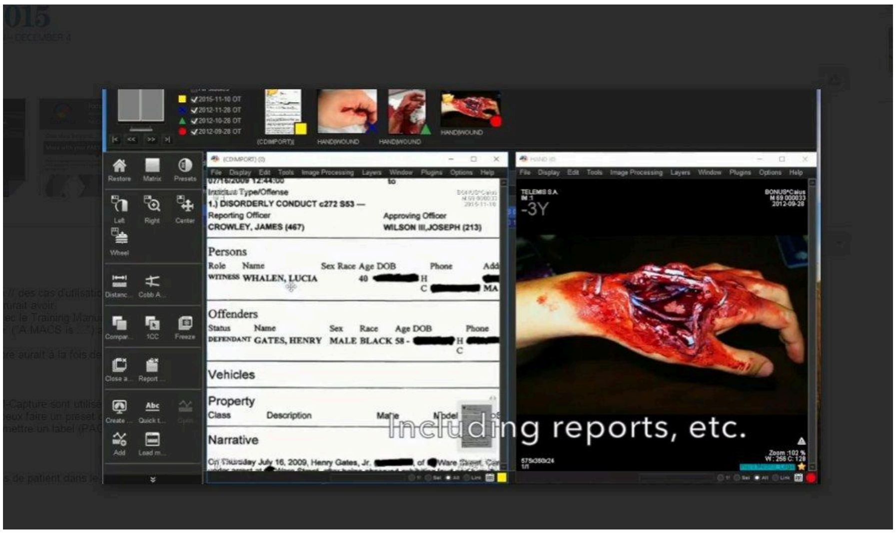
Exam: 020415/N1NA (TMC) - 2013-09-15

Telemis © 2015. Tous droits réservés. info@telemis.com | www.telemis.com

    b. Possibility of adding descriptions
    c. Archive in MACS
    d. Notification to the computerised patient file

2. Data management
   a. Image viewing in Telemis
   b. Use of tracking diagrams for better lesion locating

   c. Use of labels to centralise forensic cases
   d. Use of Scan & Go to attach expert's reports to the imagine file whilst notifying the computerised patient file.



07/16/2009 12:44:00 to

Incident Type/Offense

1.) DISORDERLY CONDUCT c272 S53 —

Reporting Officer: CROWLEY, JAMES (467)

Approving Officer: WILSON III, JOSEPH (213)

Persons

Role	Name	Sex	Race	Age	DOB	Phone	Add
WITNESS	WHALEN, LUCIA			40	[redacted]	H C [redacted]	[redacted] MA

Offenders

Status	Name	Sex	Race	Age	DOB	Phone
DEFENDANT	GATES, HENRY	MALE	BLACK	58	[redacted]	H [redacted] C

Vehicles

Property

Class	Description	Make	Model

Narrative

On Thursday July 16, 2009, Henry Gates, Jr. [redacted], of [redacted] Ware Street,

   e. Use of the provisional report to convey an initial evaluation of the lesions

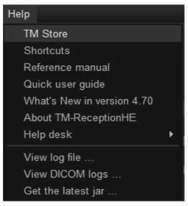
Use of notes and messages to communicate directly with one or more colleagues

4.5.3. TM Store

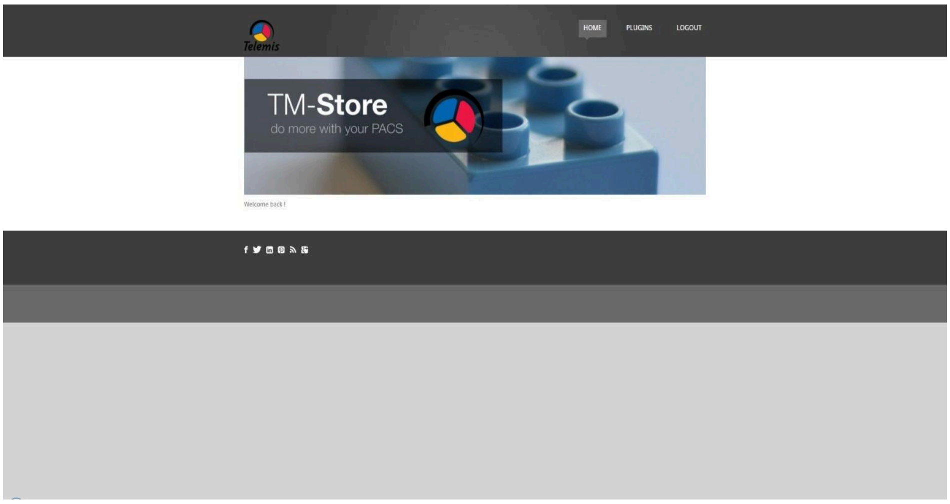
You can access a secure environment containing useful information such as:

- training videos
- user manuals
- plugins

The TM Store will only be accessible from TMRHE clients via the menu: Help => TM Store



This takes you to a web page that is updated regularly.



4.5.4. Integration

4.5.4.1. Skype

In the context of 24/7 care, teleradiology plays an increasingly important role.

For optimum treatment, we have integrated Skype, a videoconferencing tool.

You can make a videoconference call to a specific contact by clicking.

Please contact your Site Manager for implementation.

4.5.4.2. Ticket tracking tools: Zendesk

In 2015, Telemis support converted to a new incident tracking tool called Zendesk.

This tool gives users real-time access to the tracking of their request.

Each request sent by e-mail generates a ticket that is handled by the support engineers.

To bring our users closer to our Customer Support department, we have put a link in Telemis to give you direct access to your personal Zendesk page (subject to activation of your account).

For access, use the menu Help => My Telemis Helpdesk

4.5.5. MISCELLANEOUS

4.5.5.1. TMPWeb

Optimisation of the database to improve the responsiveness of the solution in anonymous mode and authenticated mode.

4.5.5.2. Storage

We have continued to upgrade our archiving solution by integrating new Dicom Enhanced and DICOM JPEG imaging types.

5. ADDON 4.70 TO 4.80

5.1. MPR - Better reconstructions

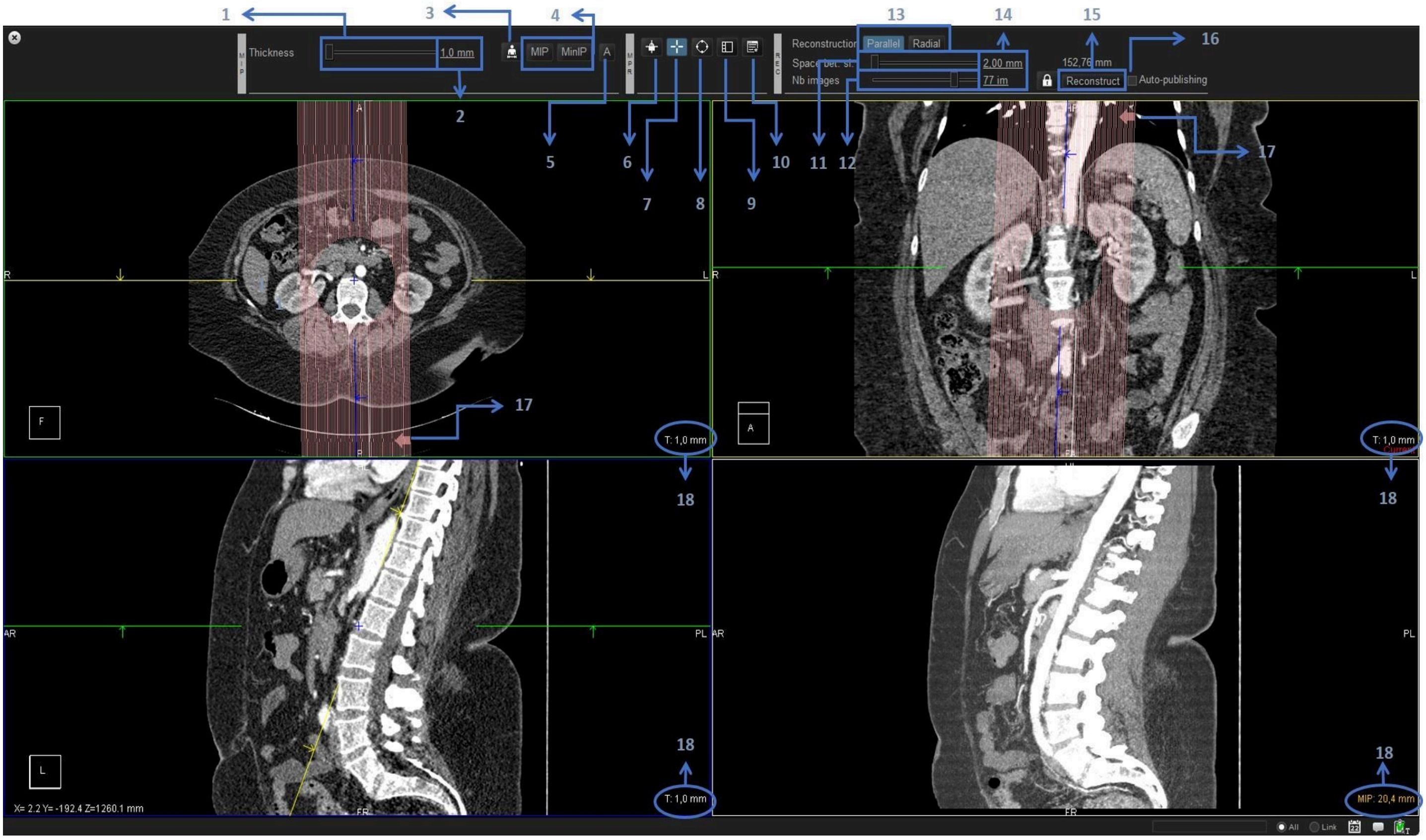
5.1.1. Description of reconstructions

In 4.80 we have reworked the ergonomics of reconstructions based on the WYSIWIG principle (What You See Is What You Get).

Simply put, all you need to do is:

- go into the desired plane
- click in the plane
- and then click the "Parallel" button

5.1.2. Summary of functions



1. Current view thickness adjustment cursor
2. Thickness value of the current view (click it to edit manually)
3. Enable a MIP with a thickness covering the whole series
4. Enable MIP or MiniMip on the current view

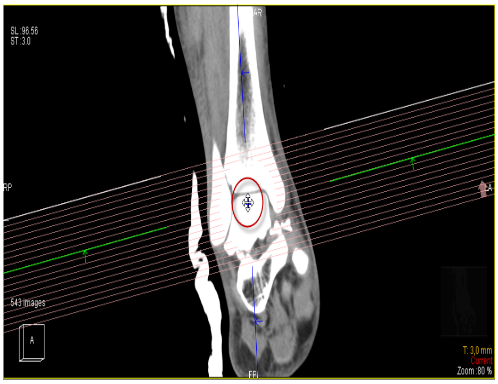
5. Propagate MIP/MiniMip/thickness of the current view to all MPR views
6. Enable or disable orthogonality between the three planes
7. Show or hide coloured axes representing the planes
8. View rotation tool
9. MPR/VRT layout menu
10. Access to reconstruction macro menu
11. Cursor to adjust the space between two reconstruction slices
12. Cursor to adjust the number of slices
13. Reconstruction mode
14. Value of the space between two reconstruction slices and the number of slices (click to edit manually)
15. Launch reconstruction in the chosen plane
16. Enable publication (send to the PACS) automatically
17. Reconstruction direction
18. Thickness of current view

5.1.3. User instructions

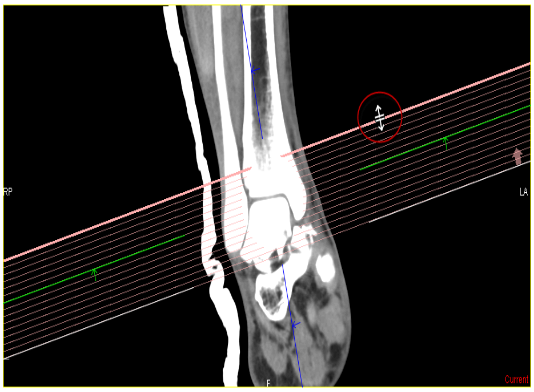
5.1.3.1. Manual reconstruction

When the "Reconstruction" button is clicked, a reconstruction comb appears.

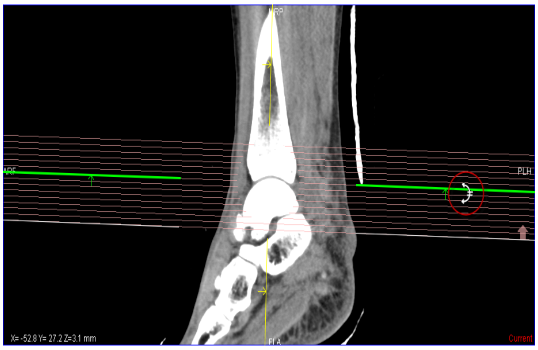
1. Move the cursor towards the middle of the comb to enable a function that moves the comb.



2. Move the cursor towards the ends of the comb to enable a mouse function that lets you extend the coverage of the region of interest.



3. Move your cursor to the central area of the comb, but off-centre to the left or right, to enable a mouse function that lets you modify the orientation of the comb


HRP
ARF
PLH
FLA
X= -52.8 Y= 27.2 Z=3.1 mm
Current

4. To modify the spacing, slice thickness, or projection type, you must:
    a. click in the reconstructed view
    b. click MIP or MiniMip to enable one of these types of projection
    c. modify the thickness and spacing via the dedicated functions
5. You can reverse the direction of the reconstructions by double-clicking the arrow provided for this purpose
6. Click one of the axes of the comb to see the result in the reconstructed view
7. When the position of your comb has been confirmed, simply click the "Reconstruction" button
8. You can also select the "auto publication" box to allow for automatic transfer of the reconstruction to the PACS
    a. enter a description of the series in the pop-up that is displayed.

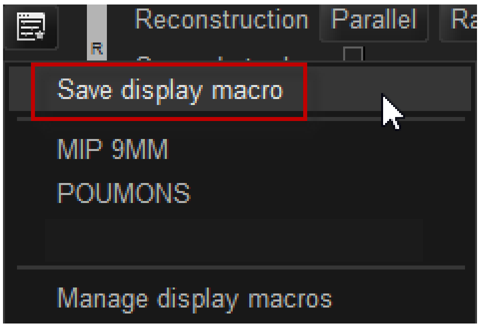
5.1.3.2. Reconstruction macro

It is now possible to save reconstruction models that you can apply at any time.

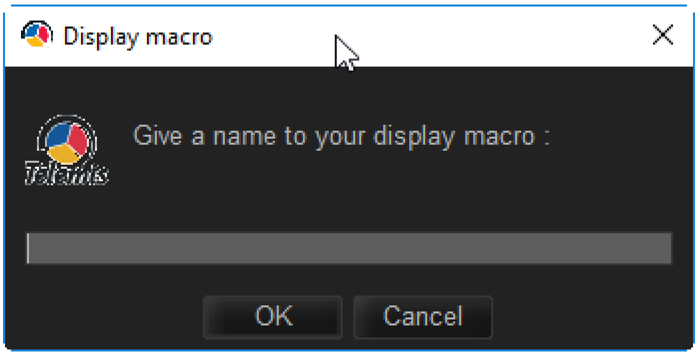
5.1.3.2.1. Saving reconstruction macros

To save a macro:

- position your comb, configure the thickness and the space between slices
- click button 10
- then click the "Save display macro" menu



- and finally, name the macro and click OK

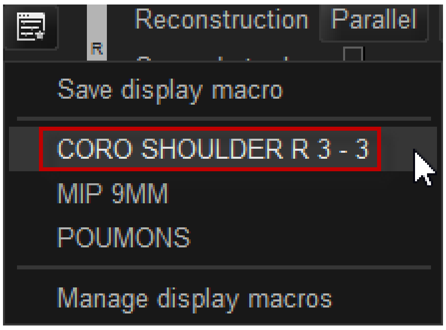


Give a name to your display macro :

5.1.3.2.2. Applying reconstruction macros

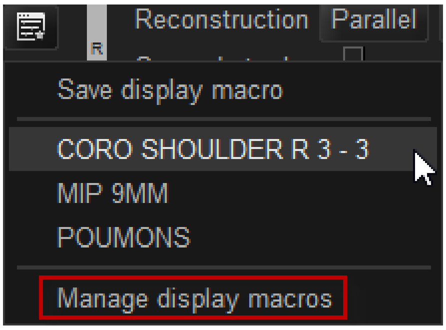
To apply a reconstruction macro:

- open a serie in MPR
- click button 10
- and then select the reconstruction macro



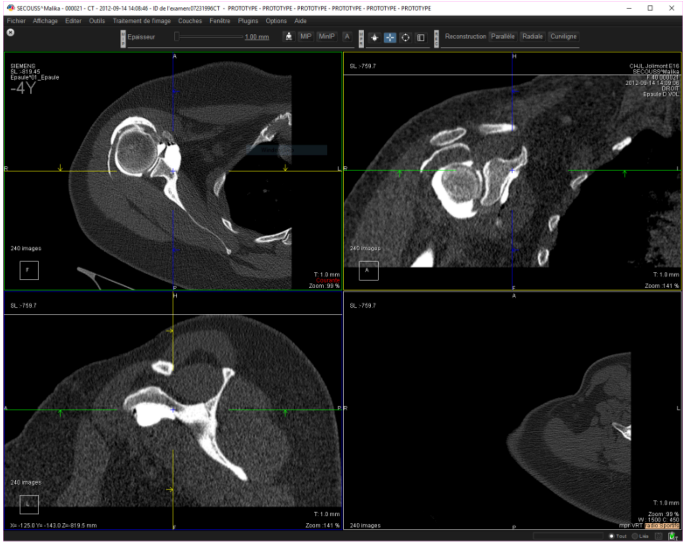
5.1.3.2.3. Managing reconstruction macros

Reconstruction macros can be deleted or renamed via the menu

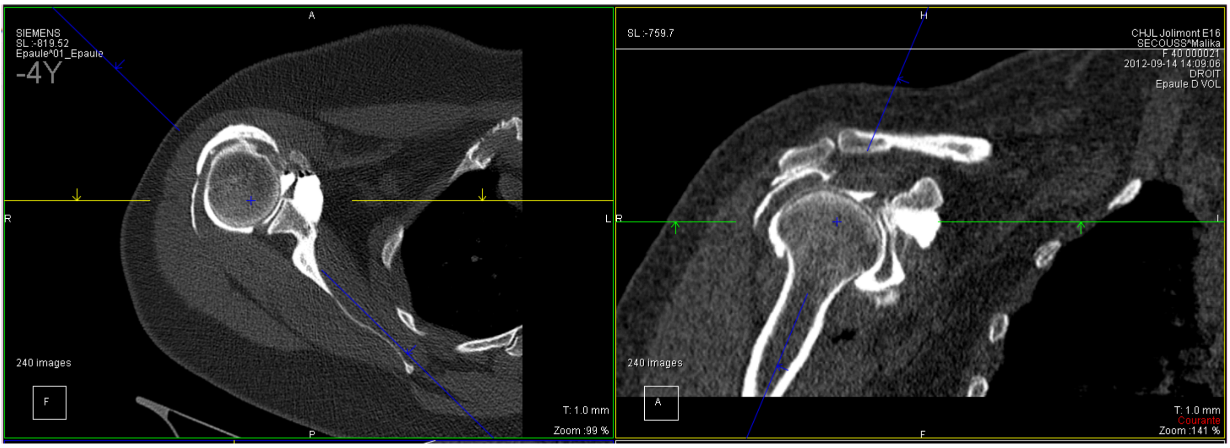


5.1.4. Application example: Coronal reconstruction of the shoulder

- Open your series in MPR
    - in this example, “MPR 4 oblique views” has been selected

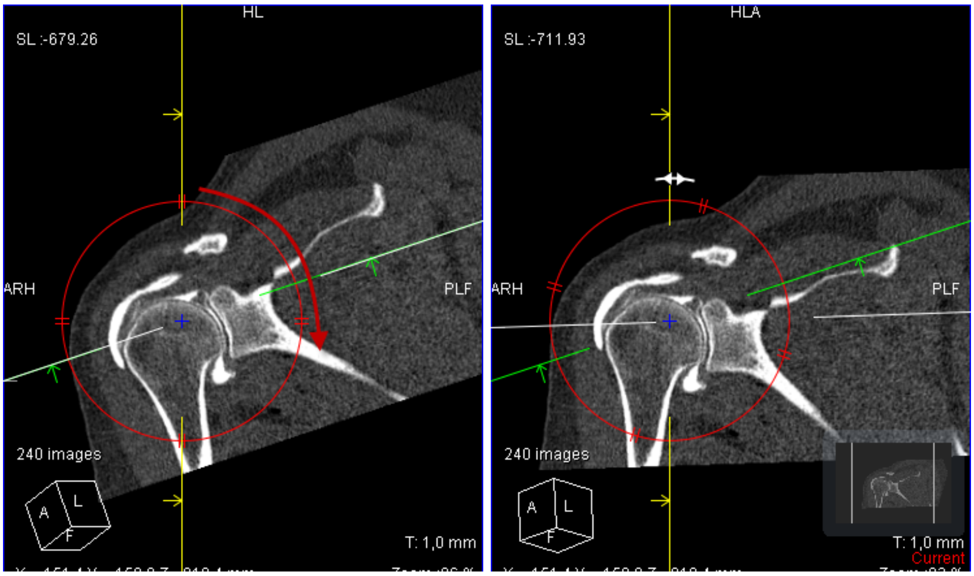


- Release the lock if you do not wish to maintain orthogonality between the three planes
- Orient the blue axis:
    - on the axial view in the plane of the fossa and clavicle
    - on the coronal view in the plane of the humerus



- Then click the lower-left view, corresponding to the coronal plane of the shoulder

- Do not hesitate to rectify your slice plane using the MPR rotation tool to produce this:



Then simply edit the settings of your comb and launch reconstruction by clicking the button

5.2. New Mammo Viewer (with Tomosynthesis)

The new Mammo viewer can integrate the following types of image into the display sequences:

- tomosynthesis
- magnetic resonance
- ultrasound

We have also implemented a new comparative concept: *Timeline comparison*

5.2.1. Timeline comparison

The timeline comparison is an option that will be enabled automatically from version 4.80.

It consists of loading the history of the selected incidence and lets you move from one exam to another using the wheel.

Image

5.2.2. Managing multimodality in display sequences

It will now be possible to natively integrate images from different modalities into the display sequences.

This will provide a better approach to the patients' senologic case.

5.2.3. Tomosynthesis management

We have worked specifically on the viewing of tomosynthesis in Telemis.

From a technical standpoint, we have ensured the compatibility of these images from most manufacturers.

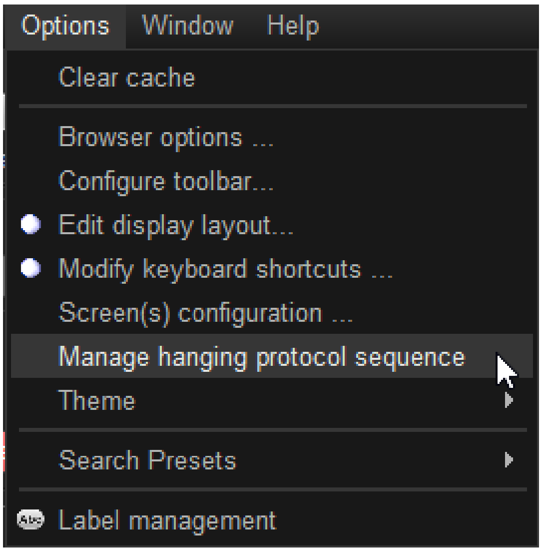
From a functionality standpoint, it will be possible to

- browse within a serie
- compare series to each other
- locate your position spatially thanks to a position indicator

Image

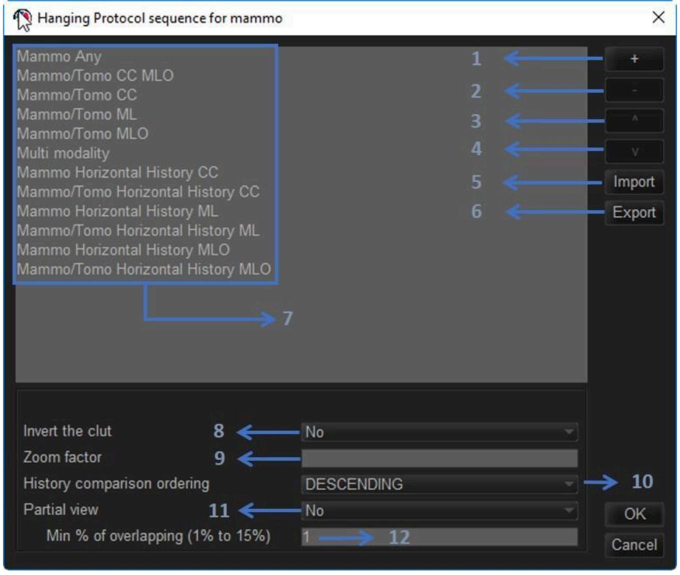
5.2.4. Configuration of display sequences

To configure the mammography display order, go to the “Options” menu and then manage the hanging protocol sequences



5.2.4.1. Description of configuration interfaces

- Select this menu. The display sequence management window appears



Invert the clut: No
Zoom factor:
History comparison ordering: DESCENDING
Partial view: No
Min % of overlapping (1% to 15%): 1

1. Button used to add a display sequence
2. Button used to delete a sequence selected in Zone 7.
3. Button used to move a sequence selected in Zone 7 upwards.
4. Button used to move a sequence selected in Zone 7 downwards.
5. Button used to import a sequence
6. Button used to export a sequence

7. Zone summarising the order of the display sequences

8. Option used to invert the contrasts of the selected sequence.

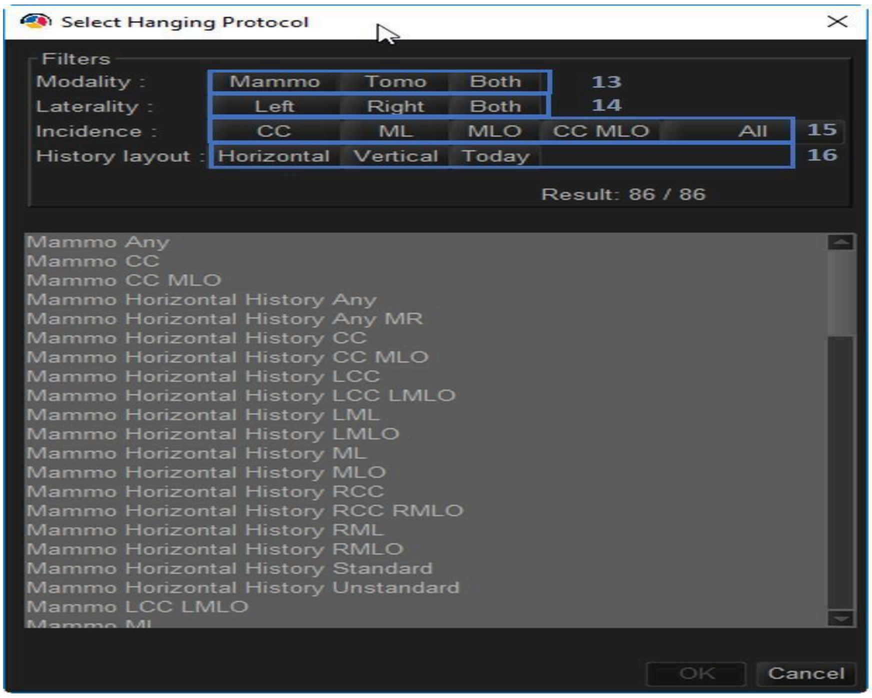
9. Applying a zoom factor to the selected sequence

10. Option used to reverse the order of the comparisons

11 Application of the partial view on the selected sequence

12. Overlap percentage when displaying the partial view

- To add a display sequence, click Button 1 for access to the display sequence search window:



13. Search filter zone on the modality

14. Search filter zone on the laterality

15. Search filter zone on the incidence

17. Search filter zone concerning the temporality and orientation of the history

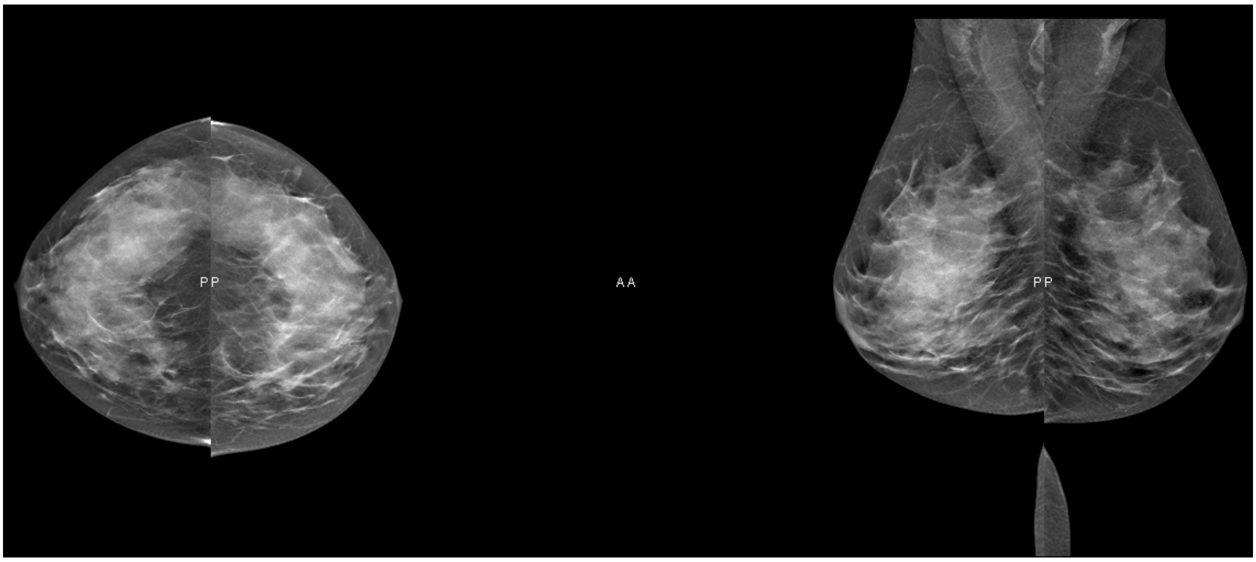
You can conduct searches by applying filters and adding the desired page layout to your display sequence

5.2.4.2. Application example: configuring a display sequence

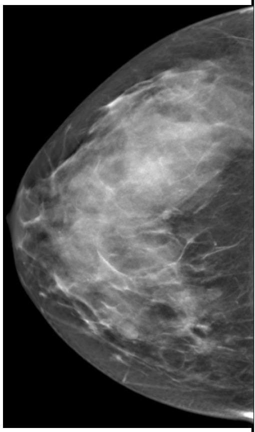
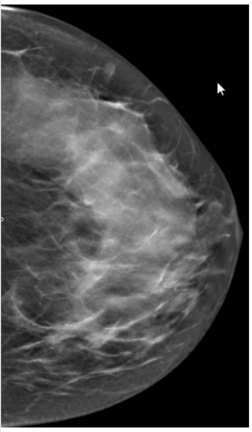
5.2.4.2.1. Standard exam of the day

The classic display order for a standard mammogram goes as follows:

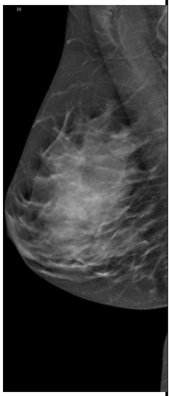
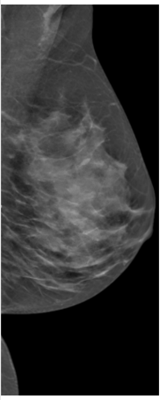
The following are displayed

<table>
<tr><th>RCC</th><th>LCC</th><th>RMLO</th><th>LMLO</th></tr>
<tr><td colspan="4">
</td></tr>
<tr><td colspan="2">SCREEN 1</td><td colspan="2">SCREEN 2</td></tr>
</table>

Next, the following are displayed

RCC	**LCC**
	
SCREEN 1	SCREEN 2

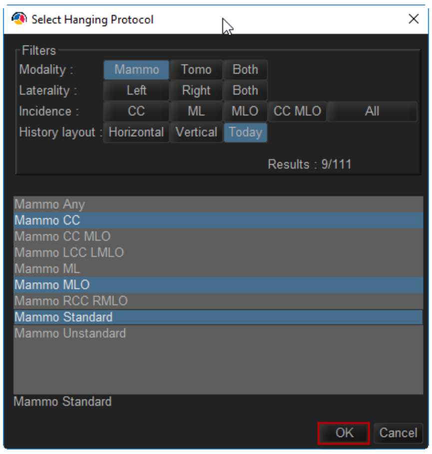
And then the following

RMLO	**LMLO**
	
SCREEN 1	SCREEN 2

To set up this display sequence, you must:

- go into the "Options" menu, and then manage the hanging protocol sequences
- click the + button
- apply a filter to the mammograms by clicking the Mammo button

- next, apply a new filter to the history by selecting Today
- you then obtain a list of nine display sequences
- select:
    - Mammo CC
    - and then ctrl - click on Mammo MLO
    - and then ctrl - click on Mammo Standard
    - and click OK

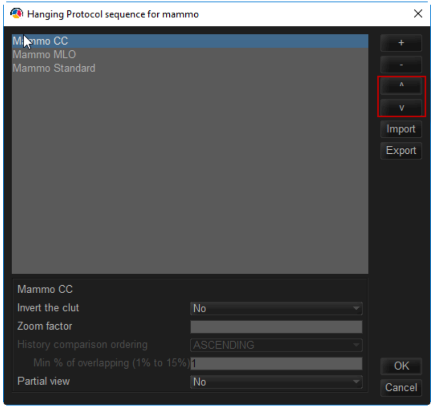


Results : 9/111

Mammo Any
Mammo CC
Mammo CC MLO
Mammo LCC LMLO
Mammo ML
Mammo MLO
Mammo RCC RMLO
Mammo Standard
Mammo Unstandard

Mammo Standard

- you will then have to order sequences in the window that appears
- to do this, use the buttons that move a selected sequence up or down



Mammo CC
Mammo MLO
Mammo Standard

Mammo CC
Invert the clut: No
Zoom factor:
History comparison ordering: ASCENDING
Min % of overlapping (1% to 15%): 1
Partial view: No

5.2.4.2.2. Advanced display

For configurations of more advanced sequences combining:

- mammo and tomosynthesis,
- contrast inversion,
- partial view, and
- history

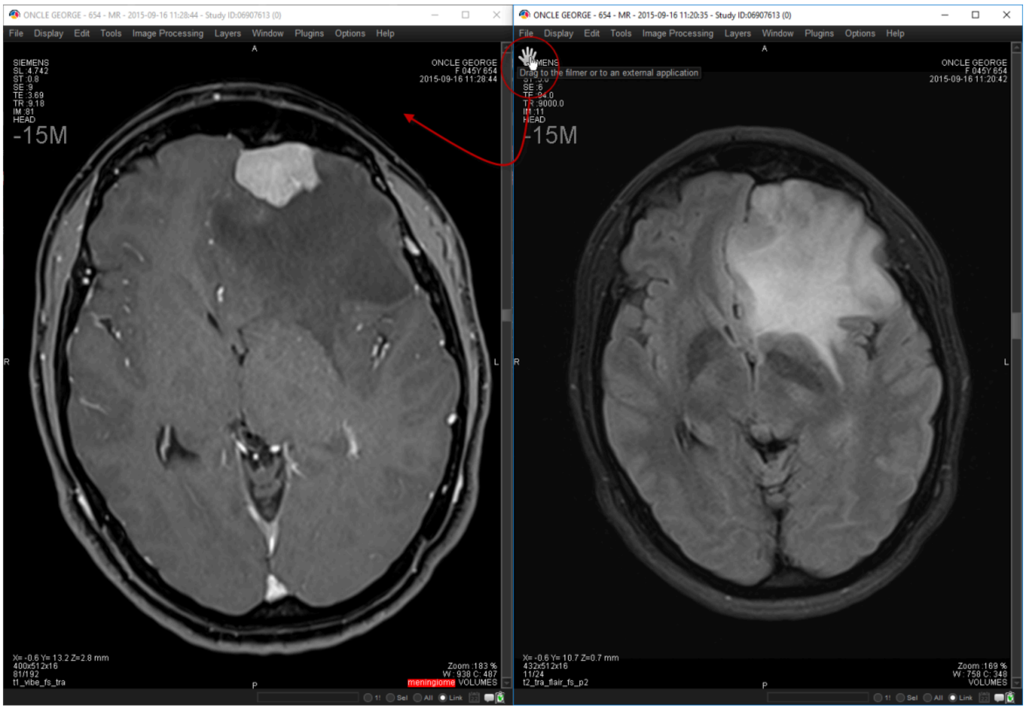
Visit the *TM-Store* to view the videos provided for this purpose.

5.3. Fusion via the drag & drop function

It is now possible to merge two series already displayed on screen using the hand that appears in the upper left-hand corner of each viewer.

5.3.1. User instructions

- Display two series on screen
- Move the cursor to the upper left of one of the two series you wish to merge
- Click the hand and hold the mouse button down, moving it to the series you wish to merge



5.3.2. Application example

5.3.2.1. Fusion of two series from the same exam

From now on, it will be easy to merge two series from the same exam at any time.

For example, in the neuro-radiological context, you can superimpose two different weightings.

The merge tool will adapt the size of the fields of view of each series, and the slice thicknesses.

You can therefore fuse 2D series with 3D series.

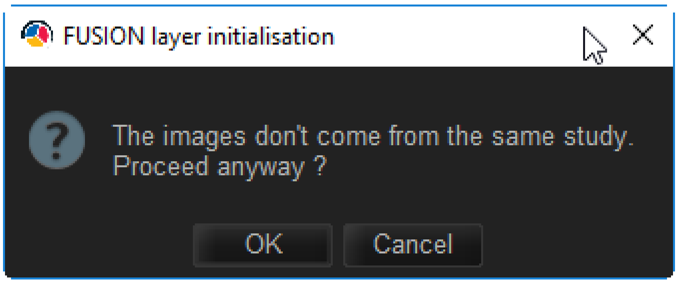
This will align the slice level.

This means that no coregistration correction will be necessary.

Next, to move gradually from one series to another, simply use the cursor that appears at the top of the merge window

5.3.2.2. Fusion of two series from different exams

When fusing two series from different exams, the system issues an alert message to notify you that these series do not come from the same exam.



FUSION layer initialisation

The images don't come from the same study. Proceed anyway ?

Simply click OK to fuse them.

The merge tool will adapt the size of the fields of view of each series, and the slice thicknesses.

You can therefore fuse 2D series with 3D series.

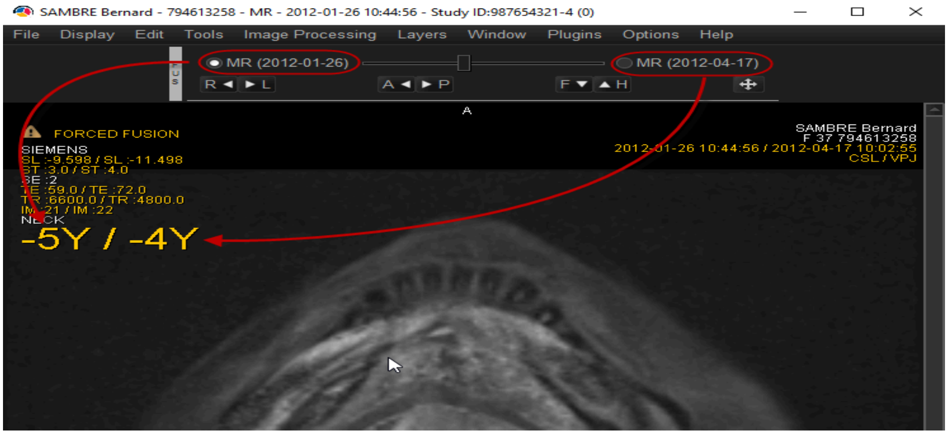
The slice level, however, will not be aligned.

A coregistration correction will therefore be necessary (see point 3.2.2.2 Coregistration correction).

5.3.2.2.1. How to tell the difference between the two series

To tell the difference between two series, you can look at:

- the date of the exams displayed in the slider
- the oldest exams are on the left
- in the fusion window, the text corresponding to the exams on the left is located to the left of the "/" symbol; likewise for the exams on the right



5.3.2.2.2. Coregistration correction

When two series from different exams are fused, a coregistration correction must be performed.

It is possible to correct the X, Y, or Z position of one series with respect to the other using the following tools:

It is also possible to move a whole series in the plane displayed without moving the other using the ✥ function

5.3.2.3. Using MPR Mode in Fusion Mode

The fusion function can be used freehand in combination with MPR Mode.

- Or you can start by opening both series in MPR Mode and then fuse them by hand.
  Or you fuse both series in 2D, and then enable MPR on the fused viewer.

5.4. Radiotherapy Module

The application contains a native module to display data from a TPS (*Treatment Planning System*).

It is also possible to generate contours called RTSTRUCT and send them to a TPS.

5.4.1. Context

5.4.1.1. Multidisciplinary meeting

During multidisciplinary team meetings, it is important for each specialist to be able to display his or her information in an optimum way.

From now on, radiotherapists will be able to display:

- treatment plans,
- irradiated zones,
- doses delivered,
- and other things

via the institutional viewing tool.

5.4.1.2. Expertise sharing: contouring complex lesions

The tool also now allows contours called RTSTRUCT to be drawn and sent to a TPS.

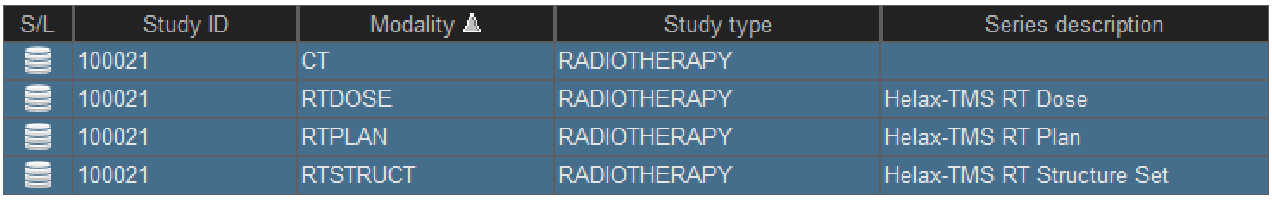
This feature will be very useful in cases of complex lesions that automatic segmentation tools do not handle well and where an input of radiological expertise seems essential.

Radiologists can therefore draw lesion contours and send them to the TPS for better patient care.

5.4.2. Display of dose data

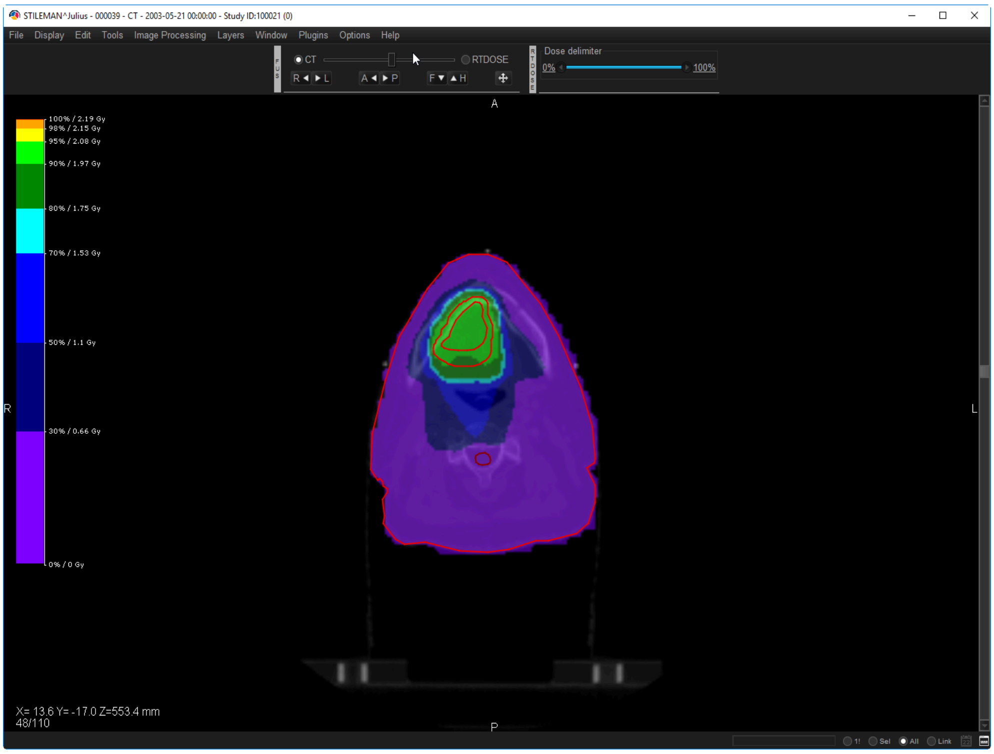
5.4.2.1. RTDOSE display

- Go to the “Series” tab of the Telemis browser
- Select all of the series concerning the radiotherapy exam, i.e.:
    - CT
    - RTDOSE
    - RTSTRUCT
    - RTPLAN
    - ...



S/L	Study ID	Modality ▲	Study type	Series description
☰	100021	CT	RADIOTHERAPY	
☰	100021	RTDOSE	RADIOTHERAPY	Helax-TMS RT Dose
☰	100021	RTPLAN	RADIOTHERAPY	Helax-TMS RT Plan
☰	100021	RTSTRUCT	RADIOTHERAPY	Helax-TMS RT Structure Set

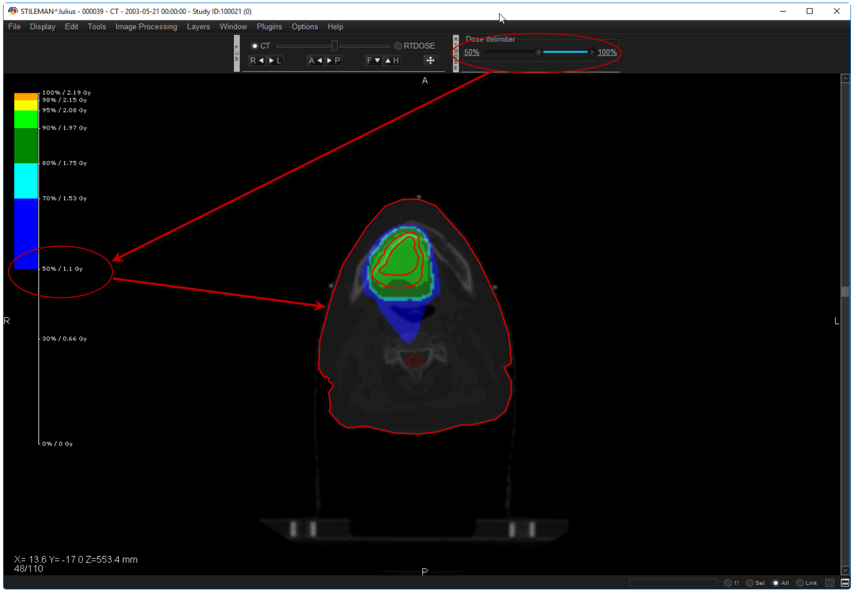
- and then press the "Enter" key on your keyboard.
- The system automatically fuses and displays the data correctly.



STILEMAN^Julius - 000039 - CT - 2003-05-21 00:00:00 - Study ID:100021 (0)

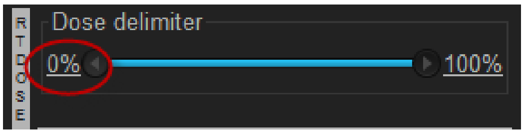
X= 13.6 Y= -17.0 Z=553.4 mm
48/110

- You can define a dose distribution threshold to be displayed on screen by setting the cursor to the minimum and maximum percentage to display.



Dose delimiter 50% 100%

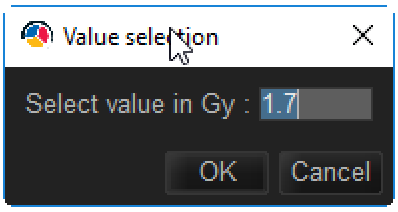
- You can also define a dose display threshold in Gy by clicking 0%



Dose delimiter

0% 100%

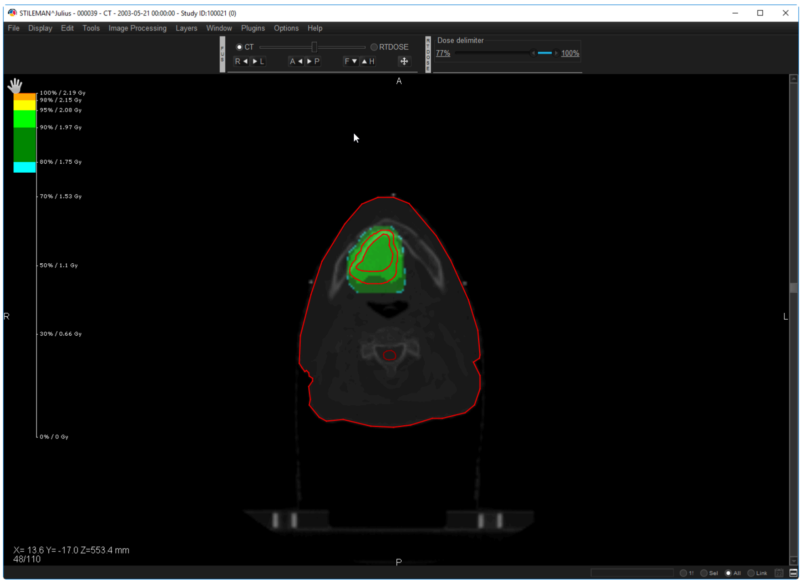
- and manually entering the minimum dose you wish to display.



Value selection

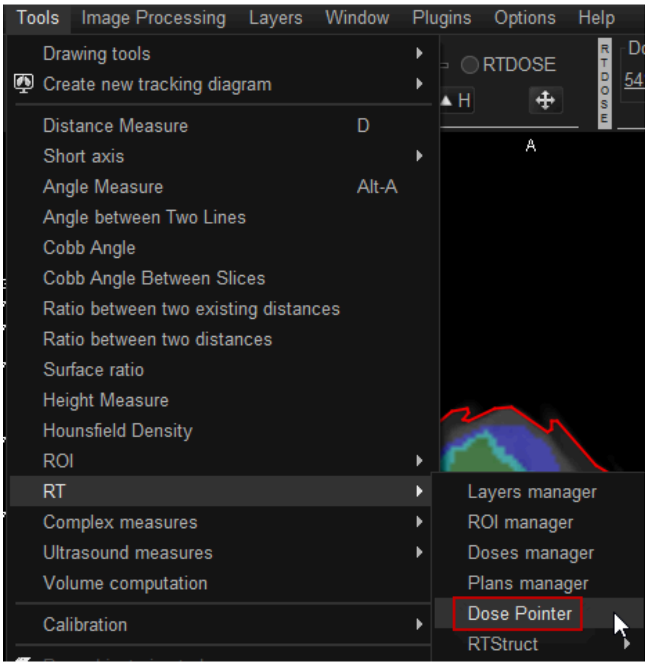
Select value in Gy : 1.7

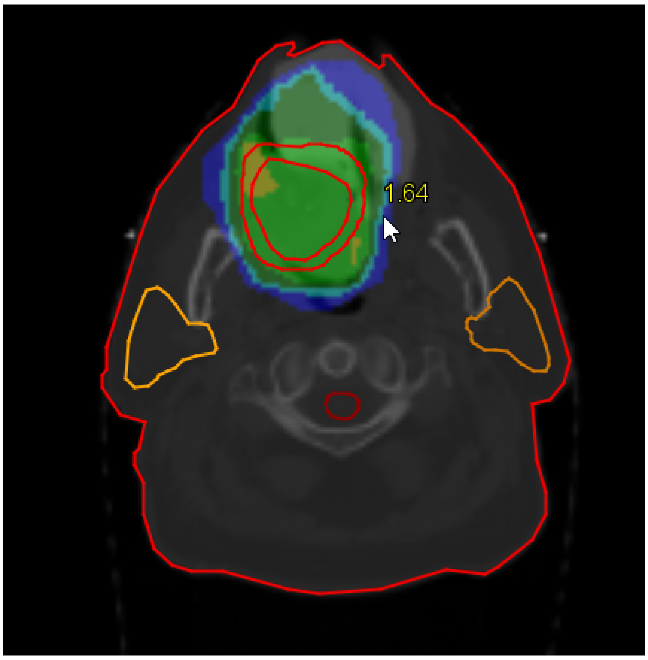
- The system will filter the dose display automatically



Dose delimiter 77% 100%

- You can also display the dose directly via the menu: “Tools => RT => Dose Pointer”



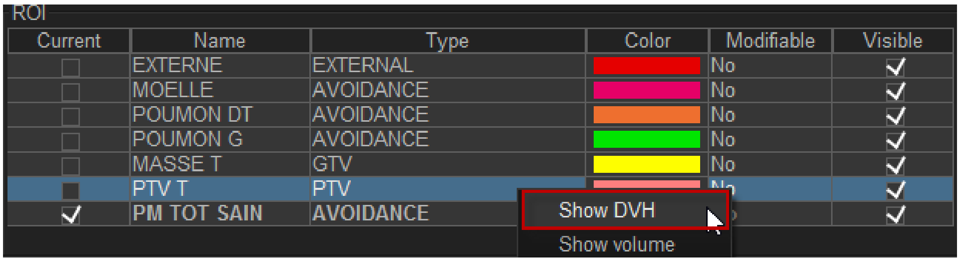


- The colour codes in the bar on the left can be configured.
- It is possible to go above 100%: this represents the excess dose administered to the patient.
    - To display more than 100% of the dose, the RTPLANs must be opened.

5.4.2.2. DVH display

- To be able to display DVH, the following must be opened:
    - CT
    - the RTDOSE layer
    - the RTSTRUCT layer
- Click the ROI management shortcut in your toolbar
    - or add it if it does not already exist.
- You will obtain a new window with all the RTSTRUCTs of the open exam:

- You may then select the structure whose DVH you wish to display, and then right-click,
- And then select the "Display DVH" menu

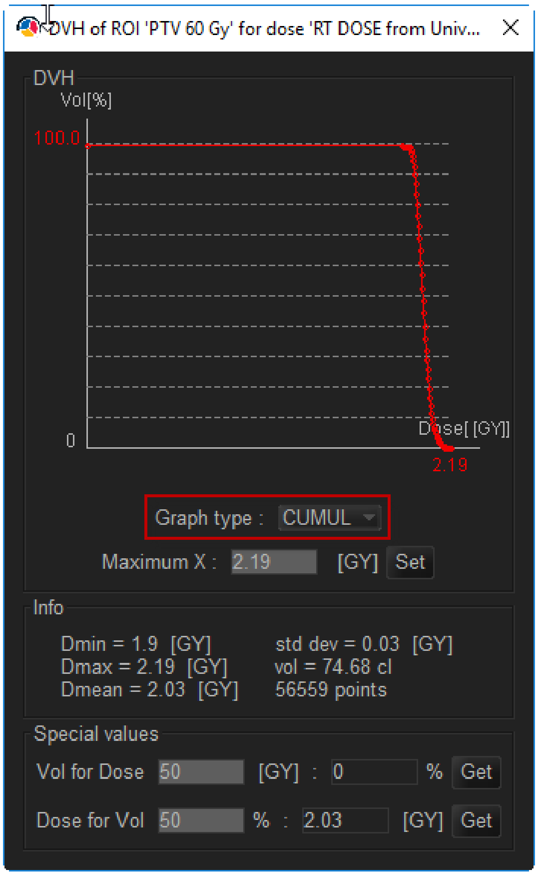
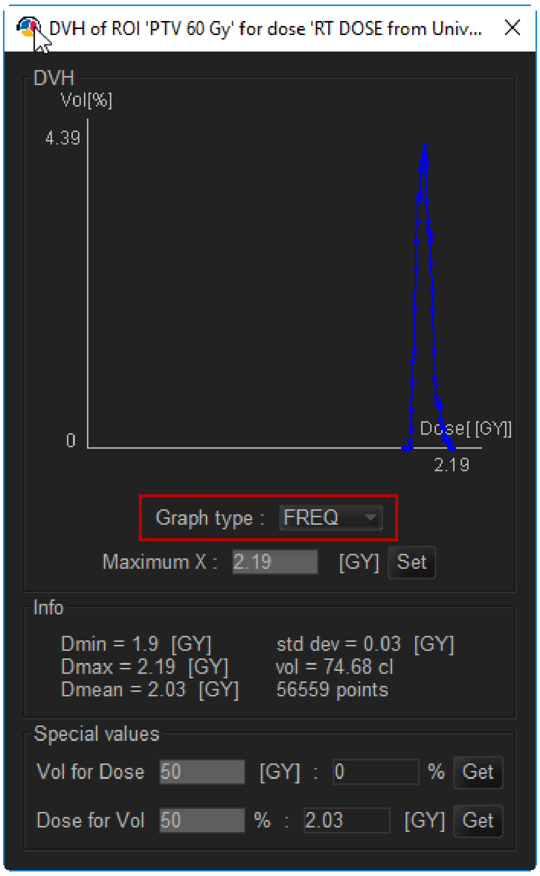


ROI

Current	Name	Type	Color	Modifiable	Visible
☐	EXTERNE	EXTERNAL	🟥	No	✓
☐	MOELLE	AVOIDANCE	🟥	No	✓
☐	POUMON DT	AVOIDANCE	🟧	No	✓
☐	POUMON G	AVOIDANCE	🟩	No	✓
☐	MASSE T	GTV	🟨	No	✓
☐	PTV T	PTV	🟥	No	✓
☑	PM TOT SAIN	AVOIDANCE			✓

It is possible to display the volume of the structure by selecting "Display the volume"

- It is possible to display the DVH as a cumulative dose or dose frequency

CUMULATIVE DOSE	DOSE FREQUENCY
	

DVH of ROI 'PTV 60 Gy' for dose 'RT DOSE from Univ...

Graph type : CUMUL

Maximum X : 2.19 [GY] Set

Info

Dmin = 1.9 [GY]
Dmax = 2.19 [GY]
Dmean = 2.03 [GY]
std dev = 0.03 [GY]
vol = 74.68 cl
56559 points

Special values

Vol for Dose 50 [GY] : 0 % Get

Dose for Vol 50 % : 2.03 [GY] Get

DVH of ROI 'PTV 60 Gy' for dose 'RT DOSE from Univ...

Graph type : FREQ

Maximum X : 2.19 [GY] Set

Info

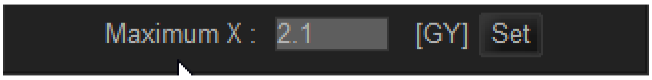
Dmin = 1.9 [GY]
Dmax = 2.19 [GY]
Dmean = 2.03 [GY]
std dev = 0.03 [GY]
vol = 74.68 cl
56559 points

Special values

Vol for Dose 50 [GY] : 0 % Get

Dose for Vol 50 % : 2.03 [GY] Get

- It is possible to define a threshold for the display of the delivered dose on this RTSTRUCT

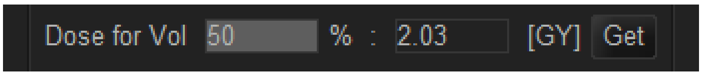


Maximum X : 2.1 [GY] Set

- It is possible to define the delivered dose percentage according to a defined dose

Vol for Dose 50 [GY] : 0 % Get

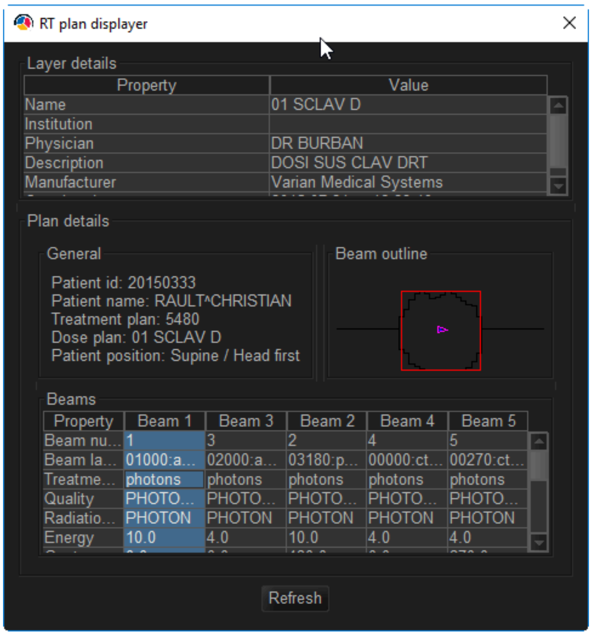
- It is possible to define the delivered dose according to a percentage of the volume defined.



Dose for Vol 50 % : 2.03 [GY]

5.4.2.3. RTPLAN display

- To be able to display the RTPLANs, the following must be opened:
  - CT
  - the RTPLAN layer
- And then click the plane management button
  - or add it if it does not already exist.
- Select one of the columns to display an irradiation plane.



Property	Value
Name	01 SCLAV D
Institution	
Physician	DR BURBAN
Description	DOSI SUS CLAV DRT
Manufacturer	Varian Medical Systems

Patient id: 20150333
Patient name: RAULT^CHRISTIAN
Treatment plan: 5480
Dose plan: 01 SCLAV D
Patient position: Supine / Head first

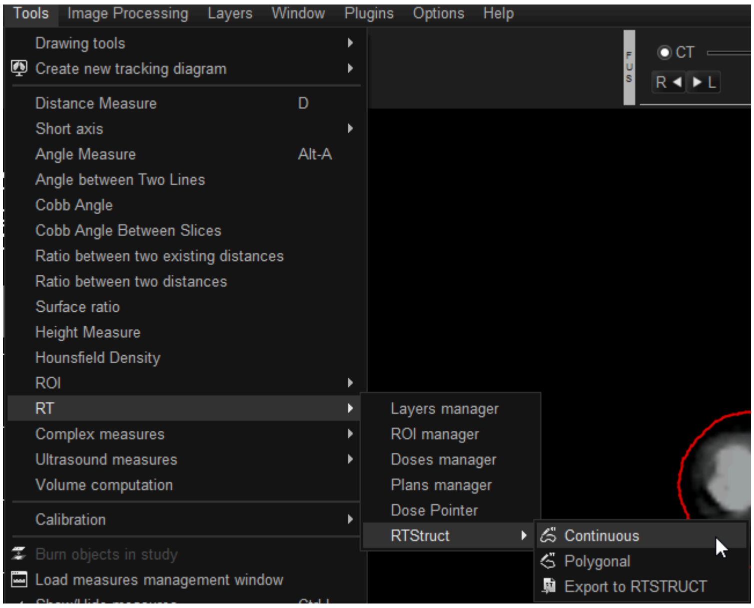
Property	Beam 1	Beam 3	Beam 2	Beam 4	Beam 5
Beam nu...	1	3	2	4	5
Beam la...	01000:a...	02000:a...	03180:p...	00000:ct...	00270:ct...
Treatme...	photons	photons	photons	photons	photons
Quality	PHOTO...	PHOTO...	PHOTO...	PHOTO...	PHOTO...
Radiatio...	PHOTON	PHOTON	PHOTON	PHOTON	PHOTON
Energy	10.0	4.0	10.0	4.0	4.0

5.4.3. RTSTRUCT management

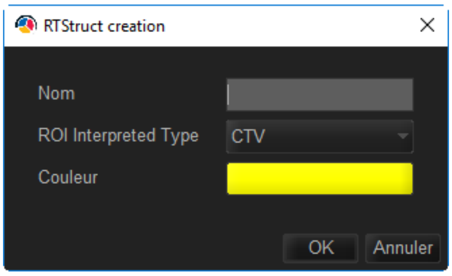
5.4.3.1. RTSTRUCT drawing

To draw an RTSTRUCT, you must:

- open a CT (generally the dosimetry one)
- Go into the “Tools - RT - RTStruct” menu and choose the type of drawing tool you wish to use.
  - The continuous tool lets you draw the contour by holding down the mouse button.
  - The polygon tool lets you draw the contour by positioning each point of the contour, click by click.



- or click the shortcut in your toolbar
    - You can add it if this has not already been done.
- Before beginning to draw, you must choose the name, type, and colour of your contour.



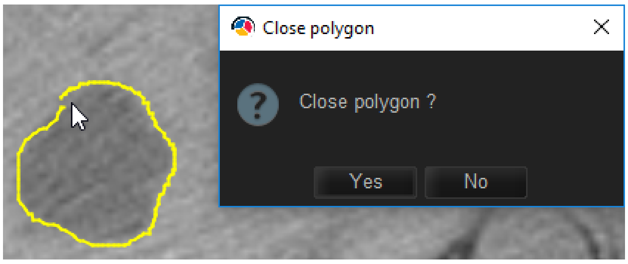
Nom

ROI Interpreted Type: CTV

Couleur

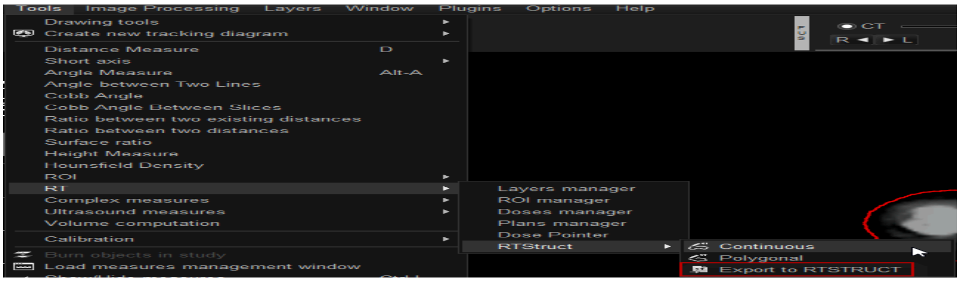
Next, you must draw the contour of the lesion manually on each slice.

- When you release the mouse, the system offers to close the polygon via this window.



Close polygon ?

- When the contour is complete, right-click anywhere in the image and then click the shortcut in your toolbar
    - You can add it if this has not already been done.
- You can also access the menu via the “Tools - RT - RTStruct” menu, in which you select “Export to RTSTRUCT”.



- Then you just need to select the DICOM destination corresponding to your TPS and click OK.

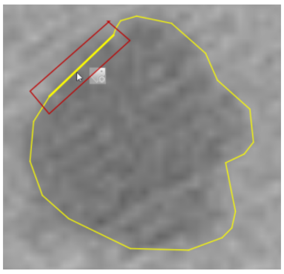
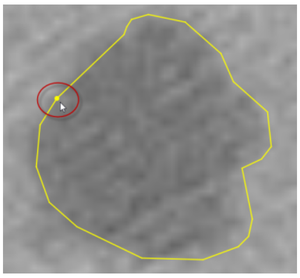
5.4.3.2. RTSTRUCT editing

You can edit an RTSTRUCT during tracing.

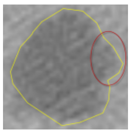
To do this, apply the following instructions:

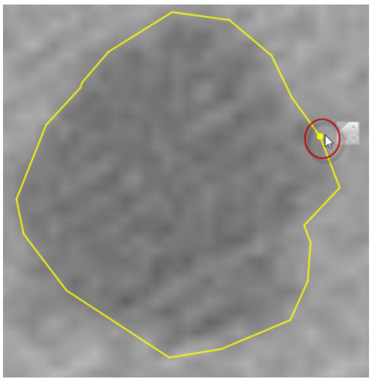
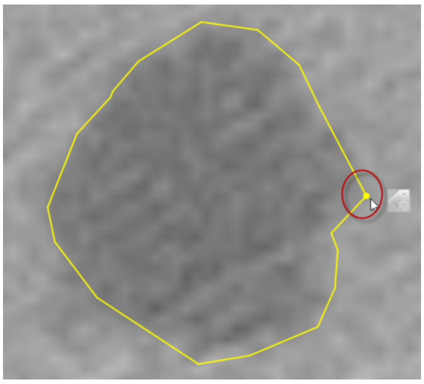
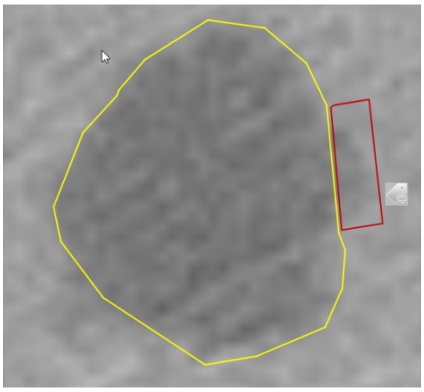
- Bring the cursor towards the contour and ctrl–left click.
- Click a segment to add intersections
- Click a point between two segments (intersection) to delete both intersecting segments

When approaching a closed contour, you will see that certain parts of the region of interest become bold

A segment of the region of interest	An intersection of the region of interest
	

5.4.3.3. Application example: Deleting part of the region of interest

To delete part of the contour, like the part circled in red here , delete all the intersecting points that constitute this bulge by doing ctrl–left click on each of the points.

Deleting the first point =>	Deleting the second point =>	Final result
		

5.5. TM-Forms

The *TM-Forms* feature lets you create personalised forms.

These forms can be completed with text input manually or using voice recognition tools.

You can also input key images from the PACS.

Once these forms have been completed, they are sent to your MACS and can then benefit from all the options available in Telemis.

Here are a few examples of the application of this feature:

5.5.1. Application Example 1: Structured Report (Prostate)

The first case is a potential example of radiological report tool in the PACS.

We have based this example on prostate exams because they are structured in terms of a report.

The idea of creating a "form" or, in this case, a report model containing all the criteria that make up a prostate exam report.

- image

Once the result is in the MACS, you can benefit from all of the transfer options in Telemis.

So, in the context of a teleradiology set-up, it would be possible to have a more generic report model and dictate any type of exam.

Then, using modules such as *TM-Satellite*, we can set up the two-way exchange of this report in DICOM PDF format.

5.5.2. Application Example 2: Multidisciplinary team meeting report (RCP)

TM-Forms are so personalisable that the scope of their application is limitless.

An example with this very concrete request from one of our clients to provide them with a form to complete to generate RCP reports.

This form is now used and takes the following form:

- image

5.5.3. Application Example 3: Request for opinion and patient transfer

Still on the basis of client requests, we have created an opinion request form in the context of patient transfer from one institution to another.

Open the case to be transferred, open the form concerned, fill in the boxes, and insert the key images.

Then simply transfer the exam and the request via a *TM-Satellite* or *6.2 TM-Community Cloud*

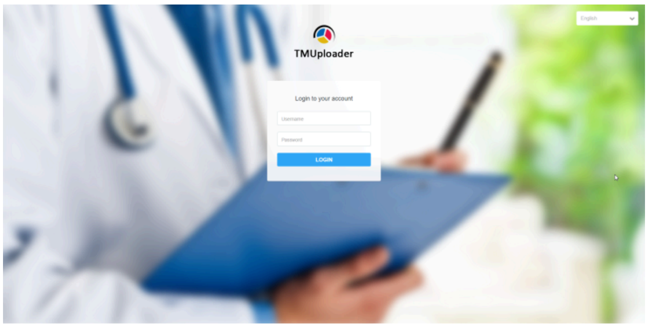
- image

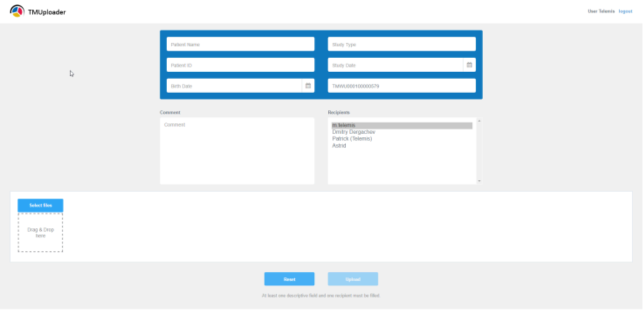
5.6. New Web and Telemis Cloud Features

5.6.1. TM-Uploader

The *TM-Uploader* is a new functionality that supplements the *TM-Publisher Web*.

This interface allows the integration of multimedia data or data from DICOM images from a web page directly into your PACS.





5.6.1.1. Application Example 1: Request for second opinion

If a colleague wants to send you a case to review, simply send him/her the download link and access codes.

Your colleague can then follow the procedure to import the whole patient file.

The file will be imported transparently into your MACS.

5.6.1.2. Application Example 2: Patient care / expert analysis

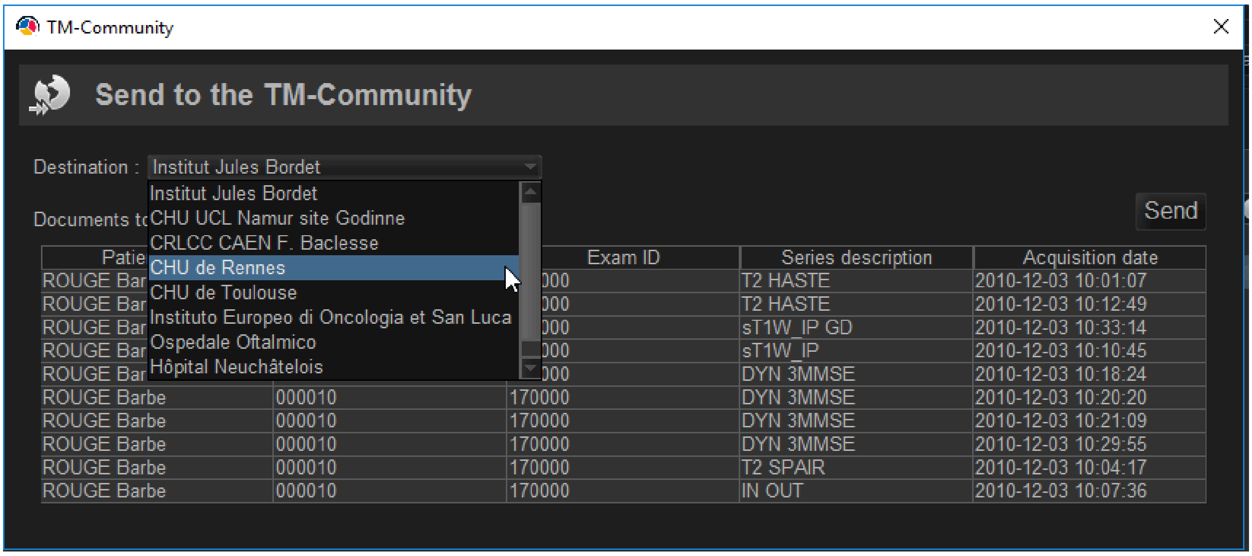
If you are taking charge of a complicated case that has been handled in different centres of expertise, it can sometimes be difficult and time-consuming to collect all the data required for optimum patient care.

In that case, simply send the link to the page concerned, and all the centres can then send you all the information you need.

5.6.2. TM-Community

This version offers you the opportunity to connect to a secure platform in the cloud for data exchange between all Telemis clients who are logged on.

All clients who are logged on can exchange their multimedia data with each other.



Destination : Institut Jules Bordet

Patie		Exam ID	Series description	Acquisition date
ROUGE Bar		000	T2 HASTE	2010-12-03 10:01:07
ROUGE Bar		000	T2 HASTE	2010-12-03 10:12:49
ROUGE Bar		000	sT1W_IP GD	2010-12-03 10:33:14
ROUGE Bar		000	sT1W_IP	2010-12-03 10:10:45
ROUGE Bar		000	DYN 3MMSE	2010-12-03 10:18:24
ROUGE Barbe	000010	170000	DYN 3MMSE	2010-12-03 10:20:20
ROUGE Barbe	000010	170000	DYN 3MMSE	2010-12-03 10:21:09
ROUGE Barbe	000010	170000	DYN 3MMSE	2010-12-03 10:29:55
ROUGE Barbe	000010	170000	T2 SPAIR	2010-12-03 10:04:17
ROUGE Barbe	000010	170000	IN OUT	2010-12-03 10:07:36

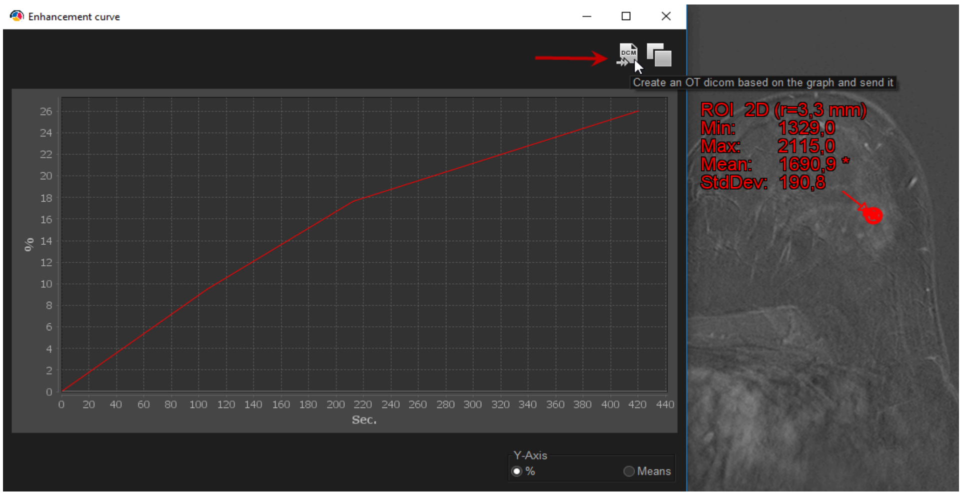
5.7. Miscellaneous

5.7.1. Saving the activity curves

From 4D viewers, activity curves or enhancement curves can be generated.

It is then possible to save these curves:

- Display your series in 4D
- Draw a ROI
- Right-click "Display enhancement curve"
- Click the button to send the curve to the PACS.



ROI 2D (r=3,3 mm)
Min: 1329,0
Max: 2115,0
Mean: 1690,9 *
StdDev: 190,8

You can display several enhancement curves and send them together. This will give a curve comparison effect.

5.7.2. VRT in the filmer

It is now possible to add different views from the VRT viewer to the filmer.

5.7.3. Virtual TMRHE

You can now have a version of your TMRHE on a tablet.

The version will be exactly the same as the home version.

To implement this on site, certain infrastructure prerequisites must be satisfied.

This case must therefore be monitored by your site manager.

5.7.4. New IRON or fatty liver measurement plugin

A new version of the "*Iron by MR*" application will be available in Version 4.80.

For more information on the use of this program, go to the *TM-Store* or contact your site manager.

5.7.5. PDF support

The Telemis viewer now incorporates an integrated DICOM PDF viewer and offers a whole set of dedicated tools.

1. Local save option
2. Printing the PDF

3. Zoom
4. Display or hide the PDF reader tab.
5. Back to first page
6. Back to previous page
7. Down to next page
8. Down to last page
9. Reduce the zoom factor
10. Increase the zoom factor
11. Display document in original size
12. Zoom to fill window
13. Zoom to fill width of window
14. Rotate clockwise
15. Rotate anticlockwise
16. Move document
17. Text selection tools
18. Zoom in on selected area
19. Dynamic zoom
20. Mask selected area

From now on, PDF documents will be managed like any Telemis viewer.

They can be managed by hanging protocols or displayed automatically in landscape mode or portrait mode, depending on the type of image.

5.7.6. Dropbox integration

We have developed integration with the Dropbox application.

5.7.6.1. Application example

It is often necessary to share documents within a department. These may be:

- Tools for the management of the department
- Diagnostic guidelines
- Anatomical references

This type of document should not be kept in the PACS.

However it is useful to be able to access it easily from the PACS.

That is why we can connect to a specific Dropbox account: so that all of these support tools at the imaging centre are accessible from any place, any time.

6. ADDON 4.80 TO 4.90

6.1. Image registration

6.1.1. The philosophy

Comparing exams carried out on different dates accounts for a large percentage of PACS system use. To accelerate the comparison process, Telemis has integrated an anatomical image registration tool that automatically aligns exams performed by different modalities, on different dates, and along different orientations.

6.1.2. How it works

The *TM-ReceptionHE* software provides three types of image registration as standard:

- anatomical: version 4.90 integrates a new algorithm to align CT images with CT, MR with MR, CT with MR, and PT/CT with PT/CT. Alignment is performed along the X, Y and Z axes and with free angle rotations.
- Table position: when two series of images belong to the same exam, the DICOM "table position" notification is used to synchronise the views.
- Free position: the user can determine the synchronisation of the viewers.

6.1.3. Default operation

For series belonging to the same exam, the *TM-ReceptionHE* software uses synchronisation on table position by default. When series from a previous exam of the same patient are displayed, anatomical comparison is enabled, to align the viewers ideally.

6.1.4. Excluding a viewer from synchronisation

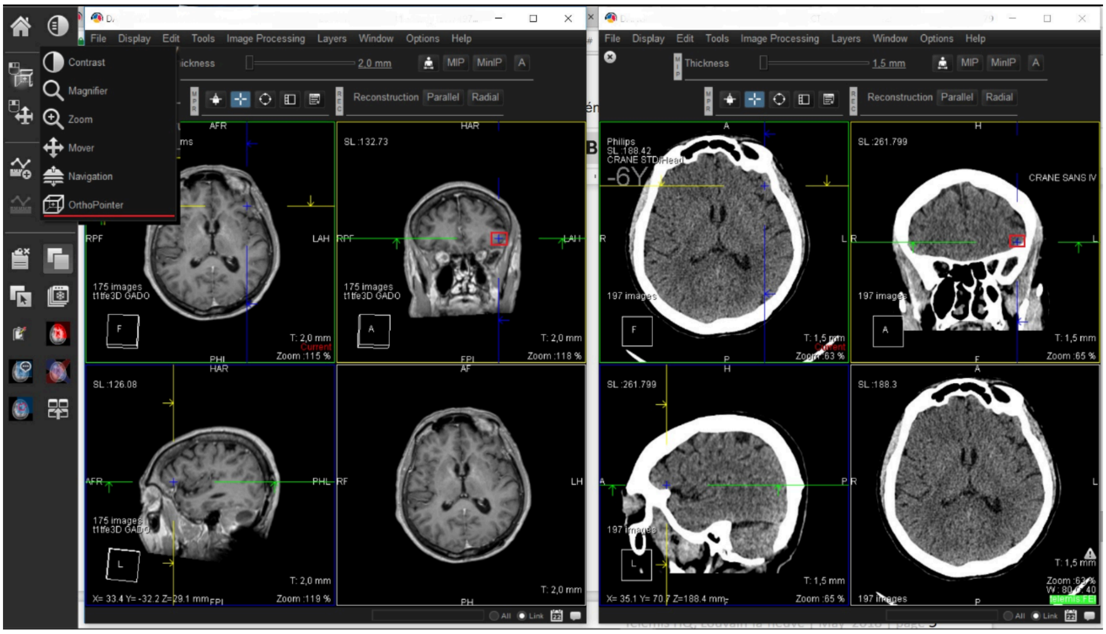
If needed, a viewer can be excluded from the synchronised view using the "compare" button in the lower right-hand part of the image window.

6.1.5. Manual registration of a viewer

According to the morphological changes in a patient, it is sometimes desirable to register one series with respect to the others, manually and quickly. To do this, when the "<" key is pressed, positioning changes in the active window are not propagated to the others. When the key is released, synchronisation is resumed with the induced offset.

6.1.6. Orthopointer tool

The orthopointer tool lets you position a marker – shown by a blue cross – on an anatomical area in a series of images, and see this pointer also appear on all open series containing the same anatomical area. This makes it easy, for example, to count the vertebrae on the two sagittal sections that are almost separated in MRI, for example.



6.2. Reporting tools

6.2.1. The philosophy

There is a global trend towards offering radiologists an all-in-one advanced image viewing and report input tool. That is why version 4.90 offers an optional report management tool combining digital dictation management and a powerful voice recognition system: a perfectly integrated text and voice tool for the radiologist.

6.2.2. Features

6.2.2.1. Status management

The ability to manage reports also implies the ability to manage one's progress status. For this purpose, we have added statuses to the exam, so that appropriate work lists can be created for junior or senior physicians and for administrative staffs.

The new statuses can be selected in the upper right-hand part of the search interface. They are:

- no report (the physician has not yet started to report the exam),
- assigned to a user for report (to transfer the case to a colleague or reserve the exam for oneself later)
- reading in progress (the physician is currently reporting the exam)
- report completed (the physician has finished the reporting task)
- report encoded (the final report is ready and sent)
- draft report (the report has been paused and is considered not to be final)
- report sent for typing (the report is in its approval phase in the administrative office)

6.2.2.2. Using the report input module

6.2.2.2.1. Opening the module

According to the configuration chosen by the user, the module is opened automatically by double-clicking the image or manually via the mic trigger button 🎙 in image viewers.

The patient context is always synchronised between the image part and the report part. Closing the images will close the report, and vice-versa.

6.2.2.2.2. Dictation or voice recognition?

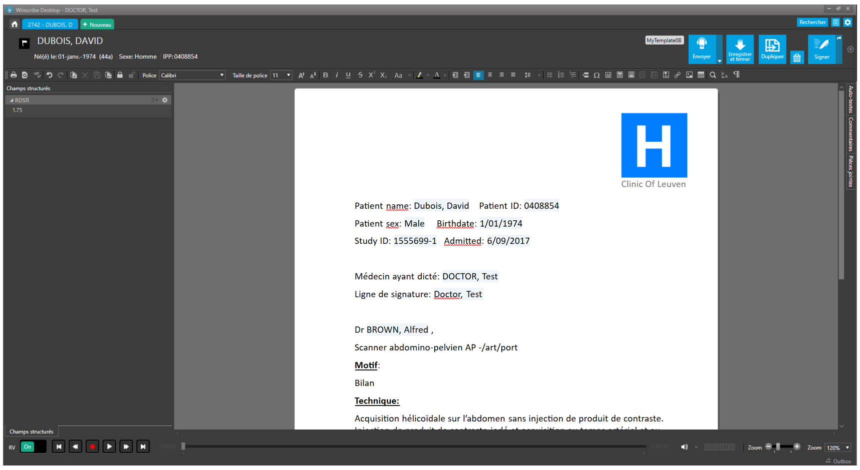
According to the time of day, the amount of work remaining or the type of exam, you can always switch to a "complete digital dictation" or "voice recognition" mode. In the first case, the digital dictation feature will send an audio file to the administrative office, where the text will be typed manually. In the second case, voice recognition eases the workload of users by transcribing the voice into text.

The VR "ON/OFF" button in the lower left-hand corner of the interface is used to switch between modes.

6.2.2.2.3. Report templates (voice recognition only)

For the convenience of the physician, report templates are associated with each type of exam. This can save precious minutes when describing the exam techniques used, for example. Similarly, structured reports, which are typically "fill-in-the-blanks" texts, mean that only the specific values for that exam need to be input, which shortens the interpretation time.

When the irradiation dose is available in DICOM-SR format, the system automatically indicates the dose values of the exam.



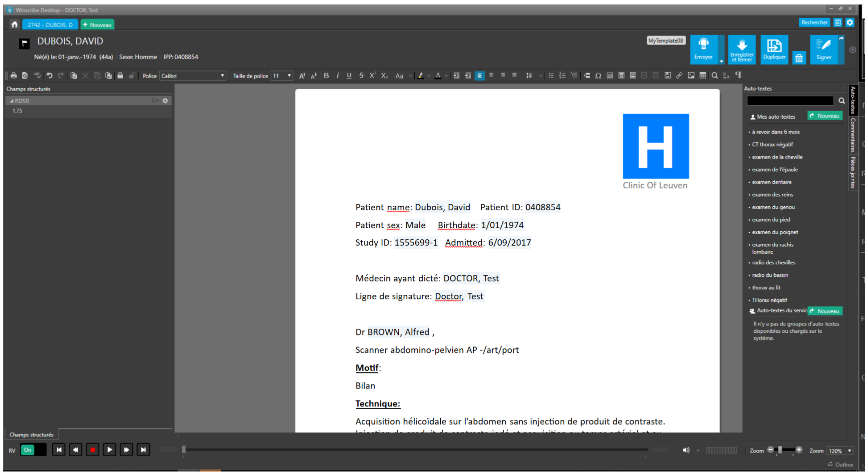
Patient name: Dubois, David Patient ID: 0408854
Patient sex: Male Birthdate: 1/01/1974
Study ID: 1555699-1 Admitted: 6/09/2017

Médecin ayant dicté: DOCTOR, Test
Ligne de signature: Doctor, Test

Dr BROWN, Alfred ,
Scanner abdomino-pelvien AP -/art/port
Motif:
Bilan
Technique:
Acquisition hélicoïdale sur l'abdomen sans injection de produit de contraste.

6.2.2.2.4. *Automatic texts (voice recognition only)*

Auto-texts let you create a library of frequently-used paragraphs in order to speed up the interpretation. The auto-texts are available either on the right-hand side of the report interface or by saying "insert" aloud, followed by the name of the auto-text to be placed in the text. For example: "*insert Negative Thorax*", places the pre-encoded paragraph(s) in the text at the cursor location.

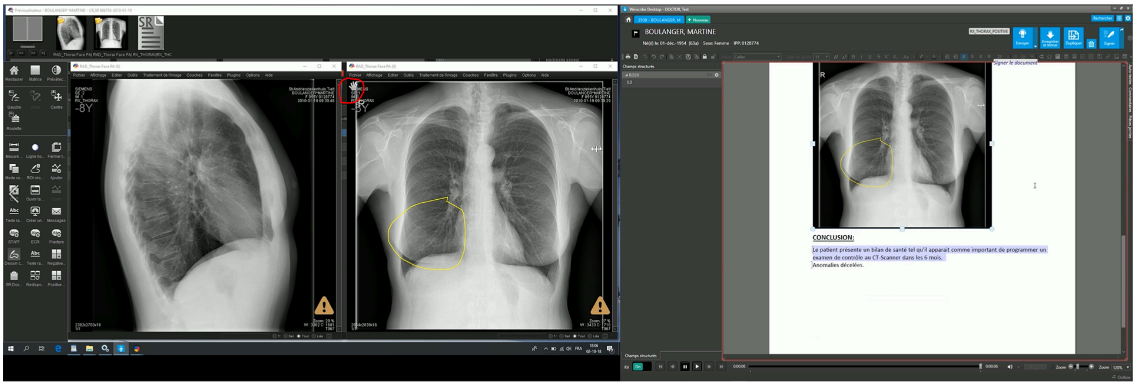

Auto-textes
Mes auto-textes
- à revoir dans 6 mois
- CT thorax négatif
- examen de la cheville
- examen de l'épaule
- examen dentaire
- examen des reins
- examen du genou
- examen du pied
- examen du poignet
- examen du rachis lombaire
- radio des chevilles
- radio du bassin
- thorax au lit
- THorax négatif

Auto-textes du servic

Il n'y a pas de groupes d'auto-textes disponibles ou chargés sur le système.

6.2.2.2.5. *Image selection (voice recognition only)*

To add some images in the report, you can use the drag & drop function in the image viewers (represented by an open hand in the upper left-hand corner of the image displayed) and place it in the text at the chosen location.



CONCLUSION:
Le patient présente un bilan de santé tel qu'il apparait comme important de programmer un examen de contrôle au CT-Scanner dans les 6 mois.
Anomalies décelées.

6.2.2.2.6. Pause

If the physician wishes to take a break from writing an exam report, the "save and close" function can be used. This changes the status of this exam in the PACS and allows the physician to resume the task later, from the exact point where the interruption occurred.

This function is especially useful for communication between junior and senior physicians in a hospital, so that the senior doctor can check and approve the reports before confirming them.

6.2.2.2.7. The "negative exam" shortcut

When an imaging exam is negative, it can sometimes seem like too much effort to dictate the whole standard report again. To save time, there is a "Negative" button in the image viewer. The purpose of this is to switch the interface from report input mode to a ready-to-use report in the event of a negative case.

6.2.2.2.8. Voice shortcuts (voice recognition only)

Several voice shortcuts are available to facilitate the radiologist's workflow. The user simply needs to speak these voice shortcuts after a short pause. The commands are as follows:

- "next field": takes you to the next paragraph or the next value field for a structured report.
- "previous field": takes you to the previous paragraph or the previous value field for a structured report.
- “conclusion”: takes you to the concluding paragraph
- “sign document”: validates the document and closes all image viewers without sending it via the administrative office.
- "send document": sends the document to the administrative office for correction.
- "insert (name of an automatic text)" is used to insert the specified automatic text.
    - You are advised to pause briefly before speaking the voice shortcuts, so that the system will understand that this is not additional text to be transcribed.

6.2.2.3. Closing the exam

When the report is in its final form, the physician can choose between

✎	sign document: the document is deemed not to require any action by the administrative office, and can be sent directly to the recipients;
🎧	send document: the document needs to be proofread by the administrative office;
⬇	save document: the document is considered to be paused;

🗑	cancel document: it is decided that the document should not be saved, and can be destroyed.

6.2.2.4. "Typing and administrative" stage

In the workflow that includes sending the document for typing and administrative actions, the exam is temporarily closed on the radiologist's console and appears on the administrative interface. Administrative personnel can listen to or read the report input by the physician and make any necessary changes.

Once this phase is complete, the list of reports for approval appears in the physician's interface. After re-reading the report, the physician simply presses the "sign" button to send the report to the recipient.

Job N.	MRN	Patient Name	Author	Created	Department	Job Type
860	11111	JONES, Michae	JAMES, Harper J	10-Jul-2013 0	Radiology	Letter
861	11111	JONES, Michae	JAMES, Harper J	10-Jul-2013 0	Radiology	Letter
867	11111	JONES, Michae	JAMES, Harper J	10-Jul-2013 1	Radiology	Letter
868	11111	JONES, Michae	JAMES, Harper J	10-Jul-2013 1	Radiology	Letter
888	48152659	WILLIAMS, Eva	HARPER, James John	10-Jul-2013 1	Radiology	CT-Scan
889	48152659	WILLIAMS, Eva	HARPER, James John	10-Jul-2013 1	Radiology	CT-Scan
906	48152659	WILLIAMS, Eva	HARPER, James John	11-Jul-2013 1	Radiology	CT-Scan

6.2.3. Module configuration

Configuration of the module is one of the services included with the purchase of this optional module. Your designated Site Manager and Sales Manager will be happy to discuss these requirements with you.

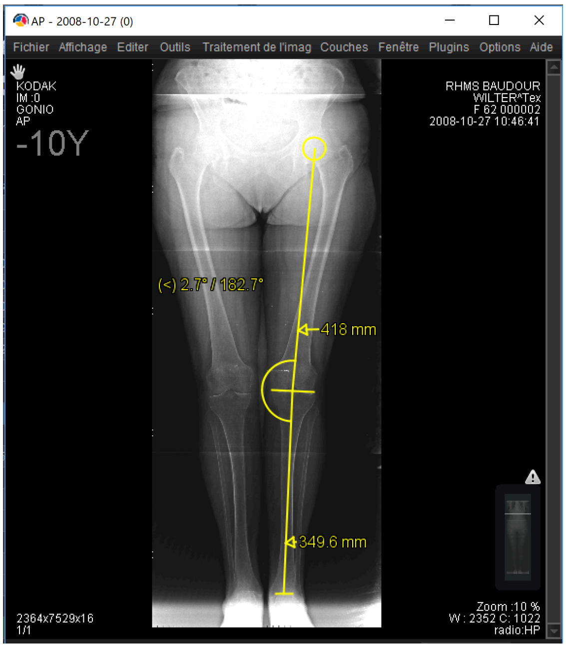
6.3. Goniometry

6.3.1. The philosophy

Telemis has had the goniometry tool for many years. In response to the needs of certain hospitals, however, we have supplemented it with another tool that presents measurements in a different and complementary way.

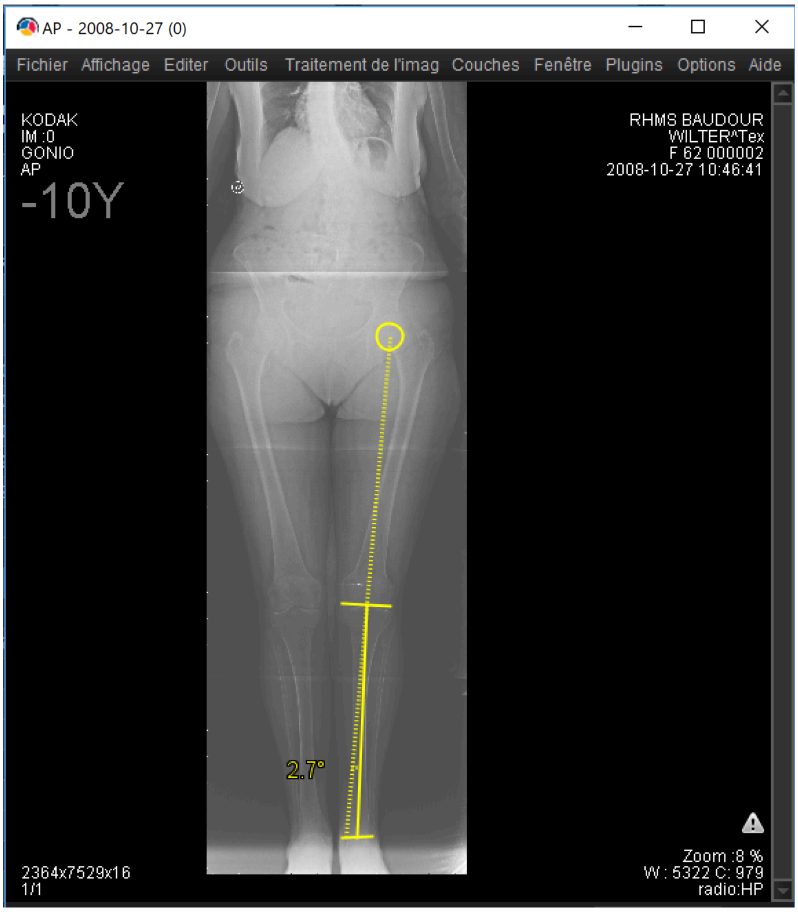
6.3.2. Goniometry tool v1

The *TM-ReceptionHE* software takes goniometric measurements via the "tool, complex measurements Goniometry v1" menu. This is the traditional Telemis tool.

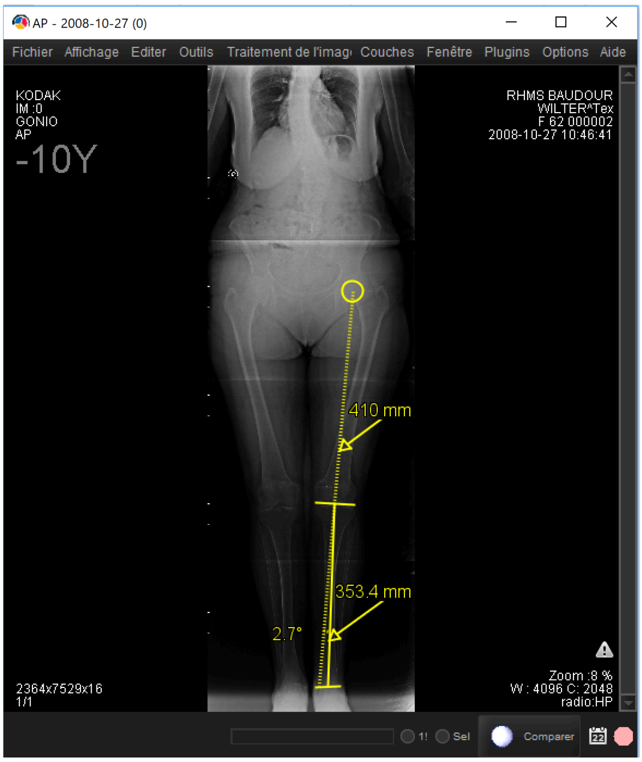

AP - 2008-10-27 (0)
Fichier
Affichage
Editer
Outils
Traitement de l'imag
Couches
Fenêtre
Plugins
Options
Aide
KODAK
IM :0
GONIO
AP
-10Y
RHMS BAUDOUR
WILTER^Tex
F 62 000002
2008-10-27 10:46:41
(<) 2.7° / 182.7°
418 mm
349.6 mm
2364x7529x16
1/1
Zoom :10 %
W : 2352 C: 1022
radio:HP

6.3.3. New tool

A "goniometry v2" tool is now available in the same menu, for users who want the measurements presented differently.



If necessary, limb lengths can also be displayed by right-clicking on the measurement drawn, and choosing the option "show/hide limb length".


AP - 2008-10-27 (0)
Fichier
Affichage
Editer
Outils
Traitement de l'imag
Couches
Fenêtre
Plugins
Options
Aide
KODAK
IM :0
GONIO
AP
-10Y
RHMS BAUDOUR
WILTER^Tex
F 62 000002
2008-10-27 10:46:41
410 mm
353.4 mm
2.7°
2364x7529x16
1/1
Zoom :8 %
W : 4096 C: 2048
radio:HP
Sel
Comparer

6.4. TM-Community

6.4.1. The philosophy

The *TM-Community* concept consists of facilitating exchanges between Telemis customers. In practice, each Telemis customer is connected to a server in a Cloud environment, which allows the user to send and receive data to and from other Telemis customers.
The exchanges are not limited to DICOM images; they can include all the data managed by Telemis (image, multimedia, PDF, DICOM-RT radiotherapy document, etc.)

Optional modules are available to connect non-Telemis customers.

6.4.2. Procedure

6.4.2.1. Sending data to a site

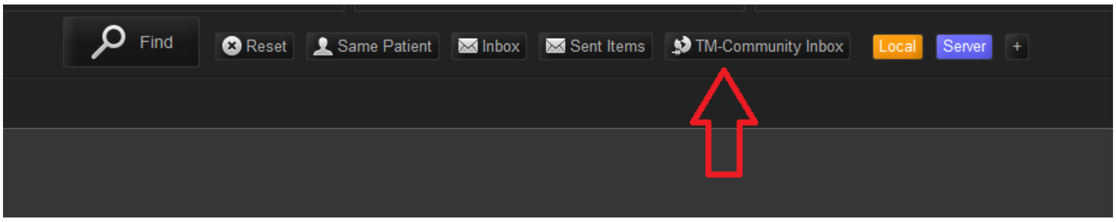
To send images from one site to another, simply:

- from the sending site, select one or more elements in the Telemis MACS and click the "*TM-Community*" button,
- select the site to which you wish to send images,
- confirm.

6.4.2.2. Receiving images from a site

When receiving images, the question of patient identity arises. To eliminate the risk of incorrectly linking an image to a similar name or falsely identical patient numbers, images received are stored in a buffer zone called "TM-Community inbox".

This box can be seen by any person holding the appropriate rights in the *TM-ReceptionHE* viewer.

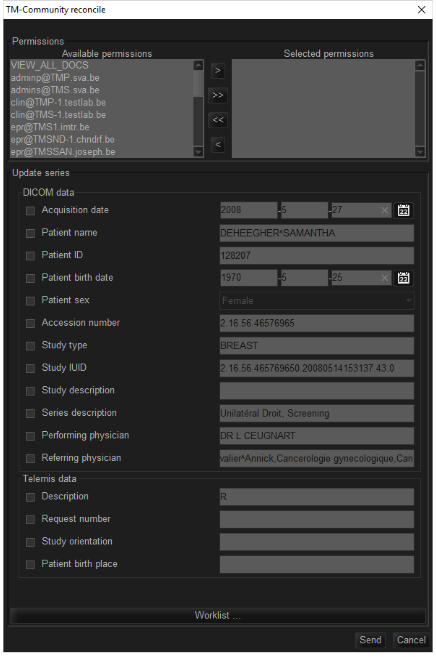


6.4.2.3. Data reconciliation

Any data in this inbox can be re-associated with the correct patient ID at the receiving site. To do this, the "Document / *TM-Community* Reconcile" menu lets you modify the necessary information. The reconciliation action is subject to authorisation.

The reconciliation window lets you

- specify which users the data is intended for
- specify the exact exam information (number, name, description, etc.)
- access the worklist (button at the bottom) to retrieve the existing identities in the system.



VIEW_ALL_DOCS
adminp@TMP.sva.be
admins@TMS.sva.be
clin@TMP-1.testlab.be
clin@TMS-1.testlab.be
epr@TMS1.imtr.be
epr@TMSND-1.chndrf.be
epr@TMSSAN.joseph.be

☐ Acquisition date: 2008 -5 -27
☐ Patient name: DEHEEGHER^SAMANTHA
☐ Patient ID: 128207
☐ Patient birth date: 1970 -5 -25
☐ Patient sex: Female
☐ Accession number: 2.16.56.46576965
☐ Study type: BREAST
☐ Study IUID: 2.16.56.465769650.20080514153137.43.0
☐ Study description:
☐ Series description: Unilatéral Droit, Screening
☐ Performing physician: DR L CEUGNART
☐ Referring physician: valier^Annick,Cancerologie gynecologique,Can
☐ Description: R
☐ Request number:
☐ Study orientation:
☐ Patient birth place:

Once the data has been associated with a patient name, the exam will automatically disappear from the *TM-Community* inbox.

6.4.2.4. Security, tracking, and traceability

A column has been added to the *TM-ReceptionHE* database. This is used to track the progress of images. According to the pictogram, the user can view:

- exams whose transfer is in progress, via the icon
- exams that have been correctly routed, via the icon
- exams with an error, via the icon

The routing status is also indicated in the notes for the exam sent.

Sending is secured every time by Telemis internal tools. Additional VPNs are however available as an option for sites that want them.

For traceability, our new *TM-Audit* tools tracks all operations and sending statuses, which can be looked up and used to compile statistics later.

6.4.2.5. Important notes

The following points are important:

- The sending speed depends on several parameters. Telemis does its utmost to ensure that exams are delivered as quickly as possible. The system does not guarantee data transfer within a certain set time.
- An authorised user wishing to send patient images to another site must first obtain the patient's informed consent.

6.5. TM-Publisher Web

6.5.1. The philosophy

TM-Publisher Web version 4.90 improves notifications and links between the producer site and external contacts and the DICOM image publication and republication workflow, whilst improving communication security and whole exam download capabilities. In addition to the "exam" view and "contact" view, a "patient" view is also available. A new HTML5 viewer complements the existing Flash viewer, whilst the *TM-Uploader* module integrated in the *TM-Publisher Web* system allows internal and external contacts to send DICOM or non-DICOM images in the system remotely for a second opinion. An optional advanced web DICOM viewer allows viewing and MPR from the platform.

6.5.2. Features

6.5.2.1. Notification to contacts

When integrated in the *Telemis-Medical* system, the *TM-Publisher* system lets you trigger the following actions from the *TM-ReceptionHE* viewing interface:

- Send a preformatted email to the contact, using your usual messaging tool.
- Send a text message containing the access codes, once a mobile phone number has been specified.
- Write an A4 page containing the exam access codes but no medical information. The page can easily be printed and used to provide access codes to a patient who wishes to see his/her exams but is not entitled to direct access to his/her medical results.

In addition, the *TM-PublisherWeb* system now supports not only the names of external contacts, but also the addition of their unique INAMI or RPPS number, etc. This allows the results to be sent to the contact physicians with greater security and confidentiality with regard to data processing.

6.5.2.2. Better workflow

There are several elements that support workflow management:

- The publication time for JPG and DICOM images has been reduced. More specifically, when a DICOM image needs to be republished, the processing time is significantly shorter.
- A "patient" view gives all the imaging exams relating to a given IPP/Patient.
- According to the configuration, a one-click download of all the image series from an exam will facilitate image retrieval between sites.

- If the site wishes, reports can be made anonymous in order to be made available in the anonymous "exam" version. Your site manager will configure this feature according to your needs.

6.5.2.3. Better security

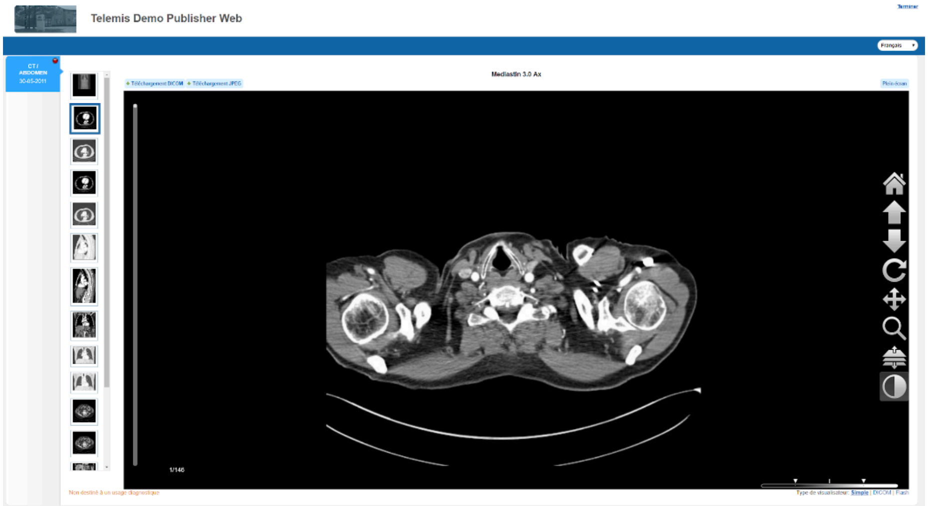
Security is an essential requirement when making imaging elements available to the outside:

- Hack protection: after a number of failures during the identification procedure, the potential attacker's IP address is blacklisted, preventing brute-force attacks on the system.
- Double identification: a double identification principle can be configured in order to secure access in "user" mode. (*)
- Identification number: management of RPPS/INAMI identification of the contact's "health professional" code.

6.5.2.4. Better viewer

6.5.2.4.1. The new HTML5 viewer

The HTML5 viewer replaces the Flash viewer by default. Because fewer and fewer web browsers now support Flash technology, it was important to be able to guarantee compatibility with the most recent tools. For older computers that do not yet support the HTML5 standard, the Flash version is still available.



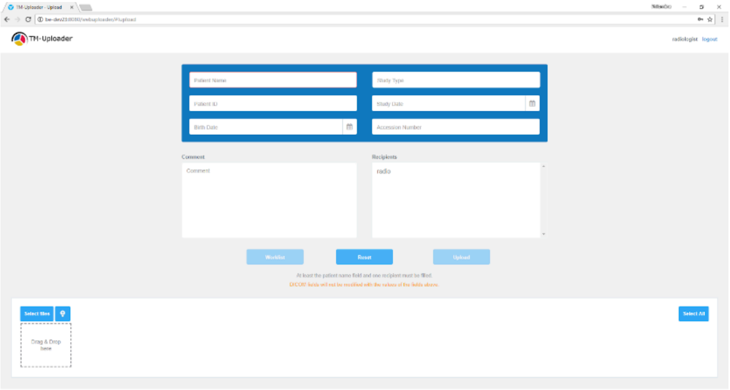
6.5.2.4.2. *Integration of TM-Home in the TM-Publisher Web*

It is important once again to insist on the perfect integration of the *TM-Home* viewers available as standard for customers with *Telemis-Medical* site licences in addition to the *TM-Publisher Web* system. This gives external contacts an extremely high-performance viewer, identical to that of radiologists, and communication tools such as labels, notes, messages, and interactivity with the hospital site. (*)

6.5.2.5. TM-Uploader

6.5.2.5.1. *The philosophy*

The *TM-Uploader* was designed to send images from an external site to the PACS. There are two cases of use: the external contact who wants a second opinion, and internal importing of CD ROMs within the organisation.



At least the patient name field and one recipient must be filled.

DICOM fields will not be modified with the values of the fields above.

6.5.2.5.2. *Importing DICOM files*

After an essential identification step, the user can drag and drop DICOM files in the appropriate space or use the "Import CD ROM" option to import files equipped with DICOMDIR and present on a storage medium.

After selecting the images, you can specify the patient name or nickname to use for these images, add a comment that will appear in the exam notes, or determine which group of users the images are intended for.

6.5.2.5.3. *Importing non-DICOM files*

The procedure is identical for non-DICOM files, except that it is essential to specify a patient name. Filtering on the at-risk file types is performed in order to minimise the risks of virus propagation as much as possible.

For more information, please refer to the specific instruction manual for the *TM-Uploader*.

6.5.2.6. Optional advanced DICOM viewer

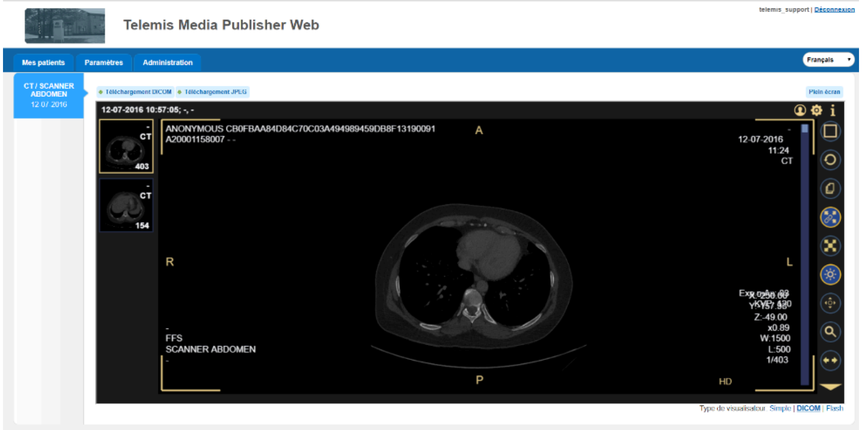
6.5.2.6.1. *The philosophy*

Advanced DICOM viewing is a paid option of the *TM-Publisher Web* system for users who are not content with HTML5 or Flash viewers and do not want to or are unable to use *TM-Home*.

6.5.2.6.2. *Using the advanced viewer*

If the option has been installed, a DICOM tab is present in the bottom right-hand corner of the image.

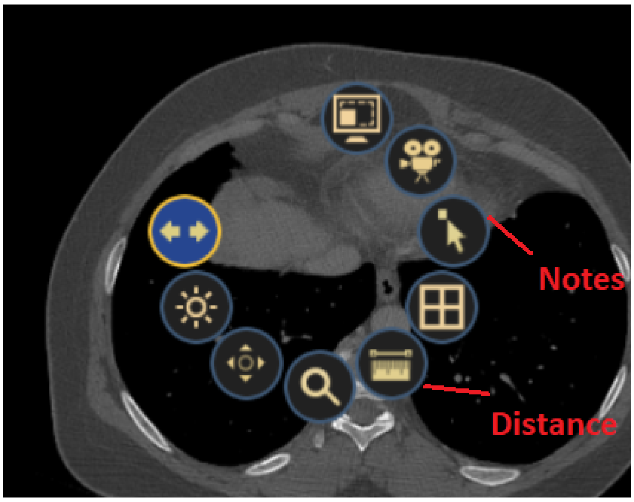
Click this tab to replace the viewer with its advanced DICOM version.



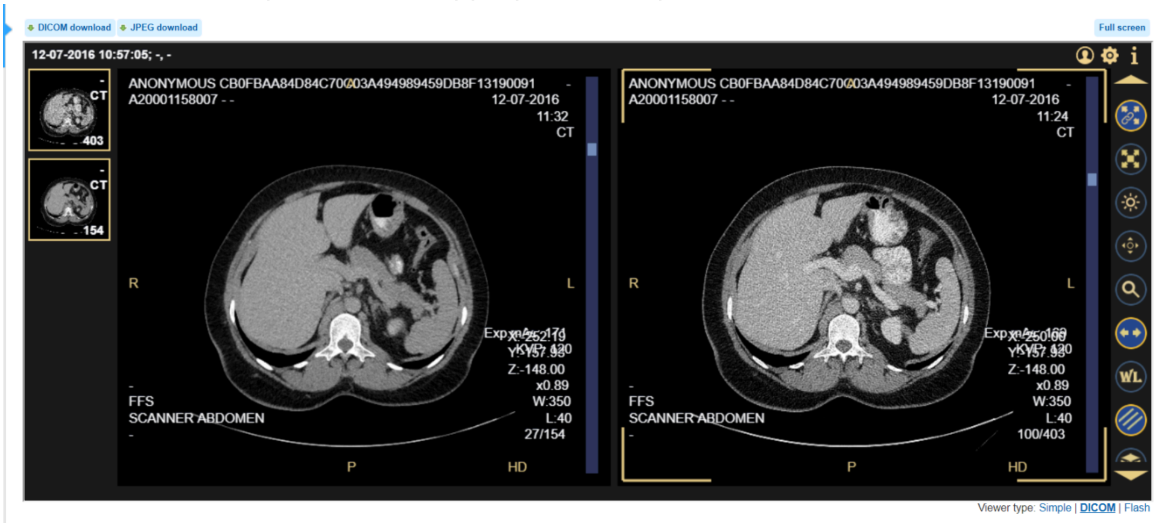
The icons to the right of the image are used to activate the various available tools:

1. Access to patient history
2. Change image layout
3. Reset
4. Comparison mode
5. Link contrast values
6. Maximise view
7. Modify window contrast and brightness values
8. Move in image tool
9. Zoom tool
10. Navigation tool
11. Contrast x-ray pre-selection
12. Reference lines
13. Activate MPR lines.
14. Back up images
15. Backup in compressed mode.

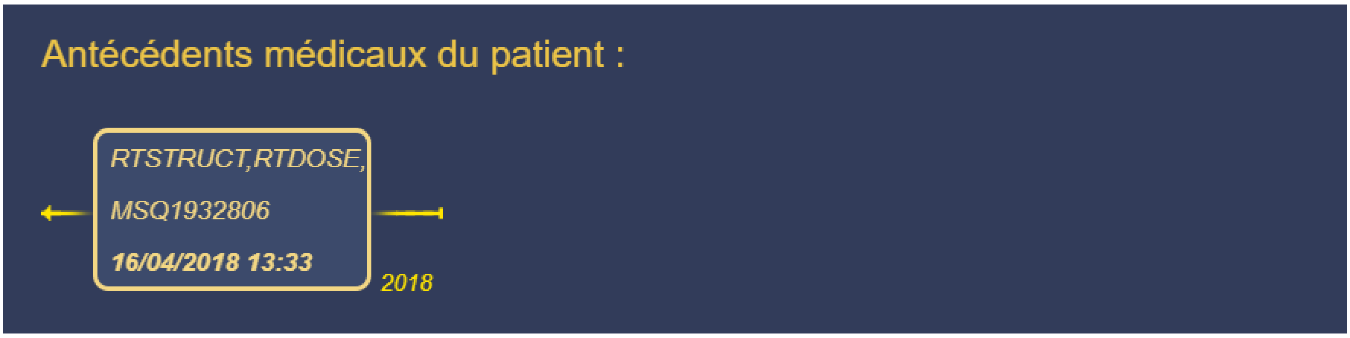
Right-click the mouse button on the image to access certain features more quickly, such as distance measurement and annotations.



To compare images, simply use the "change layout" button (2), and place the elements to be compared in the appropriate compartments

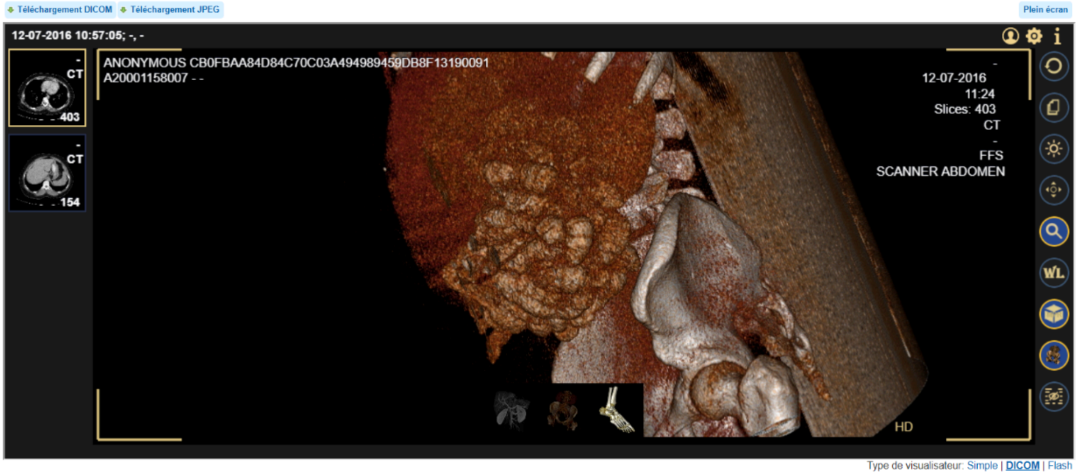


To access the patient history, click the history icon and select the relevant exams.


Antécédents médicaux du patient :
RTSTRUCT,RTDOSE,
MSQ1932806
16/04/2018 13:33
2018

To access the MPR module, click the icon

To access the VRT module (3D volume rendering), click the icon.



.

(*) Certain features need to be enabled by your designated Telemis Site Manager. Please contact him or her for more information or configurations. Certain functionality may be limited according to the country and the legislation in force.

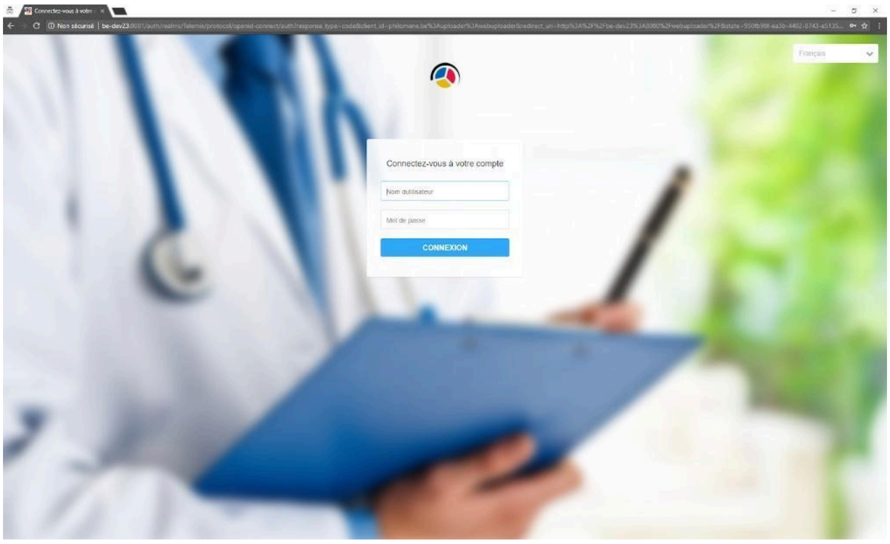
6.6. TM-Uploader

6.6.1. The philosophy

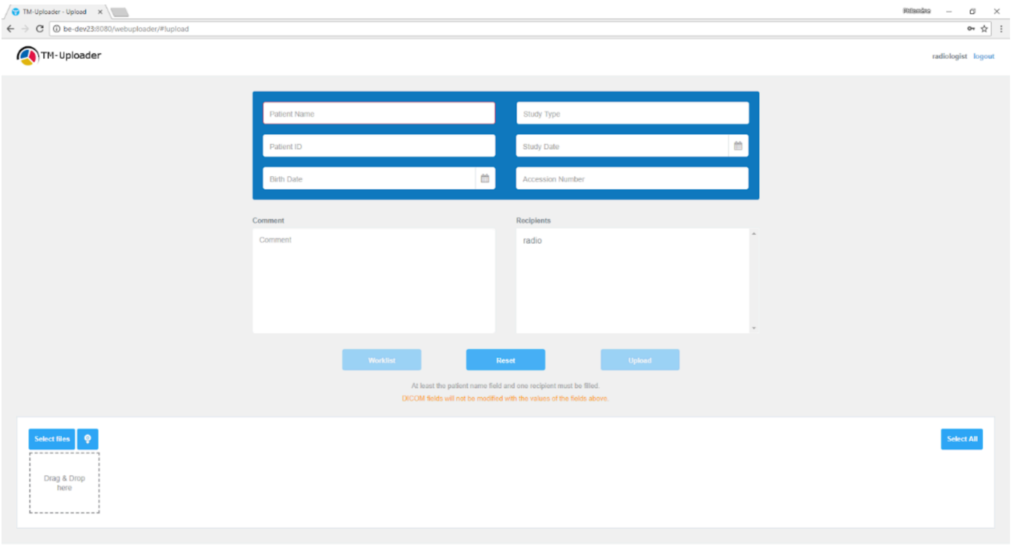
The *TM-Uploader* was designed to send images from an external workstation to the PACS. There are two cases of use: the external contact who wants a second opinion, and internal importing of CD ROMs within the organisation.

6.6.2. Identification

The first step is to log in before you can access the image sending service. To do this, you must have received access codes assigned by your PACS Manager or your designated Telemis Site Manager.



After you log in, the *TM-Uploader* window appears: the upper part of the interface is to input the patient name, whilst the lower part lets you associate images.



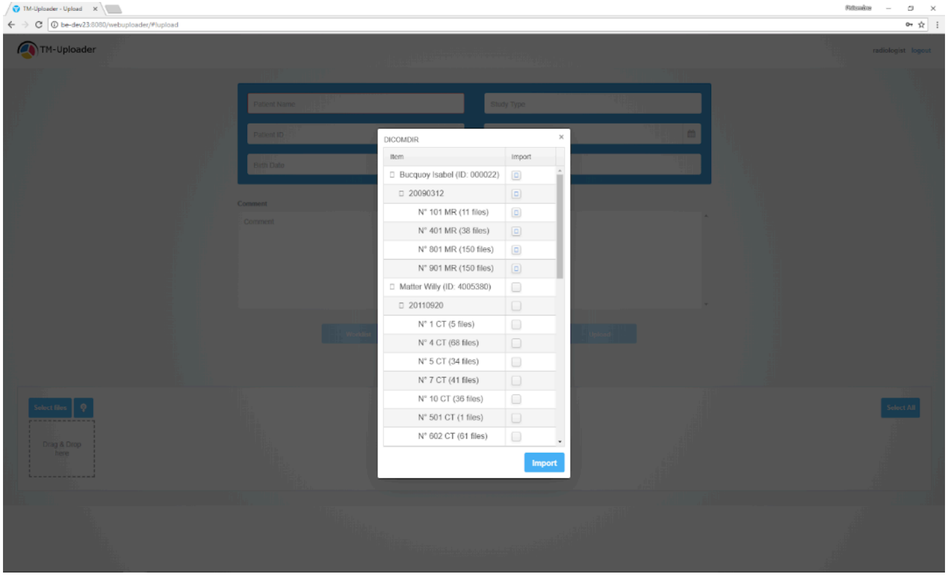
At least the patient name field and one recipient must be filled.

DICOM fields will not be modified with the values of the fields above.

6.6.3.Importing DICOM files

The user can drag and drop DICOM files in the appropriate "drag & drop here" area or use the "select" button, or use the "CD ROM import" option to import files equipped with a DICOMDIR that are present on a storage medium (USB, CD ROM, DVD, etc.) .

In the case of CD ROMs, the user can also select only a part of the image series.

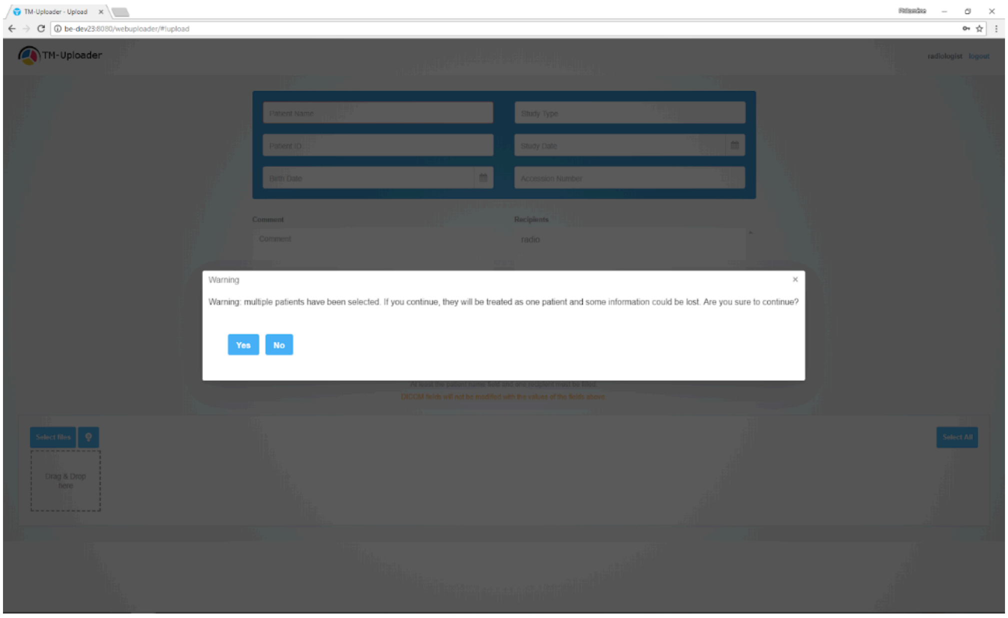


DICOMDIR

Item	Import
Bucquoy Isabel (ID: 000022)	☑
20090312	☑
N° 101 MR (11 files)	☑
N° 401 MR (38 files)	☑
N° 801 MR (150 files)	☑
N° 901 MR (150 files)	☑
Matter Willy (ID: 4005380)	☐
20110920	☐
N° 1 CT (5 files)	☐
N° 4 CT (68 files)	☐
N° 5 CT (34 files)	☐
N° 7 CT (41 files)	☐
N° 10 CT (36 files)	☐
N° 501 CT (1 files)	☐
N° 602 CT (61 files)	☐

Once the images have been selected, the system automatically fills in the patient ID and exam fields according to the information in the DICOM files.

If several patients are present on the CD ROM, a warning message requests confirmation of the multi-patient injection.



Warning

Warning: multiple patients have been selected. If you continue, they will be treated as one patient and some information could be lost. Are you sure to continue?

You can specify the patient name or nickname to use for these images, add a comment that will appear in the exam notes, or determine which group of users the images are intended for.

The group of recipient users must be selected for sending to be initiated.

6.6.4. Using the worklist

If worklist management is available, the patient identifiers can be retrieved from the site using the "Worklist" button, which makes data input more reliable at the same time.

6.6.5. Importing non-DICOM files

The procedure is identical for non-DICOM files, except that it is essential to specify a patient name. Filtering on the at-risk file types is performed in order to minimise the risks of virus propagation as much as possible.

6.7. TM-Capture

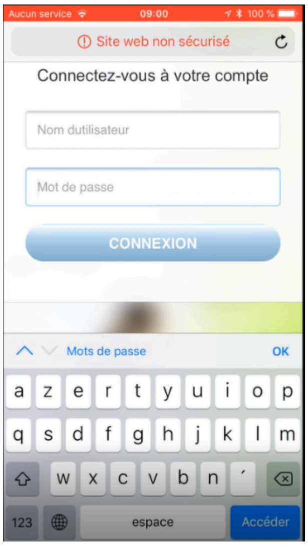
6.7.1. The philosophy

TM-Capture is designed to capture medical images via a peripheral such as a smartphone or tablet, whilst first associating a patient identity with the captured images. In addition, this version 4.90 can identify users, scan barcodes or QR codes, and facilitate the taking of multiple shots, and it operates better in multi-site environments with teaching responsibilities.

6.7.2. User identification

To track the use of the *TM-Capture* module and comply with data protection laws, it is now essential to log in before using the system.

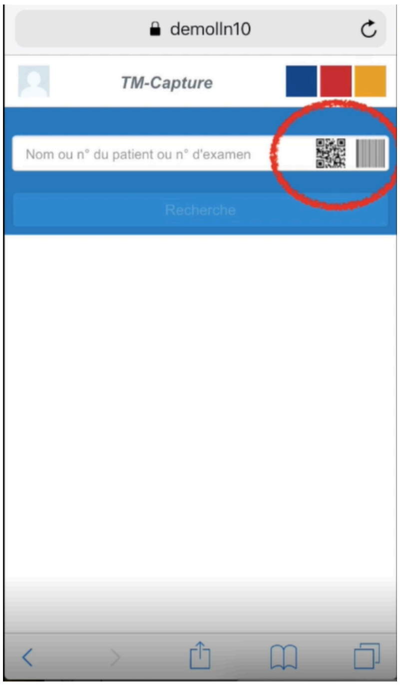
Use of *TM-Capture* is linked to user rights granted by the local manager or Telemis manager.



Connectez-vous à votre compte

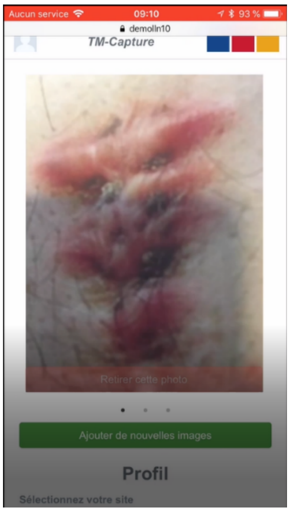
6.7.3. Scanning barcodes or QR codes

When the site uses a barcode or QR code patient ID management system, it is safer and more reliable to scan the code than to re-enter the patient number or name. According to the case, the hospital may need an ad hoc configuration or development to associate a scanned number with a patient ID number via web services. Your Telemis Site Manager will give you more information about this.



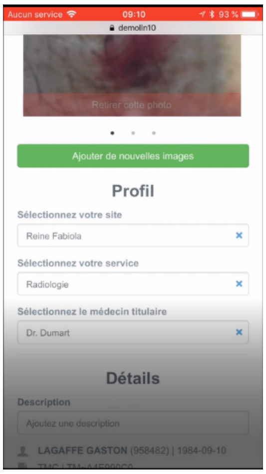
6.7.4. Multiple shots

Departments such as Dermatology regularly take several shots per patient. That is why it was important to make the system operate smoothly, allowing multiple photographs to be added quickly and irrelevant shots to be deleted. The green button is used to add a new image and the red button is used for deletion. Swipe the image to review all the images acquired.



6.7.5. Multi-site and teaching

Before sending images to the MACS system, the user can specify his or her location (geographical site and department) and, if a junior doctor, the senior doctor to whom he or she reports.



Profil

Sélectionnez votre site: Reine Fabiola

Sélectionnez votre service: Radiologie

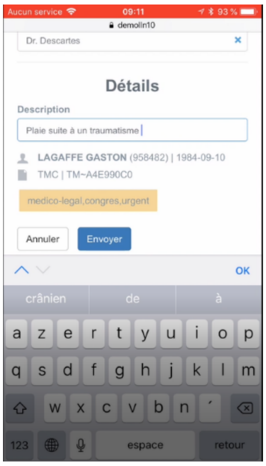
Sélectionnez le médecin titulaire: Dr. Dumart

Détails

Description: Ajoutez une description

LAGAFFE GASTON (958482) | 1984-09-10

In general, it is also useful to add a specific description to a shot or to use ready-made labels saved for specific purposes, such as forensic shots.



Dr. Descartes

Détails

Description: Plaie suite à un traumatisme

LAGAFFE GASTON (958482) | 1984-09-10

TMC | TM~A4E990C0

medico-legal,congres,urgent

6.8. The AI-Box

6.8.1. The philosophy

Artificial Intelligence has now become an essential tool in the medical sector. The current state of research, however, provides only a partial set of solutions for certain pathologies, obliging the radiologist to click several times to find out which algorithm to use according to the pathology, the exam, etc. The purpose of the AI Box is to harmonise the exchange processes between MACS and AI algorithms, as well as the display of results for the physician.

6.8.2. Directing images to the algorithms

The first essential task of the AI Box is organising the sending of series of images from the modality to the various AI algorithms on the site. Our engineers will configure automated sending as background tasks in accordance with customer requirements. This operation will be completely transparent from the physician's point of view.
The algorithms react to the images and then return the results to the AI-Box in a structured manner, in order to present a graphically homogeneous result.

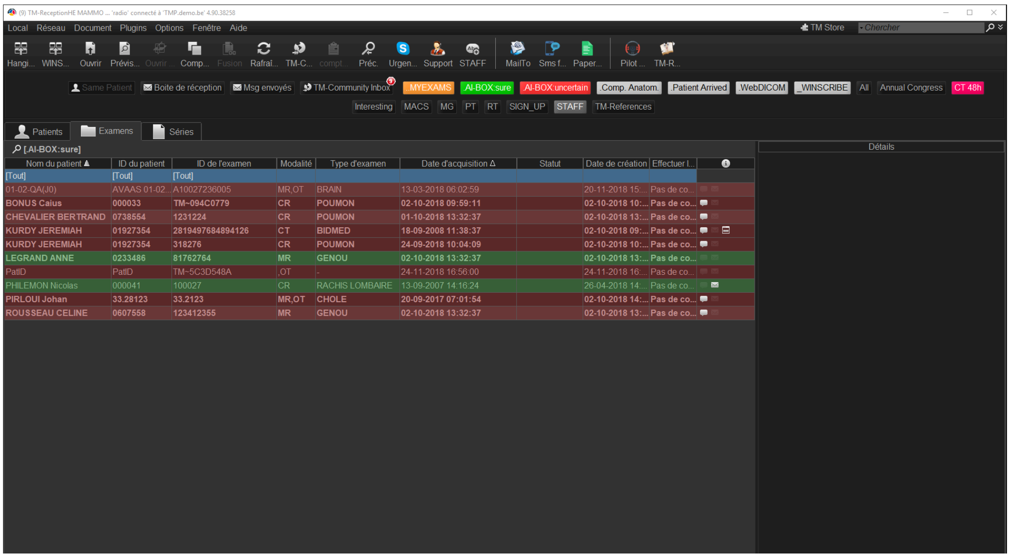
6.8.3. The Physician View

According to the configurations chosen, one or more search buttons can be added to the interface. This helps to organise the workflow according to the result of the algorithms.

The following examples could be configured:

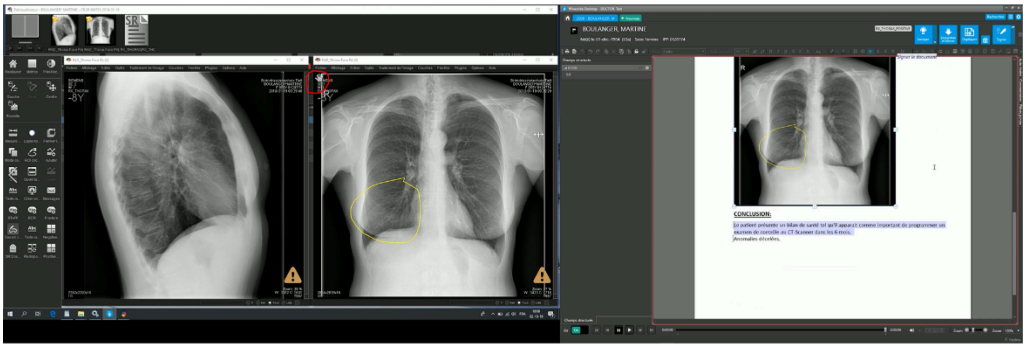
- an "AI-BOX: sure" button, indicating all the exams for which the algorithms are sure of the results;
- an "AI-BOX: positive results" button, indicating all the exams to be processed as a priority - according to the results of the algorithm.

In addition, the positive or negative results can be made visible thanks to coloured lines in the patient view, to directly highlight any problematic exams.



Nom du patient ▲	ID du patient	ID de l'examen	Modalité	Type d'examen	Date d'acquisition ∆	Statut	Date de création	Effectuer l...
[Tout]	[Tout]	[Tout]						
01-02-QA(J0)	AVAAS 01-02...	A10027236005	MR,OT	BRAIN	13-03-2018 06:02:59		20-11-2018 15:...	Pas de co...
BONUS Caius	000033	TM~094C0779	CR	POUMON	02-10-2018 09:59:11		02-10-2018 10:...	Pas de co...
CHEVALIER BERTRAND	0738554	1231224	CR	POUMON	01-10-2018 13:32:37		02-10-2018 13:...	Pas de co...
KURDY JEREMIAH	01927354	2819497684894126	CT	BIDMED	18-09-2008 11:38:37		02-10-2018 09:...	Pas de co...
KURDY JEREMIAH	01927354	318276	CR	POUMON	24-09-2018 10:04:09		02-10-2018 10:...	Pas de co...
LEGRAND ANNE	0233486	81762764	MR	GENOU	02-10-2018 13:32:37		02-10-2018 13:...	Pas de co...
PatID	PatID	TM~5C3D548A	,OT	-	24-11-2018 16:56:00		24-11-2018 16:...	Pas de co...
PHILEMON Nicolas	000041	100027	CR	RACHIS LOMBAIRE	13-09-2007 14:16:24		26-04-2018 14:...	Pas de co...
PIRLOUI Johan	33.28123	33.2123	MR,OT	CHOLE	20-09-2017 07:01:54		02-10-2018 14:...	Pas de co...
ROUSSEAU CELINE	0607558	123412355	MR	GENOU	02-10-2018 13:32:37		02-10-2018 13:...	Pas de co...

A result in the form of an additional series will also be presented every time (if the algorithm allows).



CONCLUSION:

Le patient présente un bilan de santé tel qu'il apparait comme important de programmer un examen de contrôle au CT-Scanner dans les 6 mois.

Anomalies décelées.

(thanks to CleverDoc.io for providing the search images)

The AI-Box organises and prioritises work uniformly, no matter which algorithms the institution has purchased.

7. ADDON 4.90 TO 4.95

7.1. FOREWORD

In addition to the gradual overhaul of the architecture of our PACS with a view to simplifying it and making it more robust, the new version of the TMRHE brings you improvements related to the basic everyday functions.

So, we gradually install a new PACS for you, consisting of new bricks such as TFP (Telemis Foundation Platform), the Dicom Gate, the HL7 Gate, the Site Manager, and many others (Keycloak, Watchdog, Audit), etc., with continuous rewriting of the software, that is transparent to our users.

Our aim is to ensure the continuity of our product's development, with the following watchwords: Innovation and Interoperability.

We also bear the security and maintenance of our product in mind.

In this version (4.95), we have also focused on the details, and we offer you several practical improvements that have been strongly requested by our users.

These improvements concern the Navigator, the Viewer, and the Filmer.

7.2. General information on the Navigator

7.2.1. Principle and philosophy

The TM-ReceptionHE software lets you view search results in the PACS in three tabs: Patient, Exams, and Series.
A lot of information based on search results in the PACS is displayed on your dashboard, which is called the “Navigator”.

We have developed features that aim to facilitate the visibility of some of this information in the Navigator.

7.3. Features

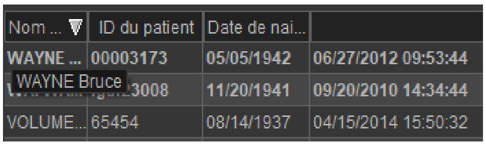
7.3.1.1. Visual alternation of lines

In the Patient view, the search result lines are now different according to whether or not they are different from each other.

Nom ...	ID du patient	Date de nai...	Dernier examen
WAYNE ...	**00003173**	**05/05/1942**	**06/27/2012 09:53:44**
WAFWA...	**fgdf23008**	**11/20/1941**	**09/20/2010 14:34:44**
VOLUME...	65454	08/14/1937	04/15/2014 15:50:32
VOLUME...	5546	11/27/1949	06/29/2015 09:01:21
VOLUME...	040325		03/19/2014 14:12:38
VGi FUL...	VGi FULL NB...	07/30/1975	03/04/2009 15:35:00
VANDER...	0778130	03/16/1957	05/11/2011 14:08:56

Information

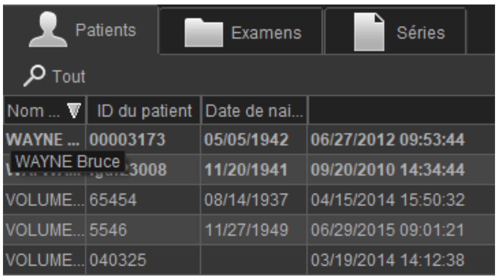
You now have the details of the information contained in each column of the Navigator: When you mouseover a cell in the Navigator, the information contained in that cell is displayed.



Nom ...	ID du patient	Date de nai...	
WAYNE ...	**00003173**	**05/05/1942**	**06/27/2012 09:53:44**
	3008	**11/20/1941**	**09/20/2010 14:34:44**
VOLUME...	65454	08/14/1937	04/15/2014 15:50:32

7.3.1.2. Dates in European format

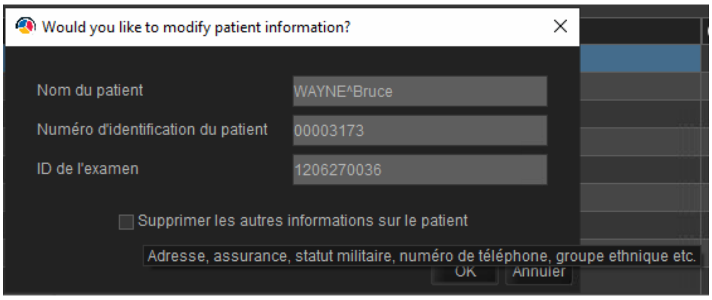
Dates in the Navigator are now automatically displayed in the user's format.



Nom ...	ID du patient	Date de nai...	
WAYNE ...	**00003173**	**05/05/1942**	**06/27/2012 09:53:44**
	3008	**11/20/1941**	**09/20/2010 14:34:44**
VOLUME...	65454	08/14/1937	04/15/2014 15:50:32
VOLUME...	5546	11/27/1949	06/29/2015 09:01:21
VOLUME...	040325		03/19/2014 14:12:38

7.3.1.3. Anonymisation before Dicom export

You can now anonymise an exam before exporting in DICOM format from the Navigator
(from the Document tab).



Would you like to modify patient information?

Nom du patient: WAYNE^Bruce

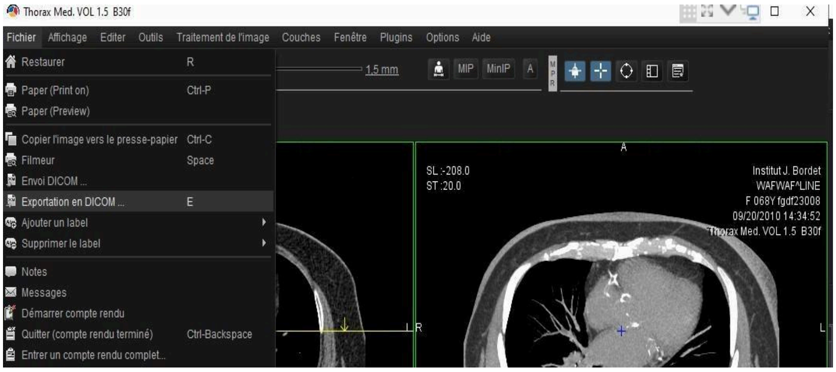
Numéro d'identification du patient: 00003173

ID de l'examen: 1206270036

☐ Supprimer les autres informations sur le patient

Adresse, assurance, statut militaire, numéro de téléphone, groupe ethnique etc.

Note that was possible to perform a Dicom export from the Viewer in the previous version :



Viewer ergonomics

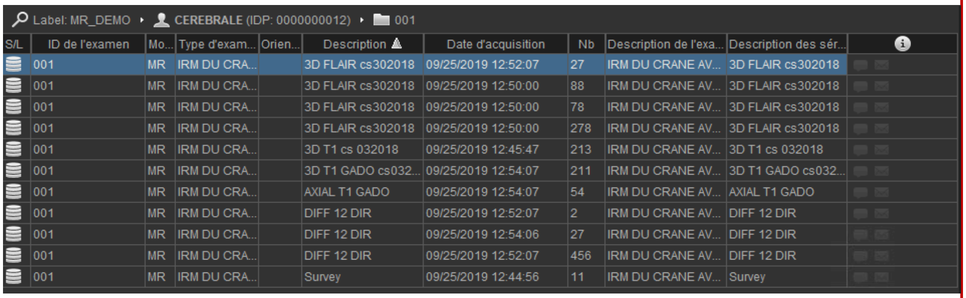
7.3.2. The philosophy

The Telemis Viewer is an essential tool for radiologists, and is continually undergoing minor improvements
intended to make it more convenient for our users to work with.

7.4. Main features

7.4.1. Optimisation of the number of open windows in an exam

When an exam consists of several series, rather than having many small windows by default, there is a new option that automatically adjusts the division of screens. By default, four windows will be displayed per screen, but if there are only two series to display, this automatic readjustment displays the two series by dividing the screen in two.



Label: MR_DEMO ▸ CEREBRALE (IDP: 0000000012) ▸ 001

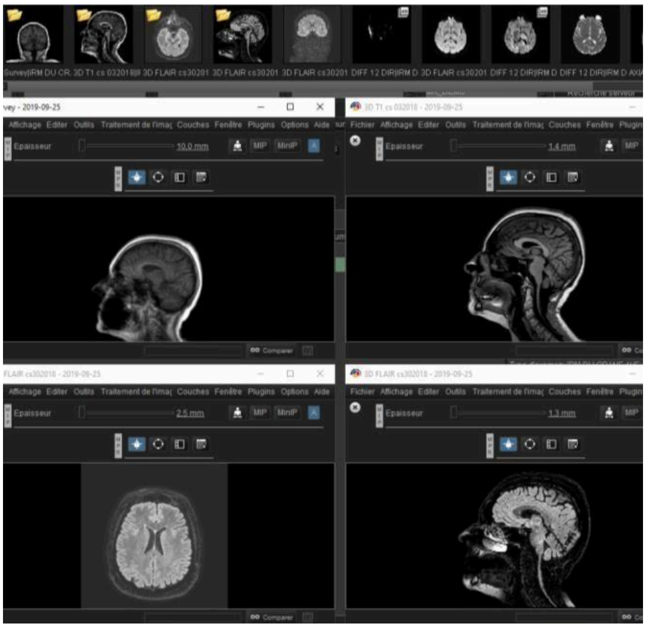
S/L	ID de l'examen	Mo...	Type d'exam...	Orien...	Description	Date d'acquisition	Nb	Description de l'exa...	Description des sér...	ⓘ
	001	MR	IRM DU CRA...		3D FLAIR cs302018	09/25/2019 12:52:07	27	IRM DU CRANE AV...	3D FLAIR cs302018	
	001	MR	IRM DU CRA...		3D FLAIR cs302018	09/25/2019 12:50:00	88	IRM DU CRANE AV...	3D FLAIR cs302018	
	001	MR	IRM DU CRA...		3D FLAIR cs302018	09/25/2019 12:50:00	78	IRM DU CRANE AV...	3D FLAIR cs302018	
	001	MR	IRM DU CRA...		3D FLAIR cs302018	09/25/2019 12:50:00	278	IRM DU CRANE AV...	3D FLAIR cs302018	
	001	MR	IRM DU CRA...		3D T1 cs 032018	09/25/2019 12:45:47	213	IRM DU CRANE AV...	3D T1 cs 032018	
	001	MR	IRM DU CRA...		3D T1 GADO cs032...	09/25/2019 12:54:07	211	IRM DU CRANE AV...	3D T1 GADO cs032...	
	001	MR	IRM DU CRA...		AXIAL T1 GADO	09/25/2019 12:54:07	54	IRM DU CRANE AV...	AXIAL T1 GADO	
	001	MR	IRM DU CRA...		DIFF 12 DIR	09/25/2019 12:52:07	2	IRM DU CRANE AV...	DIFF 12 DIR	
	001	MR	IRM DU CRA...		DIFF 12 DIR	09/25/2019 12:54:06	27	IRM DU CRANE AV...	DIFF 12 DIR	
	001	MR	IRM DU CRA...		DIFF 12 DIR	09/25/2019 12:52:07	456	IRM DU CRANE AV...	DIFF 12 DIR	
	001	MR	IRM DU CRA...		Survey	09/25/2019 12:44:56	11	IRM DU CRANE AV...	Survey	

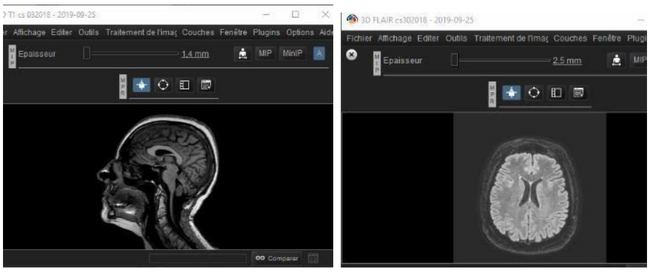
7.4.2. Simultaneous opening of a 2D and 3D viewer

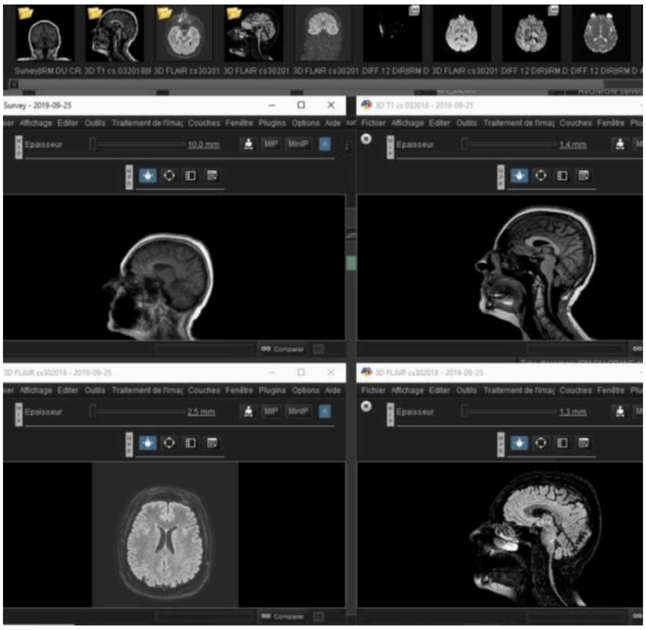
You can now open the same series in 2D and 3D, displaying them side by side, with a simple administrator configuration of the display protocols.

7.4.3. Permutation of open series

The ease of handling of the series displayed continues here, with the option to modify their positions
on the screen without having to close them first: now you can just drag and drop them.


Survey - 2019-09-25
3D T1 cs 032018 - 2019-09-25
FLAIR cs302018 - 2019-09-25
3D FLAIR cs302018 - 2019-09-25
Fichier Affichage Editer Outils Traitement de l'imag Couches Fenêtre Plugins Options Aide
Epaisseur
10.0 mm
1.4 mm
2.5 mm
1.3 mm
MIP
MinIP
Comparer


3D T1 cs 032018 - 2019-09-25
3D FLAIR cs302018 - 2019-09-25
Fichier Affichage Editer Outils Traitement de l'imag Couches Fenêtre Plugins Options Aide
Epaisseur
1.4 mm
2.5 mm
MIP
MinIP
Comparer


Survey - 2019-09-25
3D T1 cs 032018 - 2019-09-25
3D FLAIR cs302018 - 2019-09-25
Fichier Affichage Editer Outils Traitement de l'imag Couches Fenêtre Plugins Options Aide
Epaisseur
10.0 mm
1.4 mm
2.5 mm
1.3 mm
MIP
MinIP
Comparer

7.4.4. Recall your windows in one click

Show all viewers: this lets you bring all open images back to the screen when they have gone to the background, in just one click.

Historique de recherche en cours...

Show all the viewers opened via this previewer

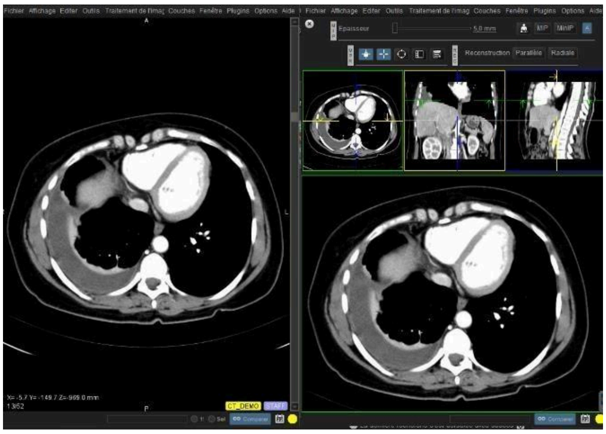
7.4.5. Improved anatomical identification between different series

- The reference lines are still displayed for just one exam at a time, but some displayed bugs have been corrected.
- Anatomical registration is used by default in “compare” mode.

  It is faster, because the coregistration calculation takes place only once in a particular study.

  As in the previous versions, you can still use the keyboard key >< to register the images manually.
- You can now compare a 2D series to a 3D series.

- Corrections applied to the 3D pointer have made it more functional, including in 2D.



- In MPR, MIP can now be applied to all views.

7.5. Secondary features

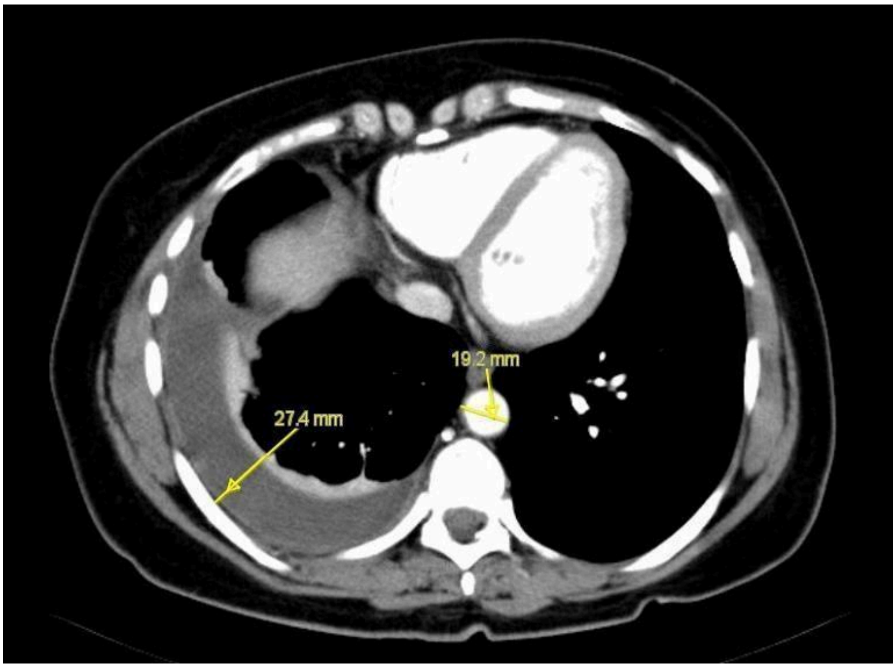
7.5.1. Critical labels in the Viewer

You can now create a label that will appear in large format on the image when it opens.
It has been created to attract the user's attention.
To do this, simply assign an order of priority to this label when creating it, by choosing the value 101.
This feature was developed for emergencies, for example, or patient errors.
When you mouseover the label, it goes to the bottom right-hand corner of the screen to avoid

hindering interpretation.

7.5.2. Visibility of measurements in the image

A new format for the measurements taken (white contours) makes them easier to read in the image.



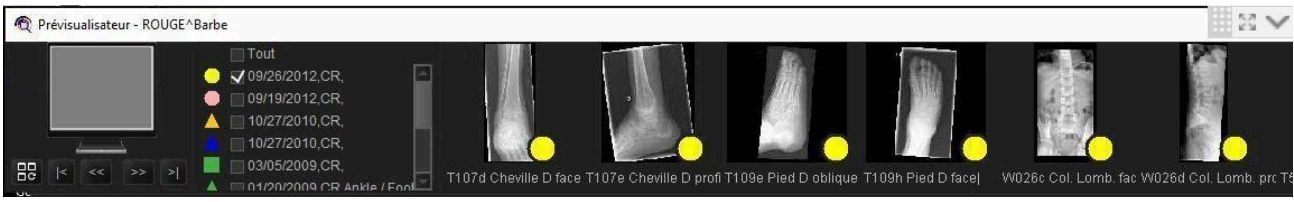
7.5.3. PDF Viewer

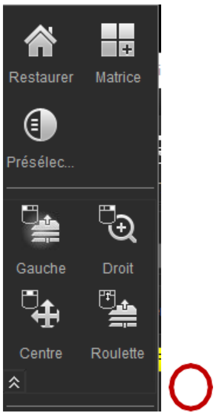
A new licence lets you manage certain special characters in some PDFs that are sometimes not readable in Telemis. This licence is included for all users.

7.6. Features of the Previewer

7.6.1. Modalities to be displayed

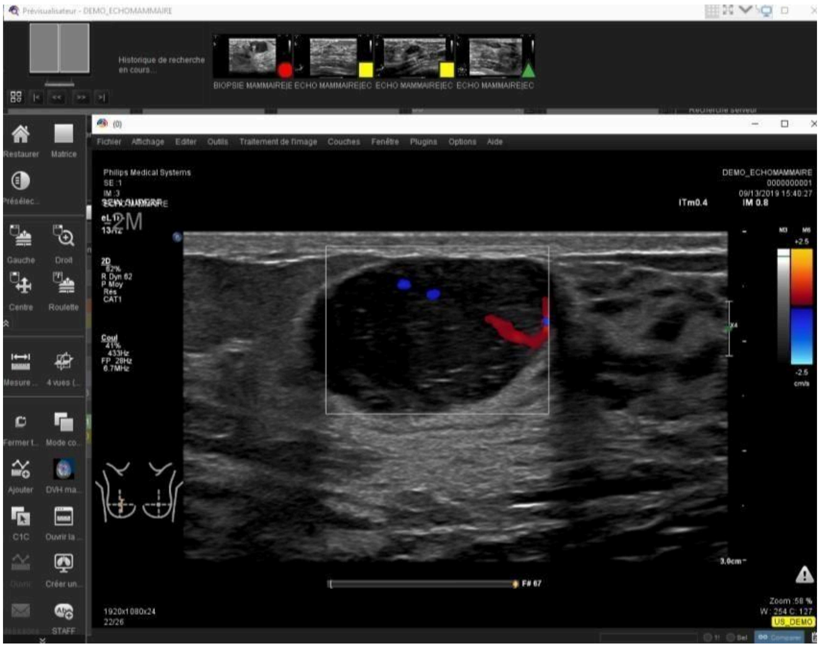
In the Previewer, you can configure the variables of the history to be displayed and therefore restrict the modalities to be displayed for a given user.





7.6.2. Ultrasound thumbnail split

For ultrasounds, which are sometimes sent as and when they are ready, there is a new auto join feature that links all the images to each other in the viewer, which facilitates the workflow. Simply drag and drop the thumbnail to view the entire series.



7.6.3. Tooltip on the previewer thumbnail

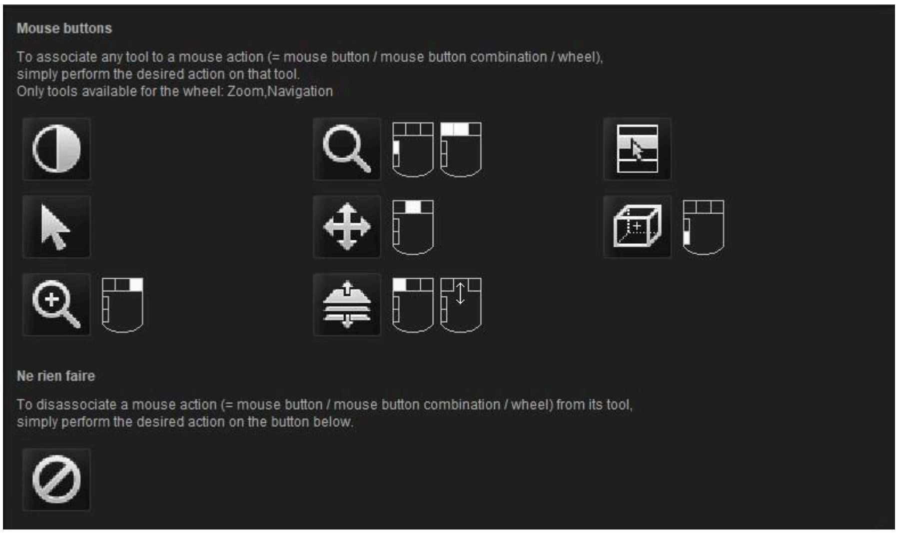
The complete information concerning the thumbnail in the previewer (series name and more) is visible by simply doing a mouseover.


US
09/20/2019
BIOPSIE MAMMAIRE BIOPSIE MAMMAIRE: 5 images

7.7. Mouse features

To avoid overloading the toolbar, you can hide the mouse features:

If you have a three-button mouse, you can now multiply its features by choosing click combinations.



Mouse buttons

To associate any tool to a mouse action (= mouse button / mouse button combination / wheel), simply perform the desired action on that tool.
Only tools available for the wheel: Zoom,Navigation

Ne rien faire

To disassociate a mouse action (= mouse button / mouse button combination / wheel) from its tool, simply perform the desired action on the button below.

If you have a multi-button mouse: the application will now support it.

7.8. Filmer

7.8.1. Philosophy

Special attention has been paid to the filmer in this new version, with several improvements aiming to make it far more functional.

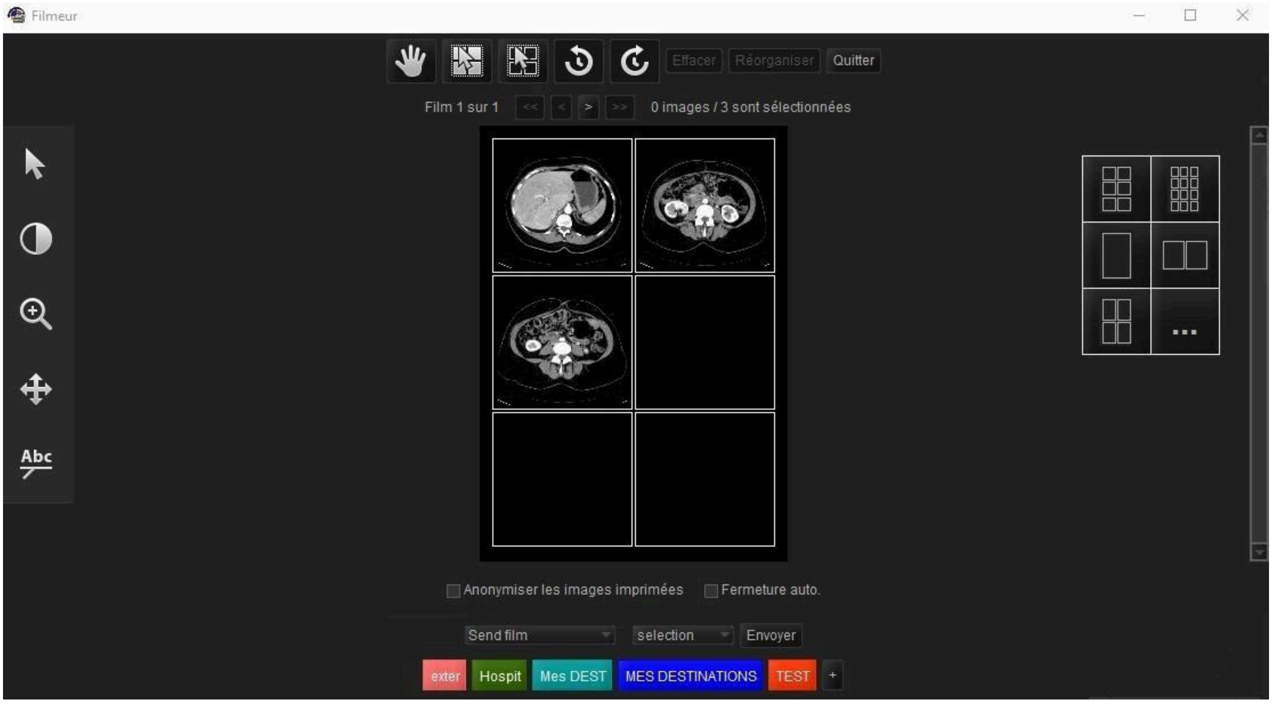
7.8.2. Basic features

7.8.2.1. Layout

- The list of available layouts is in the icon located on the right-hand side of the filmer window. ⋯

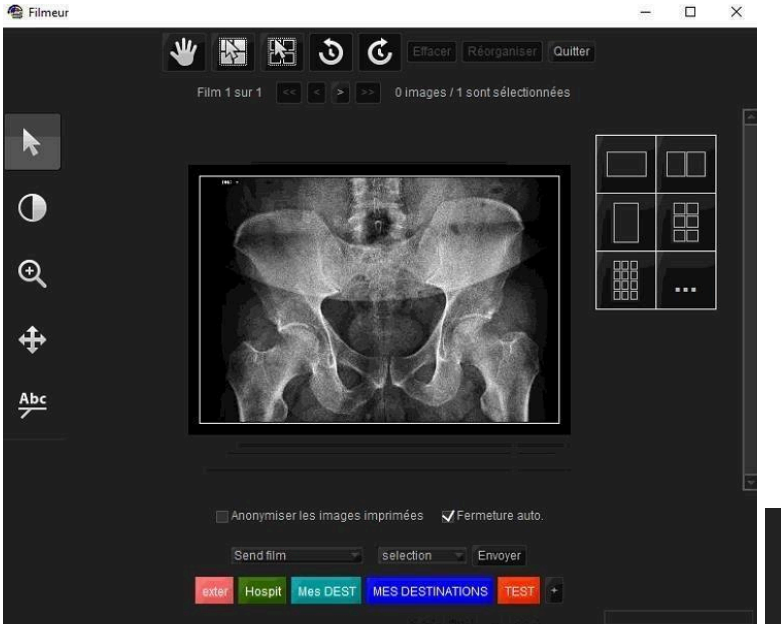
- The last layout chosen remains in the history (up to five displays can be stored in memory), and the last layout used becomes the default layout.

- When images are deleted from the filmer, the layout of the empty boxes can be reorganised.

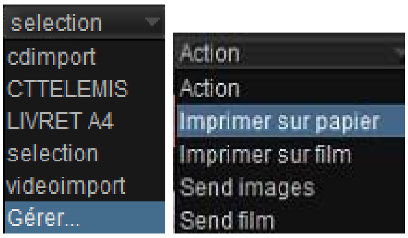


- Now the various image printing and saving destinations are available in a single tab, which means fewer clicks to send your shots.

  You can also configure as many additional destinations as necessary directly in this icon, and then create a preset of those destinations



.



Enter the name of the preset and choose the color. Then select the action(s) you want to associate to the preset.

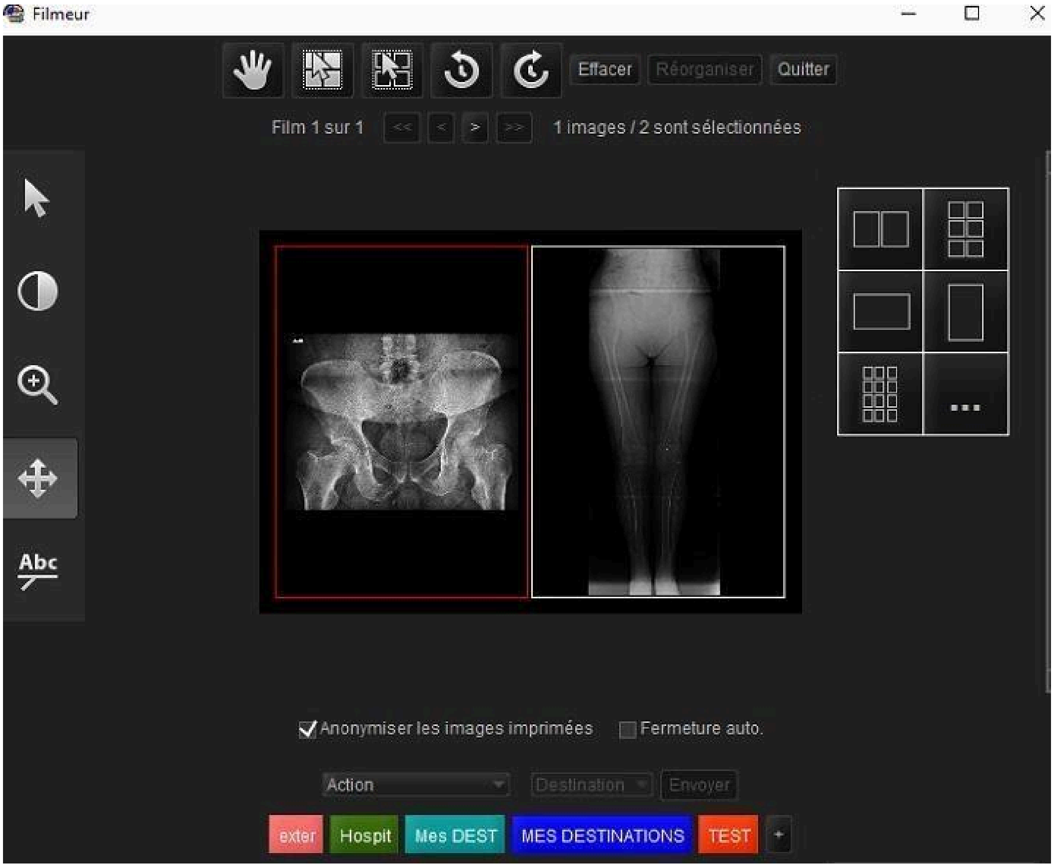
7.8.3.Image modifications in the Filmer

- Pan and Zoom are now accessible via the same mouse presets as in the Viewer.
- A correction lets you display the surface measurement in the filmer.
- You can also delete or modify annotations directly in the filmer by right-clicking → Delete annotation.

7.9. Advanced features

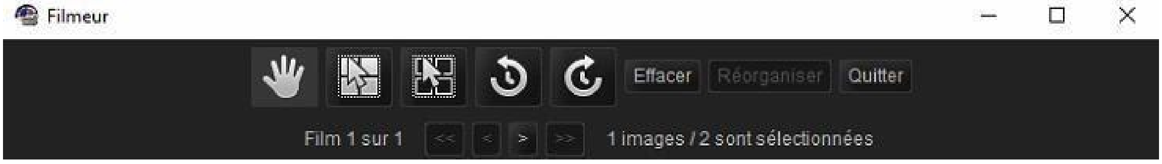
7.9.1. Anonymisation of a summary sheet

This new feature is easy to use, and it lets you export or print an anonymised summary sheet easily by ticking a box before selecting the destination of your summary sheet (PACS saving, printing on paper, etc.).



7.9.2. Export from the Filmer

Emulating its use in the Viewer, the drag-and-drop function using the '*hand*' has been developed
for the filmer in this new version.
It lets you export one or more images, or a summary sheet, very simply and intuitively in anonymised form in a Word document or the body of an email message.



7.10.Radiotherapy and DVH

7.10.1. The philosophy

Note that the application has a native module to display TPS (Treatment Planning System) data.

Since version 4.80, it is also possible to generate contours called RT Struct and send them to a TPS.

The new features in version 4.95 are found in the use of DVHs (Dose Volume Histograms), used to represent the doses received by the various organs when planning radiotherapy treatment.

7.10.2. Features

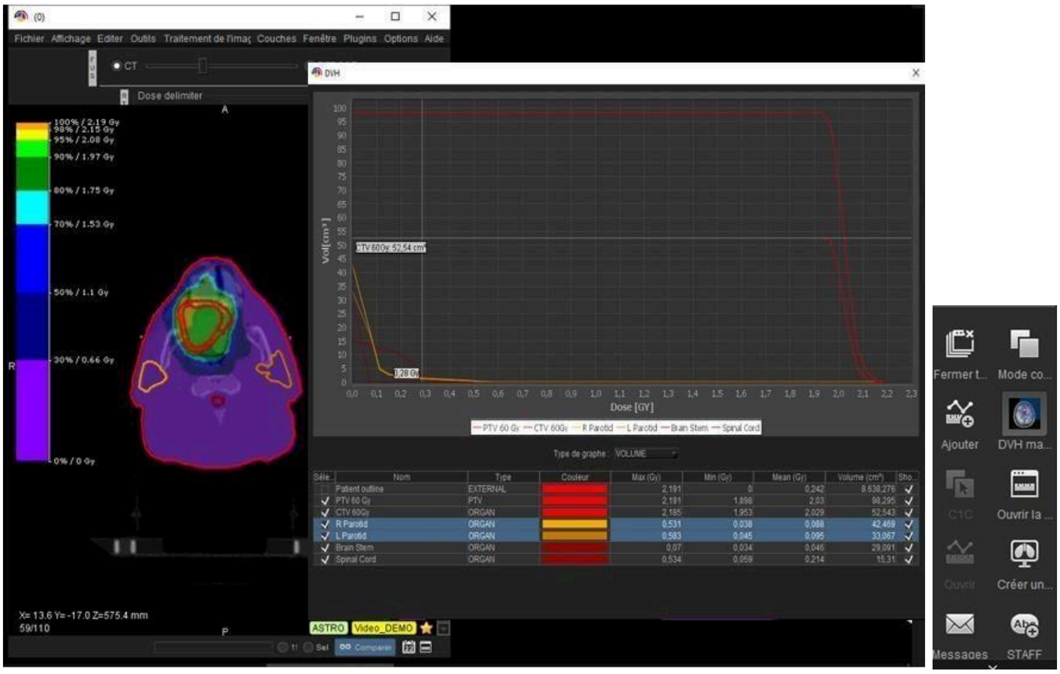
- To open the study, you used to have to select all of the ‘CT + RT Struct + RT Dose + RT Plan’ series relating to the exam.

  You can now open the whole study by selecting only the ‘RT Plan’ series (used for dose simulation), and the other series will be automatically opened by the system (including MRI, which is now handled in the study) and they will then be merged.

  Note:

- If you click RT Struct, you open only RT Struct + CT/MR; if you click RT Dose, nothing happens.
- From the Navigator, right-click an exam -> ‘RT Series analysis’ lets you see the links between these different series (the colour red indicates that the series is not linked to the study).

- The addition of a button in the DVH Manager toolbar provides fast access to the DVH graphs.

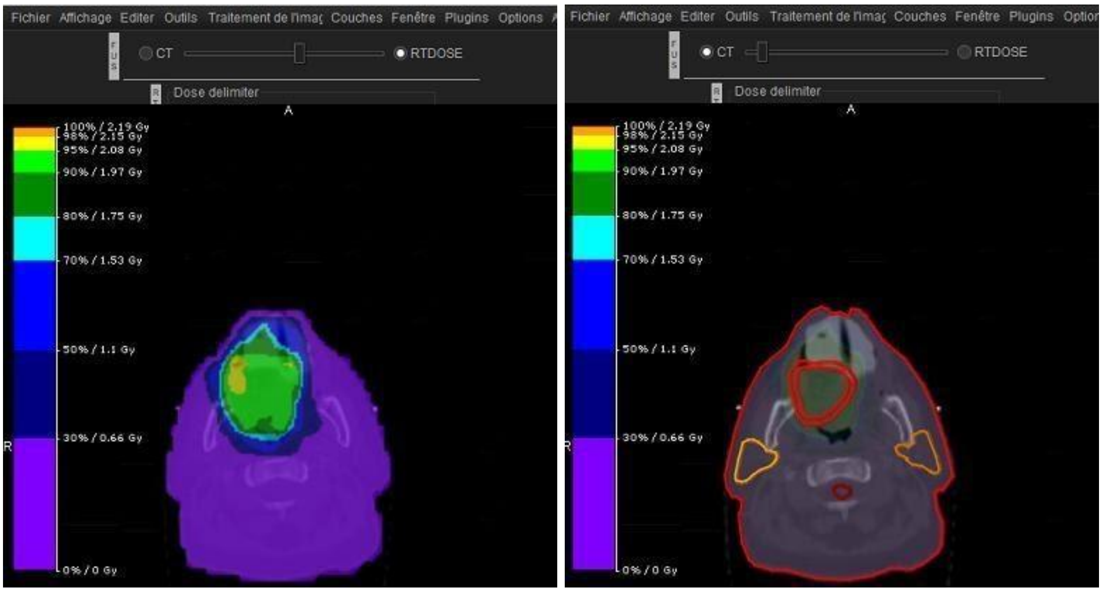


Type de graphe : VOLUME

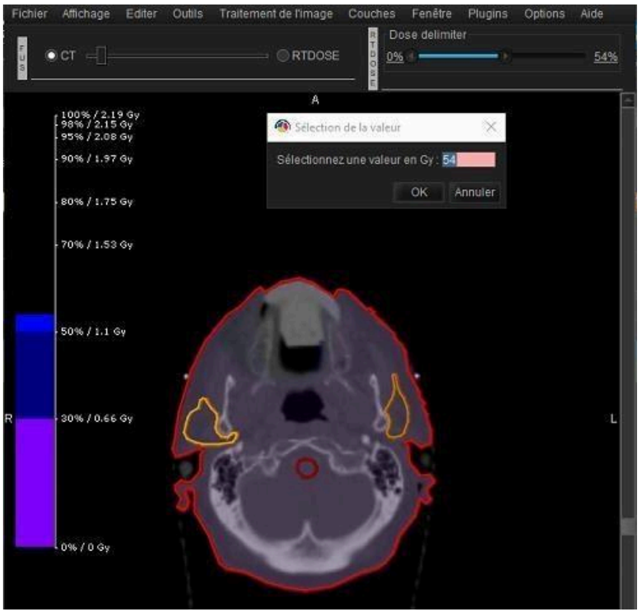
Séle...	Nom	Type	Couleur	Max (Gy)	Min (Gy)	Mean (Gy)	Volume (cm³)	Sho...
☐	Patient outline	EXTERNAL	🟥	2,191	0	0,242	8.638,276	✓
✓	PTV 60 Gy	PTV	🟥	2,191	1,898	2,03	98,295	✓
✓	CTV 60Gy	ORGAN	🟥	2,185	1,953	2,029	52,543	✓
✓	R Parotid	ORGAN	🟧	0,531	0,038	0,088	42,469	✓
✓	L Parotid	ORGAN	🟧	0,583	0,045	0,095	33,067	✓
✓	Brain Stem	ORGAN	🟥	0,07	0,034	0,046	29,091	✓
✓	Spinal Cord	ORGAN	🟥	0,534	0,059	0,214	15,31	✓

- In this new version, you can now display several DVHs on a single graph, which facilitates
  the comparison of different curves:
  - All the volumes are listed in the DVH window.
  - The colours on the graph correspond to the RT Struct colours.
  - The X and Y positions are visible on the graph.
  - The mouse pointer lets you obtain the dose value by simply passing over the curve
    (dose value in cm³).

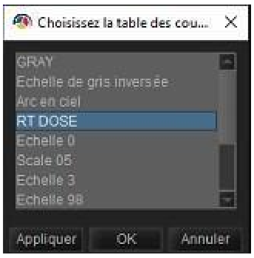
- Another improvement: easier display features.
  - Moving the cursor to the right places the emphasis on displaying regions of interest,
    whilst moving it to the left emphasises the display of DVHs.



  - You have the option of changing the CLUT (colour correspondence table) using the F2 key.
    Other CLUTs can be configured in administrator mode.
- You can now generate a new RT Struct by contouring zones directly in the PACS.
- Notes on the dose delimiter and the ROI manager:
  - The dose delimiter is available above the display window.
    You can use the cursor or manually enter the limit dose value to be displayed.

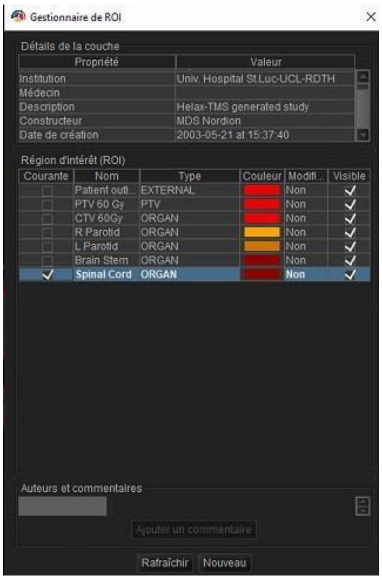


Sélectionnez une valeur en Gy : 54



In the ROI manager, you can configure the ROIs to be displayed by ticking them (on the right).

If they belong to the current layer (left-hand column), it will not be possible to disable certain ROIs.



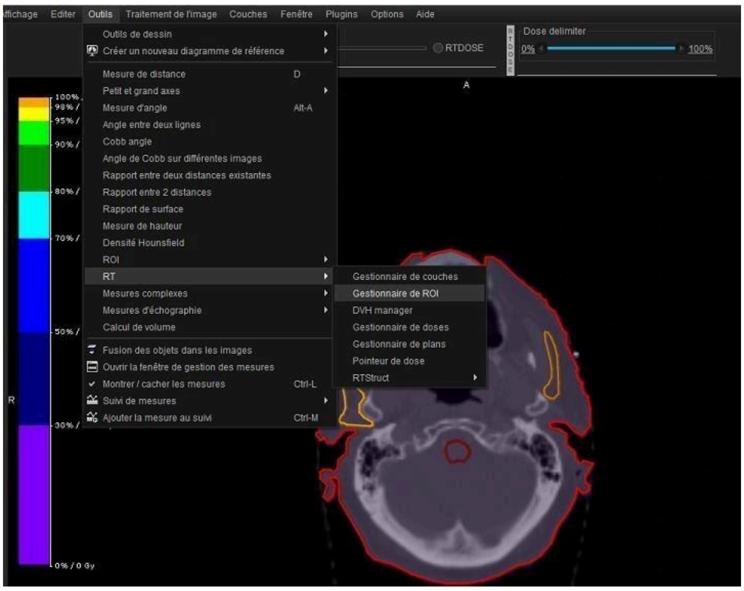
Détails de la couche

Propriété	Valeur
Institution	Univ. Hospital St.Luc-UCL-RDTH
Médecin	
Description	Helax-TMS generated study
Constructeur	MDS Nordion
Date de création	2003-05-21 at 15:37:40

Région d'intérêt (ROI)

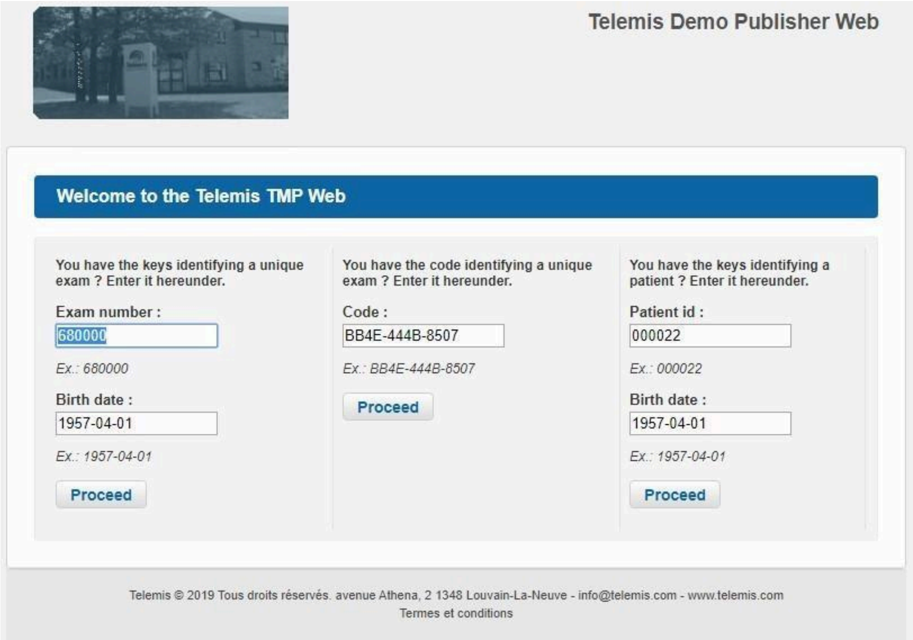
Courante	Nom	Type	Couleur	Modifi...	Visible
☐	Patient outl...	EXTERNAL	🟥	Non	✓
☐	PTV 60 Gy	PTV	🟥	Non	✓
☐	CTV 60Gy	ORGAN	🟥	Non	✓
☐	R Parotid	ORGAN	🟧	Non	✓
☐	L Parotid	ORGAN	🟧	Non	✓
☐	Brain Stem	ORGAN	🟥	Non	✓
✓	Spinal Cord	ORGAN	🟥	Non	✓

Auteurs et commentaires



7.11. TM-Publisher Web

7.11.1. The philosophy



Telemis Demo Publisher Web

Welcome to the Telemis TMP Web

You have the keys identifying a unique exam ? Enter it hereunder.

Exam number : 680000

Ex.: 680000

Birth date : 1957-04-01

Ex.: 1957-04-01

You have the code identifying a unique exam ? Enter it hereunder.

Code : BB4E-444B-8507

Ex.: BB4E-444B-8507

You have the keys identifying a patient ? Enter it hereunder.

Patient id : 000022

Ex.: 000022

Birth date : 1957-04-01

Ex.: 1957-04-01

Telemis © 2019 Tous droits réservés. avenue Athena, 2 1348 Louvain-La-Neuve - info@telemis.com - www.telemis.com
Termes et conditions

The improvements applied to TM-Publisher Web 4.95 are intended to secure the access to web data.

7.11.2. Features

7.11.2.1. Confidentiality charter

When you connect to the TMP Web, a clickable “Terms and Conditions” link appears, allowing each site
to add a solution user agreement or charter for users who are patients or GPs.

The charter must be supplied by the site.

7.11.2.2. URL parameters

The URL parameters are displayed in a way that does not contain any information related to the exam:

- Old display: http://monsite.fr/tmpweb/patient.app?patientI=387&studyI=909&serieI=5568
- New display: http://monsite.fr/tmpweb/patient.app

7.11.2.3. Patient identification

On the web portal, you can configure the random code to prevent their predictivity. Exam access codes on the web are generated randomly:

- Old type of access code: **07875725-1978-11-24**
- New type of access code: **E2FE-D3F2-0852**

7.11.2.4. Prescriber identification

Prescribing doctors are identifiable by their RPPS number (or INAMI), which prevents any confusion between similar names or different spellings in the PACS (e.g. Dr Jean Michel = Dr. Jean Michel
= Dr J. Michel = J. Michel = …).

7.11.2.5. Administrator management of patient data

For administrators of the web portal, and to comply with GDPR directives (the General Data Protection Regulation), we integrate the possibility of totally deleting all of the patient information.

8. ADDON 4.95 TO 4.96

8.1. Foreword

The TMRHE is continually being improved in order to provide users with the best possible experience, in line with Telemis's mission: "*extending human life*". This year a new tool for measuring pulmonary nodules is provided for a better comparison of such nodules over time. Some new functions are also introduced to improve everyday use of the system (more search criteria, the possibility to modify them, etc.)

Among these improvements, there is a new web interface for external distribution of images, integrating e-health for Belgian doctors, web publication in DICOM format and improved security surrounding identification.

8.2. New with TMRHE

8.2.1. Tool for calculating the volume of pulmonary nodules

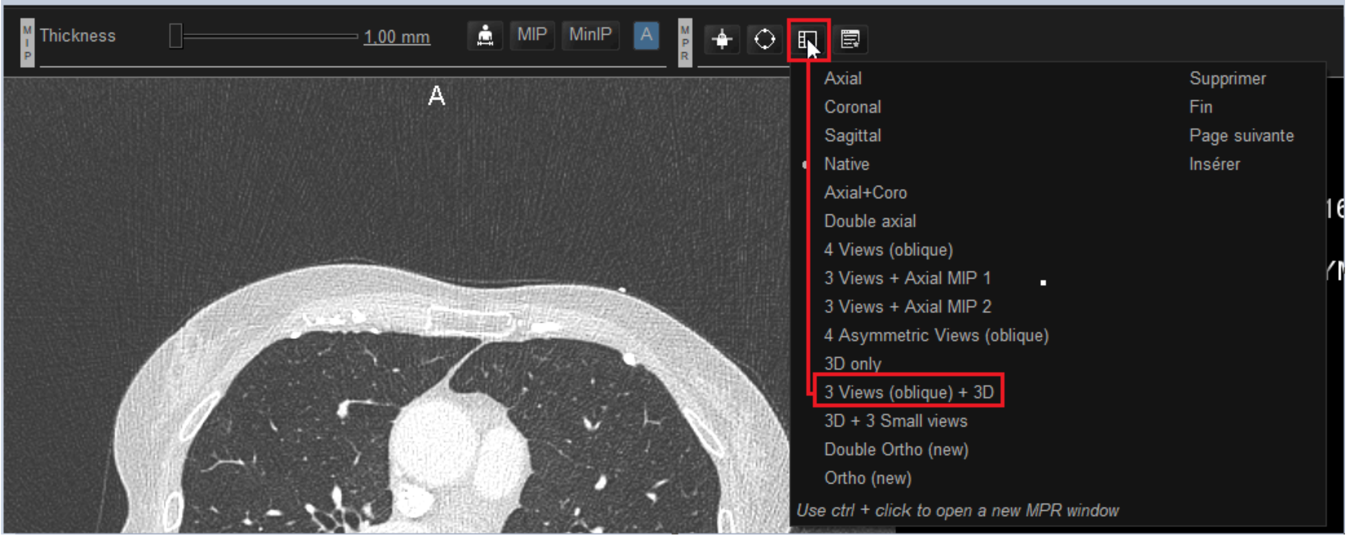
Telemis has perfected a tool for calculating the volume of pulmonary nodules. The aim of this tool is to be able to track more easily the changes in such nodules over time. The results will be useful in the follow-up tool. The tool functions with a single click which enables the algorithm to calculate automatically the nodule's limits, thus allowing the calculation to be reproducible regardless of which user is involved. It is impossible to modify the volume of the nodule.

The following notions should be understood when using the nodule volume calculation tool:

- Users remain responsible for measuring and they must validate the result visually.
- The tool is only validated for use with pulmonary nodules.
- The tool has not been validated for necrotic nodules.
- The tool must be used on parenchymal type volumes.
- Follow-up must always be carried out with the same type of windowing (parenchymal windowing).
- The tool is only usable in MPR mode on the volumes.
- Ideally, selecting the nodule should be done in the axial plane by clicking on the centre of the nodule on the slice where the nodule is at its widest.
- The tool may be activated and deactivated. Therefore, the user must request Telemis or the on-site PACS manager to activate the tool.

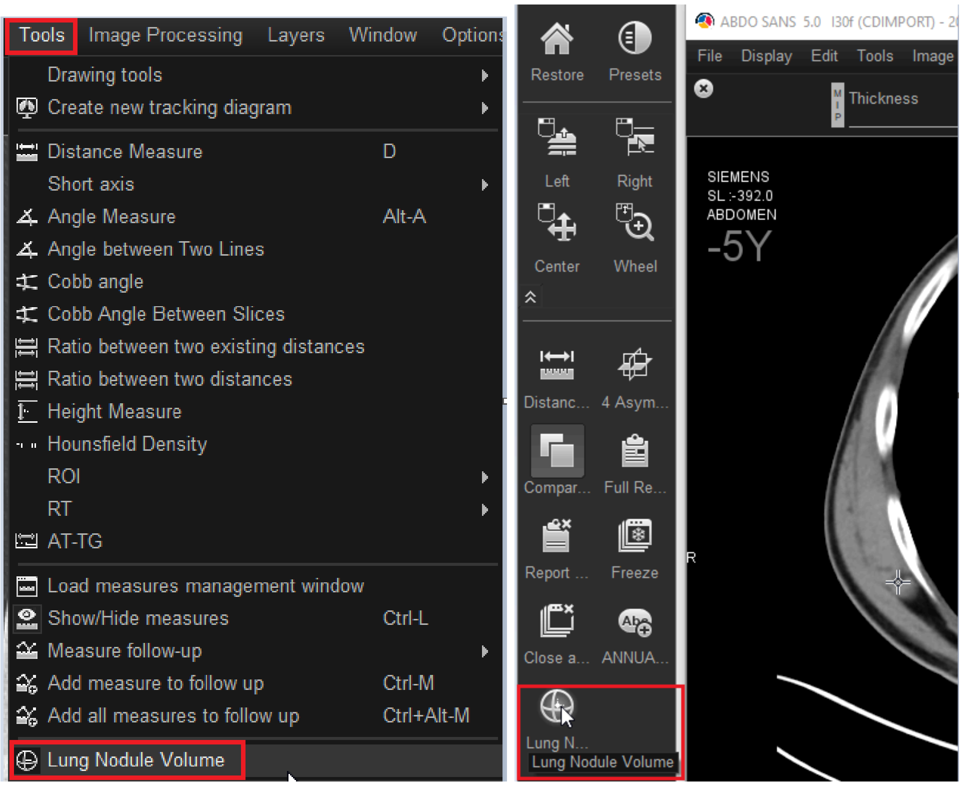
Using the tool - here an example opening in MPR with VRT views.

- Opening a series (parenchymal volume) in MPR. 3 Views + 3D (this works with all MPR views).

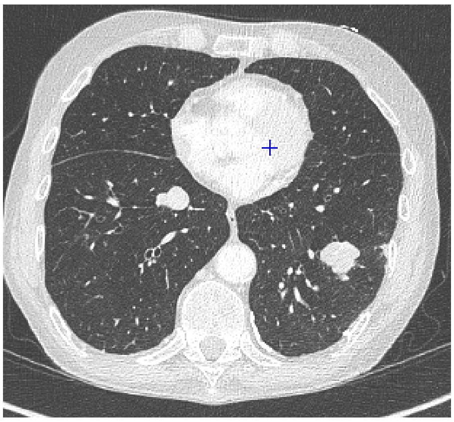


- Select the lung window for VRT.

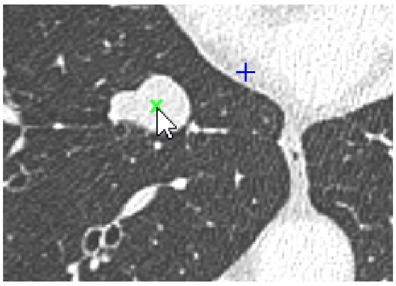
- Select the tool - beware, you need to reactivate the tool for each nodule. You may also add it to the tool bar.



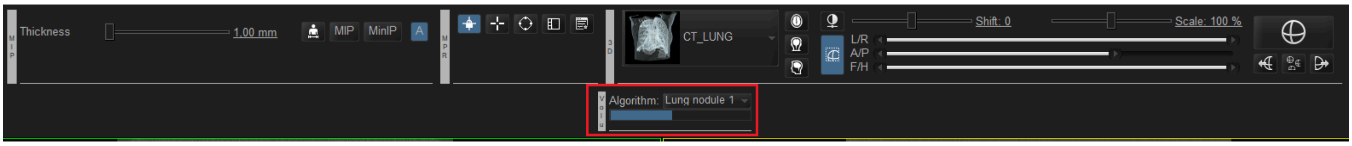
- Select an axial slice where the nodule is at its widest.



- Click on the centre of the nodule. You may zoom into the image to help.

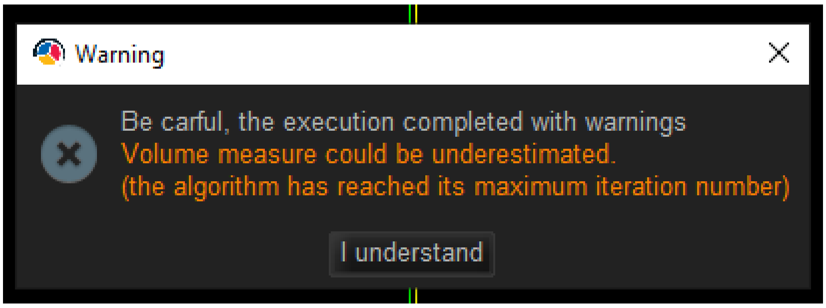


- The tool carries out the calculation and you can follow its progress on the loading bar.



Algorithm: Lung nodule 1

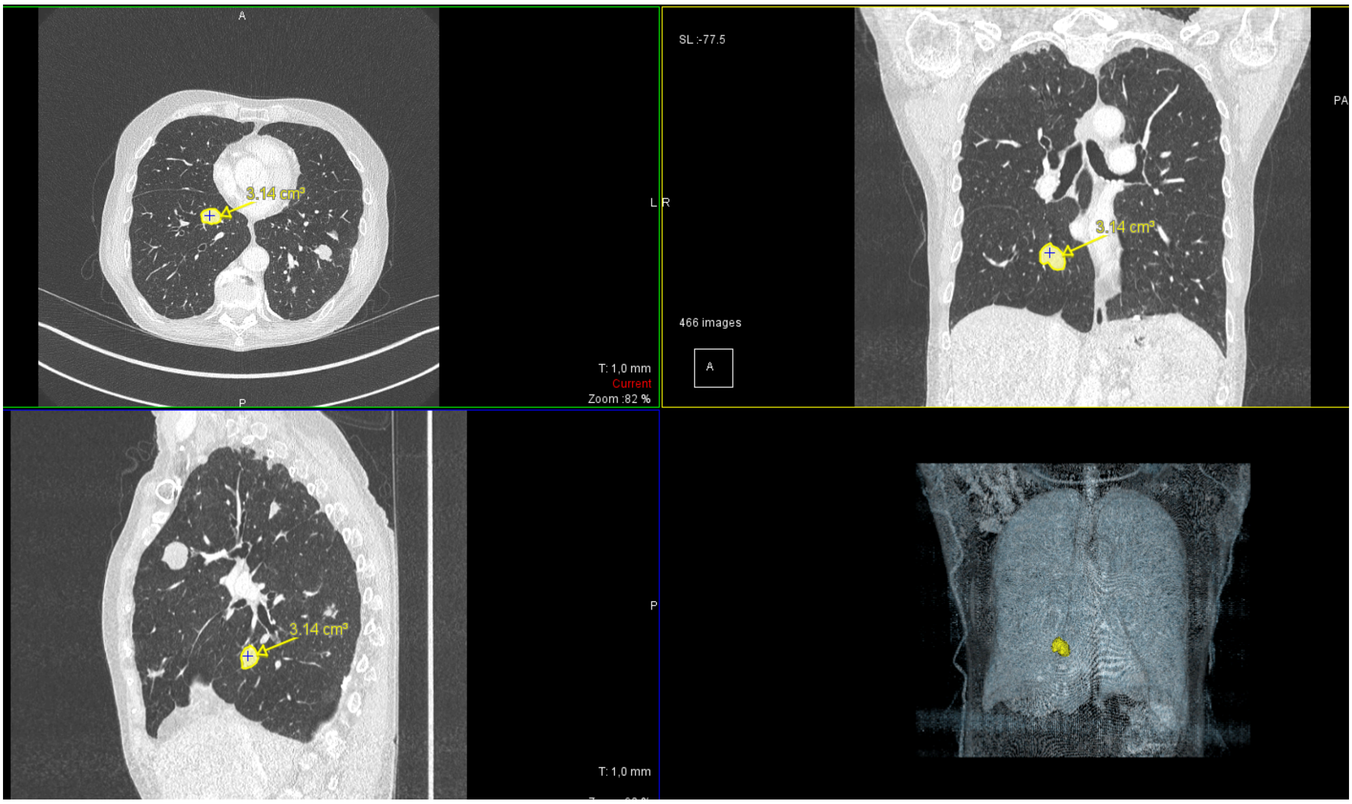
- If it's a large volume and the number of iterations of the algorithm is reached, the result may be underestimated. In this case, the following message appears to alert you.



Warning

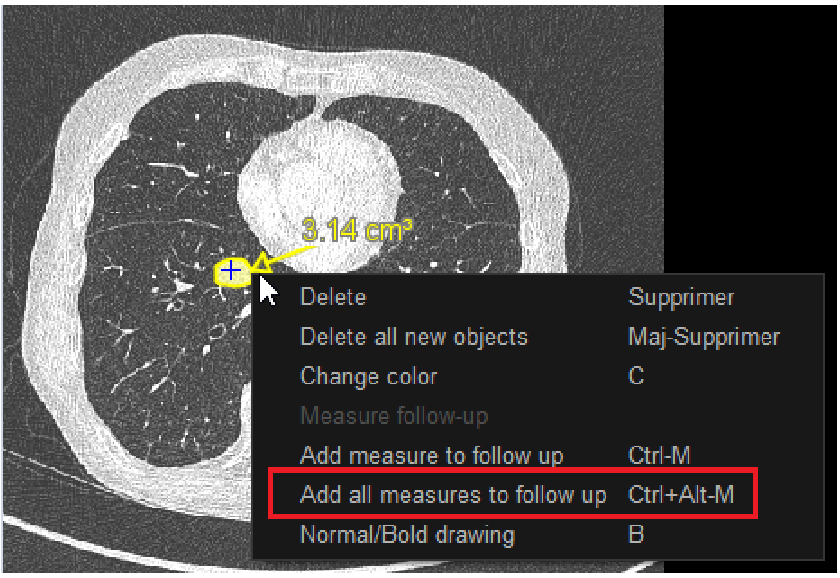
Be carful, the execution completed with warnings
Volume measure could be underestimated.
(the algorithm has reached its maximum iteration number)

- The TMRHE will indicate the nodule's measurements, the orthopointer tool will be positioned on 3 planes of the nodule being calculated and will appear in yellow in the VRT.



- To add the measurement(s) to the measurement follow-up, there are two options - 'Add measures to follow up' or 'Add all measures to follow up'. The latter is ideal when you measure several nodules in the series, because you only need to perform the add function once.

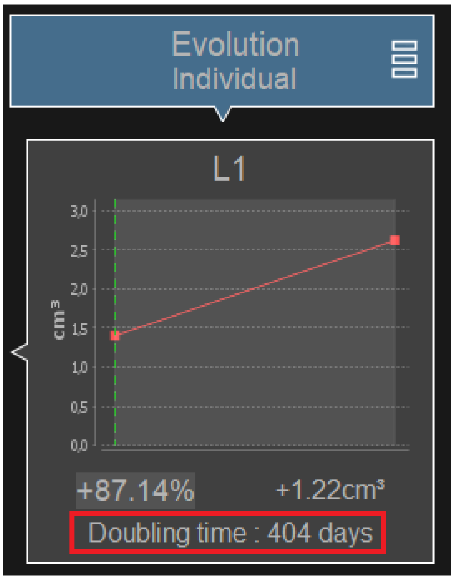
- Be careful, to be sure that all the nodules are visible to the follow-up tool, the images must not be in zoom mode when performing the add function.



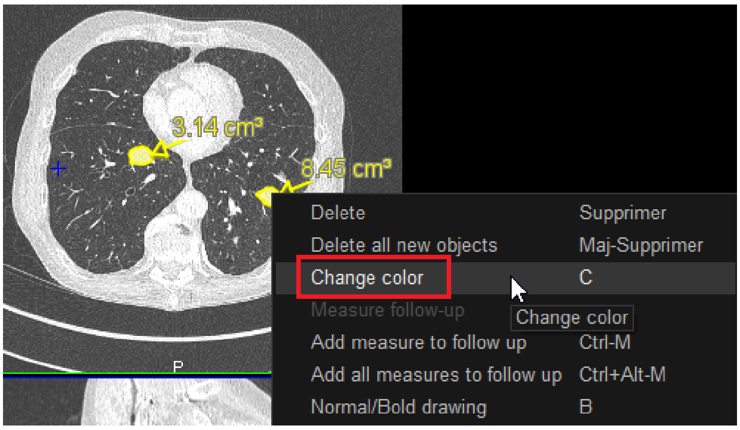
- When adding several measurements to the follow-up tool, you need to ensure that each measurement corresponds to the correct image. This is necessary because you may not have measured the images in the same order each time. To do this, use the arrows in the mini images when passing the mouse over them or drag the image to the side of the corresponding measurement.

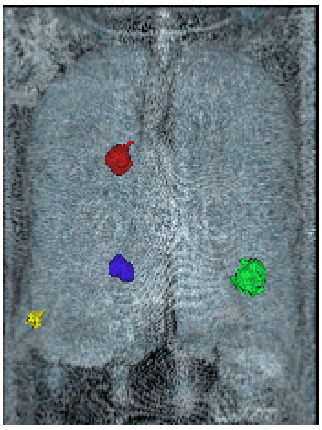
Name L1
Position 0
Type Target
Measure Volume (with mask)
Volume 5.17 cm³

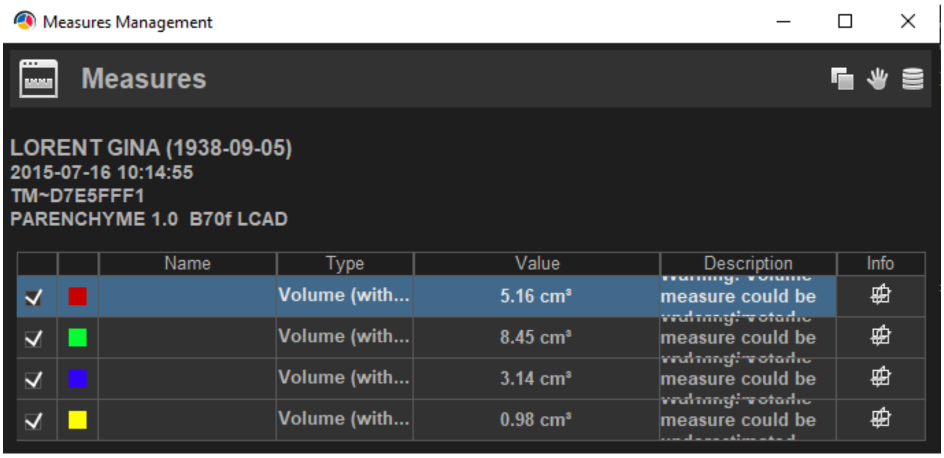
- When you have added several exams to the measurement follow-up, the evolution graphic will be displayed. This chart also shows the 'Doubling time' when you select two columns in 'Individual Evolution' mode (the value only appears in cases of an increase).



- You may change the nodules' colours to help when you are measuring several nodules.



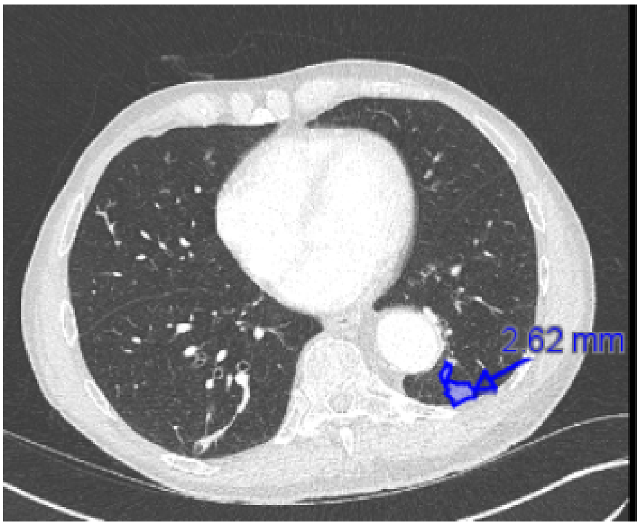




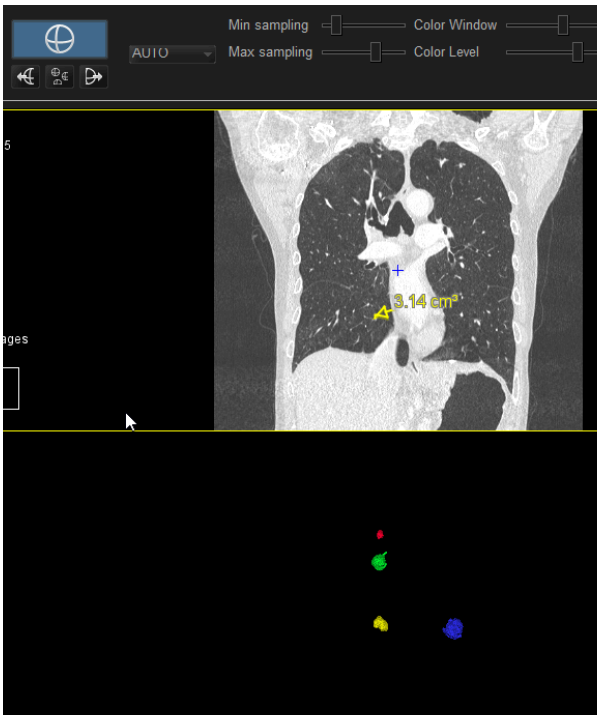
LORENT GINA (1938-09-05)
2015-07-16 10:14:55
TM~D7E5FFF1
PARENCHYME 1.0 B70f LCAD

		Name	Type	Value	Description	Info
✓	🟥		Volume (with...	5.16 cm³	measure could be	⊕
✓	🟩		Volume (with...	8.45 cm³	measure could be	⊕
✓	🟦		Volume (with...	3.14 cm³	measure could be	⊕
✓	🟨		Volume (with...	0.98 cm³	measure could be	⊕

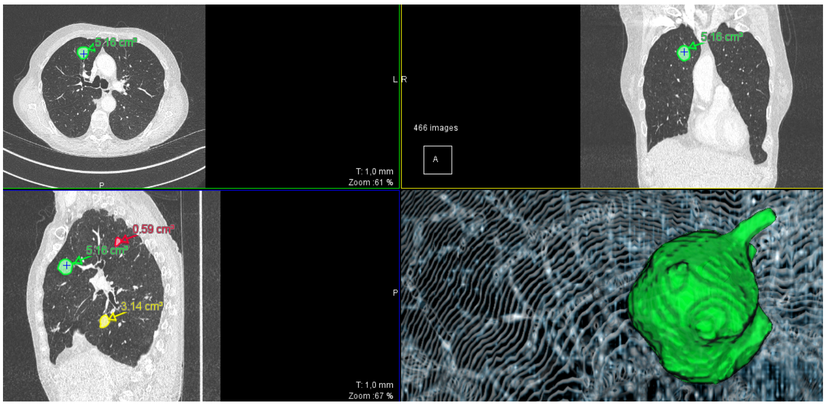
- When you call up a measurement from the measurement follow-up, the series opens on the slice for which you calculated the nodule's volume. Be careful, the volume only refers to the current slice - it is not recalculated.



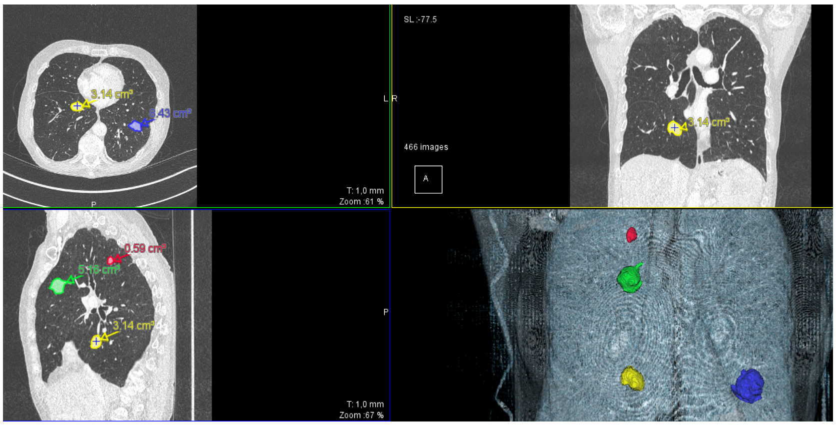
- The ⊕ button enables hiding the tissue so as to leave only the nodules appearing in the VRT visualisation.



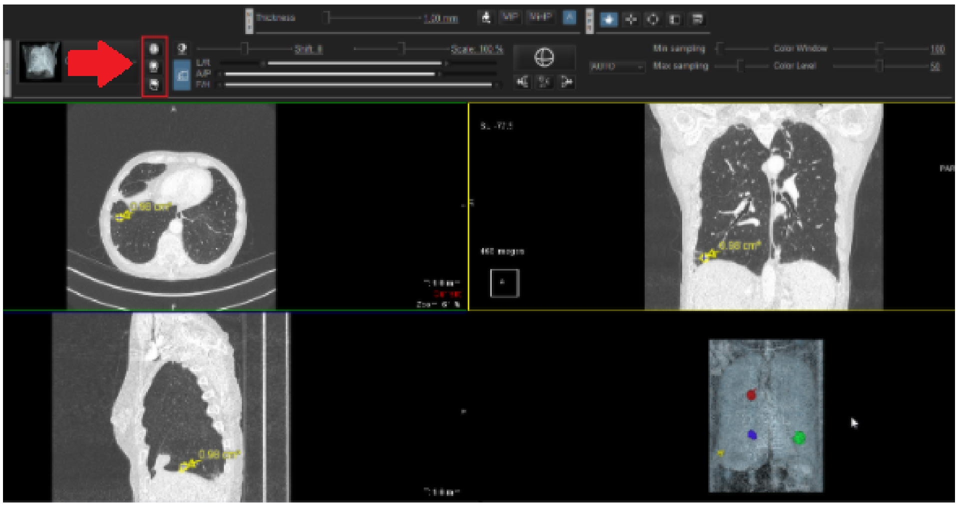
the buttons and enable zooming in on the nodules one by one, the orthopointer positioning itself on the nodule so it can be viewed in all 3 planes.



- the button zooms in on all the nodules and allows rotating around the median axis in relation to the various nodules.



- To return to the usual view, simply select one of the predefined views.



8.3. Improvements to the previewer

8.3.1. Automatic linking of a series

In the earlier version, automatic linking was implemented in the *TM-ReceptionHE* for the examinations of the day. For example, when opening an echography exam by selecting a thumbnail, all the images in the series are linked so that they open together, even if they appeared separately in the previewer.
If you don’t wish to have the full series but just one specific image, press CTRL when selecting and dragging the thumbnail, and this will load only the selected image into the viewer.

8.3.2. Modifying the stickers for examinations

Historically, Telemis usually differentiated exams using coloured geometric forms and, more recently, adding figures. These stickers appeared in the previewer as well as in the viewers, facilitating the linking of viewers by exam.

In this latest version, the stickers are configurable - figures, forms, coloured or not.

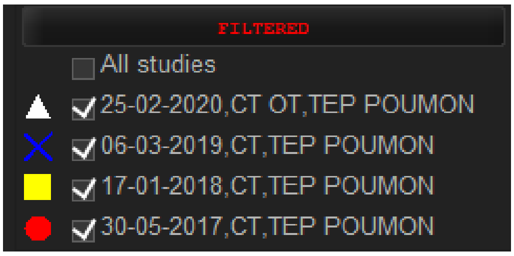
8.3.3. Minimisation of the previewer

Now, when you minimise the previewer, the patient’s images are minimised automatically at the same time, and re-open with the previewer when you select it again.

8.3.4. The previewer filter

In previous versions you have been used to being able to suppress certain modalities in the previewer. In this latest version, you may now very simply remove the filter if you have a need to access images which have been hidden by the filter.

In the example below, the previewer has been programmed not to display the PT modality.



FILTERED

☐ All studies

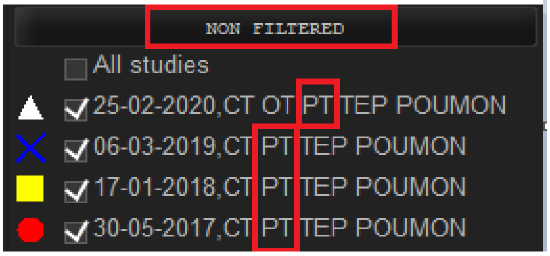
▲ ☑ 25-02-2020,CT OT,TEP POUMON

✕ ☑ 06-03-2019,CT,TEP POUMON

■ ☑ 17-01-2018,CT,TEP POUMON

● ☑ 30-05-2017,CT,TEP POUMON

To inactivate temporarily the filter, simply click on ‘FILTERED’. The modality PT is now restored.



NON FILTERED

☐ All studies

▲ ☑ 25-02-2020,CT OT,PT,TEP POUMON

✕ ☑ 06-03-2019,CT,PT,TEP POUMON

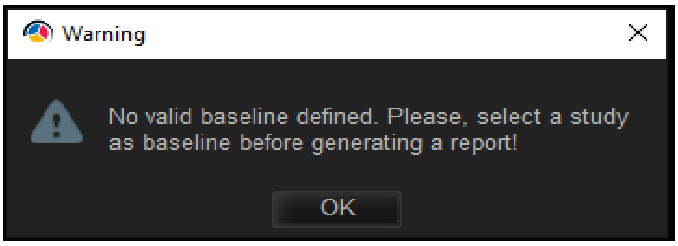
■ ☑ 17-01-2018,CT,PT,TEP POUMON

● ☑ 30-05-2017,CT,PT,TEP POUMON

8.4. Miscellaneous improvements

8.4.1. Measurement follow-up

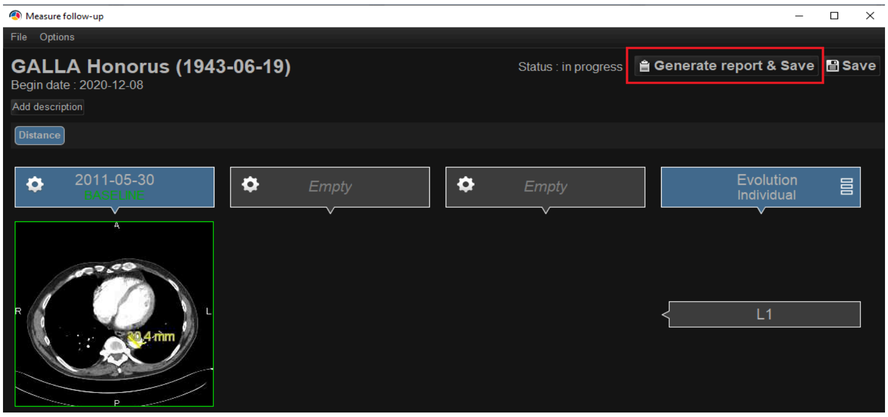
- Baseline: in earlier versions it was possible to delete the 'baseline' measurement but the follow-up of the measurement did not delete the rest, which was a source of errors. Now, if you delete the 'baseline' image, all the follow-up of this lesion is deleted and a message is displayed to suggest choosing another.



Warning

No valid baseline defined. Please, select a study as baseline before generating a report!

- Generate report and Save: in the former version of the follow-up, it was necessary first to generate the report and subsequently save using two distinct clicks. It is now possible to achieve this with just a single click using the 'Generate report and Save' button.

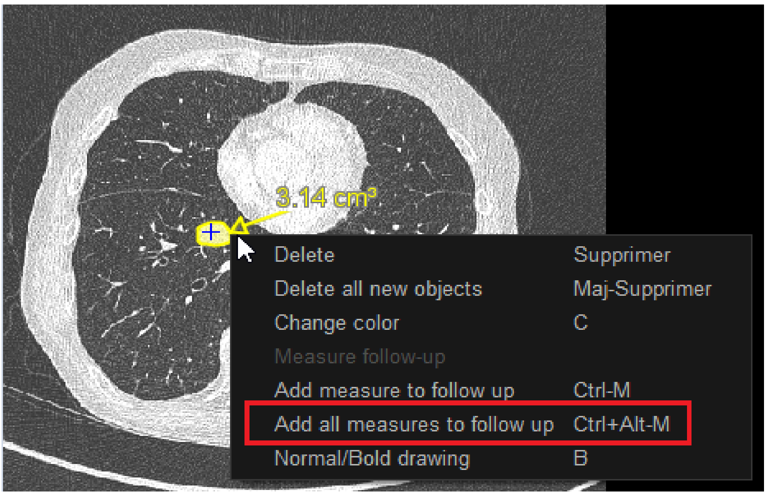


Measure follow-up

GALLA Honorus (1943-06-19)
Begin date : 2020-12-08

Status : in progress

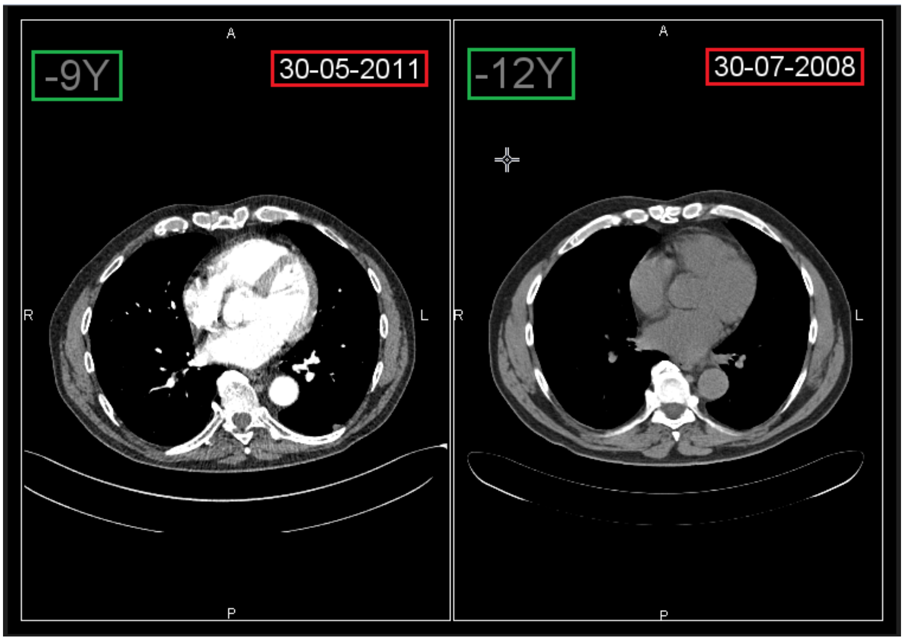
- Add all measures to follow up: it is now possible to add all measurements carried out to the measurement follow-up with a single click, providing added simplicity.



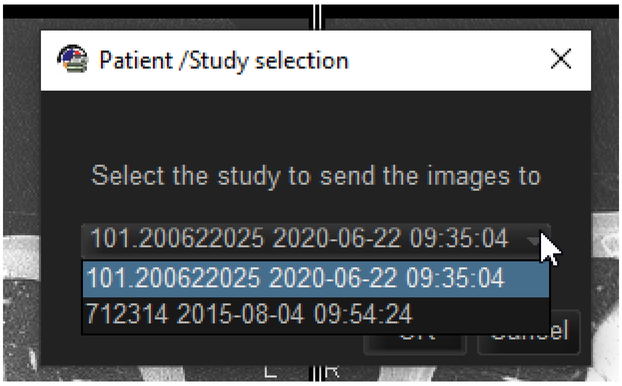
8.4.2. Filmer

Some modifications have been made to the filmer:

- Acquisition date and age of the image: the acquisition date and the age of the image at the time of filming are now displayed. The age appears top left and the acquisition date top right for each image added to the filmer.



- Choice of the summary sheet study: when sending to the PACS a filmer containing images from several exams, a window opens enabling selecting the exam in which you wish to send the summary sheet. The most recent exam is displayed at the top of the list.



Patient /Study selection

Select the study to send the images to

101.200622025 2020-06-22 09:35:04

101.200622025 2020-06-22 09:35:04

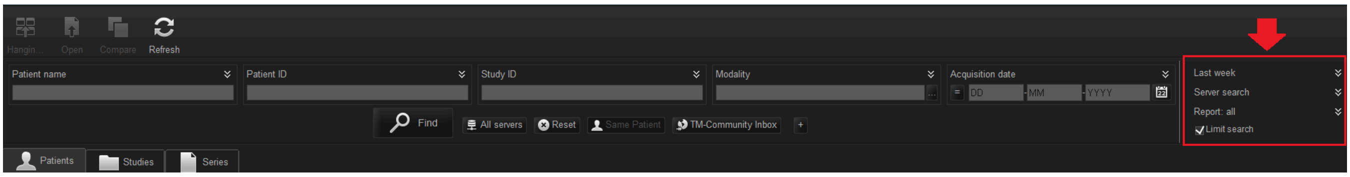
712314 2015-08-04 09:54:24

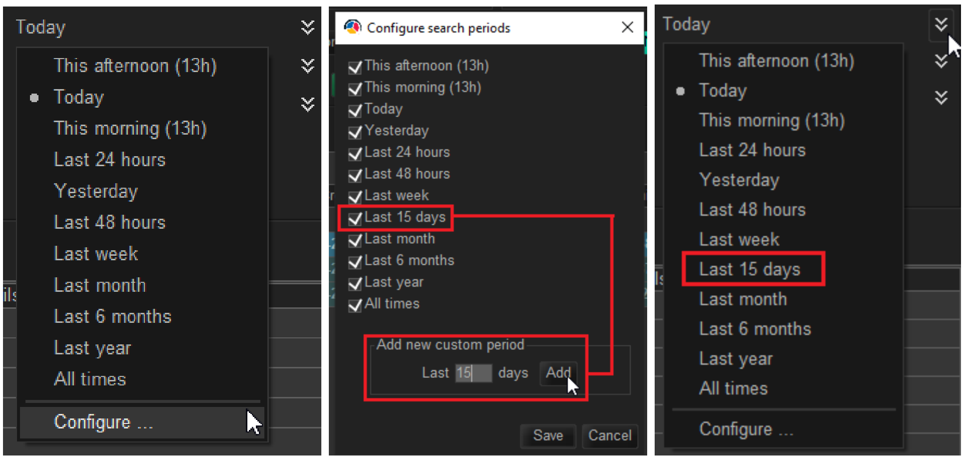
- The name of the user who sent the filmed images is retained in the images sent, in the DICOM field ‘Operator’s Name’.

0008, 1070	Operator's Name	PN	18	Telemis^Dr_Telemis

8.4.3. Search criteria for the browser

It is now possible to specify temporal criteria for searching with the browser.
Not only can you select time criteria, but you may also create new ones for yourself:





It is also possible to change the pivotal hour (Telemis to configure) to help with differentiating between morning and afternoon.

8.4.4. Delaying TM-Home updates

The number of TM-Home updates prior to a forced update has been increased in order not to oblige the back-up user to be forced into an update in emergency situations.

8.4.5. DICOM print footnote

The footnote for the DICOM print function may now be specified by Telemis according to the user’s preferred parameters.

8.5. New for the web browser (TM-Publisher Web)

8.5.1. DICOM images

Images published on the web will now all be in DICOM format. In addition to providing improved image quality, this new disposition will improve the exam re-publication function.
A transition period will be necessary for all the images for the sites to be published in DICOM format.

8.5.2. Multi-support

The new *TM-Publisher Web* is multi-platform and is compatible with Windows, Mac, Android and iPhone.

8.5.3. New interface

A new graphic interface for viewing and new functions are available in the new version of the TM-Publisher Web, and all other functions, outside the viewing window, remain unchanged. Here is a brief summary of the new items:

8.5.3.1. Identification page

Un patient

Je suis un patient ou un médecin et j'ai des codes pour visualiser des images médicales

Un docteur

Je suis médecin et je souhaite me connecter pour visualiser les images médicales de mes patients

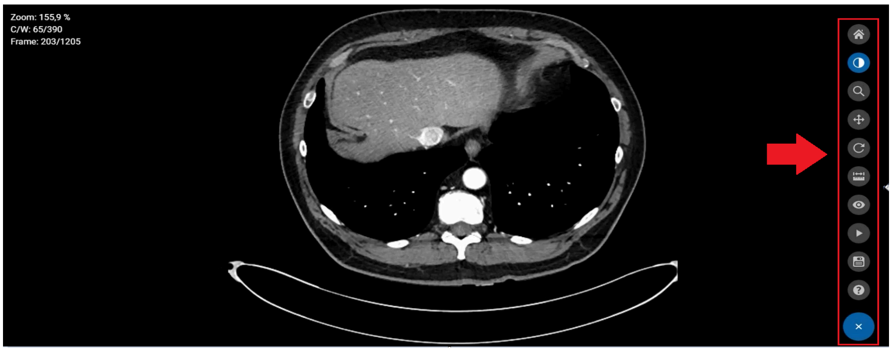
8.5.3.2. Viewing interface

- A loading bar on the right indicates the progress of loading the images into the viewer. The grey zone corresponds to the images loaded. Once all images are loaded, you may use the bar for navigating among the images.

Zoom: 100 %
C/W: -43,26/1 527,73
Frame: 16/1205

Type de visualisateur: DICOM | DICOM avancé

- A new toolbar is available to the right of the image

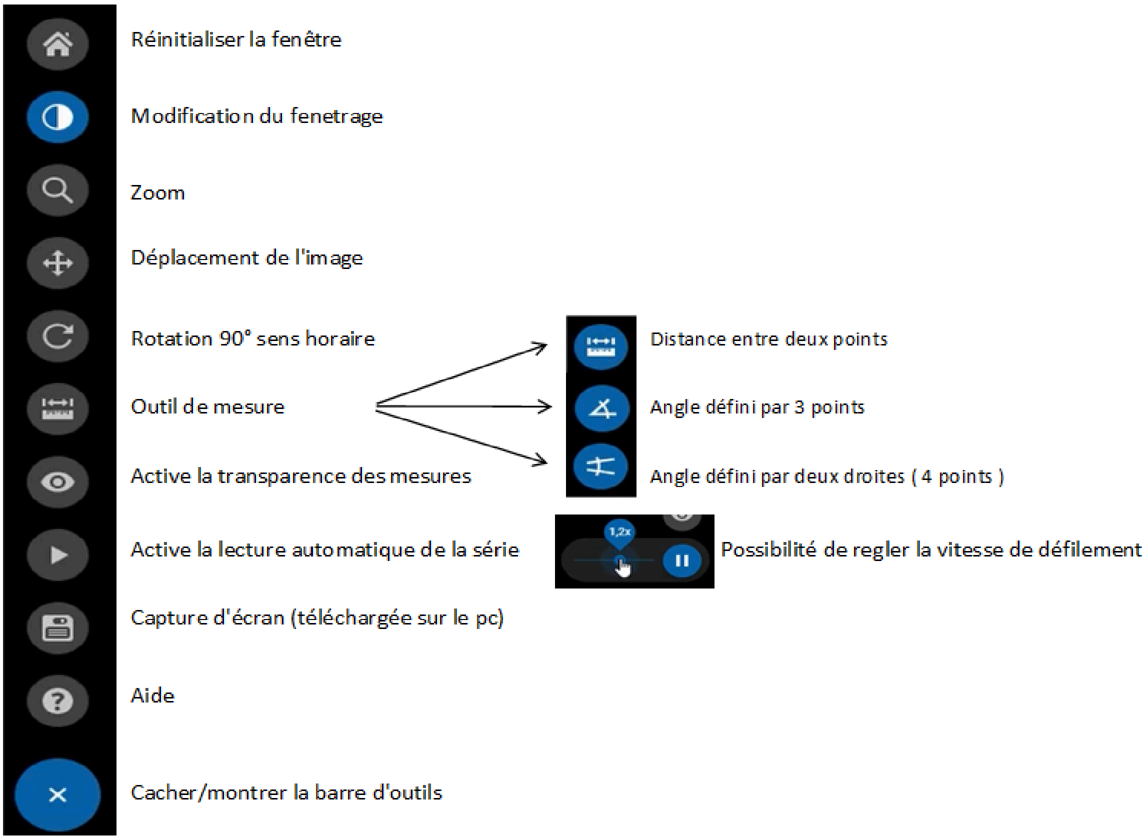


Zoom: 155,9 %
C/W: 65/390
Frame: 203/1205

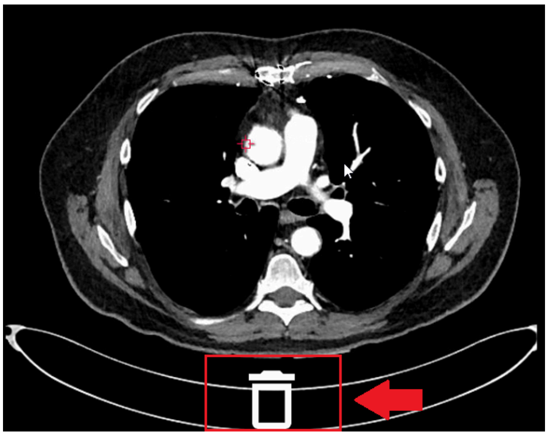
- Explication of the tools

  Default functions activated on opening the studies are:

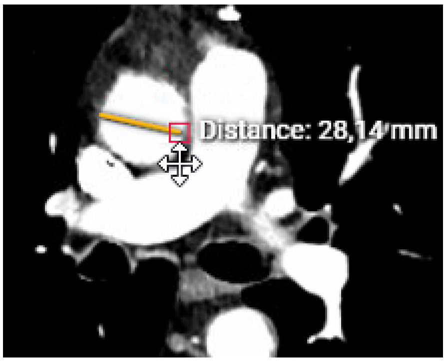
  - Left-click: windowing
  - Right-click: zoom
  - Scroll wheel: scrolling



- Measurement tools
  - General information
    - For measurement tools, when the measuring has not been completed and you wish to cancel the measurement, move the pointer to the rubbish bin which appears at the bottom of the image.



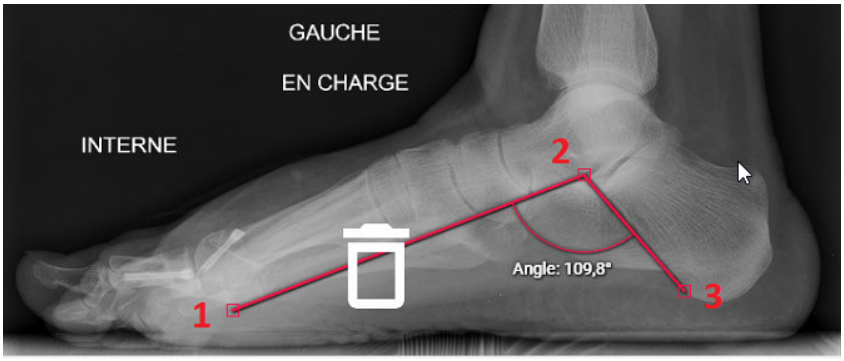
  - If you wish to modify an already completed measurement, place the cursor on the point to be modified - the point will appear as a red square - and click. It is then able to be deleted or displaced using a right-click.



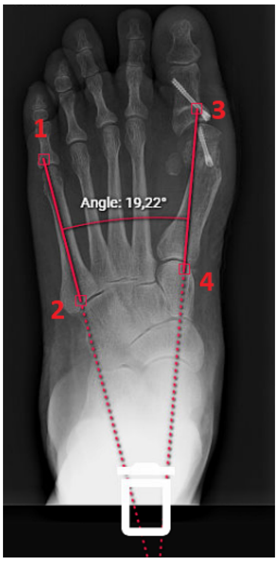
  - To delete a measurement or an angle, select the item by right clicking on any point of the said measurement or angle.
  - To de-activate the tool, right-click when the measurement is completed. If this is not done, the tool will remain active.

- Measuring distance: to do this, you may either click at the point where measuring is to start and maintain the button depressed while moving to where measuring will end and releasing the button, or click at the point where measuring is to start and then click again where measuring is to end.

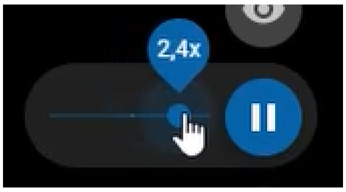
- Measuring a 3-point angle: Click at the places which form the angle in the following order: extremity, summit, extremity.



- Measuring the angle between two straight lines: define two points on the first straight line and then define two points on the second straight line. The result is the angle between the two straight lines.



- Cineloop tool: click to activate the automatic cineloop tool and click again to deactivate it. When the function is activated, a bar is displayed to help manage the reading speed. Click, move at the desired speed and release.



8.5.4. Improved security

Security for the TMPWeb interface has been improved in a manner totally transparent for the user.

For physicians in Belgium, in addition to the improvement in the identification procedure with the manual creation of a Telemis account, we have now integrated e-health. Via e-health, the application automatically creates an account and presents for viewing those exams which have the detected INAMI number associated with them. Several identification modes are available: eID card, itsme, etc.

First step, select the identification mode:

CSAM

S'identifier à l'administration en ligne

Choisissez votre clé numérique pour vous identifier.

Besoin d'aide?

Clé(s) numérique(s) avec **l'eID** ou **identité numérique**

IDENTIFICATION
avec un lecteur de cartes eID

IDENTIFICATION
via itsme

Créer votre compte itsme

Clé(s) numérique(s) avec **code de sécurité** et **nom d'utilisateur + mot de passe**

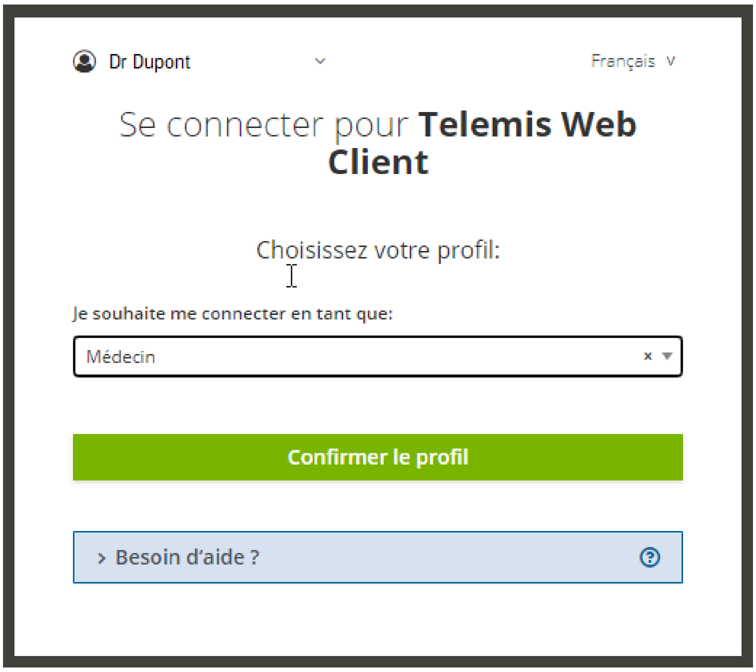
IDENTIFICATION
avec un code de sécurité envoyé par e-mail

IDENTIFICATION
avec un code de sécurité via une application mobile

Authentication européenne

IDENTIFICATION
avec une identification électronique reconnue au plan européen

Second step, select your profile:



Dr Dupont

Français

Se connecter pour **Telemis Web Client**

Choisissez votre profil:

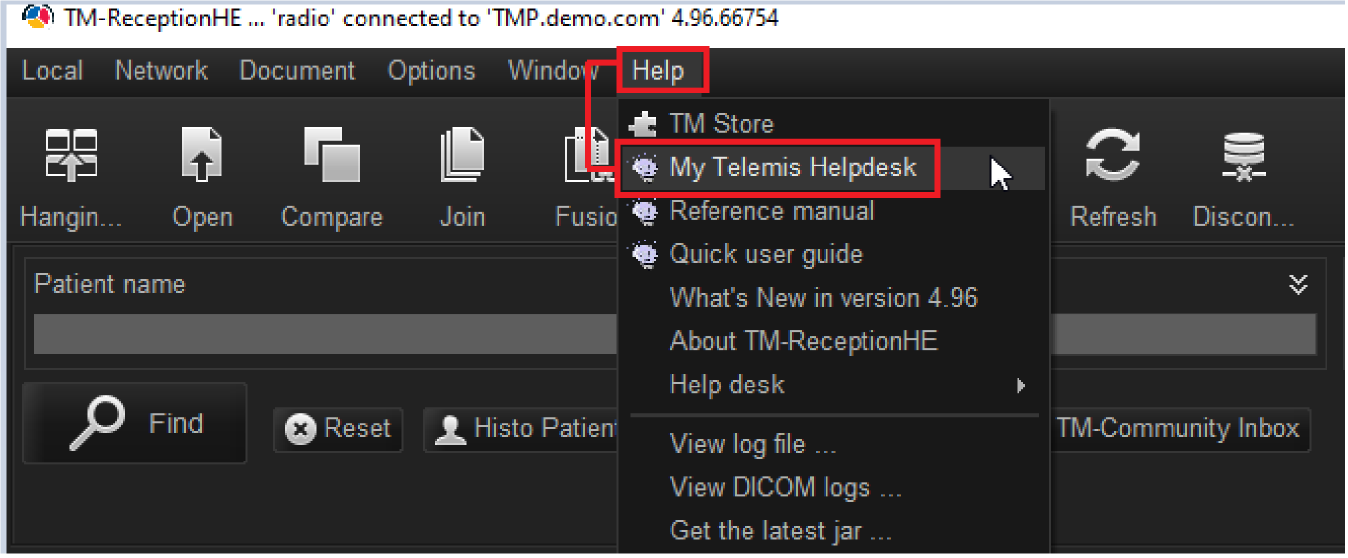
Je souhaite me connecter en tant que:

Médecin

8.6. Help

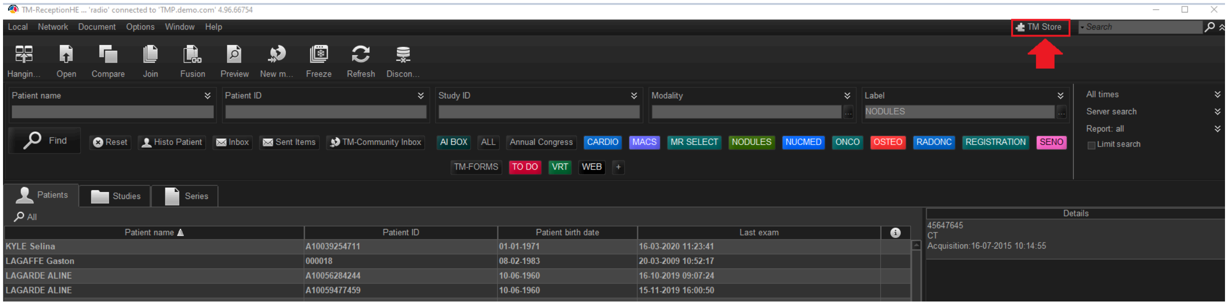
8.6.1. Support

Telemis support is accessible by telephone, but also through the TMRHE using the 'Help' tab. This will take you to our ticketing platform from where your requests will be actioned.



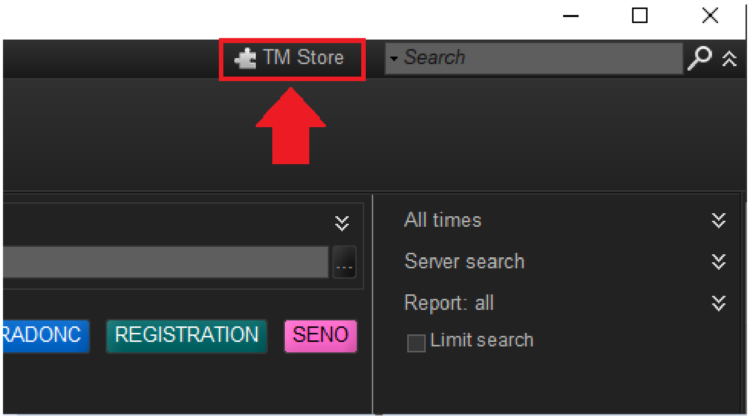
8.6.2. TM Store

TM Store is a tool made available to users by Telemis. It is a collection of videos explaining the various functions of TMRHE accessible directly from TMRHE.

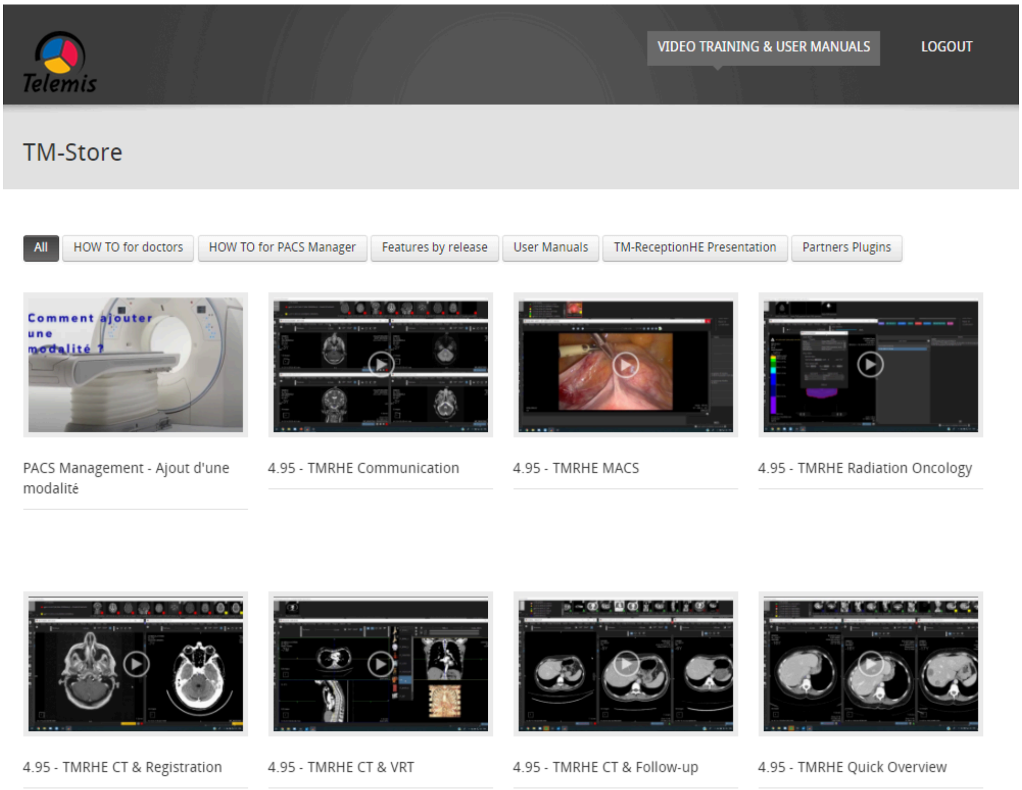


Patient name	Patient ID	Patient birth date	Last exam
KYLE Selina	A10039254711	01-01-1971	16-03-2020 11:23:41
LAGAFFE Gaston	000018	08-02-1983	20-03-2009 10:52:17
LAGARDE ALINE	A10056284244	10-06-1960	16-10-2019 09:07:24
LAGARDE ALINE	A10059477459	10-06-1960	15-11-2019 16:00:50

45647645
CT
Acquisition:16-07-2015 10:14:55



There you will find a series of videos for all the various functions which have appeared in recent updates. This new functionality is explained in a video available in several languages. It contains also certain explanatory videos concerning the actions required by the PACS manager.



TM-Store

- PACS Management - Ajout d'une modalité
- 4.95 - TMRHE Communication
- 4.95 - TMRHE MACS
- 4.95 - TMRHE Radiation Oncology
- 4.95 - TMRHE CT & Registration
- 4.95 - TMRHE CT & VRT
- 4.95 - TMRHE CT & Follow-up
- 4.95 - TMRHE Quick Overview

9. ADDON 4.96 TO 4.97

9.1. Foreword

Development of the TMRHE continues, in order to improve the user experience. Special care has gone into the details, contributing to a better overall experience (space between the windows, double-click to maximise the windows).

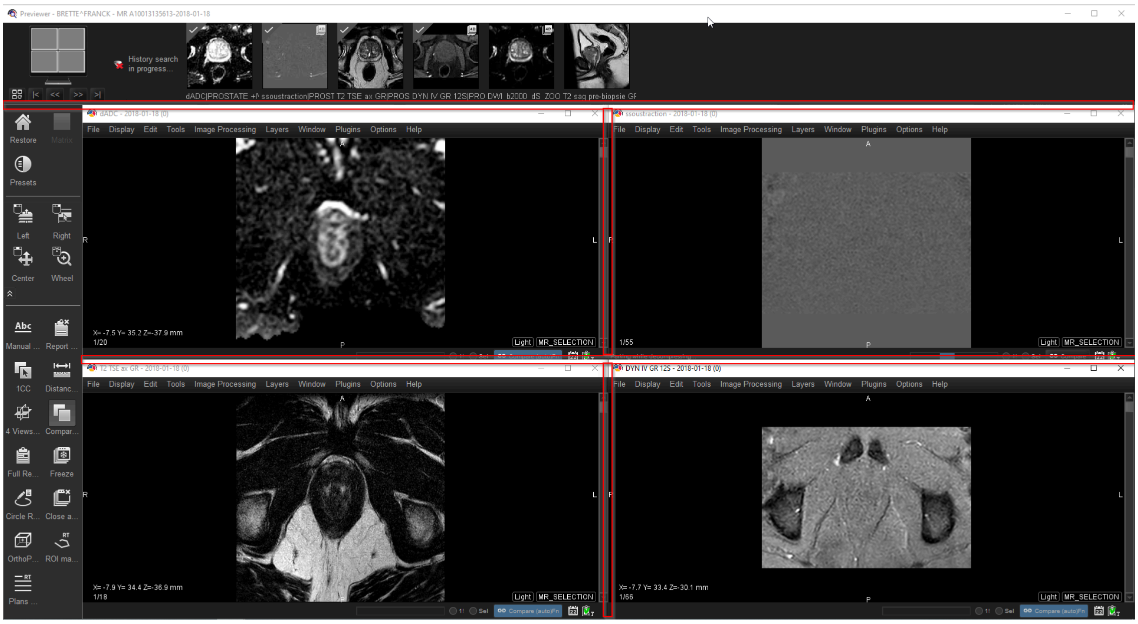
But changes have also been made to major features (MPR reference line, DVH tool, One-click compare, measurement tracking).

Some changes have also been made to aspects that are less visible to the end user, but still improve the system, such as the TM-Community system (better communication between servers and sites) and modifications to the TMP-Web (improved security, publication, multiple patient ID, notifications).

9.2. New with TMRHE

9.2.1. Space between windows eliminated

In the previous versions of TMRHE, there was always a space between the windows, which was distracting to the user if the window in the background was very bright. In the new version, those spaces have been eliminated.



9.2.2. Double-click to maximise windows

From now on, a double-click anywhere in the window toggles the window to full screen.

Double-click again to return to the normal mode.

9.2.3. MPR viewer

- The numbering of the images is now displayed in native mode.
- Reference line in native mode
- Possibility of opening a series of fewer than 10 images

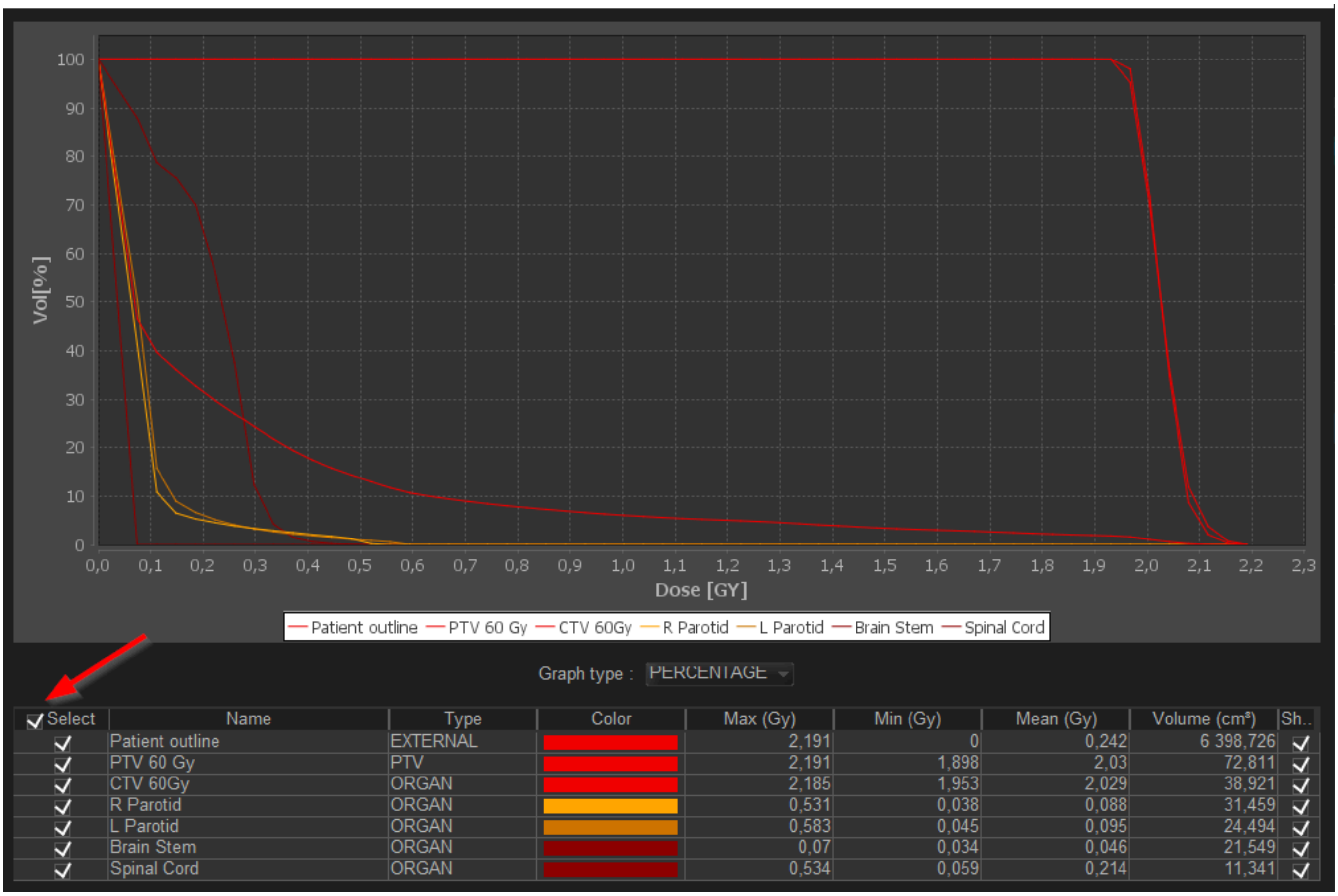
The aim was to allow the viewer to be used more often in native mode, where more features would be offered.

9.2.4. Improved management of tomosynthesis series

- Supports High-Definition Tomosynthesis (Hologic)
- Supports more incidences

9.2.5. DVH tool: curve selection

In the DVH curve management tool, you can now select or deselect all the curves with a single click.



Graph type : PERCENTAGE

☑ Select	Name	Type	Color	Max (Gy)	Min (Gy)	Mean (Gy)	Volume (cm³)	Sh..
✓	Patient outline	EXTERNAL	🟥	2,191	0	0,242	6 398,726	✓
✓	PTV 60 Gy	PTV	🟥	2,191	1,898	2,03	72,811	✓
✓	CTV 60Gy	ORGAN	🟥	2,185	1,953	2,029	38,921	✓
✓	R Parotid	ORGAN	🟧	0,531	0,038	0,088	31,459	✓
✓	L Parotid	ORGAN	🟧	0,583	0,045	0,095	24,494	✓
✓	Brain Stem	ORGAN	🟥	0,07	0,034	0,046	21,549	✓
✓	Spinal Cord	ORGAN	🟥	0,534	0,059	0,214	11,341	✓

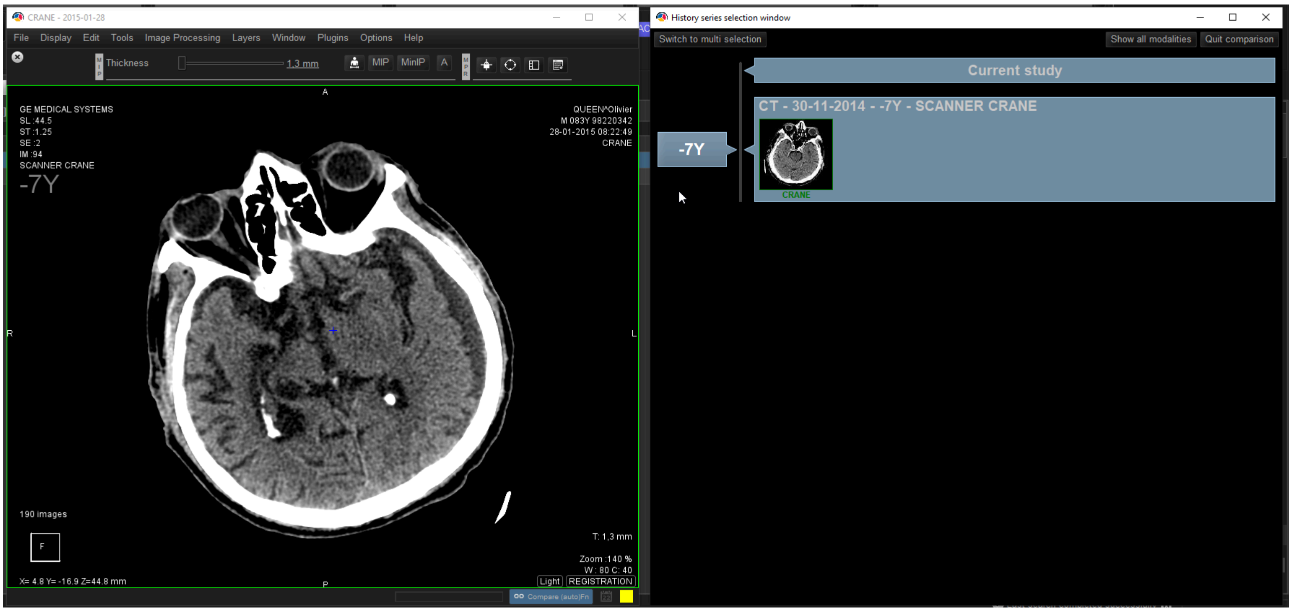
9.2.6. Comparison mode

With the comparison module being continually upgraded, this year again, the research and development team has worked on it to make it even more efficient.

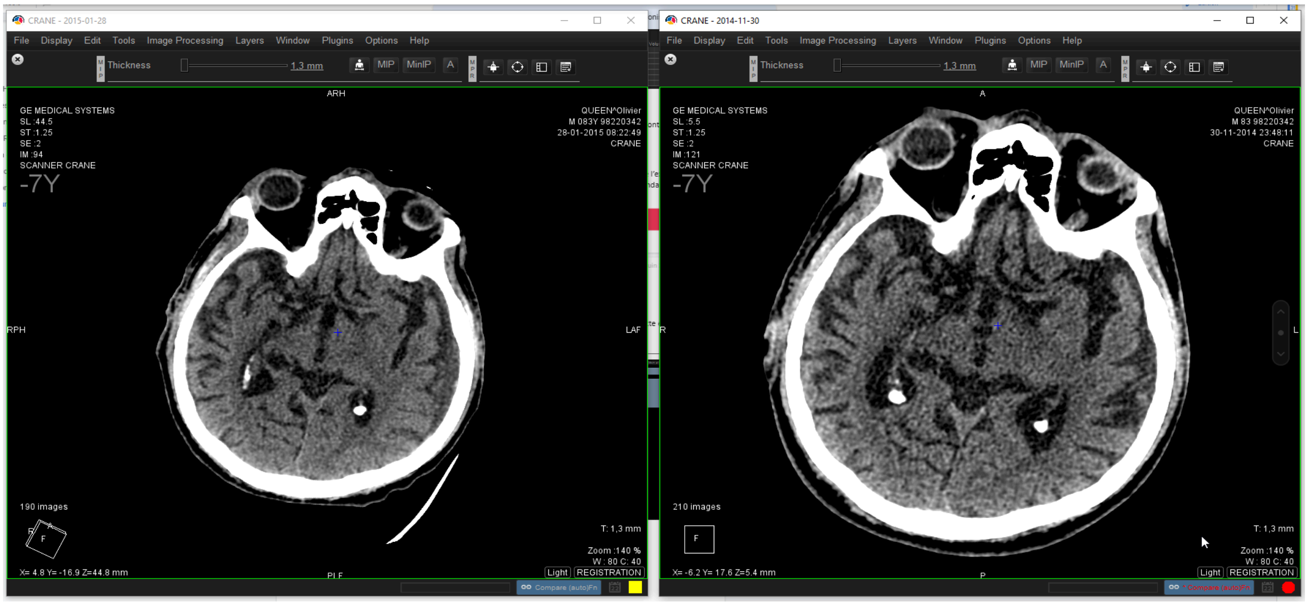
9.2.7. One-click comparison

The one-click comparison tool used to require manual selection of the exam.
In this new version, the TMRHE can select the best match from the history, and then display it directly.

Before: the system offered you the best selection in green and a potentially good one in orange, but you had to click on it.



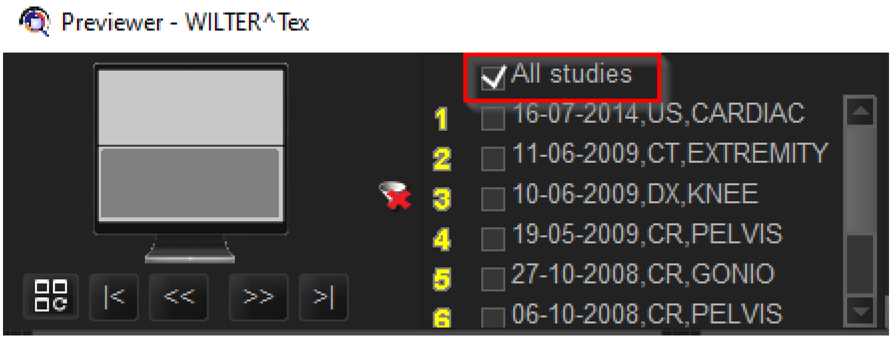
Now: the system displays the series directly if the match is good.



9.3. What's new in the previewer

9.3.1. The option to select all the exams at once

Using a new property, we can configure the TMRHE so that all the exams are selected straight away when the previewer is opened.

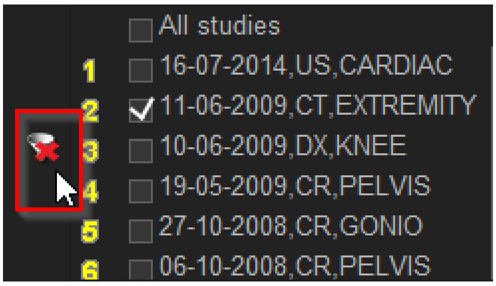


☑ All studies
1 ☐ 16-07-2014,US,CARDIAC
2 ☐ 11-06-2009,CT,EXTREMITY
3 ☐ 10-06-2009,DX,KNEE
4 ☐ 19-05-2009,CR,PELVIS
5 ☐ 27-10-2008,CR,GONIO
6 ☐ 06-10-2008,CR,PELVIS

9.3.2. Quick switch to a single exam

If several exams are selected, use the middle button (or mouse wheel) to click the exam you want to see, and only that one will be selected.

9.3.3. Option to filter the history display period



☐ All studies
1 ☐ 16-07-2014,US,CARDIAC
2 ☑ 11-06-2009,CT,EXTREMITY
3 ☐ 10-06-2009,DX,KNEE
4 ☐ 19-05-2009,CR,PELVIS
5 ☐ 27-10-2008,CR,GONIO
6 ☐ 06-10-2008,CR,PELVIS

Pending modification

9.3.4. Improved history display speed

Changes have been made in order to speed up the loading of the history in the previewer.

9.4. What's new in the filmer

9.4.1. Ability to pin the filmer

You can now pin the filmer to a location on the screen. This helps you keep an eye on it, to add the images and modify the display if necessary. It will remain in the foreground with respect to all your open windows.

To secure it in place, simply press the 📌 button.

Click it again to deactivate the feature.

9.4.2. The name of the institution is kept in the series sent

In images generated via the filmer, the name of the institution is now kept in the DICOM fields of the filmer.

9.4.3. Notification before closing

If you have not sent your filmer, a new warning message appears when you try to close it.
The purpose of this is to prevent your work from being lost.

9.5. What's new in the measurement tracking tool

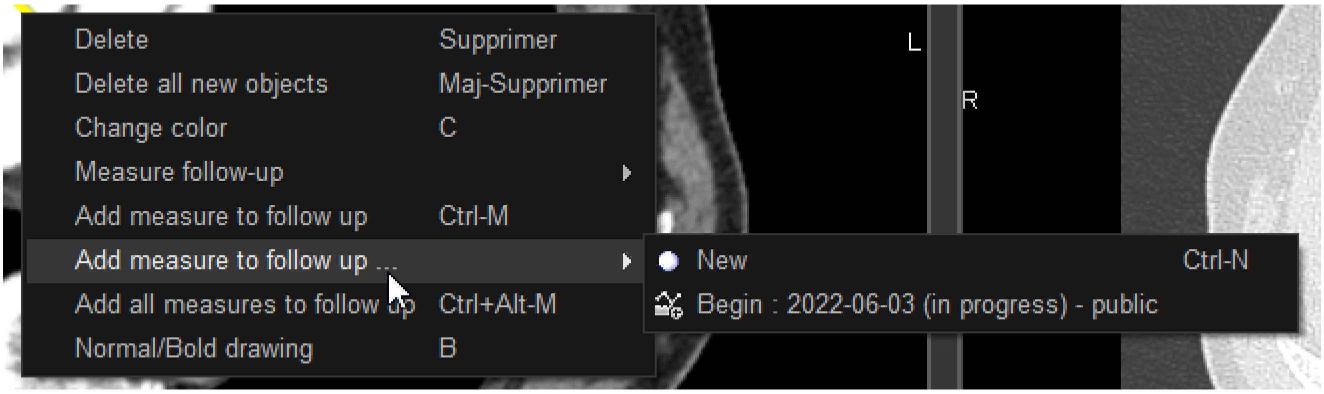
9.5.1. Simultaneous multiple tracking option

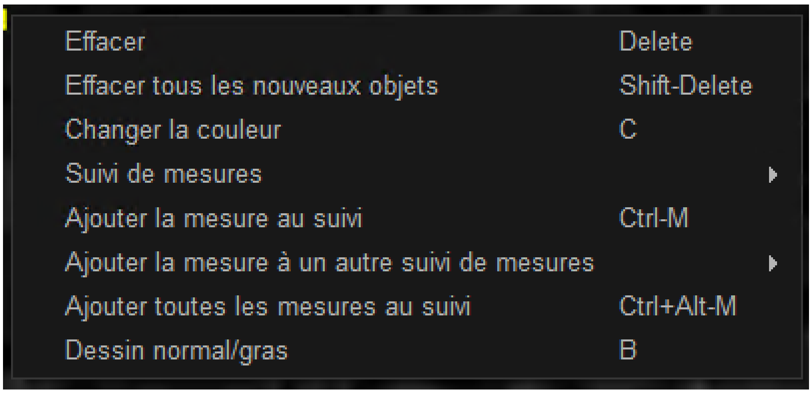
In the older versions, only one measurement could be tracked per patient. In 4.97, you can track several at the same time.

A new line, "add the measurement to measurement tracking..." lets you select tracking for the measurement of your choice.

The most common scenarios would be to monitor different lesions or different treatments in the same patient.

Or to set up a (double) blind reading.


Delete Supprimer
Delete all new objects Maj-Supprimer
Change color C
Measure follow-up
Add measure to follow up Ctrl-M
Add measure to follow up ...
Add all measures to follow up Ctrl+Alt-M
Normal/Bold drawing B
New Ctrl-N
Begin : 2022-06-03 (in progress) - public
L
R

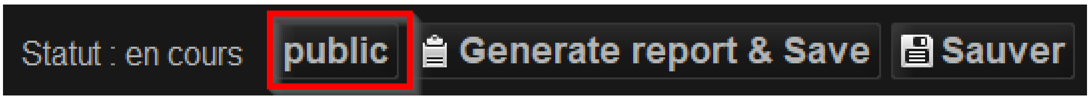

Effacer Delete
Effacer tous les nouveaux objets Shift-Delete
Changer la couleur C
Suivi de mesures
Ajouter la mesure au suivi Ctrl-M
Ajouter la mesure à un autre suivi de mesures
Ajouter toutes les mesures au suivi Ctrl+Alt-M
Dessin normal/gras B

9.5.2. Option to make measurement tracking private or public

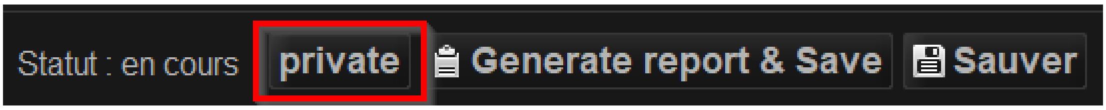
You can now make a tracked measurement private or public. This feature can be very useful for blind studies.

You can therefore have several private tracked measurements simultaneously to track the patient's progress blind.

And, if you wish, you can keep a tracked measurement public for all users.

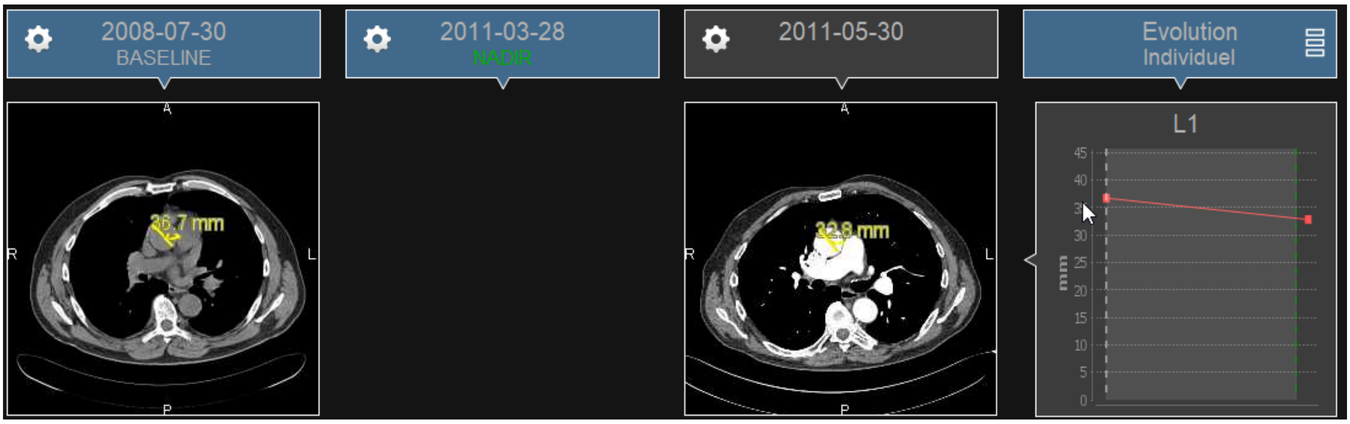


Simply click the status to toggle between private and public.



9.5.3. Improved graphs

In the measurement tracking, if there is no tracking for an intermediate examination of a measurement, the graph does not show that date.



9.6. What's new in TMP-Web

9.6.1. Multiple identifier for patients

The patient identifier can be displayed in logged-in mode according to the defined display priority.

9.6.2. Improved publication mechanism

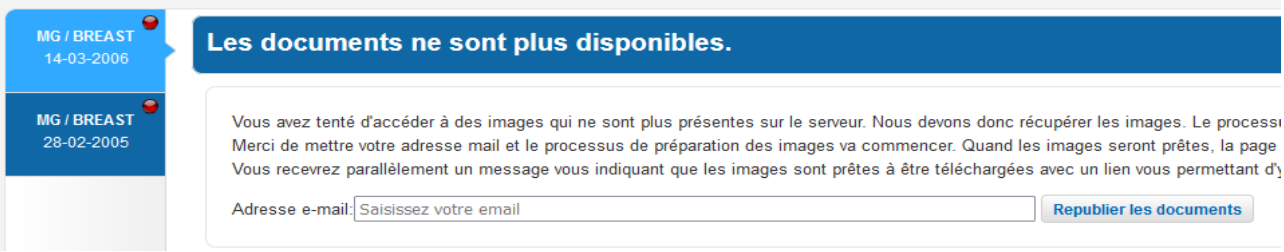
- Faster publication in case of patient changes/updates

- Priority re-publication

Re-publication takes priority over publication to avoid cases where too many publications in the acquisition folder might block the progress of re-publication.

- Re-publish all the missing exams in one click

In Patient Mode, when an access code has more than one exam, simply click "Re-publish documents" once to re-publish all the missing exams.



Les documents ne sont plus disponibles.

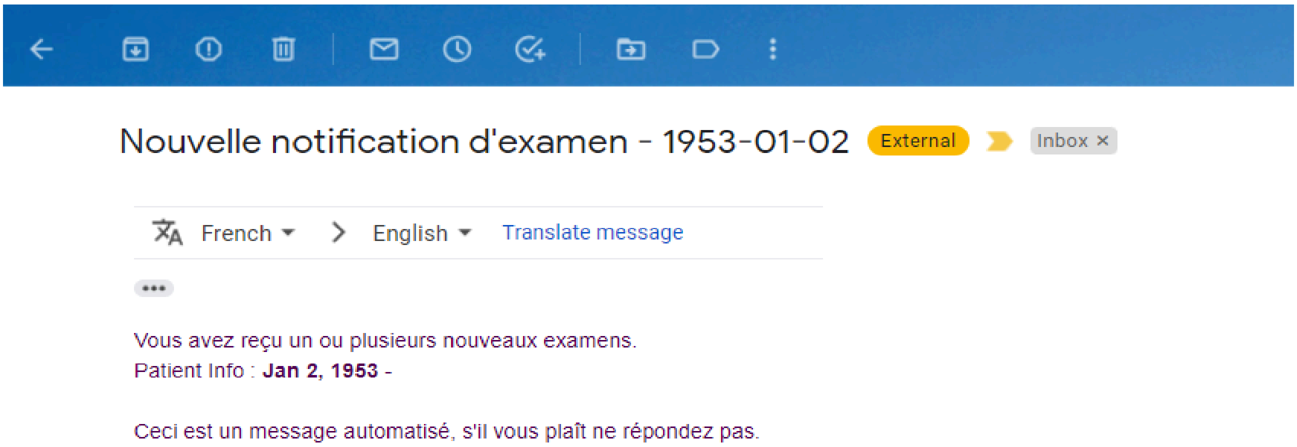
Vous avez tenté d'accéder à des images qui ne sont plus présentes sur le serveur. Nous devons donc récupérer les images. Le process
Merci de mettre votre adresse mail et le processus de préparation des images va commencer. Quand les images seront prêtes, la page
Vous recevrez parallèlement un message vous indiquant que les images sont prêtes à être téléchargées avec un lien vous permettant d'

Adresse e-mail:

9.6.3. Improved notification emails

The email notification can contain the patient information according to the web configuration.

- patient date of birth only

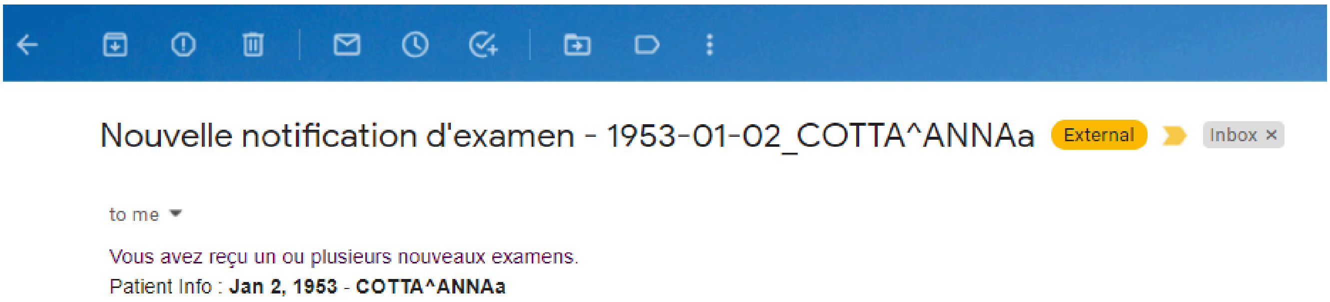


Nouvelle notification d'examen - 1953-01-02

Vous avez reçu un ou plusieurs nouveaux examens.
Patient Info : **Jan 2, 1953** -

Ceci est un message automatisé, s'il vous plaît ne répondez pas.

- patient name and date of birth



Nouvelle notification d'examen - 1953-01-02_COTTA^ANNAa

Vous avez reçu un ou plusieurs nouveaux examens.
Patient Info : **Jan 2, 1953** - **COTTA^ANNAa**

9.6.4. Improved security

Our Research & Development department has integrated a whole series of recommendations from a security certification body, to further boost the security of our portal.

9.7. Improved TM-Community system

- Ergonomic sending of exams located on remote sites
- communication mode of exams after arrival on site in automatic mode (*all documents arriving at the receiver can be automatically distributed to user groups defined in the settings*)
- Search for exams from a specific hospital

10. ADDON 4.97 TO 4.98

10.1. What's New in TMP-Web

10.1.1. Integration of a New Viewer

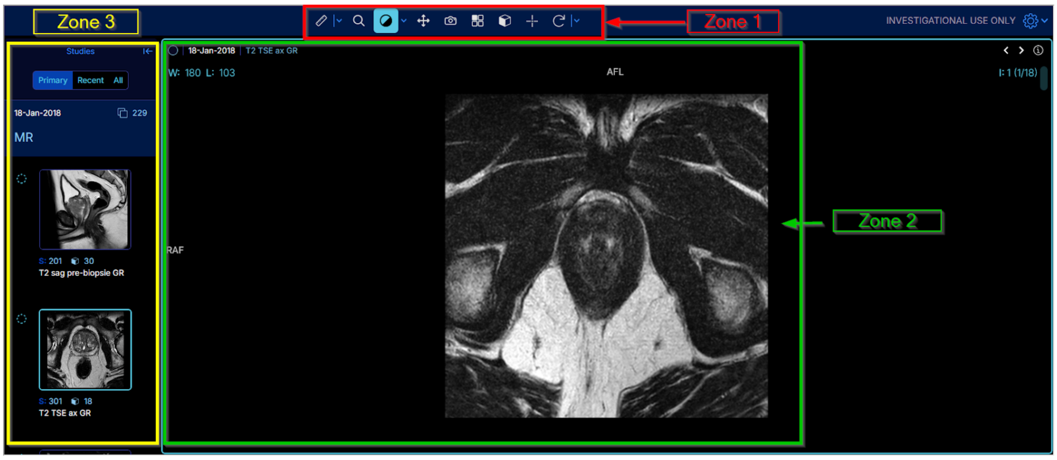
We have integrated a new viewer that provides access to a wider range of features.
To access it, you can either:

- Speak with your site manager to have this viewer set as the default
- After clicking on a thumbnail, you can click on the **"DICOM Advanced"** menu at the bottom right

10.1.2. Introduction to the New Interface

The interface of the new viewer is divided into three sections:

- **Section 1**: Series display
- **Section 2**: Tools
- **Section 3**: Preview



10.1.2.1. Section 1: Tools

The Tools section offers a variety of tools and features, which we will describe in detail below.

1	2	3	4	5	6	7	8	9

10.1.2.1.1. Measurement Tools

Several measurement tools are available to you, accessible by clicking the downward arrow to the right of the default ruler icon.

Distance Measurement
Long Axis/Short Axis Measurement
Annotation
Ellipsoidal ROI
Circular ROI

10.1.2.1.1.1. Distance Measurement

This measurement is performed in two clicks: one click on one end of the measurement, and a second click on the other end.

The measurement will be displayed in millimeters, provided the data allows for this calculation.

You can also move the displayed result.

The left-click will continue to measure distances until you assign a new function to the left-click by selecting a different tool or feature.

You can also delete the measurement by right-clicking on it.

10.1.2.1.1.2.Long Axis/Short Axis Measurement

This measurement is performed in two clicks: one clicks on one end of the measurement, and a second click on the other end.

During the measurement, a perpendicular line will appear, which you can adjust in terms of position and distance after your second click.

These two pieces of information will be useful for classifications such as RECIST, although the full methodology for this is not implemented in TMP Web.

10.1.2.1.1.3.Annotation

This tool allows you to annotate a lesion or a specific point in the image.

To do so:

- Click on the annotation tool
- Then click on the item you wish to annotate
- Next, click on the location where you want to display the arrow's tip
- A window will appear where you must fill in your annotation

10.1.2.1.1.4. Ellipsoidal ROI

This tool allows you to draw an ellipsoidal ROI.

To do so:

- Click on the ellipsoidal ROI tool
- Click at the center of your ROI
- Drag horizontally to extend your ROI from right to left
- Drag vertically to extend your ROI from top to bottom

The ROIs will provide information on:

- Density in Hounsfield units when measuring on CT images
- SUV when measuring on PET images
- Signal when measuring on MR or NM images

10.1.2.1.1.5. Circular ROI

This tool allows you to draw a circular ROI.

To do so:

- Click on the circular ROI tool
- Click at the center of your ROI
- Drag in any direction to define your radius

The ROIs will provide information on:

- Click on the circular ROI tool
- Click at the center of your ROI
- Drag in any direction to define your radius

10.1.2.1.2. Zoom

To zoom in on an image, you can:

- Click on the Zoom icon
- Click and drag upwards while holding down the click to zoom in on the image
- Click and drag downwards while holding down the click to zoom out of the image
- You can also move the image by holding down the mouse wheel and dragging the mouse

10.1.2.1.3. Contrast

By clicking on the contrast icon, your left-click will assume the usual contrast adjustment function.

By clicking on the arrow to the right of the icon, you will have access to preset windowing options, as shown in the screenshot.

10.1.2.1.4. Movement

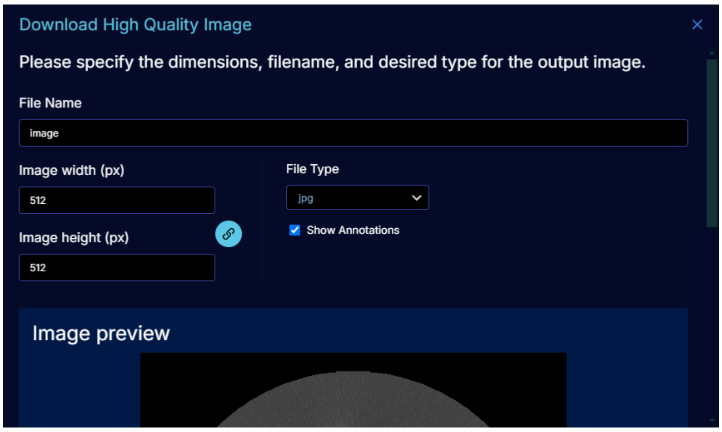
By clicking on the icon, you can move your image by holding down the left-click.

10.1.2.1.5. Screenshot

By clicking on the screenshot icon, you will access a window with a specific menu related to the screenshot options.

You will be able to:

- Manually set the name of the image file you wish to save
- Manually set the image resolution
- Manually select the image file type (JPG or PNG)
- By (de)selecting the "Show Annotations" checkbox, you can include or exclude any measurements and annotations present in the image from the screenshot



Download High Quality Image

Please specify the dimensions, filename, and desired type for the output image.

File Name: image

Image width (px): 512

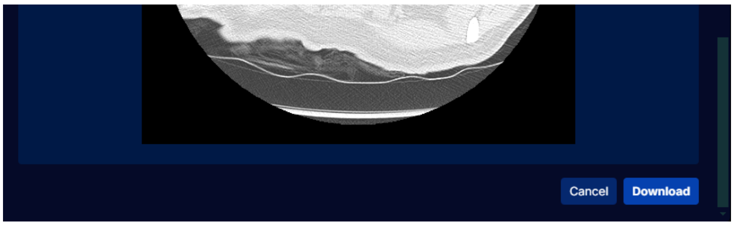
Image height (px): 512

File Type: jpg

☑ Show Annotations

Image preview

- To save the image, you will need to click on the "Download" button at the bottom right.

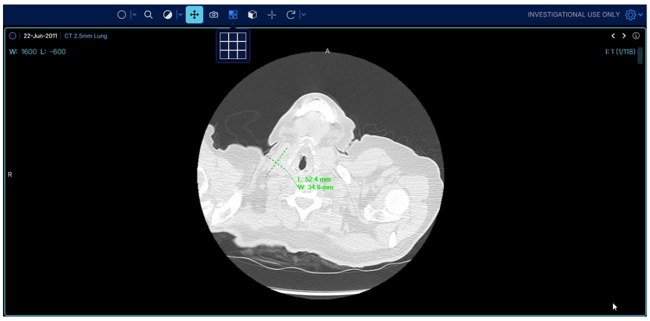
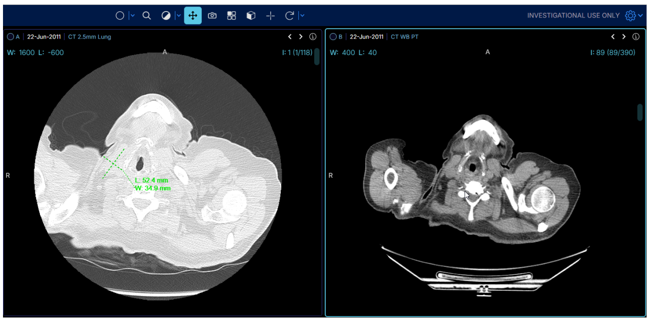


10.1.2.1.6. Display Matrix

This menu allows you to display multiple series according to the layout you desire.

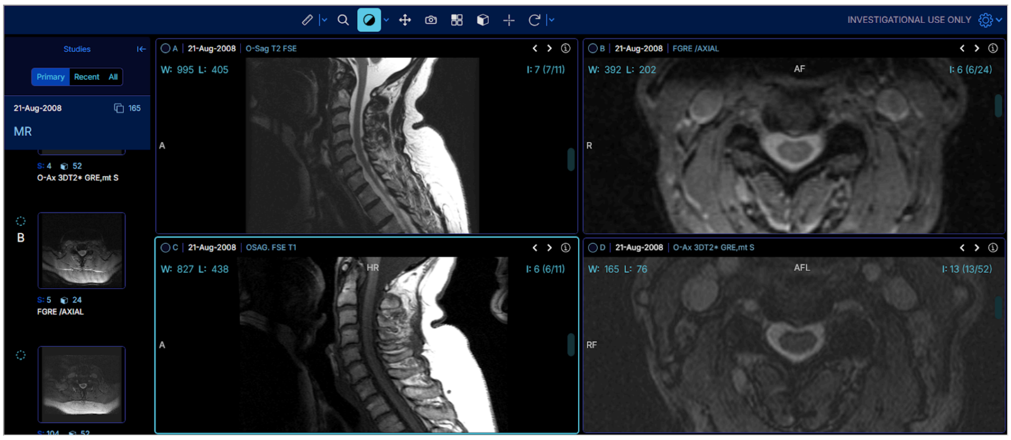
For example, if you want to display two series side by side:

- Click on the display matrix icon
- Then hover your mouse over the matrix to highlight the layout you wish to use
- Finally, click on the square
- You will then see the following result as the final display.

Matrix 1x1	Matrix 2x1
	

You can also display the series of your choice in the matrix layout of your choice.

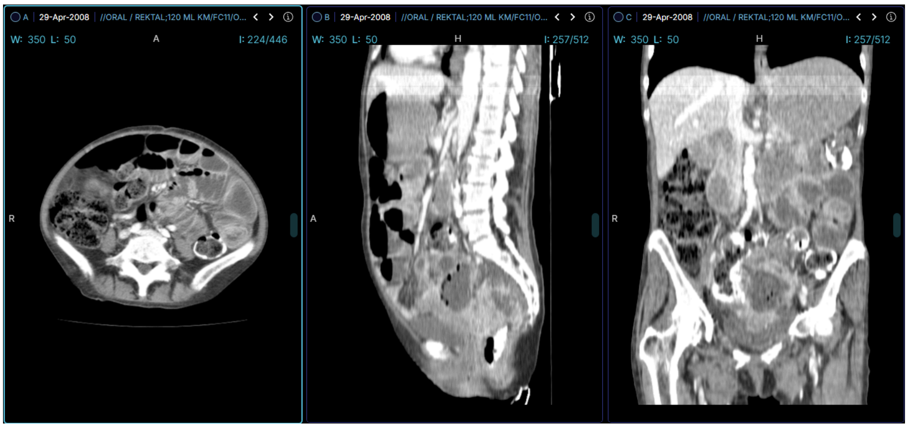
To do so, from the previewer on the left, simply drag and drop your series into the desired space.



This feature is incompatible with the MPR view.

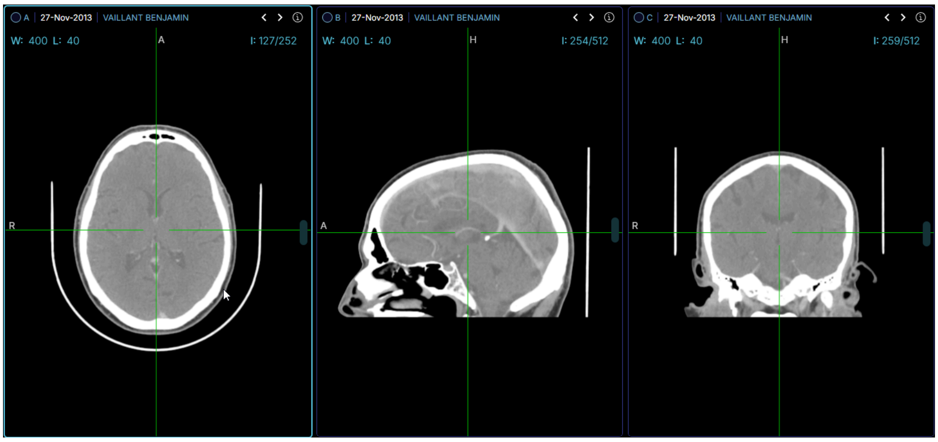
10.1.2.1.7. MPR

By clicking on the MPR icon, you will display the open series in a 3D MPR format.



10.1.2.1.8. MPR Display Plans

By clicking on this icon, the planes of the three reconstruction axes will appear in green.



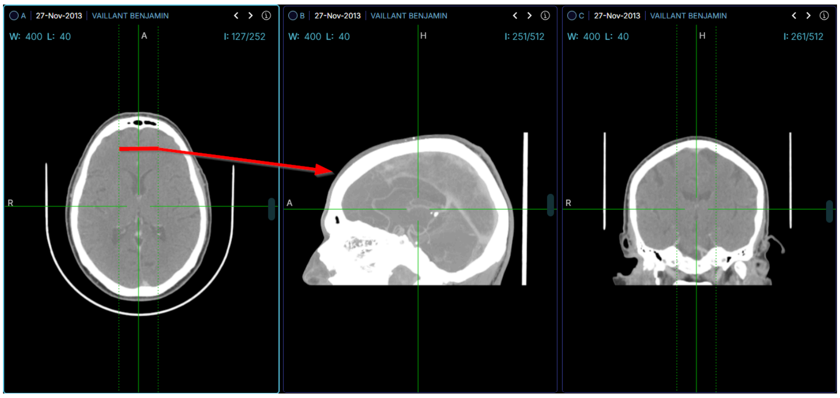
By holding down the left-click at the intersection of the planes (1), you can move the entire set, which will affect the other planes.

When you move your mouse cursor closer to one of the axes, it will highlight, and two dots will appear.

The dot (2) closest to the center (1) will allow you to adjust the thickness of the MPR for the selected axis.

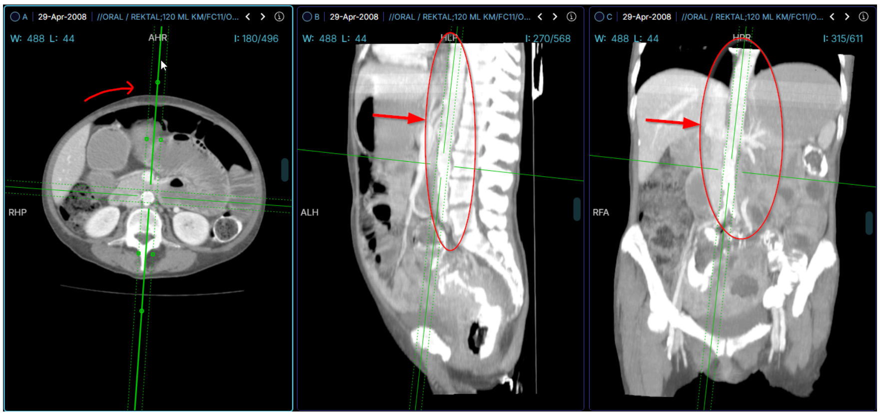
By holding down the left-click on the dot (2), you can adjust the slice thickness.

Example below: increasing the slice thickness of the sagittal plane



The dot (3), furthest from the center (1), allows you to adjust the orientation or angles of the selected axis.

In the example below, we have combined slice thickness adjustment with oblique axis orientation in order to better visualize the abdominal aorta.



10.1.2.1.9. Additional Features

Here is the list of advanced features offered by this new viewer.

10.1.2.1.9.1. Display Restoration

This feature allows the default display settings to be restored.

Default Display	Modified Image	Feature Activation
		

10.1.2.1.9.2.Rotate Image to the Right

This feature allows the image to be rotated 90° clockwise.

Default Image	Feature Activation
	

10.1.2.1.9.3.Flip Image Horizontally

This feature allows the image to be flipped horizontally on its axis.

Default Image	Feature Activation
	

10.1.2.1.9.4.Series Synchronization/Comparison

This feature allows you to manually synchronize series in order to compare examinations.

To activate it, you will need to:

- Split your display matrix to show the series you wish to compare (see point 10.1.2.1.6),
- Then manually align the series at the same level if you are comparing examinations from different dates,
- And finally, activate the feature.

You will then be able to navigate through the two series in a synchronized manner.

Users logged in with a user account can also compare series from examinations conducted on different dates.

10.1.2.1.9.5.Reference Line

This feature allows the reference line to be displayed across the other visible planes.

To activate this feature, you will need to:

- Split your display matrix to show the series you wish to view (see point 10.1.2.1.6),
- Then activate the feature.

10.1.2.1.9.6.Image Overlay

This feature allows you to show or hide image overlays, when available.

10.1.2.1.9.7.Series Navigation

This feature enables navigation through the series using the left click.

10.1.2.1.9.8.Invert Contrast

This feature inverts the contrast of the displayed image.

Default Display	Feature Activation
	

10.1.2.1.9.9.Probe

This feature allows real-time display of Hounsfield density values (for CT images) or signal intensity (for MR images) by holding down the left mouse button.

10.1.2.1.9.10. Cine Mode

This feature enables dynamic display of the images within the selected series.

When the feature is activated, a menu appears at the bottom of the image.

You must start the playback loop by clicking the left-hand button, and you can adjust the playback speed by increasing or decreasing the FPS using the arrows on either side of the displayed value.

10.1.2.1.9.11. Angle

This feature allows you to perform angle measurements. The measurement is carried out using three clicks, as illustrated in the image below.

10.1.2.1.9.12. Magnifier

This feature applies a magnifying effect to the area currently hovered over by the mouse cursor.

10.1.2.1.9.13. Rectangle

This tool allows you to draw a rectangular ROI.

To do so:

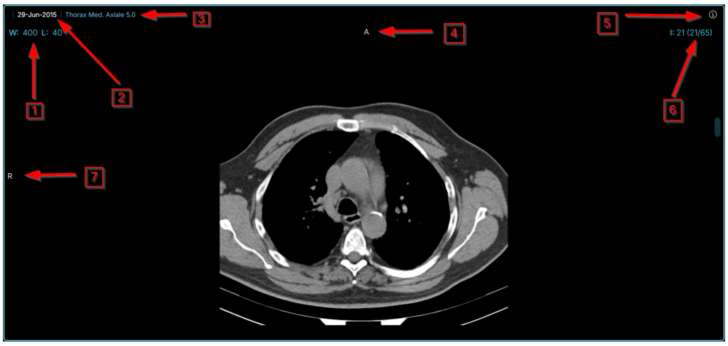
- Click on the Rectangle tool,
- Click next to the area you wish to measure,
- Drag in any direction to draw your rectangle.

10.1.2.1.9.14. DICOM Fields Browser

This feature allows you to display the DICOM fields of the series.

10.1.2.2. Section 2: Series Display

Here is a description of the useful information you will find in this area:



1. Image Windowing
2. Acquisition Date
3. Series Description
4. Image Orientation Indicator
5. Additional Information Button
6. Slice Number
7. Image Orientation Indicator

10.1.2.3. Section 3: Preview

1. This menu allows you to access the patient's history (functional only when logged in)
2. By clicking on this arrow, you can hide the entire preview area
3. Total number of images for the examination
4. Acquisition date
5. Examination modality
6. Number of images in the series
7. 2D or 3D series indicator
8. Series description

10.2.TM-Capture Enhancement

The TM-Capture solution is now compatible with the Datamatrix barcode format, a high-density two-dimensional barcode that allows a large amount of information to be represented on a small surface.

11. APPENDIX

11.1. Keyboard and mouse summary

To get the list of all the available shortcuts in the *TM-Reception*,

√ Select *[Help]* *[Shortcuts]* from the Browser or any viewer menu.

11.1.1. Browser shortcuts

11.1.1.1. Keyboard

Key	Action
F1	Import new images into *TM-Reception HE*
Ctrl F4	Arrange viewers
F5	Refresh
F12	Hide browser
Alt C	Compare selected documents
Ctrl C	Open default connection
Ctrl D	Delete document(s)
Ctrl F	Forward document(s)
Ctrl J	Join document(s)
Ctrl O	Open document(s)
Alt P	Open preview pane on the selected documents
Ctrl S	Save current document in database
Cursor left	Go from “Series” to “Studies” and from “Studies” to “Patients”
Cursor right	Go from “Patients” to “Studies” and from “Studies” to “Series”
Backspace	Same as cursor left
+	Join document(s)
Ctrl -	Go to previous exam
Ctrl +	Go to next exam
Escape	Cancel network operation
Enter	Idem as cursor right
Enter	Open the selected exams, from the “Series” viewer

11.1.1.2. Mouse

Mouse action	Action location	action performed
Left click	list column header	Sort the column alphabetically
Shift left click	list column header	Sort the column reverse-alphabetically
Ctrl left click	List column header	Set this column as a secondary sort key, alphabetically
Shift Ctrl left click	List column header	Set this column as a secondary sort key, reverse-alphabetically.
Double click	’Patients’ or ‘Studies’ list	Display the ’Studies’ or ‘Series’ list for the patient or study of the line clicked
Double click	’Series’ list	Open the series displayed in the clicked line
Double click	details of the 'Patients' list	Open the ‘Series’ view for the study displayed in this detail line
Double click	Details of the ‘Studies’ list	Open the series displayed in this detail line.

11.1.2. Viewer shortcuts

As a general rule, measure tools are associated with the 'Alt' key; Single key press associates a tool with the left mouse button, the same key in association with 'Shift' associates the tool with the right mouse button.

11.1.2.1. Keyboard

Key	Action
F1	Brightness & contrast presets
F2	Color Look-Up Table (CLUT)
F3	Text on screen
F4	Show examination preview pane
Ctrl F4	Arrange viewers
F5	Refresh the view
Ctrl F5	Exchange position with another viewer
F6	Show main toolbar (2D viewer)
F6	Set the offset position between viewers for the comparison (orthogonal viewer)
F7	Show/hide toolbars
Shift F7	Change the comparison code
Alt F7	Show/Hide the toolbars, information line and menu
Ctrl F7	Show next toolbar
F8	Display selected images only

F9	Open new viewer
F10	Maximize on one screen
F11	Maximize on all the screens
F12	Display main browser
Shift F12	Close all the viewers
1	Send viewer to first screen (in a multi-screen environment with TMR-HE)
2	Send viewer to second screen (in a multi-screen environment with TMR-HE)
3	Send viewer to third screen (in a multi-screen environment with TMR-HE)
4	Send viewer to fourth screen (in a multi-screen environment with TMR-HE)
A	auto-contrast
Alt A	Angle measure on left mouse button
Ctrl A	Select all images
C (Shift C)	Contrast tool on left (right) mouse button
Alt C	Start cine viewer
Alt D	Distance measure on left mouse button
E	Export selected images as
Alt H	Horizontal flip of the images
I	Invert grey scale
M (Shift M)	Magnifier tool on left (right) mouse button
N (Shift N)	Navigation tool on left (right) mouse button
P (Shift P)	3D Pointer tool on the left (right) mouse button
Alt P	Recall the previewer
Ctrl P	Print current viewer
Alt R	Clockwise rotation
Alt Shift R	Anti-clockwise rotation
S (Shift S)	Image Selection tool on left (right) mouse button
Alt S (Alt Shift S)	Select drawn items tool on left (right) mouse button
Ctrl S	Save current document in database
T	Toggle between the Tools application domains
V (Shift V)	Mover tool on left (right) mouse button
Alt V	Vertical flip of the images
Z (Shift Z)	Zoom tool on left (right) mouse button
Back space	Exit from the viewer
Shift back space	Exit from all the viewers of this study
Delete	Delete the selected items (drawings)

Shift Delete	Delete all the items (drawings)
Cursor Up	Navigate on line up in the viewer
Cursor Down	Navigate on line down in the viewer
Page Up	Navigate on page up in the viewer
Page Down	Navigate on page down in the viewer
Home	Navigate to the first image of the viewer
End	Navigate to the last image of the viewer
-	Smaller display matrix
+	Bigger display matrix
/ (num pad)	Zoom 100%
Esc	When using a measurement tool, cancel the measure
Space	Send images into the filmer

11.2. Table of figures

11.3. Index

🏭	Telemis S.A. Avenue Athena, 2 B-1348 Louvain-la-Neuve Belgium http://www.telemis.com
SN	<serial number with date of manufacture>*
ⓘ	See instructions for use Access via “Help” menu or www.telemisstore.com
REF	Telemis-Medical
UDI	(01) 05430003032008 (8012) V4.98
MD	
CE 0476	Kiwa Cermet Italia Spa

* See the software “About” dialog box for exact serial number and manufacture date.

Telemis