Starviewer
Medical Imaging Software

USER MANUAL

v1.0

Information and help: support@starviewer.udg.edu

1. STARVIEWER

Starviewer is a medical imaging visualisation application that satisfies DICOM protocol.
It supports different modalities: X-ray, CT, magnetic resonance, mammography, radio fluoroscopy, and ultrasound, amongst others.
It can communicate with any PACS server, or obtain images from external files.
It can also be integrated into a RIS.

Starviewer is made by:

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2. CONTACT US

For any doubt, suggestion, please send an email to:

support@starviewer.udg.edu

3. ELECTRONIC INSTRUCTIONS FOR USE

You can self-print a copy of these instructions for use using the printing function of your PDF reader, nonetheless, you can request a printed copy them at support@starviewer.udg.edu which will be served free of charge within 7 days.

Newer, current and older versions of instructions can be downloaded at https://starviewer.org/eifu. We recommend accessing the instructions from the “help” menu in order to ensure the right ones are visualized.

4. SAFETY INFORMATION

Read this user manual.

You must read this user manual before using Starviewer for diagnosis purposes.

Do not rely solely on Starviewer for critical decisions.

Medical imaging devices are not bug free, and the images and data you are presented arise from a complex chain of devices, each one adding risks. Whenever you make a critical decision for a patient you should consider supporting it with additional information from other sources in order to minimize as much as possible a scenario where a software bug that is unnoticed and shows plausible data to the user which ends up founding a critical decision to the patient that may lead to death or irreversible damage.

Contact support if you observe suspicious results.

If you are using Starviewer and you observe strange results that you suspect may be wrong, you should contact support at support@starviewer.udg.edu to report the potential problem as soon as possible. You should also try to open the same study with an alternative software if possible to check if the same result is obtained.

Do not rely solely on Starviewer in emergency situations.

If you need high availability in order to respond in emergency situations, you shall have a contingency plan in order to continue diagnosing in case some parts in your chain of devices fail. This can range from your capturing devices, the network, up to the visualization workstations.

In the specific case of Starviewer, recommended contingency measures could range from having the ability to diagnose from the capturing devices workstations to being able to transfer studies to USB drives in case of network/PACS failure. Unlike centralized/cloud visualization solutions, Starviewer is a decentralized piece of software, where each visualization workstation is independent from each other.

Calibrate your displays to ensure a correct visualization.

The correct visualization of medical images requires taking measures in order to ensure that what you display is consistent with what the human user perceives. You shall calibrate your displays, ensure their performance, use medical displays, do periodic checks, etc.

Do not use the hardware above its specified limits.

Starviewer is a software piece that needs to be executed in a general purpose computer hardware. You need to ensure that the hardware operates within the specified manufacturer parameters such as vibration, altitude, environmental radio interference, temperature, humidity, radioactivity, etc.

Image quality may temporally degrade during interaction.

For the sake of performance and interactivity, image quality may be temporally degraded during interactions. It will be reversed to the maximum quality when the interaction finishes.

5. SPECIAL OPERATING INSTRUCTIONS

No special operation is required, just normal operation following this user manual.

6. STUDY MANAGEMENT

6.1. SEARCHING FOR AND RETRIEVING STUDIES

The application allows users to search for studies from three different sources:

- Local database: It allows users to search for retrieved or imported studies on the computer.
  Menu: File > Local Database Studies...
  Shortcut: CONTROL+L

- PACS server: It allows users to search for studies from one or more PACS.
  Menu: File > PACS...
  Shortcut: CONTROL+P

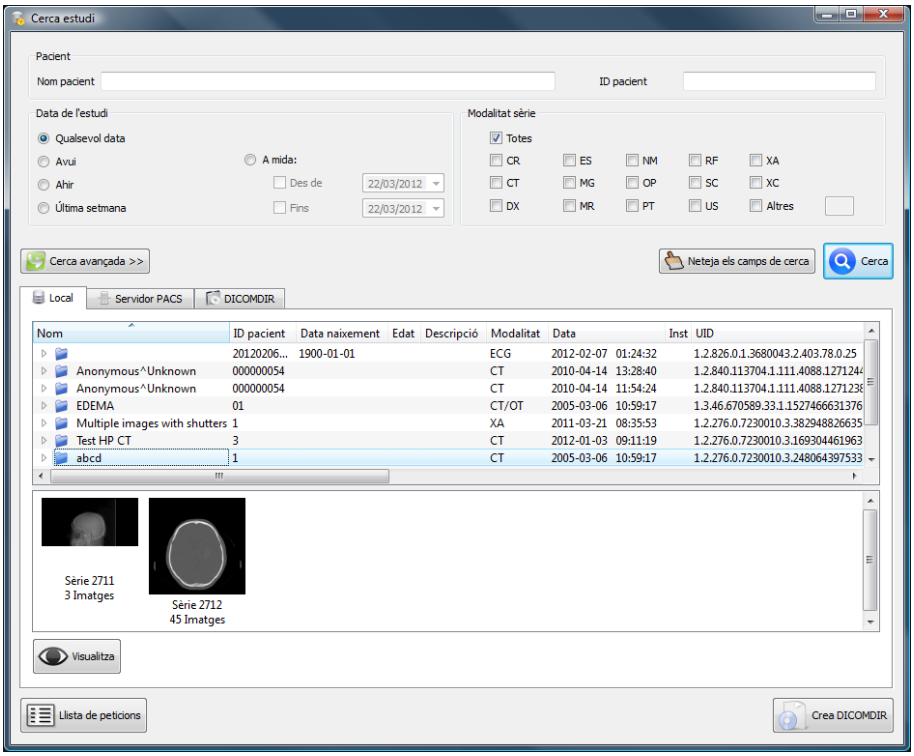
- DICOMDIR: It allows users to search for studies that are stored in a DICOMDIR to the computer, or to any other device (USB, CD, DVD).
  Menu: File > Open DICOMDIR...
  Shortcut: CONTROL+D

From the same window that appears when searching in any of the three options, users can search in any of the other options by simply selecting the tab corresponding to the place where they want to search for the studies.

6.1.1. Local database

In order to search for studies in the local database, it can be accessed in two different ways:
- From menu File > Local Database Studies...
- Pressing the shortcut keys CONTROL+L

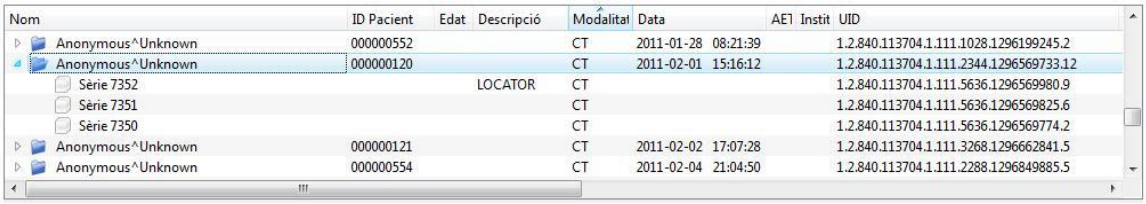
And a dialogue box appears as the one shown below:



This tab shows the studies that are stored in the computer where users are working, and that have been retrieved from a PACS or from a DICOMDIR.

In order to search in the local database, different filters can be applied, such as: patient name, patient ID, date of the study or modality.

Studies are displayed in the form of a list, where they can be selected using the arrow on the left of the folder in order to expand the information about the series they contain. The studies can be sorted by any of the attributes shown in the list by clicking on the title of the corresponding column. The sorting option is saved according to the last configuration applied.



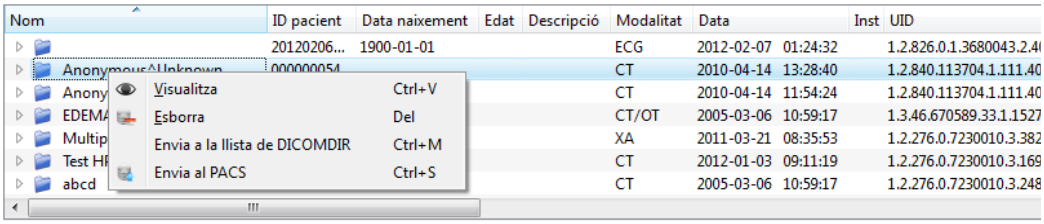
To perform a multiple selection of studies, the CONTROL key must be held down while performing the selection of the list. If there is more than one selected study, the operations carried out will affect all the selected studies.

By selecting one or more studies, different operations are allowed:
- View: It opens the selected studies, organising the viewers and the series automatically in the case it finds an appropriate viewers layout (Hanging Protocols).

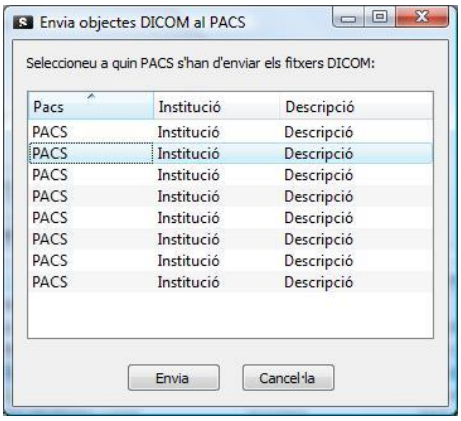
RIGHT BUTTON

This operation can also be performed by using the keyword with the CONTROL+V keys, by clicking with the RIGHT BUTTON of the mouse on the study, or by double clicking on any series of the study.

By clicking with the RIGHT BUTTON of the mouse on a study or a series, different actions can also be performed:



- View: It performs the same operation as the View button: it visualises the selected studies, organising the viewers and the series automatically in the case it finds an appropriate viewers layout (Hanging Protocols).
- Delete: It deletes the selected studies or series of the list from the studies locally stored. This operation can also be performed by selecting and pressing the Delete key.
- Send to DICOMDIR List: It exports the files (the data) of the study in DICOMDIR format in order to record it on a USB, CD, DVD, hard disk... To do so, first it is necessary to send all the studies to the DICOMDIR list by using this functionality, and then export it together (see section Exportation of studies). This operation can also be performed by selecting the study and pressing the CONTROL+M keys.
- Send to PACS: It sends the selected studies or series to the selected PACS. By selecting the option Send to PACS, or by pressing the CONTROL+S keys, a dialogue box with the PACS we have configured appears such as the one shown below:



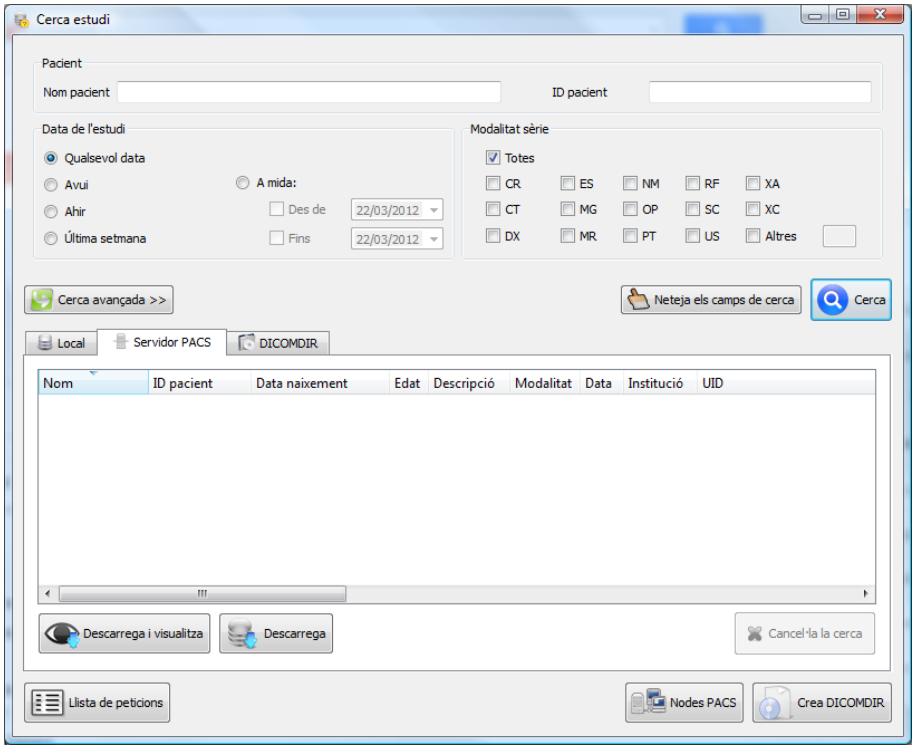
From this dialogue box we will be able to choose the PACS where we are going to send the selected elements. Once the selection has been performed, we will send the elements by clicking the Send button. If the PACS does not appear in the list, it can be configured as a new PACS (see section PACS configuration).

6.1.2. PACS servers

In order to search for studies in one or several PACS servers, they can be accessed in two different ways:

- From menu File > PACS...
- Pressing the shortcut keys CONTROL+P

And a dialogue box appears as the one shown below:



From the PACS Server tab, users can search for patient studies that are stored in the configured PACS list. To configure new PACS, see section PACS configuration.

ICON 1

By default, searches are carried out in the PACS that, when configured, have been flagged with the option Default Query PACS**.** In order to visualise in which PACS is searched by default, users have to choose the option PACS Nodes (ICON 1), and the list of activated PACS appears in the upper-right corner of the window. The selected PACS are the ones that are activated and, hence, the ones where the studies will be searched in.

Different filters can be applied to perform the search, such as: patient name, patient ID, date of the study and series modalities.

ICON 2

ICON 3

By selecting the option Advanced Search (ICON 2), it is allowed to apply other criteria such as: patient birth date, patient age, study time, study UID, study modality, series UID, SOP Instance UID...
Once the parameters have been specified, we have to select the option Search (ICON 3) and all the results that match the chosen options will appear.

If during a search users want to cancel it, they will have to click the Cancel query (ICON 4) button.

ICON 4

Once the search is completed, different actions can be performed:
- Retrieve & View: It retrieves the study locally and visualises it automatically once retrieved. This operation can also be performed directly by clicking with the RIGHT BUTTON of the mouse on the study that has to be visualised, and selecting the option Retrieve & View, or by using the CONTROL+V keys.
- Retrieve: It retrieves the selected study/series/image (one or more) and stores it locally. This operation can also be performed by clicking with the RIGHT BUTTON of the mouse on the study that has to be visualised and selecting the option Retrieve, or by using the CONTROL+R keys.

RIGHT BUTTON

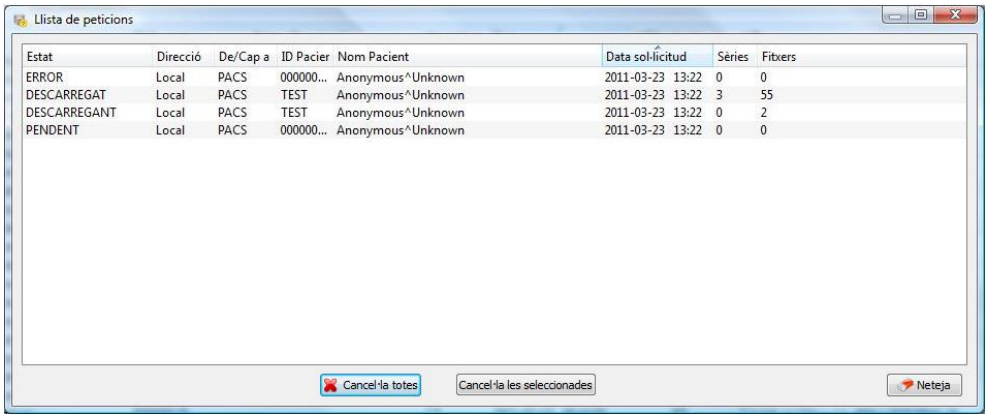
The retrieving status of each requested study can also be checked by selecting the option of the ICON 5, Operation List (see next section Operation list).

ICON 5

6.1.2.1. Operation list

All the studies that are being retrieved, the ones pending to be retrieved, the retrieved ones, the ones that are being sent, the ones pending to be sent, the sent ones, the ones that are being cancelled, the ones pending to be cancelled and the cancelled ones can be consulted in the operation list by pressing ICON 5 from the PACS Server tab (see previous section PACS servers).

The operation list window shows the status of each study that has been selected to be retrieved or sent.



The different statuses are:
- Retrieved: The study has already been retrieved and it can be found in the local database, where it is ready to be visualised.
- Retrieving: This study is being retrieved.
- Pending: The study is waiting to be retrieved (only one study can be retrieved at a time).
- Error: There was an error while retrieving the study.
- Sent: The study has been sent to the PACS.
- Sending: The study is being sent to the PACS.
- Cancelling: The study operation is being cancelled.
- Cancelled: The operation related to the study has been cancelled.

There are also different operations available to perform with the elements of the list:
- Cancel All: It cancels all the pending operations and the ones that are being executed.

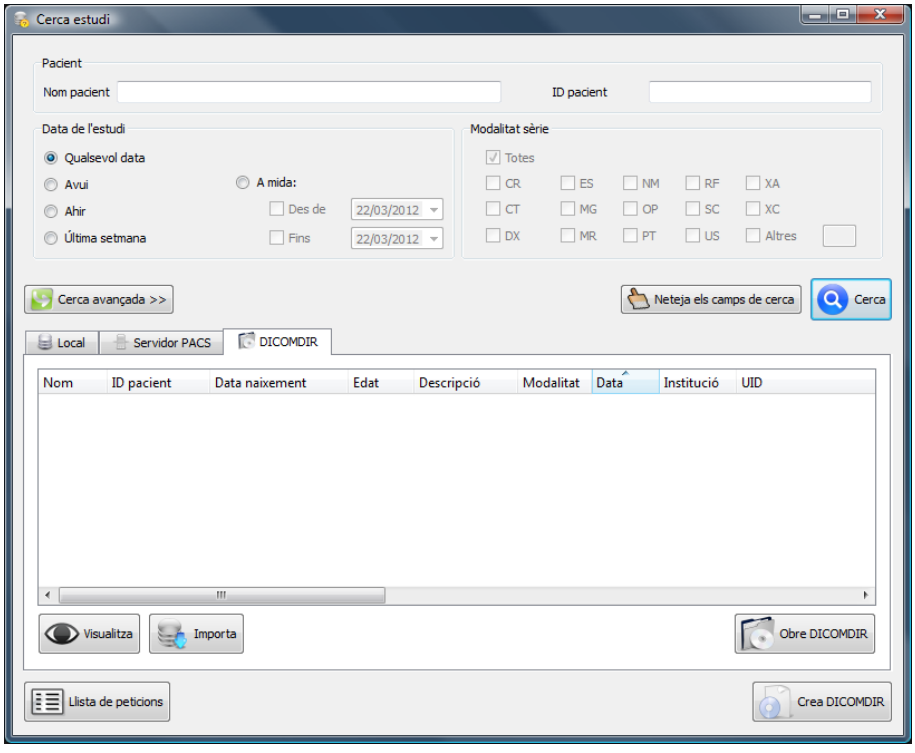
- Cancel Selected: It only cancels the selected operations.
- Clear: Removes from the list all the studies with a retrieved, sent, cancelled or error status.

6.1.3. DICOMDIR

In order to search for studies from a CD/DVD, USB, or a hard disk, we have the functionality of importing from DICOMDIR.

It can be accessed in two different ways:
- From menu File > Open DICOMDIR...
- Pressing the shortcut keys CONTROL+D

A dialogue box is shown that allows users to search for the DICOMDIR file in any directory. Once the DICOMDIR has been opened, the DICOMDIR tab is shown with all the studies that it contains, such as the one shown below:



Different actions can be performed with the elements of the list:

RIGHT BUTTON

- View: Visualises the selected study. This operation can also be performed directly by clicking with the RIGHT BUTTON of the mouse on the study that has to be visualised, and selecting the option View, or by pressing the CONTROL+V keys.

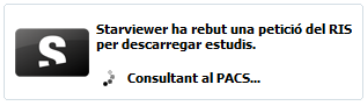
- Import: It imports the selected study/series/image (one or more) storing it locally. This operation can also be performed directly by clicking with the RIGHT BUTTON of the mouse on the study that has to be imported, and selecting the option Import, or by pressing the CONTROL+R keys.

6.1.4. Access from RIS

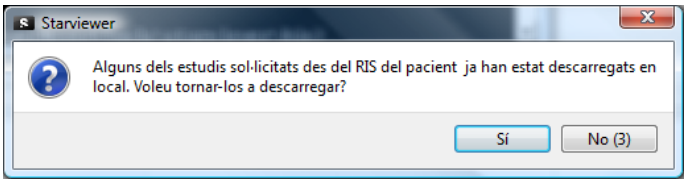
Starviewer can be integrated with a RIS, so that users can choose the study they want to visualise from the RIS without the need for doing the search manually.

The connection between Starviewer and the RIS must be well configured. Section RIS configuration contains information about how to configure this connection.

To open a study from the RIS, users have to select the button of the study from the RIS. After that, the Starviewer application starts (if it was not previously initialised) and a dialogue box is shown that indicates that the search for the studies that have been requested from the RIS has begun.



Once the studies have been found, and before retrieving them, the application checks whether they have already been retrieved in the local database. In case they are already retrieved in the local database, users are asked whether they want to retrieve them again.



If users reply in the affirmative, the study is retrieved again by updating the study located in the local database, and then the study is opened; otherwise, if users reply in the negative, or they remain silent for some seconds, the application automatically visualises the study of the local database without retrieving it again.
In case the study does not exist in the local database, it is retrieved and automatically visualised.

When a study is being retrieved, the initial dialogue box indicates the evolution of the retrieval, that is, the studies that have been retrieved and the ones pending to be retrieved.

This dialogue box automatically disappears once the retrieval is complete. If users want to make it disappear during the retrieval process, they can click with the left button of the mouse on the dialogue box.

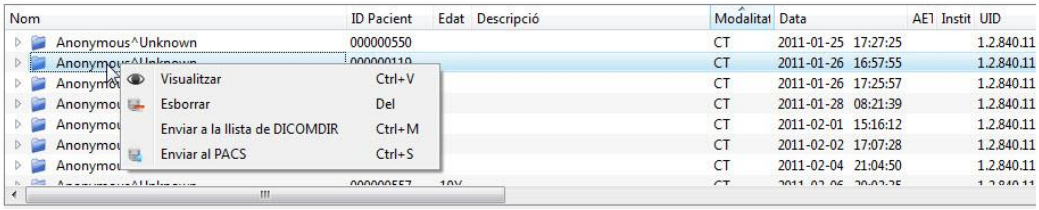
If for some reason the retrieval cannot be carried out (the study does not exist...), the same dialogue box reports the error.

6.2. EXPORTATION OF STUDIES

In order to export the data of one or more patients in DICOM format, it is first necessary to select which studies will be exported. To select the studies to be exported, the local database has to be opened through File>Local Database Studies... or by pressing the shortcut keys CONTROL+L.

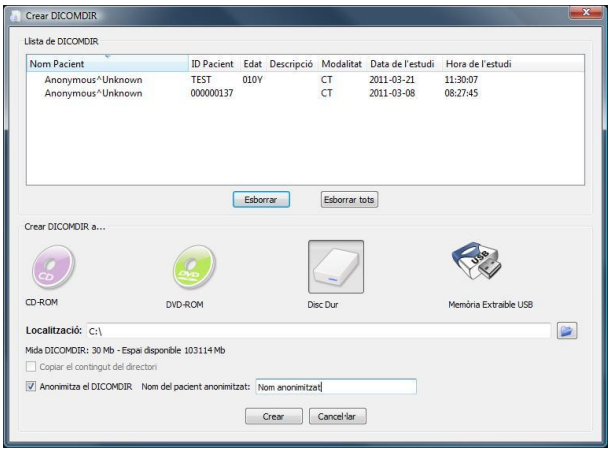
A list with the studies we have in the local database appears, so these are all the studies we can export. We need to select all the studies we want to export; to select more than one study of the list at the same time, we have to press the CONTROL key while selecting studies from the list. Once they are selected, we have to click with the RIGHT BUTTON of the mouse on one of the selected studies and choose the option Send to DICOMDIR List, or press the shortcut keys CONTROL+M.

RIGHT BUTTON



Once sent, we have to select the option Create DICOMDIR (ICON 1), and the following window appears:

ICON 1



This window allows us to select the device where we want to export the data:

- CD/DVD
- USB
- Hard disk

The application allows us to add the whole content of a specific folder into the exported data, such as a viewer that allows the visualisation of the images, or additional information to the study, in any format (reports, for example). This directory is previously configured, and the information about how to do so can be consulted in section DICOMDIR configuration.

6.2.1. Anonymisation of studies

It is possible to convert the patient data into anonymous data when exporting them. To anonymise the

data, the option Anonymize DICOMDIR studies has to be selected, and a new name for the patient (maximum 64 characters) has to be chosen. This name will be applied to all the patients being exported at that time; it can also be left blank. It is recommended to anonymise the studies if they have to be sent outside the hospital.

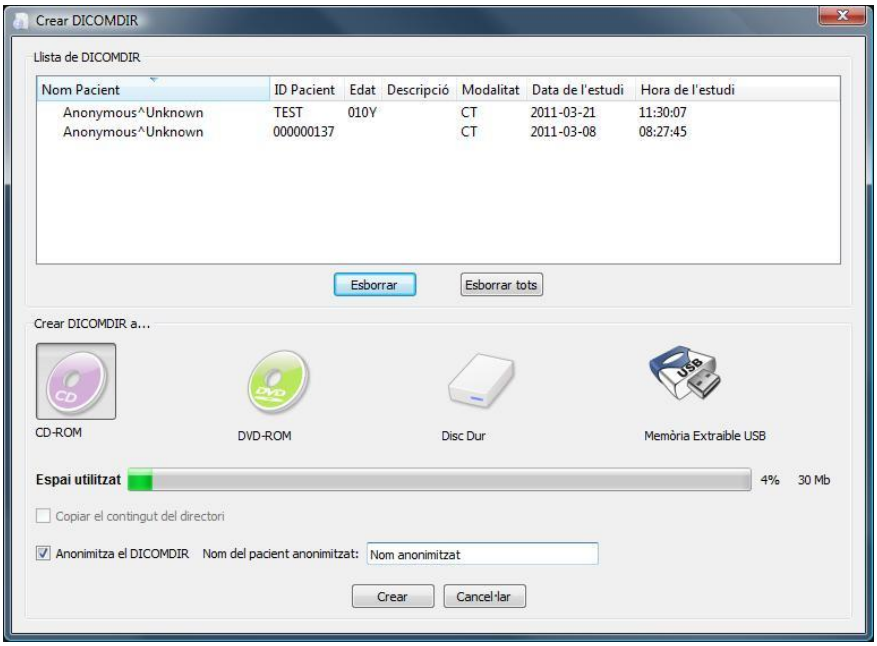
6.2.2. Recording to CD/DVD

Please follow the steps of section Exportation of studies.

Once we see the list of studies in the queue to record in DICOM format, we have to choose ICON 1 (CD) or ICON 2 (DVD) and select the option Create.

ICON 1

ICON 2



The program that has been configured to create the CD or the DVD, whose configuration can be found in the panel of DICOMDIR configuration, automatically opens.

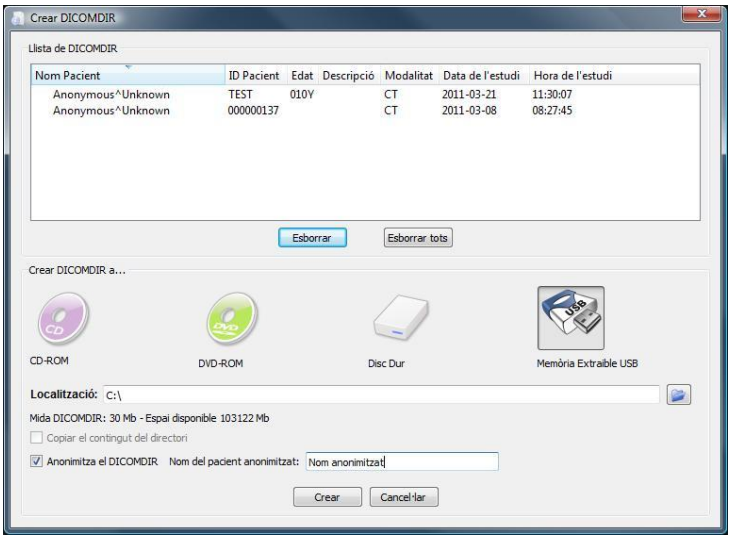
6.2.3. Recording to USB

Please follow the steps of section Exportation of studies.

Once we see the list of studies in the queue to record in DICOM format, we have to choose ICON 3 and then select ICON 4 to find the location within the USB where we want to save the studies of the list. Once the location to save the DICOMDIR has been selected, we have to select the option Create.

ICON 3

ICON 4



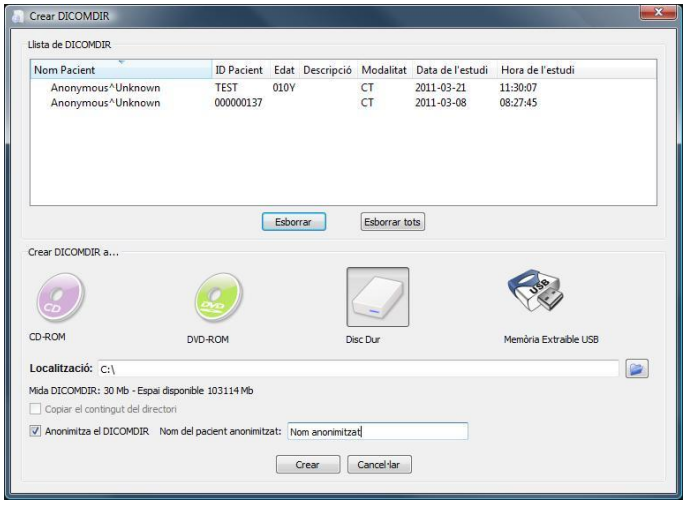
6.2.4. Recording to hard disk

Please follow the steps of section Exportation of studies.

ICON 1

ICON 2

Once we see the list of studies in the queue to record in DICOM format, we have to choose ICON 1 and then select ICON 2 to find the location within the hard disk where we want to save the studies of the list. Once the location to save the DICOMDIR has been selected, we have to select the option Create.



7. IMAGE VISUALISATION: 2D VIEWER

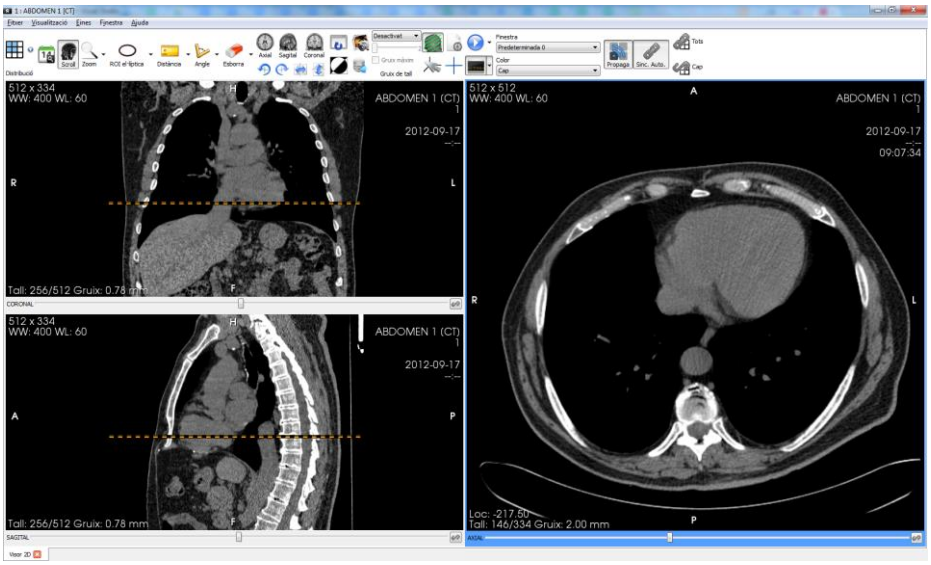
The 2D viewer is the module that allows us to visualise the images from the studies of practically every kind of image modality such as CT, MR, MG, RF, CR, and US, amongst others. It allows us to perform a wide range of basic and advanced actions on the loaded images. A summary of the most outstanding functions is shown below:

Visualisation management
- Choosing the visualisation mode in a custom way (number of opened studies, placement of images...)
- Visualising the list of related studies that the patient has

Basic manipulation
- Images movement in spatial and temporal dimension
- Zooming
- Magnifying glass
- Image rotation
- Image flipping: vertical and horizontal
- Reversing colours
- Reset a viewer to its initial state
- Hide patient information from the viewer
- Save a screenshot in image format (.jpg, .png, .bmp, .tiff)
- Send images to a PACS

Performing different measurements:
- Distances, TA-GT
- Angles, Open angles
- Elliptic ROI, Polygonal ROI, Magic ROI, Circle (Regions of interest) to compute areas and average grey values
- Erasing performed measurements

Advanced functions:
- Orthogonal reconstructions: Axial, Sagittal, Coronal
- Thick Slab (MIP, MinIP, average)
- Reference lines
- 3D cursor
- Visualising images as a video
- Checking the information of a single voxel
- DICOM additional information
- Synchronisation: automatic and manual
- Propagation of zooming, window, orientation, panning...
- Fusion of PET-CT and SPECT-CT images



To learn more about each function, please check Basic visualisation and Advanced visualisation chapters.

8. BASIC VISUALISATION

8.1. IMAGE NAVIGATION AND LAYOUT

8.1.1. Opening studies

When we load a study, the application is responsible for automatically distributing its content in a set of viewers. To carry out this procedure, there are two complementary mechanisms: the Hanging Protocols and the automatic layout. Details are explained below.

8.1.1.1. Hanging Protocols

The Hanging Protocols are templates that allow us to define a layout for the viewers where the content of each viewer is given by a series of restrictions and conditions that the images of the studies we load must comply with.

This allows us to perform automatic layouts in accordance with almost any study. The most typical example would be the mammographies, where the Hanging Protocols allow us to create several templates to show the different projections with the layout we want, such as the comparison with craniocaudal, oblique or even prior mammographies. The same is applicable to any image protocol.

8.1.1.2. Automatic layout

This mechanism creates a regular viewers layout according to the image modality of the study, so that the maximum amount of sequences or images can be placed if desired.

Starviewer provides a default configuration for each modality, which is summarised below:
- It will create as many viewers as images or series contained in the study, up to a maximum of 48 viewers distributed in 6 rows and 8 columns
- The layout direction will be from left to right, in ascending order, starting from the sequences with the oldest date
- For plain X-ray images (CR, DX, RF, ES, OP, XA, XC, etc.), the layout will be done by images
- For the rest of modalities (CT, MR, PT, etc.) the layout will be done by series, excluding Surveys (MR) and Locators (CT)

The layout configuration is adjustable and we can have a specific one for each image modality. The options that we can modify for each modality are the following:
- Distributing by images or by series
- Layout direction (from left to right or from top to bottom)
- Maximum number of viewers (it can be set between 2 and 48, or as many as possible up to a maximum of 48)
- Exclusion of Surveys (MR) and/or Locators (CT)

All these parameters can be modified from the configuration menu of the 2D viewers layout.

8.1.1.3. Criteria for the selection of the layout mechanism

Every time a new study is loaded, it is necessary to choose whether to apply a Hanging Protocol or an automatic layout. Next, the criteria followed to determine the layout system applied is explained.

When a new study is loaded, the internal library of Hanging Protocols templates is checked and, according to the properties of the loaded study, those that can be candidates for being applied according to the restrictions defined in each template are filtered. In this case, two scenarios are possible:

- The filtering process results in one or more candidate Hanging Protocols. In this case, the Hanging Protocol that better complies with the restrictions is applied. The rest of candidate Hanging Protocols can be chosen later by users through the viewers layout tool if they want.
- The filtering process results in no candidate Hanging Protocol. In this case, the automatic layout according to the content of the study is applied.

On the other hand, we can also choose that, even if there are candidate Hanging Protocols, these can only be applied for the modalities we choose through the 2D viewers layout configuration options. In this case, the automatic layout according to the content of the study is applied. Additionally, we will have the candidate Hanging Protocols available and we will be able to apply them later using the viewers layout tool. By default, the modalities where the application of Hanging Protocols will be a priority will be CR, CT, MG, MR and US.

If we load studies from different modalities, the best Hanging Protocol from those modalities that have it as a preferential layout will be applied. In the event that we have no Hanging Protocols, the automatic layout applied will be the result of the combination of the automatic layout configurations of each modality. The criteria to combine the properties of the automatic layout configurations will be the following ones:
- If the layout criterion (by images or by series) is different, the series criterion will be applied.
- If the layout direction criterion (from left to right or from top to bottom) is different, the left to right criterion will be applied.
- The maximum number of viewers will be the minimum of the set of configurations to be combined.
- All the excluding criteria that have been included in each configuration will be included.

8.1.2. Comparison of studies
Function: It allows the visualisation of two studies of the same patient side by side to compare them. The most recent study is considered as the current one, and the oldest study as the prior one.

Shortcut to activate it: F10

Mode of operation: The comparison mode is activated by selecting a prior study in the related studies tool, and it is disabled by unselecting the prior study in the same tool. Alternatively, if the current study is a mammography or a CR of the thorax, the comparison mode can be activated and disabled by pressing the shortcut key F10. In this case, the most recent prior study of the same type (mammography or CR of the thorax) is selected automatically, and if none exists, the comparison mode is not activated.

When the comparison mode is activated or when the current or prior study is changed while it is activated, the application first looks for an existing combined Hanging Protocol (that is, that combines images from two studies at the same time) that is applicable to both selected studies, and if it is found it is applied. If no applicable combined Hanging Protocol is found, then the Starviewer window is divided in two halves where the left half corresponds to the current study and the right half to the prior one; for each study, a regular layout or an individual Hanging Protocol is applied in accordance with the criteria explained in section 5.1.1.3.

Viewer where it is applied: All of them; when the comparison mode is activated, the layout of the whole window changes.

8.1.3. Related studies

Function: It shows the list of related studies of the current patient that can be found in the local database, in the PACS selected by default, and in the PACS where the study comes from, and it allows users to change the current and prior studies.

Mode of operation: When clicking on the icon, the list of related studies that have been found appears. From this list users can change the displayed study and activate or disable the comparison with a prior study. The selection buttons of the Current and Prior columns allow users to change respectively the current and prior studies that are displayed at every moment. Only a more recent study than the prior one selected can be chosen as the current study, and only an older study than the current one selected can be chosen as the prior one; in any other case the selection button does not appear.

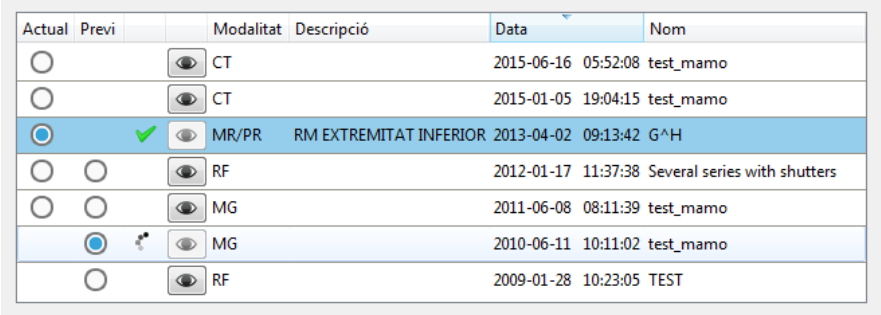
To change the current study, users must click on the selection button corresponding to the new study in the Current column. To add or change a prior study to compare, users must click on the selection button corresponding to the new study in the Prior column. When a study is selected as current or prior, if it is not in memory, it is automatically retrieved from the PACS or it is loaded from the local database. To disable the comparison and view only the current study, users must click on the marked selection button in the Prior column. To load a study from the list to memory without viewing it, users have to select ICON 1 of the desired study.

ICON 1

The list is sorted by study date in descending order (from newest to oldest). The order can be changed by clicking on the desired column (Name, Modality, Description...).

The search for related studies is performed in the local database, in the PACS selected by default, and in the PACS where the study comes from (see section PACS configuration). All the studies that have the same patient ID are considered as related studies. It is possible to change the configuration by including also the studies with the same patient name; in this case, users have to contact the Starviewer administrator in order to activate this functionality.

The studies from the list may be in different statuses:



ICON 1

ICON 2

ICON 3

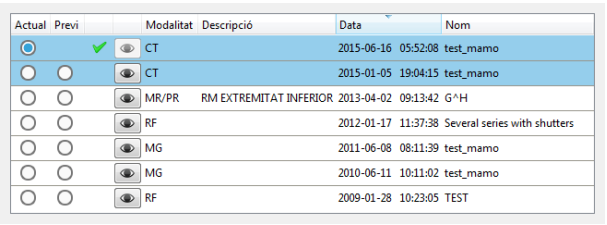
ICON 4

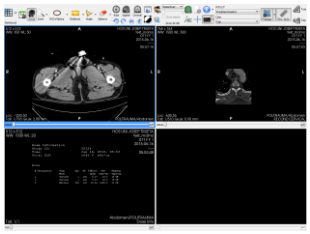
- Selected as current or prior: Selection button checked in the Current or Prior column (ICON 1).
- Available to be selected as current or prior: Selection button unchecked in the Current or Prior column (ICON 2).
- Not available to be selected as current or prior: No selection button in the Current or Prior column.
- In memory: ICON 3 in the third column.
- Retrieving or pending retrieval: ICON 4 in the third column.
- Available to be retrieved from the PACS or loaded from the database: No icon in the third column.

The studies with the same modality as the displayed study are highlighted.

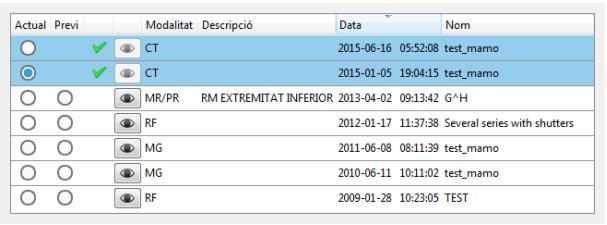
Viewer where it is applied: Once the current or prior study selected has been retrieved, it is automatically loaded. If only one study is visualised, without a prior one, the new images layout and placement of viewers is decided as explained in the section Criteria for the selection of the layout mechanism. If two studies are shown, the current and the prior ones, the criteria explained in the section Comparison of studies are followed.

Example:
We open a study, we click on the related studies icon, and a list of found cases appears.

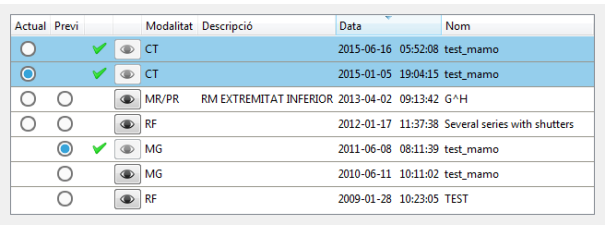


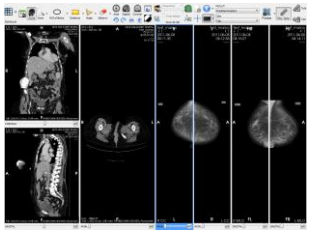


We select another study as the current one by clicking on its selection button in the Current column. Once opened, it applies the default viewers layout to the new study.

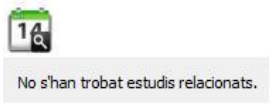


We select a prior study to compare it by clicking on its selection button in the Prior column. Once opened, it applies a layout combining both studies.





If no related studies of the patient are found, the following message is shown:



If the application reports that no related studies have been found, it does not mean that there is none. It may be that in a PACS not configured to search for by default some studies can be found, or that the name contains typographical errors and they are not found either.

8.1.4. Manipulation of the layout and content of viewers

Once the studies have been loaded, we have some tools to modify the applied layout and adjust both the content and their layout. Below, we explain which these tools are.

8.1.4.1. Layout manipulation tools

Function: It creates a viewers layout in accordance with the chosen specification. Two types of specifications can be chosen:

- Custom regular layouts: It allows users to select the number of rows and columns to generate a regular grid of viewers. The viewers are filled following the automatic layout criteria.
- Hanging Protocols layouts: If the study has candidate Hanging Protocols, it allows us to choose which one we want to apply.

Shortcut keys to activate it: F11 and F12

Mode of operation:

ICON 1

ICON 2

Mouse:

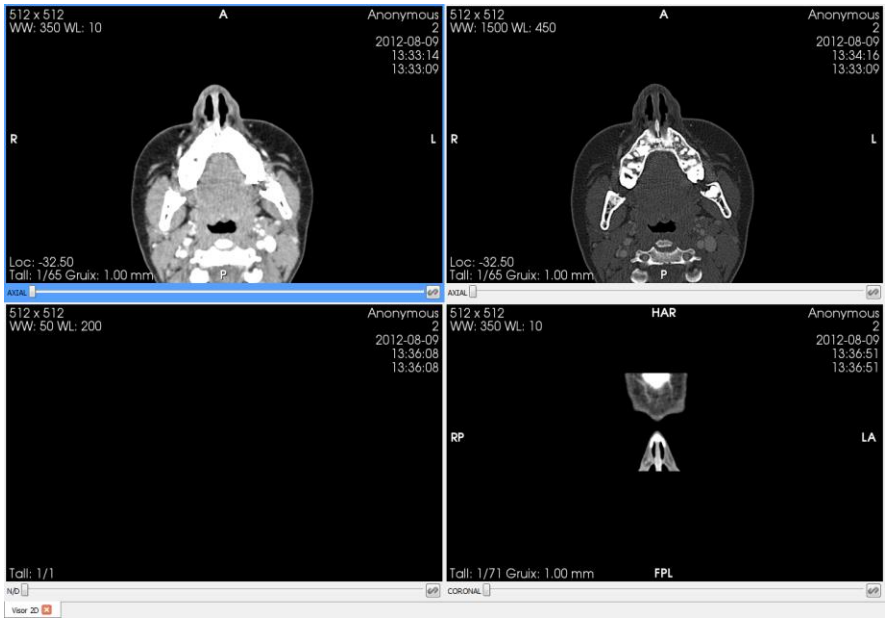
- Custom regular layouts: Select ICON 1 and move the mouse over the dynamic grid of squares that appears. When the highlighted grid is the desired one, press the left button of the mouse.
- Hanging Protocols layouts: Select ICON 2 and select an element within the Hanging Protocols section. The Hanging Protocols are divided in three groups: Hanging Protocols for the current study, Hanging Protocols for the prior study, and combined Hanging Protocols. The last two groups are only displayed if the

comparison mode is active.

Keyboard: With the F11 and F12 keys the previous and next Hanging Protocol can be applied, respectively, inside the same group and following the order in which they appear in the menu.

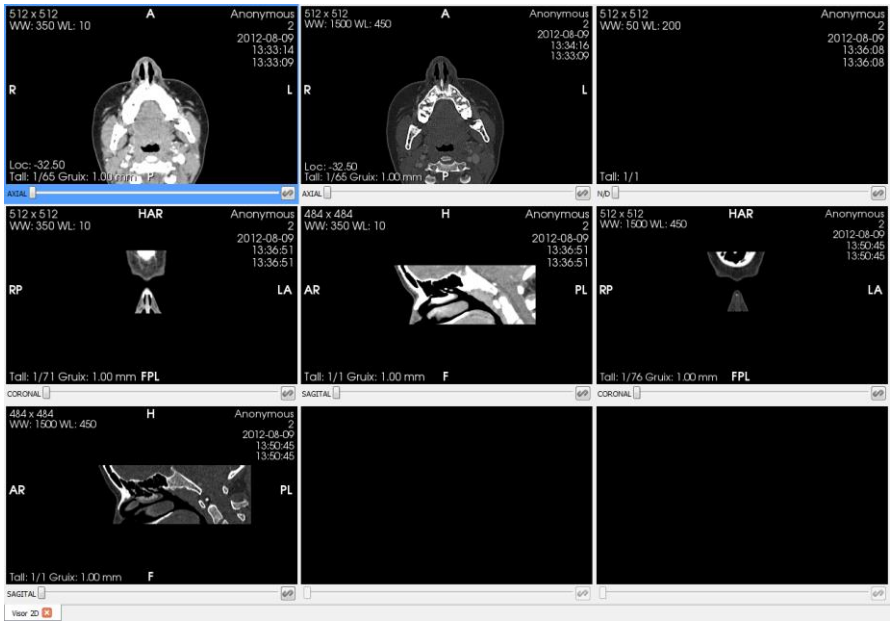
Viewer where it is applied: When only one study is displayed: all of them; the application replaces the whole current layout by the selected one. When two studies are compared: if a combined Hanging Protocol is applied, or if there was one already applied, all of them; if a regular layout or a Hanging Protocol from a study is applied and there was no combined Hanging Protocol applied, only half of the window corresponding to the study in question is affected.

Example of a custom regular layout
1. Initial viewers layout:



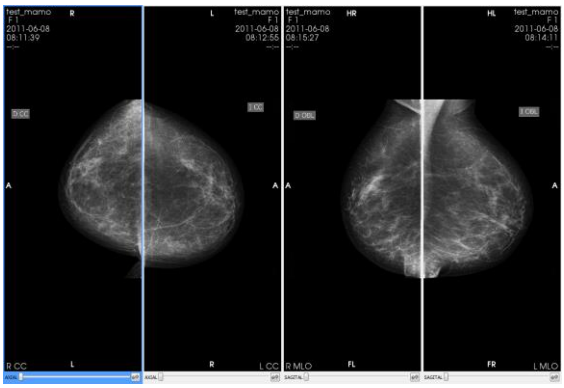
2. Selection of a different layout, for example a 3x3 layout:

3. Result obtained:

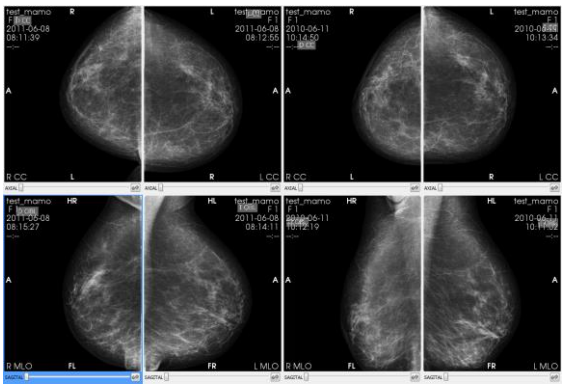

512 x 512
WW: 350 WL: 10
A
Anonymous
2
2012-08-09
13:33:14
13:33:09
R
L
Loc: -32.50
Tall: 1/65 Gruix: 1.00 mm
P
AXIAL
512 x 512
WW: 1500 WL: 450
A
Anonymous
2
2012-08-09
13:34:16
13:33:09
R
L
Loc: -32.50
Tall: 1/65 Gruix: 1.00 mm
P
AXIAL
512 x 512
WW: 50 WL: 200
Anonymous
2
2012-08-09
13:36:08
13:36:08
Tall: 1/1
N/D
512 x 512
WW: 350 WL: 10
HAR
Anonymous
2
2012-08-09
13:36:51
13:36:51
RP
LA
Tall: 1/71 Gruix: 1.00 mm FPL
CORONAL
484 x 484
WW: 350 WL: 10
H
Anonymous
2
2012-08-09
13:36:51
13:36:51
AR
PL
Tall: 1/1 Gruix: 1.00 mm
F
SAGITAL
512 x 512
WW: 1500 WL: 450
HAR
Anonymous
2
2012-08-09
13:50:45
13:50:45
RP
LA
Tall: 1/76 Gruix: 1.00 mm FPL
CORONAL
484 x 484
WW: 1500 WL: 450
H
Anonymous
2
2012-08-09
13:50:45
13:50:45
AR
PL
Tall: 1/1 Gruix: 1.00 mm
F
SAGITAL
Visor 2D

Example of a Hanging Protocols layout

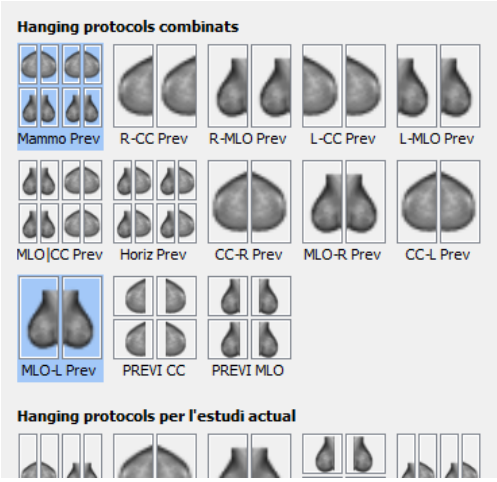
1. Initial viewers layout:



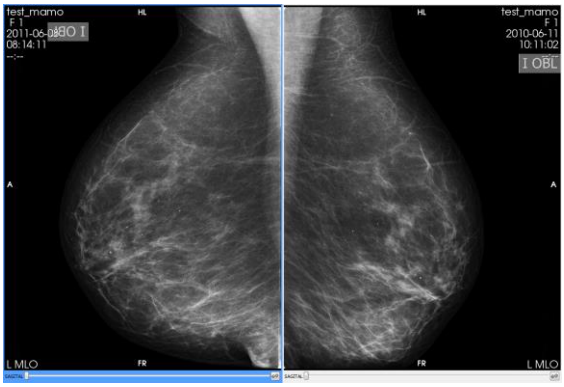
2. Activation of the comparison with a prior study. A combined Hanging Protocol is applied by default, in this case Mammo Prev:



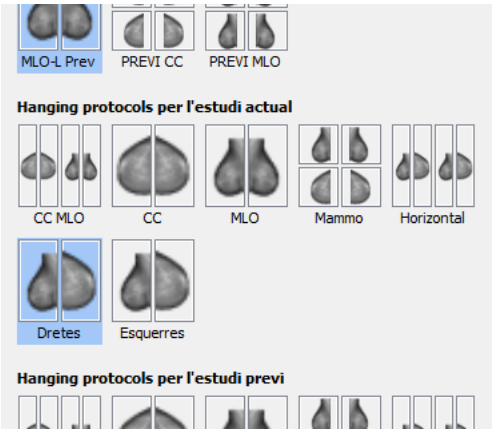
3. Selection of another combined Hanging Protocol, for example MLO-L Prev:



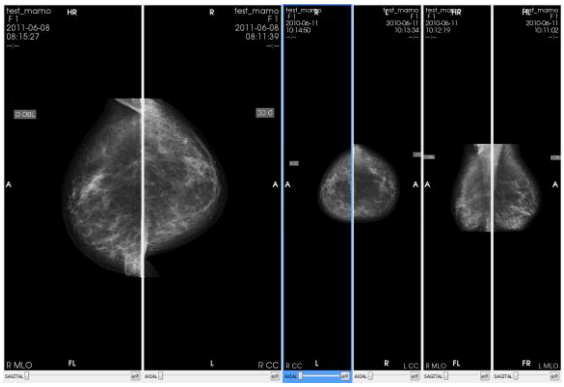
4. Result obtained:



5. Selection of an individual Hanging Protocol for the current study, for example Rights:



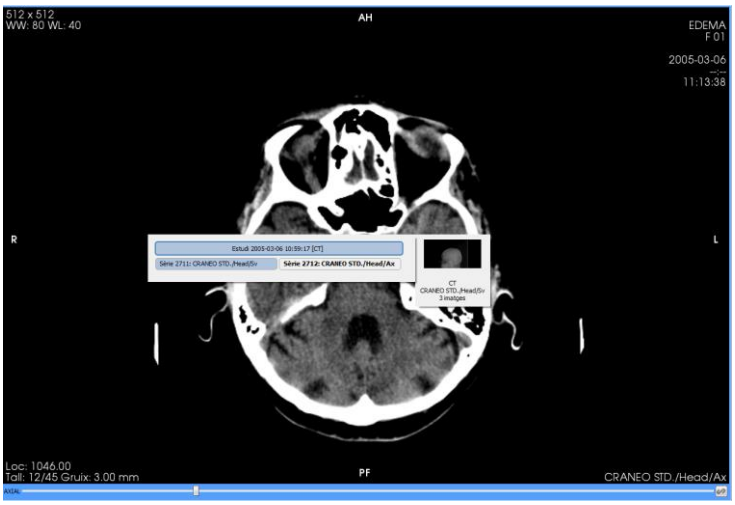
6. Result obtained: the selected Hanging Protocol is applied to the current study and the default one, in this case CC MLO, is applied to the prior one:



8.1.4.2. Tools to select the content of the viewer

RIGHT BUTTON

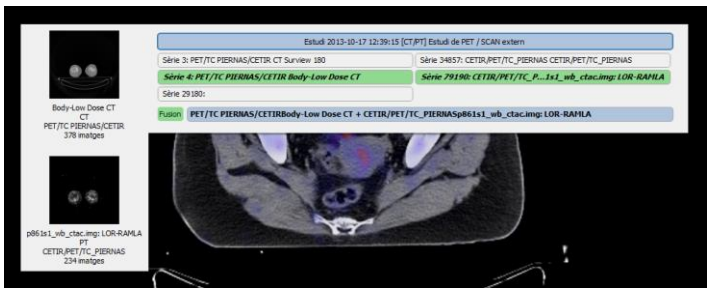
In order to change the series displayed in a viewer, users have to click with the RIGHT BUTTON of the mouse inside the viewer (without moving the mouse), and a list appears with all series available to be shown.



To change the series of the viewer, users only need to select an element of the list (the one highlighted in blue or in a darker colour). The element displayed in bold is the series that the viewer contains.

If we load a study from the same patient, either from a PACS, from local studies, or from the Related studies tool, it automatically appears in the list of available series, and therefore it can be placed in any of the viewers. The studies are ordered from the most recent to the oldest.

If there are series from different modalities that can be merged, the possible fusion combinations that we can visualise will appear after the conventional series, flagged with the label Fusion. When we move the mouse over a possible fusion combination, the series combined in this fusion will also be highlighted. To know more about the conditions under which the fusion options will appear, see chapter Fusion.



On the other hand, if we are in the last image of the series and we press the + key, the next series will be loaded. If we are in the first image of the series and we press the – key, the previous series will be loaded instead. This navigation is circular and consecutive within the studies; for example, if we are in the last image of the last series of the last study and we press +, we will go to the first image of the first series of

the first study. For more information about the images movement, see chapter Scroll.

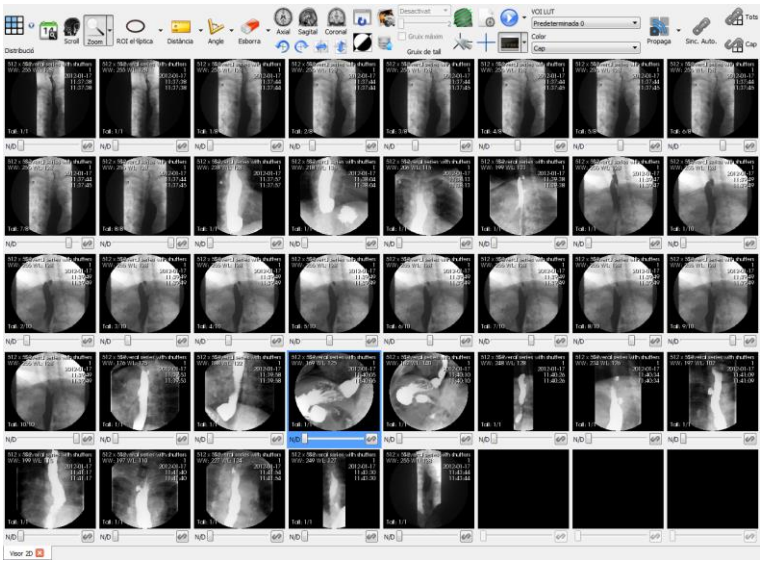
8.1.5. Viewer enlargement

A viewer can be temporarily enlarged at any time to visualise the image in greater detail. By double clicking on a viewer, it is enlarged to fill the whole window or solely one half, depending on whether the main window of Starviewer is on a single screen or two, respectively. By double clicking again on an enlarged viewer, it returns to its normal size.

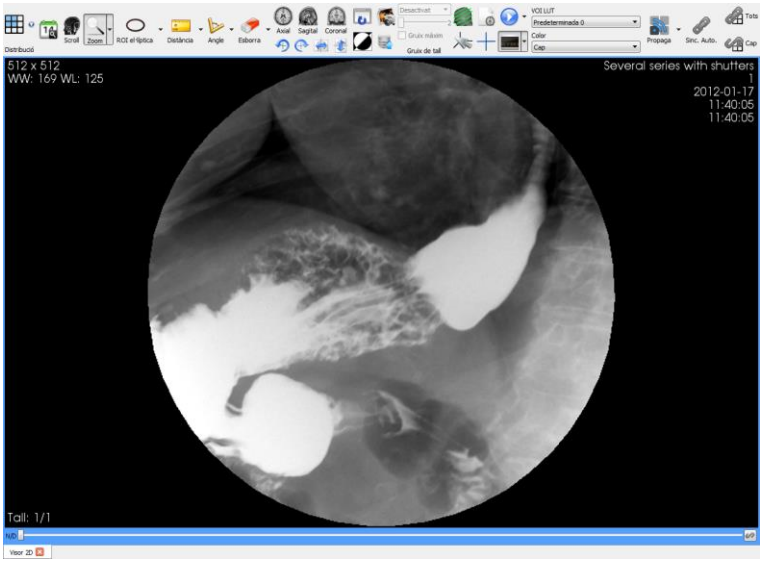
This functionality is always available except when the distance, TA-GT, angle, open angle, polygonal ROI and magic ROI measurement tools are enabled.

Example

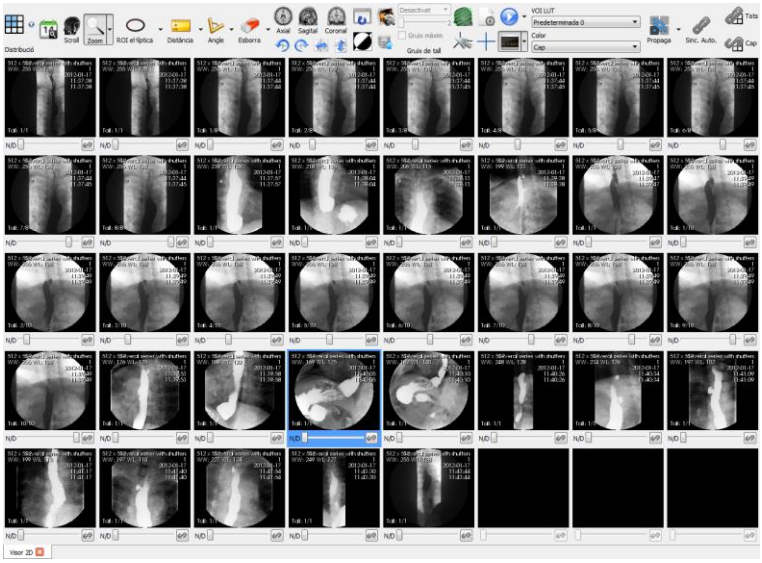
1. Normal viewers layout:



2. Double click on one of the viewers:



3. Double click on the viewer:



8.2. IMAGE MANIPULATION TOOLS

8.2.1. Scrolling

Function: It changes the image of the different slices that form the displayed patient series. The slice number of the displayed slice is shown below each viewer on the left side, as well as the total number of slices contained in the series.

Shortcut keys to activate it: S

Mode of operation:
Mouse: Press the left button while moving the mouse up and down within a 2D viewer. It can also be used by spinning the mouse wheel in order to have a higher accuracy. While it is enabled, the icon appears next to the mouse cursor. If we activate another tool, the scroll functionality with the mouse wheel remains enabled.


Left button


Wheel

Keyboard:

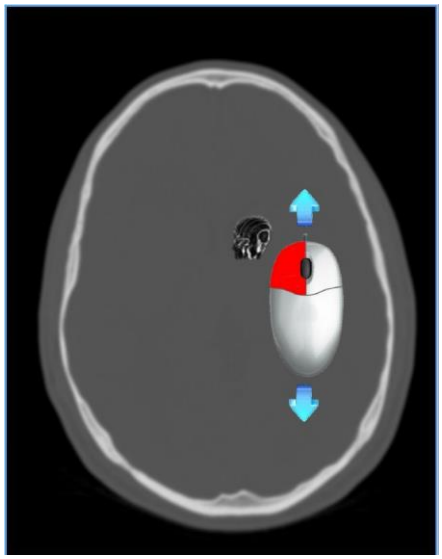
OPTIONS	DESCRIPTION
Next / Previous image	Keys ↑ / ↓
Next / Previous image going through all series	Keys + / -
First image	Key HOME
Last image	Key END

Interface: Using the slider placed below each viewer (highlighted in red in the figure).

This tool can also be configured to make a cyclic scroll. The configuration process is explained in section 2D viewer configuration.

Viewer where it is applied: Viewer over which the mouse is moved while the left button is pressed or the mouse wheel is spun, or the active viewer while the keys are pressed.

Example:




Left button

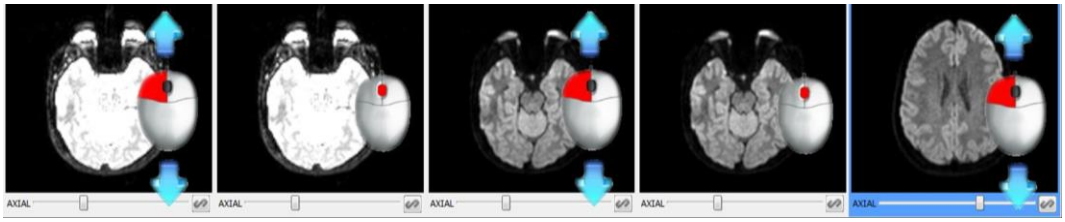

Middle button

8.2.2. Phase change

In dynamic models, where there is more than one image per slice, the phase can be changed at any time.

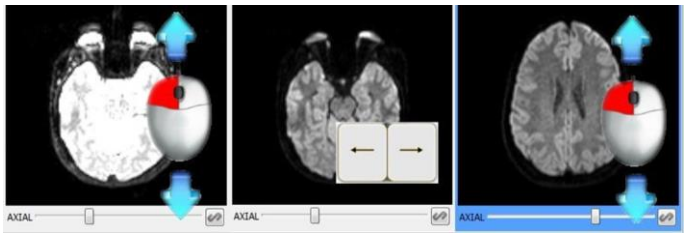
To perform this operation, the following ways are possible:

Mouse: By using the mouse, and placing the cursor on the active viewer, a click with the middle button of the mouse is done (without moving it) and the phase change mode is enabled. From this point, the slice changes (scrolling) are converted to phase changes (moving the mouse wheel, or pressing the left button and moving the mouse at the same time). To enable the scrolling mode again, the middle button of the mouse must be pressed again.



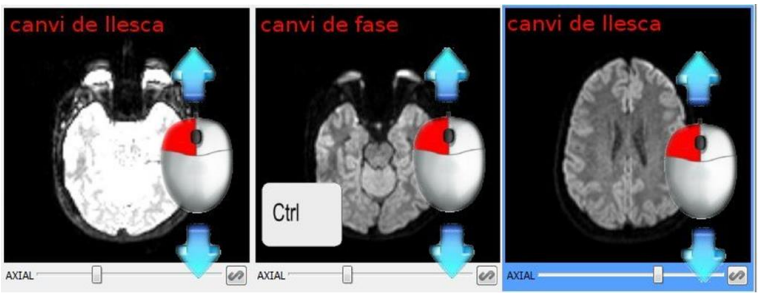
Initial state | To phase change | Phase change | To scrolling | Scrolling

Keyboard: By pressing the ← and → keys the phase is decreased and increased, respectively.



Scrolling Phase change Scrolling

Keyboard + Mouse: If the CONTROL key is held down while the scrolling tool is enabled, the phase is changed instead of the slice.



Scrolling Phase change Scrolling

Left button

8.2.3. Zooming

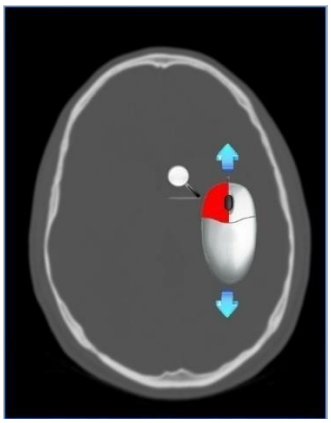
Function: Increase/Reduce image size

Shortcut key to activate it: Z

Mode of operation:
Mouse: Pressing the left button of the mouse while moving the mouse up and down within a 2D viewer.

Viewer where it is applied: Viewer where the mouse is moved on while pressing its left button.

Example:



8.2.4. Magnifying glass

Function: It creates a new window, where it magnifies the area of the image pointed out with the mouse.

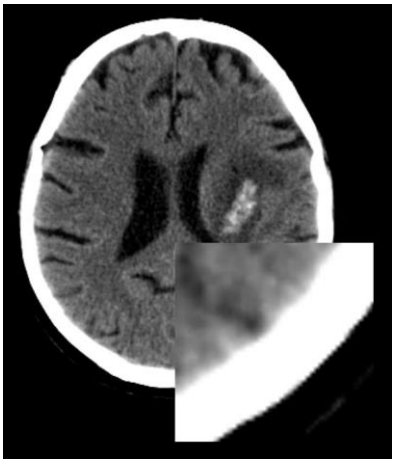
Shortcut key to activate it: SHIFT+Z


Left button

Mode of operation:
Mouse: Press the left button while moving the mouse over the image. A new window appears, where the area where the mouse points out is magnified. The mouse can be moved within the image, but if the mouse is placed outside, the magnifying window disappears.

Viewer where it is applied: Viewer where the mouse is moved on while pressing its left button.

Example:



8.2.5. Panning

The icon does not appear in the toolbar; it is always available using the mouse.

Function: Moves the image towards the point where the mouse cursor is moved.

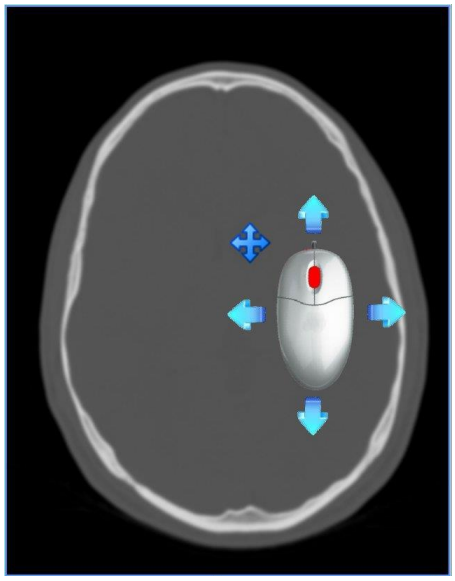
Mode of operation:

Mouse: Holding down the middle button while moving the mouse in the direction where the image has to be moved.

Press the left button and move the mouse

Viewer where it is applied: Viewer that contains the image where the mouse click has been performed.

Example:



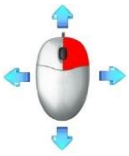
8.2.6. Changing the window

For the extensions 2D Viewer and MPR 2D Viewer the icon does not appear in the toolbar; it is always available using the mouse.

Function: Changing the greyscale of the viewer. See also the Selection of default windows tool.

Shortcut key to activate it: W

Mode of operation:
Mouse: Holding down the right button of the mouse while performing a vertical and/or horizontal movement.

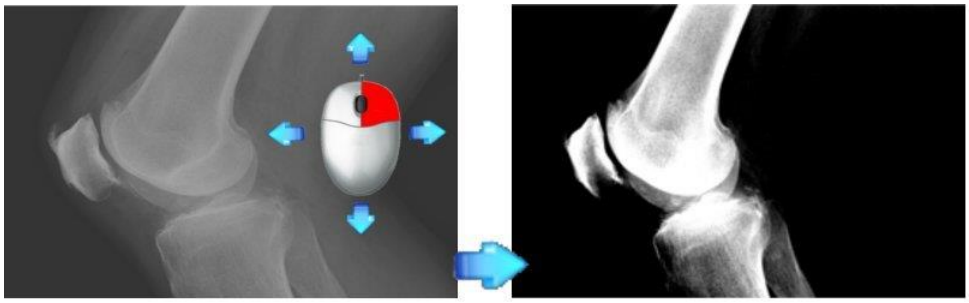


Press the right button and move the mouse

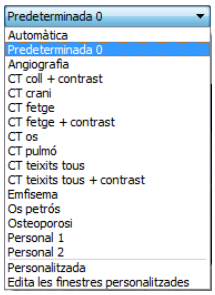
Viewer where it is applied: Viewer that contains the image where the mouse click has been performed.

The default window of each image before applying the window change tool corresponds to the value defined in the DICOM image, and it can different for each image. Once the window change tool has been used, all the images will have the same window.

Example:



8.2.7. Selection of default windows



Function: It changes the greyscale of a viewer according to some previously predetermined windows. Each window is suitable to visualise a particular type of study. There are 4 types of default windows:

WINDOW TYPE	DESCRIPTION
Automatic	Formed by the element “Auto”, which is available for any type of image. It applies a normalised window based on the range of values of the current image.
Default by DICOM	It contains the values defined within the DICOM of the image. A DICOM image may contain zero or more default windows. The name of these values is also defined in the DICOM file, and if not, they are defined as “Default” plus an ordering number.
Default by modality	It contains values previously defined by the application, and they are designed to visualise studies of certain modalities, such as for CT. There are different default values: Emphysema, Angiography, CT Neck+Contrast, CT Head, CT Liver, CT Soft Tissues, etc.
Default by users	Formed by the specific and custom values that users have saved. See the functioning in the next section Custom defined windows.

Mode of operation: Selecting the viewer where the window change has to be applied and, using the keyboard or the drop-down menu, performing one of the steps described below.

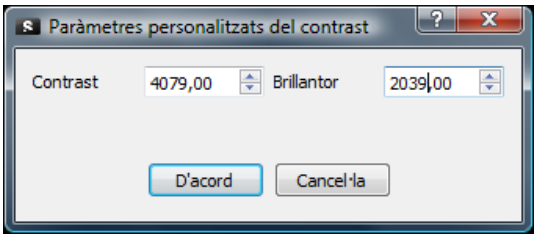
Keyboard: Selecting the number that corresponds to the window that has to be applied.

- º: It alternates in a sequential way the automatic windows and the DICOM default ones (Auto, Default 0, Default 1...)
- 0: Emphysema
- 1: Angiography
- 2: CT Neck+Contrast
- 3: CT Head
- 4: CT Liver
- 5: CT Liver+Contrast
- 6: CT Bone
- 7: CT Lung
- 8: CT Soft Tissues
- 9: CT Soft Tissues+Contrast
- SHIFT+1: Petrous Bone

SHIFT+2: Osteoporosis

Interface: Selecting an element from the drop-down menu, either a value automatically defined, defined in the DICOM, defined by the application or defined by the users.

The option “Custom” (at the end of the drop-down menu) allows us to choose the exact values of contrast and brightness to be applied to the image. To do so, we have to select the “Custom” option from the drop-down menu, which will display a dialogue box such as the one shown in the next image.

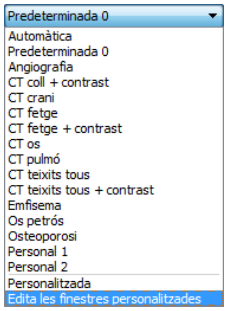


Introduce the values corresponding to the contrast and the brightness, and press the OK button. After that, the chosen values are applied to the selected viewer.

To define new values, and keep them permanently, choose the option Edit Custom WW/WL from the drop-down menu. See the functioning of this option in the next section Custom defined windows.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

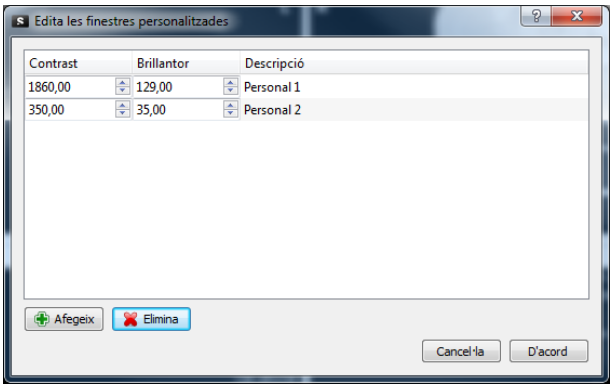
8.2.8. Custom defined windows



Option: Edit Custom WW/WL, within the default windows drop-down menu.

Function: It allows users to save, edit and delete new WW/WL values so that they are available each time the application starts.

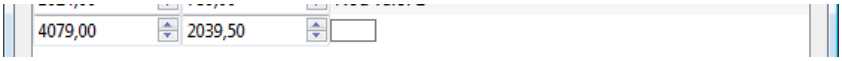
Mode of operation: Select the option Edit Custom WW/WL from the drop-down menu. A window such as the one shown below is displayed:

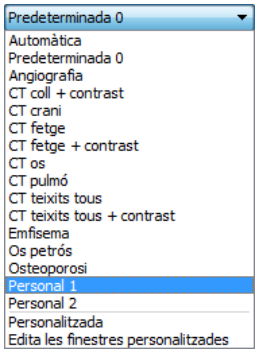


All the values we have stored are displayed in this window. Different options are possible:

Add New**:** It allows users to add a new value to be stored.

By selecting this option or by pressing the RETURN key, a new line is displayed with the current WW/WL values of the selected viewer. We can replace these values by the desired ones, and we can also give them a new name by writing it in the last box. Once defined, we have to select **OK.**

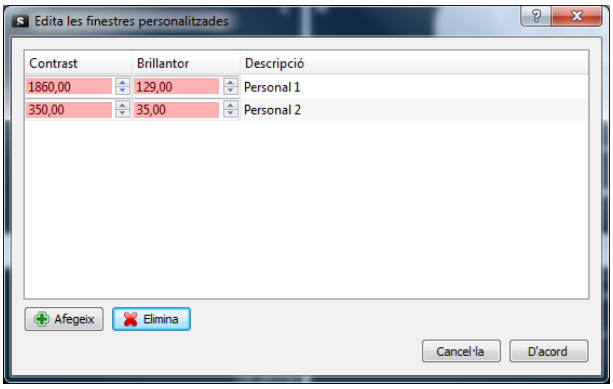




The new stored values appear at the end of the default values list.

Remove: It allows users to remove one or more of the stored values. The list allows the selection of multiple values at the same time by pressing the control key while clicking on the description field of each value. To remove the elements, select one or more elements of the list and press Remove. A dialogue box is displayed asking for a removal confirmation. Press OK to remove the value.

Edit: To edit the values the users simply have to change the value in the text box that shows the current value (areas highlighted in red in the next image).

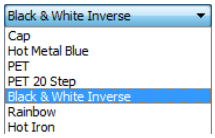


To finish the changes, and save them permanently, press the OK button. If we have a description without text, or the text is repeated, the application will report the error and the changes will not be saved until the error is solved.

If we exit by pressing Cancel or by pressing the red cross of the window, none of the performed changes will be saved.

Viewer where it is applied: New value available to all viewers.

8.2.9. Selection of colour functions

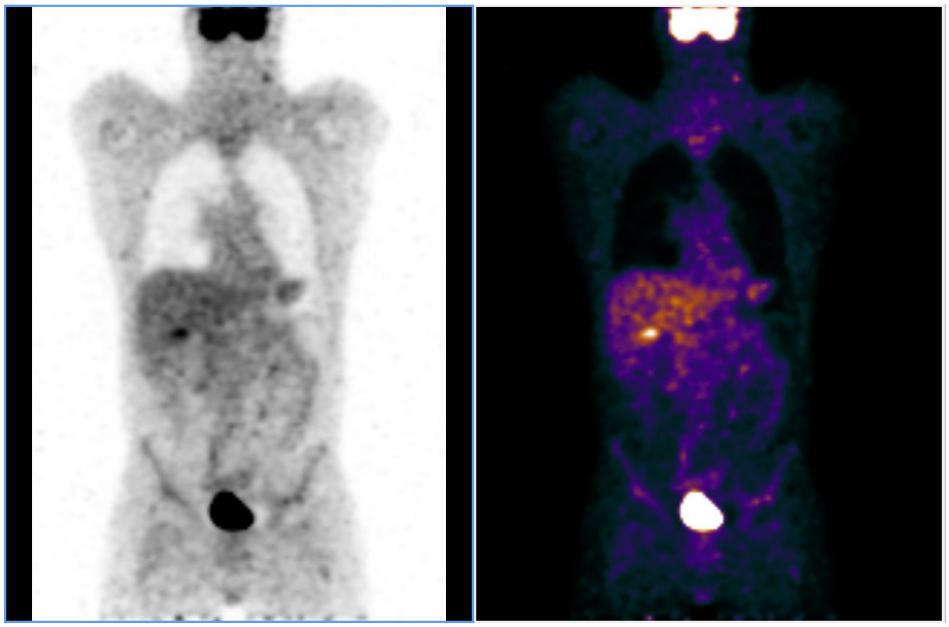


Function: It changes the colour function of a viewer according to some default colour functions. Each function is suitable to visualise a specific type of study. Currently, there are only colour functions available for studies of PET and SPECT modalities. In PET or SPECT images the monochrome inverse colour function (Black & White Inverse) will be applied by default. In PET-CT or SPECT-CT fusion images, the PET Osirix colour function will be applied over the PET or SPECT image by default.

Mode of operation: Select the viewer where the colour function has to be applied (if it is not selected yet) and select an element of the drop-down menu.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:
The same series of PET with different colour functions (Black & White Inverse and PET).



8.2.10. Reversing colours

Function: It inverts the colour scale of the image, that is, the blacks turn white and the whites turn black, the yellows turn blue and the blues turn yellow, and so on.

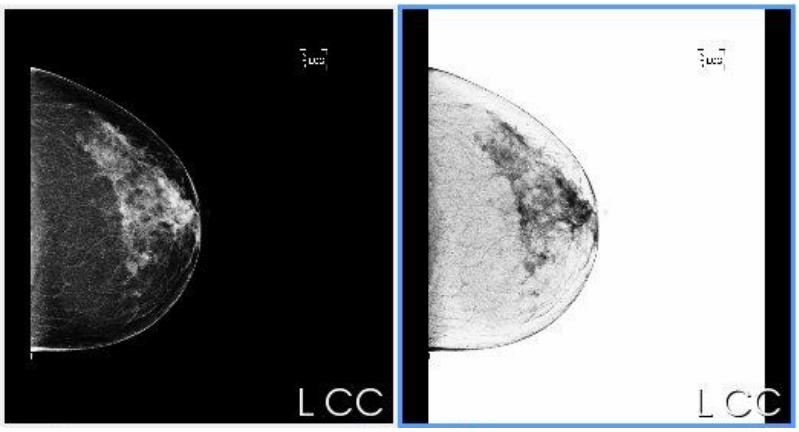
Shortcut key: I

Mode of operation: Select the viewer where the colour transformation has to be applied (if it is not selected yet) and press the icon or the corresponding shortcut key.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:

The image on the left is the original one, and the image on the right corresponds to the original image after applying the colour reversal.



8.2.11. Changing orientation

8.2.11.1. Image flipping

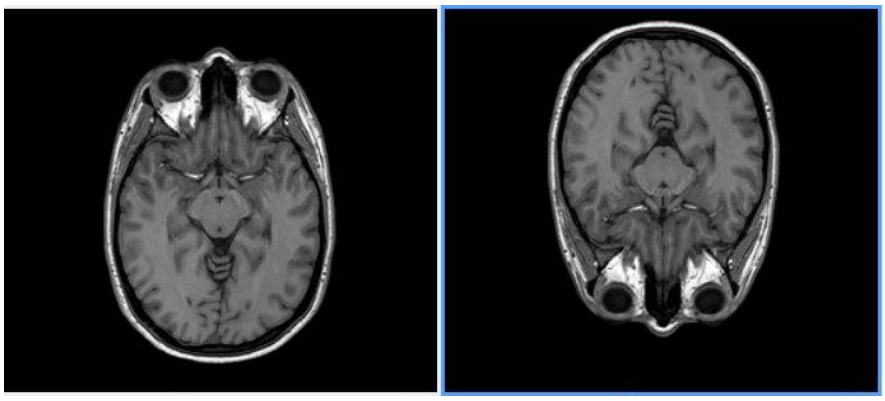
Function: It applies a vertical or horizontal flipping to the image.

Shortcut keys**:** J (vertical), H (horizontal)

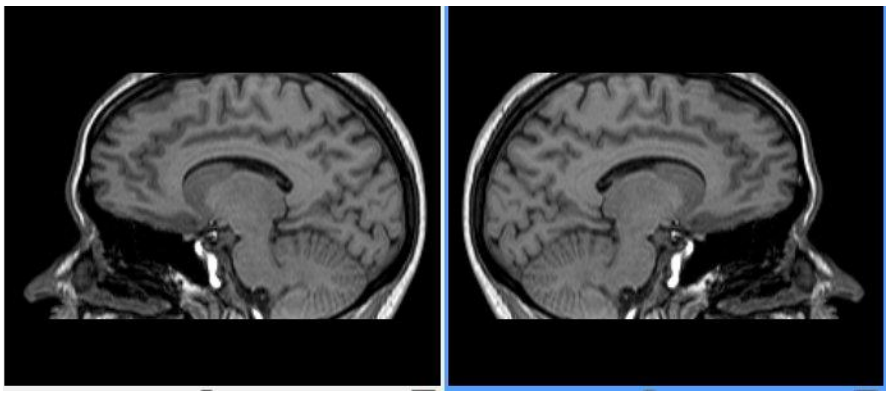
Mode of operation: Select the viewer where the transformation has to be applied (if it is not selected yet) and press the icon or the corresponding shortcut key.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example (vertical):



Example (horizontal):



8.2.11.2. Image rotation

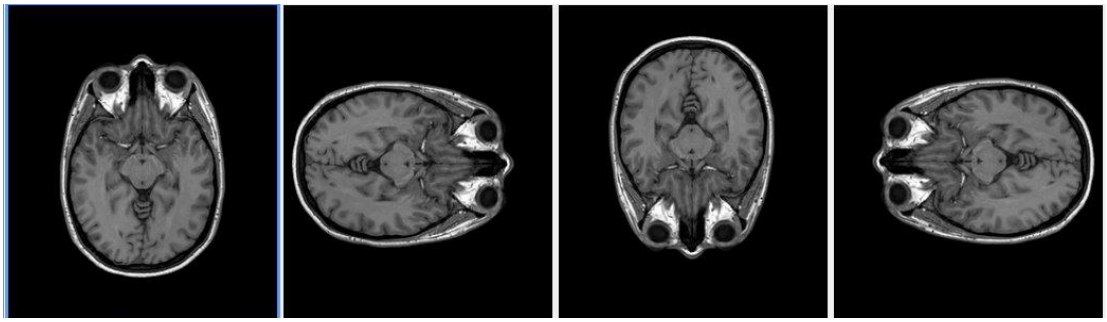
Function: It applies rotations of 90º to the image clockwise and anti-clockwise.

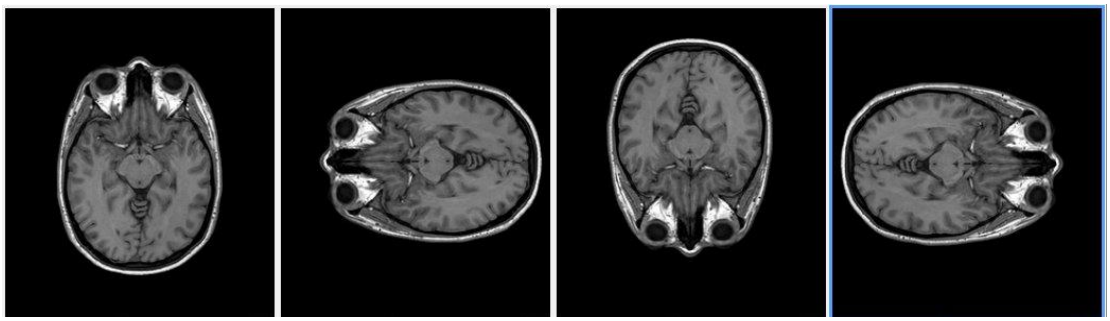
Shortcut keys: G (clockwise), F (anti-clockwise)

Mode of operation: Select the viewer that contains the image to which the rotation has to be applied (if it is not selected yet) and press the icon or the corresponding shortcut key for each turn of 90º needed.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:
The first row of images shows the result of applying the rotation clockwise consecutively. In the second row of images we see the effect of applying the rotation anti-clockwise. After applying the action four times, the result returns to the initial state.





8.2.12. Reset to initial state

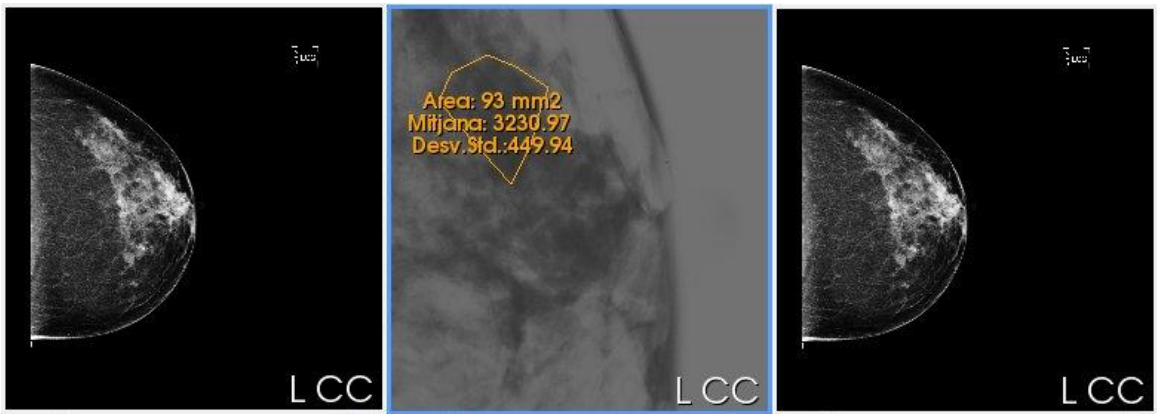
Function: It returns the image of the viewer to its initial state as if it was reloaded from the beginning.

Shortcut key: CONTROL+R

Mode of operation: Select the viewer that has to be restored (if it is not selected yet) and press the icon or the corresponding shortcut key.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:
The leftmost image is the original image, the image in the middle is the original image after applying a zooming operation, a change of scale, adding annotations, etc., and the rightmost image is the result of applying the restoration of the viewer to the middle image. We can see that the image is exactly the same it was at the beginning.



8.2.13. Information layers management

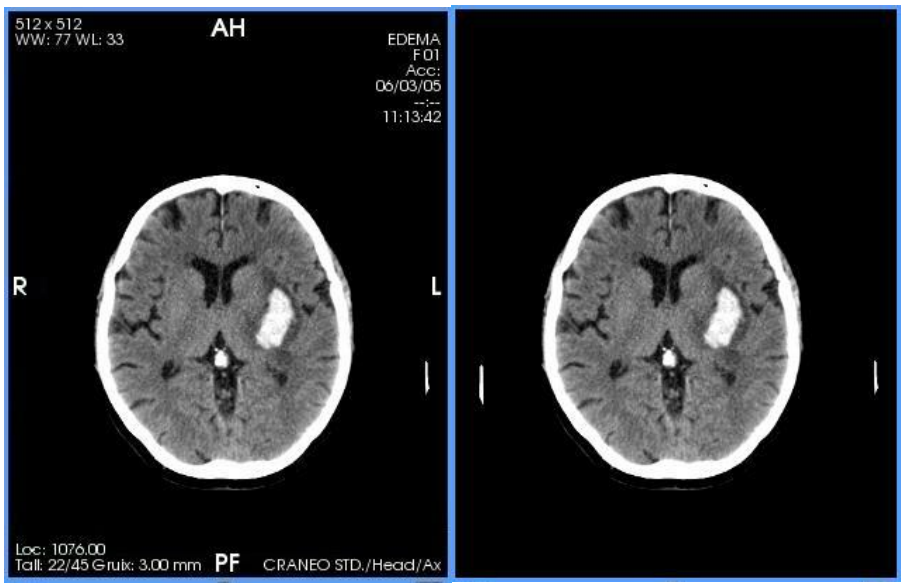
8.2.13.1. Textual information

Function: It hides or shows the textual information in the viewers (amongst these, patient and study data). If there is information printed on the image itself, this information cannot be hidden.

Mode of operation: Select the icon to hide the information, and select it again so that the information reappears.

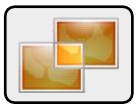
Viewer where it is applied: All.

Example:
The image on the left shows a viewer with all the patient information; the image on the right shows the same viewer, but hiding the patient information.



This feature is useful if users need to create an image for a presentation and the patient information should not appear, since by using the Screenshot tool this information also disappears.

8.2.13.2. Overlays



ICON 1

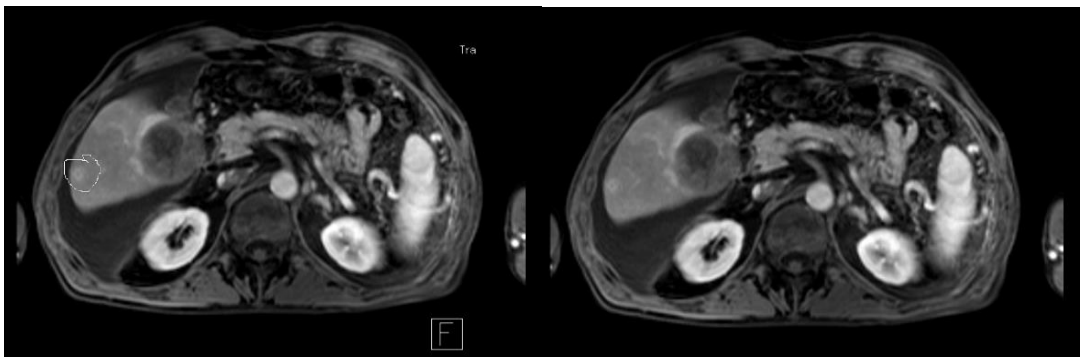
This feature can be found in the menu of the button to manage textual information (ICON 1).

Function: It shows/hides the information of the overlays. The overlays are a layer of information that contains annotations performed over the image. It is a deprecated annotations format, but there are still modalities that use it and it may contain important information for the diagnosis.

Mode of operation: Select the icon to hide the information, and select it again so that the information of the overlays reappears.
They are enabled by default.

Viewer where it is applied: All.

Example:
The image on the left shows a viewer where the overlays are enabled (we can see a ROI, annotation “F” and “Tra” in white); the image on the right shows the same viewer, but removing the overlays information.



8.2.13.3. Shutters

This feature can be found in the menu of the button to manage textual information (ICON 1).

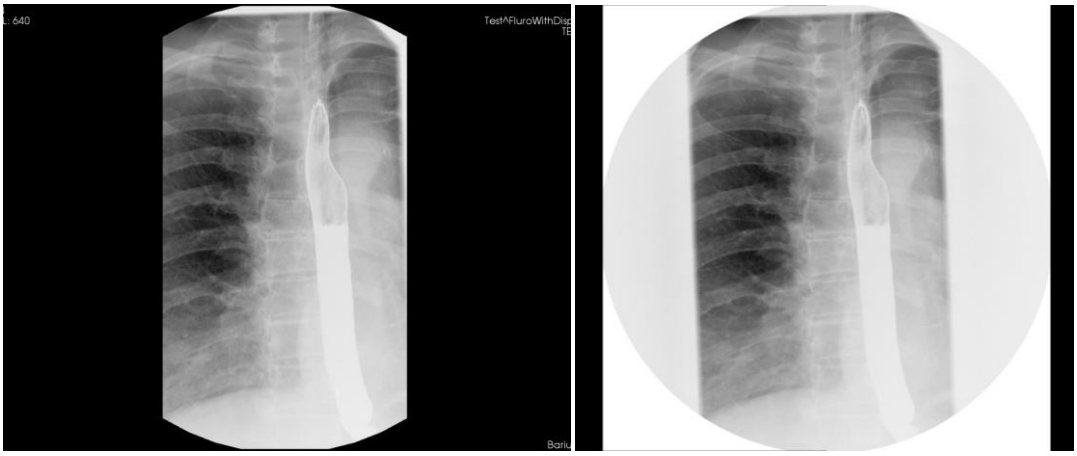
ICON 1

Function: It cuts out non-important areas of the image to facilitate the diagnosis. They are usually white areas that can disturb users when visualising the image. They are common in images of RF modality and plain X-ray.

Mode of operation: Select the icon to show the entire image without removing the margins. Select it again to enable the shutters again and, therefore, to remove the margins of the image that may be a nuisance.
They are enabled by default.

Viewer where it is applied: All.

Example:
The image on the left shows a viewer where the shutters are enabled; the image on the right shows a viewer where the shutters are disabled.



8.2.14. Screenshot

Function: It saves one or all the images contained in the active viewer in photography format (therefore, DICOM information is deleted) anywhere to the computer, or to an external device (USB, hard drive...). The export formats are: PNG, JPG, BMP and TIFF. All of them are image formats that can be opened with any machine without the need for specific software.

Shortcut keys**:** CONTROL+S (current image), CONTROL+A (all the images).

Mode of operation:

Mouse: Select the viewer from which the image or images have to saved, select the screenshot tool, and choose one of the two options: Save an image from the current series, Save all images from the current series. A dialogue box is displayed that allows users to choose the directory where the image or images will be saved, which is confirmed by selecting Save.

Keyboard:
- Save an image: Select the viewer from which the image has to be saved (if it is not selected yet), and press the CONTROL+S keys. A dialogue box is displayed that allows users to choose the directory where the image will be saved and, after specifying a folder and a filename, select Save.
- Save all images: Select the viewer from which all images have to be saved (if it is not selected yet), and press the CONTROL+A keys. A dialogue box is displayed that allows users to choose the directory where the images have to be saved and, after specifying a folder and a prefix for the filenames, select Save.
- It is recommended to save the images in an empty folder, since if the series contains many images, a file is created for each one.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

8.2.15. Exporting DICOM images

Function: It generates a new DICOM series from a capture of the series that is currently displayed. It is stored within the same study. The new series can only be stored locally, or sent to one or several PACS. It saves the annotations embedded in the images of the series.

Mode of operation: Select the viewer that contains the series that has to be exported (if it is not selected yet) and press the icon for creating a new series**.** A window is opened, which provides different options:

Series description**:** It is the description the new series will have.

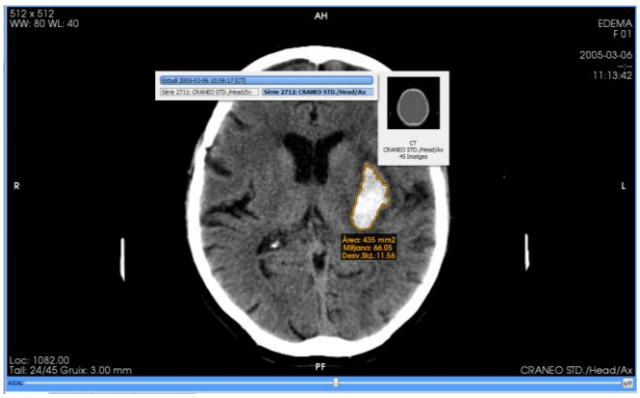
Images to export: It allows users to choose the images that will be saved. Depending on the series, different options can be chosen:
- Current image only: Only the displayed image is saved.
- All images of the series (available if it contains more than one image): It saves all the images that form the series, that is, all the slices.
- All images of the current phase (available if it contains more than one phase and image): It saves the images of all the slices that form the displayed phase.
- All phases of the current image (available if it contains more than one phase and image): It saves the images of all the phases corresponding to the displayed slice.
At the bottom of the image preview, the total number of images to be saved is displayed.

The right part of the dialogue box reports that the images will be stored in the local database and in the selected PACS.
- If no PACS is selected, images are only stored in the local database and, therefore, they will only be accessible from the machine where they have been generated.
- If one or more PACS are selected, images are stored in the local database and they are also sent to the selected PACS; therefore, the images can obtained if they are needed in the future, and they can be accessed from any machine connected to the selected PACS.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:

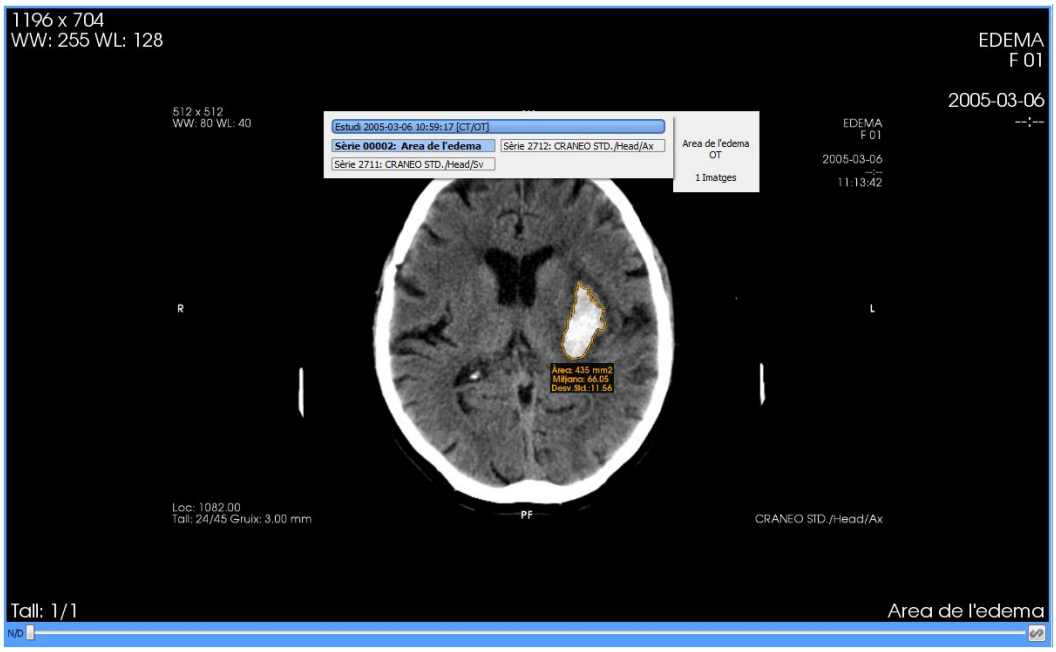
1- We perform, for example, an area in one of the viewers, which is the one that will be saved. We can see that we can only choose two series from the study.



2- We select ICON 1 to export the image, and we add a description. We only want to save the current image, and only locally, so that we do not select any PACS. Finally, we select Export.

ICON 1

3- In the patient menu, the new captured series is displayed, and it is available to be visualised in any viewer.


1196 x 704
WW: 255 WL: 128
EDEMA
F 01
2005-03-06
512 x 512
WW: 80 WL: 40
Estudi 2005-03-06 10:59:17 [CT/OT]
Sèrie 00002: Area de l'edema
Sèrie 2712: CRANEO STD./Head/Ax
Sèrie 2711: CRANEO STD./Head/Sv
Area de l'edema
OT
1 Imatges
EDEMA
F 01
2005-03-06
11:13:42
R
L
Àrea: 435 mm2
Mitjana: 66.05
Desv.Std.:11.56
Loc: 1082.00
Tall: 24/45 Gruix: 3.00 mm
PF
CRANEO STD./Head/Ax
Tall: 1/1
Area de l'edema
N/D

8.3. MEASUREMENT TOOLS

8.3.1. Distance

Function: It allows users to compute the minimum distance between two points.

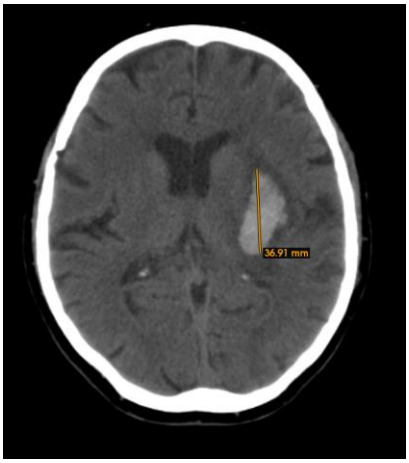
Shortcut key to activate it: D

Mode of operation:
Mouse: Make a first click with the mouse to assign the starting point, move the mouse, and make a second click to assign the ending point. The annotation of the measurement will be placed next to the second point. To cancel the measurement when it is still not finished, press the ESC key.


Left button

Viewer where it is applied: Viewer over which the mouse cursor is located. The viewer can be changed while creating a distance.

Example:



8.3.2. TA-GT

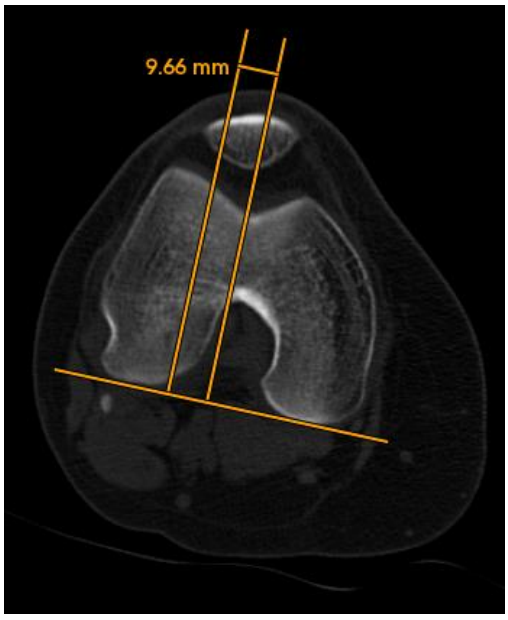
Function: It allows users to perform a TA-GT measurement.

Mode of operation:
Mouse: Make a first click with the mouse to assign the starting point of the line, move the mouse, and make a second click to assign the ending point of the line; this line will be the reference line. Once we have created this line, we need to create two more lines perpendicular to it. To do so, we have to move the mouse and set the point where the second line ends, and repeat the process for the third line. When completing the measurement, the line that joins the last two lines, which indicates the distance between them, is displayed.
To cancel the measurement when it is still not finished, press the ESC key.


Left button

Viewer where it is applied: Viewer over which the mouse cursor is located. The viewer can be changed while creating the TA-GT measurement.

Example:



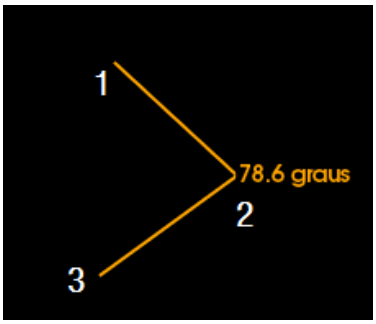
8.3.3. Angle

Function: It allows users to compute the angle formed by three points.

Shortcut key to activate it: A

Mode of operation:
Mouse: Make a first click to assign the first point, make a second click to assign the second point ("inflection point"), move the mouse until the third point is located, and make a third click to set this last point. The result of the measurement will be placed at the origin of the angle.
To cancel the measurement when it is still not finished, press the ESC key.


Left button



Viewer where it is applied: Viewer where the clicks are made. The viewer can be changed while creating an angle.

Example:

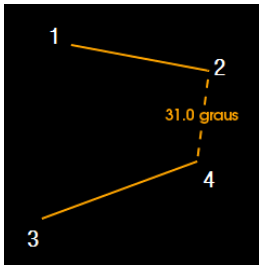
8.3.4. Open angle

Function: It allows users to create angles without setting the “inflection point”, since it is computed from two lines.

Shortcut key to activate it: SHIFT+A

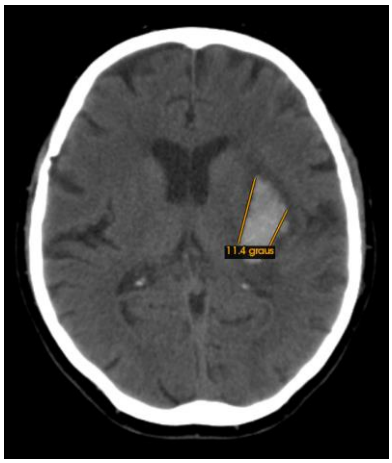
Mode of operation:
Mouse: It consists in drawing two lines. Make a first click to assign the first point of the first line, and a second click to assign the second point of the first line. Once the first two points are set, the same process is repeated to assign the two points of the second line. The application computes the angle formed by the two drawn lines. The order of the points in the first and the second line is irrelevant. The result will be placed in the dashed line that joins the two lines, that is, the place where the angle would be formed.
To cancel the measurement when it is still not finished, press the ESC key.


Left button



Viewer where it is applied: Viewer where the clicks are made. The viewer can be changed while creating an angle.

Example:



8.3.5. Regions of interest (ROI)

Starviewer provides different tools to draw regions of interest with different shapes. Once the region of interest is drawn, the area is computed in mm^2 (if the image does not have spacing information, it will be computed in $pixels^2$), as well as some statistical data such as the mean and the standard deviation. For images with more than one component per pixel (colour image), only the area is computed. If the image has specific units, these will be indicated in the statistical data. For images of PET modality, the maximum and average SUV will be also computed in the drawn region. In PET-CT fusion images, the SUV of the PET image and the statistical data of the CT image will be displayed. To learn more about how the SUV is computed and which methods exist, see chapter Standardized Uptake Value (SUV) measurement.

The ROI tools are grouped in the same button in the toolbar. Below, we explain each of the existing ROI tools.

8.3.5.1. Elliptic ROI

Function: It allows users to create an elliptic region.

Shortcut key to activate it: R

Mode of operation:
Mouse: While pressing the left button, move the mouse until the ellipse has the desired size; then, stop pressing the button of the mouse. If the movement is done horizontally, the ellipse changes the horizontal diameter; if the movement is done vertically, the vertical diameter is changed instead. The result of the measurement is placed at the lower side of the ellipse if it grows from top to bottom, and it is placed at the upper side if it grows inversely.
To cancel the measurement when it is still not finished, press the ESC key.

Viewer where it is applied: Viewer where the click is made.

Example:

Left button

8.3.5.2. Polygonal ROI

Function: It allows users to create a polygonal region.

Shortcut key to activate it: SHIFT+R

Mode of operation:
Mouse: Make different clicks with the left button of the mouse, drawing the shape of the area that has to be computed. Double click to automatically close the area. The result will be placed outside the polygon as close as possible to the last created point.
To cancel the measurement when it is still not finished, press the ESC key.

Viewer where it is applied: Each point has an effect in the viewer where the left button of the mouse is pressed. The viewer can be changed even if a ROI is not finished, and when the mouse enters the viewer again, it is possible to continue with the creation of the ROI.


Left button

Example:

8.3.5.3. Magic ROI

Function: It allows users to delimit a region with similar intensity values within a threshold starting at an initial point.

Shortcut key to activate it: M

Mode of operation:
Mouse: Click with the left button of the mouse inside the area where the ROI has to be created. Then, while still pressing the mouse button, move the mouse vertically up or down until the size of the ROI fits the desired area. When the drawn area is the desired one, stop pressing the mouse button, and the information of the chosen area will be displayed at the lower side of the ROI.
To cancel the measurement when it is still not finished, press the ESC key.


Left button

Viewer where it is applied: Viewer that contains the image where the click is made.

Example:

8.3.6. Circle

The icon is located in the ROI tools drop-down menu.

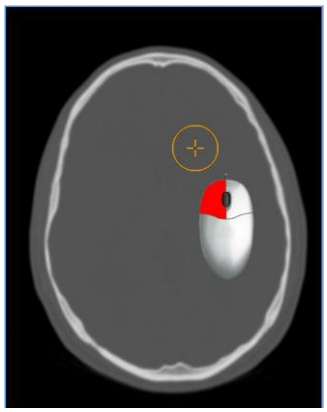
Function: It allows users to create a circular region by indicating its centre.

Mode of operation:

Mouse: Move the mouse while pressing its left button, and stop pressing it when the circle has the desired shape. The tool does not take into account whether the movement is made horizontally or vertically, since it always keeps the circular shape. The diameter of the circle will be the maximum distance between the initial point and the movement made.
To cancel the measurement when it is still not finished, press the ESC key.

Viewer where it is applied: Viewer where the click is made.

Example:




Left button

8.3.7. Erasing

Function: It erases the annotations (distances, ROI, angles, open angles...) displayed in a viewer. It allows users to:
- Erase objects one by one
- Erase objects in a region
- Erase all objects of a viewer

Shortcut key to activate it: E

Mode of operation:

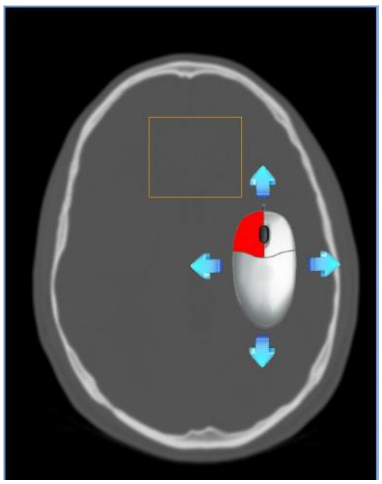
Mouse:

ACTION	DESCRIPTION
Erase objects one by one	Click with the left button of the mouse on the annotation to be erased.
Erase objects in a region	Hold down the left button of the mouse while moving it to draw the region to be erased. All the objects that are completely inside the box are erased.
Erase all objects of a viewer	Select the viewer that has to be cleared (with the margin painted), select the arrow next to the rubber icon, and select the option All of current viewer.

Keyboard: The action of erasing all objects of a viewer is available by pressing the CONTROL+E keys.

Viewer where it is applied: Viewer that contains the mouse, or the active viewer (with a darker or blue colour frame).

Example:



8.3.8. Considerations on geometric measurements

8.3.8.1. Units and types of measurements

The units displayed in the geometric measurements, mainly distances and ROI, may vary depending on the presence of certain DICOM attributes. Additionally, depending on the image modality and according to the present attributes, the application may give one or more results for the same measurement, each one with its corresponding meaning. When needed, the type of measurement will be explicitly indicated to avoid confusion with the type of measurement omitted.

Next, we explain in which cases each unit and type of measurement may appear.

All the geometric measurements will always be displayed together with their corresponding unit, whether pixels (px) or millimetres (mm).

8.3.8.2. Measurements in pixels

The measurements are displayed in pixels (px) when it is not possible to determine the physical space between two consecutive pixels. This scenario occurs when the following image attributes are not present:
- Pixel Spacing (0028,0030)
- Imager Pixel Spacing (0018,1164)

8.3.8.3. Measurements in millimetres

In order for the measurements to be shown in millimetres (mm), we need at least one of the following pixel spacing attributes are present in the image:
- Pixel Spacing (0028,0030)
- Imager Pixel Spacing (0018,1164)

In this case, additionally, and depending on the modality, the present attributes and the corresponding values, more than one value may be computed in the same measurement, where each one may have a specific meaning. The different types of measurement values that may appear and their possible conditions are detailed below.

Physical measurements
Measurements will be considered as physical when the following conditions are met:
- the image modality is CT, MR, PT, SC, US or NM
- the presence of the Pixel Spacing (0028,0030) attribute in the image with a valid value

The Pixel Spacing attribute determines the physical space between two consecutive pixels, which is why the measurement taken on the image corresponds to the actual physical measurement of the patient it represents.

Measurements in projection radiography images
When dealing with projection radiography images (those with CR, DX, RF, MG, XA, XC, IO, OP or ES modality), their own nature implies that different spacing attributes can be provided, which makes it possible to interpret different types of measurements. Below, the possible scenarios are described.

Measurement in detector

Measurements will be considered relative to the detector's plane when one of the following conditions is met:

- The Imager Pixel Spacing (0018,1164) attribute is the only present spacing attribute, or
- The Imager Pixel Spacing (0018,1164) and Pixel Spacing (0028,0030) attributes are present and have the same value.

For projection radiography images, if no type is explicitly stated, the default measurement is relative to the detector.

Calibrated measurement

These measurements are possible when the following condition is met:
- The Imager Pixel Spacing (0018,1164) and Pixel Spacing (0028,0030) attributes are present and have different values.

In this case, Imager Pixel Spacing (0018,1164) will have the spacing corresponding to the detector's plane, and Pixel Spacing (0028,0030) will have a calibrated spacing that will approximate the spacing in the image plane.

This case will allow us to give both measurements, the one from the detector and the calibrated one. If the calibrated one is displayed, whether or not together with the measurement from the detector, it will always be displayed together with a label that explicitly indicates that the value of the measurements corresponds to the calibration.

Magnified measurement

This case is similar to that of calibrated measurements, but it is specific to MG modality images. Measurements may be magnified when the following conditions are met:

- The image modality is MG
- The Imager Pixel Spacing (0018,1164) and Estimated Radiographic Magnification Factor (0018,1114) attributes are present in the image

In this case, the calibration between the detector and the image plane is done by dividing the value of the Imager Pixel Spacing by the value of the Estimated Radiographic Magnification Factor.

This case will also allow us to give both measurements, the one from the detector and the magnified one. If the magnified one is displayed, whether or not together with the measurement from the detector, it will always be displayed together with a label that explicitly indicates that the value of the measurement corresponds to the magnified one.

Unknown meaning measurement

This scenario occurs when, according to the modality and the present attributes, the meaning of the measurement cannot be determined due to the lack of complementary information. For a measure to be considered that way, the following conditions must be met:

- The image modality is of projection radiography: CR, DX, RF, XA, XC, MG, IO, OP or ES
- The only present spacing attribute is Pixel Spacing (0028,0030)

If these conditions are met, the measurement will always be displayed together with a label that explicitly indicates this condition of the measurement.

Obtaining such a measurement is not normal and would indicate that there is an error or a problem in the data generation of the acquired image. This problem should be reported to the technical team of the modality to correct it and generate the data properly.

8.3.8.4. Priority of the measurements

Given the possible types of measurements, in some cases we will have to decide which values we want to show and how. Next, we describe the measurements that are computed first according to each case and how they are displayed.

- If the image is of projection radiography:
    - If the measurement comes with no label and is displayed in mm, it will be, by omission, a measurement relative to the detector's spacing.
    - If the measurement can be calibrated or magnified, the calibrated or magnified value will be given as a priority and it will always be displayed together with the corresponding label that explicitly indicates its condition.
- If the image is not of projection radiography (CT, MR, PT, US, etc.), it will be a physical measurement (mm) by omission and it will not be displayed together with any label.
- If the conditions for an unknown meaning measurement are met, the measurement will always be displayed together with the corresponding label that explicitly indicates its condition.

8.3.8.5. Measurements verbosity

Since sometimes we can have more than one result for the same measurement, we might want to have more or less information depending on the case. For this reason, we can define the verbosity for the measurements that are computed. By default, the verbosity will be the minimal. This option can be configured in the 2D viewer configuration options.

The options about the verbosity we can choose are the following:

- Minimal: One single measurement will always be displayed. Only the labels for calibrated and magnified measurements will be displayed. This is the option set by default.
- Minimal Explicit: The same as in the Minimal option, but also displaying labels in detector measurements.
- Verbose: There will be as many labels as the present attributes allow. Only the labels for calibrated and magnified measurements will be displayed.
- Verbose Explicit: The same as in the Verbose option, but also displaying labels in detector measurements.

8.3.8.6. Accuracy and precision

In simple terms, accuracy measures how close the results are to the reality, while precision measures how much they vary when performing repeated measures of the same thing.[1]

In Starviewer, precision of measures is limited mainly by the precision of the user or the input device (i.e. the mouse) when trying to perform the same measure, and also by the image resolution. On a lower degree, it is also limited by the precision of the DICOM DS (Decimal String) Value Representation[2], the precision of the C++ double type[3][4] and the precision of the FPU in the specific CPU[5].

On the other hand, accuracy depends on the calibration of the scanning device and the image resolution.

Accuracy has been verified with several measuring tests, including testing with reference images.[6]

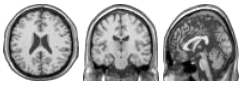
Numbers in Starviewer are displayed with the following precisions:

- Distances, areas, statistical values and SUV are displayed rounded to 2 decimal places
- Angles are displayed rounded to 1 decimal place
- Window width and level values are displayed rounded to integers
- Pixel values are displayed with as many decimal places as needed (following the default C++ behaviour)

[1] https://en.wikipedia.org/wiki/Accuracy_and_precision
[2] http://dicom.nema.org/medical/dicom/current/output/chtml/part05/sect_6.2.html
[3] https://en.cppreference.com/w/cpp/language/types#Floating_point_types
[4] https://en.wikipedia.org/wiki/IEEE_754
[5] https://en.wikipedia.org/wiki/Floating-point_unit
[6] http://www.dclunie.com/

9. ADVANCED VISUALISATION

9.1. RECONSTRUCTIONS



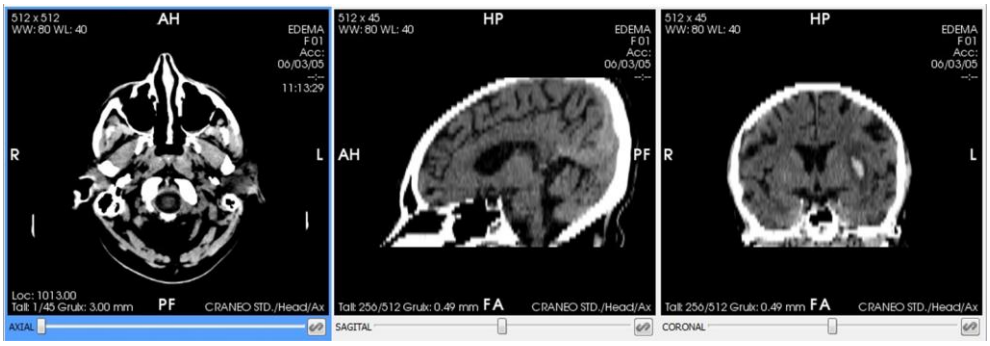
Function: It changes the cutting plane of the images.

Shortcut keys: CONTROL+1 (axial), CONTROL+2 (sagittal), CONTROL+3 (coronal).

Mode of operation: Click on the corresponding icon, and the series contained in the active viewer will be reconstructed according to the chosen view (axial, sagittal or coronal).

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:



Axial Sagittal Coronal

9.2. THICK SLAB

(initial state)

(available options)

Function: It assembles the information of a range of images in a single one. The available compositions are MIP (Maximum intensity projection), MinIP (Minimum intensity projection) and Average.

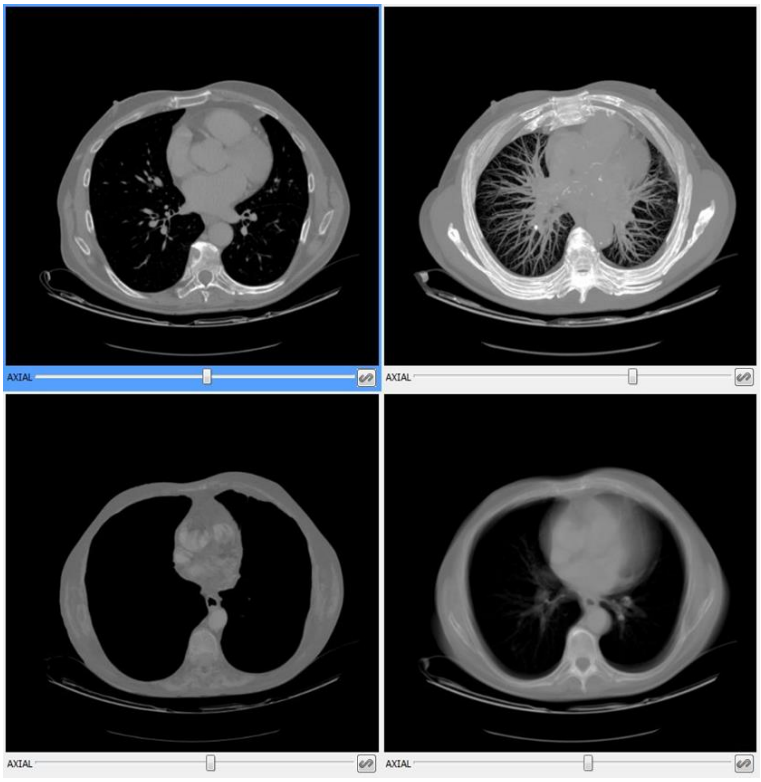
Mode of operation: Select the viewer where the Thick Slab has to be applied (if it is not selected yet), select an option from the drop-down menu (Disabled, MIP, MinIP, Average), and select the number of images to assemble or select the option Maximum

Thickness. Changes are immediately applied to the selected viewer.

If the view of a viewer is changed while the Thick Slab is enabled, then the physical thickness is kept in the new view. For example, if we have a viewer in axial view with a MIP with a total thickness of 10 mm and we change to a sagittal view, in the new view a MIP will be applied with the necessary number of images so that the total thickness remains 10 mm or the closest possible. However, when the Maximum Thickness option is enabled, the maximum thickness accepted by the view we have changed will be applied.

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:
The top-left viewer contains the original image. The top-right one is the result of applying a Thick Slab with a MIP of 65 images, the bottom-left one is the result of applying a MinIP with a thickness of 65 images, and the bottom-right one is the result of computing the average also with 65 images.



9.3. REFERENCE LINES

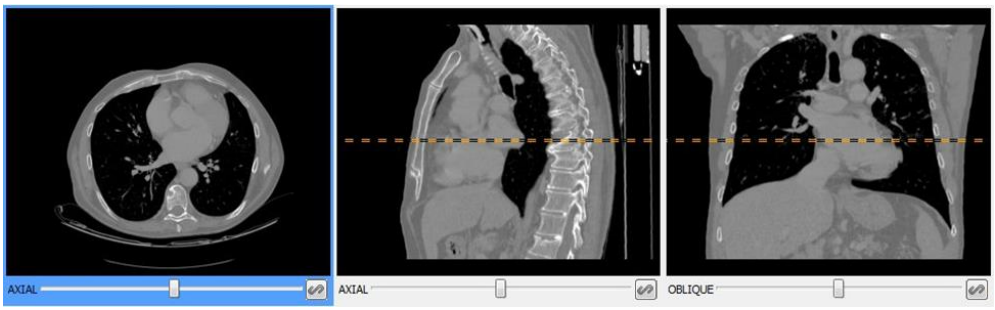
Function: It allows users to visualise which area of the remaining viewers corresponds to a specific cutting plane.

Shortcut key to activate it: L

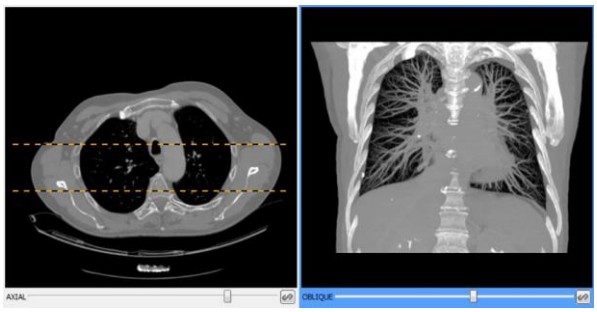
Mode of operation: Select the reference lines icon and, from now on, for all the image changes performed to any viewer, if it is possible (same study, the patient has not moved...), the cutting plane in reference to the rest of viewers will be displayed.

Viewer where it is applied: All the viewers that contain a series of the same patient study, where the patient has not moved.

Example:
In the first example, the leftmost viewer is the selected one, and the other viewers show a line that corresponds to the slice displayed in the main viewer.



In the second example, the main viewer is the one on the right, and it shows how the tool works with a viewer where we have enabled the Thick Slab; as the viewer displays more than one image at the same time, the cutting plane has a thickness, which is what the viewer on the left shows. The entire area between the two parallel lines is what is displayed in the main viewer.



In order for the reference lines to be displayed, the angle between the reference image planes and the projected one must be between 45º and 135º.

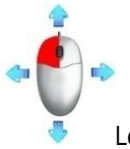
9.4. 3D CURSOR

Function: It allows users to choose a point of an image, and the other viewers automatically check whether they contain the point and position themselves in order to show the point it corresponds to.

Shortcut key to activate it: C

Mode of operation:

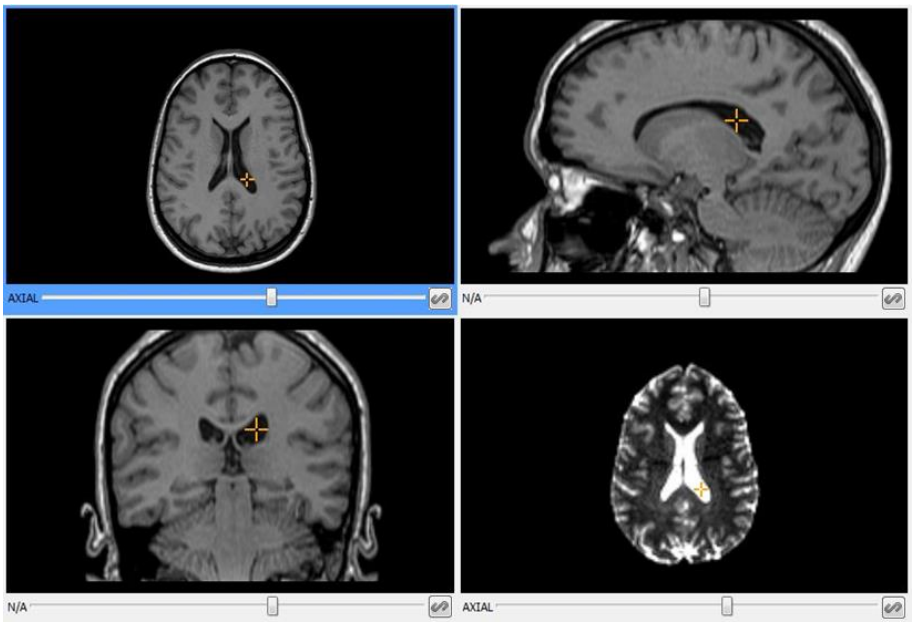
Select the 3D cursor icon, and select a point of an image from a viewer; the rest of the viewers, if possible (same study, the patient has not moved...), will show the image that contains the same point. The point can be changed by clicking on another point of the image, or by holding down the left button and moving the cursor. Images are automatically updated.



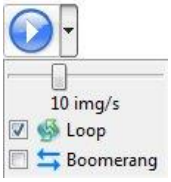
Left button

Viewer where it is applied: All the viewers that contain a series of the same patient study, where the patient has not moved.

Example:
A point has been selected in one of the viewers, and the other viewers automatically show the same point. If the viewer is displaying a reconstruction (sagittal or coronal), it will keep on showing the point according to the reconstruction.



9.5. VIDEO



(when selecting the right arrow, the other options are displayed)

Function: It displays the images one after the other automatically, as if it was a video.

Mode of operation: Select the viewer where the video has to be displayed (if it is not selected yet) and press the start icon ICON 1.
The slider allows users to control the speed at which images are displayed.
If ICON 2 is enabled, when it is finished it starts again, so that the video is repeated continuously.
If this option is enabled together with ICON 3, the video moves backwards instead of returning to the beginning when it arrives at the end.

ICON 1

ICON 2

ICON 3

Viewer where it is applied: Active viewer (with a darker or blue colour frame).

9.6. VOXEL INFORMATION

Function: It shows the value of a specific point (voxel). As many values as voxel components will be displayed. If the image is monochrome, a single value will be displayed; if the image is RGB, the values of each channel will be displayed. The value can be displayed together with the corresponding units depending on the modality, e.g. HU for Hounsfield units in CT images.

Shortcut key to activate it: V

Mode of operation:

Mouse: Select the voxel information icon, and move the mouse over the image, and the value of the point where the cursor is placed is displayed.

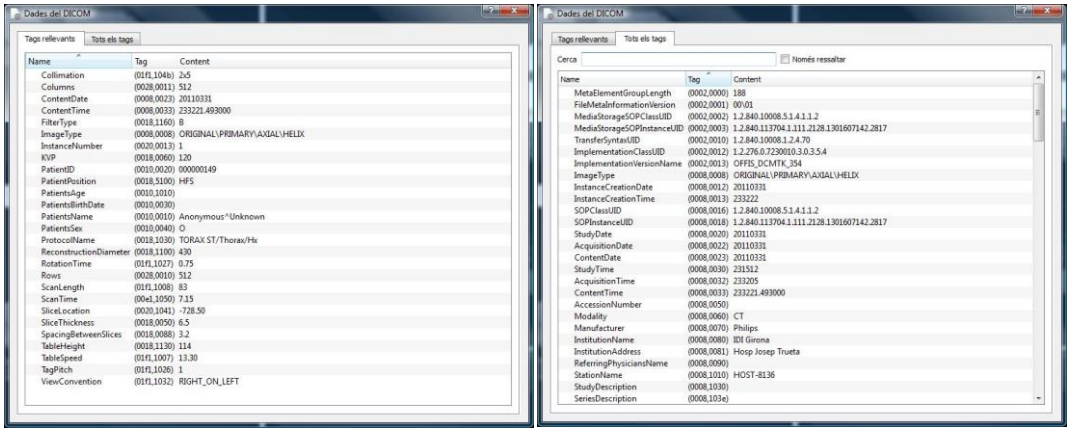
Viewer where it is applied: Viewer under the cursor.

Example:
We select the tool and we move the cursor over the image, and the value of each position is displayed.

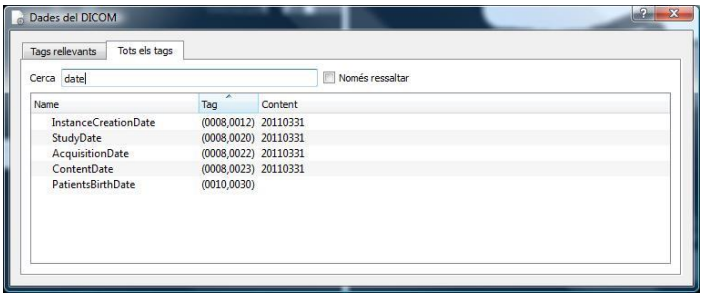
9.7. DICOM INFORMATION

Function: It shows additional information contained in the DICOM file of the image displayed in the selected viewer. Users can consult the most relevant information, but also any other information not defined as relevant.

Mode of operation: Select the viewer from which the information has to be displayed, and also the desired image. Then, press the additional information button and the information of the selected image is displayed in the main viewer.
If the relevant information has been defined for the image modality, the content will be displayed in the Meaningful Tags tab. Otherwise, select the All Tags tab to consult all available information.

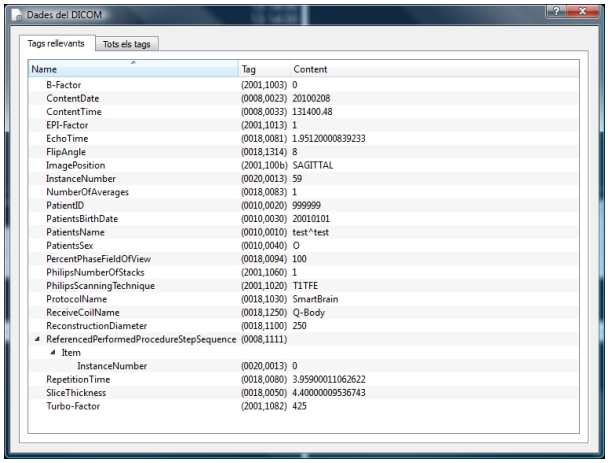


From the All Tags tab, searches are allowed to filter the information, either by showing the results that match the search or by highlighting them.

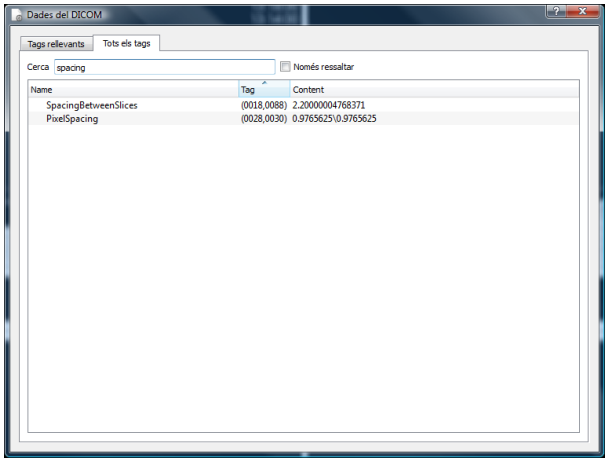


Viewer where it is applied: Active viewer (with a darker or blue colour frame).

Example:
If we want to consult the content of the SpacingBetweenImages tag of a magnetic resonance study, we select the DICOM information tool and the relevant tags are displayed.



Since the tag we are looking for is not relevant, we select the All Tags tab, and we perform a search by introducing the text spacing; all the tags that contain this text are displayed.



9.8. MANUAL SYNCHRONISATION

The icon is placed at the bottom-right corner of each viewer:

Function: Each image change (spatial jump) that is performed in a viewer has an effect to the rest of viewers when the synchronisation tool is enabled. To perform the jump, the distance travelled is considered instead of the amount of images.

Mode of operation: Press the synchronisation button of all the viewers that have to be synchronised (at least 2 viewers). From this point, each movement made when changing an image will have an effect to the rest of synchronised viewers as long as they display the same view, that is, if we make a movement in a viewer displaying an axial view, only the viewers with the manual synchronisation enabled that display an axial view will be automatically changed. The chain icon indicates whether the viewer in manually synchronised (closed) or not (opened).
This tool considers the distance travelled and not the amount of images, so that there is always the same jump with different viewers.
Enabling the manual synchronisation disables the automatic synchronisation. See the section Automatic synchronisation.

Viewer where it is applied: All the viewers selected with the synchronisation button.

9.9. MANUAL SYNCHRONISATION IN ALL VIEWERS

Function: It activates the manual synchronisation to all viewers at the same time. See tool Manual synchronisation.

Shortcut key to activate it: U

Mode of operation: Press the Activate manual synchronisation in all viewers button. From this point, the behaviour is the same as if the manual synchronisation would have been selected in each viewer. See section Manual synchronisation.

Viewer where it is applied: All viewers that contain a loaded image.

9.10. DEACTIVATING MANUAL SYNCHRONISATION IN ALL VIEWERS

Function: It disables the manual synchronisation to all viewers at the same time. See tool Manual synchronisation.

Shortcut key to activate it: SHIFT+U

Mode of operation: Press the Deactivate manual synchronisation in all viewers button. From this point, the behaviour is the same as if manual synchronisation would have been disabled in each viewer. See section Manual synchronisation.

Viewer where it is applied: All viewers that contain a loaded image.

9.11. AUTOMATIC SYNCHRONISATION

Auto-Sync

Function: It automatically synchronises all the viewers, placing them at the same position when activating the tool, and causing each jump made in a viewer to have an effect to the rest of viewers (as long as it is possible: same study, the patient has not moved...).

Shortcut key to activate it: O

Mode of operation: Press the automatic synchronisation button. From this point, each movement made when changing an image will have an effect to the rest of viewers automatically, as long as it is possible: same patient and study, the patient has not moved...
This tool takes into account the image acquisition plane; therefore, changes in axial view will only have an effect to the viewers in axial view. The same is applied for sagittal and coronal views.
Enabling the automatic synchronisation disables the manual synchronisation. See section Manual synchronisation.

Viewer where it is applied: All.

9.12. PROPAGATION

Propagate

Function: It propagates a set of visualisation properties of the active viewer, so that these properties can be synchronised with the viewers that have a series of common attributes with it. These attributes may vary depending on property modified in the active viewer.

Shortcut key to activate it: P

Mode of operation: Propagation can be manually activated or deactivated through the toolbar button or the shortcut key P. When it is activated, an initial propagation of the properties is made between all the viewers, where the active viewer in that moment has priority, so that they are synchronised from the beginning.

Below, the properties that can be synchronised and the conditions that have to be met in each case for the synchronisation to be effective are detailed.

- Window: the window of the active viewer is propagated. If we select a default window (the ones included in the DICOM heading, the standard and the automatic ones), the equivalent window corresponding to the image they are displaying is selected in the other viewers. For default windows, the absolute window values are propagated.
Synchronised viewers: those that contain the same series as the active viewer. For fused models, it will only be applied on the matching series.

- Zooming: the zooming absolute value from the active viewer is propagated.
Synchronised viewers: those that have the same anatomical plane and modality as the active viewer. Exception: if modalities are PET-CT or SPECT-CT and they have the same anatomical plane, there is synchronisation as well.

- Scrolling: the position of the image within the active viewer is propagated if the series between viewers share the same coordinate system (that is, they are from the same study, the patient has not moved, etc.). If the coordinate system is different, it cannot be guaranteed that the same position is displayed between viewers; therefore, propagation of scrolling is not allowed.
Synchronised viewers: those that have the same anatomical plane as the active viewer and share a coordinate system.

- Orientation: the orientation (rotation and flipping) of the image from the active viewer is propagated.
Synchronised viewers: those that have the same anatomical plane and modality as the active viewer. Exception: if modalities are PET-CT or SPECT-CT and they have the same anatomical plane, there is synchronisation as well.

- Phase: the phase of the active viewer is propagated.
Synchronised viewers: those that have fused series. It is only applied on the secondary series as long as it is the same as the one from the active viewer.

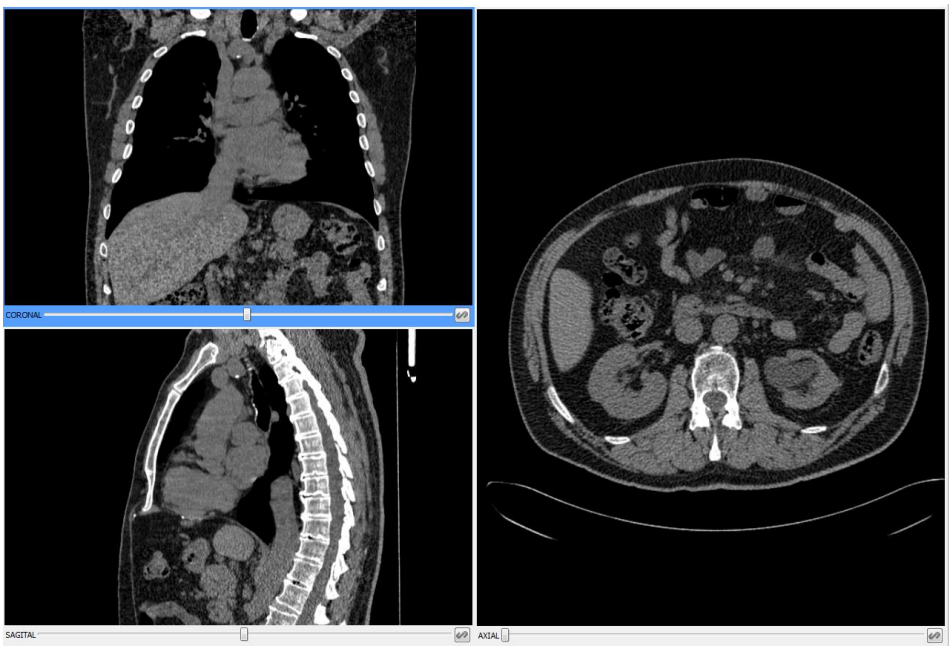
- Thick slab: the projection type and the thickness of the thick slab of the active viewer are propagated.
Synchronised viewers: those that have fused series and the same anatomical plane as the active viewer. It is only applied on the secondary series as long as it is the same as the one from the active viewer.

Others: Propagation can be automatically activated for certain modalities. With the default configuration the propagation is activated for the CT, MR and PET modalities. To learn how to configure the default modalities, see section 2D viewer configuration. In addition, we can also choose which properties are propagated and which are not. If we display the menu attached to the propagation icon, we will see the list of active properties. By clicking on these, we will activate or deactivate them. By default, all available properties are propagated. The selection of properties applies to all the modalities equally.

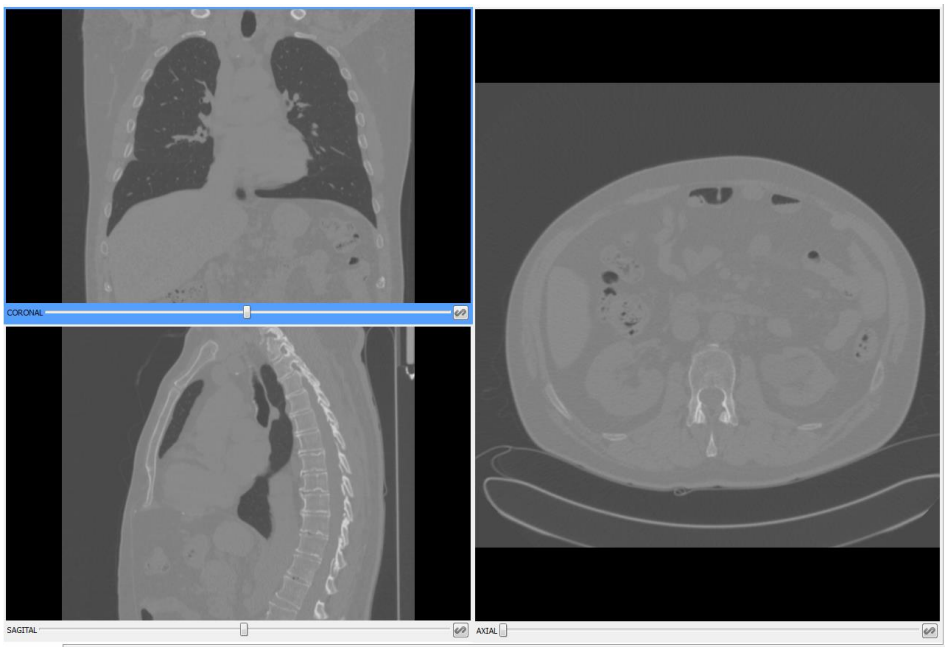
Examples:

Window

We have the following viewers layout, where all the viewers have the same series:

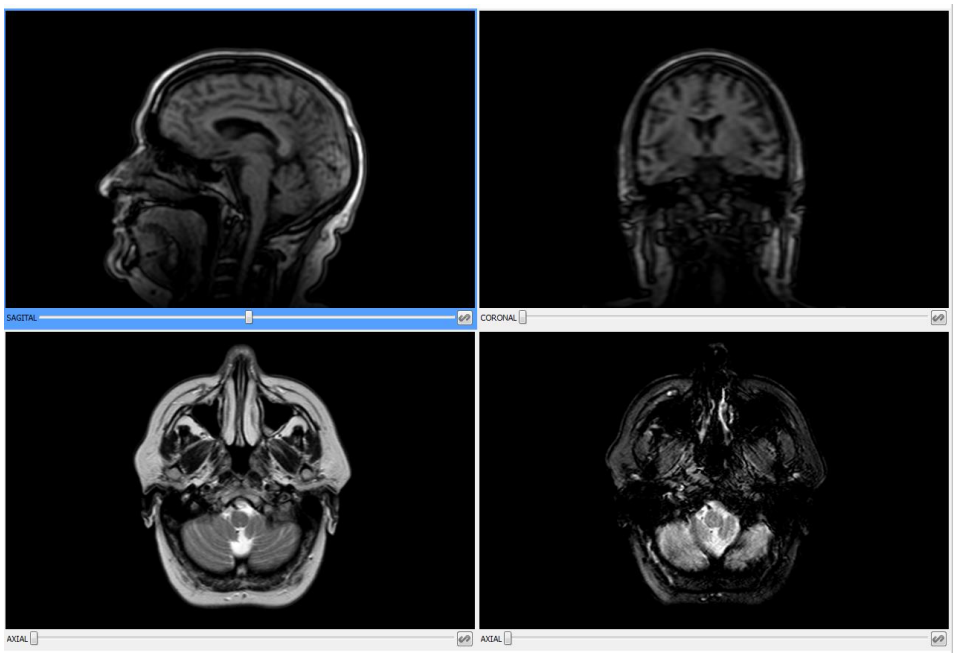


If we change the window in the viewer with coronal view using the window tool the window values are propagated to the other viewers.

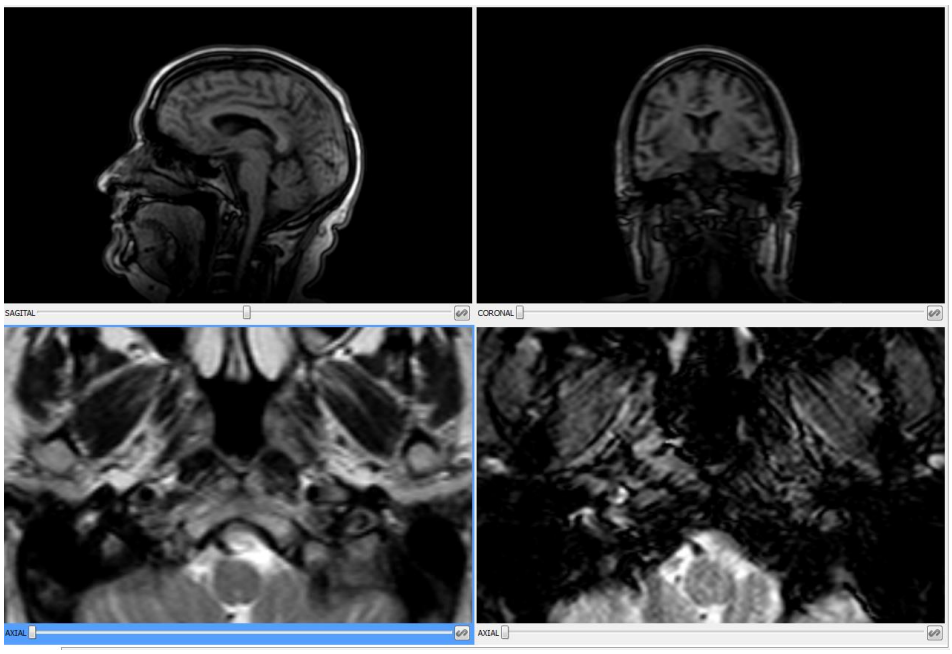


Zooming, scrolling and orientation

We have the following viewers layout:

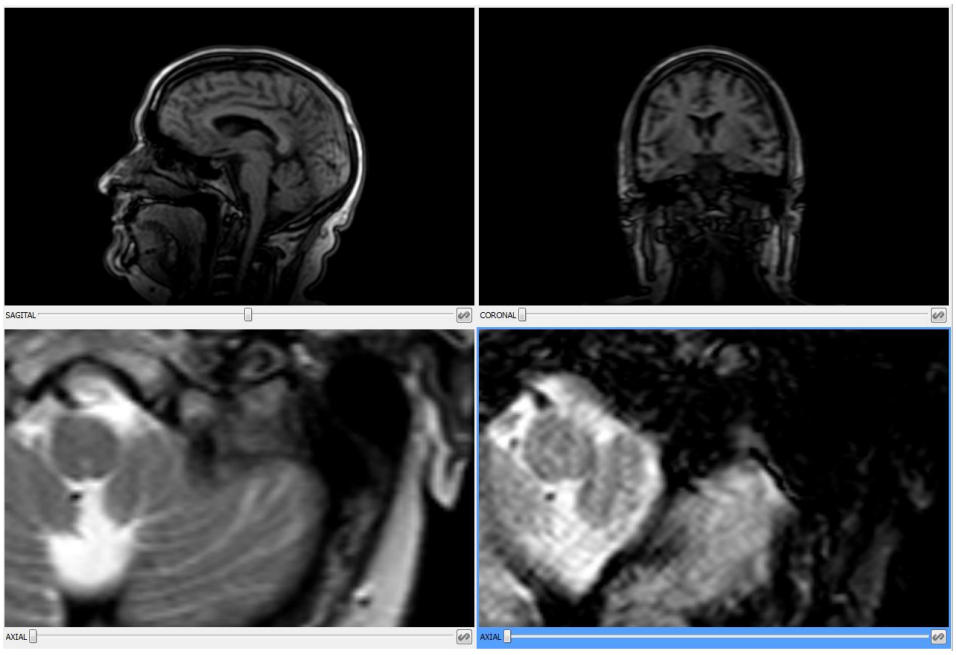


If we zoom in the axial viewer on the left, the action is absolutely propagated to the axial viewer on the right, so that the same object looks the same size in both viewers.

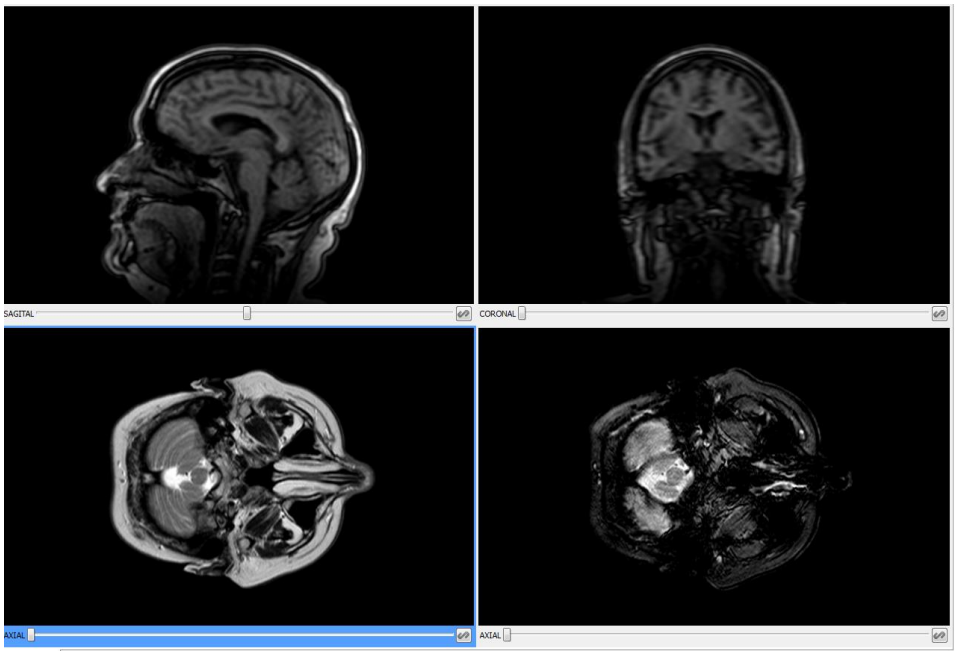


If we scroll the image in the axial viewer on the right, the new position is propagated to the axial viewer on the left, so that the same

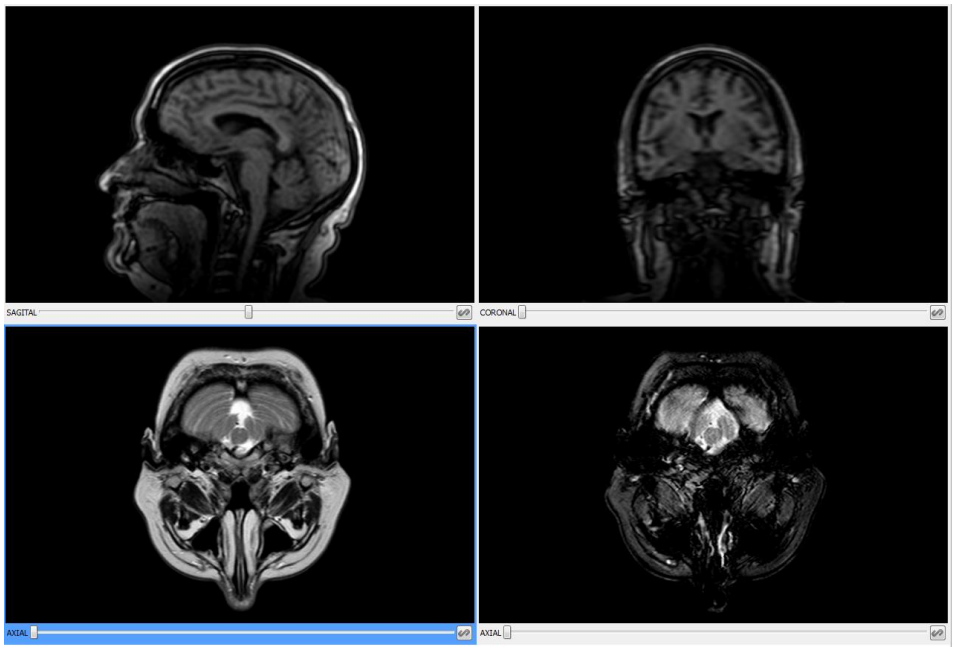
object is displayed in the same position in both viewers if they share the same coordinate system; if they have different coordinate systems there will be no propagation.



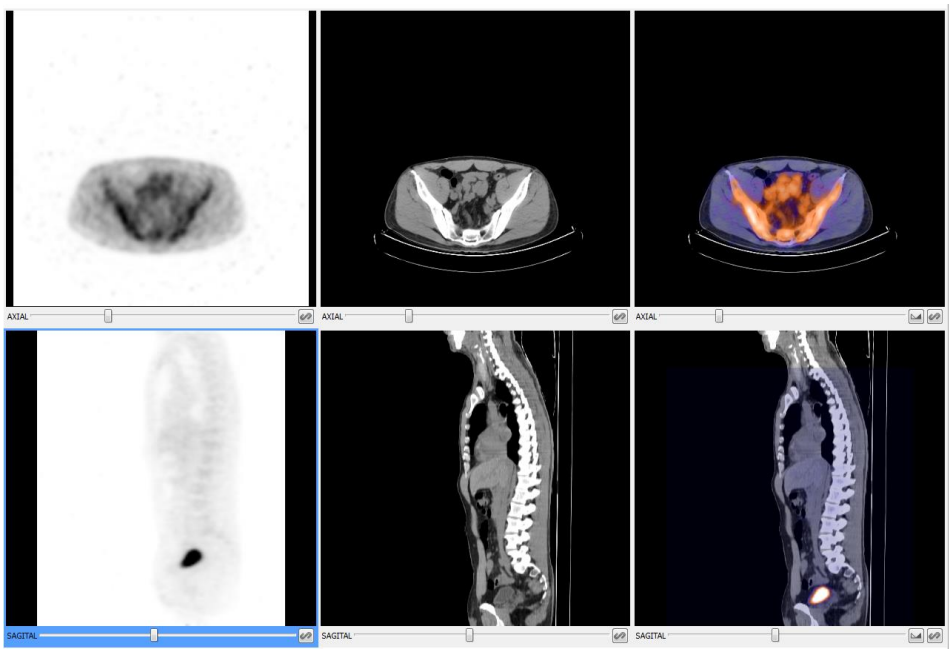
If we rotate the image in the axial viewer on the left, the same orientation is propagated to the axial viewer on the right.



If we vertically flip the image in the axial viewer on the left, the same flipping is propagated to the axial viewer on the right.

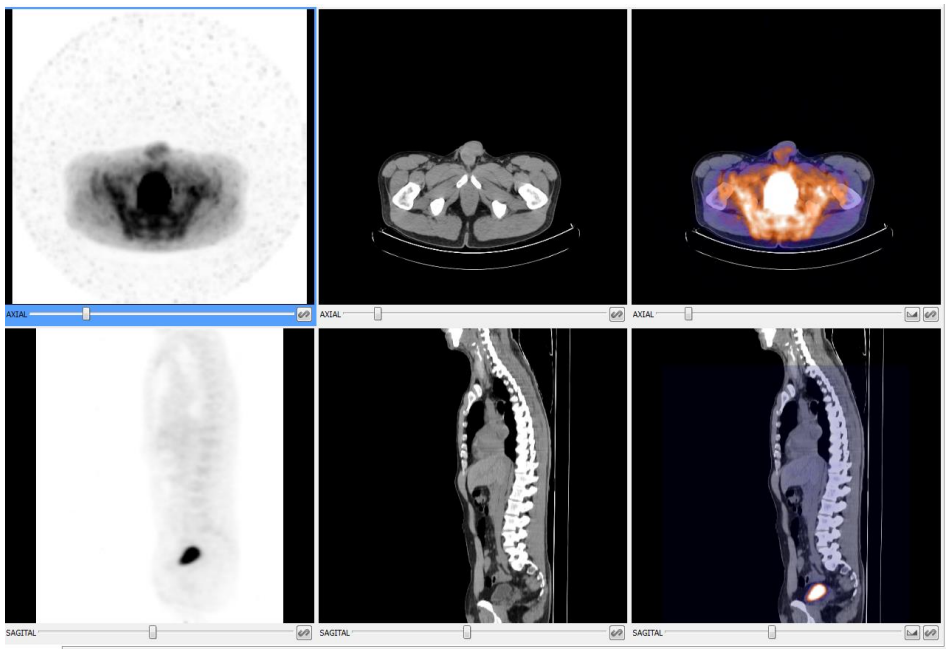


Thick slab
We have the following viewers layout:

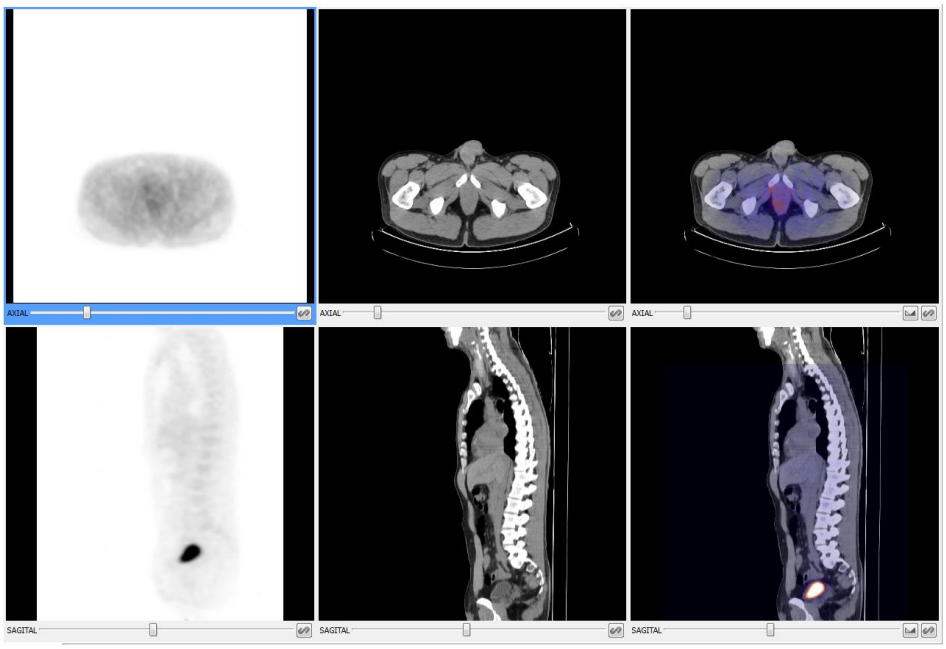


If we activate the thick slab with a MIP projection and we increase the thickness in the axial viewer with a PET series, it is propagated to the axial viewer with fusion applying the same projection and thickness to the secondary image (PET), but not to the

primary one (CT).



If we change the projection type to MinIP in the axial viewer with the PET series, it is propagated to the axial viewer with fusion by changing the projection of the secondary image (PET) to MinIP.



9.13. FUSION

The fusion function allows users to display a fused visualisation of PET-CT or SPECT-CT. A fusion can be loaded from the same patient studies menu, where all the possible fusion combinations are shown after the individual series. For a CT series to be fused with PET or SPECT one, the following conditions must be met:

- Both series have to share the same spatial identifier (Frame of Reference UID), that is, they are acquired in the same coordinate system.
- The CT series has to be contained in the space occupied by the PET or SPECT series, or vice versa.

In a PET-CT or SPECT-CT fusion, the CT series is seen as the main series over which the PET or SPECT series is superimposed as the secondary one, partially transparent and with a colour function. Both series are permanently synchronised to show the same region of space. If an area only available in the CT is explored, the PET or SPECT will not be displayed.
The contribution of each series to the final fused image is, by default, 50% of each series, but it can be adjusted through the Fusion balance tool, which is displayed at the bottom of the viewer, next to the manual synchronisation button. The current balance can be seen at all times in the lower-right corner of the viewer.

Some tools behave differently when a PET-CT or SPECT-CT fusion is displayed or when a single series is displayed:

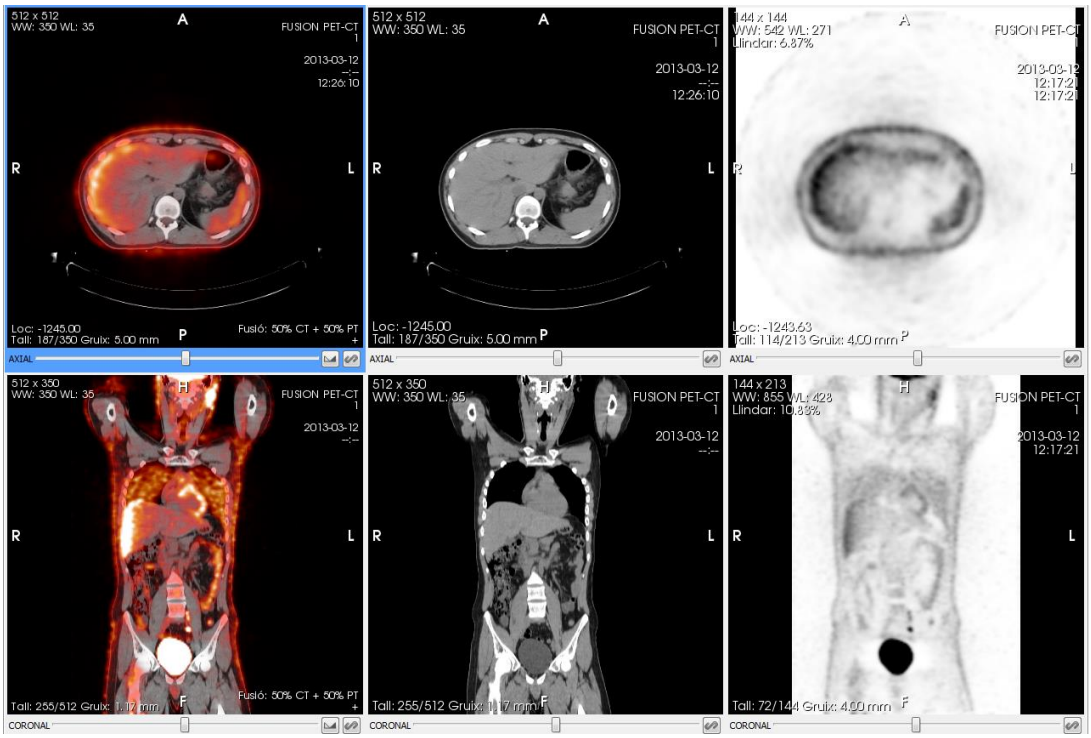
- The selection of a colour function changes the colour of the PET or SPECT series instead of that of the main series.
- The voxel information tool displays two values, one of each series. For the PET image, the SUV value will be displayed whenever possible.
- The ROI tools, in addition to the corresponding values of ROI of the CT image, show the maximum and average value of SUV, computed according to the selected method in the Starviewer configuration.

On the other hand, there are certain functionalities and tools that are not synchronised between the CT and PET or SPECT fused images, and must be applied separately. When we interact on the viewer with fusion, the change of window, the change of phase and the thick slab function are only applied to the main series, that is, the CT one. To interact on the secondary series, the PET or SPECT one, we need the propagation through a secondary viewer. We must have the PET or SPECT series loaded in another viewer; then, through this viewer and enabling the propagation, we can synchronise and change the phase, the window or the thick slab of the fused PET or SPECT series.

ACTION	TO APPLY ON CT IMAGE (FUSION)	TO APPLY ON PET IMAGE (FUSION)
Change of window Change of phase Thick Slab	Apply the action on the viewer with fusion	Apply the action on the secondary viewer with the same PET or SPECT series as the viewer with fusion. Propagation must be enabled.
Colour function	Not applicable	Select the colour function on the viewer with fusion

Finally, the other functionalities and tools do not depend on the content of the image, so that they behave exactly the same as with a simple visualisation.

Example:
In the following image we see an example of a PET-CT fusion where, from left to right, we have the fused image, the CT image and the PT image. At the top we see the axial projection, and at the bottom the coronal projection of the same series.

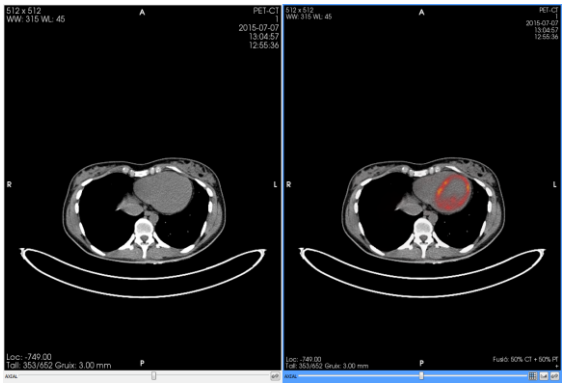


9.13.1. Fusion layout

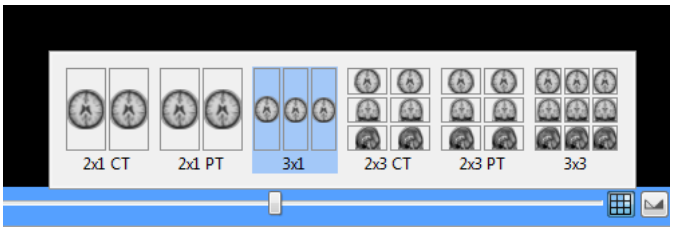
A custom fusion layout can be created by applying a regular layout and then assigning the desired series to each viewer, or by applying one of the default fusion layouts. In the viewers that visualise a fusion, a button is displayed in the lower-right corner that allows users to apply a fusion layout of 2x1, 3x1, 2x3 or 3x3 that replaces the current layout of the window.

Example:

1. We load a fusion into a viewer:



2. We apply a fusion layout:



3. Result:

9.14. FUSION BALANCE

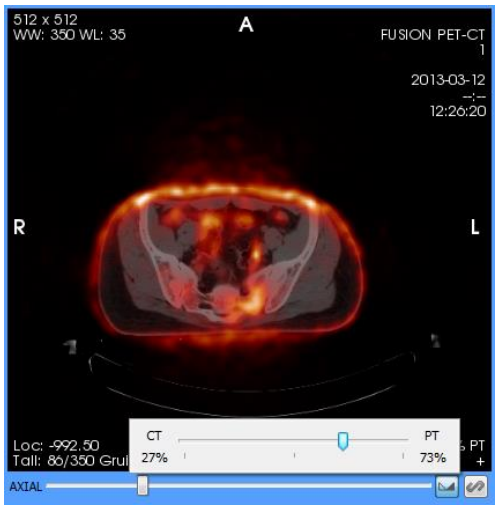
The icon is placed in the lower-right corner of each viewer:

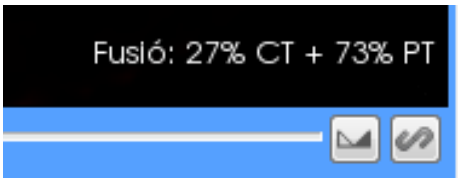
Function: It controls the percentage of fusion that each image contributes with to the final fused image. This allows us to see only the primary or secondary image (balance 100%-0% or 0%-100%, respectively), or that the contribution of one of the two images is greater with respect to the final image. By default, both fused images are balanced at 50%.

Mode of operation: Press the fusion balance button in a viewer with fused images. A slider will be displayed where we can balance the fusion percentage of each image. This button will only be displayed in viewers that have fused images.

Viewer where it is applied: In the selected viewer with fusion.

Example:
In the following example we see an example of how the slider is displayed, and of the annotations of the viewers that indicate at all times the current fusion balance of each image.





9.15. STANDARDISED UPTAKE VALUE (SUV) MEASUREMENT

The SUV is a value commonly used in the PET modality image analysis. It is commonly defined as the relationship of the radioactive concentration *C* of the tissue (Bq/ml) in instant *t*, and the injected activity, multiplied by a normalisation factor, such as the body weight.

The SUV is computed when we draw a ROI on a PET image or a fused PET-CT image. The SUV will be computed over the maximum and the average value of the drawn ROI with respect only to the values of the PET image, whether it is fused or not. There are three normalisation methods:
- Body weight
- Lean body mass
- Body surface area

The selection of which normalisation method is used can be configured in the 2D viewer configuration options. The method used by default will be that of body weight.

In the annotation of the measurement, a label will indicate the applied normalisation method:
- bw: Body weight
- lbm: Lean body mass
- bsa: Body surface area

Each measurement (maximum and average value) will be displayed together with the corresponding units, which may be the following according to the normalisation method:
- g/ml: For weight and lean body mass
- cm2/ml: For body surface area

9.15.1. Formulae

In this section we detail the formulae used, as well as the required parameters for is computation.

9.15.1.1. SUV

$$SUV = \frac{C(t)}{D_i \times d} \times N$$

PARAMETER	DESCRIPTION	UNIT
C(t)	Radioactive concentration	Bq/ml
D_i	Injected radioactive dose	Bq
d	Decay correction factor	
N	Normalisation factor chosen (weight, lean body mass or body surface area)	g: Weight and lean body mass cm^2: Body surface area

9.15.1.2. Decay correction factor

The injected dose D_i to compute the SUV is corrected by the radioactive decay factor between the injection time and the beginning

of the acquisition through the formula[1]

$$Decay\ factor = 2^{\left(\frac{-\Delta t}{T_{1/2}}\right)}$$

Where:
$T_{1/2}$: Half-life in seconds
The computation of Δt depends on the value of the Decay Correction (0054, 1102) DICOM attribute:
- If it is START: Δt will be the time interval between the administration of the dose and the acquisition of the image, in seconds
- If it is ADMIN: Δt will be 0

(*) The computation of the time interval will preferably be done with the Series Date (0008, 0021), Series Time (0008, 0031) and Radiopharmaceutical Start Date Time (0018, 1078) attributes. If they are not available, it would be done with the Series Time (0008, 0031) and Radiopharmaceutical Start Time (0018, 1072) attributes assuming that the administration and the acquisition of images are done the same day. If any of these attributes is missing, the computation of the SUV cannot be carried out.

9.15.1.3. Lean body mass

The lean body mass is computed with two formulae, Morgan's[2] or James'[3], depending on the patient sex:

Men (Morgan)

$$1.1 \times W - 120 \times \left(\frac{W}{H}\right)^2$$

Women (James)

$$1.07\ \times W - 148 \times \left(\frac{W}{H}\right)^2$$

Where:
W: Weight of the patient in kg.
H: Height of the patient in cm.

9.15.1.4. Body surface area

To obtain this value we use the formula from Du Bois[4]

$$BSA_{cm^2} = 71.84 \times H^{0.725} \times W^{0.425}$$

Where:
W: Weight of the patient in kg.
H: Height of the patient in cm.

9.15.1.5. Bibliographical sources

[1] "Radioactivitat." *Wikipedia: The Free Encyclopedia.* Wikimedia Foundation, Inc., December 8, 2013. Web. January 21, 2014. <http://ca.wikipedia.org/wiki/Radioactivitat#Llei_fonamental_de_la_desintegraci.C3.B3_radioactiva)>
[2] Morgan, Denis J. and Bray, Kelly M. Lean Body Mass as a Predictor of Drug Dosage: Implications for Drug Therapy. *Clinical Pharmacokinetics.* 1994, Vol. 26, 4, pp. 292-307.
[3] James, W. Philip T. *Research on obesity.* London: Her Majesty's Stationery Office, 1976. ISBN 0114500347.
[4] Du Bois, Delafield and Du Bois, Eugene F. A formula to estimate the approximate surface area if height and weight be known. *Archives of Internal Medicine.* 1916, Vol. 17, 6-2, pp. 863-871.

9.15.2. Required data

The following list presents the required DICOM attributes to compute the SUV. The lack of any of these attributes may cause the SUV value or some type of normalisation cannot be computed.

ATTRIBUTE	DESCRIPTION	NEEDED FOR
(0010,1030)	Patient's weight	Any SUV (bw, lbm, bsa)
(0010,1020)	Patient's height	lbm, bsa
(0010,1040)	Patient's sex	lbm
(0008,0021)	Series date	Decay correction factor
(0008,0031)	Series time	Decay correction factor
(0018,0078)	Date and time of dose administration	Decay correction factor
(0018,0072)	Time of dose administration	Decay correction factor
(0018,0075)	Half-life	Decay correction factor
(0018,0074)	Radioactive dose administered to the patient at the moment of administration	Injected radioactive dose
(0054,1001)	Units of pixel values	SUV. Depending on the units it will determine whether it can be computed or not.

9.15.2.1. Manufacturer exclusive attributes

Depending on the manufacturer of the modality we will need to use additional private attributes to compute the SUV.

MANUFACTURER	ATTRIBUTE	DESCRIPTION	NEEDED FOR
Philips	(7053,1009)	Pixel conversion factor	Converting pixel values to Bq/ml

9.16. MPR 2D VIEWER

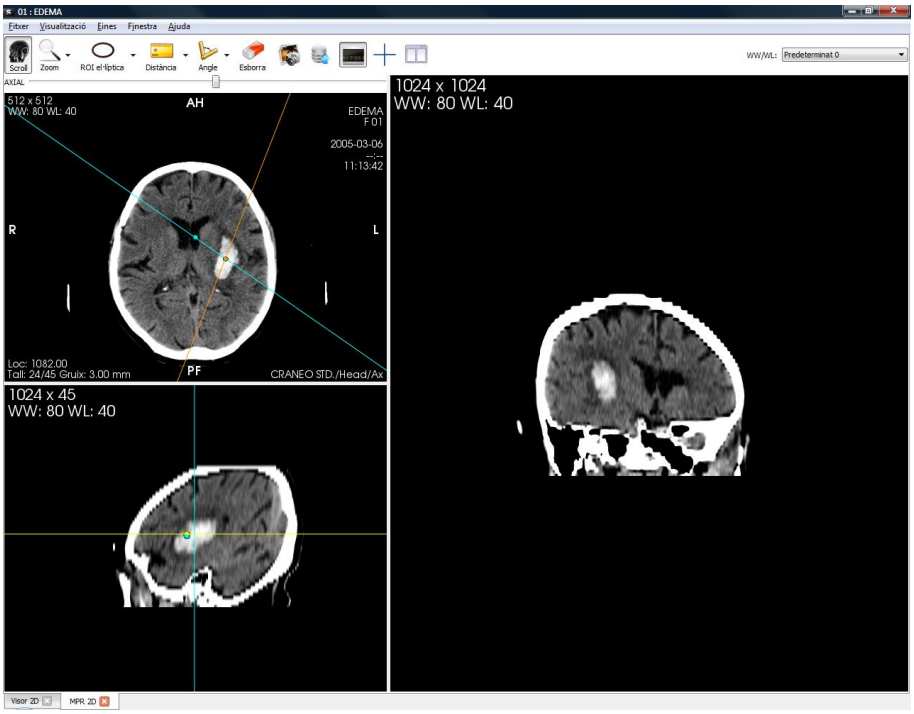
The MPR 2D viewer allows users to perform reconstructions of a series in any cutting plane, whether it is orthogonal or not.

It allows users to manipulate two additional cutting planes that form the resulting images, thus seeing images in acquisition planes that are different from those acquired by the modality.

To move the cutting planes, follow the instructions below:

OPTIONS	DESCRIPTION
Rotation	The cursor is placed on one of the lines and, while holding down the left button of the mouse, the

	mouse is moved in the direction where the cutting plane has to be rotated.
Movement	The cursor is placed on one of the lines and, while holding down the CONTROL key and the left button of the mouse, the mouse is moved in the direction where the cutting plane has to be moved.



The two spheres placed on the two lines indicate the rotation centre of the cutting planes.

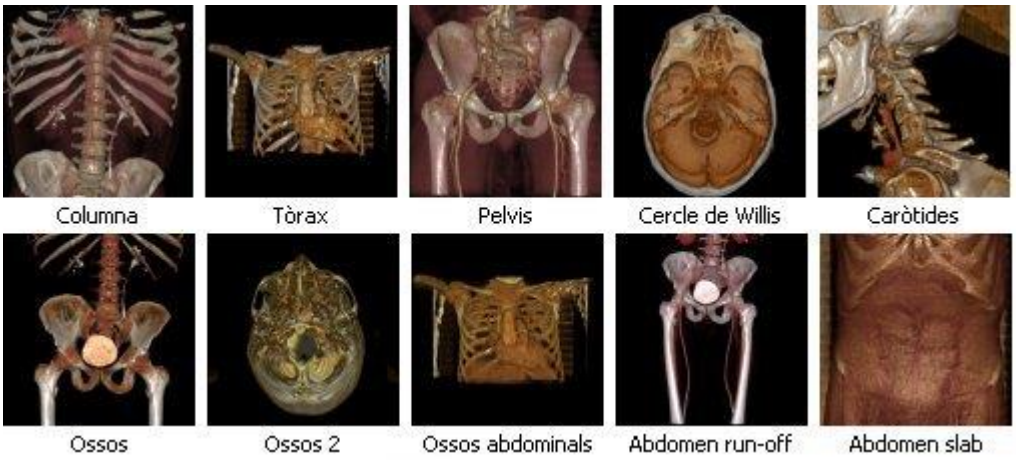
It also has different computation tools:
- Distances, TA-GT
- Angles
- Open angles
- Elliptic ROI, Polygonal ROI, Magic ROI, Circle (Regions of interest) to compute areas and average grey values
- Erasing performed measurements

And other tools:
- Scrolling
- Zooming
- Magnifying glass
- Erasing annotations
- Save a screenshot in image format (.jpg, .png, .bmp)
- Exporting to PACS
- Removing patient's information from the viewer
- Visualise the information of a single voxel (position, value)

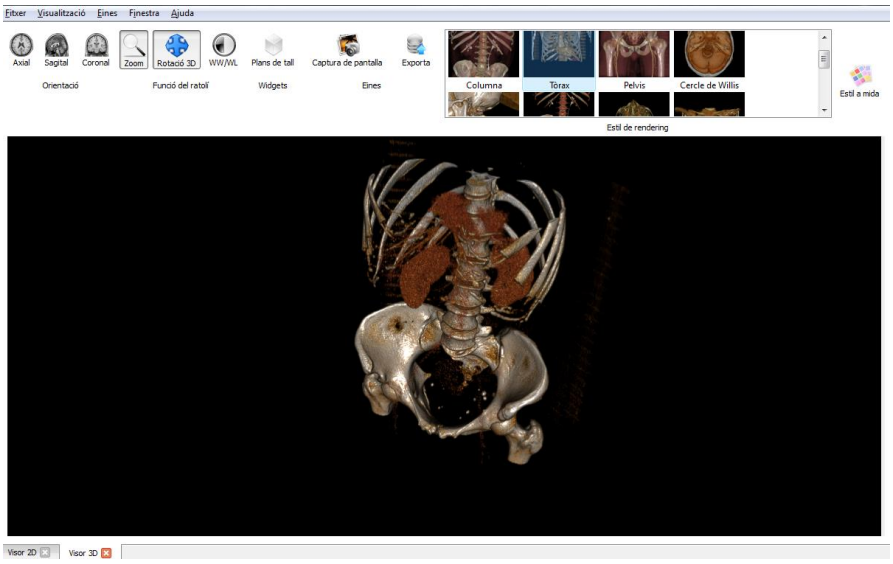
9.17. 3D VIEWER

It visualises all the information of the volume in 3D (volume rendering), with the option of adding or removing information or applying different colour functions (transfer function).

The defined transfer functions are the following ones:



To apply one of the previous functions, users just need to double-click on the corresponding image with the mouse.



It has different tools:

- Visualising the volume from the axial, sagittal or coronal view
- Zooming
- 3D rotation
- Changing the window
- Panning
- Trimming a volume (cutting planes)

- Screenshot
- Sending image to PACS

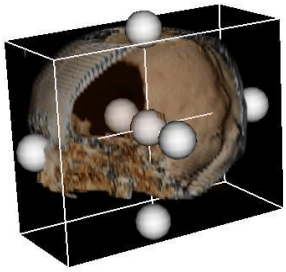
9.18. CUTTING PLANES

Function: It allows users to trim a volume within a 3D viewer to remove areas of the volume that users do not want to visualise. These areas are simply hidden, and the information is never deleted permanently.

Shortcut key to activate it: B

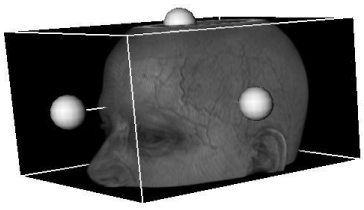
Mode of operation: It consists in a box that includes the volume. All the information that remains inside the box will be visible, and what remains outside will be trimmed, so that it will be non-visible information. The trimmed information is not lost, it simply remains hidden. Users can unhide it by modifying the size of the box so that it does not hide any part of the volume.

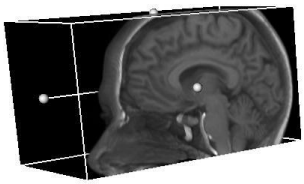
There are different actions that can be performed with this cutting box, which are explained below. To manipulate the different faces users have to use the spheres drawn on each face (6 faces – 6 spheres). Furthermore, there is a central sphere used to manipulate the whole box at the same time.



LEFT BUTTON

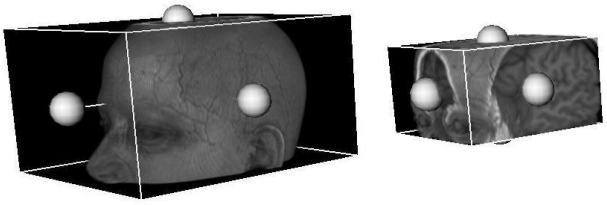
Cropping on one face: Hold down the LEFT BUTTON of the mouse on one of the spheres that are displayed when selecting the cutting planes tool, and move the mouse in the direction where the information has to be removed. Cuts can be made on each side of the white-framed box that is displayed around the whole volume.





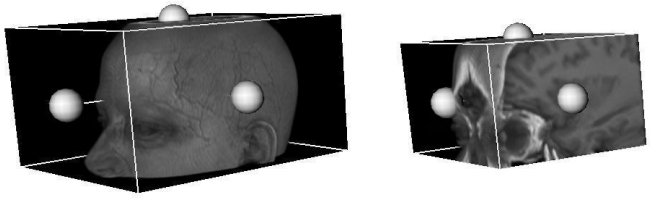
RIGHT BUTTON

Increasing/Reducing the cutting box: Hold down the RIGHT BUTTON of the mouse inside the box that includes the volume and move the mouse up (if increasing) or down (if reducing).



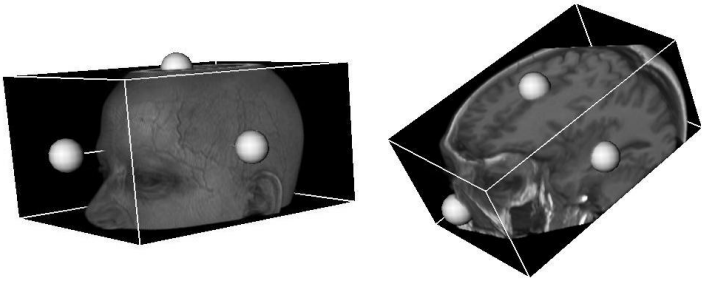
Moving the cutting box: Hold down the MIDDLE BUTTON of the mouse inside the box that includes the volume and move the mouse in the direction where the box has to be moved. This operation can also be done by selecting the central sphere of the container box.

MIDDLE BUTTON



Rotating the cutting box: Hold down the LEFT BUTTON of the mouse on one of the faces (without selecting any sphere) that are displayed when selecting the cutting planes tool, and move the mouse in the direction where the box has to be rotated.

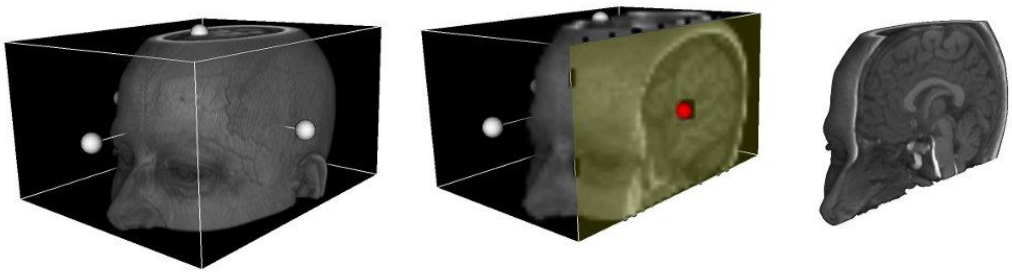
LEFT BUTTON



If we deactivate the cutting planes tool we will see the trimmed volume. To display all the information of the volume, we need to activate the tool again to display the box and increase it until we see the initial information.

Viewer where it is applied: 3D viewer.

Example:
The volume on the left shows the initial state, once the tool has been activated. Three of the spheres that belong to each face where the volume can be trimmed are displayed.
The volume in the middle shows the action of trimming one of the faces (the one that contains the red sphere).
The volume on the right shows the final state, after trimming one of the faces, and also after deactivating the cutting planes tool, thus hiding the box that includes the volume.



9.19. 3D ROTATION

Function: It allows users to rotate a volume within a 3D viewer to visualise it from different points of view.

Shortcut key to activate it: Q

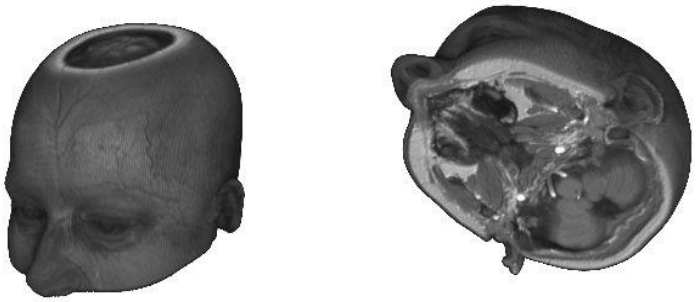
Mode of operation:

Mouse: Hold down the right button of the mouse while moving the mouse in the direction where the volume has to be rotated.
To rotate the axis **perpendicular** to the image, press the CONTROL key while rotating with the mouse.

Click the right button and move the mouse

Viewer where it is applied: 3D viewer.

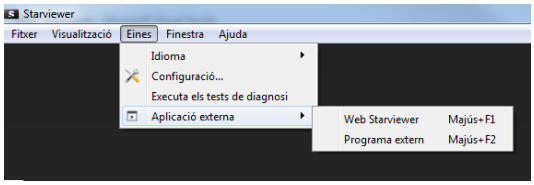
Example:
The volume on the left would be the initial position, and with a rotation we can see it from the point of view displayed in the volume on the right.



9.20. EXTERNAL APPLICATIONS

If external applications have been defined in the Starviewer configuration, these will be displayed in the Tools > External applications

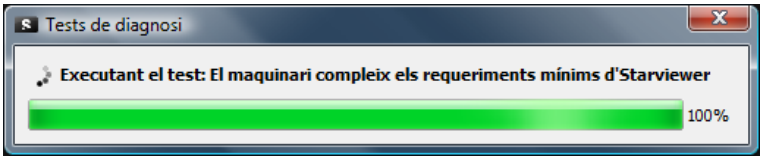
menu. For more information, check the section for the external applications configuration. When clicking on it, it is possible that some information (if this is how it has been configured) is transmitted from the active viewer to this application. In this way, the application that is opened can know the current working context and act properly (for example, by showing the same study opened in Starviewer).



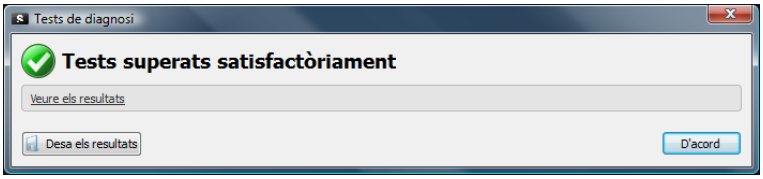
10. DIAGNOSIS TESTS

To access the diagnosis tests, users have to open the Tools > Run Diagnosis Tests menu.
Its functionality is to verify a series of system parameters and run a series of tests that allow users to evaluate whether the system is well configured and fulfils the recommended requirements, and to diagnose errors and possible problems.

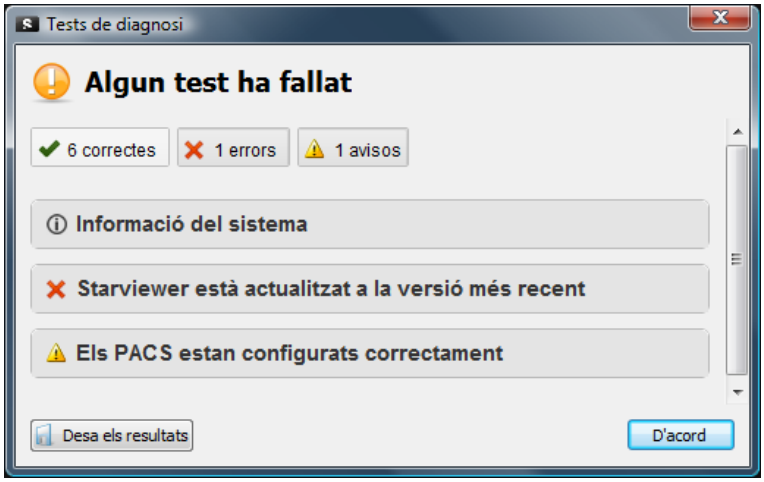
When selecting the menu, a window is opened that indicates that the tests are running, where the percentage of tests executed so far is displayed.



Once the test is completed, two types of messages may be displayed reporting the results.



If no test fails, a message is displayed indicating that all tests have worked correctly. We have the option to see which tests have been executed with the See results button, and also the option to save the results through the Save Results button. Press OK to close the window.



If, on the contrary, a test fails, a window is displayed with information of the system, reporting the errors found, warnings to be taken into account, and tests that have worked correctly. By default, the errors and warnings are displayed. To see also those that have worked correctly, users must select the succeeded button; to hide them, use the same procedure.

By selecting ICON 1, the system information is displayed.

ICON 1

ICON 2

ICON 3

ICON 4

Each of the rest of messages corresponds to a specific type: Succeeded, Error or Warning.

The correct results, represented with ICON 2, simply indicate that it has been executed correctly and that the results are the expected ones.

The warnings, represented with ICON 3, indicate that something is not well configured or that the application may not work as expected, but users can still use it. It is recommended that no warning message is displayed.

If there is an error, it is indicated with ICON 4. If we get an error, it may be that the test could not be executed or that the result of the test is incorrect.

If the result is an error or a warning, we can open it to see the detailed description of the problem by clicking on the header of the problem. It also allows us to see a solution to solve the problem and, therefore, to have the application well configured.

Finally, at the bottom-left corner of the window, we have the option Save Results, which allows us to save the results in a text file and send them by email as an attached document to support@starviewer.udg.edu in order to get support for solving the problem.
By pressing the OK button, the window is closed.

11. DICOM PRINTING

Extension that allows users to print images in DICOM format in DICOM printers.
To print an image, users have to open the Visualization menu and choose the option DICOM Print.

In this window, the printing preferences are displayed on the left, and the image to be printed on the right. The viewer allows users to change the image, the series and the patient study by using the patient menu (right button). It also allows users to change the window of the images to be printed by using the Changing the window tool and the Selection of default windows tool. If we want to restore the image to the initial image, we have to press the restoration button (ICON 1).

ICON 1

The panel on the left allows users to choose different parameters such as:
- Printer (see section Adding a printer for more information)
- Number of copies
- Film size
- Film type
- Orientation
- Printing grid size
- Images to be printed: current, or range of images (see section Selecting images to print for more information)

11.1. SELECTING IMAGES TO PRINT

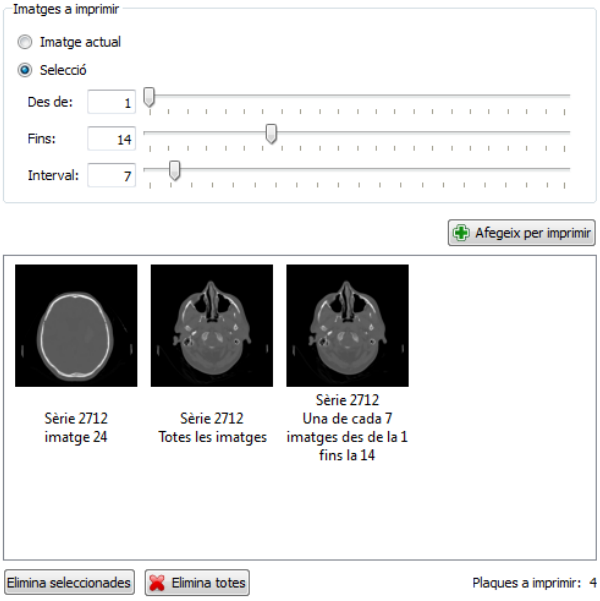
With the printing tool users can print more than one image from different series of the same film. To select the images to be printed, the following steps will be followed as many times as necessary until all images in the printing list are obtained:

1. Select the series that contains the images in the viewer on the right.
2. Select the images to be printed through the section Images to print.
   Images can be selected in different ways:
   - Current Image: It adds only the current image to the list of images to be printed.
   - Selection: It selects the images to be printed according to the chosen criteria (see example below):
     - Interval: Image leap (e.g. Printing 1 image out of 7).
     - From: Initial image of the selection to be added to the list.
     - To: Final image of the list to be added to the list.
3. Select Add to print.

Finally, once the list of images is created, select the Print option.

If any of the images added to the list has to be removed, select the element of the list (image) and click Remove selection. It is also possible to remove all of them by selecting the Clear option.

Example about how to select images:



In this example we have decided to print the current image, which corresponds to image 24, we have also decided to print all the images from the series, and finally we have added to the printing list images from 1 to 14 with a leap of 7 images, so that images 1 and 8 are added to the list. Total number of films that will be printed: 4, since we have chosen that there are 12 images for each film.

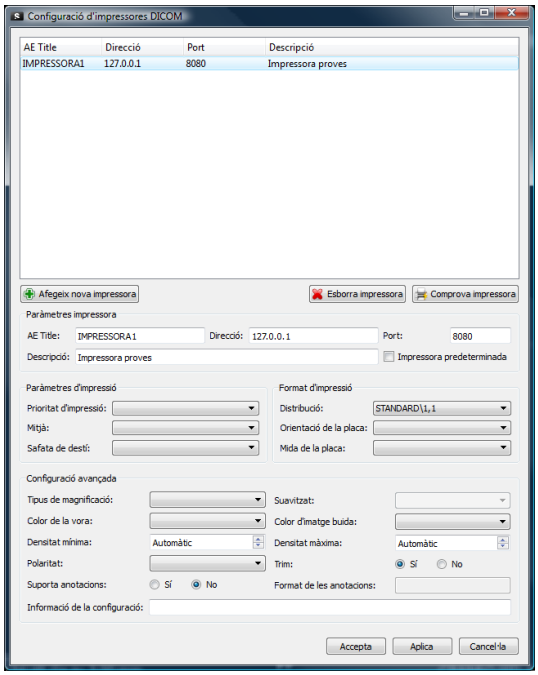
11.2. ADDING A PRINTER

ICON 1

ICON 1

ICON 2

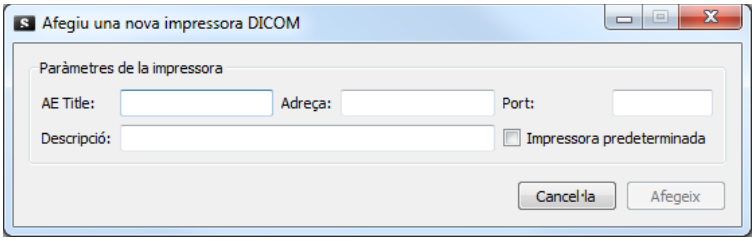
To add a printer, users have to select ICON 1 from the DICOM Print extension, and the following window is displayed:



Different actions can be carried out:

- Add New Printer: Click ICON 2 to add a new printer.

ICON 2



OPTIONS	DESCRIPTION
AE Title	Name of the printer
Hostname	IP address of the printer
Port	Connection port with the printer
Description	Short description of the printer
Default printer	Whether it is or not the printer configured by default (only one printer can be configured by default)

- Remove Printer: To remove a printer from the list click ICON 1.

- Test Printer: Click ICON 2 to check the connection with the printer. If the test fails, it may be that the printer is not available, or that some of the configuration parameters such as the AE Title or the port are incorrect.

To make an advanced printer configuration, check the administrator's manual of the application.

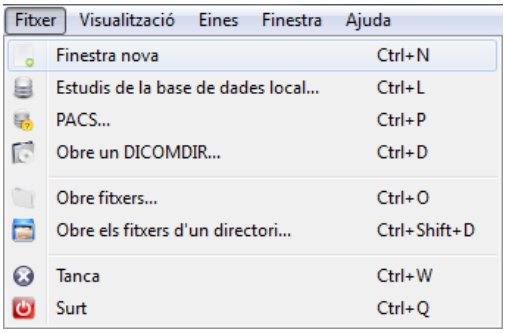
12. THE MENUS

From the menu bar, we find different options:

- File menu
- Visualisation menu
- Tools menu
- Window menu
- Help menu

12.1. FILE MENU

Menu from where users can manage the data sources to be consulted and perform a basic management of the application.



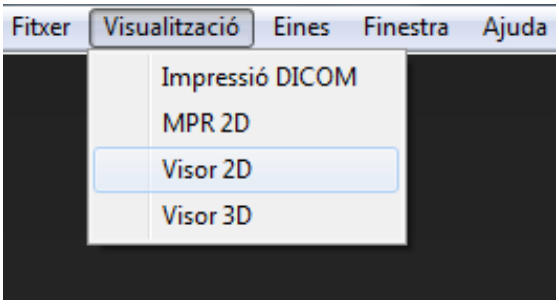
OPTIONS	DESCRIPTION
New Window	It allows users to open a new instance of Starviewer. Shortcut keys: CONTROL+N
Local Database Studies...	It allows users to access and open studies that been retrieved to the local database (to the computer). Shortcut keys: CONTROL+L
PACS...	It allows users to access a PACS, retrieve and visualise studies. Shortcut keys: CONTROL+P
Open DICOMDIR...	It allows users to open files from patients that are stored in another place (user's folder, CD, DVD, external drive, USB...). Shortcut keys: CONTROL+D
Open Files...	It allows users to open studies that are not in DICOM format, such as an MHD... Shortcut keys: CONTROL+O
Open Files from a Directory...	It opens all files that are in the same folder. Shortcut keys: CONTROL+SHIFT+D
Close	It closes the current tab. Shortcut keys: CONTROL+W
Exit	It closes the application. Shortcut keys: CONTROL+Q

12.2. VISUALISATION MENU

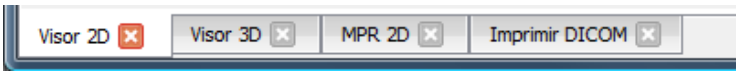
Once a study has been opened, different viewer types to display the patient's studies can be chosen, or extensions to use different

resources:

- 2D Viewer (by default when a study is chosen)
- MPR 2D Viewer
- 3D Viewer
- DICOM Print

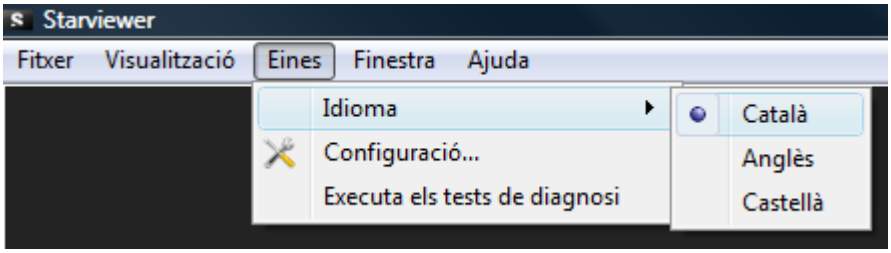


To choose one of the viewers, users only need to select the element within the Visualisation menu. A new tab is displayed with the new selected viewer.



12.3. TOOLS MENU

From the Tools menu users can select the language, and also access to different configurations such as PACS, Database, etc.



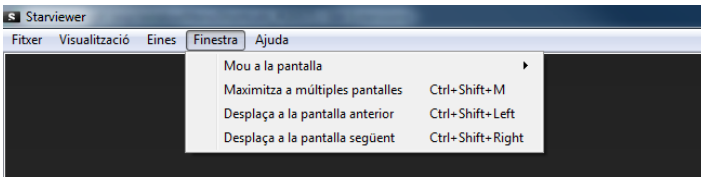
From the Language option there are three possibilities: Catalan, English or Spanish. Each time the language is changed, the application must be restarted in order for the changes to take effect.

From the Configuration menu different elements can be configured:
- 2D Viewer
- 2D Viewer Layout
- PACS
- Local Database
- RIS Listener
- DICOMDIR

Finally, the tools menu contains a tool to verify the state of the system to check that the application works correctly. See section Diagnosis tests.

12.4. WINDOW MENU

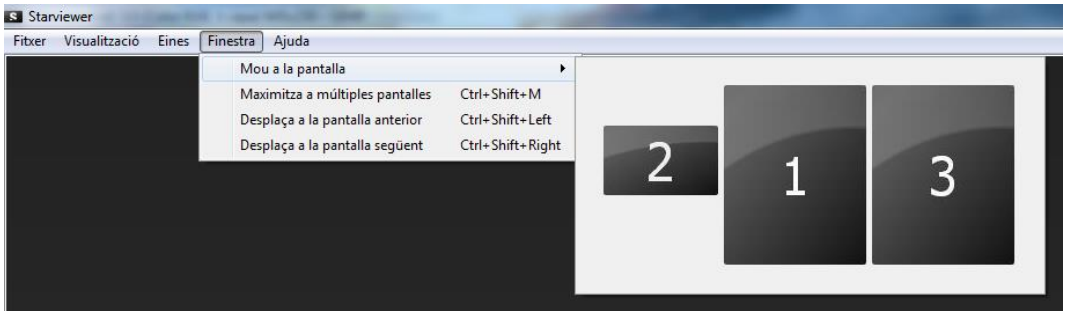
The Window menu allows users to choose four options as shown in the following image:



Below we detail each of these functions.

12.4.1. Move to screen

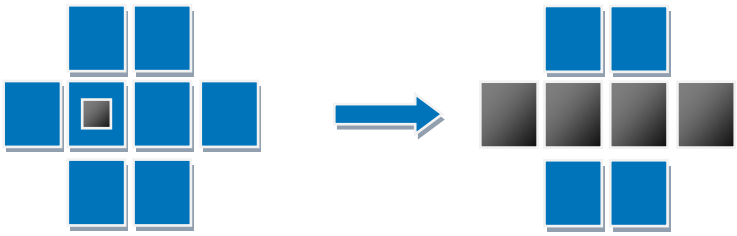
It allows users to move the window of the application to a specific screen. The menu shows the current screen configuration and, by selecting the desired screen, the application is placed on it.



12.4.2. Maximise to multiple screens

Shortcut: CONTROL+SHIFT+M

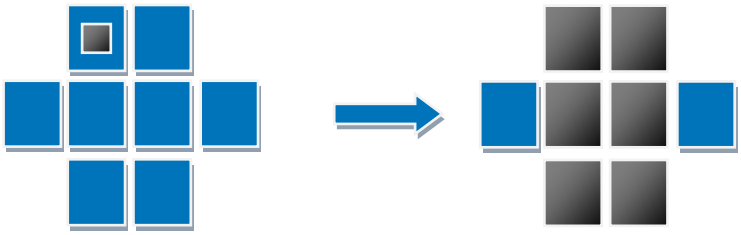
The application window is maximised to occupy the maximum number of screens as long as the rectangular shape of the window can be maintained. The horizontal expansion is first considered, and then the vertical expansion.



In the previous drawing the application window and the screen where it is located are displayed in black, while the rest of screens are displayed in blue. If we maximise, it is horizontally expanded as much as possible.

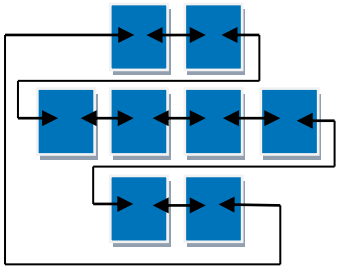
In the following drawing, the application window and the screen where it is located are also displayed in black, and the same for the rest of the screens, which are displayed in blue. In this case, if we maximise it is vertically expanded as much as possible, but it is

also horizontally expanded to the maximum.



12.4.3. Move to adjacent screen

With the Move to previous screen and Move to next screen options we can move the window to the previous and next screens in a sequential and circular way, as it is shown in the following drawing.



12.4.3.1. Move to previous screen

Shortcut: CONTROL+SHIFT+←

When it reaches the leftmost screen, if there are no more screens, it is placed to the rightmost screen that is below the current one. If there are no more screens below, it is placed to the topmost and rightmost screen.

12.4.3.2. Move to next screen

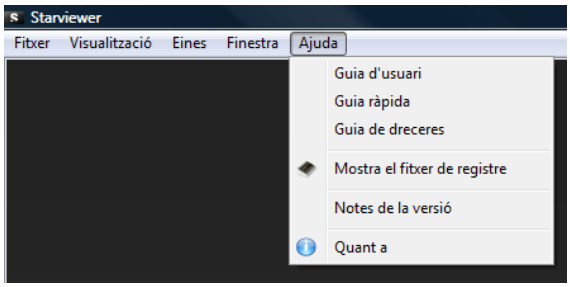
Shortcut: CONTROL+SHIFT+→

When it reaches the rightmost screen, if there are no more screens, it is placed to the leftmost screen that is below the current one. If there are no more screens below, it is placed to the topmost and leftmost screen.

12.5. HELP MENU

From the Help, we can access this user manual, a quick start guide of the application, the shortcuts guide and the log file of the application (it shows different information related to the activity of the application, and also whether an error has been detected).

It also allows us to check general information of the application, such as the platform version.



To show this user manual, select the User Guide option. A .pdf file is opened.

To show a quick start guide of the application, select the Quick Start Guide option. A .pdf file is opened.

To show the shortcuts guide, select the Shortcuts Guide option. A .pdf file is opened with a diagram of the shortcuts. This diagram can also be found in this manual in the section Shortcuts.

To show the log file, select the Show Log File option, and a window is displayed with a list of information that the application has been saving.

Updates, improvements, corrections... of the current version can be checked with the Release Notes option.

To show general information of the platform, choose the About option. It shows the version of the application, the support and contact address, the web page...

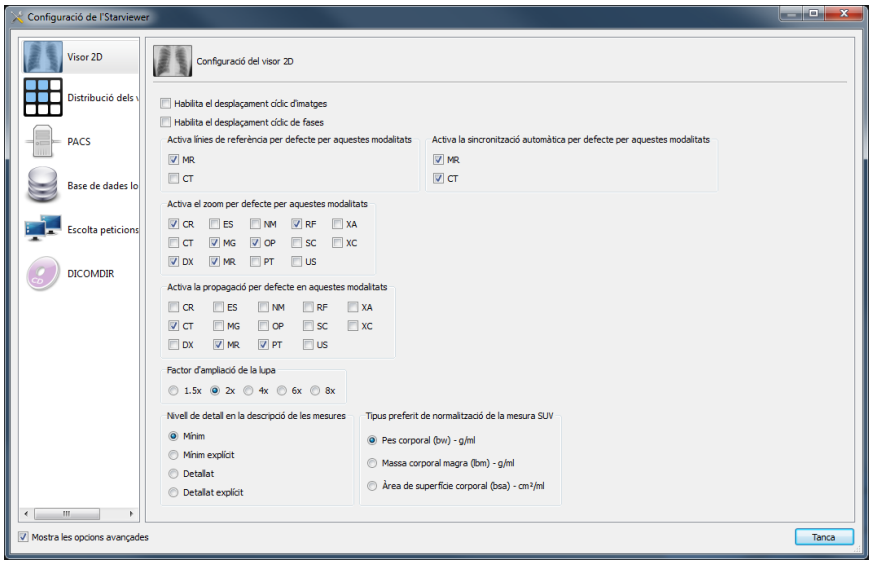
13. CONFIGURATIONS

13.1. 2D VIEWER CONFIGURATION

To access the 2D viewer configuration, users have to access the Tools > Configuration menu and select the 2D Viewer ICON 1.

ICON 1

The 2D viewer configuration window is displayed:

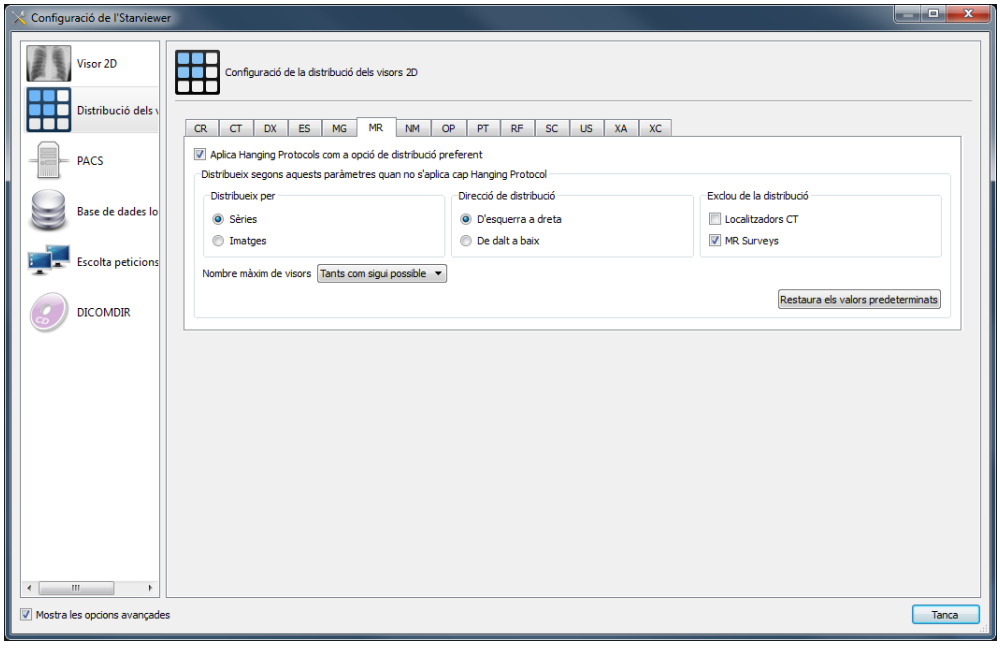


Different parameters can be configured:

OPTIONS	DESCRIPTION
Enable slice scroll loop	It modifies the behaviour of the Scrolling tool so that the images scrolling is continuous in both directions. From the last image we can advance to the first one, and from the first one we can go backwards to the last one. This option is disabled by default.
Enable phase scroll loop	It modifies the behaviour of the Scrolling tool so that the scrolling between phases is continuous in both directions. From the last phase we can advance to the first one, and from the first one we can go backwards to the last one. This option is disabled by default.
Enable reference lines by default for these modalities	It configures the Reference lines tool to be enabled by default when opening studies of the selected modalities: MR and/or CT. It is enabled by default for the MR modality.
Enable automatic synchronisation by default for these modalities	It configures the Automatic synchronisation tool to be enabled by default when opening studies of the selected modalities: MR and/or CT. It is

	enabled by default for the MR modality.
Enable zoom by default for these modalities	It configures the Zooming tool to be enabled by default in the left button of the mouse when opening studies of the selected modalities. For the modalities that are not selected, the tool assigned to left button will be the Scrolling. By default, the following modalities are assigned: CR, DX, MG, MR and RF.
Enable propagation by default on these modalities	It configures the Propagation tool to be enabled by default when opening studies of the selected modalities. By default, the following modalities are assigned: CT, MR and PT.
Magnifying glass tool zoom factor	It allows users to choose which is the zoom factor of the image when the Magnifying glass tool is being used.
Measurements description verbosity	It allows users to choose the verbosity for measurements that may give more than one result according to the present image attributes. For more details, see section Measurements verbosity. By default, the verbosity will be Minimal.
Preferred SUV measurement normalisation type	It allows users to choose the normalisation factor used in SUV measurements. By default it will be Body weight. For more details about the SUV measurements, see section Standardised Uptake Value (SUV) measurement.

13.2. 2D VIEWERS LAYOUT CONFIGURATION



From this configuration section we can configure the studies layout options. Each study modality can be configured independently and their options are found in the corresponding tab. The parameters we can configure for each modality are the following:

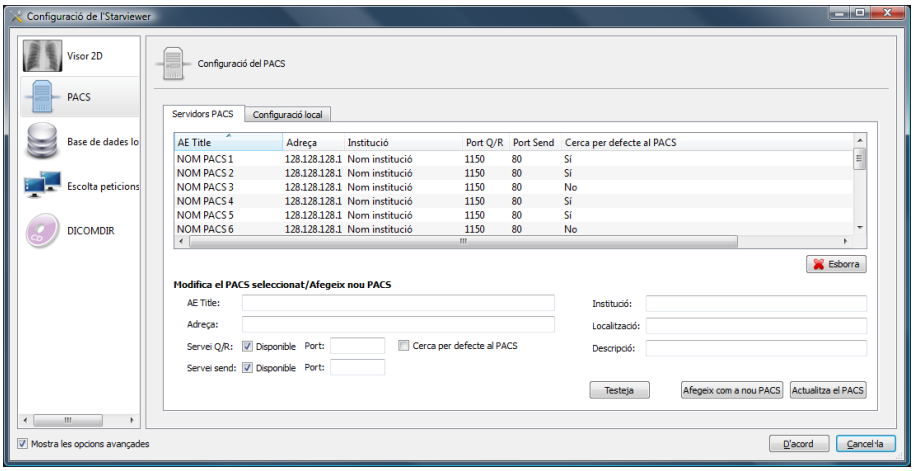
OPTIONS	DESCRIPTION
Apply Hanging Protocols as preferential layout option	With this option selected, if there are Hanging Protocols available for the study of the indicated modality, the best possible Hanging Protocol will be applied as preferential option when loading a study. If there are no candidate Hanging Protocols, the layout criteria indicated in the lower box will be applied (Layout according to these parameters when no Hanging Protocol is applied). By default, the modalities in which the application of Hanging Protocols will be preferential are CR, CT, MG, MR and US.
Layout according to these parameters when no Hanging Protocol is applied	In this box we can define the parameters of the automatic layout for the selected modality.
Layout by	It configures whether the assignment sequence in each viewer is made by series or by images.
Layout direction	It configures the direction in which the series or the images will be assigned in each viewer within the layout.
Exclude from layout	It configures which images and/or series of the study are excluded in the assignment. Useful for not showing images or series that are not relevant.
Maximum number of viewers	Maximum number of viewers that will be created in the layout, regardless of the total number of images or series. It allows us to set a number between 2 and 48 viewers, or the possibility to create as many viewers as possible (up to a maximum of 48), adapting to the content of the study.
Restore defaults	It restores the default values of the selected modality.

13.3. PACS CONFIGURATION

Within the configuration of a PACS we find two tabs: PACS Servers and Local Configuration:

13.3.1. PACS servers

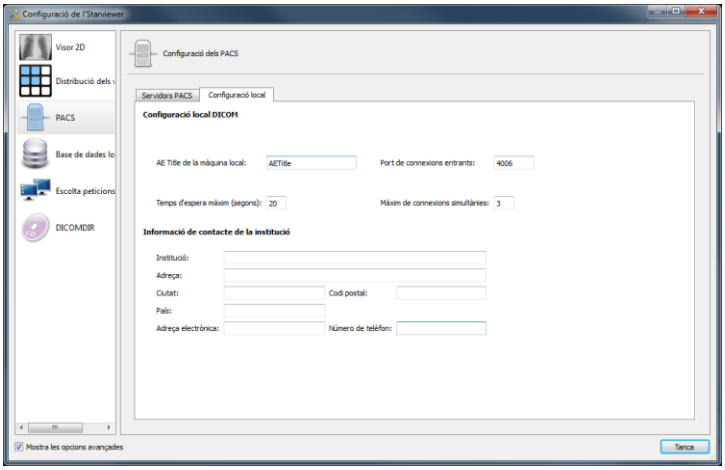
The configuration of the PACS servers allows us to add, delete and test the different PACS queried by the application.



OPTIONS	DESCRIPTION
Add a server	Fill the fields AE Title, Address (IP), Ports, Institution, Location, Description... and press the Add as New PACS button. If the Default Query PACS is selected, the PACS selected with this option will always be queried when performing any search.
Delete a server	Select an element of the list and select the Delete option.
Update a server	Select an element of the list, change the fields to be updated: AE Title, Address (IP), Ports, Institution, Location, Description... and press the Update PACS button.
Test a server	Select an element of the list of PACS, and select the Test option.

13.3.2. Local Configuration

It allows users to configure the machine parameters required for the communication with the different PACS servers.



OPTIONS	DESCRIPTION

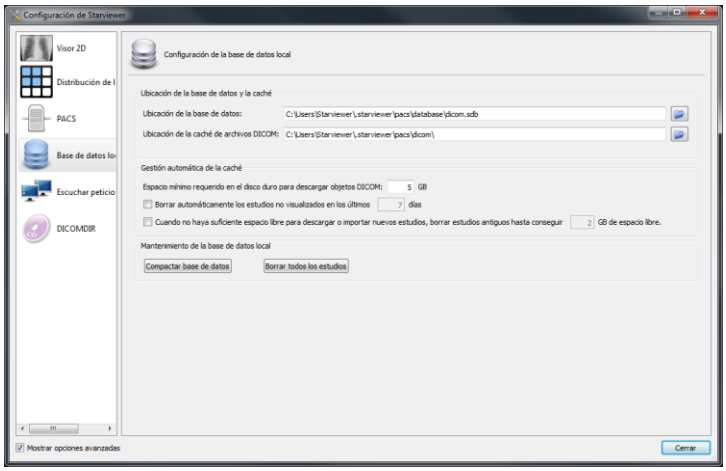
Local machine AE Title	AE Title that the machine must have.
Incoming connections port	Communication port of the machine for DICOM incoming connections.
Maximum seconds for timeout	Maximum waiting time for PACS responses.
Maximum simultaneous connections	Maximum number of connections that may exist at the same time, either by making a query or by saving a study in the PACS. We can only have a single simultaneous retrieval.
Institution contact information	It allows users to add information about the institution. This institution information will be displayed in the readme.txt file in the DICOMDIR that are created.

13.4. LOCAL DATABASE CONFIGURATION

To access the local database configuration, users have to open the Tools > Configuration menu and select the local database ICON 1.

ICON 1

The local database configuration window is displayed:



Different parameters can be configured:

OPTIONS	DESCRIPTION
Database location	File where the local database is stored.
DICOM files cache location	Directory where the images of the local database studies are stored.
Minimum space required in hard disk to retrieve DICOM objects	It allows users to define the minimum space necessary for the system to retrieve DICOM objects; if there is not enough free space the application does not allow users to retrieve studies. (See table footnote)
Automatically delete studies not viewed in the last X days	Each time Starviewer is opened, it deletes the studies that have not been visualised during the last indicated days to free disk space automatically.
When there is not enough free space to retrieve or import new studies, delete old studies until XGB of free space are obtained	When the minimum space in hard disk to retrieve DICOM objects is smaller than the one indicated, the studies that have not been visualised for a longer time will be automatically deleted until XGB of free space in hard disk are reached.

(*) If when new studies are imported or retrieved to the system there is less free space than the one indicated by the Minimum space required in hard disk to retrieve DICOM objects parameter, the application deletes the studies that have not been visualised for a longer time until the XGB indicated by the When there is not enough free space... option are reached.

Maintenance of the local database can also be performed:

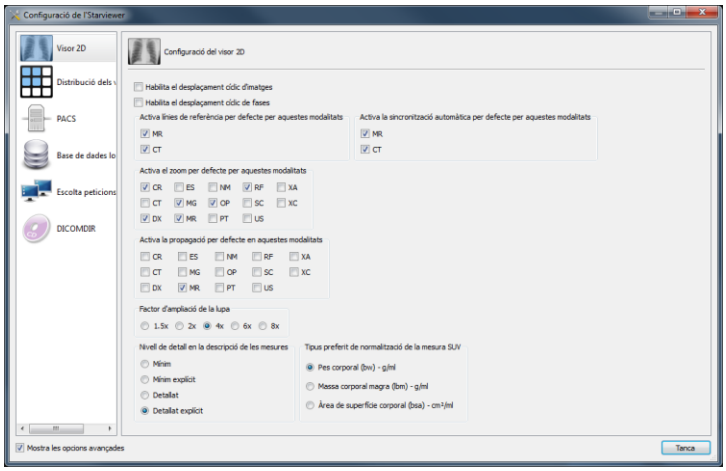
OPTIONS	DESCRIPTION
Create database	It creates the database indicated in the database location again.
Compact database	It compacts the current database, that is, it reduces its size and makes the local queries faster.
Delete all studies	It deletes all studies that are stored locally.

13.5. RIS CONFIGURATION

To configure the RIS parameters, users have to open the Tools > Configuration menu and select the RIS Listener option (ICON 1).

ICON 1

A configuration option will be displayed as the one shown below:



Users can enable or disable the option for the Starviewer to be integrated with a RIS.

To enable it, users have to select the Listen to RIS requests on port option and configure the port through which the RIS will send the retrieval requests.

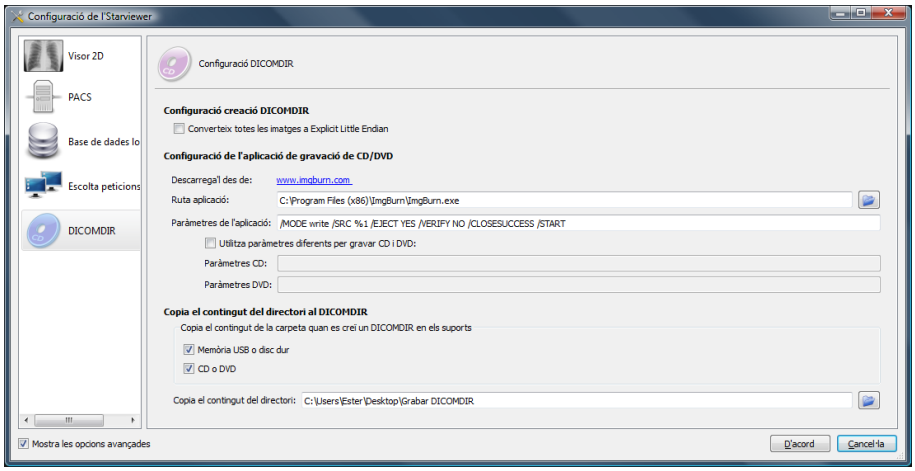
It is possible to indicate that a study requested by the RIS is automatically displayed once it has been retrieved by checking the Automatically view the studies upon reception option.

13.6. DICOMDIR CONFIGURATION

To access the DICOMDIR configuration, users have to open the Tools > Configuration menu and select the DICOMDIR option (ICON 1).

ICON 1

The configuration window is displayed:



Different parameters can be configured:

13.6.1. DICOMDIR creation configuration

OPTIONS	DESCRIPTION
Convert all images to Explicit Little Endian	If enabled, it automatically converts all images to Explicit Little Endian when creating a DICOMDIR.

13.6.2. CD/DVD burning application configuration

OPTIONS	DESCRIPTION
Application path	It is the directory where the program to burn CD and DVD is installed.
Application parameters	They are the parameters that allow users to configure the CD and DVD burning application.

13.6.3. Copy folder content to DICOMDIR

Starviewer can be configured so that each time a DICOMDIR is created it automatically adds the content of a folder (files and subfolders). Users can choose in which case the folder content has to be copied: when creating a USB

and/or when creating a CD/DVD. The path of the folder to be copied has to be indicated in Folder path to copy content, and the application has to be restarted.

13.7. EXTERNAL APPLICATIONS CONFIGURATION

To access the external applications configuration, users have to open the Tools > Configuration menu and select the External application option (ICON 1).

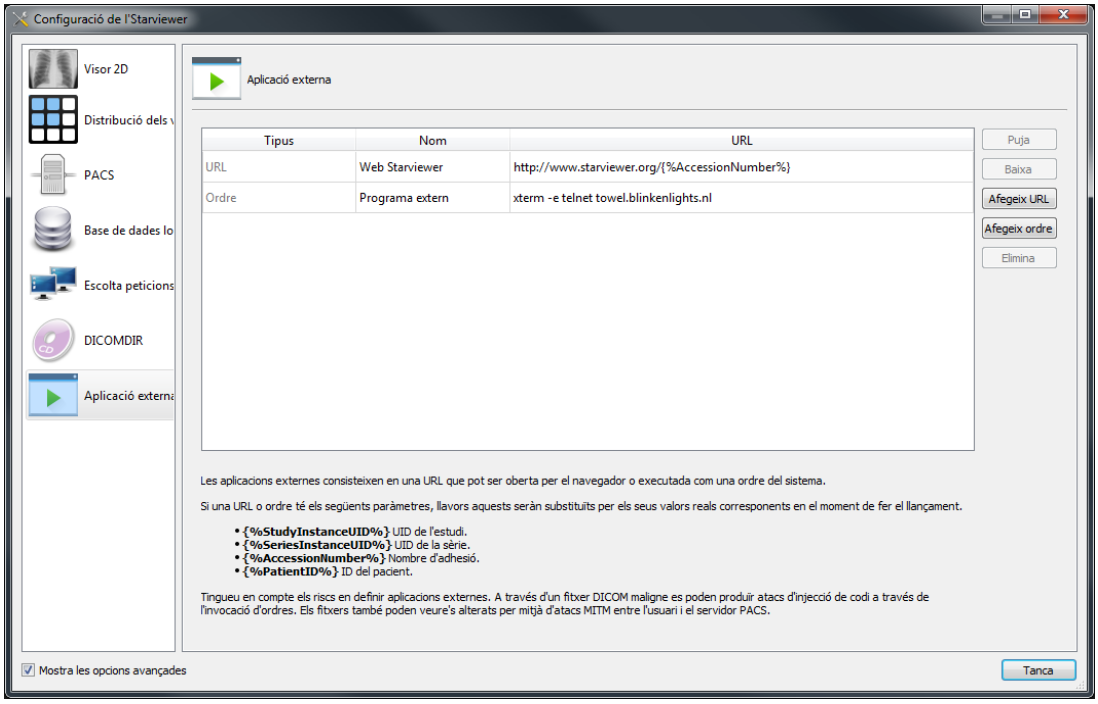
ICON 1

External applications consist in a URL that can be opened in the browser or executed as a system command. Users can add new ones with the “Add URL” or “Add command” buttons. If a URL or command has the following parameters, then these will be replaced by their corresponding actual values at the time of execution. If it is opened with the browser, then the special characters will be encoded with the percentage method (also known as “url encoding”).

- {%StudyInstanceUID%} Study UID.
- {%SeriesInstanceUID%} Series UID.
- {%AccessionNumber%} Accession number.
- {%PatientID%} Patient ID.

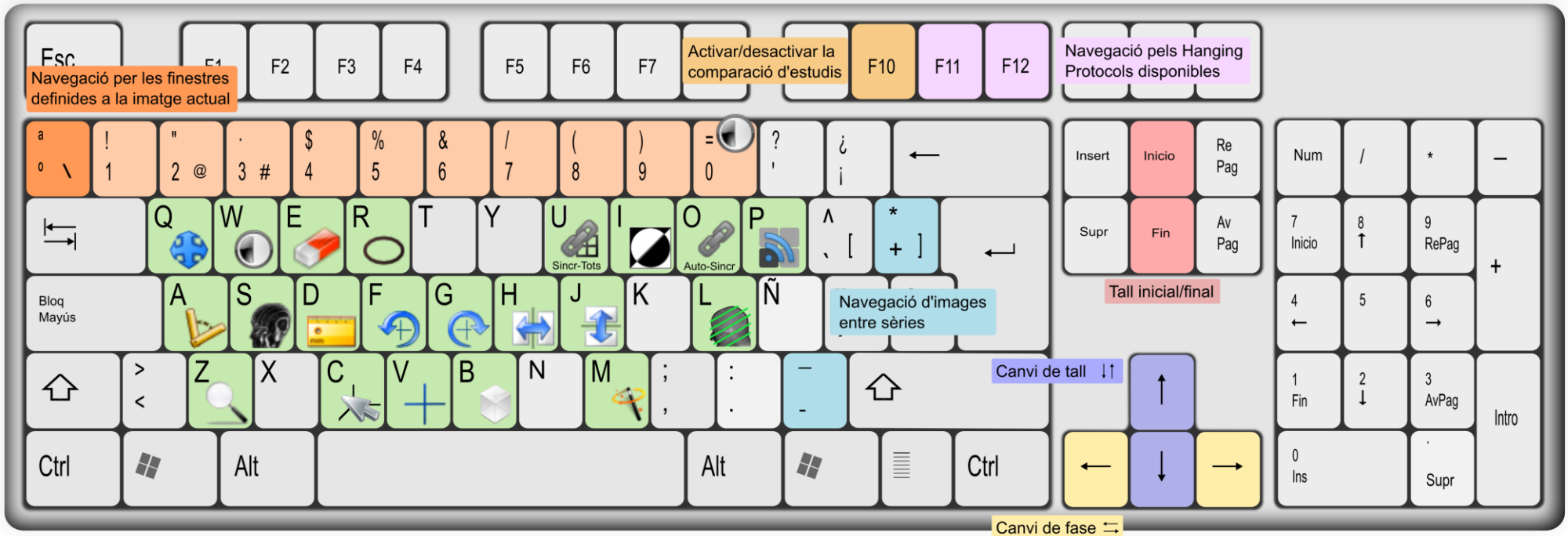
The risks when defining external applications must be taken into account. Through a malicious DICOM file, code injection attacks can occur through the invocation of commands. Files can also be altered through MITM attacks between the user and the PACS server.

The order of the external applications is taken into account when generating the menu and the assignment of the keyboard shortcuts. To change it, users have to select a row from the table and use the “Up” and “Down” buttons.



14. SHORTCUTS

14.1. MAIN SHORTCUTS



14.2. OTHER IMPORTANT SHORTCUTS

	Axial view	Ctrl + 1		New window	Ctrl + N		Open angle	⇧ + A
	Sagittal view	Ctrl + 2		Open files	Ctrl + O		Polygonal area	⇧ + R
	Coronal view	Ctrl + 3		Open DICOMDIR	Ctrl + D		Erase all annotations	Ctrl + E
	Capture current image	Ctrl + S		Explore local studies	Ctrl + L		Restore	Ctrl + R
	Capture the whole series	Ctrl + A		Search the PACS	Ctrl + P		Maximise to multiple screens	Ctrl + ⇧ + M
	Unsynchronise all viewers	⇧ + U		Magnifying glass	⇧ + Z		Move window to another screen	Ctrl + ⇧ + →
	External applications	⇧ + F1 ... F12						

15. GLOSSARY

AE Title: The AE Title (from Association Entity Title) is the identifier used by the DICOM protocol to recognise the parts implied in communication and image transfer operations. Therefore, each PACS and workstation has its own AE Title associated to a TCP/IP address with which the communications between them are negotiated.

DICOM: DICOM (from Digital Imaging and Communications in Medicine) is a standard for manipulating, storing and transmitting medical imaging information. The standard includes a definition of the DICOM file format and the communication protocols, based in TCP/IP, which allow the exchange of information between two entities that have the ability to send and receive information in DICOM format. DICOM was developed to allow the integration and communication of scanners, radiographic devices, servers, workstations and a large variety of hardware from different vendors.

PACS: PACS (from Picture Archiving and Communication System) is a system formed by the combination of hardware and software dedicated to the storage, retrieval, administration, distribution and presentation of medical imaging. The universal format for the storage and transfer of images is DICOM.

Query/Retrieve: DICOM service that allows a workstation to search for images and retrieve them from a PACS.

Store: DICOM service used for sending images or other persistent objects to a PACS or to a workstation.