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Annex I

of MedDream USER MANUAL (version 8.9.1)

MedDream viewing functionalities

version 8.9.1

The annex describes the usage and configuration of MedDream Viewing functionalities.

See the MedDream USER MANUAL document for the general information about the MedDream product, installation requirements and verification, IT security measures.

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MedDream viewing functionalities

The annex describes the usage and configuration of MedDream Viewing functionalities.

See the MedDream USER MANUAL document (https://www.meddream.com/files/meddreamviewer/doc/MedDream-User-Manual.pdf) for more information about MedDream product:

- general information about the MedDream product,
- list of applicable standards,
- warnings regarding residual risks,
- installation requirements and verification,
- IT security measures .

Minimum hardware requirements for client-side MedDream viewing functions

The table describes the requirements for computer, that uses MedDream viewing functionalities from remote MedDream server through the internet:

Parameter	Minimal Requirements
Desktop Web	
CPU	Intel® Core™ i3 4 core CPU or better
RAM*	8+ GB, 256+ MB of video memory
Storage space	10+ GB
Network Bandwidth	100+ Mbit/s
Web Browsers	Chrome 148+, Firefox 151+, Microsoft Edge 148+, Safari 26+
Mobile device iOS Web	
RAM*	2+ GB
Storage space	2+ GB
Network Bandwidth	100+ Mbit/s
Web Browsers	Safari 26+, Chrome 148+
Mobile device Android Web	
RAM*	2+ GB
Storage space	2+ GB
Network Bandwidth	100+ Mbit/s
Web Browsers	Chrome 148+, Firefox 151+

* For CT, MRI, PET-CT client side MPR/MIP rendering:

  - 64bit CPU and 64bit operating system;
  - Graphic board with >=1 GB video memory (hardware acceleration is enabled on the browser);
  - 12 GB of RAM to open more than 800 images;
  - 16 GB of RAM to open more than 1500 images;
  - 24 GB of RAM to open more than 3000 images (cardiac or functional imaging, MG Tomosynthesis).

* For MG Mammography:

  - 64bit CPU and 64bit operating system;
  - Graphic board with >=1 GB video memory (hardware acceleration is enabled on the browser);
  - 16 GB of RAM.

* For MG Tomosynthesis:

  - 64bit CPU and 64bit operating system;
  - Graphic board with >=1 GB video memory (hardware acceleration is enabled on the browser);

- 16 GB of RAM.

* Depending on the total amount of RAM on user's workstation, the browser is allowed to allocate the restricted amount of memory, and therefore MedDream application may load not more than 16 GBytes of data. Due to these limitations, browser may run out of memory, if the user loads several large computed tomography, mammography or tomosynthesis studies.

⚠ **NOTE!** Hardware acceleration should be enabled in web browser for better performance.

⚠ **NOTE!** Mozilla Firefox browser has certain memory limitations: MIST MPR functionality will fail on series where uncompressed DICOM data is larger than 2 GB.

⚠ **NOTE!** MedDream enables users to view all data stored with a bit depth of up to 16 bits per color channel. However, it displays 8 bits per color channel at a time due to web browser limitations (maximum display of 256 values per color channel). You can utilize the Window leveling tool to explore the entire data range within the images.

⚠ **NOTE!** The MedDream viewing functionalities server system requirements are detailed in the Install Manual of the MedDream viewing functionalities.

Logging on to MedDream

⚠ **NOTE!** If integrated Viewer is used, the login window may be disabled in configuration.

⚠ **NOTE!** The login page may not displayed, if automatic authentication is configured.

To log on to MedDream, please do the following:

Enter the address given by your administrator in your Internet Browser. The following screen will appear:

- Enter the username you were given in the field Username.
- Enter the password in the field Password. If you forgot your password, please contact your system administrator.
- Press Log in button.

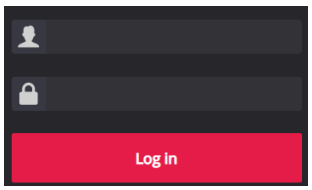


Figure 1. Log in window

⚠ **NOTE!** Login may be blocked in case of several failed login attempts, if restrictions are configured.

⚠ **NOTE!** Contact your system administrator, if you can not access the login page from outside the regular workplace. Access to login page only from a particular IP range or host name may be configured.

⚠ **NOTE!** Search window should be displayed after successful login. If the error about forbidden functionality is displayed instead, press the Log Off button, in case it is displayed on the error page, and contact your system administrator to verify the system configuration and user rights.

⚠ **NOTE!** On the right upper corner of the login window you can change the language by selecting the language code from drop-down list.

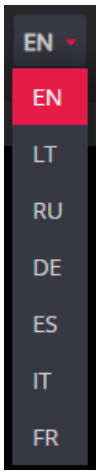


Figure 2. Language selection in a log in window

⚠ **NOTE!** The list of supported language is defined in configuration.

⚠ **NOTE!** The language selection is saved in browser local storage.

Displaying notifications

The **Notification** menu  is displayed in the system menu area of Viewer, Search and Settings window.

The messages that are issued by the system in the currently viewed window are temporary displayed in the top right corner of the window, and may later be access through notification menu:

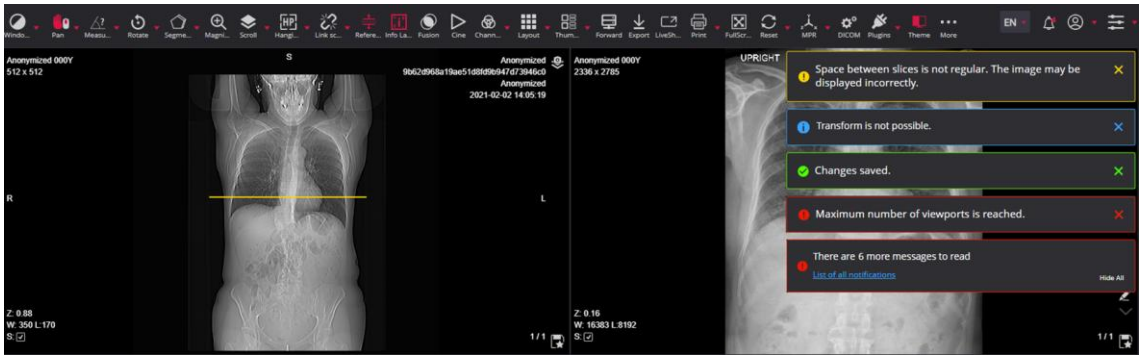


Figure 3. Notifications temporary displayed in the viewer window

If the current notifications list contains errors, the number of error messages is displayed at the top right corner of the icon:  .

⚠ **NOTE!** Viewer, Search and Settings windows have separate notifications lists.

⚠ **NOTE!** If a new identical notification is delivered, the previous notification is deleted from the list, and the latest is added to end of the list.

Rules for displaying notifications in the window:

- Each message has a severity sign at the left side of the notification window, as described below in the order of increasing severity:

success message indicates, that action was successfully performed,

info message notifies the user about system possibilities or system actions,

warning message notifies that user should be more cautious and possibly take additional actions to prevent any damage,

error message informs that something went not as expected;

- Notifications in the window are displayed temporary. The system automatically hides the message window after 5 seconds. Each notification has the close button at the right side, and can also be closed by the user.
- Up to four notifications may be displayed at a time in the window, with the earliest messages displayed at the top of the list. If there was more than four messaged popped, the system displays the summary message:

the summary message shows the number and the highest severity sign of not displayed notifications,

the messages from the summary notification will automatically be displayed one by one, as the notifications in the window is closed by the system or user,

the user can remove all the displayed and still not displayed messages from the window by clicking the **Hide All** link in summary message window.

Notifications window may be opened by either clicking the **List of all notifications** link in summary notifications window, or Notifications icon in toolbar. The **Notifications** window lists all the messages that were hidden from the window, and were not cleared from the notifications list:

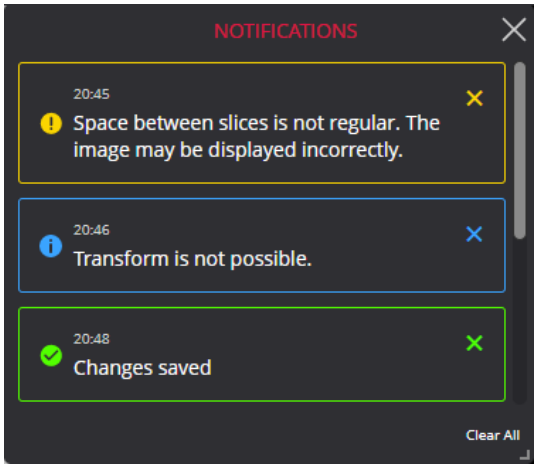


Figure 4. Notifications window

Besides the above-described message content, the time, when message was issued, is displayed.

NOTE! Pressing **Close** button for the message displayed in **Notification** window, deletes this message from the notifications list. Pressing **Clear All** link deletes all the messages at once.

License & Password Warnings

The system can be configured to check password strength and license expiration, notifying the user of each condition. For configuration details, refer to the installation documentation.

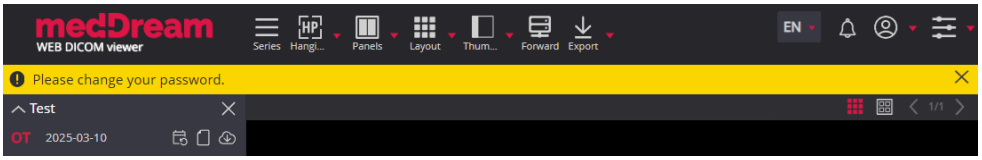


Figure 5. Password warning line

The user can close the notification by selecting ✕. However, the warning message will appear each time a new view window is opened.

The system displays a license expiry warning when there are 7 days or fewer remaining until the license expiration date (*ValidTo - Now ≤ 7 days*).

If the first one or two days of this period fall on a weekend, the notification is postponed until the next working day.

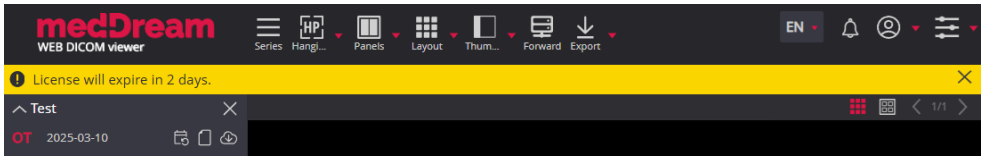


Figure 6. License expiry warning line

Search of studies

The Search menu will help you quickly find the studies you need. We recommend using all possible search menu options in order to get the most accurate search results and save your time. Search parameters are accessible from Search window that is opened after the successful login.

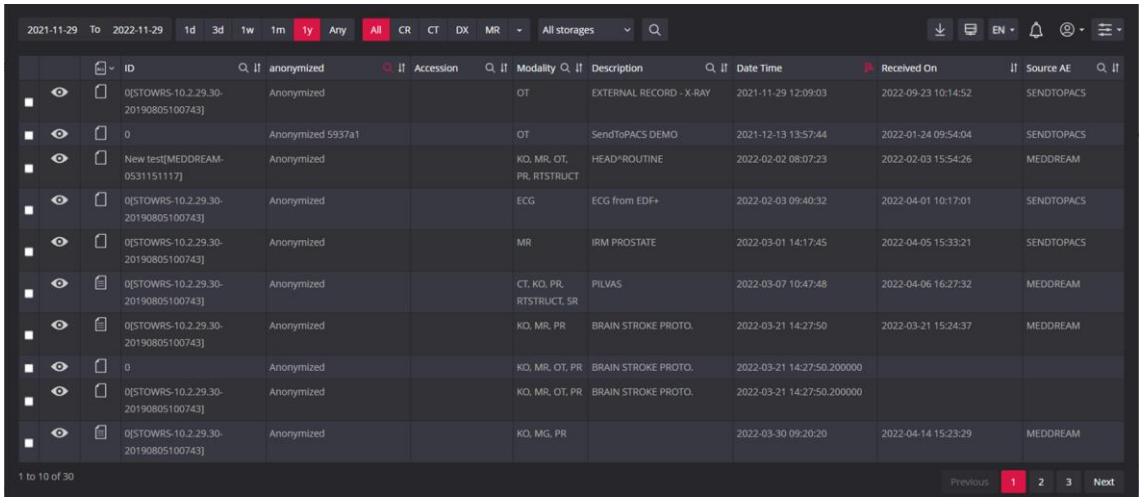


Figure 7. Search window

NOTE! If integrated Viewer is used, the search window may be disabled in configuration.

NOTE! If the error about forbidden functionality is displayed after login, press the Log Off button, in case it is displayed on the error page, and contact your system administrator to verify the system configuration and user rights.

Description of search menu parameters:

1. Search for studies according the search criteria listed below can be done by selecting the criteria entry field and entering the text in it:

- **ID** - enter patient's ID number
- **Name -** enter the patient's name or surname
- **Accession** – enter the study accession number
- **Modality** - enter the method which was used to obtain the study images
- **Description** – enter a few keywords from the study description
- **Source AE** – enter title of the device from where the study was sent to the PACS.



Figure 8. Search criteria entry fields in search window

NOTE! It is not possible to search for Ideographic and Phonetic versions of patient names. The search is performed only against the basic version (Alphabetic), even if the image contains the other two versions and the PACS supports them.

NOTE! Search criteria entry field is marked with a loupe sign at the right. The loupe sign is highlighted when the field is selected, or the search criteria is applied.

NOTE! To perform the search, press **Enter** key after the criteria is entered.

2. Search for studies having the study date in the specified date interval can be done. There are two ways for defining the date interval:

- To select the **date interval** from the quick pick list: "**1d"** (current day), "**3d"** (3 days interval), "**1w"** (1 week interval), "**1m"** (1 month interval), "**1y**" (1 year interval) or "**Any"** (no specific date interval):

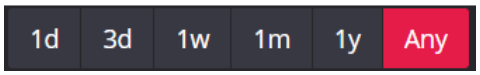


Figure 9. Quick pick list for choosing the study date interval

⚠ **NOTE!** One date interval value can be picked at a time. The ends of picked interval are displayed in the date fields on the left of the interval pick list. The fields are empty if no specific interval (**Any)** is picked.

⚠ **NOTE!** The default **date interval** is defined in "Settings". The search according the picked date interval is performed automatically on search window open and on any interval change in pick list.

- To specify one or both ends of the **date interval** in the date fields on the left of the interval pick list: click on the interval start or end entry field and choose the date from the pop-up window.

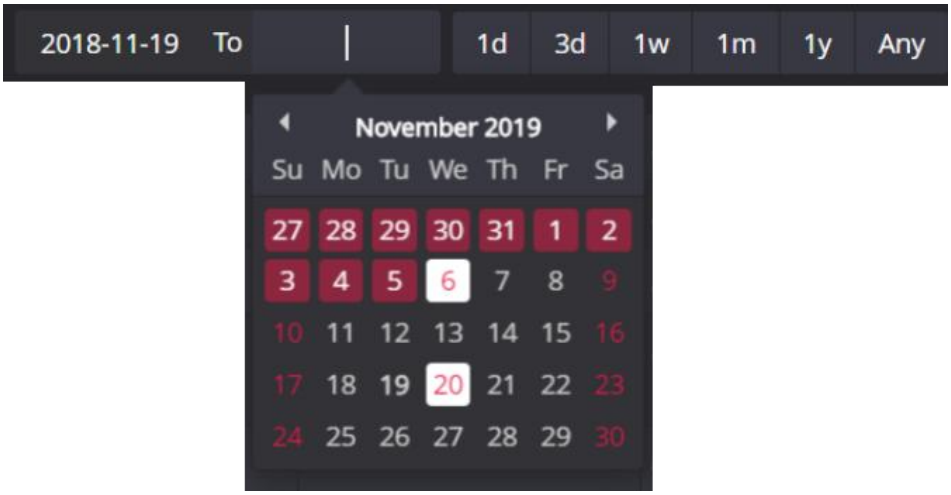


Figure 10. Study date interval entry fields

⚠ **NOTE!** To perform the search according the entered date interval click **Search** icon after the interval ends are entered.

3. The search can also be done by the method which was used to obtain the study images (modalities). You can pick one or more modalities from the modalities that are visible in modalities pick list:

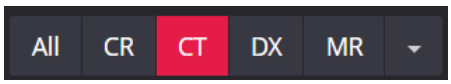


Figure 11. Pick list for choosing modality: CT is chosen

⚠ **NOTE!** Only one modality may be selected in list, if single modality search is enabled in Settings.

⚠ **NOTE!** The search according the picked **modalities** is performed automatically on any change in pick list.

⚠ **WARNING!** The picked modalities are saved in browsers local storage and search according these modalities is automatically performed on search window open next time.

You can customize the modalities pick list: expand the modalities list with triangle on the right side of the list and pick the modalities that you want to appear in modalities pick list.

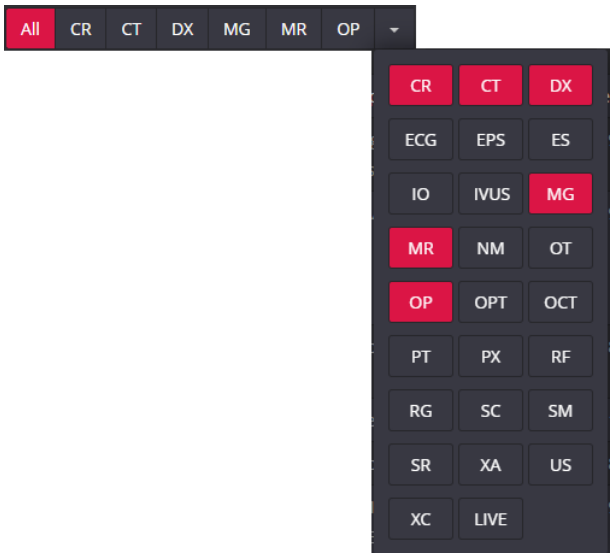


Figure 12. Customization of modalities pick list

The list of modalities:

CR – *Computed Radiography*

CT – *Computed Tomography*

DX – *Digital Radiography*

ECG – *Electrocardiography*

EPS – *Cardiac Electrophysiology*

ES – *Endoscopy*

IO – *Intra-Oral Radiography*

IVUS – *Intravascular Ultrasound*

MG – *Mammography*

MR – *Magnetic Resonance*

NM – *Nuclear Medicine*

OT – *Other*

OP – *Ophthalmic Photography*

OPT – *Ophthalmic Tomography*

OCT – *Optical Coherence Tomography (non-Ophthalmic)*

PT – *Positron emission tomography (PET)*

PX – *Panoramic X-Ray*

RF – *Radio Fluoroscopy*

RG – *Radiographic Imaging*

SM - *Slide Microscopy*

SR- *Structured Report Document*

SC – *Secondary Capture*

XA – *X-Ray Angiography*

US – *Ultra Sound*

XC – *External camera photography*

LIVE – live stream

⚠ **NOTE!** If you are searching for some rare modality that has no corresponding button here, try to enter its abbreviation directly into the search criteria **Modality**. The system searches for all the modalities that are picked in modalities control and entered in Modality search criteria.

⚠ **NOTE!** The primary list of modalities that are displayed in modalities selection control is defined in “Settings”. The customized modalities list is saved in browser local storage after the customization is done.

4. The search for study in particular storage can be done. You can pick a particular storage from drop-down storage list:

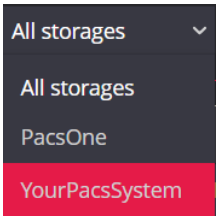


Figure 13. Picking the storage

The search according the picked **storage** is performed automatically on selection change.

⚠ **NOTE!** The storage selection control is visible only if multiple storages are configured.

⚠ **NOTE**! The storage selection is saved in browsers local storage and search in this storage is automatically performed on search window open next time.

⚠ **CAUTION!** Be aware, that access to the storages may be restricted by the user rights. The storages list contains only the storages, that are granted for the user. Searching is performed only in the granted storages, if the **All storages** option is selected.

5. The search for reported or not reported studies be done. By default, the system searches all, reported and not reported, studies. You can pick a particular option from drop-down list:

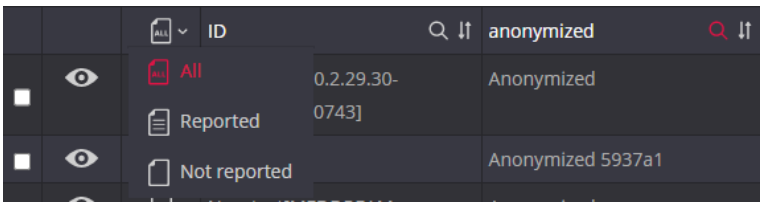


Figure 14. Picking the reporting criteria

The search according the picked criteria is performed automatically on selection change.

After the search is performed, the studies, that correspond to the search parameters, are displayed in search results list. The results list displays the following study information:

- **ID** - patient's ID number.
- **Name -** patient's name and surname.
- **Accession** – study accession number.
- **Modality** - method which was used to obtain the study images.
- **Description** –study description.
- **Date Time** – study date and time.
- **Received On** – the date and time when the study was received by PACS.
- **Source AE** – title of the device from where the study was sent to the PACS.

⚠ **NOTE!** The field is empty if the DICOM file or PACS does not have the particular data.

In the search results list, you can do the following:

1. To sort the result list by any of data fields. Each field has **Ascending/Descending** button . You can arrange each of them in ascending or descending order. Click once and the order of the selected field will change from ascending to descending and vice versa.

NOTE! By default the system sorts the dada as text. Contact your system administrator to configure the number sort for numeric data columns.

2. To navigate through result list by picking the required page or using **Previous** and **Next** in page navigation controls:

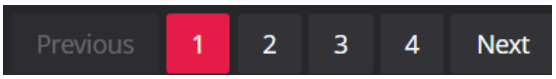


Figure 15. Page navigation in the search results list

NOTE! The number of studies per page is defined in Settings. If the search results of the page do not fit to the window, you can scroll the list with the scrollbar at the right side of the results table, or with the mouse wheel while hovering over results list.

3. To mark the studies for forward or export by checking the tick box in first column of the results list:

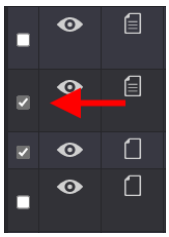


Figure 16. Marking the study

The forward and export functionality is activated by selecting the appropriate menu in the search window. See detailed description in section “Export and Forward”.

NOTE! The Tick box selection status is reset to unselected on Search window reload, for example when the sort order is changed, the page is refreshed, the user navigates to the other page.

4. To open the study in viewer by clicking the study in the search results list. See detailed description in section “Opening studies”.

5. To open the Report window by clicking the Create report icon, or Edit report icon in the search results list. See detailed description in section “Report module”.

You can do the following using the buttons in the top right corner of the search window:

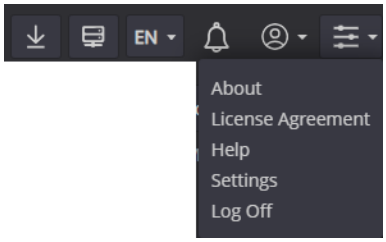


Figure 17. The other menu in Search window

1. Clicking the **Export** button opens the export window. Before doing so, mark the studies you want to export. See detailed description in section “Export and Forward”.

2. Clicking the **Forward** button opens the forward window. Before doing so, mark the studies you want to forward. See detailed description in section “Export and Forward”.

3. **Language** menu enables language change by picking language code in expandable list.

4. Clicking **Notifications** button opens the notification window. The notifications functionality is explained in the section “Displaying notifications”.

5. **User details** menu allows to see the login name, login time, and the user name, if provided.

6. **System** menu in Search window contains the following options: About; License Agreement; Help; Setting; Log Off. See detailed description in section “System menu functions”.

⚠ **CAUTION!** Export, and Forward functionality may be disabled. Contact the system administrator to verify the configuration, if export or forward is missing.

MedDream DICOM Viewer

Viewer window

Viewing and analyzing the study images is done in Viewer window. Viewer window contains several zones.

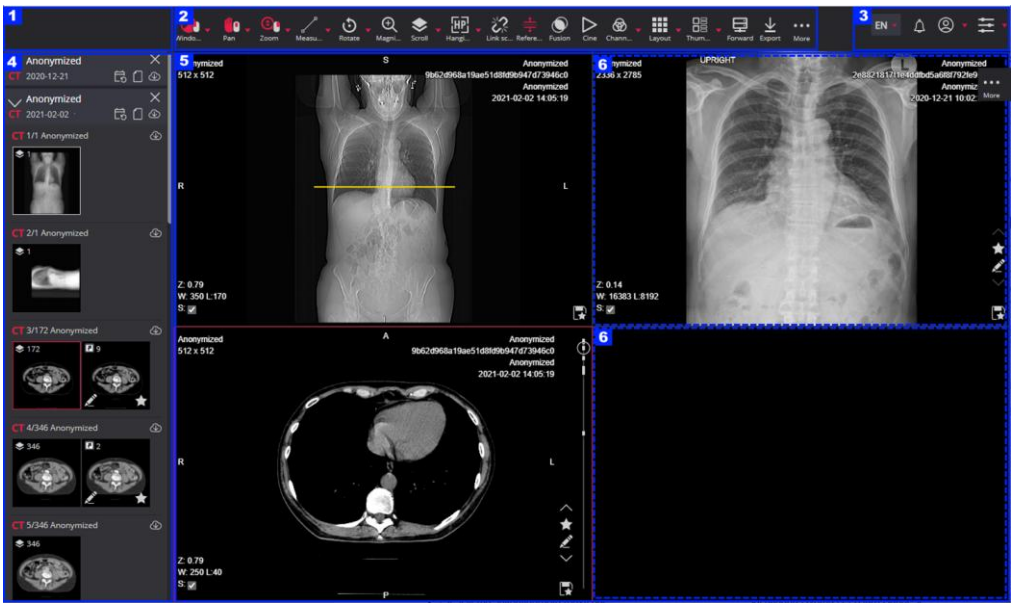


Figure 18. Viewer window zones

The Viewer window zones, with blue border and number in the top left corner, as displayed in the figure above:

- Zone 1 in the left corner of the Viewer window header row displays system logo;
- Zone 2 on the right of the system logo in the Viewer window header row displays toolbar with image manipulation tools;
- Zone 3 in the right corner of the Viewer window header row displays the system tools;
- Zone 4 displays the thumbnails. Thumbnails zone is displayed on the left side of the window in the figure, but may be displayed in another place as well or temporary hidden (see description in section “Thumbnails”);

⚠ **NOTE!** By default, system is configured to not show the image thumbnails for CT, MR, PT and NM series, and also the for the multiframe that is displayed as series of images, in order to decrease the study loading time. The system administrator should change the configuration, if all thumbnails are needed for these series, as displayed in picture.

- The view zone 5 takes the largest part of the Viewer window in the figure, and may be divided to several panels and/or viewports (zone 6 with dashed line border in figure).

The description of Viewer window zones follows in the subsection of this section.

Toolbar

Image manipulation tools are displayed at the top of the Viewer window. In section “Toolbar Properties” you can configure what buttons and in what order are shown on toolbar. In addition, you can customize what buttons are displayed directly in toolbar (pinned), and what goes under the expandable **More** tools list. The **More** button is displayed at the end of the tools list. If there is not enough space for the buttons to be displayed, including the pinned buttons, the system automatically places the not fitting tools under the **More** button. Click the **More** button to see the missing tool buttons.

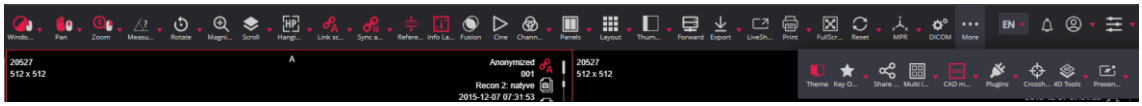


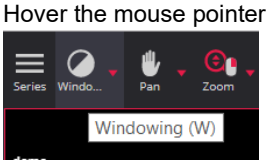
Figure 19. Expanded toolbar.

⚠ **NOTE!** The tools displayed on the toolbar depend on the image being uploaded in the active viewport.

⚠ **NOTE!** Hiding of toolbar button or button’s menu option may be configured in panels toolbar settings (see section “Panel toolbar settings”).

In the toolbar you can also enable mouse usage for a particular tool. To enable the mouse usage for a tool, perform the following:

- Hover the mouse pointer over the tool icon: in the example, the cursor is over the Windowing icon

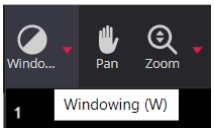


- Press the mouse key that you want to use for the mouse action
- Tool icon displays the activated mouse button: in example 

, the left mouse button is activated to change the brightness level.

⚠ **NOTE!** The mouse button assignment is saved in browser's local storage. If local storage does not contain the saved values, the default assignment is used: left mouse button is assigned to **Windowing** tool, middle mouse button is assigned to **Pan** tool, and right mouse button is assigned for **Zoom** tool.

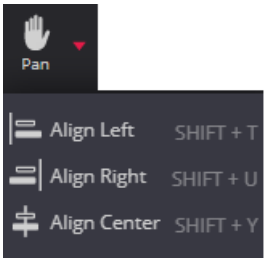
The active mouse key is deleted by pressing the same key over the tool icon once more or by activating the same mouse key for another tool.

You can activate and deactivate the left mouse button usage for tools' mouse action with keyboard: press the letter displayed in tooltip 

. Pressing 'W' activates the left mouse button usage for windowing function 

.

Clicking the triangle on the right of tool icon expands the tool menu:



You can activate the menu option by clicking it. If the option has an assigned shortcut, the key combination is written on the right: for example, pressing 'SHIFT' and 'T' keys simultaneously, aligns the active image left.

The toolbar can be set to display only icons without function names. When you hover the mouse pointer over an icon, the function name is shown in a tooltip. More information is available in the System Settings section.

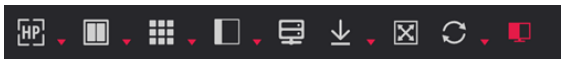


Figure 20. Toolbar. Icons only.

⚠ **NOTE!** When installing a new version of the system, the Toolbar order is changed by default. It is possible to specify that the current order is kept and that new menus are added to the end of the Toolbar. See the installation instructions for details.

System tools

The system tools zone contains four buttons:

- **Language** menu that enables language change by selecting the language in expandable list.
- Expandable **System** menu with the following options: About; License Agreement; Help; Shortcuts; Settings; Log Off. See detailed description in section "System menu functions".

  ⚠ **NOTE!** System menu options may be disabled in "Settings". The Settings option may also be not allowed by user rights.

  ⚠ **NOTE!** Log Off functionality in Viewer window is available only for integrated viewer with disabled Search window. If the Log Off is not available in Viewer window, use Log Off in Search window.

- **Notifications** menu opens the notification window. The notifications functionality is explained in the section “Displaying notifications”.
- **User details** menu allows to see the login name and time. If provided, the user name is also displayed.

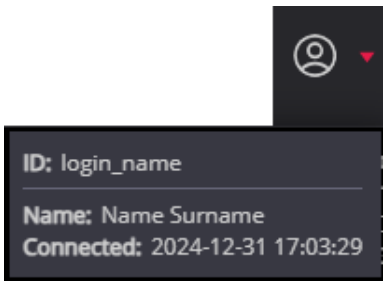


Figure 21. User information expanded

⚠ **NOTE!** User details menu may be disabled in “Settings”.

⚠ **NOTE!** In case of Mobile display mode, the system places all the system tools under one Grouped system tools button with expandable menu for accessing each tool.

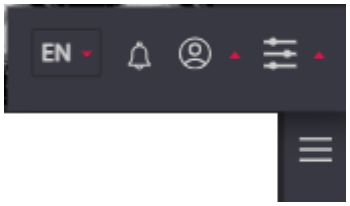


Figure 22. Expandable Grouped system tools button menu in Mobile display mode

Thumbnails bar

The Thumbnail holds the studies that are opened in Viewer window. By default, the patient’s name, study modality and study date are displayed in the study description section of the thumbnail. The additional label, date highlighting for comparison studies, and number indicator can be configured in the system settings:

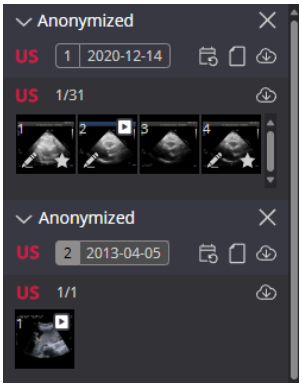


Figure 23. Study description section with additional label and highlighted comparison study date

If study description is expanded, the series description and series images thumbnails are displayed.

⚠ **NOTE!** In the new horizontal thumbnails bar (Top BETA and Bottom BETA options) the study description is displayed in the expandable studies list instead of tabs. See subsection “Horizontal thumbnails bar” for description.

⚠ **NOTE!** By default the series are listed in the same order as returned from the storage, but moving the series of the particular modalities to the end of the series list may be configured. Contact your system administrator for changing the default system configuration.

⚠ **NOTE!** By default all the series of the study are displayed in the Viewer, but blacklisting of series may be configured. The blacklisted series are not displayed in the Viewer but are included when archiving, exporting or forwarding the study.

For video and multi-frame images, the type indicator is displayed at the top right thumbnail’s corner. The Presentation state icon is displayed at the bottom left thumbnail’s corner, if presentation state is saved for the image. The Key object icon is displayed at the bottom right thumbnail’s corner, if the image is marked as key object.

In order to decrease the study loading time, the system may be configured to not show all the image thumbnails for the series with large number of images:

- The series of CT, PT, and MR modality, that in general has large number of images;
- The series of MG, OPT, and NM modality, that are created from primary multi-frame image.

In such cases only one series thumbnail image is displayed, and thumbnail is generated from the first or middle image in the series.

If a series has images with saved presentation state or marked as key objects, icons with the quantities of these objects are shown next to the series thumbnail: - saved key objects, - unsaved key objects, - presentation states. If a segment has been created in the series, the segmentation icon appears . The segmentation icon can be highlighted if a segmentation is selected in the action window (see the Segmentation section for details).

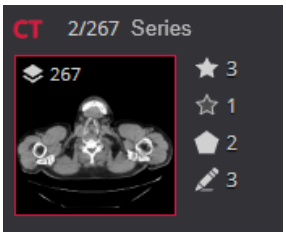


Figure 24. Study description section with additional label

⚠ **NOTE!** By default, system is configured to not show the image thumbnails for CT, MR, PT and NM series, and also the for the multiframe that is displayed as series of images.

⚠ **NOTE!** By default, series thumbnail is generated from the first image in series.

⚠ **NOTE!** Be aware, that viewing and saving the key objects and presentation states may be restricted by the user rights.

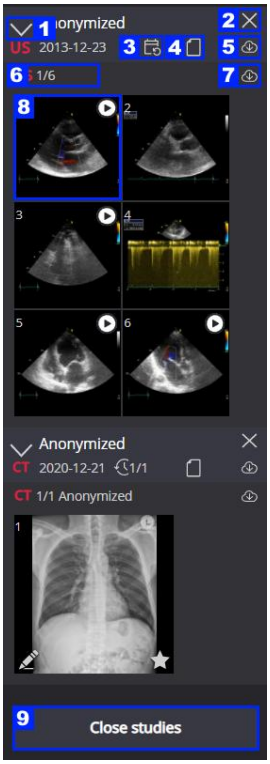


Figure 25. Action controls in Thumbnail

In thumbnail zone you can perform the following (see control numbers in Figure 25 and Figure 27):

- Expand or collapse the study description by clicking the chevron icon (number 1) at the top left corner of the study description.
- Remove the study from Viewer window if you are done with it. If not configured to hide the closing buttons, to remove the study from Viewer window, click on close study button (number 2) at the top right corner of the study description.
- Open patients' studies modal (dee detail description in section "Patient history") by clicking the patient's history icon (number 3) in the study description.
- Open Report window by clicking the Create report icon, or Edit report icon (number 4) in study description. See detail description in section "Report module".
- Preload the data by clicking the preload icon. Clicking the preload icon on the right side of study description (number 5), preloads the whole study. Clicking the preload icon on the right side of series description (number 7), preloads the series. You can also initiate the preload of the series or the whole by dragging the series or study header to the viewport. Study or series preload allows to scroll through the images much faster.

⚠ **NOTE!** Automatic start of the study instances preload on study opening, and the series instances preload on the opening of the series image, and progressive instances preload around the viewed image may be configured in settings.

⚠ **NOTE!** The preload icon is not displayed, if the series or study images are loaded.

Once you click the preload icon, preloading starts and progress bar is displayed. The stored *series* can be scrolled interactively in the form of scrollable image stacks.

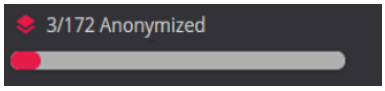


Figure 26. Preload progress bar

⚠ **NOTE!** The system checks the loaded CT, MR, or PT series, or NM multiframe image, and displays the phase filter, if series or multiframe contains images of several phases.

⚠ **NOTE!** The system may be configured to display the cardiac phases for the ECG guided cardiac CT or MR series. Contact your system administrator to configure returning the cardiac phase metadata, if you do not see the cardiac phase icon in the series header, or see the cardiac series divided to phases by acquisition instead.

⚠ **NOTE!** The localizer images are separated as phase, if included in series. Contact your system administrator to configure moving the localizer images to separate series at data preparation.

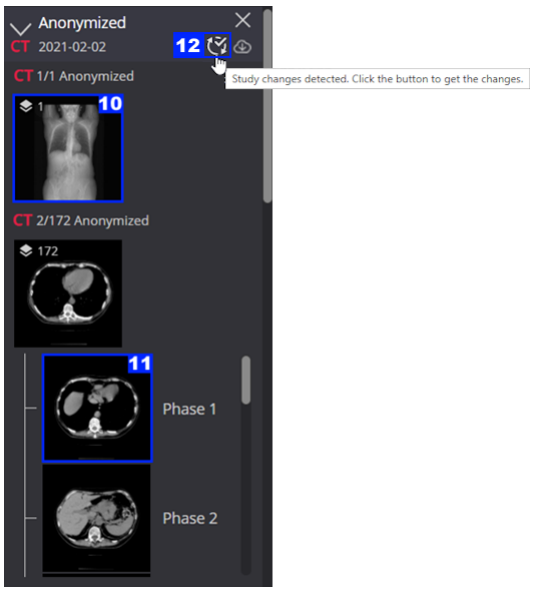


Figure 27. CT series default view without images thumbnails, and with phase filter

- If not configured to hide the closing buttons, remove all the studies from Viewer window by clicking on **Close studies** button (number 9) at the bottom of the Thumbnail zone.

⚠ **NOTE!** By default, the close buttons for a single study or all studies are available. It is possible to change the system settings so that a confirmation dialogue displays before the close action or the close buttons are completely unavailable. Contact your system administrator regarding the system configuration.

- If study changes tracking is supported by studies storage and is configured, the system regularly tracks the changes in study structure and displays the Get study changes icon, if changes are detected. Clicking the Get study changes icon (number 12) adds the missing series or images to the study structure and hides the icon until more changes are detected.
- Open images in the following ways:
  - To open any series in the viewport, drag the series description (number 6) to that viewport. System displays the first series image in the viewport, and automatically starts series images preload;

- To open any image from series with images thumbnails (number 8), find the image thumbnail and click it to open in active viewport, or drag it to selected viewport. If the image is currently viewed, the image picture is highlighted;
- To open series with only one series thumbnail image in the active viewport, click the series thumbnail (number 10), or drag it to selected viewport. In the viewport system displays the image which was used for generating thumbnail, that is first or middle image in series. The series thumbnail image is highlighted, if at least one series image is displayed in viewer;

  ⚠ **NOTE!** Quick series images preview cannot be done for CT, MR, PT and NM series, and also the for the multiframe that is displayed as series of images, if not displaying thumbnails is configured. Use scrollbar cursor dragging in viewport for quick series images preview.

  ⚠ **NOTE!** The automatic series preload for better scrolling performance may be done on CT, PT, MR series opening, if not displaying thumbnails is configured (see in section “Scroll”).
- To open the phase images in the active viewport, click the selected phase thumbnail (number 11), or drag it to selected viewport. The middle of the phase images is displayed, and you can see images of the phase by scrolling forward and backward;
- To open a study, press and hold the study header without clicking on the active header element, then drag and drop the study header into the panel. If the system is configured with Hanging protocols version v2, and HP for Study drag protocols are enabled, the system searches for the applicable drag hanging protocol and lays the study accordingly. The study is not opened, if the applicable protocol is not found. If the HP for Study drag protocols are not enabled and the study header is dragged into the panel with the active overview layout, the system opens the study series or images in the overview layout.

By default, you can open the image in the active viewport with single left mouse button click on the thumbnail.

⚠ **NOTE!** If image opening with single left mouse button click is disabled in settings, the left mouse button double click should be used.

You also may open the image in the empty viewport, instead of opening it in the active viewport, with right mouse button click. The system searches for the empty viewport, and opens the image in this viewport. If there is no empty viewports available, the system automatically extends the layout, and than opens the image in an empty viewport.

⚠ **NOTE!** The automatic layout extension is done only if the current layout has not more than 16 viewports.

⚠ **NOTE!** By default configuration, image opening in empty viewport is disable. The option should be enabled it in system settings, if needed.

Horizontal thumbnails bar

The horizontal thumbnails bar has the study headers placed in the horizontal tabs, and the series of the expanded study are listed horizontally, from the left to the right. Except for the limit, that only one study may be expanded at a time, all the other information and controls may be found in the same place of the study header, and series header, and works identically as in vertical thumbnails bar.

With a new horizontal thumbnails bar design (Top BETA and Bottom BETA) the following changes in location of information and icons are introduced:

- The headers of all the studies that are opened in the Viewer are displayed not in the tabs, but in the expandable list:

The same information as in tab with the study header is displayed in the list for each study: modality of the study, patient ID, study date, study description.

The icons for accessing study reports, study preload, and study close are available for each study. Note that you do not have to change the currently viewed study (the highlighted one) for activating the preload or closing the other study from the list.

The studies are grouped by the patient. The studies of the different patients start from the record with the patient icon.

Button for closing all the studies is displayed at the bottom of the list.

The currently expanded study is highlighted. Clicking the other study automatically closes the list and displays the thumbnails of the selected study in the thumbnails bar. Note, that clicking the icon activates the corresponding action for the study, but does not load the study thumbnails and does not close the list.

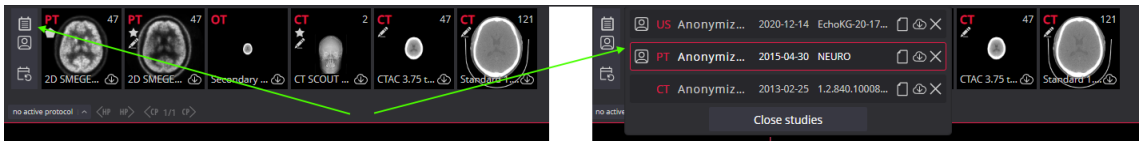


Figure 28. Studies list in horizontal thumbnails bar (BETA)

- The series header is not available. The modality of the series and the series description is displayed directly either on the first or only thumbnail image for the series.
- The additional data for the currently expanded study may be accessed by clicking the corresponding icon on the left of the thumbnails bar:

patient icon  expands the detailed patient information,

and patient's history icon  opens the list of patient studies.

View zone

The view zone takes the largest part of the Viewer window and is designated to view and analyze the images. The view zone may be divided to panels and the panel may also be divided to several sections, each section (dashed line in Figure 18) working as separate viewport. It is possible to have the panel toolbar and different layout per panel, what adds flexibility and allows using the parts of the view zone for different purposes. The figure below demonstrates the window with two vertical panels configured. The left panel with 1x2 layout is used for diagnostics, and the right panel with 4x2 overview layout is used for study series overview. See section "Panels, Layout, and Multi image/series" for detailed view zone dividing and panels toolbar description.

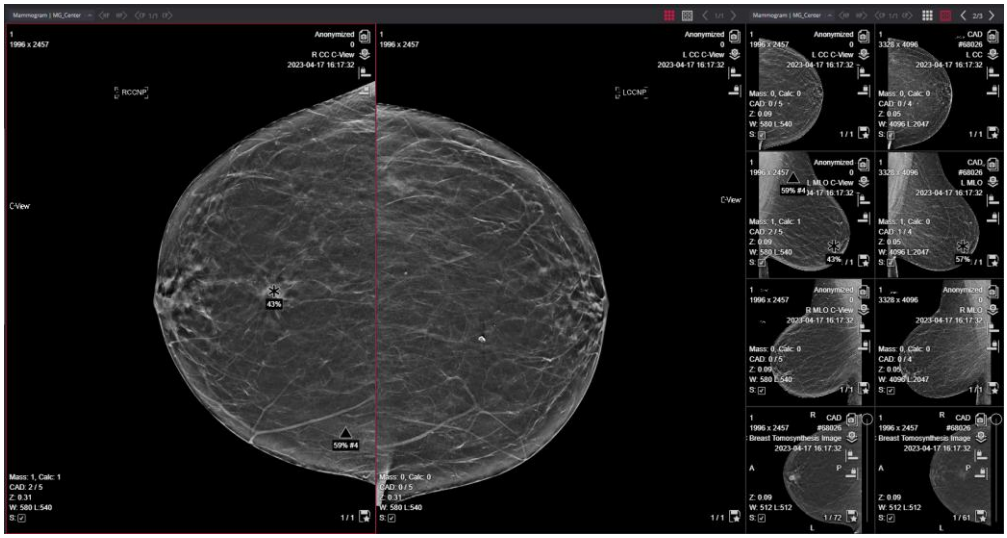


Figure 29. 1x2 Panel with panel toolbar and different layout per panel configured

The manipulation is allowed in one active viewport at a time. To activate the viewport, click on the viewport area – the active viewport is highlighted. The toolbar and quick menu are automatically adjusted according the content of the active viewport.

At the right side of the viewport a scroll bar is shown. A scroll cursor is scrolled according to the position of the active image in the series. At the bottom of the scroll bar the total number of images in the series and the number of the active image are shown. Dragging the cursor along the scroll bar scrolls through the images of the series. Clicking on scroll bar displays the image corresponding to the scroll position.

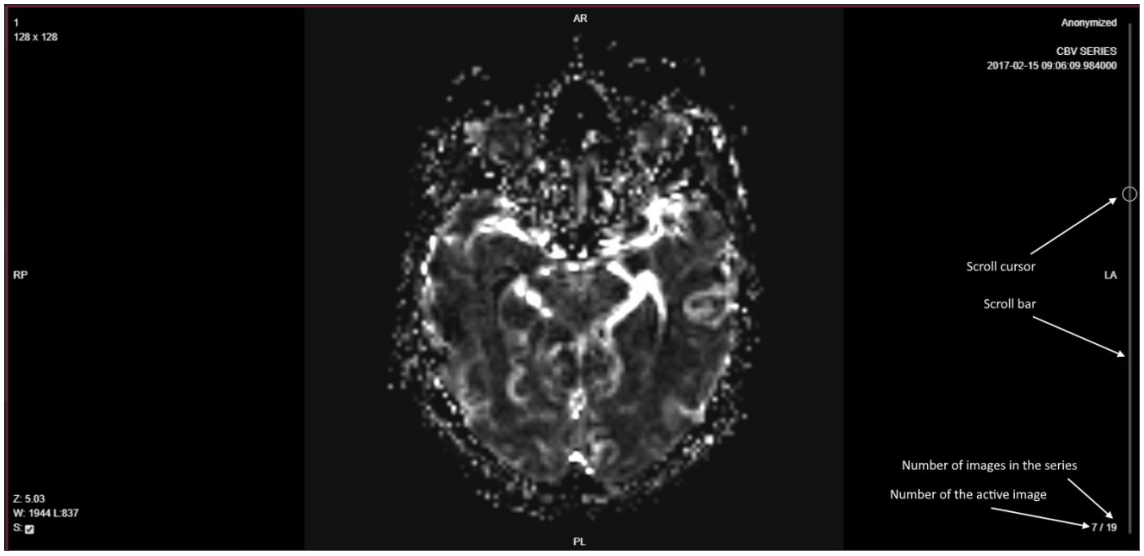
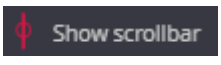


Figure 30. Image scroll bar

⚠ **NOTE!** By default configuration, the scrollbar is displayed for the series of CT, MR, PT, OPT, NM, MG, OT, and OCT modalities, and having two or more images. Contact your system administrator for system configuration.

⚠ **NOTE!** To hide the scroll bar, clear the **"Show Scrollbar"** option in the **"Scroll"** menu 

. To show it again, select this option once more.

The system shows the additional information about the displayed image in the viewport info labels:

- The data from the image DICOM file may be displayed at the top right and top left corner of the image. Fields to be displayed are configurable. Label highlighting may be configured for marking the comparison studies. See settings section “Label Properties” for configuration description.

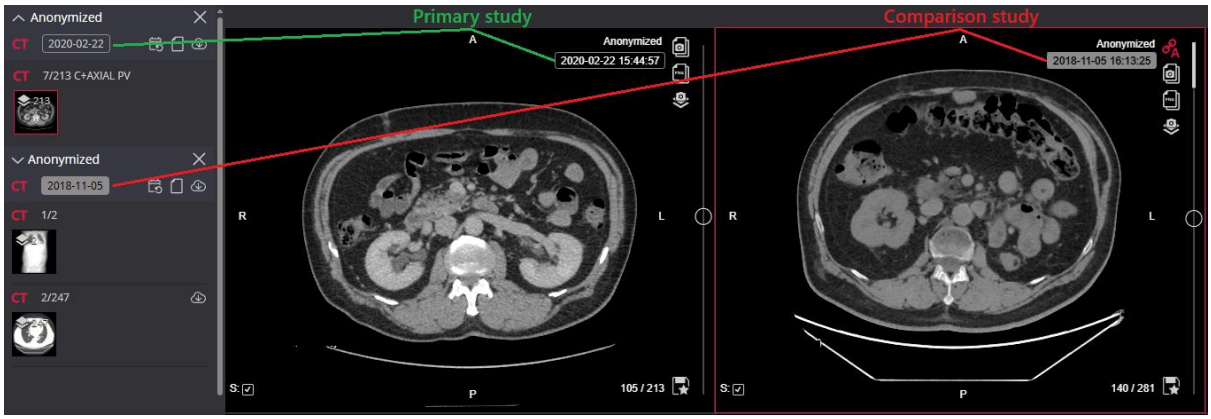


Figure 31. Comparison studies marking

- Number indicators can be shown in thumbnails and the viewport. If header highlighting is on (for comparison studies), the number appears on the highlighted row. If not, it appears in the first line of the right-side header. The numbering ranges from 1 to 99. Open studies are not renumbered even if one of the studies is closed during the session. When “Close Studies” is selected, the numbering starts again from 1. The number indicator is displayed when any of the thumbnail bars is enabled – on the left, right, top, or bottom. See settings section “Thumbnails” for configuration description.

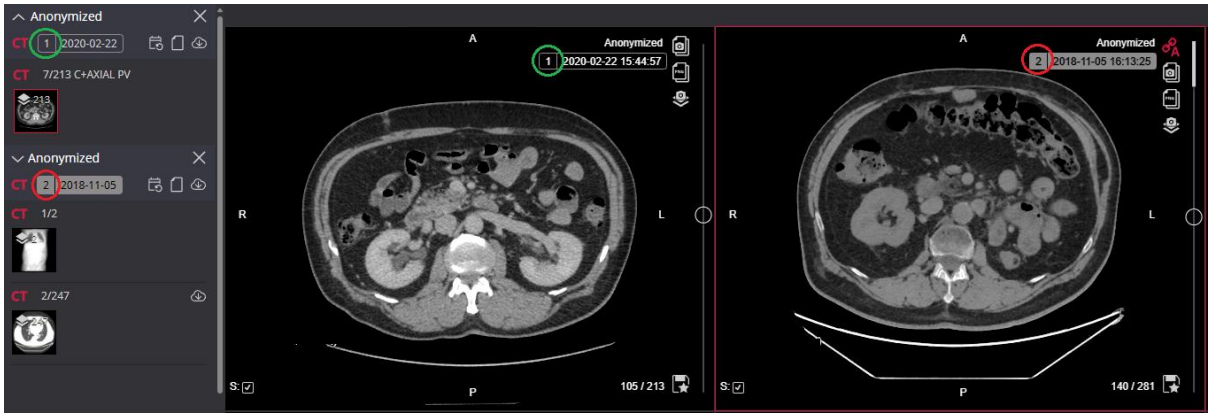


Figure 32. Number indicator in thumbnail and viewport

- The anatomical directions, if available in the DICOM data, are displayed in the middle of each viewport side. The directions are automatically recalculated, if the image is rotated or flipped.

⚠ **NOTE!** The anatomical direction is not displayed on the aligned and locked side of the mammography image.

- The number of displayed images, and the total number of images in series are displayed in the bottom right corner of the viewport.
- The labels in the bottom left corner of the viewport notifies about applied transformations:
  - Applied brightness and contrast values. For positron emission tomography (PET) images, the brightness and contrast is not displayed. Instead, the maximum pixel value is displayed, and the standardized uptake value (SUV) may be calculated and displayed: Max: BQML 14636.00, SUV 5.05;
  - Applied VOI LUT value;

- Applied color palette;
- Image zoom level;
- User entered calibration value;
- Intensity of the point, if intensity measuring is switched on;
- Magnification coefficient, if magnification tool is used;
- Rotation and flip values;
- Plane of reconstructed series, if reconstructed series is displayed;
- Actual calculated frame rate, if multi-frame is playing and showing actual fps is configured;
- Series scan direction and slice distance (position) in scan axis. The function should be enabled in settings and is displayed only for CT, MR, PT, and NM series.
- The number of the currently viewed matched series, and the total number of the matched series for the Hanging protocol viewport, if more than one matched series found.
- Warning about lossy compression with type and ratio of the latest compression, if this data is available: 

.
- The CAD label with number of findings in current image and total number of findings in all the mammography CAD SRs of the study. If current image has findings, the label with numbers of mass and calcification of findings in current image is also displayed.

⚠ **NOTE!** Use **Info Labels** tool to hide or show the viewport labels (see in section “Info Labels”).

⚠ **NOTE!** System automatically adjusts font size of the label and truncates or hides the labels to fit the smaller viewport.

⚠ **CAUTION!** Use the patient’s name, dates, anatomical direction and other information, which is displayed in the viewport labels, to ensure that you are viewing the right image.

Viewport toolbar

Viewport toolbar holds the tools, that are accessible directly from the viewport. The area for the toolbar is allocated at the right side of the viewport, on the left of the scroll bar, if scroll bar is displayed in the viewport.



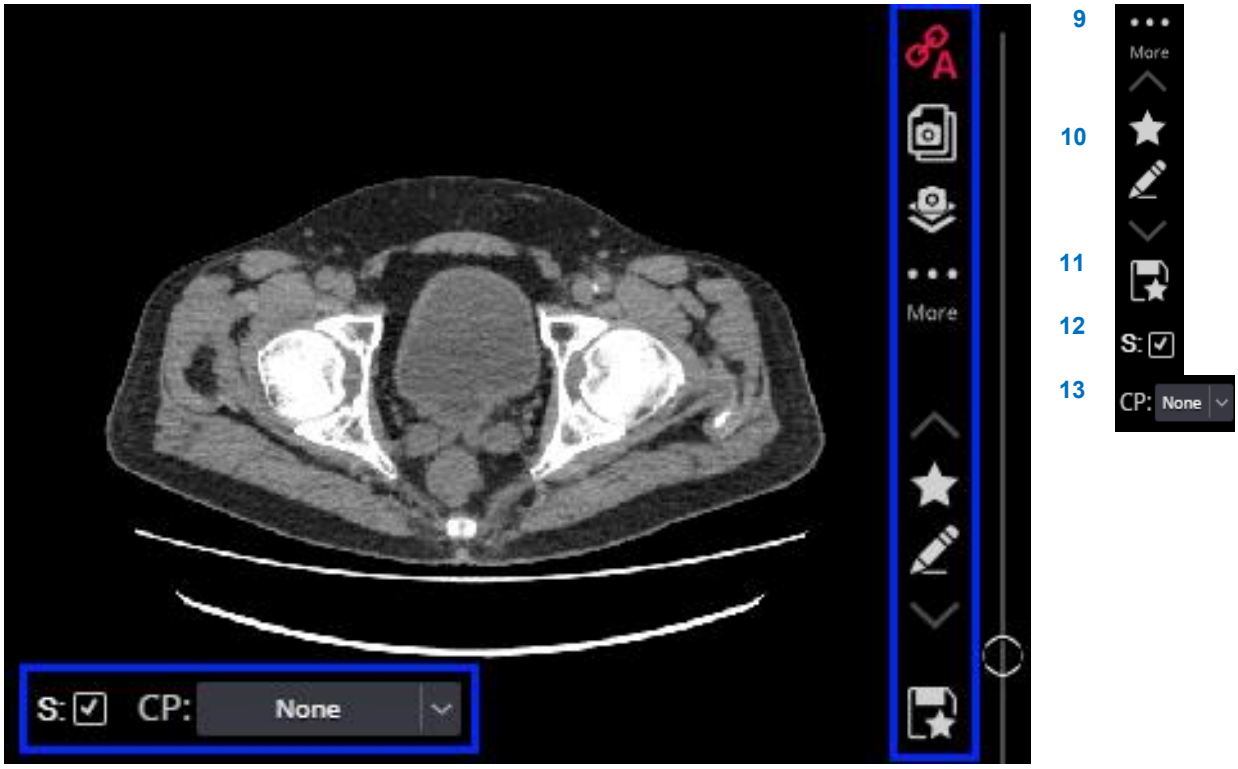


Figure 33. Viewport toolbar

The following tools are accessible from the Viewport toolbar (see control numbers in figure “Viewport toolbar”):



1. Enable or disable the synchronous scrolling for a particular series by tapping the manual or automatic link button (number 1) in the Viewport toolbar. See detail functionality description in section “Link scrolled series”.



2. Paste the copied measurement on the image by tapping the Paste measurement button (number 2) in the Viewport toolbar. See detail functionality description in section “Copy and paste measurement”.



3. Copy the image and other content, that is displayed in the viewport, to the clipboard by tapping Copy viewport content to the clipboard button (number 3) in the Viewport toolbar. See detail functionality description in section “Copy viewport content”.



4. Copy the image, that is displayed in the viewport, to the clipboard by tapping Copy original image to the clipboard button (number 4) in the Viewport toolbar. See detail functionality description in section “Copy original image to the clipboard”.



5. Save the image and other content, that is displayed in the viewport, as secondary capture image by tapping Save viewport content as secondary capture DICOM button (number 5) in the Viewport toolbar. See detail functionality description in section “Copy viewport content”.



6. The button is used to detect the orientation of the current view plane and to generate a MIST MPR image based on that plane. In the generated image, the user can adjust the Intensity Projection value (MIP/MinIP/AVG). For a detailed description of the functions, see the section “Generate Intensity Projection (MIP)”.



7. Align and Lock Left aligns the image to the left and keeps it aligned when working with all images in a series.



8. Align and Lock Right aligns the image to the right and keeps it aligned when working with all images in a series.



9. If there is not enough space for the buttons to be displayed, the More button is displayed. Click the More button to see the missing buttons.



10. View the additional data of the image using the Quick access to additional data buttons (number 10) in the Viewport toolbar. See detail functionality description in section “Quick access to additional data”.



11. Quickly save the key object and presentation state by tapping Quick save button (number 11) in the Viewport toolbar. See detail functionality description in sections “Presentation states” and “Key Objects”.

⚠ **NOTE!** System displays notification about ongoing process and temporary deactivates buttons **Copy original image to the clipboard**, **Save viewport content as secondary capture DICOM**, and **Quick save** to prevent the repeated clicks.

⚠ **NOTE!** System deactivates buttons **Copy original image to the clipboard**, **Save viewport content as secondary capture DICOM**, and **Quick save** in order to prevent the unintentional clicks while other mouse workflows, like measurements, are activated in the viewport.

⚠ **NOTE!** The tool button in the Viewport toolbar is displayed only if it is applicable according to the Viewer configuration, the user actions, or the viewport content.

The following controls may be displayed in the viewport (see controls at the bottom left corner in Figure 33):



12. Smooth thick-box for image and multi-frame image. By default, smooth should be applied when the image is opened. If the user unchecks the smooth tick-box, the system displays the image without smoothing and saves the information in browser’s local storage. The smooth will not be applied for the images of this modality until the smooth option is not changes once more, or the browser’s local storage is not cleared.

⚠ **NOTE!** The text and symbols may be distorted when smooth is applied on reports saved as secondary capture images.

⚠ **NOTE!** The smooth is not applied, and the smooth check box is not displayed, if the smooth is switched off in system configuration.

⚠ **NOTE!** The image sharpening and edge filters may be configured and accessed in Plugins tool menu.



13. Color palette selection box for monochrome images. The displaying of the color palette selection box is controlled from Windowing tool menu, and allows to apply the color palette to monochrome image (see in section “Color palette for monochrome images”).

Copy viewport content

If image, video or multi-frame is viewed in the viewport, the system provides two options for copying and saving of the viewport content:

- The Copy viewport content to the clipboard  button in the Viewport toolbar converts the viewport content to png format and copies it to the clipboard. When copied, the clipboard content may be pasted to any source, that supports png format.

- Save viewport content as secondary capture DICOM  button in the Viewport toolbar converts the copied viewport content to secondary capture DICOM and stores it on the PACS. JPEG baseline transfer syntax is used for storing the captured content. The stored image is automatically displayed as a new instance in the **Secondary captures** series, which is typically the last series in the study.

  ⚠ **NOTE!** Content of the viewport, that displayes the 2D or 3D recontructed series, may also be copied to the clipboard or saves as secondary capture.

⚠ **NOTE!** Saving viewport content to DICOM function is available only if the used study storage provides DICOM saving functionality.

The viewport content is copied as described:

- The size of the clipboard image is the same as the size of the viewport's area;
- The viewport's pixels are copied as follows:
  - The currently viewed image or frame, as it is displayed in viewport after all the transformations, like rotation, zoom, windowing, is copied;
  - The fused PET image pixels are copied;
  - If copying to the clipboard, all the viewport labels, as displayed in the viewport, are copied. For the viewport labels with active control (like smooth check box), the current selection is displayed instead of the control. If you want to copy without info labels, before copying hide the labels with Info Labels tool (see section "Info Labels");
  - All the measurements with labels, text (comments), as displayed in the viewport, are copied;
  - All the segments, as displayed in the viewport, are copied;
- The following viewport's elements are not copied:
  - Scroll bar is not copied;
  - Viewport toolbar tools (icons) are not copied;
  - Other toolbars (like fusion toolbar, multi-frame toolbar) are not copied;
  - If saving viewport content as secondary capture DICOM, the viewport labels and the viewport labels with the controls (like smooth check box) are not copied.

Copy original image to the clipboard

If image is viewed in the viewport, the Copy original image to the clipboard  button is displayed in the Viewport toolbar. Clicking the button converts the original content of the image, that is currently displayed in the viewport, to png format and copies this png image to the clipboard.

⚠ **NOTE!** Copying of the original image to the clipboard function is disabled in default system configuration.

Generate Intensity Projection (MIP)

When the button  is selected, the system detects the orientation of the current view plane and generates a MIST MPR image based on that plane. In the generated image, the user can adjust the Intensity Projection value (MIP/MinIP/AVG).

After the action is performed, the icon is highlighted  . Clicking the highlighted action icon returns the user to the original view.

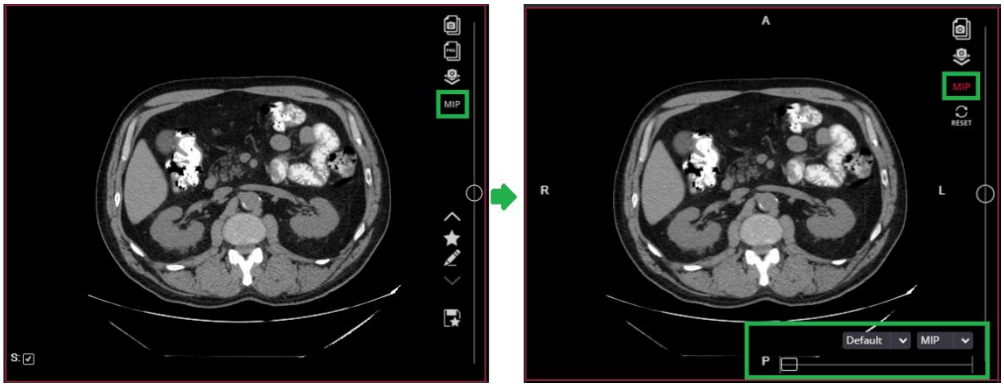


Figure 34. Quick access to additional data controls

⚠ **NOTE!** The visibility of the MIP button in the viewing area is configured in the system settings.

Quick access to additional data

⚠ **NOTE!** Medical image is qualified as image with additional data if either there is at least one presentation state saved for the image, or the image is marked as belonging to at least one saved or not saved Key object, or both conditions are met.

⚠ **NOTE!** Be aware, that viewing and saving the key objects and presentation states may be restricted by the user rights.

If series, that is viewed in the viewport, contains images with additional data, the controls for quick access to additional data are displayed in the Viewport toolbar:

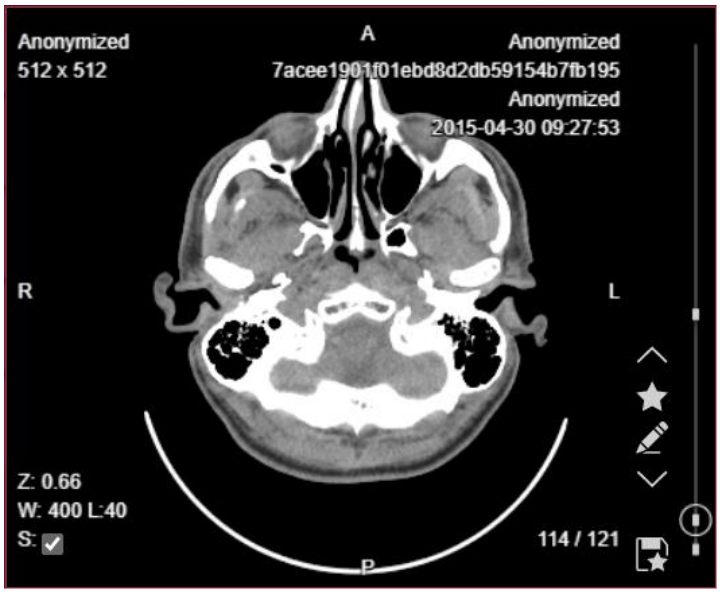


Figure 35. Quick access to additional data controls

To access the images with additional data and additional data, use quick access controls as described below:

- If scrollbar is displayed, marks on scrollbar  indicates the place of images with additional data within series. Click on marked place of the scrollbar to open the image with additional data.

- Use up-pointing chevron button, and down-pointing chevron button to navigate through the images with additional data in currently viewed series:
    - The chevron buttons are displayed only if series contains more than one image;
    - Click the up-pointing chevron button to navigate from the currently displayed image to the previous image with additional data in the series. The chevron button is grayed and inactive, if there isn't any image with additional data from the currently displayed image to the begin of the series;
    - Click the down-pointing chevron button to navigate from the currently displayed image to the next image with additional data in the series. The chevron button is grayed and inactive, if there isn't any image with additional data from the currently displayed image to the end of the series.
- Use Key object button to view the series Key objects and to set the Key object filter (see in section “Key Objects” for detail description). Key object button is grayed and inactive, if currently displayed image does not belong to any Key object.
- Use Presentation state button to view and to open the saved presentation state (see in section “Presentation states” for detail description). Presentation state button is grayed and inactive, if currently displayed image hasn't any saved presentation state.

Color palette for monochrome images

If monochrome image is viewed in the viewport, and the user enables the color palette selection for the series, that is displayed in the active viewport (see in section “Windowing”), the system displays the color palette selection field in the viewport. By default, the image opens in grayscale, and none color palette is applied. The user can apply the color palette:

- Expand the color palette selection field and select the palette, if you want the color palette to be applied:

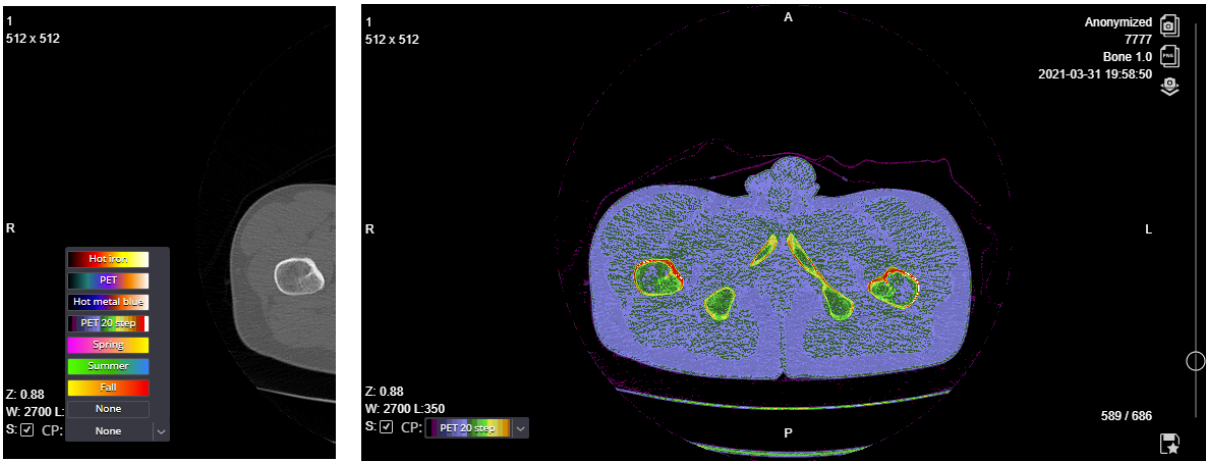


Figure 36. Color palette selection and applying

- Select do not apply color palette (“None” options) to see again the grayscale image in the viewport.

NOTE! Disabling the Color palette selection in windowing menu automatically clears the applied color pallete in the active viewport.

NOTE! The color palette is automatically disabled if the other series is opened in the viewport, or the other instance type is opened for the same series.

By applying the color palette, inversion can be applied too. The color set of an inverted CP is the same, but the start and end of the color gamut are reversed (for example if the first color was yellow and the last color was red, after the inversion the first color be red and the last color yellow).

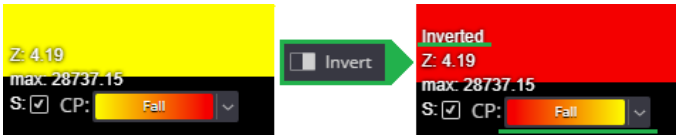


Figure 37. Inverted color palette

⚠ **NOTE!** If the color palette is applied to an inverted image for the first time, inversion is automatically switched off. If inversion is switched on after applying the CP, inversion is kept switched on.

⚠ **NOTE!** The color palettes list is not complete – in addition to the default palette set, a system administrator can add more. For more information, see the installation documentation.

Quick menu

A **quick menu** appears with a right-click mouse operation on the viewports' area. A quick menu offers tools that have been chosen to be included in a quick menu via Settings. Separate tools may be configured to be included in quick menu for Desktop display mode and for Mobile display mode. Refer to the "Panel toolbar settings" chapter for more information.

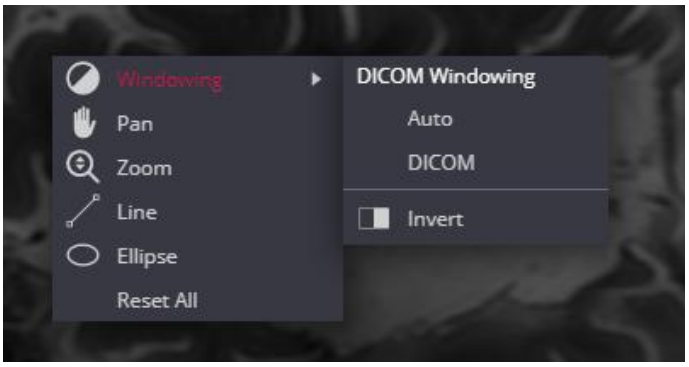


Figure 38. Quick menu

If it is specified via Settings that the thumbnail zone is accessed from the quick menu, right-click mouse operation at a selected point in the viewport displays the thumbnail zone on the right of the click point, and the quick menu on the left of the click point.

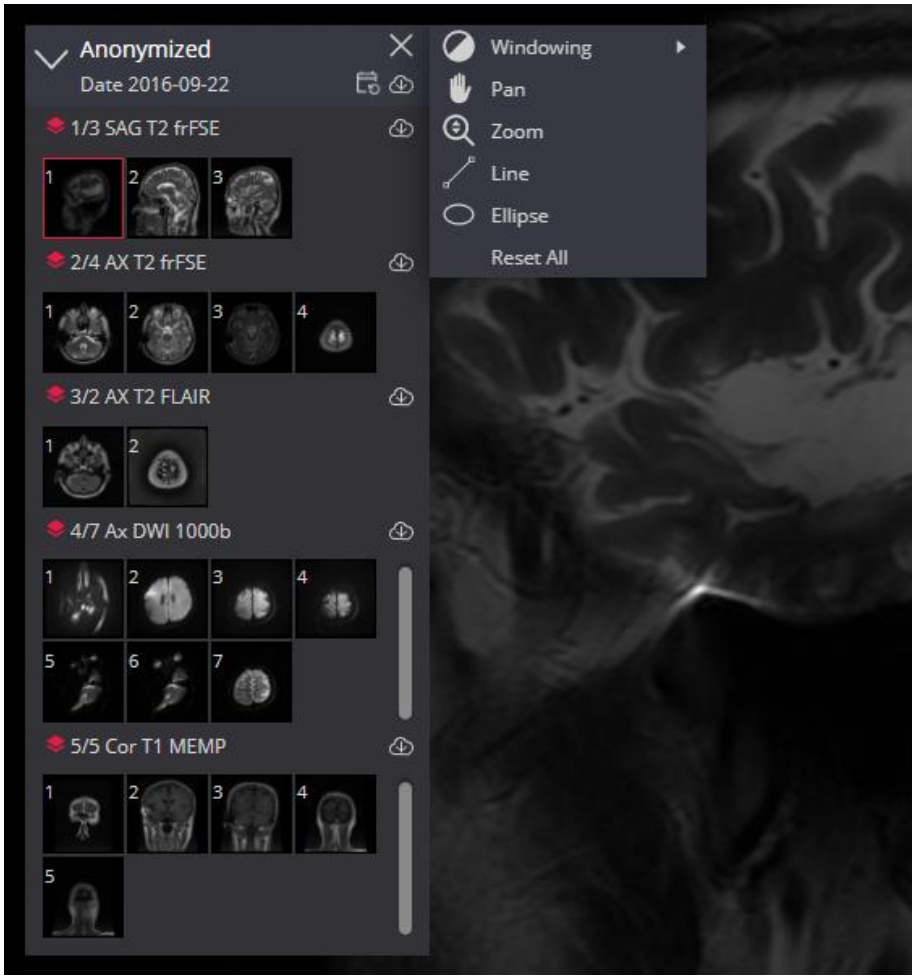


Figure 39. Quick menu with thumbnail zone

Opening studies

⚠ **NOTE!** The section described how to open the studies in Viewer window from the Search results list in Search window. For a description of opening studies in mobile mode, see in section “Opening studies in MedDream Mobile mode”. If Viewer is used in an integrated solution, the window is opened by an integrating information system, such as a hospital information system or a patient portal.

⚠ **NOTE!** See in sections "Patient studies window" and "Patient history" for detail description how to open the studies from the Patient studies list.

⚠ **NOTE!** To view the image of the study that is already opened in Viewer’s window, drag the image picture from thumbnail.

If you need to open the study, please do the following:

1. Find the study in search results list (the active line is highlighted when scrolling through list) and click on it.

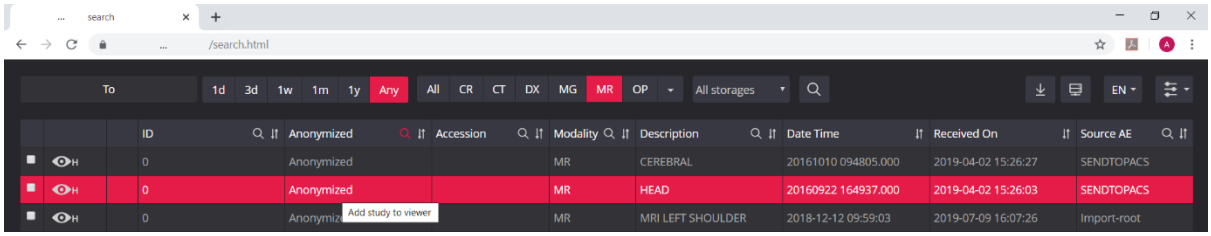


Figure 40. Study selection in the search results list

2. A new browser tab will pop up and Viewer window with selected study opens in it:

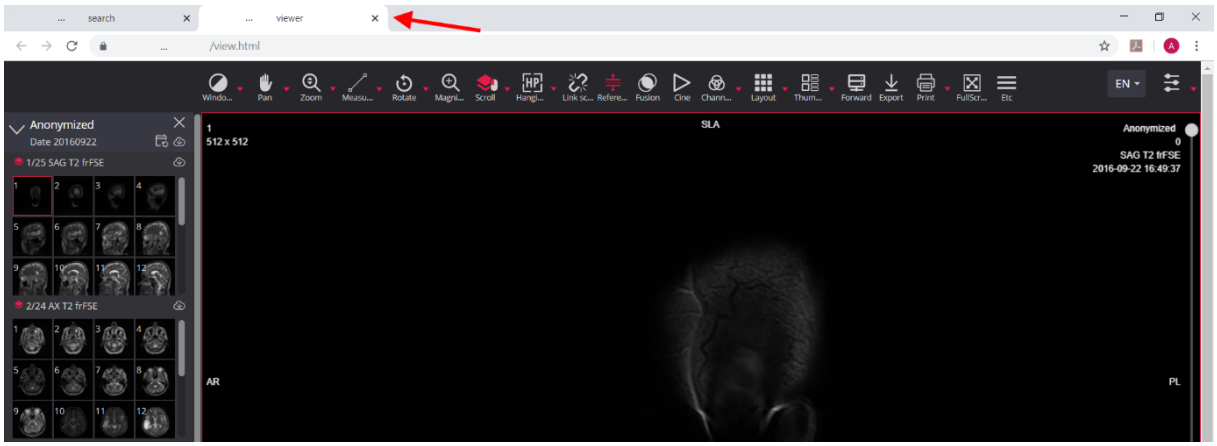


Figure 41. Viewer window in new tab

⚠ **NOTE!** The image of the first series opens, if Auto Open Image conditions are met (see description in the settings section).

⚠ **NOTE!** If one series thumbnail is configured for modality, the first or middle instance is opened depending on configuration.

3a. If you need to open more than one study in the same Viewer window (e.g. to compare images from different studies), please do the following:

- From Viewer window tab go back to the Search window tab.
- Find and click the study in search results, as described in step 1.
- The Viewer tab automatically activates and the selected study is opened in Viewer window. The study description is displayed at the bottom of the thumbnail zone and expanded. Descriptions of all the previously added studies are collapsed:

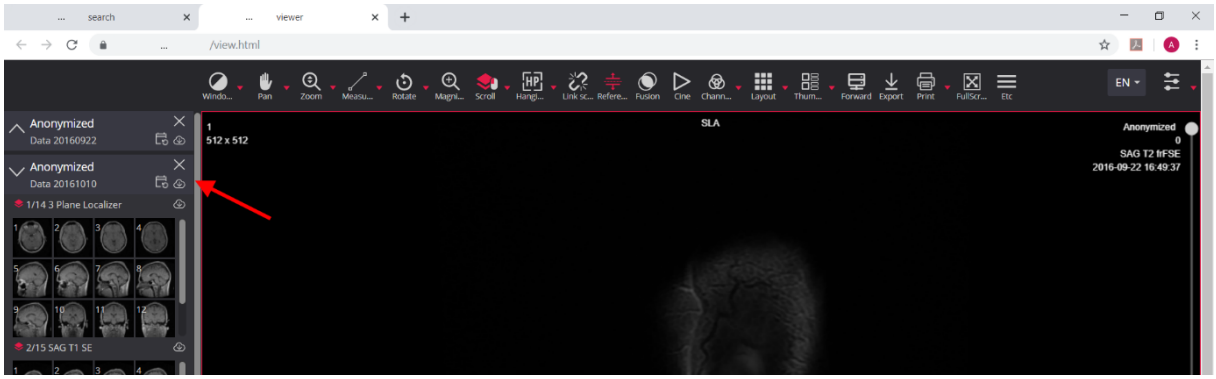


Figure 42. New study opened in the same Viewer window

⚠ **NOTE!** In case the first study image should be opened according to Settings, the image is opened in the first (top right) viewport and only if this viewport is empty.

⚠ **NOTE!** Repeat the actions of this step, if you need to open the third or more studies in the same Viewer window.

⚠ **NOTE!** By default, studies of multiple patiens may be viewed in the same Viewer window. However the system may be configured to close all the studies of previous patient before opening the study of a new patient. Contact your system administrator regarding the system configuration.

3b. If you need to open the study in a new Viewer window, please do the following:

- From Viewer window tab go back to the Search window tab.
- Find the study in search results and click it holding the CTRL key pressed down.
- The new browser tab pops-up and the new Viewer window with selected study opens in it.

Patient studies window

Patient studies window is displayed in the following conditions:

- URL with parameters is used for opening the studies in the Viewer,
- the passed URL parameter is patient ID for only one patient,
- and the system is configured to show Patient studies window instead of directly opening the studies in the Viewer window.

Patient studies window displays the **Patient studies list**, that is retrieved based on patient ID and storage data in URL:

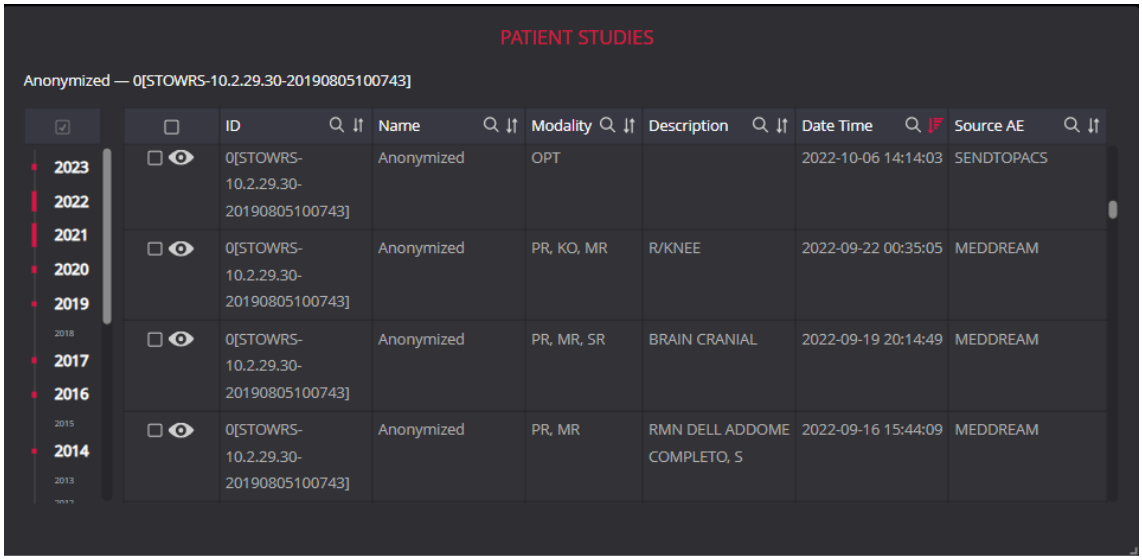


Figure 43. Patient studies window

You can sort, search, and open studies from Patient studies list (see detail functionality description in section “Patient history “).

NOTE! The system may be configured to return the patient studies for a limited number of days.

NOTE! The system may be configured to display the different study information in patient studies window and patient history window.

NOTE! It is not possible to sort and filter the patient’s studies list if working in mobile mode.

NOTE! You won’t be able to reopen the Patient studies window from the Viewer. But the patient studies list may be accessed in Patient history window, if the patient history viewing is allowed.

CAUTION! The integrating hospital system may have and use different patient ID from different sources for the same patient. Be cautious and note that patient studies history from the particular source will not be accessible from the Viewer, if you do not initially open at least one study with each different patient ID.

In case there is more than one patient returned, the warning mark will be displayed near the patient information. Use the chevron icon on the right to expand the list and view all the patients’ information:



Figure 44. Multiple patients’ information in Patient studies window

Patient history

Patient studies list provides a quick overview of all patient research history. The Patient history window opens by clicking the displayed patient’s history icon in thumbnail zone, or Study modal of the Viewer window:

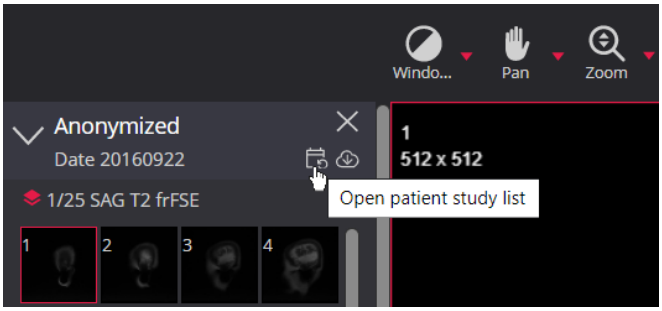


Figure 45. Opening the Patient history window from the header of viewed studies

⚠ **NOTE!** The patient's history icon is visible only if the viewing patient's history is allowed by system configuration, and the user rights.

⚠ **NOTE!** It is possible to configure that patient's studies are automatically opened in thumbnail panel in settings (see Settings section). By default, this function is disabled.

Patient history window displays the patient studies:

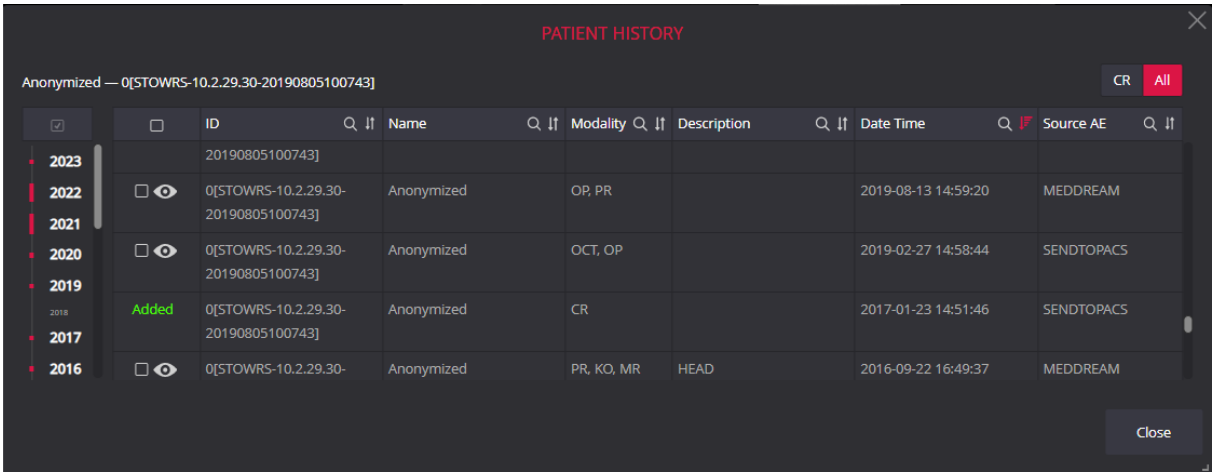


Figure 46. Patient history window

⚠ **NOTE!** The system may be configured to return the patient studies for a limited number of days.

⚠ **NOTE!** The system may be configured to search for patient studies either in all storages, or in the storage of the viewed studies.

⚠ **CAUTION!** Be aware, that access to the storages may be restricted by the user rights. If search for patient studies is configured in all storages, searching is performed in the storages, that are granted for the user.

By default, the following study information is provided in **Patient studies list**:

- **ID** - patient's identification number,
- **Name** - patient's name and surname,
- **Modality** - the method which was used to obtain the study images (modality),

- **Description** – the study description,
- **Date Time** – study date and time,
- **Source AE** – device from where the study was sent to the PACS.

⚠ **NOTE!** The system may be configured to display other study information in patient studies list.

You can use the modality filter at the top right corner of the Patient history window. Possible filter options:

- The modality of the study from which the Patient history window was opened (**CR** in the figure, 

);
- **All** patient historical studies. This option is the default value when you open history window.

You can do the following action in **Patient studies list**:

- Sort the patient studies list. Sorting is possible by all columns. The sort-related functionality:
  - By default, the list is sorted in descending order by **Date Time** when patient studies list is displayed.
  - To sort the list according to the selected column, or to change the sorting order, you need to click the sort button in the in the heading of the selected column. The action performs the sort and changes the sort icon as follows:  sorted ascending,  sorted descending,  unsorted.
  - It is allowed to sort only by one column at a time. Sorting by another column automatically cancels the previous sort.
- To filter or search the studies list:

To apply the modality filter, click the modality button in the top right corner of the patient history window 

. The highlighted button indicates, that modality filter is applied. Click "All" to reset modality filtering.

To view the studies for a particular year, use year filter on the left of the window. Click the year that has studies indicator on the left, and the highlighted year 

indicates, that year filter is applied. You may filter the studies for several years by holding CTRL button pressed and clicking the years in the year filter. The option "NA" is available at the end of the filter, if there are studies without study date. To remove the particular year filter, click on the highlighted year. The check box at the top of the filter removes all the year filters.

  - Filter/search is possible by all columns with a search icon  . To perform a search, click on the column name – the system highlights the search icon and search criteria input field. Enter a search phrase in the highlighted input field - the system automatically filters the list based on the text you enter. The columns with an active filter have highlighted search icon  in the column header.
  - Note, that it is allowed to have different filter applied at a time.
- Open the patient study for viewing:
  - To open one study, click on the eye icon  in the first column of the studies list.
  - To open multiple studies at once, mark the tick-box next to the studies you want to open and click the **Add studies to viewer** button. All the studies, that currently displayed in the list, may be marked or unmarked at once by clicking the tick-box in the header of the first column.
  - All the studies, that are already opened in Viewer, are highlighted as **Added** and haven't controls for opening.



Figure 47. Searching and opening several studies from Patient history window

NOTE! It is not possible to sort and filter the patient's studies list if working in mobile mode.

NOTE! By default, patient history search is performed according to the *Patient ID*. Contact your system administrator regarding the system configuration, if multiple patients ID are displayed.

Tools for image manipulation and analysis

NOTE! In section "Toolbar Properties" you can configure, what buttons and in what order are shown in toolbar.

To adjust and to analyze the study images according to the criteria you need, use the image manipulation tools:

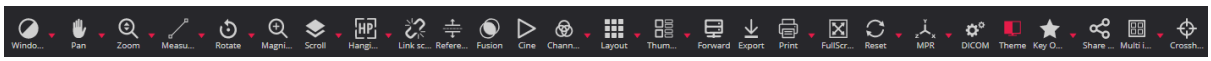
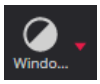


Figure 48. Image manipulation tools

Windowing



Windowing button is used to adjust image contrast and brightness (Level and Window values). You can change the brightness using the mouse or from menu.

For changing the brightness with mouse, assign the mouse button to Windowing function 

. Hold down the assigned button and drag the mouse upwards or downwards (to change Level values), and right or left to change Window values. You also may change the windowing value with mouse middle button drag and holding the Shift button pressed.

The windowing values may be applied for the same series in different viewports. By default, this feature is disabled, and you should use the **Sync Windowing for Same Series** menu to enable it.

NOTE! Sync Windowing feature is also applicable for the reconstructed orthogonal series.

Also, you can click the red triangle on the right of the button and select the windowing from the menu:

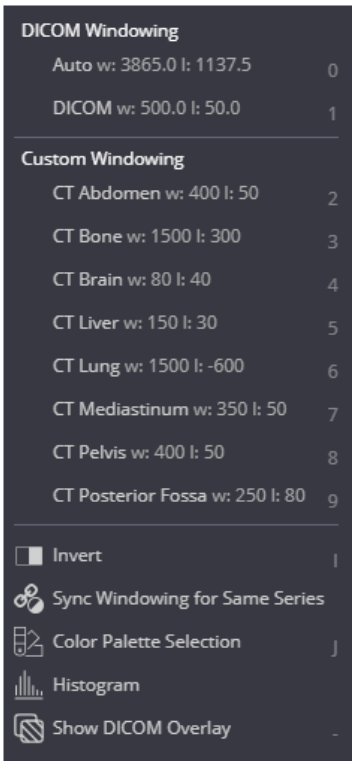


Figure 49. Windowing button menu example

The brightness level menu consists of static and dynamic elements - groups and options. Dynamic menu elements are only displayed if they are applicable to the active image.

The description of Windowing menu elements:

- Static group **DICOM Windowing**. Group contains the following options:

Auto – the system analyses the image and adjusts the brightness and contrast automatically. Static menu option. Auto windowing is applied, if no other options available in DICOM Windowing group.

Dynamic menu options - all the Window and Level value pairs from image DICOM data: windowing title, w value, and l value are displayed. The first option is automatically applied, if available.

- **VOI LUT** (*Value Of Interest Look-Up Table*) dynamic group is displayed only if VOI LUT configurations are found in image DICOM file. This transformation gives greater weight to the range of values of interest. The DICOM Standard Window Center and Window Width are linear VOI LUT where only 2 parameters are specified - center and width of the interval. Meanwhile, the non-linear VOI LUT uses a free shape curve in the form of a table. In MedDream user environment VOI LUT is called non-linear transformation.

The VOI LUT group displays all VOI LUT configurations that are available in the active image DICOM file. The names of VOI LUT configurations specified in the DICOM file are displayed. If VOI LUT configurations exist, the first VOI LUT configuration is automatically applied, along with Auto w and l values.

- The **Color LUT** group displays the **COLOR PALETTE** menu, if COLOR PALETTE is found in image DICOM file. If there is a Color Palette, it will be applied during the study loading process. After changing the Window Leveling through the menu for an open image, the Color palette will not be applied automatically. To apply the color palette after changing the windowing level, click the **COLOR PALETTE** menu.

- **Custom Windowing** dynamic group holds the custom windowing options that are define in settings (see in section “Windowing settings”), if the active image modality adheres to settings.

- **Invert** – the static option that is used to invert the image.

- **Sync Windowing for Same Series** – static option that allows applying windowing values for the for the same series displayed in different viewports (including MPR projections). Windowing synchronization is

enabled if the synchronized windowing icon on the left side of the menu is highlighted . Windowing synchronization settings are stored in your browser's local storage and only apply to the same browser.

- **Color Palette Selection** – static option that enables applying color palette for the series in the active viewport (see in section “Color palette for monochrome images”). Color palette selection is enabled, if icon on the left side of the menu is highlighted .
- **Show DICOM Overlay** – static option that shows or hides the overlay on the image. Overlay is displayed, if icon on the left side of the menu is highlighted .

NOTE! To view the overlay, the overlay layer data should be available in DICOM, and displaying overlay should be configured.

NOTE! Showing of retired built-in overlay may be additionally disabled in the configuration. Contact your system administrator, if overlay data is not displayed.

NOTE! The overlay layer is automatically inverted, if displayed on inverted image.



Figure 50. Image with DICOM overlay layer displayed (left) and not displayed (right)

Shortcuts can be used to change values of windowing:

- The **Auto** is linked to shortcut [**0**] by default;
- The **DICOM** value is linked to shortcut [**1**] by default; if there is more than one value in the DICOM, the shortcut is linked to the first value and the next value has no shortcut.
- **Custom Windowing** shortcuts values are created dynamically from [**2**] to [**9**] the order in which the values in the menu are displayed. If you want to change the order of the shortcuts, you have to change the order of the custom values in the settings window.

Auto and DICOM-first values can be assigned additional shortcuts values. For more information see in chapter "Shortcuts".

Histogram



The **Histogram** can be opened from the Windowing menu by selecting the item **Histogram** or by pressing a keyboard shortcut (if one has been assigned by the system administrator).

Histogram - a bar graph showing the distribution of pixel intensity data in an image: the horizontal axis of the graph represents the change in values and the vertical axis represents the total number of pixels for that value. The yellow curve crossing the graph represents the windowing W/L values.

Three graph scales can be selected 

:

1. “HU” - fixed scale HU units from -1500 to 2500;
2. “Min-Max range” - scale from the actual smallest pixel value to the actual largest value in the image (scale width and values depend on the open image data);
3. “Full range” - the maximum possible set of values under the pixel intensity storage tag “Bits Stored” ("16": [-32768, 32767]; “12”: [-2048, 2047]; “8”: [-128, 127]).

It is possible to specify how many bins the data should be split - **Number of bins** (possible values from 32 to 1024).

In positron emission tomography (PT) studies, a scale with SUV units is displayed 

. If the study data are sufficient for SUV calculation, this scale is selected. If the data are anonymized in such a way that SUV values cannot be calculated, the SUV scale is still shown but cannot be selected.

⚠ **NOTE!** There are cases when scales of histogram bins and windowing values do not match, what makes the histogram diagram unusable. The warning message will be displayed in histogram window in such case.

The user can change:

- the center of the range - the **Window Level** (L);
- the range of the numbers is referred to as the **Window Width** (W);
- the **lower bounder** of width;
- the **upper bounder** of width.

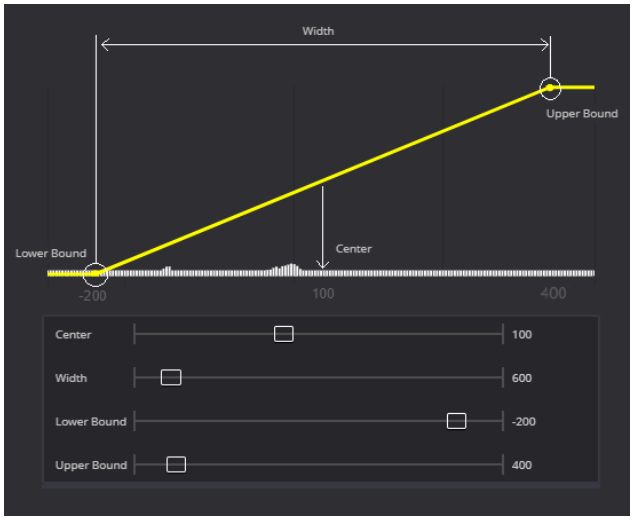


Figure 51. Managing W/L values in the histogram

Values can be changed with the slider bar, by entering values from the keyboard, or by using the arrows to change values within 10 

.

NOTE! When entering a value from the keyboard, the system will only apply the entered value when Enter is pressed or when the cursor focus is changed.

NOTE! If the user enters a value lower than the possible value, the system automatically selects the lowest possible value. The system automatically selects the maximum possible value if a value greater than the possible value is entered.

NOTE! You can see the maximum and minimum values in the tooltip that appears when you hover the mouse over the input field.

In the Histogram window it is possible to select DICOM file, Auto and Custom values, in the same way as in the Windowing menu item. It is also possible to invert the image and activate the color palette.

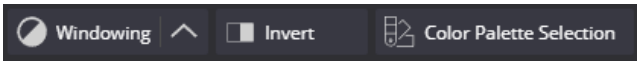


Figure 52. Additional buttons in the histogram window

In the histogram window of fused images, two tabs are available. By switching between the tabs, the user can view the values of both layers and control windowing for each layer separately.

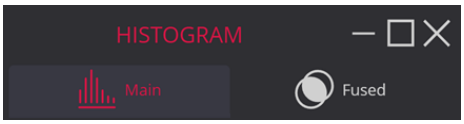
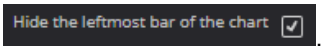


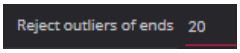
Figure 53. Histogram of fused images

The window contains a group of additional information 

.

This part contains additional options:

- to unmark the flag to not hide the leftmost bar of the chart 

.
- the option to specify that reject outliers from ends less than 

(the maximum possible value 20).

NOTE! If multiple viewports are open with different studies or different images, the histogram represents the information of the image on which is active.

Rotate the mouse wheel to zoom in on the histogram graph. Zooming in shows a more detailed range of values. The enlarged graph can be viewed by dragging it to any edge of the graph.

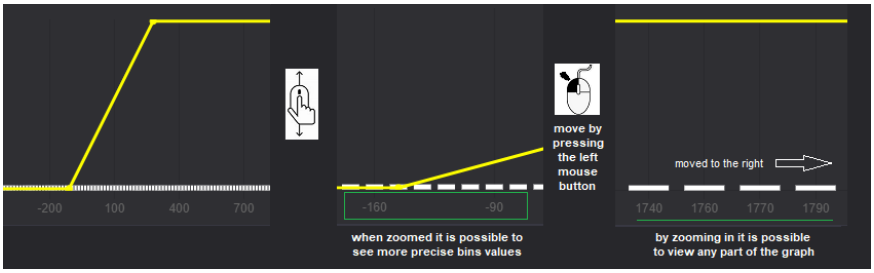


Figure 54. Zoom the histogram graph

For a more detailed view of the number of pixels with specific values, you can scroll the Y-axis slider bar.

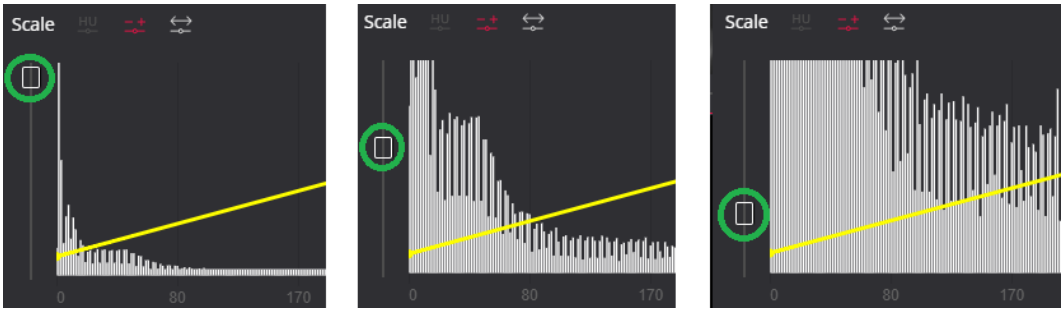


Figure 55. Zooming the Y-axis of the histogram graph

To cancel the zoom, select the button 

.

Pan



Pan button allows you to position images within the pane. You can change the image position using the mouse or alignment option from menu. This feature is especially useful when the image is larger than the pane, as it usually is after zooming in.

For changing the image position with mouse, assign the mouse button to Pan function 

. To move an image within the pane:

- press the selected mouse button on the image and drag the cursor to desired place or position;
- release the mouse button to leave the image in its new position.

You also may change the position with mouse middle button drag and holding the Ctrl button pressed.

You can use the Pan menu for changing the image alignment, the highlighted icon indicates that alignment is activated 

:

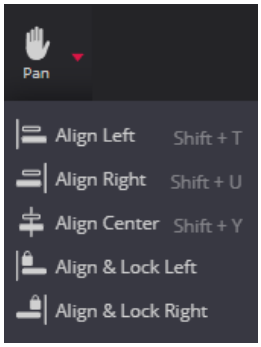


Figure 56. Image alignment options in Pan menu

The system maintains the current vertical image positioning in the viewport in case the left or right horizontal alignment is applied. However, the image is centered horizontally and vertically, if Align Center is chosen.

Menu actions with the additional Lock function  not only align the image but also keep it aligned while working on images of the series. The lock does not allow the images to be moved away from the selected border when changing the image scale or place. When the Lock menu is activated, icons are highlighted  .

To turn off locking, press the highlighted menu item again.

The system automatically turns off locking when you select alignment without locking or when you perform a Rotate action (either with the mouse or by selecting from the menu).

Align & Lock buttons available on the viewport in **MG** images.

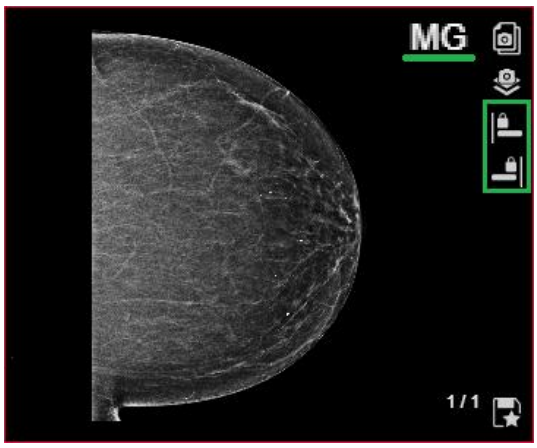


Figure 57. Align & Lock buttons on the viewport

Functionality can be activated which, when Align & Lock is activated, displays all labels and controls (buttons, slider bar, etc.) on the opposite side of the alignment image.

⚠ **NOTE!** Functionality may be enabled or disabled in the settings.

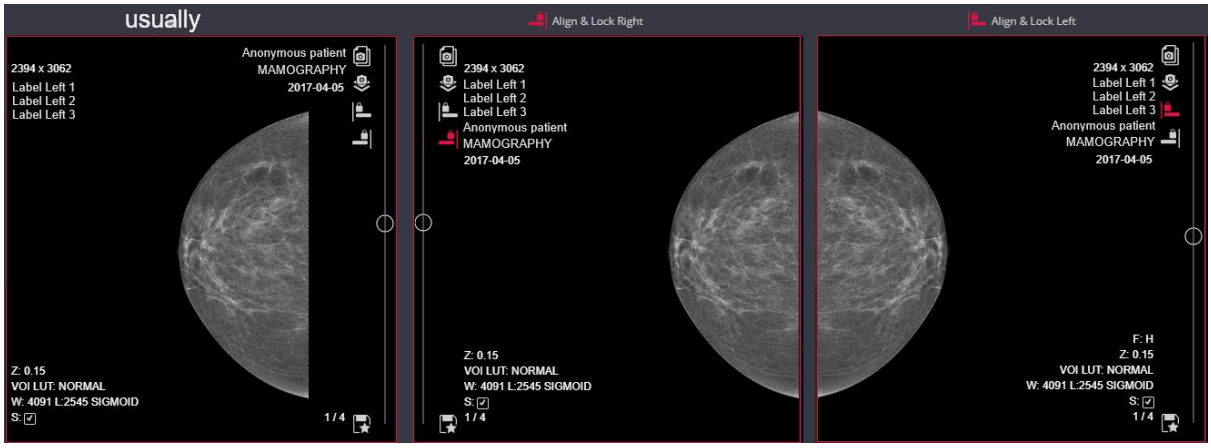


Figure 58. Align & Lock. Control buttons on the opposite side of the alignment

In addition, it is possible to define in the settings which labels must be displayed if the viewport height is small and all labels do not fit. For example, if you specify date and patient name as mandatory and if all labels don't fit, only defined labels are displayed, other labels are not displayed, but "..." is indicated

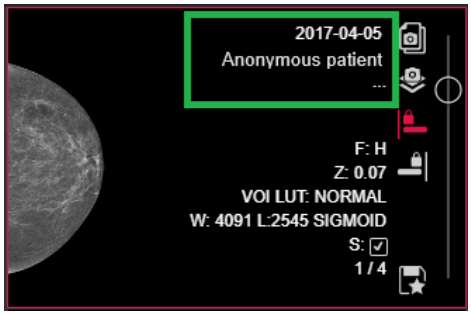
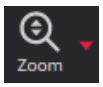


Figure 59. Align & Lock. Mandatory labels to be displayed

Zoom



Zoom button allows you to enlarge or reduce the image size. You can change the image size using the mouse or zoom option from menu.

For changing the image size with mouse, assign the mouse button to Zoom function 

. To zoom the image, do the following:

- choose which part of the image you want to zoom in/out,
- place the mouse cursor on the chosen part,
- click the selected mouse button and drag up or down,
- the chosen part will be zoomed in/out.

You also may zoom by scrolling the mouse wheel and holding the Ctrl button pressed.

By default settings, the zoom is done to or from the start position of the mouse cursor. See Settings section, howto configure the zoom to or from the viewport center.

⚠ **CAUTION!** Be cautious and ensure, that you are viewing the right place, if working with a zoomed image.

⚠ **NOTE!** If Align and Lock function is on, the alignment to the selected side is maintained while zooming.

Zoom button menu may have the following options:

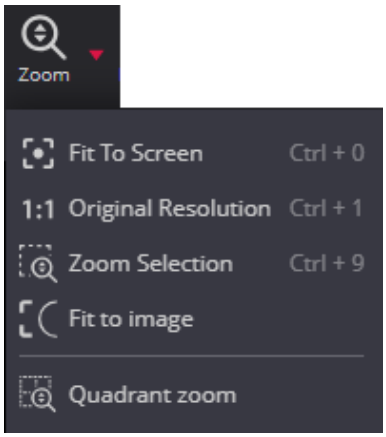


Figure 60. Zoom button menu

When you click **Fit to Screen** option, the size of the image is automatically adjusted so that the image would fill the entire viewport. So, if the image is too large, it is zoomed out, and if it is too small, it is zoomed in.

Clicking **Original Resolution** option, the size of the image changes into original size.

Clicking **Zoom Selection** option activates the area selection workflow in the active viewport:

- press the mouse button, that is assigned to the Zoom tool, at the corner of the region, which you want to zoom;
- drag the mouse to the opposite corner of the region, which you want to view – the system automatically draws the bounding rectangular;
- release the mouse button when the rectangular bounds the region, which you want to be viewed in the viewport;
- the system fits the selected region to the viewport.

⚠ **NOTE!** Rotation, flip, and horizontal alignment is maintained when zooming the selected region.

⚠ **NOTE!** Access **Zoom Selection** and **Fit to Screen** options from quick menu, or by shortcuts for quickly zooming to the region of interest and going back to whole image.

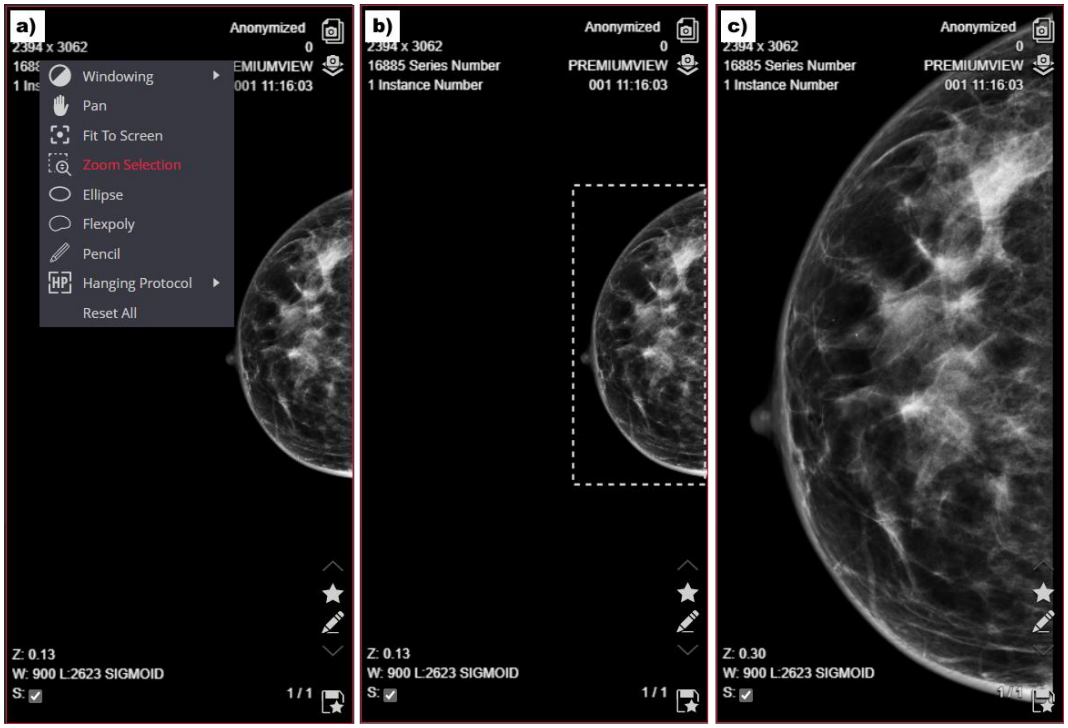


Figure 61. Zoom selection

Zoom selection steps: a) select Zoom Selection in quick menu; b) press and drag mouse to select region in viewport; c) release the mouse button to zoom the selected region.

Fit to image option is available only for mammography images. When you click Fit to image option, the system detects the actual mammography image boundaries and excludes the empty background and then displays the actual image to fill the entire viewport.

⚠ **NOTE!** In case of tomosynthesis multiframe images, the actual image boundaries are calculated based on current frame image and are used for all the frames. Apply Fit to image several times, if the image placement becomes not acceptable when scrolling the frames.

Quadrant zoom for mammography

⚠ **NOTE!** The **Quadrant zoom** functionality is available only if allowed by license and system configuration.

The **Quadrant zoom** option will be displayed only if the active panel has 1x2 layout with one or two aligned and locked to the panel center line mammography images. In case of two images, these images must be of a similar size and divide to the equal number of quadrants.

⚠ **NOTE!** If image play mode is on (see section “Cine mode” for example), the Quadrant zoom is automatically switched off or not allowed. Switch off image playing mode to use the Quadrant zoom functionality.

Clicking **Quadrant zoom** option starts the browse through both mammography images in original resolution, and displays the quadrant zoom support menu options in the expandable Zoom tool menu:

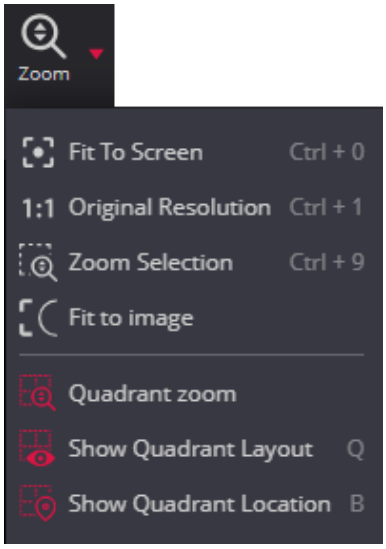


Figure 62. Zoom button menu when Quadrant zoom is active

By default, the system displays overview images in both viewports with the location of the quadrants marked with a green frame and the location of the currently enlarged quadrant marked with red frame.

⚠ **NOTE!** By default, the **Q** shortcut is assigned to Show Quadrant Layout menu option, and **B** shortcut is assigned to Show Quadrant Location menu option. The shortcuts may be changed or assigned in the Shortcuts window (see section "Shortcuts").

The quadrant location is calculated by separating the part with image from the empty background and automatically enabled, but the user can select to navigate the whole image by clicking the highlighted Show Quadrant Location option in the Zoom menu and disabling it. If the Show Quadrant Location option is disabled, the green quadrant location frame will be placed at the border of the overview window. You can change the quadrant location selection with the shortcut key **B**.

The user can navigate the images sequentially moving through the quadrants:

- Buttons to navigate the quadrants with number of currently viewed quadrant and total number of quadrants are displayed in panel toolbar.
- The default shortcuts are assigned to the quadrants navigation buttons. **PageDown** shortcut displays the next quadrant enlarged, and the **PageUp** shortcut returns to the previous quadrant.
- The system also provides the possibility to use the same shortcuts for hanging protocols and quadrant navigation. If the hanging protocol with quadrant zoom is opened, the shortcut assigned to both functions moves to the next quadrant until the last quadrant is viewed and then goes to the next hanging protocol. By default, the **Alt+V** shortcut displays next hanging protocol or next quadrant, and **Alt+C** shortcut displays previous hanging protocol or previous quadrant. This behavior may be disabled by assigning the different shortcuts for shortcuts pairs Next HP and Next Quadrant with priority, and Prev. HP and Previous Quadrant with priority in 2D shortcuts section of Keyboard shortcuts (see section "Shortcuts").

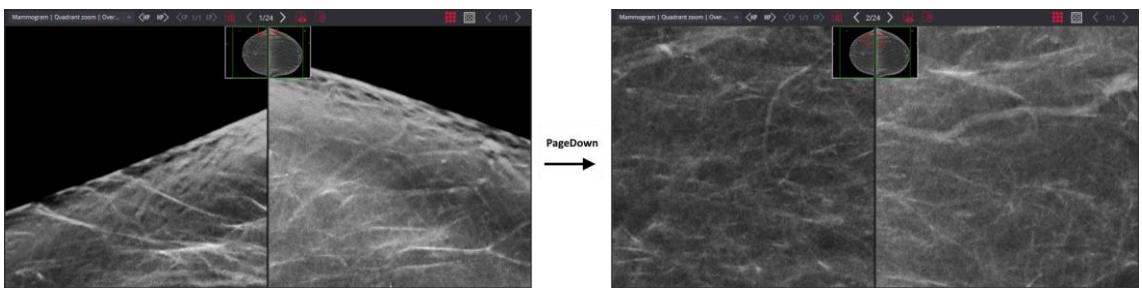


Figure 63. Browse mammography images with quadrant zoom function

The user can hide the overview window with shortcut **Q** or by clicking the highlighted Show Quadrant Layout option  in the Zoom menu and disabling it  .

NOTE! The system keeps the same windowing, inversion and color palette values when showing quadrant in original resolution. The user can change the windowing and inversion for the viewport with active quadrant zoom. However, the color palette selection component is hidden, and color palette may not be changed without switching the quadrant zoom off or using color palette sync functionality.

The system automatically switches the Quadrant zoom off, if the user interrupts the ongoing mammography images browsing, for example by placing the other image in the viewport, resizing the image, or changing the panel layout. In case the viewports are resized, the system may propose or force the user to restart the browsing from the first quadrant in order that any part of the image is not overlooked.

The user can also stop the Quadrant zoom by clicking the highlighted Quadrant zoom option  in the Zoom menu and disabling it  .

NOTE! The Quadrant zoom menu options and navigation component may be configured to be displayed in the Panel toolbar. See sections “Panels, Layout, and Multi image/series” and “Panel toolbar settings” for detailed description.

Channels



Channels highlights a color component or two colors combination component in the image by showing selected color in white shades and other colors in black. This tool is enabled for image view. By default, no color component is highlighted. Click the red arrow in order to choose color(s) from the list:

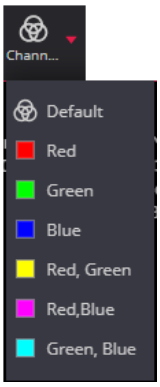
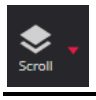


Figure 64. Color selection in Channels button menu

The selected channel is applied and its icon is displayed on Channels button  . To remove the color highlighting, select the **Default** menu option in Channels button menu.

Scroll



Scroll tool enables easy image scrolling with mouse and changing the active series using button’s drop-down menu. You can scroll the series images by scrolling the mouse wheel in the desired direction.

For scrolling the series images with mouse without wheel function, assign the mouse button to Scroll function 

. Once tapped it enables you to scroll through the series of images by using a vertical drag gesture: drag upwards to scroll towards the series beginning, and drag downwards to scroll towards the series ending.

You also may scroll the series images by scrolling mouse wheel.

By default, scrolling is done in scope of current series. To enable the scroll between series, use the **Activate fast scroll between series** menu.

NOTE! Scrolling between series apply for scrolling with mouse and does not apply for scroll bar function.

Scroll button can be extended:

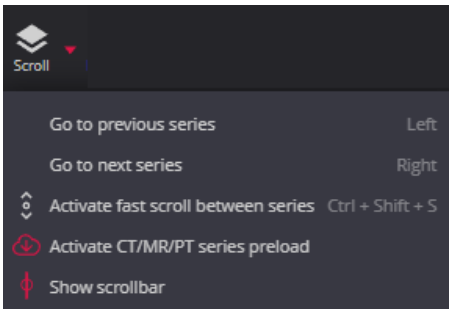


Figure 65. Scroll button menu

- To change the active series, use menu option **Go to previous series** (shortcut - Left Arrow in keyboard) or **Go to next series** (shortcut - Right Arrow in keyboard). In settings this functionality can be included in quick menu, for faster browsing through study series.
- To activate/deactivate of fast scrolling between series with mouse, use **Activate fast scroll between series** option. Series scrolling is enabled if the scroll icon on the left side of the menu is highlighted  . The initial value is taken from Activate fast scroll between series setting. If changed, series scrolling settings are stored in your browser's local storage and apply instead of system settings.
- To automatically start series images preload on CT/MR/PT series opening, use **Activate CT/MR/PT series preload** option. Menu option is displayed, only if the not displaying series images thumbnails and automatic preload is configured for CT/MR/PT series, and progressive instances preload is not configures in settings. Automatic series preload is enabled if the preload icon on the left side of the menu is highlighted  . Automatic preload settings are stored in your browser's local storage and only apply to the same browser.
- The **Show Scrollbar** option is enabled by default  . It defines that a scroll bar is displayed on the right side of the viewing area. When this option is unchecked  , the scroll bar is no longer displayed.

Magnifier



Magnifier button is used to magnify (enlarge) a certain area of the image.

Assign the mouse button to Magnifier function 

. Click the selected mouse button on the desired image place - image area is enlarged. The enlarged area can be dragged to other place of the image in order to magnify it. The small circle shows the center of enlarged area.

You can change magnification in this area with the help of mouse wheel from 1 time (no enlargement) to 50 times. In order to enlarge, press the selected mouse button and scroll the mouse wheel until the desired

magnification is reached. The actual magnification value is displayed on the bottom left corner of the active viewport (M x [magnification coefecient]):

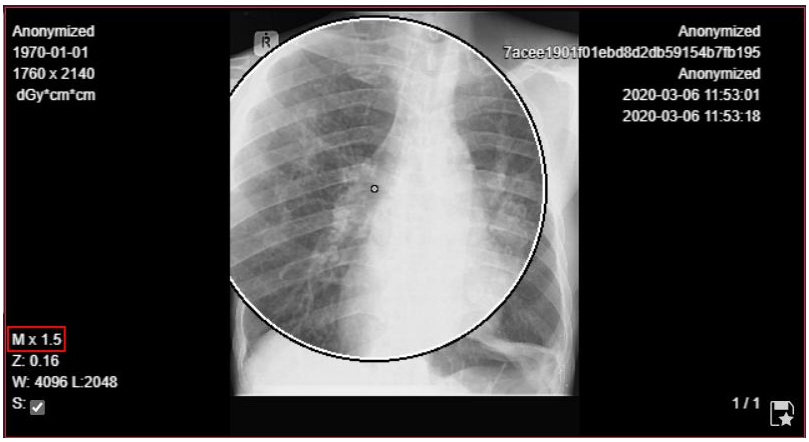


Figure 66. Magnification coefficient of Magnifier tool

To change the magnifier radius, press the selected mouse button, press Alt and scroll the mouse wheel till will reach the required size.

Tool magnification and radius can be different in different viewports.

The last changed values the system will apply in the newly opened viewport and the new session.

Digital Subtraction



Digital Subtraction button is used to subtract a pre-contrast mask image from subsequent images for better visualization of blood vessels in angiography series.

The Digital Subtraction tool is displayed in toolbar only if the active angiography image series or multiframe has the mask data, and the digital subtraction is enabled in configuration.

⚠ **NOTE!** By default, configuration the digital subtraction function is disabled. Contact your system administrator, if you want to use the digital subtraction for angiography series with mask data.

The automatic applying of digital subtraction at image opening may be configured, if subtracted is recommended viewing mode for angiography image series or multiframe. The digital subtraction icon is highlighted  , if the digital subtraction is currently applied.



Figure 67. The angiography multiframe image without (on the left), and after the mask subtraction (on the right)

The digital subtraction also can be applied or cleared manually.

Click the highlighted Digital Subtraction button in the toolbar to revert the mask subtraction, and view the original series in the viewport.

Click the not highlighted Digital Subtraction button to subtract the mask from the displayed angiography series. The image tools like windowing, zoom, pan, may be applied for viewing and analyzing the subtracted series.

Montage



Montage button opens the Montage dialog window, in which the user can create the montage from the currently viewed images, and save this montage image as secondary capture DICOM.

To do the montage, click the Montage button with the selected mouse button. The system allows assigning the left, and the middle mouse button for montage tool. The right mouse button may not be assigned for montage tool. The mouse pictogram with assigned button is displayed  , and the montage window is opened.

You can add the content of any not empty Viewer viewport to the montage by clicking on the viewport with the assigned mouse button:

- The system copies the viewport content to the first empty viewport in the montage image, if an empty viewport is available.
- If maximum montage layout size not reached, and empty viewport is not available, the system extends the montage layout, and copies the viewport content to the first empty montage viewport. The maximum allowed montage layout is 20 viewports.
- The system copies image pixels, measurements and text (comments). The patient identifier, name, study date with highlighting for comparison study, labels are also copied. Other labels, and the other content, like reference lines, segmentation, fused layer pixels, are not copied.

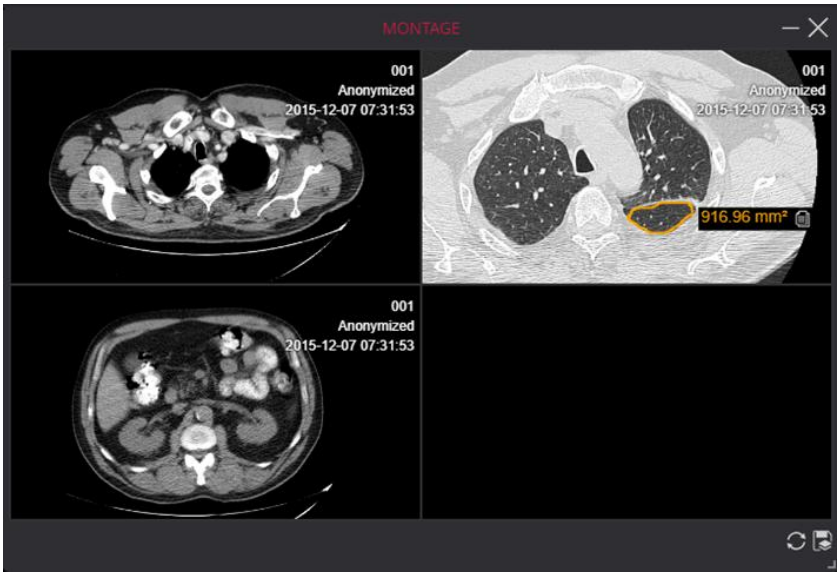


Figure 68. Montage window

⚠ **NOTE!** If shortcut is assigned to the Montage button, it opens the Montage dialog window if not opened, or adds the image from the active viewport to Montage dialog, if the Montage dialog is already opened.

⚠ **NOTE!** To minimize risk of image mismatch, the system displays the patient identification code, patient name, and study date on each displayed or saved montage image.

With the buttons in the top right corner of the Montage window, you can do the following:

- Delete the image from the montage by selecting the montage viewport ant then pressing the Delete button. The montage layout is not changed and the empty viewports is left after deleting the particular image from montage.
- Reset all the montage by pressing the Reset button. All the images are cleared, and montage layout is set to one viewport.
- Save the current montage image as secondary capture DICOM by pressing the Save button. The system converts the montage image to secondary capture DICOM and stores it on the PACS. The default background color is black, but it may be changed in settings. The stored image is automatically displayed as a new instance in the **Secondary captures** series, which is typically the last series in the study.

  ⚠ **NOTE!** Saving viewport content to DICOM function is available only if the used study storage provides DICOM saving functionality.

- Close the Montage window by pressing the Close window button.

Sync actions



The **Sync Actions** function allows performing certain actions simultaneously across multiple viewports. The user can choose which viewports the synchronization should be applied to.

Synchronization of Window Level, Color Palette, Zoom, and Pan

The first five function groups in the **Sync Actions** menu provide the ability to perform Window Level, Color Palette, Zoom, and Pan operations across multiple viewports: for the same series or for all viewports where are open images, or for the viewports with Auto synchronized series (see section Link scrolled series for more iformation). By default Synchronization settings Pan and Zoom is synchronized for auto synchronized CT, PT, NM, and MR series (see Settings section for more information).

Select the menu and check in the drop-down list of actions that want to synchronize. If you want to synchronize all actions - Windowing, Color Pallete, Zoom, and Pan - mark the first group.

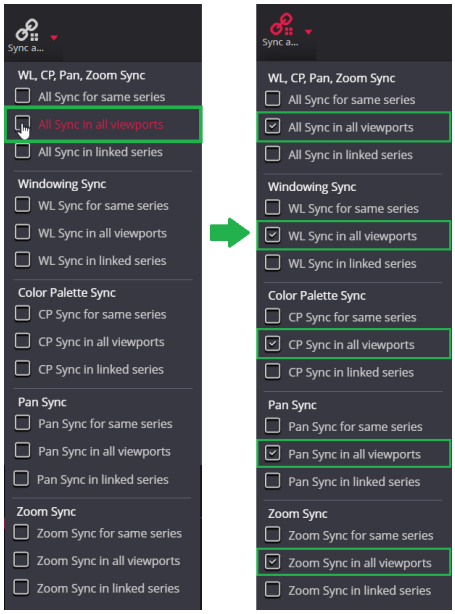


Figure 69. Sync all action

If you need not all actions or different selections, e.g. for Zoom in all viewports and Windowing only in open views in the same series, then select the required items one at a time by reopening the menu.

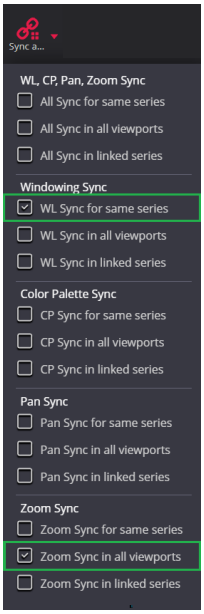


Figure 70. Sync some actions

The selection is saved in the browser's local storage and will be set when starting the viewer next time, but it may be configured to use the Synchronization settings instead of local storage values (see Settings section for more information).

When the attribute is checked, the action is performed synchronously in the same series or in all viewports, or Auto synchronized viewports. For example, the Color Palette will be enabled in all of them, and changing the value in one viewport will change it in the others (or in the same series, or in all).

⚠ **NOTE!** Pan actions "Align & lock Left" and "Align & lock Right" are not applied to the MG images despite the Pan Sync is selected and applicable for the viewport.

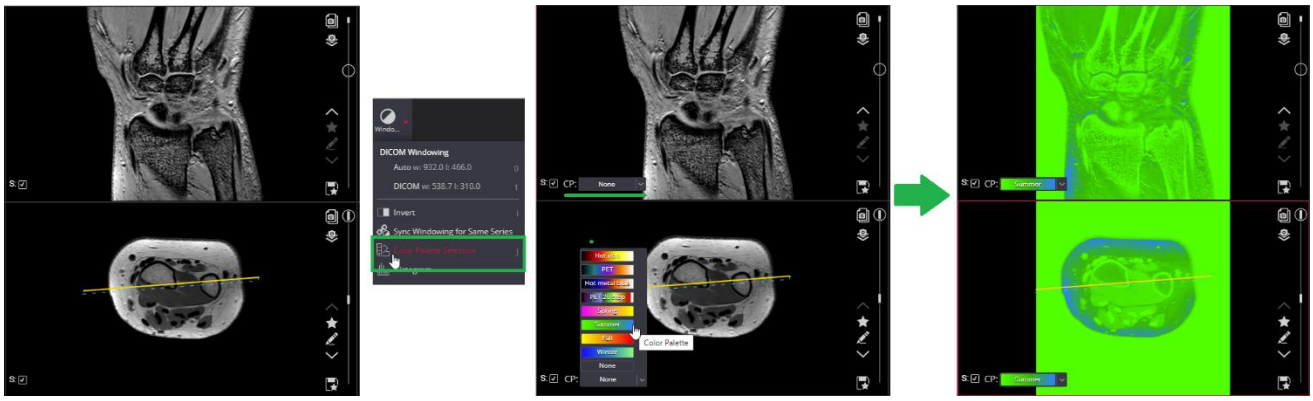


Figure 71. Sync CP in all viewports

⚠ **NOTE!** If the functionality is activated in different view states, e.g. Windowing has already been changed, or has already been moved, or has already been enlarged, or the viewport sizes are different, then the resulting visuals may be different because the action is performed in proportion to the current view state. It is not synchronized in absolute values.

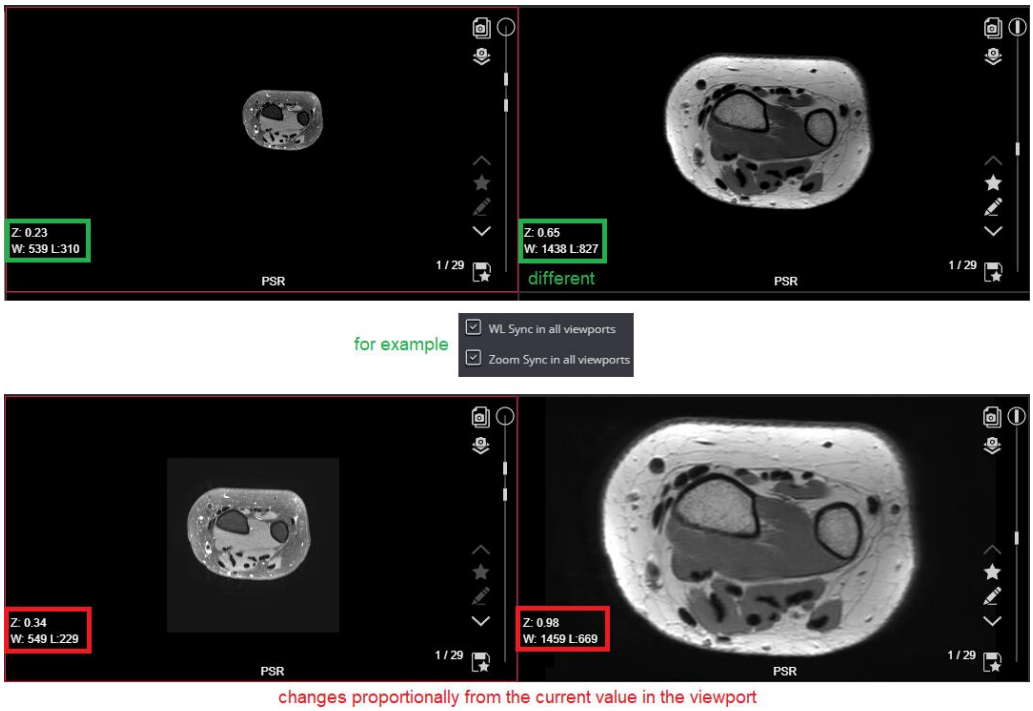


Figure 72. Proportional synchronization of actions

Multiframe Sync (All Viewports)

The system allows synchronized control of multi-frame image playback across all viewports.

Two modes are available:

- **Play Sync Start** – all images are synchronized based on the active viewport and played at the same speed, starting from a synchronized frame.
- **Sync Playback** – all images start playing simultaneously, but continue independently, each at its own speed and from the current frame.

Detailed information is provided in the section **"Synchronized multi-frame image playback".**

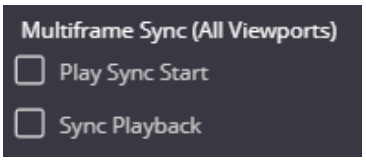


Figure 73. Multi-frame Playback Synchronization Modes

MIST MPR Sync

When the MIST MPR synchronization mode is enabled, in all viewports displaying generated MIST projections, changes to the MIP type (projection type – min / avg / max) and thickness (by selecting a value from the list or adjusting it with a slider) / number of slices are synchronized across all viewports.

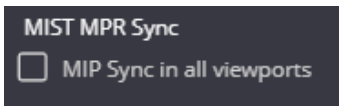


Figure 74. MIST MPR Sync

More information about how this function works is provided in the section "MPR. MIST Oblique".

Panels, Layout, and Multi image/series

Panels, **Layout,** and **Multi image/series** (**Overview layout**) functions allow dividing the view zone of the Viewer window for displaying the separate images in each division. It helps in analyzing and comparing the images.



Panels and Layout allows to optimize the Viewer window for specific tasks. The Viewer's view zone may be organized in one or more panels, with the possibility to select and apply the different layout for each panel. Select the desired panels layout under the extendible **Panels** menu and the view zone will be divided into the selected number of identical size panels.

⚠ **NOTE!** The current panels selection is highlighted in the expandable **Panels** menu.

⚠ **NOTE!** 1x1 layout is by default applied to the panel.

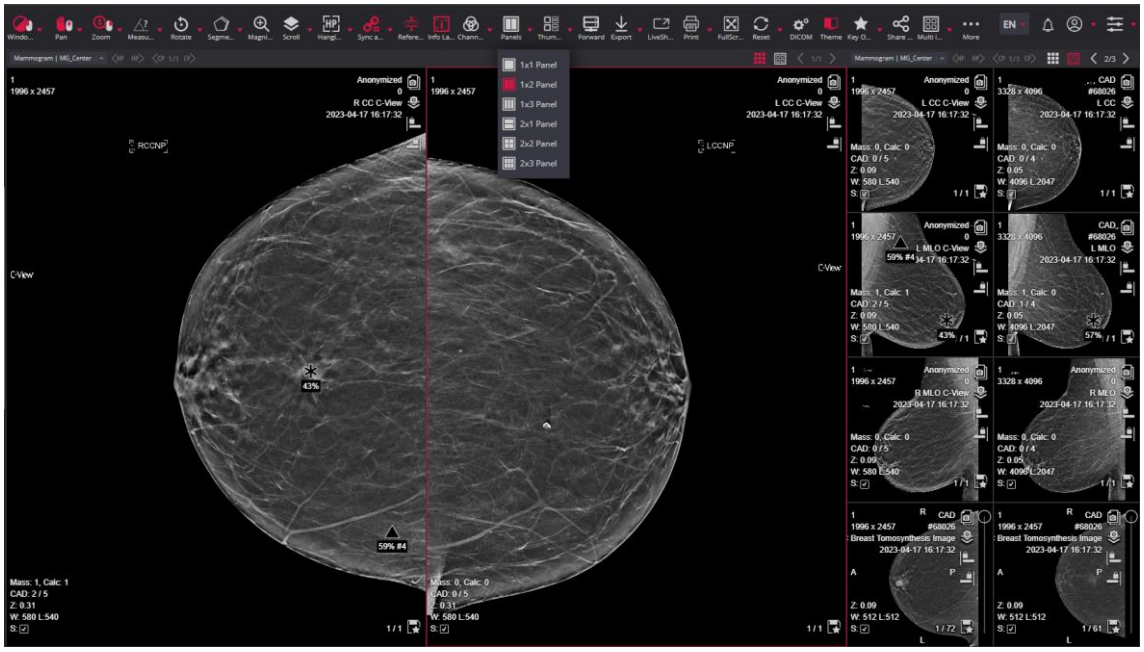


Figure 75. 2x1 panel selected for the Viewer window

By default, the panel toolbar is displayed and allows quick access to the layout, hanging protocol and quadrant zoom functions as described below. See the section “Panel toolbar settings” for detailed description how to configure or hide the panel toolbar. Note, that if the tool is configured, but currently not applicable, it is disabled in panel toolbar.

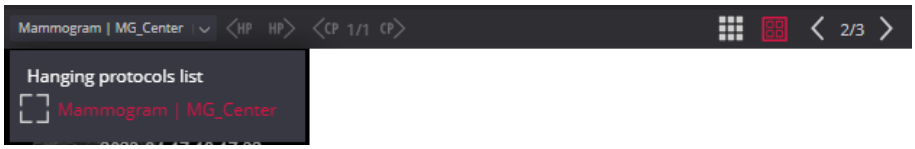


Figure 76. Panel toolbar with applicable hanging protocols list expanded

The hanging protocol tools are displayed on the left side of the panel toolbar:

- expandable list of applicable hanging protocols,
- buttons to navigate the hanging protocols list,
- buttons to navigate the comparison studies list of the currently applied hanging protocol,
- the number of current comparison study or comparison studies page and the total pages.

Note, that one hanging protocol may be applied in the Viewer, and the hanging protocols list is the same for all panels. See the detailed description of these components in the section “Hanging protocols”.

The layout tools are displayed on the right side of the panel toolbar:

- expandable list of available layouts,
- expandable list of overview layouts (multi series/multi-image layout),
- buttons to navigate the overview layout pages,
- the number of current overview layout page and the total pages.

Either regular layout, or overview layout may be applied for the panel, and the actual selection is highlighted. The previous layout is automatically destroyed, and the images are closed, when changing layout type for panel. See the detailed description of these components below in this.

The Quadrant zoom tools are displayed in panel toolbar if quadrant zoom activation conditions are met (see section “Quadrant zoom for mammography” for detailed description):

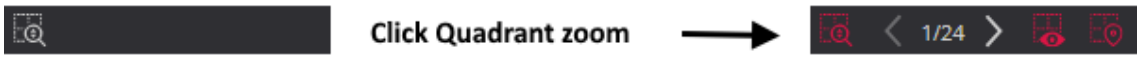


Figure 77. Panel toolbar with Quadrant zoom tools

- Quadrant zoom option switch the function on and off,
- buttons to navigate the quadrants with number of currently viewed quadrant and total number of quadrants,
- Show Quadrant Layout option,
- Show Quadrant Location option.

The navigation, Quadrant Layout and Quadrant Location tools are displayed only if the Quadrant zoom is switched on  .



Layout button divides the active panel into viewports. Select the panel, and then choose the desired layout under the extendible **Layout** menu. The active panel will be divided into the selected number of identical size viewports.

⚠ **NOTE!** The system may be configured to display Layout button with expandable layouts list either in Viewer main toolbar, or in Panel toolbar, or in both toolbars.

If the layout is changed, the system tries to keep as many the images as possible from the previous layout in a new layout, and displays them either in the same viewport, or in the empty viewport. But only the active image is opened, if layout is created from multi image or multi series layout, or changed to 1x1 layout.

The panel or viewports size may be adjusted. To change the size of the panel or the viewports inside the panel, point the mouse cursor to the division line (the cursor should obtain the divider look), hold the mouse button down and drag the line.

The layout of the panel to which belongs the active viewport is highlighted in the expandable Layout menu.

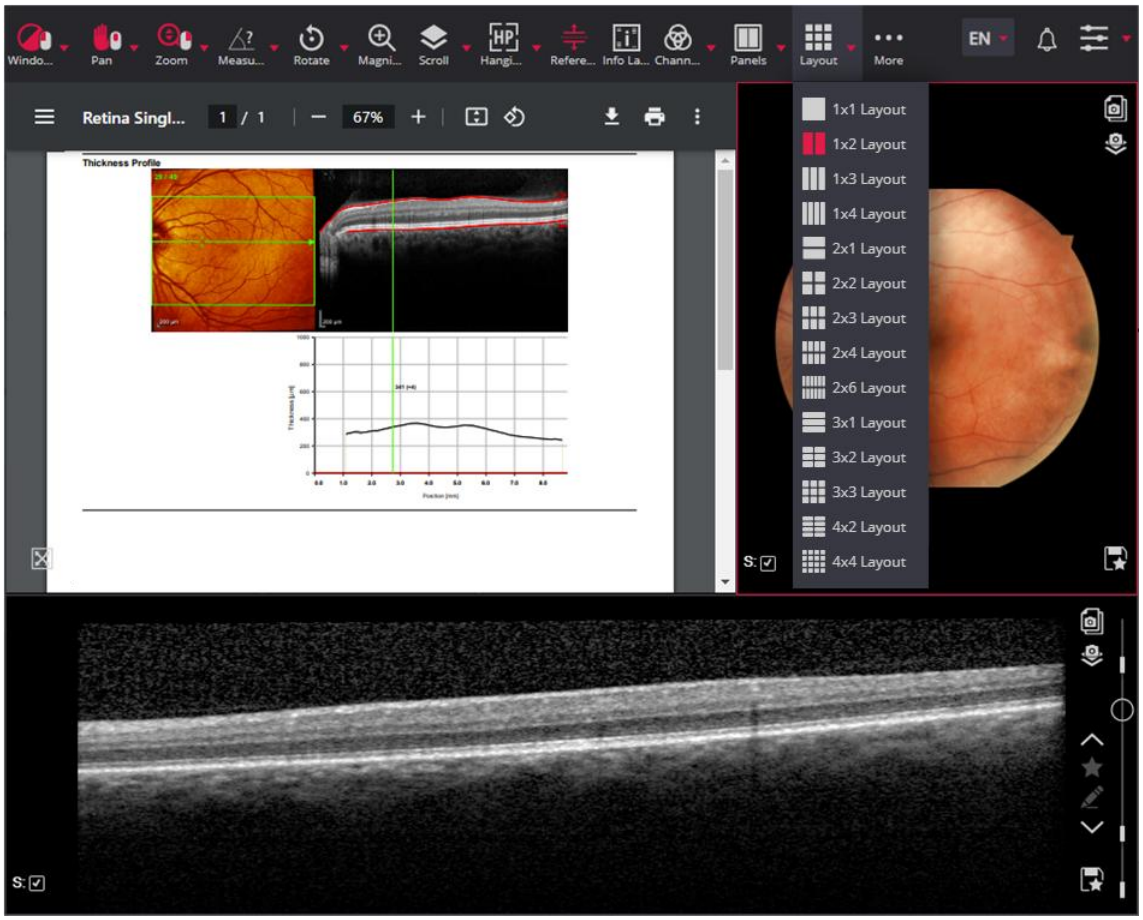
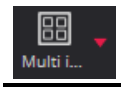


Figure 78. Two panels with 1x2 layout applied for top panel and manually adjusted panels and viewports size

⚠ **NOTE!** If one extended view is set in settings, then double-click the left mouse button on the image for temporary viewing it on top of layout. Double-clicking the right mouse button on the enlarged image, returns to the previous layout. . If two extended views are set in settings, the image is enlarged in corresponding extended view, and the other part of the viewer window stays visible.

⚠ **NOTE!** The panels and layout per each panel selection is saved in browser's local storage. If local storage does not contain the layout value, the one panel with layout according the system settings is displayed.



Select the menu from **Multi image/series** (**Overview layout**) button drop down list to open the selected number of series images or series in the active panel. The panel is automatically divided to required number of sections. Each section has the same size and shows the separate image.

If any of the Multi image layouts is selected from the menu, the system applies the layout and opens the images of the current series in each section starting from the active image and following towards the end of the series. You can scroll the series in any of the multi image viewports using scroll bar or mouse. Opening the other image in the multi image viewport from the thumbnail bar automatically closes the multi image mode and opens the image in single viewport. Multi image or Multi series layout can also be closed manually by selecting the 1x1 Single image/series menu.

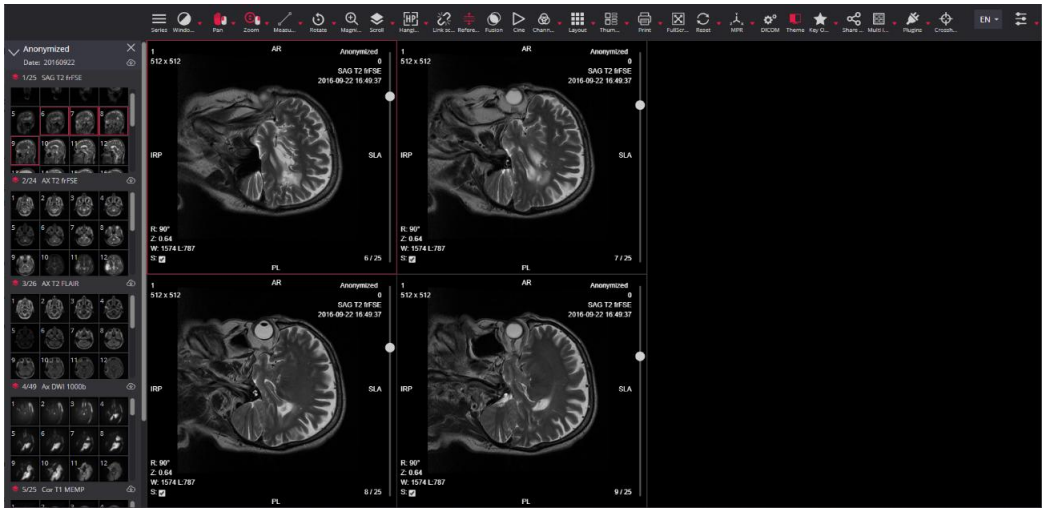


Figure 79. 2x2 Multi image menu applied in the first viewport of 1x2 layout

⚠ **NOTE!** Image manipulation functions (ex. **Scroll, Windowing, Rotate, Pan, Zoom**) affect the entire set of multi images that are opened in one viewport. For example, if you select **Bone** contrast mode for one of multi images, it will apply the **Bone** mode to all images that are viewed as multiple images in viewport though the changes do not apply to the image in other viewports.

If any of the Multi series layouts (overview layouts) is selected from the menu, the system applies the layout and opens the first or middle images of the different series in each section starting from the first series and following towards the end of the study.

⚠ **NOTE!** The system may be configured to display Overview layout button with expandable overview layouts (multi series layouts) list either in Viewer main toolbar, or in Panel toolbar, or in both toolbars.

⚠ **NOTE!** The system allows to configure opening of all the images of all the series sequentially in the multi series layout. By default settings this behavior is configured for CR, DX, US, XA, and RX studies (see the “Settings” section for configuration description). In such cases the mouse wheel scrolls to the next page instead of the next image.

You can scroll the series in any of the multi series viewports using scroll bar or mouse or open the other series from the thumbnail bar. You can quickly navigate through all the series of the study using shortcuts or navigation buttons in panel toolbar. By default, configuration, the **PageUp** shortcut opens the previous set of study’s series or images, and the **PageDown** shortcut opens the next set of study’s series or images in the multi series layout of the active viewport.

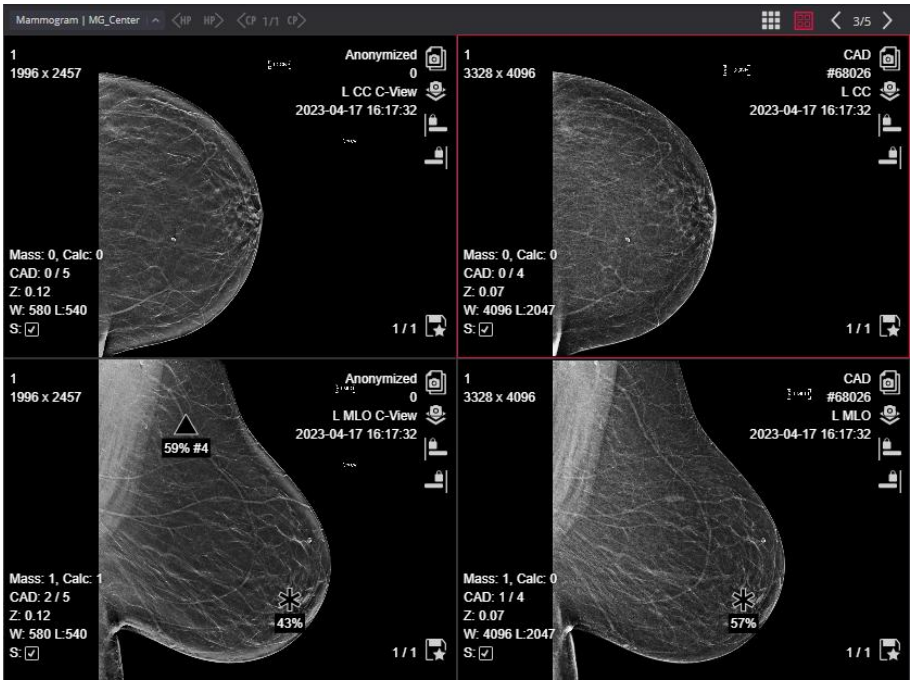


Figure 80. 2x2 Multi series (overview layout) menu applied in the panel and the 3rd page from 5 opened

⚠ **NOTE!** If not more than two (2) Multi series layouts are opened in the viewer window, the **Alt+PageUp** and **Alt+PageDown** default shortcuts may be used for navigating through all the series of the study in the in the multi series layout of the other not active panel.

Note, that default values of the shortcuts can be change. For more information see in chapter "Shortcuts".

Extended Views

Provides the possibility to have two extended views (enlargment regions) in the Viewer window, in which case a double-click on an open image will temporary enlarged it inside one extended view instead of the full Viewer window.

⚠ **NOTE!** Feature must be activated in the settings.

When the user double-clicks on an open image, the image is temporarily enlarged inside extended view.

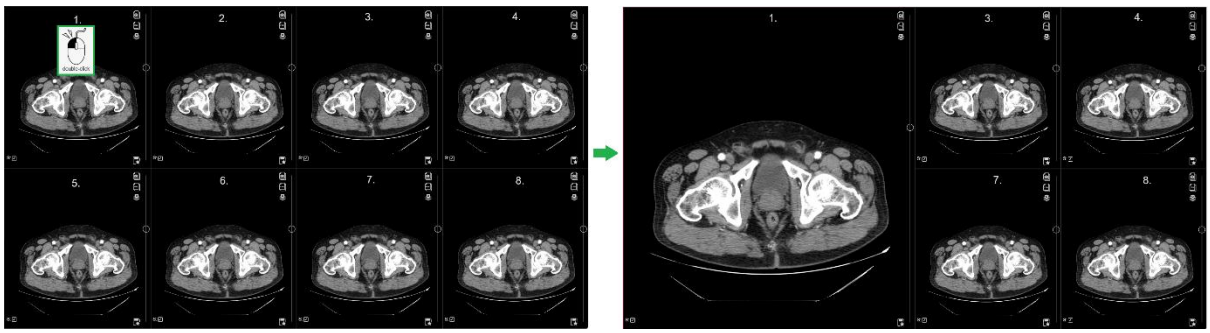


Figure 81. Two extended views. Enlarged inside one extended view of two

Double-clicking on a zoomed image returns to the original layout.

When the user holds down Alt and double-clicks an open image, the image is temporarily enlarged in the opposite extended view.

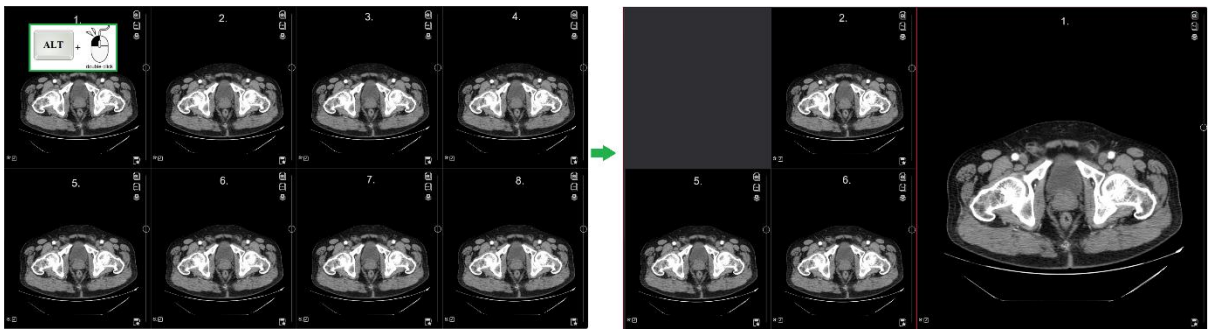


Figure 82. Two extended views. Enlarged in the opposite extended view

Allows you to enlarge adjacent views in a single action by double-clicking on the edge of the viewport: by double-clicking on vertically or horizontally neighboring viewport edges.

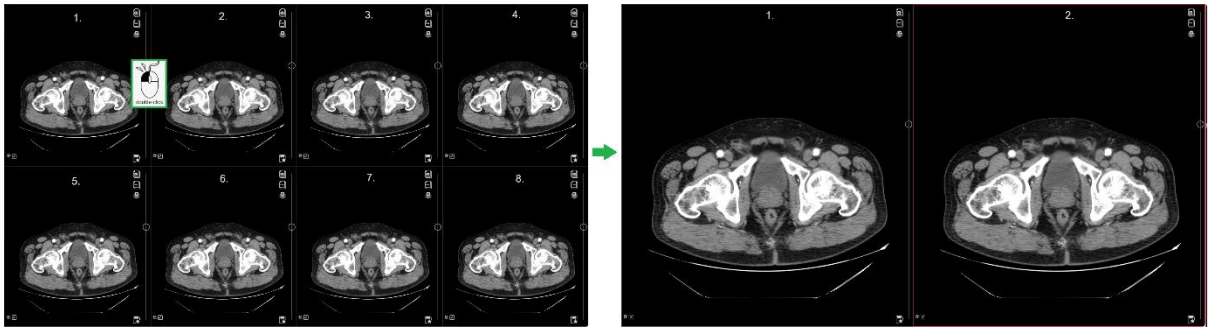


Figure 83. Two extended views. Enlarging two images. Side-by-side images

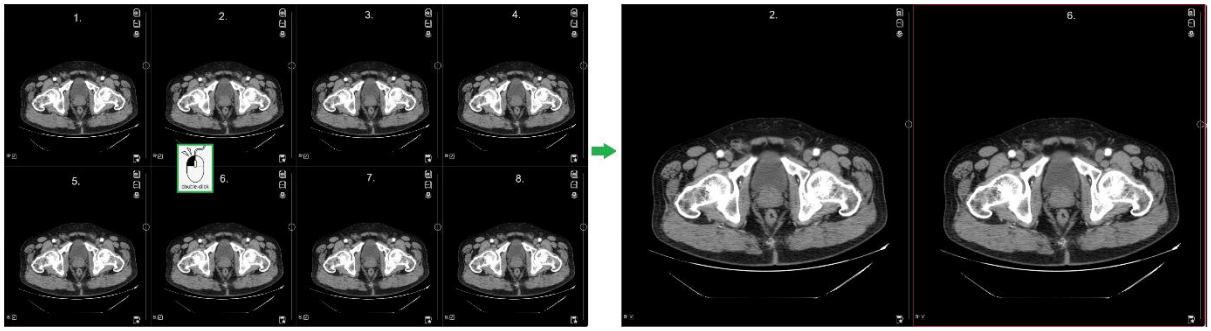


Figure 84. Two extended views. Two extended views. Enlarging two images. One image on top of another

Allows you to enlarge four images in one action: double-click on the corner connecting the four viewports.

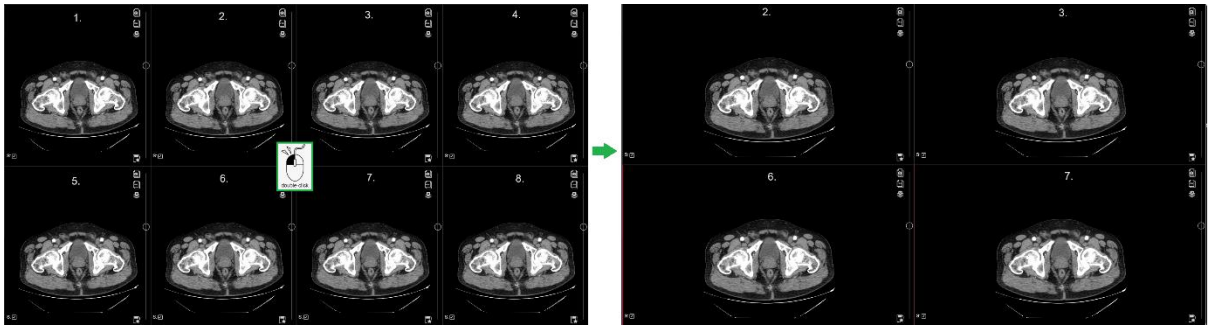


Figure 85. Two extended views. Enlarge four images

Double-clicking on any enlarged image returns you to the original layout.

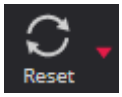
With two extended views and 1x1 layout, the performance is the same as with one extended view, i.e. the image is magnified in full window.

If the layout has an odd number of columns, e.g. 1X3, then the first two columns are mapped to the first extended view and the third to the second.

⚠ **NOTE!** With two extended views functionality enabled, it is no longer possible to manually resize the viewport by manually dragging the viewport edge.

⚠ **NOTE!** When working with two monitors, one extended view is on each monitor. Functionality not suitable for use with more than two monitors.

Reset



Reset button is used to reset the image, after using manipulations like **Windowing, Rotate, Pan, Zoom**, and clear measurements that you have been working on. You can choose to reset all images (**Reset All**), or to reset only active image (**Reset Selected**).

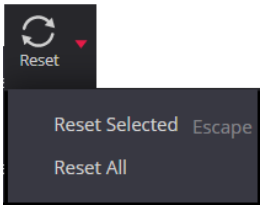


Figure 86. Reset button menu

Exception that **Reset** does not deactivate Align&Lock mode.

MPR



To start the multi-planar reconstruction, expand the **MPR** button menu and select the desired option in it:



Figure 87. MPR button menu

⚠ **NOTE!** Multi-planar reconstruction (MPR) may be applied for CT, PT, NM and MR series having more than 2 images in series. Contact your system administrator if you want to configure MPR functionality for other modalities or SOP classes.

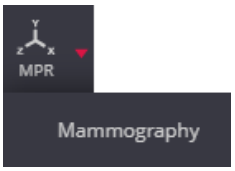
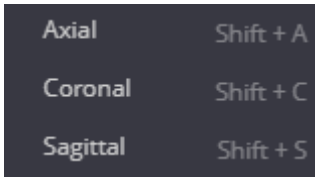


Figure 88. MPR button menu for breast tomosynthesis series

⚠ **NOTE!** The system generates reconstructed series from the original series having images with gantry tilt, irregular spacing, or not parallel, but the reconstructed series have inaccurate spacing and proportions. In such cases the notification to not use the reconstructed series for medical purposes is displayed, and the measurements are disabled.

Axial, Coronal, or Sagittal



By selecting the corresponding menu option, you can launch the series image reconstruction in one of three planes: **Axial**, **Coronal**, or **Sagittal**. The program performs the following steps:

- Preloads the series images. The progress bar appears in the viewport during the image preload process.

- Applies the required image transformation, if the selected plane differs from the original series data set. The transformation tag is displayed in the viewport, if applied.
- Displays the selected view (**Axial**, **Coronal**, or **Sagittal**) in active viewport. The scroll cursor is moved in the middle of the initial or calculated set of images.

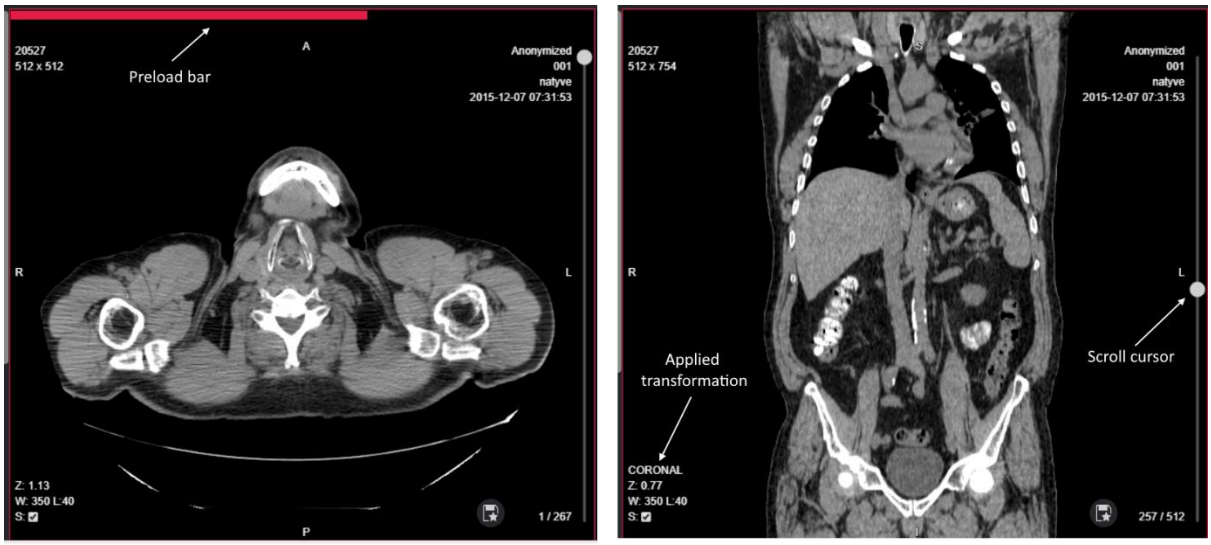


Figure 89. Steps of Coronal image reconstruction from axial series of images: axial series preload and calculated coronal view

Once the image reconstruction process is finished, you can use the scroll bar or scroll function to see the images (slices) of the view (axial, sagittal, coronal) you have selected.

⚠ **NOTE!** When displaying any of the selected projections in the viewport, it is possible to choose the next plane transformation function without additional loading of the original series. For example: coronal is the first choice and then sagittal can be selected (from the menu bar or by shortcut) in the same viewport.

Orthogonal



Selecting the **Orthogonal** menu allows to get the series image reconstruction in two planes that are perpendicular to the original series plane. The program automatically applies the layout for displaying the original series and two reconstructed planes in separate viewports:



Figure 90. Orthogonal reconstruction from axial series of images

⚠ **NOTE!** To analyze images of the reconstructed series, use tools: **Windowing**, **Zoom**, **Pan**, **Scroll, Measure**, **Reference Lines**, **Crosshair and Fusion**.

⚠ **NOTE!** Orthogonal reconstruction is not allowed in the viewport of the Multi series layout.

MIST Oblique



MIST (Medical Image Streeming Technology) **Oblique** is used for 3D reconstruction.

Images from one selected series are used for three-dimensional reconstruction. To perform a 3D reconstruction, load any image in the series into the selected viewport and press **MIST Oblique** from the **MPR** drop-down menu. The system divides the viewing area into four parts and starts the loading of the series of images and the image reconstruction process.
The reconstruction action **MIST Oblique** can be initiated with shortcut. By system value by default, the shortcut is Shift + Q. This value of shortcut can be change. For more information see in chapter "Shortcuts".

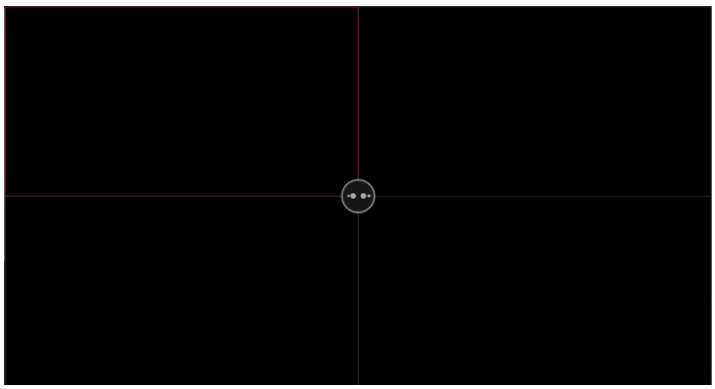


Figure 91. MPR MIST Oblique 3D indicator of the reconstruction process

The image data of the original series is converted to a spatial image. After the reconstruction process, parts of the viewport display the 3D image and slices of the transformed images in three perpendicular planes.

⚠ **NOTE!** Mozilla Firefox browser has certain memory limitations: MIST MPR functionality will fail on series where uncompressed DICOM data is larger than 2 GB.

⚠ **NOTE!** The system can be set to not generate a 3D image. In the case of such a system configuration, only sections of the transformed images in three perpendicular planes are visible in the result.

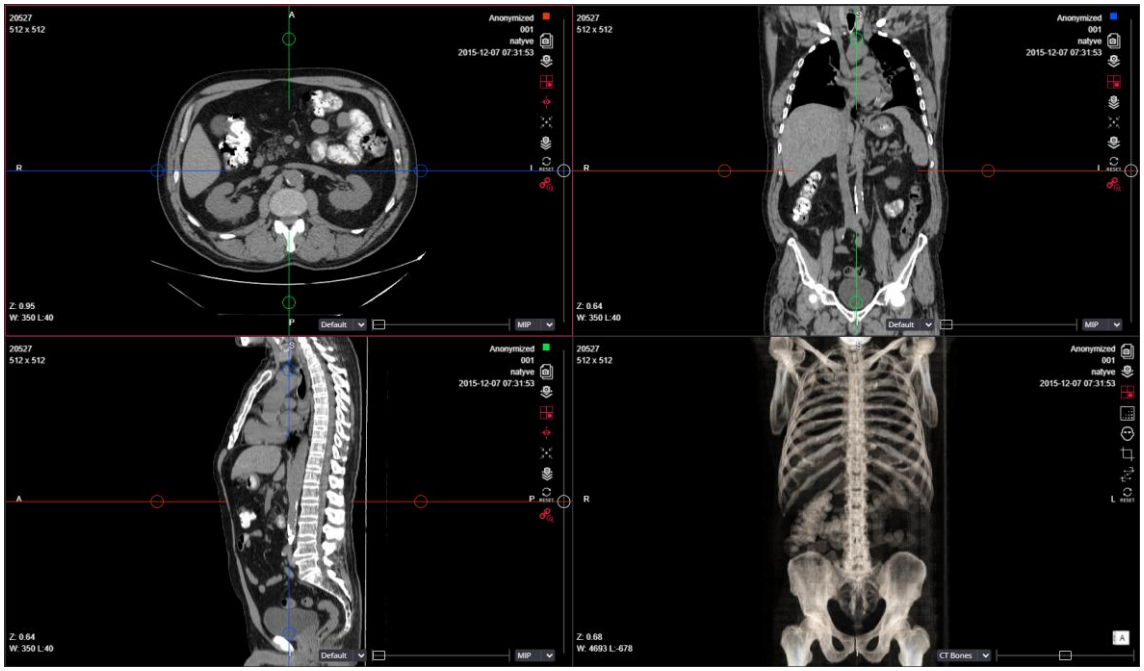


Figure 92. The reconstruction result of MPR MIST Oblique

Series of transformed images are displayed in the main anatomical planes: axial, coronal and sagittal.

- The first viewport (first row left column) shows a series of transformed images in the axial plane. The axial plane is indicated by a red square in the upper right corner of the viewport.
- The second viewport (first row right column) shows a series of transformed images in the coronal plane. The coronal plane is indicated by the blue square in the upper right corner of the viewport.
- The third viewport (second row left column) shows a series of transformed images in the sagittal plane. The sagittal plane is indicated by the green square in the upper right corner of the viewport.

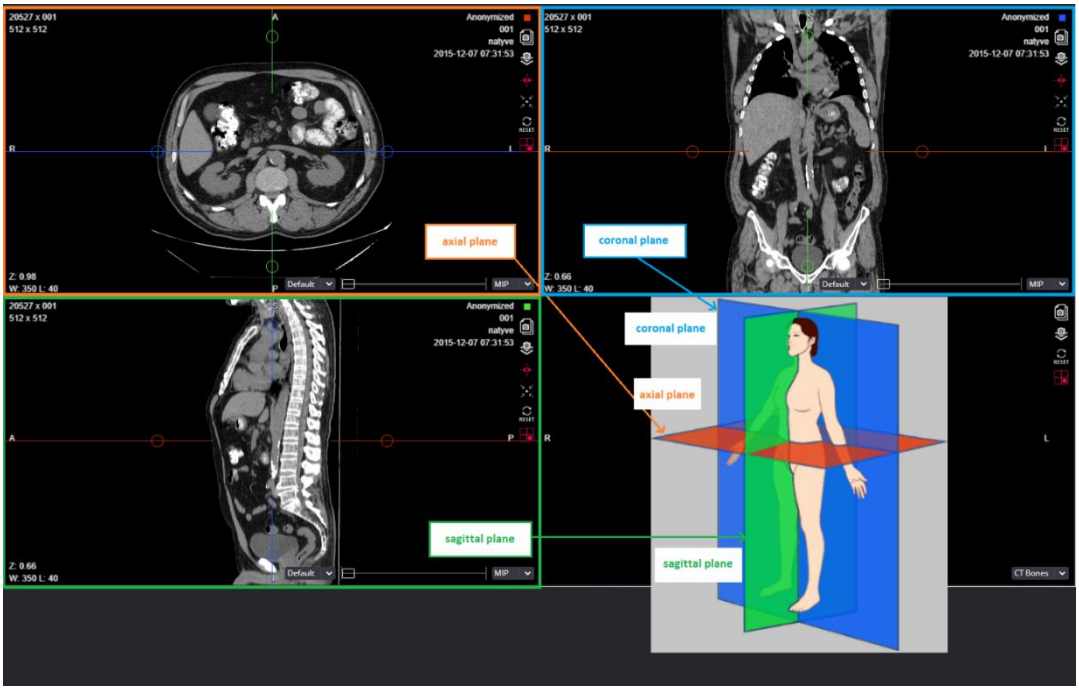


Figure 93. The Scheme of planes of transformed images

The anatomical direction of the transformed images in the viewing area is from left to right and from top to bottom:

- axial plane series images are displayed in the direction from R (left) to L (right) and from A (top) to P (bottom);
- coronal plane serial images are displayed in the direction from R (left) to L (right) and from S (top) to I (bottom);
- the sagittal plane serial images are shown in the direction from A (left) to P (right) and from S (top) to I (bottom).

The thickness of the slice

The lower right corner of each plane image shows the thickness of the slice used for image preparation in millimeters and the method of image preparation.



Figure 94. The thickness of the section used for image preparation in millimeters and the method of image preparation

Slice thickness 

by default is 0.01 mm.

The slice thickness can be changed:

a) selecting the thickness value from the list;

b) by moving the cursor in the scroll bar

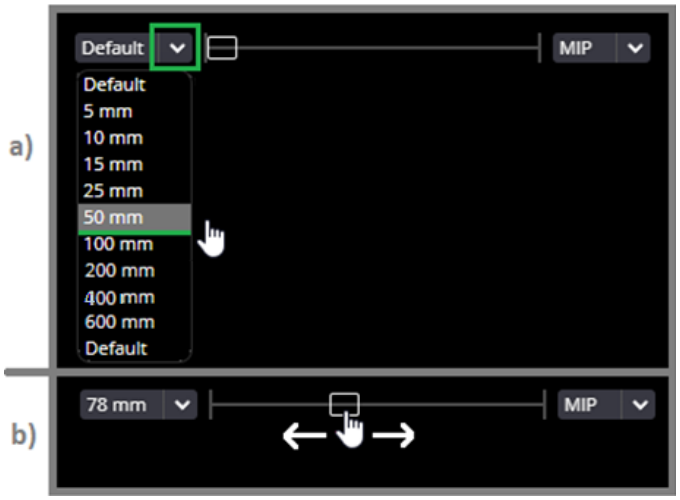


Figure 95. Changing the slice thickness

Slice Thickness Synchronization

When the “MIP Sync in all viewports” mode is enabled, slice thickness changes are applied simultaneously across all viewports displaying generated MIST projections. More information about this menu option is provided in the section “Sync Actions. MIST MPR Sync”.

When the slice thickness is changed in one viewport (by selecting a value from the list or using the slider), the same setting is automatically applied to all other synchronized viewports.



Figure 96. Sync Slice Thickness Adjustment Across All Viewports

The image preparation method

The image preparation method can be changed by selecting a value from the drop-down list.



Figure 97. Changing the image preparation method

The values:

- **MIP** (Maximum Intensity Projection): the pixel of the generated image is assigned the maximum value from the images (layers) entering the section;
- **AVG** (Average Intensity Projection): the pixel of the generated image is assigned an average value calculated from the images (layers) entering the section;
- **MinIP** (Minimum Intensity Projection): the pixel of the generated image is assigned the smallest value from the images (layers) entering the slice.

Image Preparation Method Sync

When the "**MIP Sync in all viewports**" mode is enabled, slice thickness changes are applied simultaneously across all viewports displaying generated MIST projections. More information about this menu option is provided in the section "Sync Actions. MIP MPR Sync".

When the slice thickness is changed in one viewport (by selecting one of the three available values from the list), the same setting is automatically applied to all other synchronized viewports.

Rotation of intersecting planes

To rotate the intersecting planes:

- place the mouse cursor on any axis rotation element - a circle,
- press the left mouse button
- while holding the button down, rotate the axis around the center point.

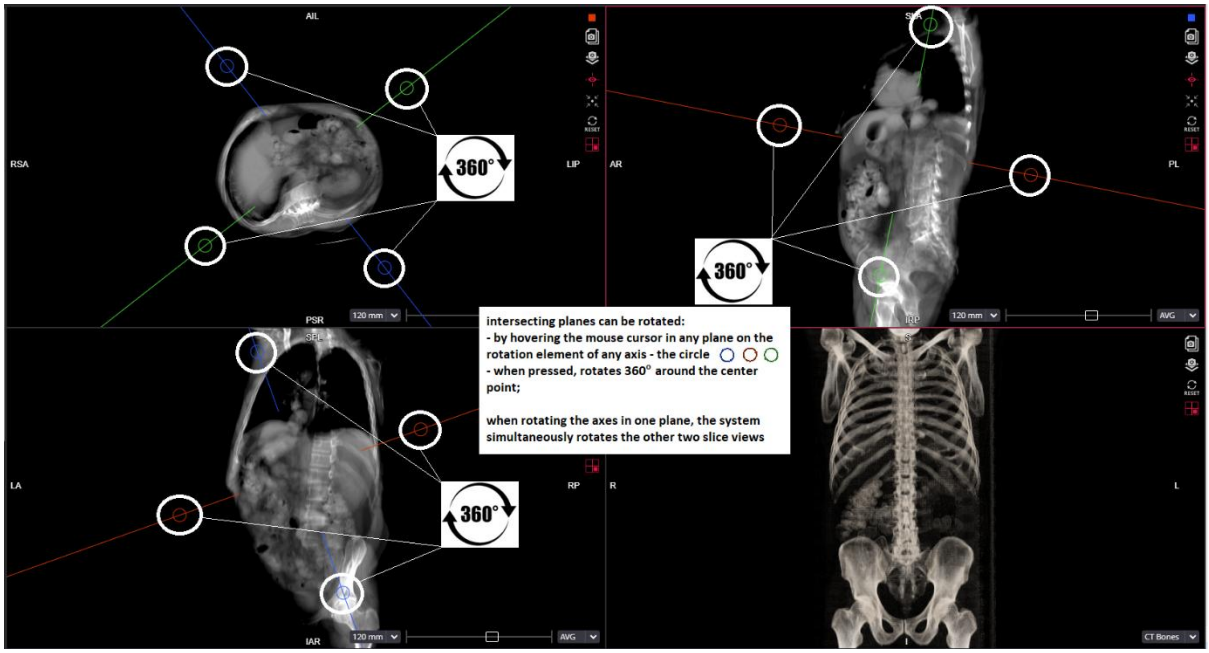


Figure 98. Rotation of intersecting planes

⚠ **NOTE!** When the user rotates the intersecting planes in one of the transformed image slices, the system rotates the other two slice images.

⚠ **NOTE!** As the plane is rotated, the system automatically updates the anatomical direction indicators displayed in the view areas of the rotated planes, which can be used to judge the direction of the cut in the patient's body.

Scrolling along the intersecting planes

To scroll along the intersecting planes:

- place the mouse cursor on the axis line in the selected section view;
- press the left mouse button,
- scroll the axis while holding the button down.



Figure 99. Longitudinal displacement of intersecting planes

⚠ **NOTE!** As the user longitudinally scrolls the intersecting planes in one of the transformed image slices, the system scrolls the images in the other two planes.

⚠ **NOTE!** The action can be performed after the axes have been rotated. Then you don't scroll up/down or left / right, but diagonally, depending on how the rotation was done.

⚠ **NOTE!** If a normal crosshair is activated in an overlapping image opened in another viewport and the user changes its position, the dedicated MIST Obligue crosshair is automatically synchronised. However, when changing the dedicated MIST Oblique crosshair, there is no synchronisation with the normal crosshair.

Carrying intersecting planes

To carry intersecting planes:

- place the mouse cursor on the intersection center of the axis lines in the selected section view;

⚠ **NOTE!** To avoid covering the viewed image, the center does not normally show the lines of axis crossing. When the left mouse button is pressed, the axis lines are redrawn in all projections to show the point of crossing.

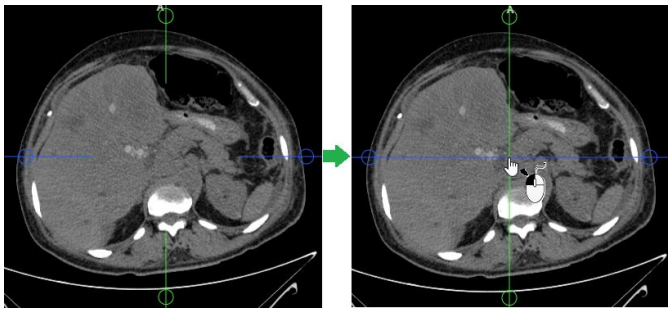


Figure 100. The center point of the intersecting planes

- press the left mouse button,
- the system redraws the axes to show the point of crossing of the axes in all projections,
- hold down the button and drag the intersecting planes in any direction.

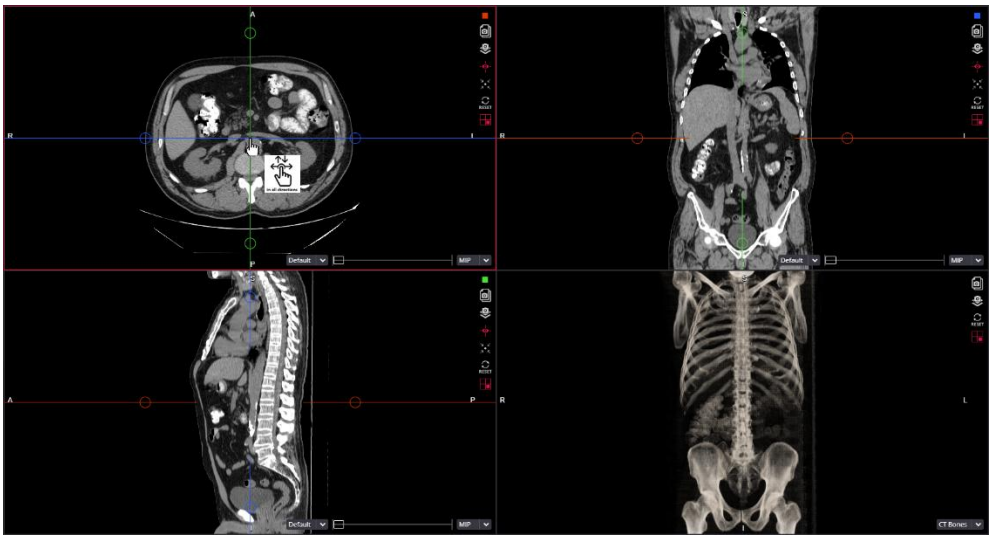


Figure 101. To carry the intersecting planes

⚠ **NOTE!** As the user moves the intersecting planes in one of the slices of the transformed images, the system scrolls the images in the other two planes.

The action buttons in the viewport

Actions can be performed by selecting an action button in the viewport.



Figure 102. Action buttons in the viewport

⚠ **NOTE!** Menu actions not described in this section work the same as opening an untransformed image in the viewport. Detailed descriptions of the actions in other sections of the document.

⚠ **NOTE!** If there is not enough space for the buttons to be displayed, the More button 

is displayed. Click it to see the missing buttons.

Copy viewport content to the clipboard

The action  converts the content of the viewport to png format and copies it to the clipboard (see section “Copy viewport content” for detailed description). After copying, the clipboard image can be pasted into any resource that supports the png format.

Save as secondary capture

The action  converts the copied content of the viewport to a DICOM sub-input file and saves it to the PACS.

For a detailed description of actions  and  , see in section “Copy viewport content”.

Show/hide axes

Show/hide axes. To hide the axes of transformed images, select  . After the action, the button icon will change to white  .

If the axes are not visible, selecting  makes the axes visible.

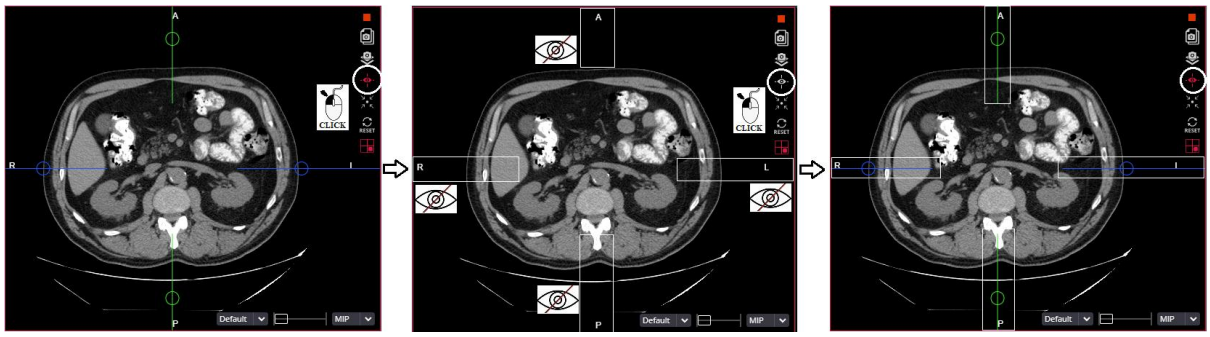


Figure 103. Show/hide axes

⚠ **NOTE!** There is no action in the transformed spatial 3D view.

⚠ **NOTE!** Selecting an action on any plane of the transformed image shows or hides the axes in all three planes: axial, coronal, and sagittal.

Centering the axes

To center the axes. To see the transformed axial sections centered, to see the axial lines passing through the centers of the images, select  .

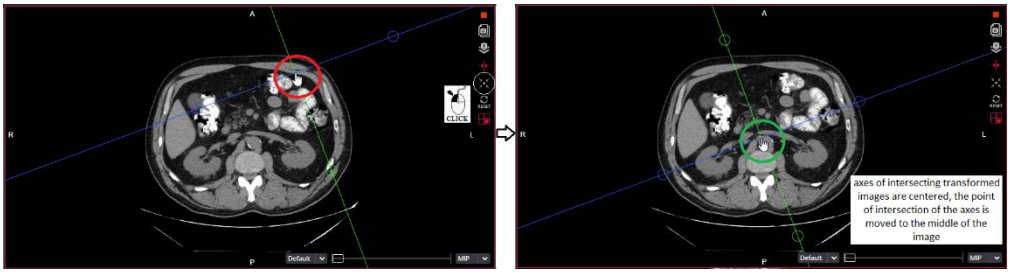


Figure 104. To center Axis

⚠ **NOTE!** There is no action in the transformed spatial 3D view.

⚠ **NOTE!** Selecting an action on any plane of the transformed image centers the axes in all three planes: axial, coronal, and sagittal.

⚠ **NOTE!** If the axes of the transformed images have been rotated, the Center Axis action does not restore the rotation.

Export MPR to PACS

The action  converts the reconstructed 2D series to DICOM and saves it to the PACS.

The current series orientation, rendering method and slice thickness are used when rendering the derived reconstructed series. The rendering process may take some time and is done on server side in order not to disturb the work. The **Export MPR to PACS** icon is disabled and status is displayed near it while saving is in progress.

The saved derived series is automatically sent to the Viewer and displayed in the thumbnail panel. The series description starts with “MPR…” string, followed by rendering method and series orientation, example: “MPR MIP SAG”.

Reset

Restore the original image. After completing the actions with the axial sections of the transformed images, select 

. The system will reset the images to their original state.

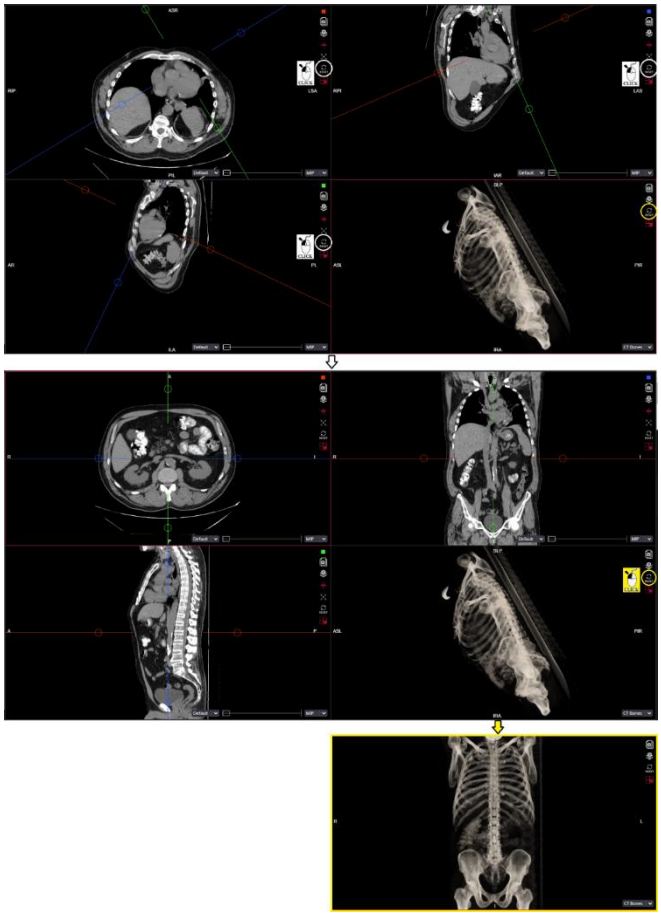


Figure 105. Action of restoring the original image

⚠ **NOTE!** Selecting an action in any plane of the transformed image restores images in all three planes: axial, coronal, and sagittal.

⚠ **NOTE!** Action 

is also in the transformed spatial 3D image viewer. This action button works separately from the axial section view buttons.

Changing the layout

To **Change the layout of transformed images in the viewport**, press  . The system displays a list of possible image layout values.



Figure 106. The list of values for the layout of transformed images

⚠ **NOTE!** After changing the layout of the images, the icon of the action button  changes to the icon of the selected layout, e.g. .

The layout  is applied when opening the transformed image. The **MIST Oblique** layout divides the field of view into four equal sections, three showing axial, coronal, and sagittal sections, and the fourth a three-dimensional view.

Layouts  represent axial, coronal, and sagittal sections, do not represent a three-dimensional image. The order of arrangement of axial sections can be changed by selecting  .

The layout  shows axial, coronal and sagittal slices, in the right part of the MIST viewing window shows a three-dimensional view.

When selected  , only the 3D spatial image is displayed. Axial views of the sections are not depicted.

When selected  , the active image is magnified over the entire **MIST Oblique** viewport.

3D image render quality

The system performance may be increased by reducing the quality of the 3D image rendering. By default, the system tries to render the 3D image of high quality. In case the user does not need or cannot benefit from high 3D image quality, for example due to small viewport size, the user can lower render quality and so increase the performance. To change 3D image render quality, press the render quality icon  in 3D image viewport and select the value from the expanded values list. Note that selected value is highlighted, saved in browser storage and reused next time when rendering the 3D image. The Reset button does not change the render quality, so you should change the render quality by selecting a different value from the render quality expandable menu.



Figure 107. 3D image render quality changed from high to low

Change 3D image orientation

By default, the 3D image is displayed with anterior body side towards the viewer. To change 3D image orientation , press the orientation icon  in 3D image viewport to expand the list of body anatomical sides and select the needed orientation:

- Press  for showing the anterior side.
- Press  for showing the posterior side.
- Press  for showing the left side.
- Press  for showing the right side.
- Press  for showing the inferior side
- Press  for showing the superior side.

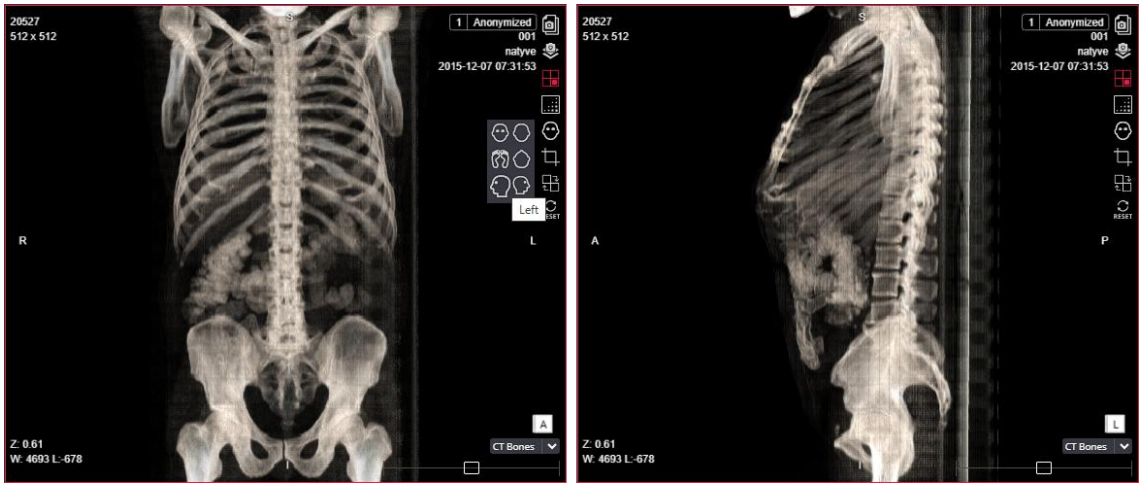


Figure 108. Changing orientation from the anterior side to the left side

3D image cropping

You can crop the 3D image to remove the background elements or focus on a specific object. Press the show/hide cropping icon  in 3D image viewport and the system highlights the cropping tool  and creates the rectangular cropping box around the image. The cropping tool has handling points at the box corners, and in the center of the box sides. You can grab the selected point (the point color changes) and drag it to trim the outer part of the 3D image. You also can use the Rotate tool  in main toolbar, or Orientation tool  in 3D viewport toolbar to change the 3D image position for better viewing the parts that need to be cut. See the picture below for cropping the lungs in the human body.

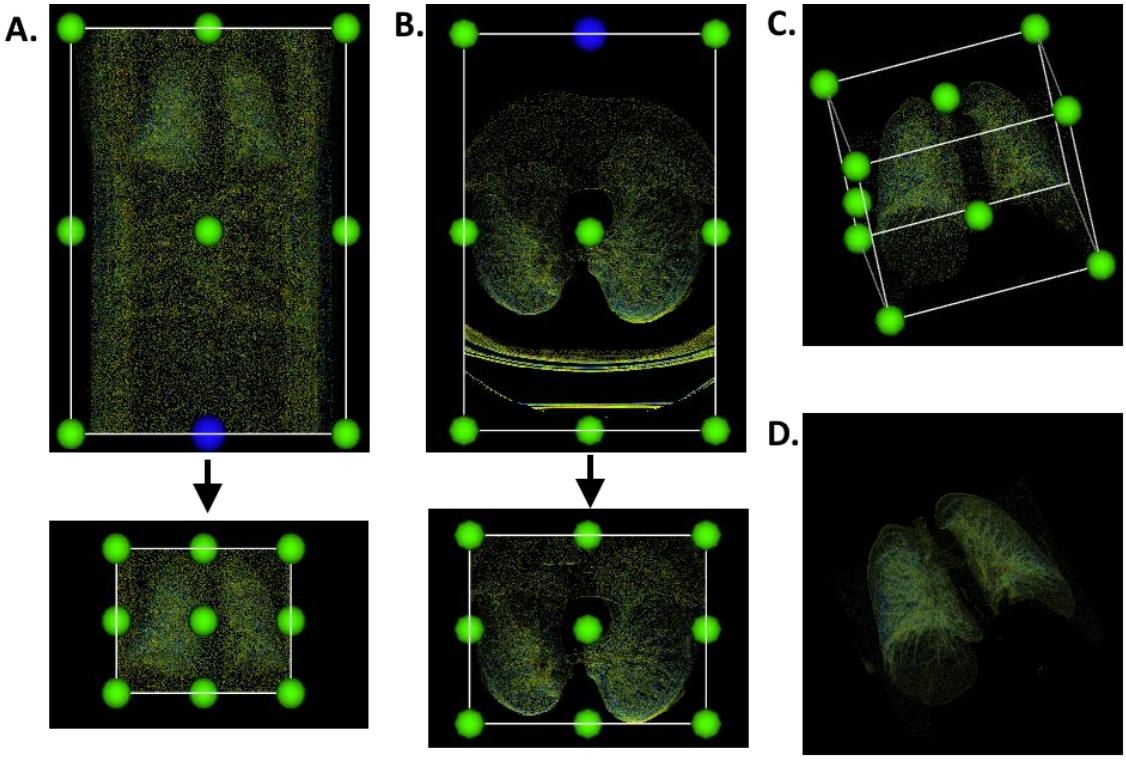


Figure 109. A. 3D image from anterior side viewed (top) and cropped (bottom). B. Image orientation changed to view from superior side (top) and cropped (bottom). C. 3D image free rotation to view and/or adjust cropping. D. Final 3D lung image after hiding the cropping box.

Note, that system automatically applies the low 3D image render quality to ensure the smooth and quick image render at trim process. The render quality will be automatically restored when you hide the cropping box by pressing the highlighted cropping icon  .

Switch to Curved Planar Reconstruction (CPR) viewport

To **Switch to Curved Planar Reconstruction (CPR) viewport**, press  in 3D image viewport. The system converts the 3D viewport to 2D CPR viewport and displays information on how to do the curved planar reconstruction. The CPR line tool button is displayed in each 2D viewport to start with curved planar reconstruction:

- Click the CPR line tool to activate it in any 2D viewport, the icon is highlighted  in all viewports.
- Draw the polyline for the plane you want to be straightened:
  - position the mouse pointer on the point from which you want to start, click and release the left mouse button;
  - then move the cursor to the second, third, fourth, etc. points and each time click the left mouse button once and release it;
  - when the cursor is moved to the last point, double click the left mouse button.
- The system straightens the curved plane and displays the reconstructed 2D view in CPR viewport. The first point of the polyline is the top of the image.

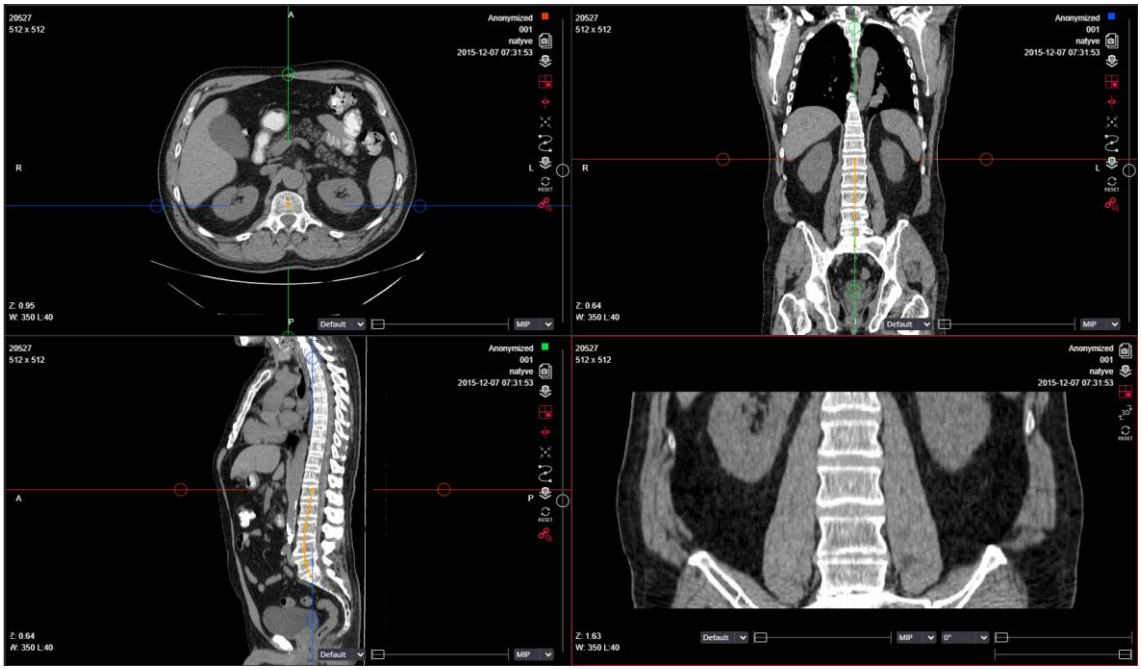


Figure 110. Curved plane reconstruction

- You can move the polyline points or the whole line in any of the 2D viewports to adjust the curved plane view.
- You can change the thickness of the slice, image preparation method, image width, rotate the reconstructed curved plane around the straightened polyline with corresponding extendable list or slider.

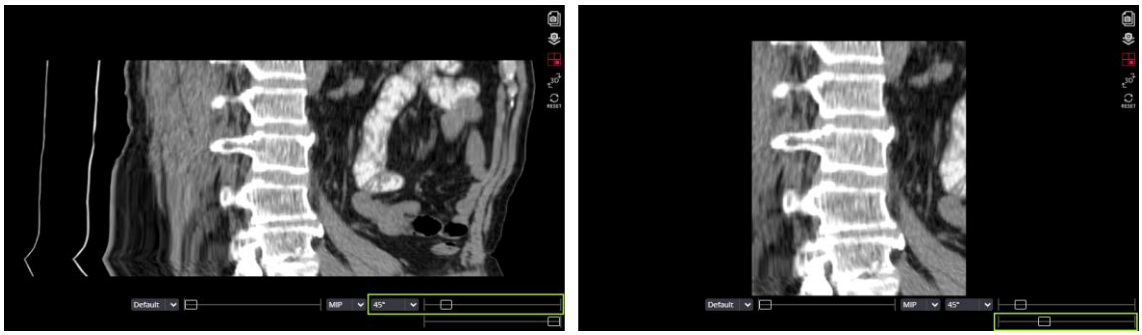
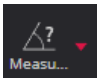


Figure 111. Reconstructed curved plane rotation and width changing

When you have finished working with CPR, press icon Switch to 3D view  to return to 3D image viewport.

Implemented the possibility to perform actions with transformed series of images and with formed spatial image, **the buttons of which are available in the menu bar**: to change Windowing level, to move, to zoom in, to rotate, etc.

⚠ **NOTE!** The actions that are selected in the menu bar are different when one of the slice views and the 3D view are active. Actions **Measure**  and Fusion  can only be performed in axial, coronal and sagittal planes.

⚠ **NOTE!** The menu is controlled by the system settings, so the use of some functions may be restricted, the menu buttons may be unavailable.

Sync-Zoom in MIST Oblique Viewports

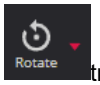


MIST Oblique viewports support sync-zoom — when the user zooms in one viewport, all synced viewports zoom together. Each viewport has an individual sync-zoom icon. By default, the icon is highlighted  in the axial, coronal, and sagittal viewports, indicating that sync-zoom is enabled.

To desync a specific viewport, click the icon — it becomes deselected  and that viewport no longer responds to zoom actions from other viewports. The

3D viewport does not support sync-zoom.

Rotate

Rotate 

transformed image planes and 3D images in all directions. The system does not update other planes when rotating.

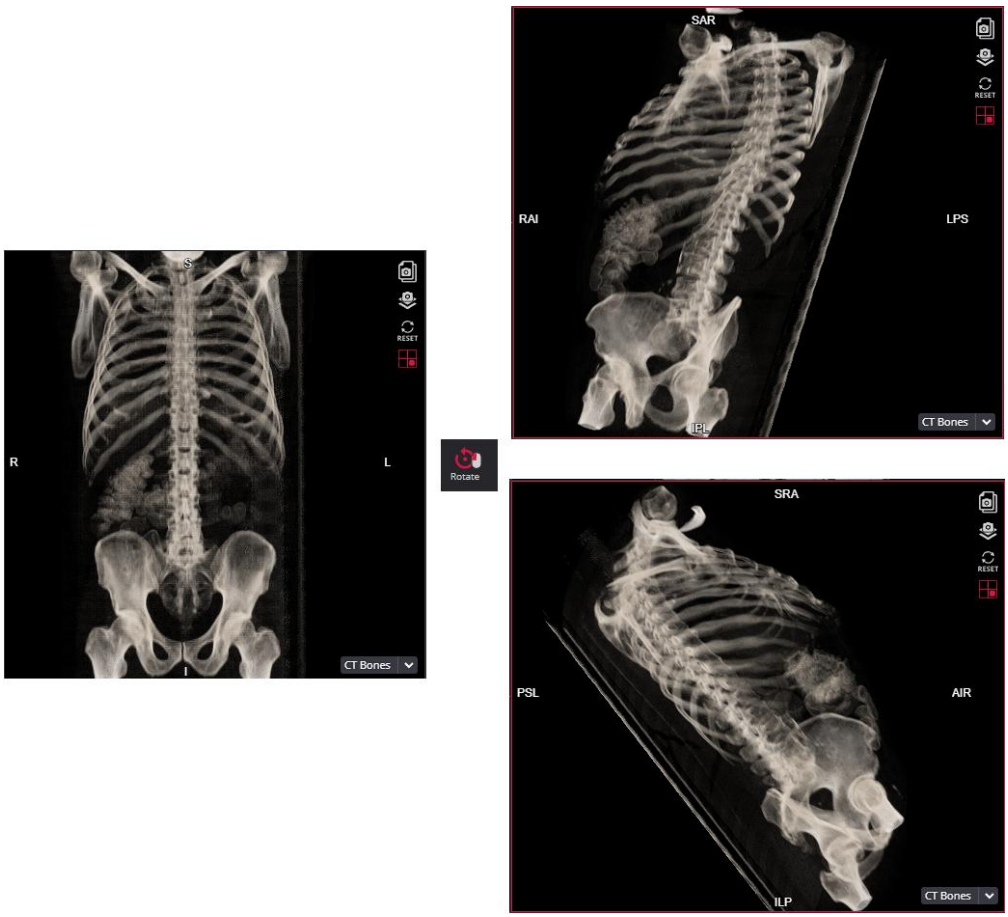
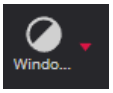


Figure 112. Rotation of the spatial image

In the axial, coronal and sagittal planes, the Rotate action menu additionally allows the selection of the **Flip Horizontal** and **Flip Vertical** functions.

Changing the Windowing level

It is possible to change the Windowing level by selecting an action 

in the menu. It is described in detail in the “Windowing” section.

In the lower right corner of the spatial 3D image viewing window, it is possible to select programmed Windowing level presets, each preset representing the map of density values to color and opacity values.

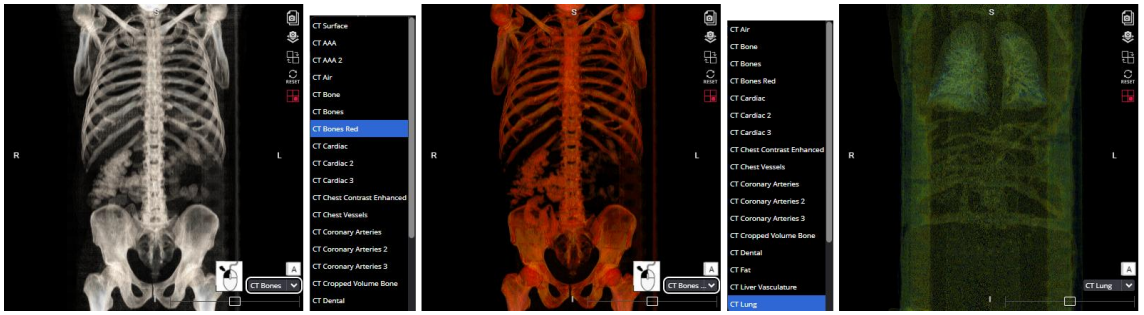


Figure 113. Selection of expected Windowing levels in a spatial 3D image

NOTE! The list of programmed presets Windowing levels and default preset are configured in the settings. Contact your system administrator regarding the system configuration.

NOTE! After selecting default 3D Windowing levels, the default values can be adjusted by selecting an action 

.

NOTE! After selecting default 3D Windowing levels, the opacity values can be adjusted with the slider at the bottom of the viewport.



Figure 114. Changing the Windowing level and opacity

The special CTSurface preset may be included in the Windowing level presets list. The CTSurface preset visualizes values of the same density as surface, and dragging the slider at the bottom of the viewport the predefined color and opacity values are applied.



Figure 115. Changing the color and opacity values for the CTSurface preset

Measuring 2D reconstructed images

Measure button 

allows you to measure and analyze the 2D reconstructed images. To pick the measure tool, use the **Measure** button drop-down menu:

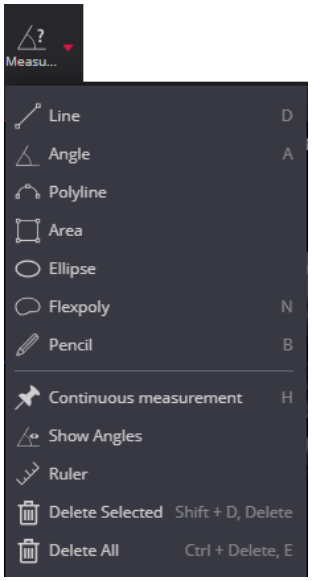


Figure 116. Measure button menu for 2D reconstructed series

The list of tools for 2D reconstructed series is limited: Line, Angle, Polyline, Area, Ellipse, Flexpoly, and Pencil. The Continuous measurement, Show Angles, Ruler, and measurement delete supported functions are also available for 2D reconstructed series. The measure tools and supportive functions are described in detail in the “Measuring images” section.

⚠ **NOTE!** Due to memory limitations that are applicable for browser applications, the pixel values, that are loaded for reconstruction, are stored in variables of the optimal size to meet the memory constraints and most use cases. However, in rare cases the actual pixel value may exceed the size of the storage variable and is automatically cropped to maximum supported value. This cropped pixel value is displayed on screen and used in pixel intensity statistics calculations. Warning about such cases is displayed in the Viewer window when initiating the reconstruction.

MIST Axial, MIST Coronal, MIST Sagittal



By selecting the corresponding menu option, you can launch the series image reconstruction in one of three planes: **MIST Axial**, **MIST Coronal**, or **MIST Sagittal**. The program performs the following steps:

- Preloads the series images. The progress bar appears in the viewport during image preload process.
- Applies the required image transformation, if the selected plane differs from the original series data set. The transformation tag is displayed in the viewport, if applied.
- Displays the selected view (**Axial**, **Coronal**, or **Sagittal**) in active viewport. The scroll cursor is moved in the middle of the initial or calculated set of images.

⚠ **NOTE!** Mozilla Firefox browser has certain memory limitations: MIST MPR functionality will fail on series where uncompressed DICOM data is larger than 2 GB.



Figure 117. MIST axial, MIST coronal, MIST sagittal

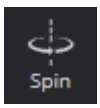
The reconstruction action can be initiated with shortcuts. By system value by default, the shortcuts are:

- MIST Axial – Shift + I
- MIST Coronal – Shift + O
- MIST Sagittal – Shift + P

These values of shortcuts can be change. For more information see in chapter "Shortcuts".

The functionalities on transformed images are same that on MIST Oblique. See the section above.

Spin



The reconstruction of the serial image in MIST coronal, MIST oblique allows to rotate the projections around the Y-axis. The operation is technically possible to perform also MIST axial.

For spining with mouse, assign the mouse button to Spin function 

(or other mouse buttons 

or 

): press the selected mouse button on the image and drag the cursor from right to left (or from left to right) until the projection spined to the desired position.

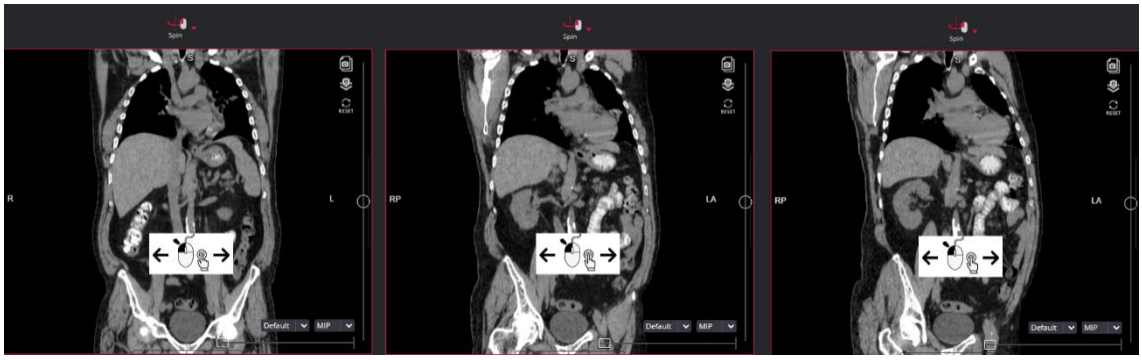


Figure 118. Spin around Y axis

Selecting one of the drop-down menu items Auto Spin Forward or Auto Spin Backward will automatically rotate the projection around the Y-axis. The rotation continues until the next action is selected or mouse click in the viewport. More than one projection can be automatically rotated at a time.

MIST Orthogonal

MIST Orthogonal

When the **MIST Orthogonal** (Medical Image Streaming Technology) menu item is selected, the image data of the primary series is converted into a volumetric image, while reconstructions are simultaneously generated in two planes perpendicular to the original series. The reconstructed series are always displayed in a single row in the following order: axial → coronal → sagittal.

The application automatically selects an appropriate layout and opens the original series together with the two reconstructed series in separate viewing areas. If the current layout contains fewer than 3 columns, it is automatically changed to a layout with the same number of rows and 3 columns. If the layout already contains 3 or more columns, it remains unchanged.

The series are arranged starting from the active viewing area to the right. If there is not enough space on the right side for all three series, the remaining series are placed to the left of the active viewing area.

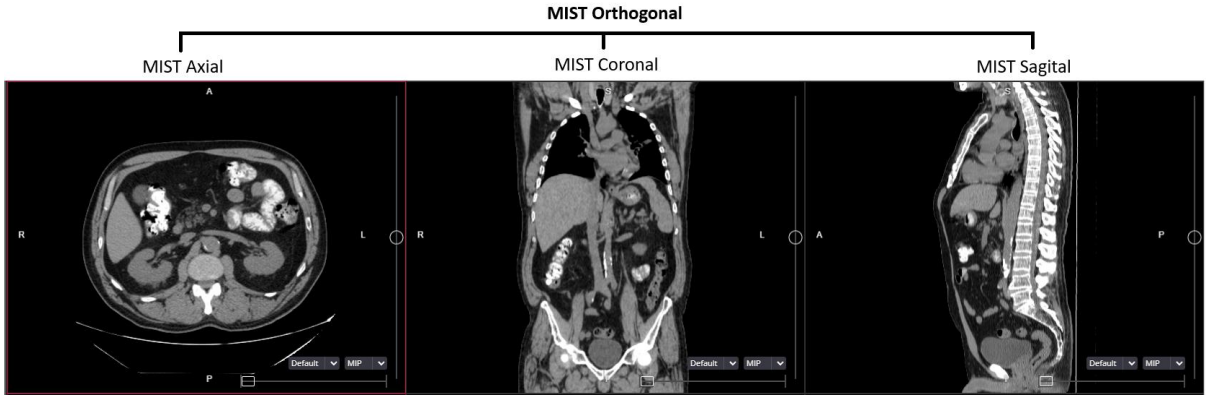


Figure 119. Spin around Y axis

⚠ **NOTE!** If the target viewports, selected according to the rules described above, already contain images, the reconstructed series will replace the existing content.

MIST Advanced PET



The action button to perform the Fusion action and to generate MIST projections in a 2x3 layout: first row with fusion and bottom row without fusion.

Open the series in the viewer for viewing. Select the action button in the menu bar **MPR**; sub-menu **MIST Advanced PET**.

The system opens a fusion action dialog where the user has to select the series with which to perform the fusion (for more details on Fusion, see the relevant section). If a fusion action has already been performed, this step is skipped.

⚠ **NOTE!** When Advanced PET is applied by the hanging protocol, the series to be fused is selected automatically from the same study as background series according to the selection criteria in hanging protocol. It is possible to change the fused series in the Fusion dialog.

The system generates axial, coronal and sagittal MIST projections and lays them out in a 2x3 layout, with fusion in the top row and without in the bottom row.

For the lower right sagittal projection, automatic rotation around the y-axis (also called Spin) is switched on and a slice thickness of 400 mm is selected. All actions in the viewport are the same as in normal MIST projections.

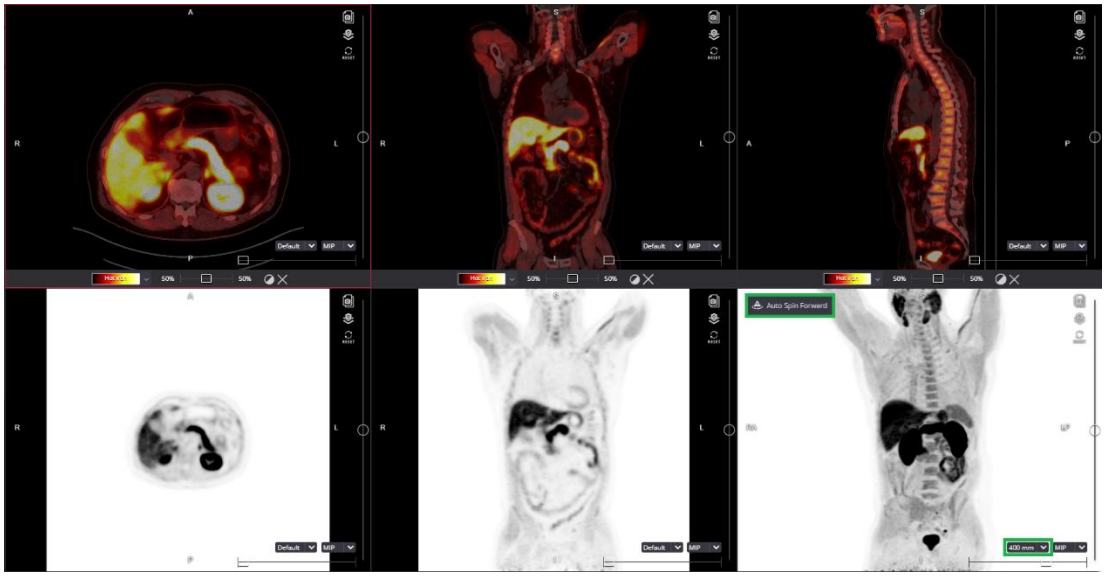


Figure 120. MIST Advanced PET

Dental MPR



⚠ **NOTE!** Dental functionality is Optional. Please contact sales@meddream.com to get Dental functionality license.

The action **Dental MPR** may be used to perform panoramic image reconstruction and provide image analysis tools for dentistry.

If the axial CT or MR series is viewed in the active viewport, you can launch the dental MPR layout by selecting the **Dental MPR** menu option from **MPR** tool menu. The system loads the axial series, generates the 3D image and displays it in Dental layout.

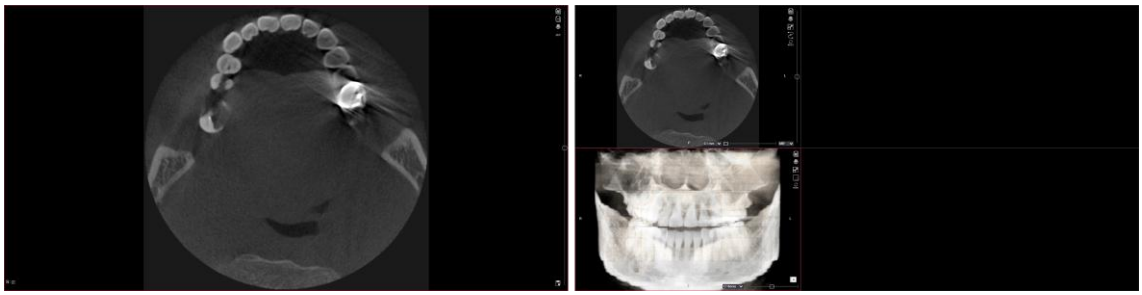


Figure 121. Initial dental layout displayed for axial CT series

Work with spatial 3D image

The system automatically creates and displays a spatial 3D image. For 3D images you can change the windowing level and programmed windowing preset, apply rotation, zoom and pan, copy the image to clipboard, or save the image as secondary capture DICOM. See example below in this section and the detailed description how to use the tools in section “MIST Oblique”.

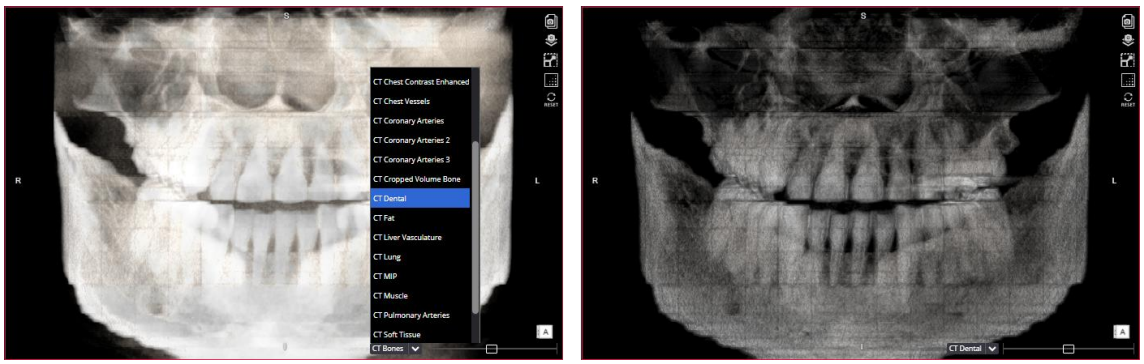


Figure 122. Changing Windowing level preset for 3D image

⚠ **NOTE!** List of Windowing level presets may be configured in system Settings.

⚠ **NOTE!** The Windowing values for 3D image are displayed in the bottom left corner of the 3D image viewport and may be adjusted using Windowing tool 

from the main Viewer window toolbar.

Rotate tool  from the main Viewer window toolbar may be used for free 3D image rotation with mouse.



Figure 123. Rotation of the 3D image

Anatomical direction letters and cube in the 3D viewport indicate the orientation of the rotated 3D view plane relative to the main anatomical planes.

⚠ **NOTE!** In dental MPR, the Rotate tool is available for 3D image, but not for 2D reconstructed series.

⚠ **NOTE!** Use the Reset button RESET in the 3D viewport toolbar to clear the rotation and other visual or spatial transformation and reset the 3D image to initial state.

Generate panoramic image

To generate the panoramic view and perpendicular tooth views, you need to draw the panoramic curve (polyline).

First, adjust the axial series view for better visualization of the dental arches:

- You can change the thickness and rendering method in the bottom right corner of the axial image viewport.
- You can scroll the series with a mouse wheel and select the best place for dental arches visualization.

Then click the CPR line tool to activate it, the icon is highlighted when active , and draw the polyline for the plane you want to be straightened as panoramic view:

- Position the mouse pointer on the point from which you want to start, click and release the left mouse button.
- Then move the cursor to the second, third, fourth, etc. points and each time click the left mouse button once and release it.
- When the cursor is moved to the last point, double click the left mouse button.

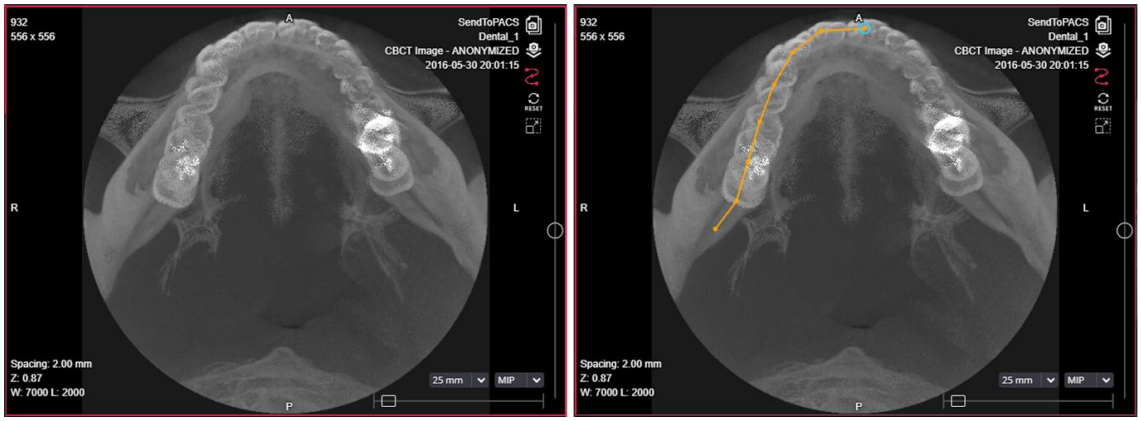


Figure 124. Panoramic polyline drawing

The system generates the panoramic series based on the panoramic polyline and displays it in panoramic viewport (top right viewport in the dental layout). By default, the 20 mm thickness and MIP rendering method is selected for the panoramic view. The width of the panoramic image equals the length of the panoramic polyline and is displayed at the bottom left corner of the panoramic image.

The system generates three tooth images in the planes, that are perpendicular to axial view and panoramic view and displays the images in the bottom right viewport. By default, the middle image is placed in the middle of the panoramic view, and the default spacing between tooth images is 2 mm. The spacing values are displayed at the bottom left corner of the axial image, and in the spacing selection box in each tooth image. The intersection lines with tooth planes are displayed in the axial and panoramic viewports. And the current position of the tooth image in the panoramic view is displayed at the bottom left side of each tooth view. Note, that position is metered as distance from the right side of the panoramic image which by default is in the left side of the panoramic image viewport.

The system shows anatomical directions on reconstructed images. Left (L) and Right (R) anatomical directions are displayed on the panoramic image. Lingual (L) and Buccal (B) anatomical directions are displayed on the tooth image.

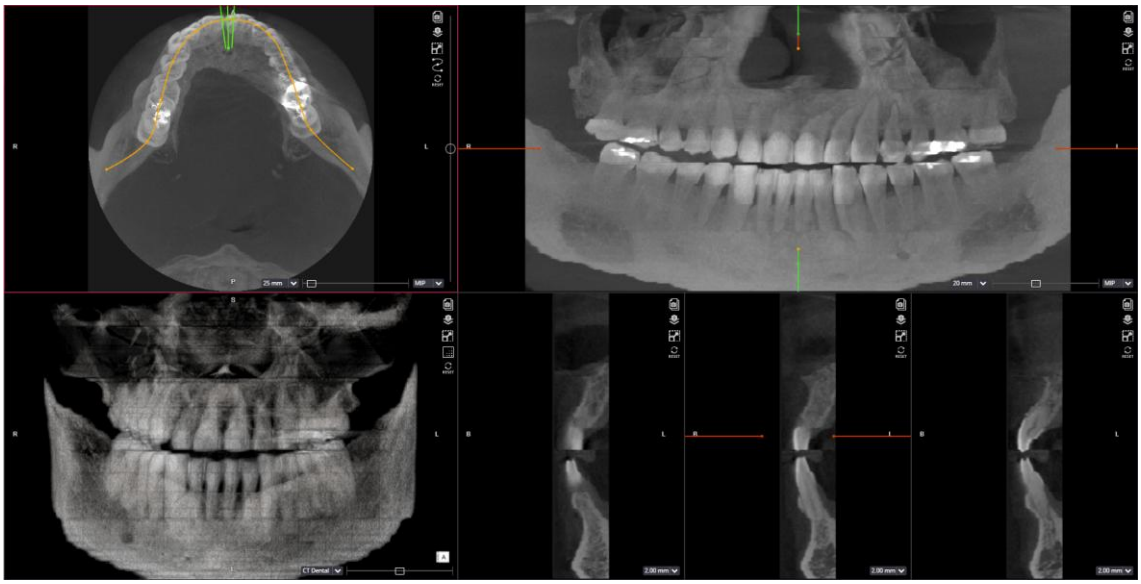


Figure 125. Panoramic and tooth views generated

Automated tools

The system does not provide automated tools for panoramic curve drawing. However, the system may be with 3rd party automated tools to obtain the polyline and other data, like nerve channels or sinuses.

If the integration is configured, and required data is received for the study, the automated tools icon  is displayed below the polyline tool in the generated initial dental layout. Instead of manual polyline drawing, the user can click the automated tools icon, and the system automatically draws the panoramic curve, generates the panoramic images based on this curve, and marks the nerve channel, sinuses in axial, panoramic and 3D image:

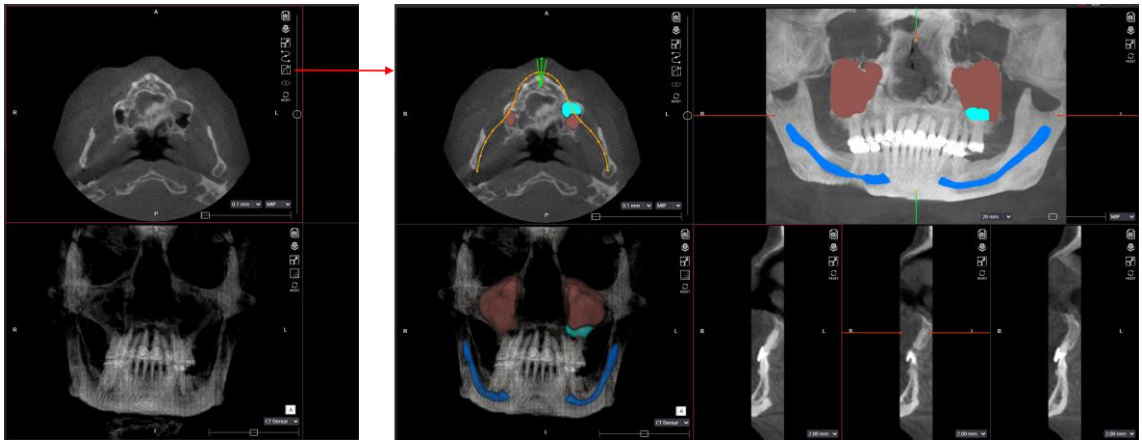


Figure 126. Automatic tools used to show dental curve, nerve channels, and sinuses

The automatically generated dental curve has points and may be adjusted by dragging any of the points.

The view icon  is displayed below automated tools icon and allows you to hide or show the other finding.

Dental layout modification

The default dental layout has four viewports with axial and panoramic images in the top row, and 3D and teeth images in bottom row. Any of the viewport may be enlarged by clicking the Show bigger image icon  in the

viewport toolbar. The enlarged image is displayed in top row and the icon for this image is changed to Show smaller image  . The other viewports are made smaller and displayed in the bottom row.

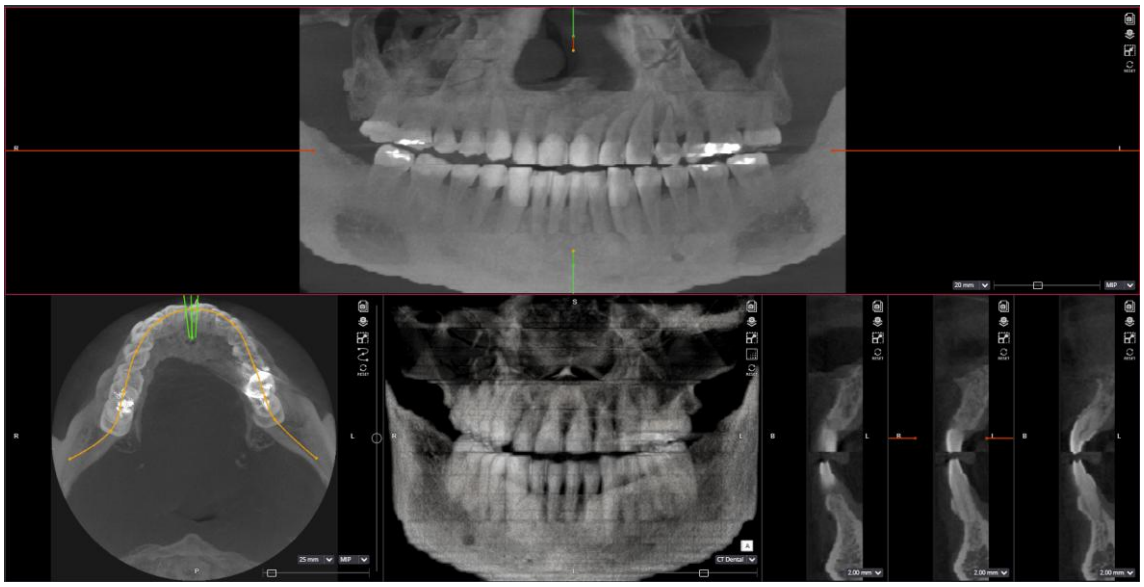


Figure 127. Dental layout with enlarged panoramic image

You can enlarge other image by clicking the Show bigger image icon  in it. Note, that three tooth images are enlarged together.

You can return to default dental layout by clicking the Show smaller image icon  in the enlarged image.

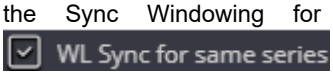
⚠ **NOTE!** You also can temporarily maximize the any image in the whole window by double clicking on the image. Each tooth image is maximized separately in this case.

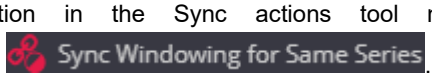
Work with panoramic image

The system provides below listed possibilities to adjust the panoramic image:

- You can change the thickness and image rendering method in the bottom right corner of the panoramic image viewport with corresponding extendable list or slider. See detailed description of how to use these tools in section “MIST Oblique”.
- You can change the windowing values for the panoramic view. Use the Windowing menu or mouse to change the windowing for the panoramic image. A detailed description of how to use windowing tools is in section “Windowing”.

  ⚠ **NOTE!** Currently applied windowing values are displayed in bottom left corner of the panoramic viewport, if info labels are switched on in Viewer window.

  ⚠ **NOTE!** You can change the windowing for axial, panoramic and tooth images at once by marking the Sync Windowing for the same series option in the Sync actions tool menu 

  or in Windowing tool menu 

  .
- You can change the generated panoramic image by editing the panoramic polyline in the axial viewport. You can point to the line segment (the line should become highlighted) and drag the whole polyline. Or you can point to the polyline point (the point should become highlighted) and drag the point. The following picture shows the adjustment of panoramic polyline to better display the tooth in the upper

arch. The axial series is scrolled to display the image of the upper arch: the position of the currently viewed axial image is marked as red intersection line in panoramic image and moves while scrolling the axial series. Then the points of the polyline are slightly moved down to the tooth. The system automatically generates a new panoramic image when the panoramic polyline is changed.

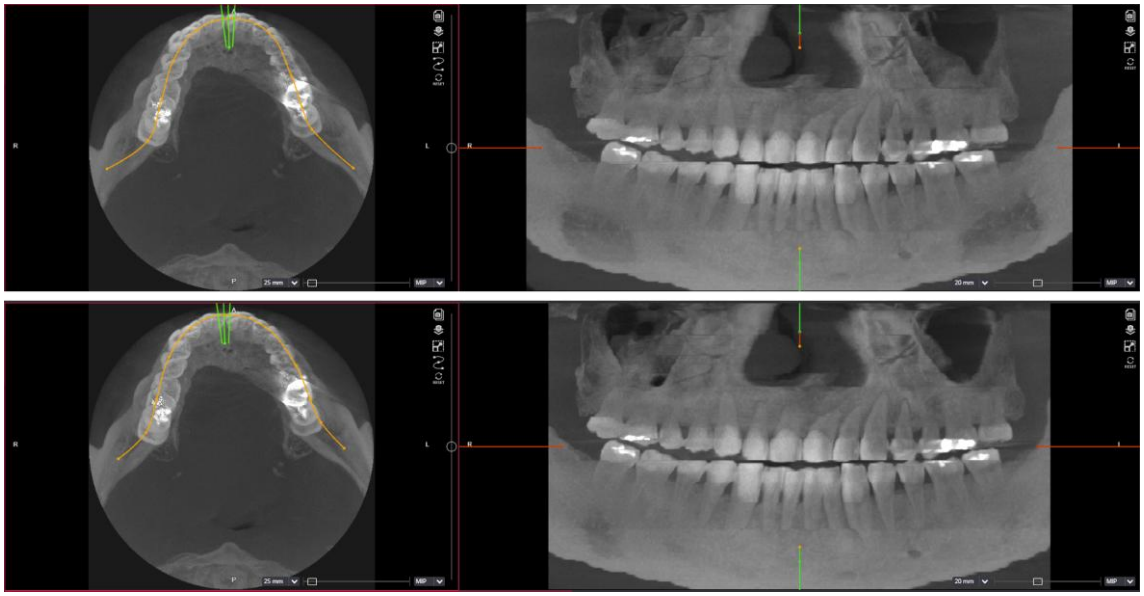


Figure 128. Changing the panoramic polyline to regenerate the panoramic images

- The generated panoramic plane is perpendicular to the axial plane while the teeth normally grow at an angle to the axial plane. Instead of changing the panoramic polyline and regenerating the panoramic view, you can scroll the panoramic images with mouse wheel to see the various regions of interest. The yellow dotted panoramic and axial plane intersection line on axial images moves while scrolling the panoramic images.

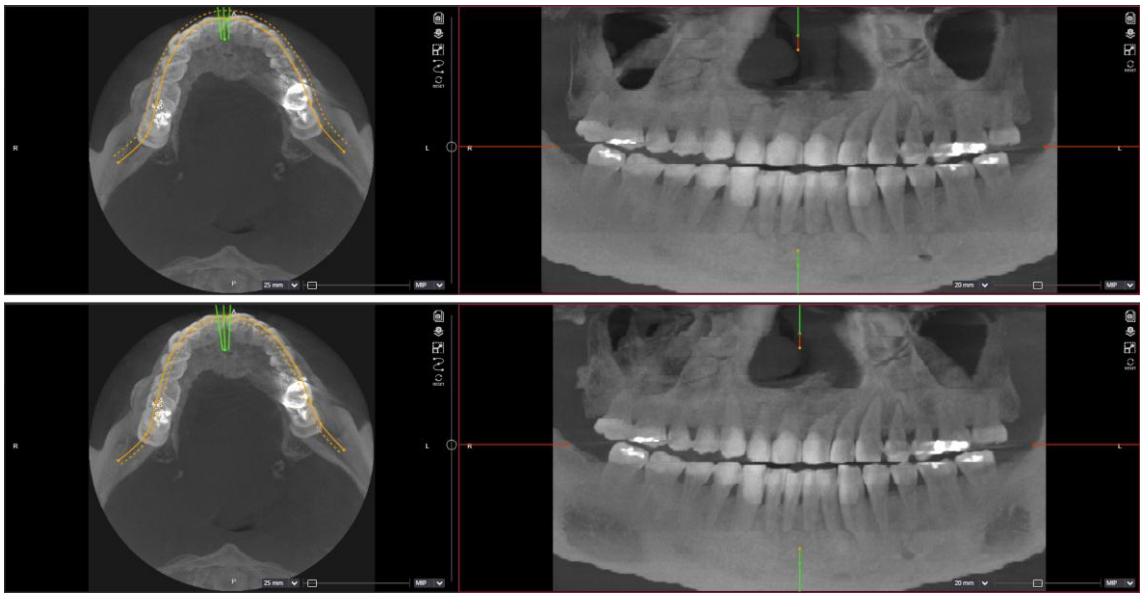


Figure 129. Scrolling the panoramic images to view the different regions of interest

- You can enlarge and view the different parts of panoramic image using the Pan and Zoom tools from the Viewer's main toolbar.

Work with tooth images

In the tooth viewport you can locate the interested tooth, view tooth images in three planes, and measure the tooth angle to the axial plane.

- You can change the position of the tooth images and locate the tooth in three ways:

In the axial image you can point the mouse cursor to the middle tooth image intersection line (the line should become highlighted) and drag the line to the wanted position. The tooth images and image position at the bottom left corner of each image are automatically updated.

In the panoramic view you can point the mouse cursor to the green dot at the bottom of the tooth image intersection line (the intersection line should become visible) and drag the line to the wanted position. The tooth images and image position at the bottom left corner of each image are automatically updated.

You can scroll any of the tooth images. All the three tooth images scroll together. The position numbers at the bottom left corner of each tooth image and the intersection lines in axial and panoramic images are updated correspondingly.

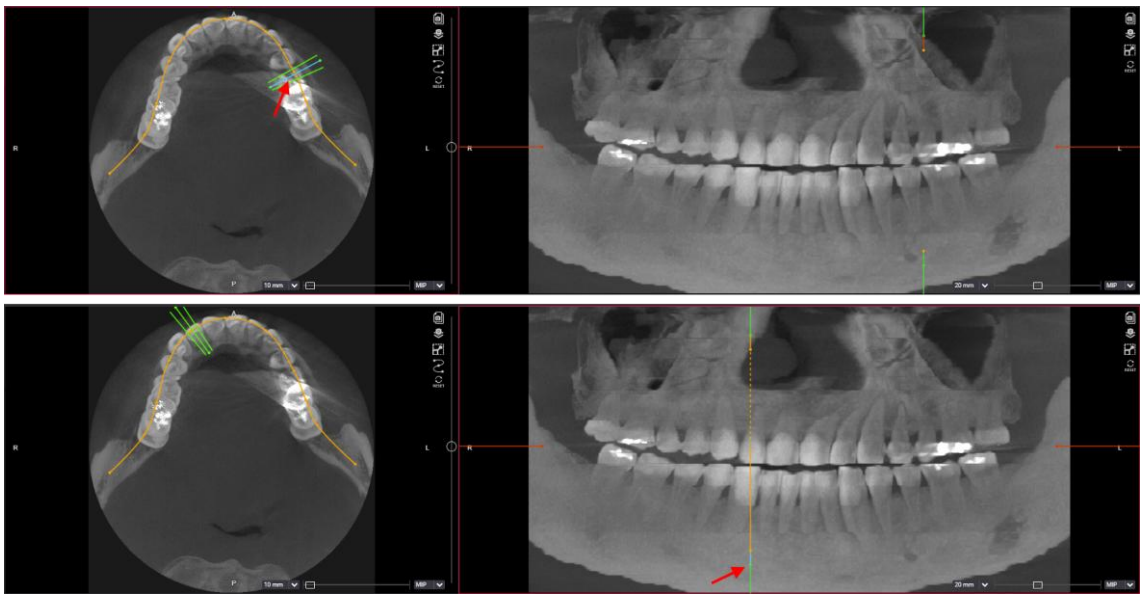


Figure 130. Changing tooth images position by dragging intersection line in top axial image or bottom panoramic image

- You can change the angle of the tooth image to the axial plane by rotating the tooth image intersection line in panoramic view. Point the mouse cursor to the yellow dot at the bottom or the top of the tooth plane intersection axis (the intersection line should become visible, and the dot should become highlighted) and drag the dot to the wanted position. The tooth images are automatically updated, and the angle is displayed in each tooth image near the image position.

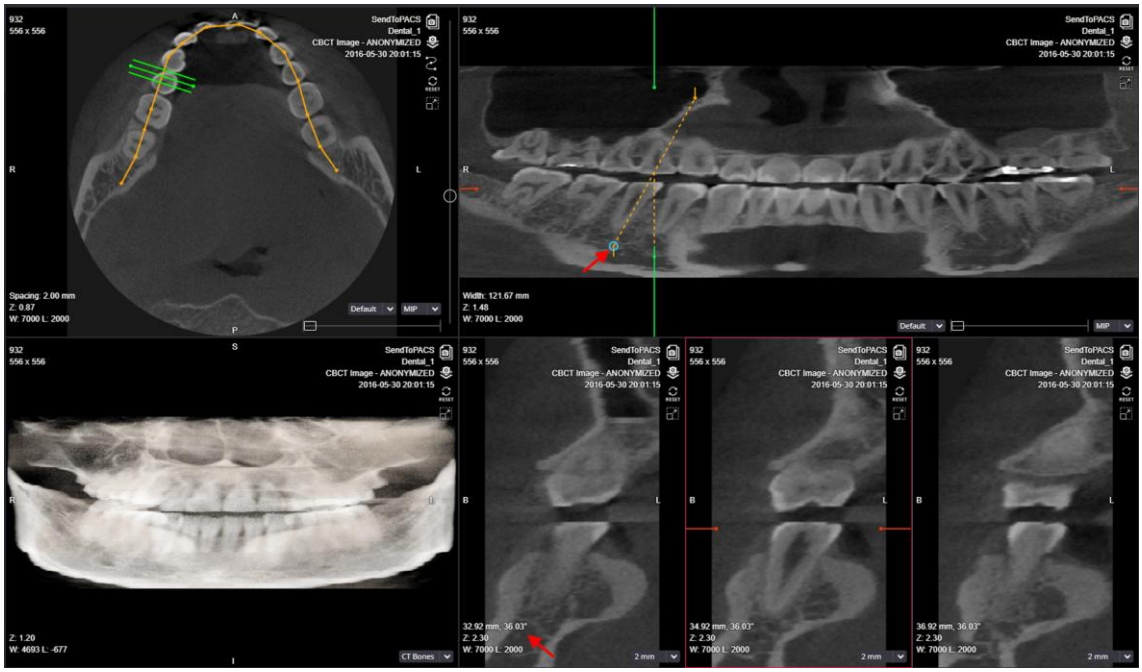


Figure 131. Changing the angle of the tooth images

- You can change the spacing between tooth images in two ways:

In the axial image you can point the mouse cursor to not middle intersection line of the tooth image (both side lines should become highlighted) and drag the line to the wanted position. The side tooth images, their position, and the spacing are automatically updated.

You can select the spacing between the tooth images from the expandable list, that is displayed at the bottom right corner of each tooth image. The side tooth images, their position, and the intersection lines with spacing in axial image are automatically updated.

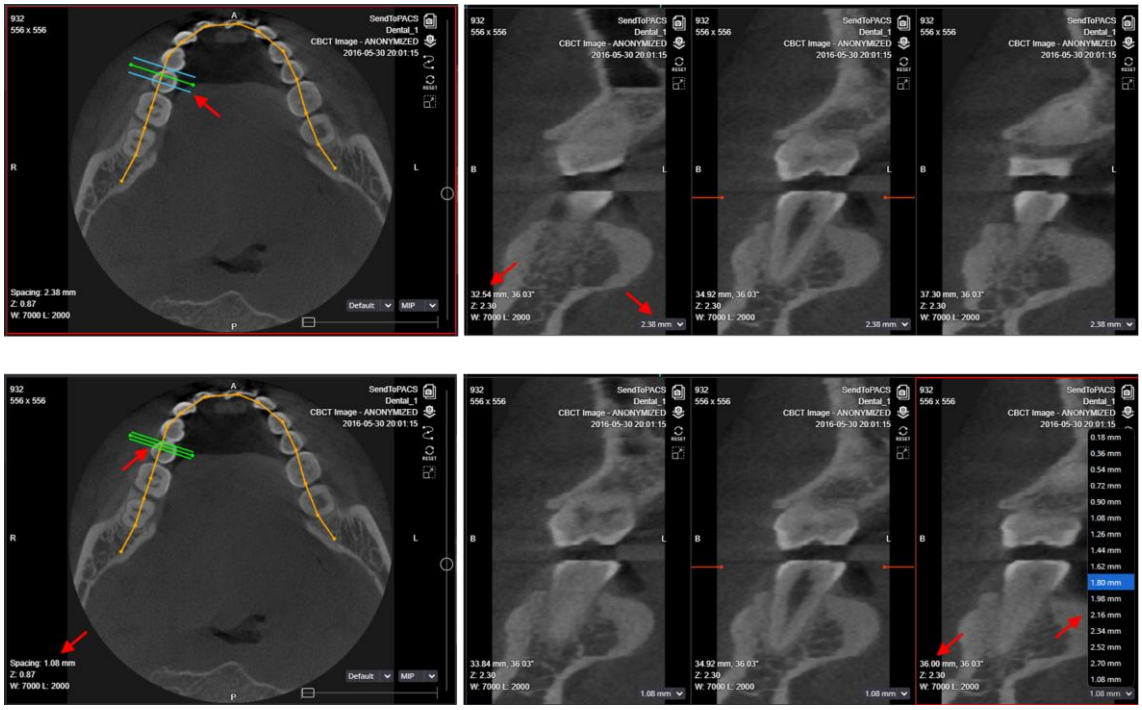


Figure 132. Changing tooth images spacing by dragging intersection line in top axial image or selecting from the list on bottom right

- You can enlarge and view the different parts of tooth image using the Pan and Zoom tools from the Viewer's main toolbar.

  ⚠ **NOTE!** The same scaling, position and windowing is applied for all the three tooth images, if changed in one of the tooth images.

Tools for 2D reconstructed images

The section describes the tools that are available for all reconstructed 2D images: axial series, panoramic series, and tooth series.

The tools for copying the image to clipboard or saving the image as secondary capture DICOM are available in viewport toolbar. See detailed description in the section "The action buttons in the viewport" of MIST Oblique functionality.

The measuring tools for 2D reconstructed image may be selected from the Measuring tool in the Viewer window toolbar. See detailed description in the section "Measuring 2D reconstructed images" of MIST Oblique functionality.

Mammography reconstruction

If breast tomosynthesis multiframe image is configured to be displayed as series of images, and MG modality is added to multi-planar reconstruction configuration, the user can initiate the reconstruction of the MG series.

The reconstruction of breast tomosynthesis series may be initiated by selecting the **Mammography** menu option from **MPR** tool menu or **MIP** button, which is displayed in viewport vertical toolbar, if the multi-planar reconstruction is configured for mammography.

⚠ **NOTE!** The breast tomosynthesis images often exceed the WebGL texture limit (see section "WebGL 3D Texture Limit"), and system displays MPR data cropping window and tries to set the used image area to include the whole image without the empty background. If the image excluding background is still to large, the rectangular of maximum possible size is set in the center of the image.

The reconstructed 2D breast tomosynthesis series is displayed in the same oriented 2D plane and as the original series, but highlighted **MIP** button indicates that the viewport displays reconstructed series.

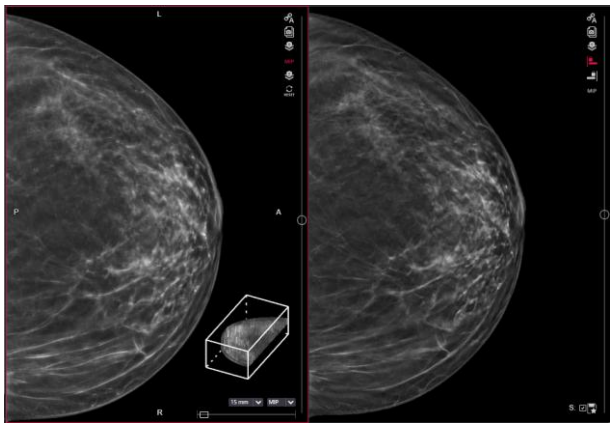


Figure 133. Breast tomosynthesis original series on the right and reconstructed series on the left

The tools of 2D reconstructed series, like slice thickness or rendering method, are available and may be applied to the reconstructed series. The thickness and position of rendered image is also visualized in cube that is displayed in the corner of the viewport.

Clicking the highlighted **MIP** button in the viewport with reconstructed series, displays the original series.

⚠ **NOTE!** The other reconstruction tools from MPR menu by default display the reconstructed series in axial, coronal and sagittal planes what is not convenient for mammography series analysis.

Close MPR



After the MPR has been generated, it is possible to close the projection and return to the original series. To do this, activate the viewport where the MPR is projected and select Close MPR from the MPR menu item. The action can be assigned to a combination of shortcut buttons (see section "Shortcuts" for details).

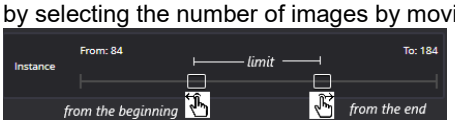
⚠ **NOTE!** To close all projections that are generated by Orthogonal, the action should be performed on each viewport. The window layout is not changed.

WebGL 3D Texture Limit

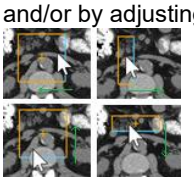
WebGL 3D Texture Limit – this is the maximum data size (texture volume) that the browser can process using WebGL. If this limit is exceeded, a 3D projection cannot be generated, and the data must be reduced to the allowed size.

When the WebGL 3D texture limit is reached, the system automatically opens a dialog window where the user can reduce the data set:

- by selecting the number of images by moving the slider to the beginning or the end



- and/or by specifying which image area to use for generating the 3D projection by moving the defining square 
- and/or by adjusting the image width and/or height by moving the edges of the defining square



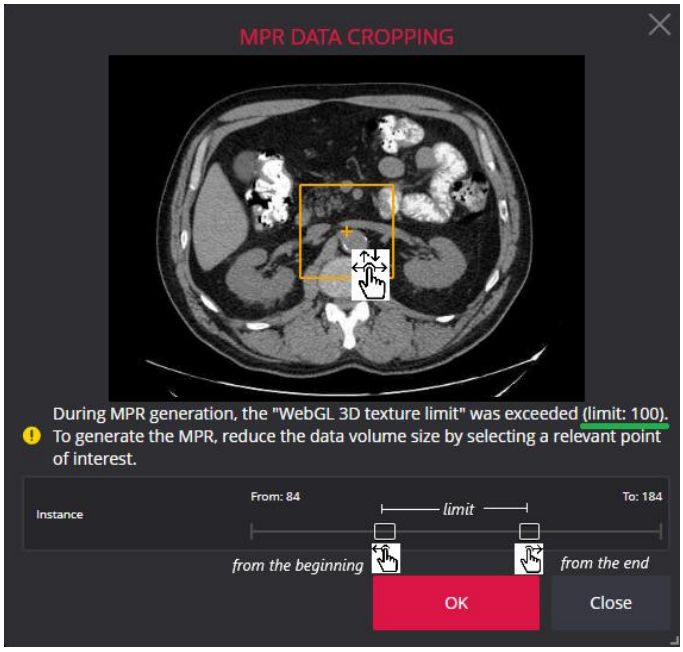


Figure 134. WebGL 3D Texture Limit. Data Reduction

Reference Line and Crosshair

Reference Line and **Crosshair** tools helps to localize the images in intersecting planes.

⚠ **NOTE!** The localization tools are mainly used for CT, MR and PT studies, that contains several series taken in several planes.



Overlaying reference lines allow you to indicate the location of an image slice on another image of an intersecting plane:

- Prepare Layout for image comparison. Move into viewports the images that you want to compare.
- Activate viewport with the image you want to know the location of in regard to other images.
- Click the button Reference Line. The button highlights  that indicates activation of reference line function in all the opened viewports.
- Lines, indicating the location of the active series, appear in the images that are in the planes intersecting with an active image plane. The gray lines indicate the location of the first and the last image of the active series. By default, showing the first and the last series image location is enabled, but may be disabled using the expandable menu of the reference line tool. The yellow line indicates the location of the currently viewed image:

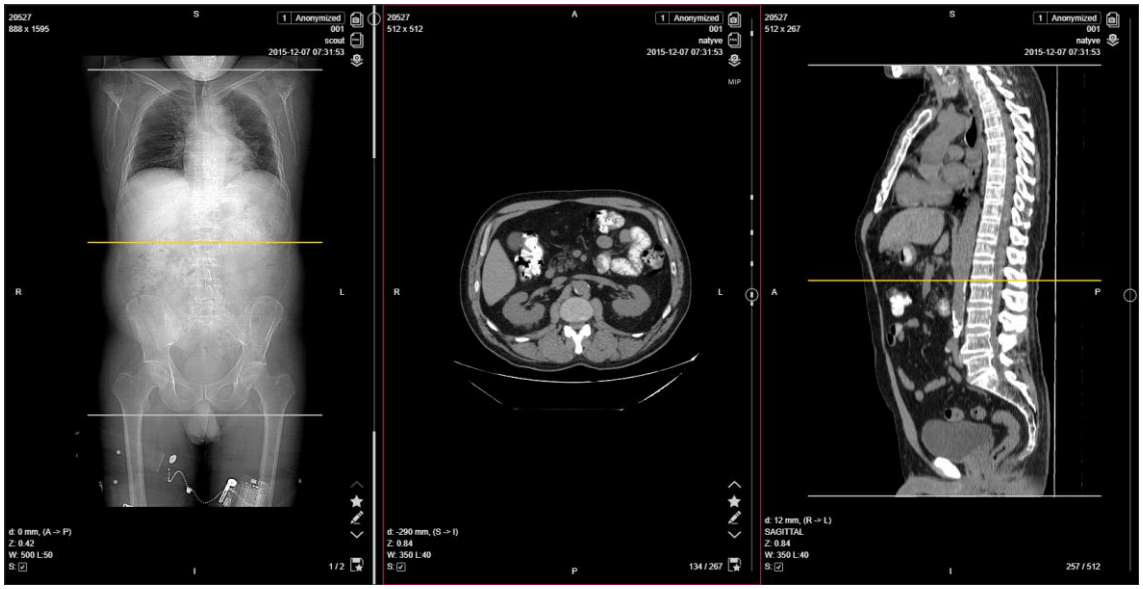


Figure 135. Image reference line in intersecting planes

- Scroll the active image series to see the reference line of the currently viewed image moving in intersecting planes.

⚠ **NOTE!** Reference line function is automatically applied in all active viewports if **Reference line** tool is activated (tool icon is highlighted). If the function is not needed, click the highlighted **Reference line** button to deactivate the tool.

The reference line may be configured using expandable menu:

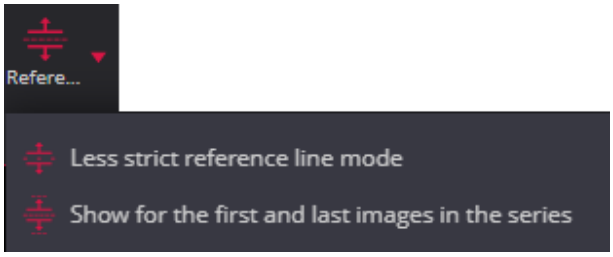
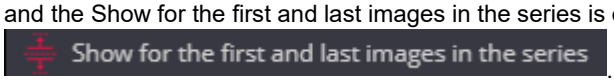


Figure 136. Reference line tool menu

Gray lines indicating the location of the first and the last image in the active series may be hidden by disabling the Show for the first and last images in the series in the Reference line tool menu. By default, the icon is highlighted, and the Show for the first and last images in the series is enabled:



. The default value can be changed in the system settings so that this menu option is not enabled.

If the series or the same study do not have the same frame of reference, the system calculates the reference line based on the image position in patient coordinates system. Such reference lines are displayed in gray color and may be hidden by disabling the Less strict reference line mode in the Reference line tool menu. By default, the icon is highlighted, and the Less strict reference line mode is enabled:



.

⚠ **NOTE!** For ophthalmology and mammography images the system does not calculate intersection based on the image position in patient coordinate system.

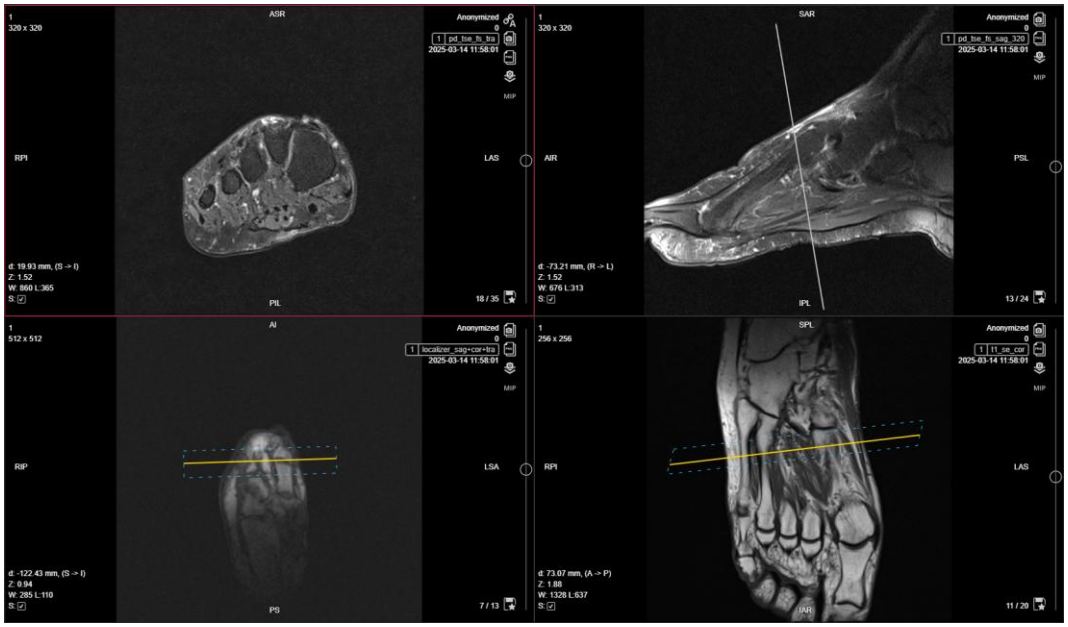


Figure 137. Less strict reference line enabled and displayed in the top right viewport

The dashed rectangle near the reference line indicates the slope of intersecting plane in case the image plane and intersecting plane is not orthogonal.

⚠ **NOTE!** The system shows the slope the slope of intersecting plane only for the active image intersection line and does not show it for the first and the last series image intersection lines.

⚠ **NOTE!** The system does not show planes slope and intersection line for almost parallel images, whose plane orientations differ by less than two degrees.



Crosshair tool allow you to locate the images (slices) of the intersecting planes for the selected point on the active image:

- Prepare Layout for image comparison. Select the images from series that you are interested in and move them into viewports. You can also use the MPR function to generate the wanted axial reconstruction from the series.
- Activate the crosshair function by assigning the wanted mouse button  . Hover over the point of interest for the image being analyzed and click the selected mouse button.
- The system automatically displays the intersection lines and locates the corresponding images (slices) in the viewports displaying series from intersecting planes. The intersection plane and plane's intersection line are marked with the same color (red, green or blue).

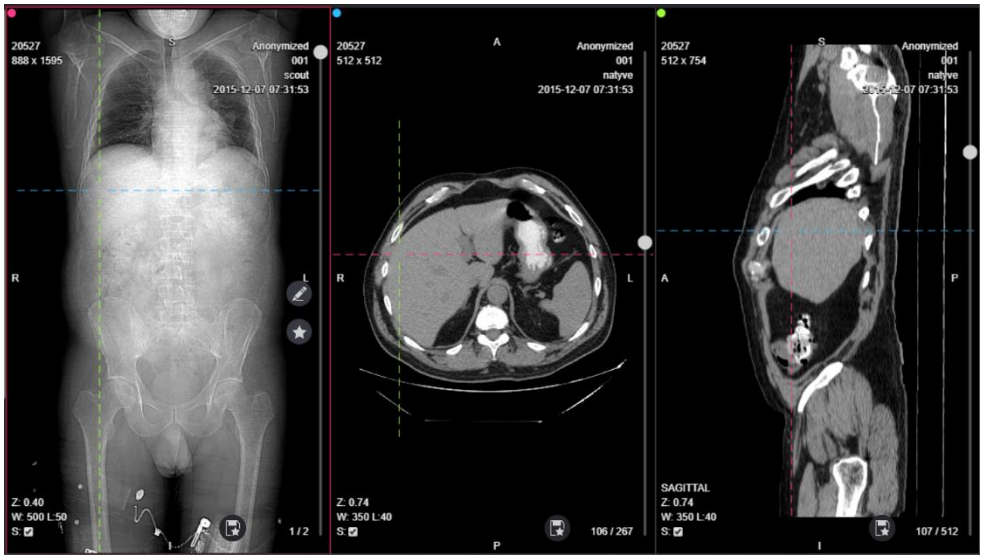


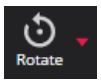
Figure 138. Crosshair tool

- Hold the mouse button pressed and drag the crosshair through the image to see the slices changing in intersecting planes.
- Crosshair lines dotted . When the assigned mouse button is clicked, the lines connect at the center point .

NOTE! In Oblique views, you can rotate the crosshair by holding the mouse button pressed and dragging one of the lines. The crosshair position and axes orientation should be maintained relative to the image, if the user rotates or flips the image.

NOTE! Crosshair is automatically switched off if navigation is selected in the segmentation dialogue. See the segmentation section for details.

Rotate



Rotate button allows you to rotate and flip the image. You can rotate the image using the mouse or rotate option from menu.

To rotate the image with mouse, assign the mouse button to Rotate function . To rotate the image, hold the selected mouse button pressed on the any side of the image and drag it clockwise or counterclockwise wise. The rotation angle is displayed on the bottom left corner and changes when the image is rotated.

Use the **Rotate** button menu to rotate or flip the image:

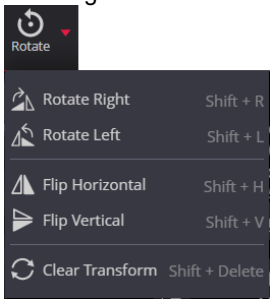


Figure 139. Rotate button menu

- **Rotate Right** – to rotate the image 90° clockwise.
- **Rotate Left** – to rotate the image 90° counter-clockwise.
- **Flip Horizontal** – to flip an image 180° about the horizontal axis.
- **Flip Vertical** – to flip an image 180° about the vertical axis.
- **Clear Transform** – revert to original image orientation.

DICOM



Click **DICOM** button to open the modal with DICOM tags of the active image:

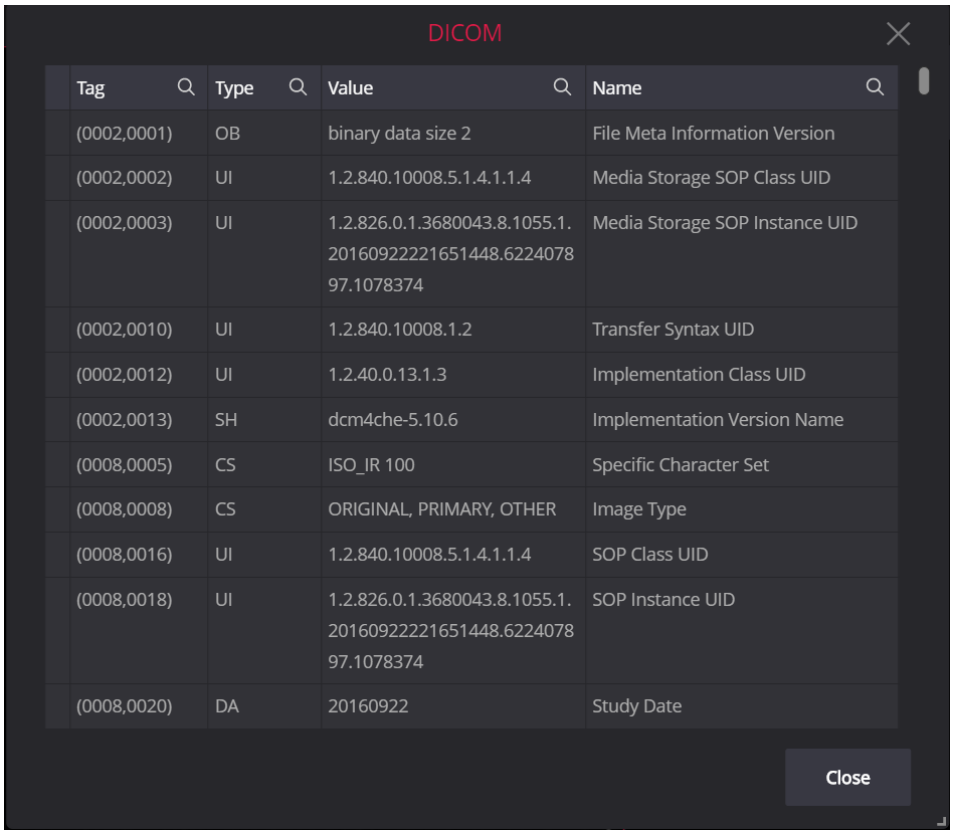


Figure 140. DICOM tag window

You can search the DICOM tag by selecting the appropriate criteria entry field and entering the text in it. Search according to **Tag**, **Value**, **Type**, and **Name** parameters can be done. The system filters the data automatically at the text entry:

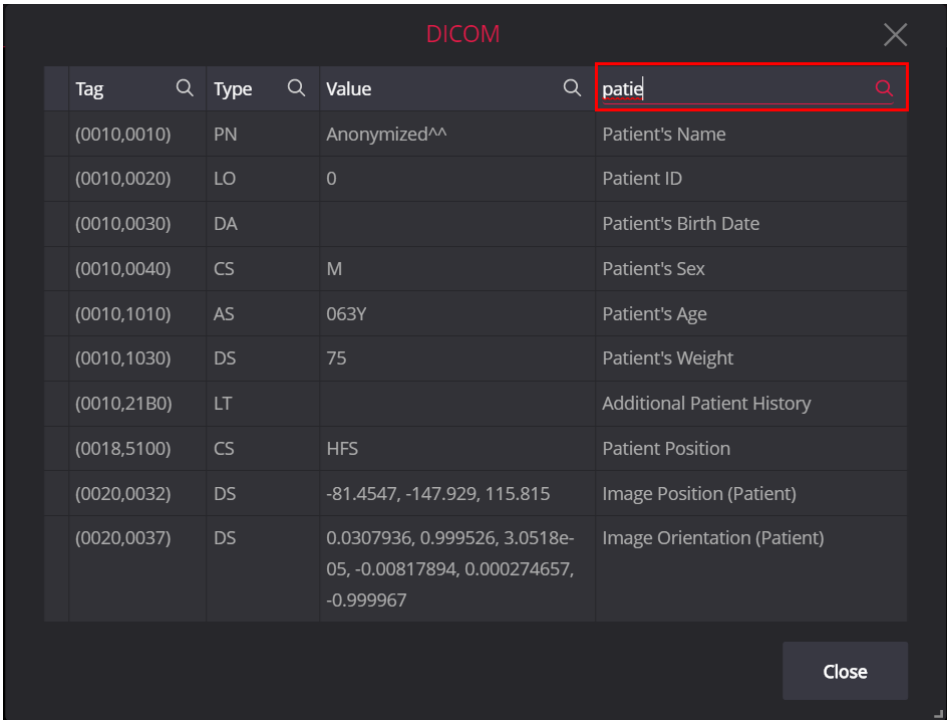


Figure 141. Search according DICOM tag name in DICOM tag window

'+' sign on the left of SQ tags indicates the container tag, that holds the other tags. Click the '+' sign to expanded the list and see the internal tags:

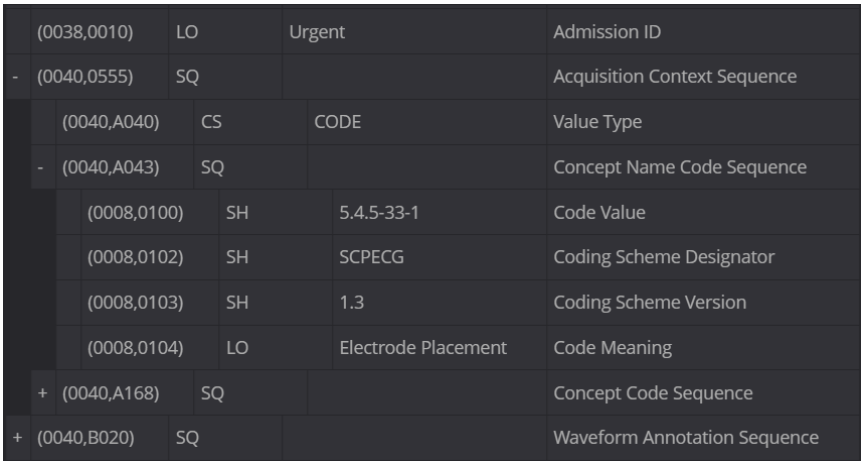
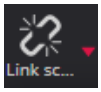


Figure 142. Expanding the SQ tags in DICOM tag window

Link scrolled series



Link scrolled series button is intended for making comparison on image slice location. Linking may be applied to currently viewed series with more than one image in series. There are four types of synchronization: **Non-synchronize**, **Manual synchronize (M)**, **Automatic synchronize (A), and Distance synchronize(d)**.



Non-synchronize mode indicates that scroll is not synchronized.



In the **Manual synchronize** mode, the active series and all the other series having multiple images are linked for scrolling. System displays manual series link button in the top right corner of the viewport and switches scrolling on for all series by default.



In the **Automatic synchronize** mode, the active CT or MR series and all the other series with identical modality, frame of reference UID, and image orientation (patient) values and having multiple images are linked for scrolling. System displays automatic series link button in the top right corner of the viewport and switches scrolling on for all series by default.



In the **Distance synchronize** mode, the active series and all the other series of the same anatomical axis and having data for calculating the slice distance from the referenced position are linked for scrolling. System displays distance series link button in the top right corner of the viewport and switches scrolling on for all series by default. The currently opened instance in all linked series is treated as the same body place and reference position.

⚠ **NOTE!** To change the reference position for the series, disable the distance link in the viewport, scroll to the corresponding image, and then enable the distance link.

By default, Synchronization settings (see Settings section for more information) Viewer window opens with Link scrolled series mode set to **Auto synchronize**, and you may change it manually by clicking the button. The icon is changed to the Distance synchronize mode, Non-synchronize mode, Manual synchronize mode and back to the Automatic synchronize mode correspondingly. You can also select the synchronization mode by selecting the corresponding menu option in the **Link scrolled series** button's menu, or using the shortcut assigned to the menu option.

You can change the default Link scrolled series mode to Auto synchronize in **Link scrolled series** button menu:

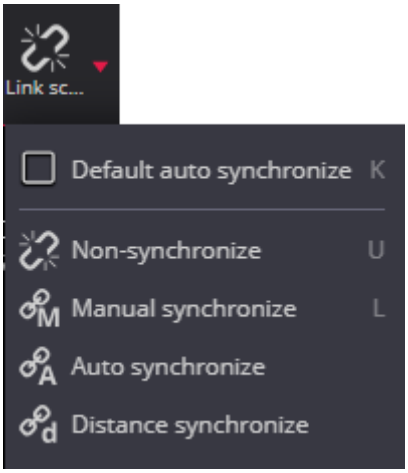


Figure 143. Link scrolled series button menu

Click the **Default auto synchronize** menu option or use shortcut K to change the status. The marked checkbox on the left side of the menu indicates, that default **Link scrolled series** mode is changed to **Auto synchronize**, the current mode is also set to Auto synchronize and the menu icon is highlighted  . The selection is saved in browser's local storage and **Auto synchronize** Link scrolled series mode will be set when starting the viewer next time.

⚠ **NOTE!** The **Auto synchronize** can also be set as default mode of the **Link scrolled series** button in the Synchronization settings (see Settings section for more information).

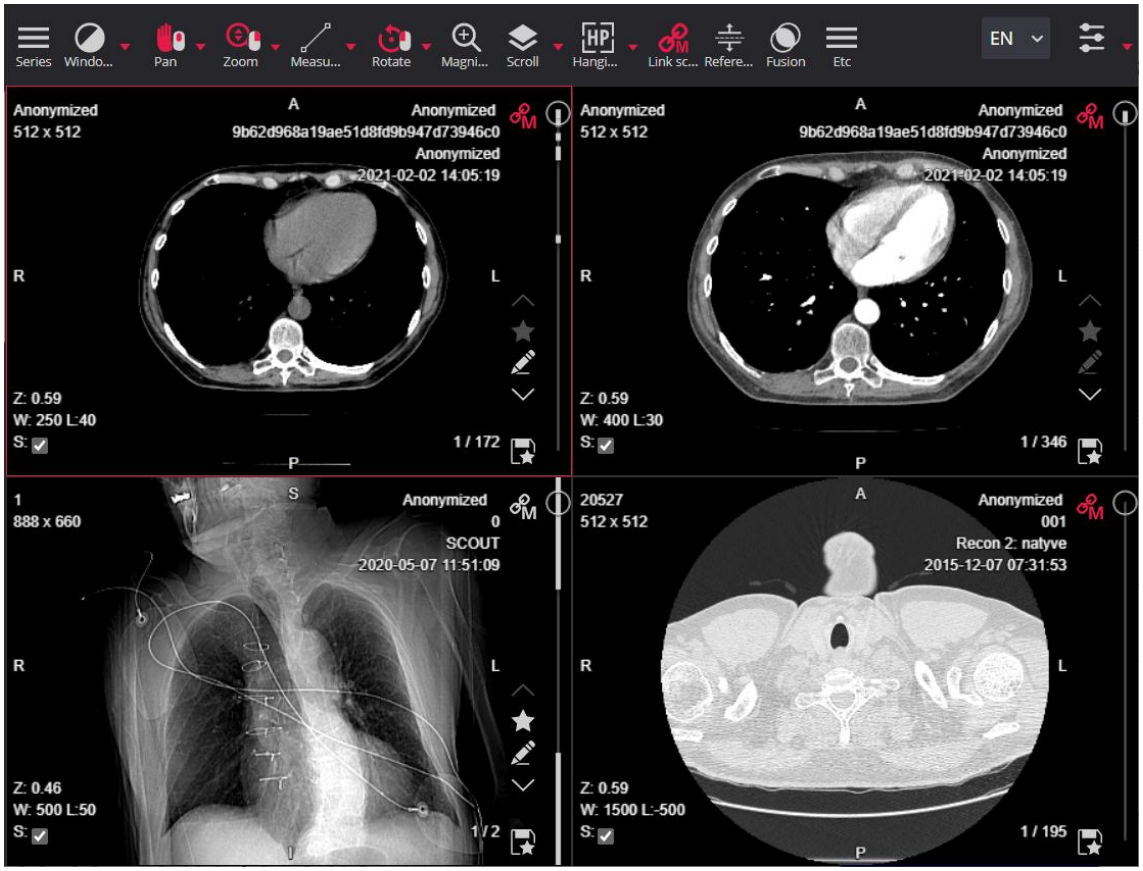


Figure 144. Manual link mode in Viewer with the disabled linked scrolling for one of the series

When automatic or manual link is enabled, and one or more viewports contains series with link button, you can do the following:

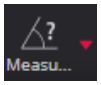
- Scroll the images of the linked series simultaneously:
  - In automatic mode, when scrolling images in the active series, the image in the linked series is selected according to the image position and slice thickness;
  - In manual mode, when scrolling images in the active series, the images in the linked series are scrolled one by one;
  - In distance mode, when scrolling images in the active series, the image in the linked series is selected according to the image position and distance from the reference image.
- Enable or disable the synchronous scrolling for a particular series by tapping the manual, automatic, or distance link button in the viewport. Highlighted icon indicates, that linking is enabled for the series.
- Open a new linked series in the viewer, if opening series meets the link criteria. The link button is displayed in the viewport, either with default value, or previous state, if the previous series was linked and the viewport already had link button displayed.

⚠ **CAUTION!** Note, that MedDream cannot guarantee that the manual series linking displays the images of the same patient and at the corresponding position.

⚠ **NOTE! Link scrolling** functionality works more efficiently when the series are preloaded.

Tools for measuring, and presentation state saving

Measuring images



Measure button allows you to measure and analyze the images in number of ways. To pick the measure tool, use the **Measure** button drop-down menu:

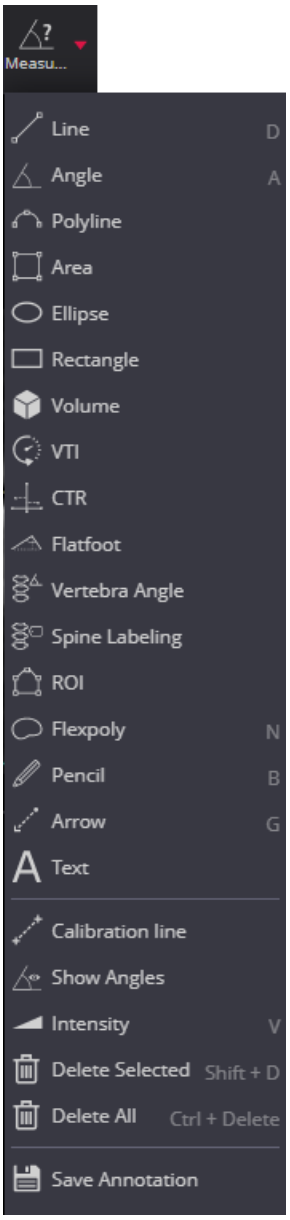


Figure 145. Measure button menu

NOTE! The tools in **Measure** button menu may vary depending on license type, active image type and system settings:

- **Measure** button is not displayed for structure reports (SR).
- ECG studies has different set of Measure tools.

- **TPA**, **Norberg Angle**, **VHS, Hip DI,** and **TTA** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.
- **VTI** measuring is applicable and displayed only for US modality.
- The limited list of tools is supported for 2D reconstructed series, see section " Measuring 2D reconstructed images" for details.

⚠ **NOTE!** By default system configuration, the measurement is displayed on the frame on which it was drawn. Contact your system administrator to change the configuration to see the measurement on all the frames of the multiframe image.

The top group of **Measure** menu contains the measuring tools. To use the measuring tool, assign mouse button to measure function: the mouse pictogram with assigned button is displayed  . The system allows assigning the left, and the middle mouse button for measuring tool. The right mouse button may not be assigned for measuring tool. The highlighted tool pictogram indicates that tool is ready for measuring. You can change the active measuring tool by selecting the other tool in menu – the selected tool icon is displayed in Measure button:  .

⚠ **NOTE!** You can use the tools, like zoom or pan, that are assigned to other mouse buttons, to adjust the image while performing the measurement.

⚠ **NOTE!** The measuring tools is automatically deactivated after one measurement is finished:  . To measure with the same tool several times, use the Continuous measurement function.

The divider line in expandable **Measure** button menu separates the measuring tools from supporting functions. The detail measuring tools and supporting functions description is provided in following sub-sections.

⚠ **WARNING!** MedDream cannot guarantee the accuracy of calibration data received from the modality. Note, that MedDream cannot guarantee that the manual calibration which is performed by users is done accurately.

⚠ **WARNING!** The accuracy of the measurements is affected by the calibration status of the monitor. Monitor calibration ensures that tones that are lighter than black are displayed clearly separately from true black, and tones that are darker than white are clearly distinguished from true white. How to calibrate the monitors is described in the software installation instructions, which are provided separately in this user guide.

⚠ **WARNING!** Note, that measuring functions in MedDream is approximate.

Line



The **Line** tool helps to measure the distance between objects:

- select **Line** tool in **Measure** menu;
- place the mouse cursor on the starting point, click and release the selected mouse button;
- move the cursor to the end point, click the selected mouse button and release it;

- the distance will be displayed in yellow:

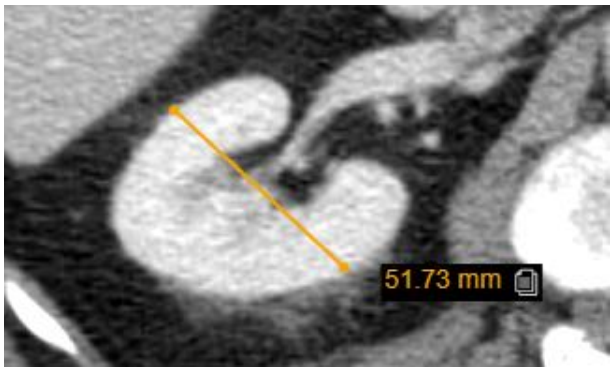


Figure 146. Distance measurement

Use „Alt“ key to draw vertical or horizontal lines. Hold the „Alt“ key pressed while drawing the line measurement. The system automatically aligns line horizontally or vertically, depending which direction is closer to current cursor position. Do not release the “Alt” key until line measurement is not finished.

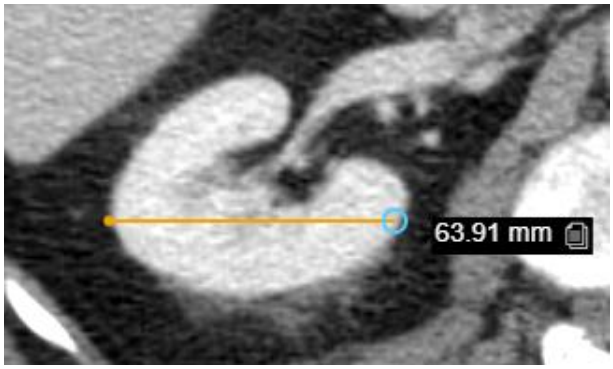


Figure 147. Horizontal line drawing, holding the "Alt" key pressed

If Line tool is used in motion mode or spectral doppler region of the cardiac ultrasound image, drawing the line that is not parallel to x or y axe shows three measurements: deltaY, deltaX, and ration deltaY/deltaX.

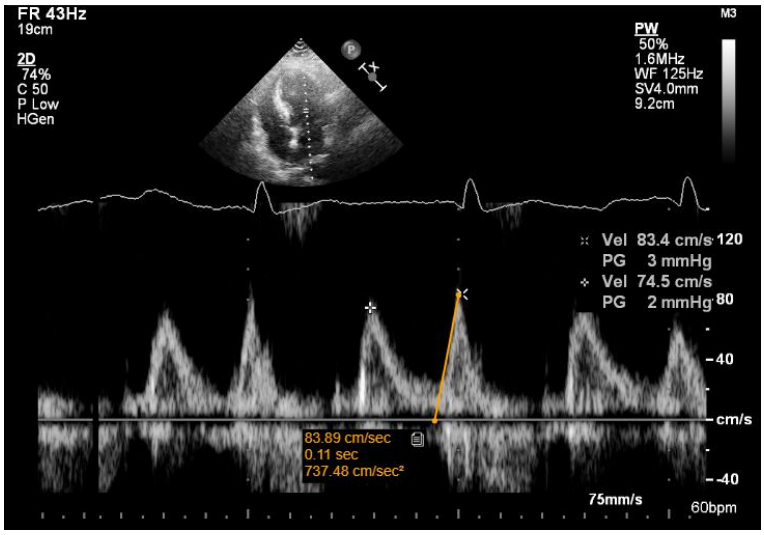
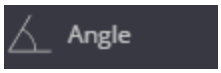


Figure 148. Line measurement in doppler region on cardiac ultrasound image

Angle



Angle tool is used to measure the angle:

- select **Angle** tool in **Measure** menu;
- position the mouse pointer on the point from which you want to measure the angle, click and release the selected mouse button;
- move the pointer to the second point (the apex), click and release the selected mouse button again;
- move the pointer to the end point and click the selected mouse button again – the angle is displayed on the image:

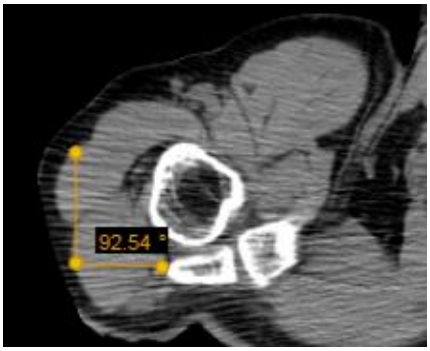


Figure 149. Angle measurement

Cobb Angle



The **Cobb angle** button is used to measure angle between lines. To measure angle:

- select **Cobb angle** tool in **Measure** menu;
- click on image and draw two lines, parallel to the most tilted vertebrae,
- the system measures and displays:
  - the corner; the angle is measured at the point where two lines drawn by the user would intersect if they were extended as straight lines;
  - the distance between the midpoints of the lines drawn by the user;
- you can drag lines and line points, or the whole measurement object by dragging the white dotted line.

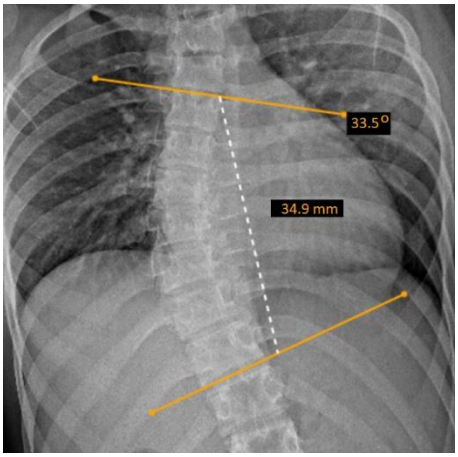
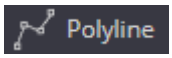


Figure 150. Cobb angle measurement

Polyline



The **Polyline** tool is used to measure the distance or perimeter of a region of interest:

- select **Polyline** tool in **Measure** menu;
- position the mouse pointer on the point from which you want to start measuring, click and release the selected mouse button;
- then move the cursor to the second, third, fourth, etc. points and each time click the selected mouse button once and release it;
- when the cursor is moved to the last point, double click the selected mouse button, and the total length of all the lines is displayed. If you place the last point on top of the first point, you will get the perimeter:

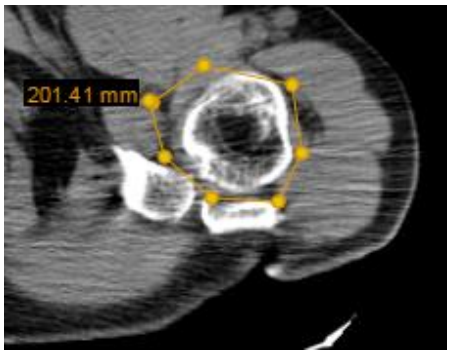
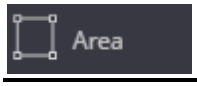


Figure 151. Perimeter measurement

Area



The **Area** tool is used to measure the area of a region of interest:

- select **Area** tool in **Measure** menu;
- mark points around the area of interest, as described in Polyline tool section;

⚠ **NOTE!** For proper calculation of measurement values the polyline should not intersect itself.

- when you reach the last point, double click the selected mouse button twice - the area (in square millimeters) will be displayed:

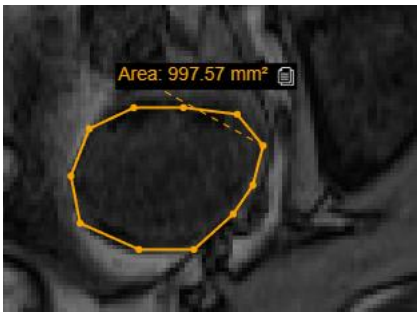


Figure 152. Area measurement

The system can be configured to display additional intensity values: medium brightness (marked Mean), the standard deviation (marked SD), which gives the variance of the random variables about the mean, sum value and minimum, maximum values. The units of measurement depend on the type of study.

⚠ **NOTE!** If the intensity values may not be calculated, only the area value will be displayed.

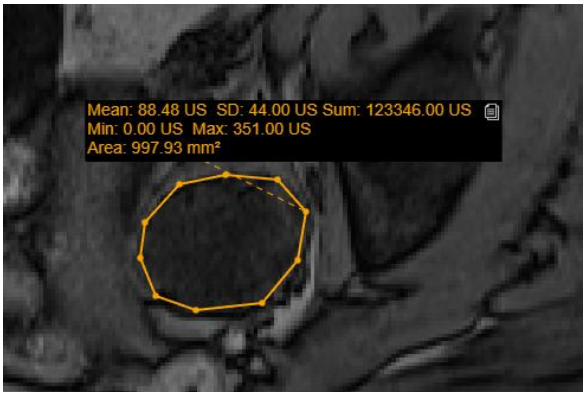
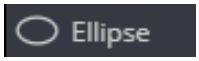


Figure 153. Area measurement with brightness values

Ellipse and Rectangle





Ellipse and **Rectangle** is used to measure area in cm^2 units, length and width in *cm* units, minimum, maximum and medium brightness (marked *Mean*) in *HU* units and for the standard deviation (marked SD), which gives the variance of the random variables about the mean and sum value, in *HU* units:

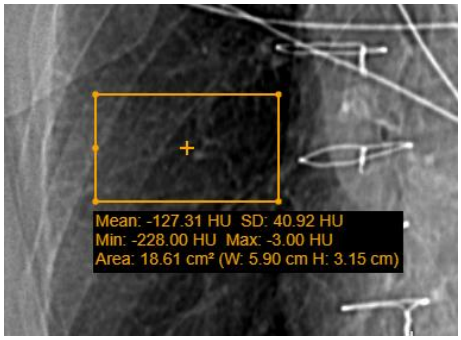


Figure 154. Rectangle measurement

⚠ **NOTE!** If the intensity values may not be calculated, only the area value will be displayed.

To measure an area of interest using **Ellipse** or **Rectangle**, you can measure in two ways:

- press the left mouse button at the point that will be the starting point of the measurement, and immediately release the left mouse button; then move the mouse cursor to the opposite point of the **Ellipse** or **Rectangle** and click the left mouse button again to complete the measurement;

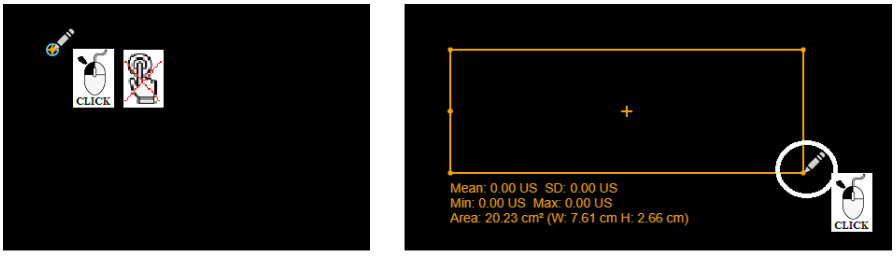


Figure 155. The first way to measure Ellipse or Rectangle

- press the left mouse button on the point that will be the starting point of the measurement, and without releasing the left mouse button, drag the cursor to the opposite point of the **Ellipse** or **Rectangle**, then release the left mouse button, thus completing the measurement.

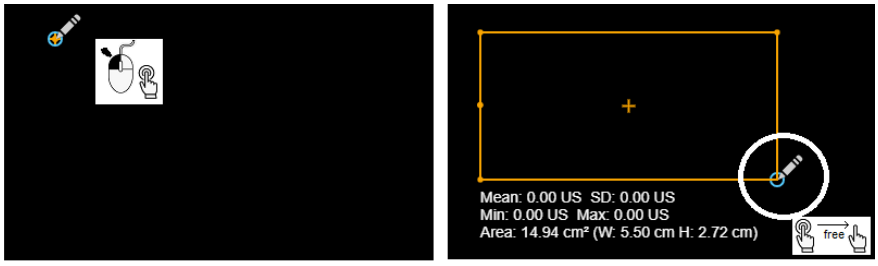


Figure 156. The second way to measure Ellipse or Rectangle

To mark the area of interest as **Circle** or **Square**, press the **ALT** key during the measurement. The system automatically:

- **Ellipse** will be changed to **Circle** whose diameter is equal to the length of the shortest axis of the ellipse;
- **Rectangle** will be changed to a **Square** whose sides are equal to the length of the shortest axis of the rectangle.

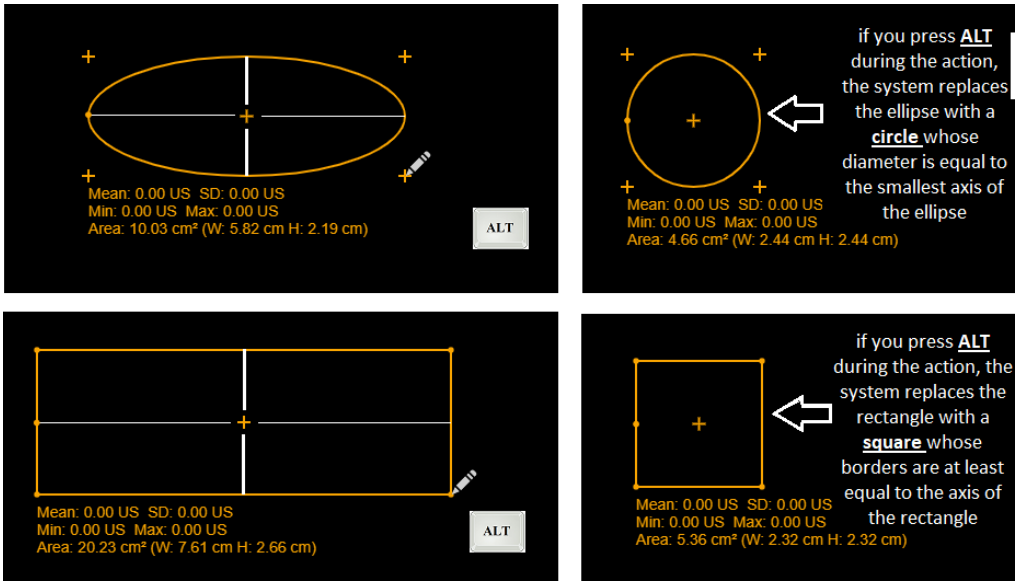


Figure 157. Replacing an ellipse with a circle. Replacing a rectangle with a square

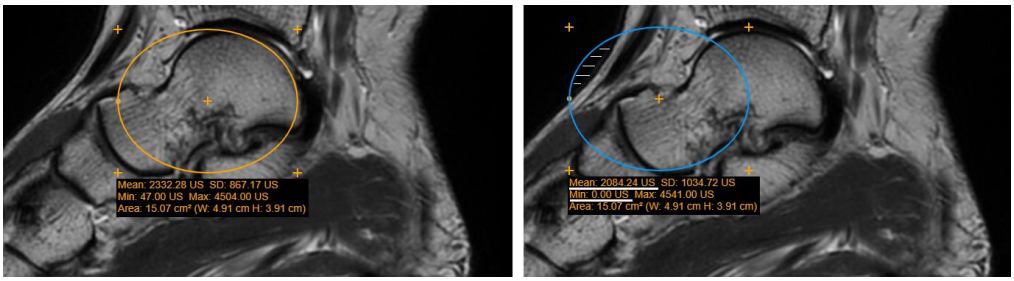


Figure 158. Ellipse measurement

⚠ **NOTE!** If the **Ellipse** or the **Rectangle** measurement range is defined beyond the body contour then the minimum brightness will be 0 and the average brightness may decrease significantly.

To resize **Ellipse**, mouse over any point outside the measurement that is marked with a plus . The icon will change to a blue circle . Press the left mouse button and without releasing move the point in any direction, decreasing or increasing **Ellipse**.

If you press the **ALT** key during editing, the system will change **Ellipse** to **Circle** with a diameter at least equal to the axis of the ellipse.

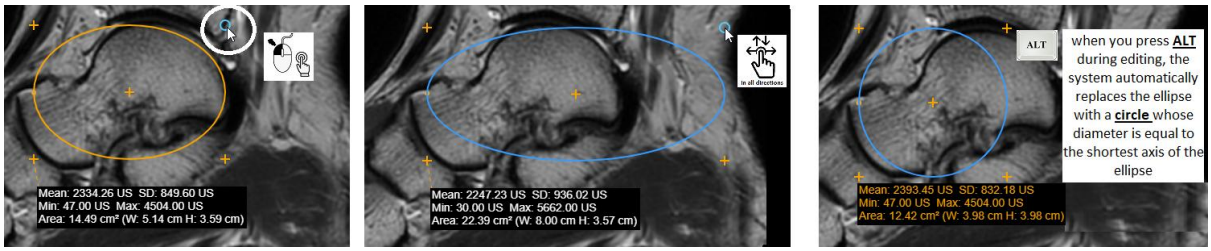


Figure 159. Ellipse editing

To change **Rectangle**, mouse over any corner point, the icon will change to a blue circle  . Press the left mouse button and without releasing the point move the point in any direction, decreasing or increasing **Rectangle**.

If you press the **ALT** key during editing, the system will change **Rectangle** to **Square** with sides equal to the shortest axis of the rectangle.

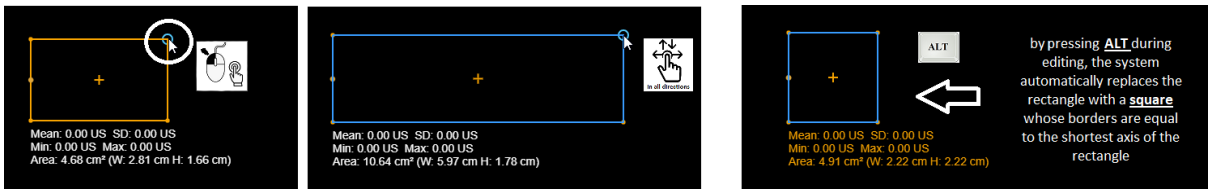


Figure 160. Rectangle editing

To change the position of the **Ellipse** or **Rectangle**, move the mouse cursor to the center point, which is marked with a plus  . The center icon will change to a blue circle  . Press the left mouse button and without releasing move the **Ellipse** or **Rectangle** to another place in the image.

To rotate **Ellipse** or **Rectangle**, move the mouse cursor to the point , which is placed on the line  , and when the point changes to blue circle, press the left mouse button and without releasing move the point.

Volume



The **Volume** button is used to measure the volume of the object.

The volume is calculated from a three-dimensional shape, which is obtained by rotating the left and right plane shapes around the axis of rotation by 180 degrees.

⚠ **NOTE**! The user must predict the axis of rotation, the upper and lower points of the axis of rotation. The easiest way is to use other tools to draw perpendicular axes through the center of the area. The start and end points of one of the axes would be the upper and lower points of the axis of rotation.

With skill, it is possible not to use additional tools and the center and to predict the start and end points by eye.

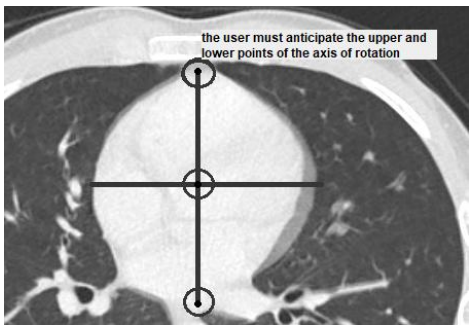


Figure 161. Volume measurement

In the **Measure** menu, select the **Volume** tool:

- place the mouse cursor on the upper point of the axis of rotation, click once and release the selected mouse button;
- then move the cursor to the second, third, fourth, etc. points by clicking and releasing the selected mouse button once on each of them;

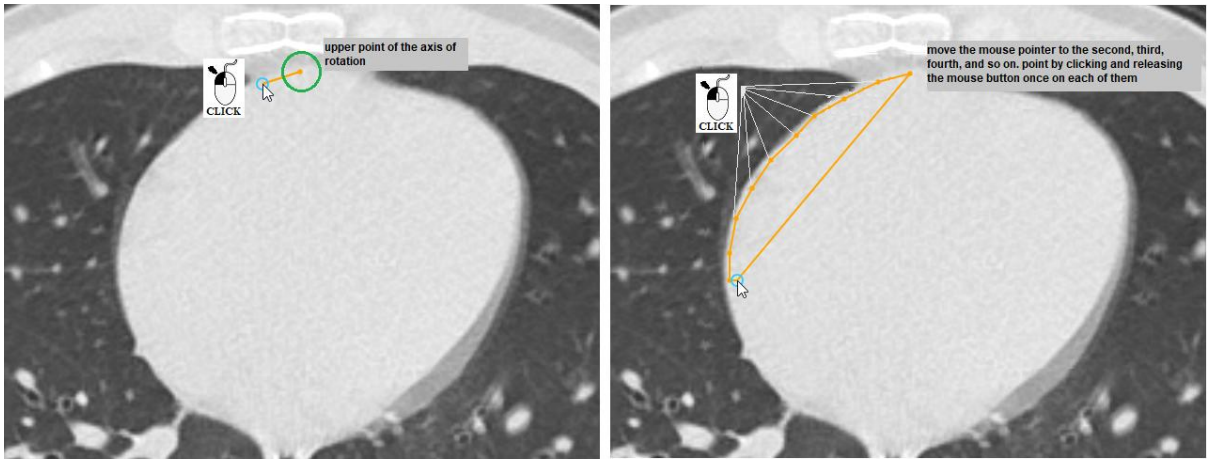


Figure 162. Start of marking the contour of the measuring area

- when you reach the bottom point of the axis of rotation, press the selected mouse button twice - the program marks the axis of rotation;

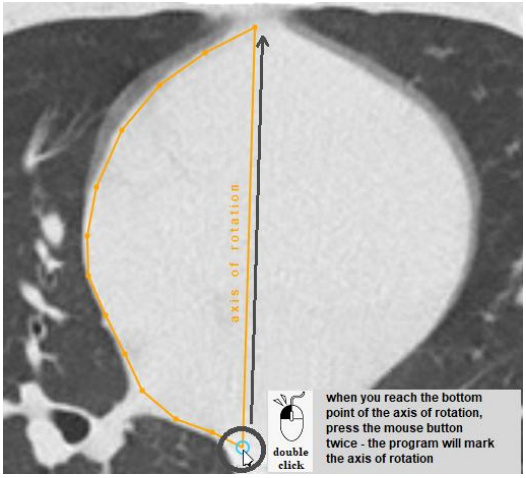


Figure 163. The axis of rotation

- continue marking points on the other side of the axis of rotation by clicking and releasing the selected mouse button once on each of the points;
- when you reach the last point, press the selected mouse button twice;

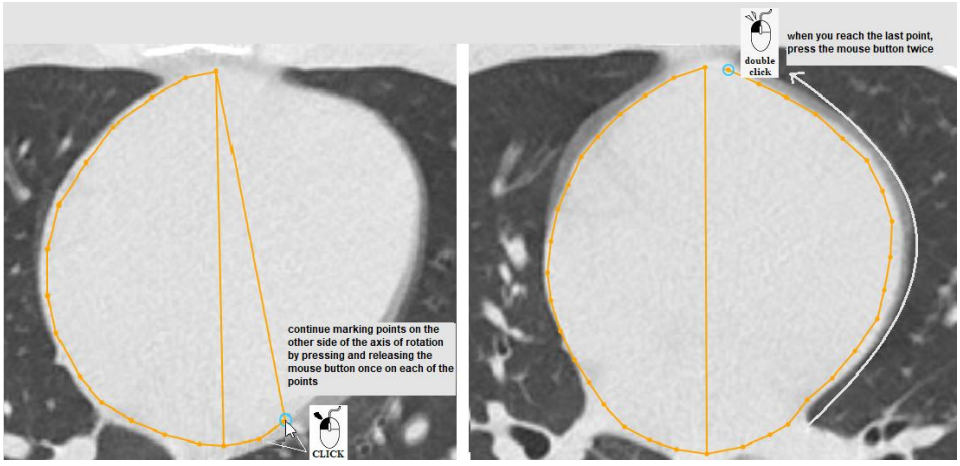


Figure 164. End of contour marking of the measuring area

- the last point is connected to the starting point of the axis of rotation; the left and right sides of the figure are rotated 180 degrees in space around the axis of rotation, at + 90° and -90°; the resulting three-dimensional figure;

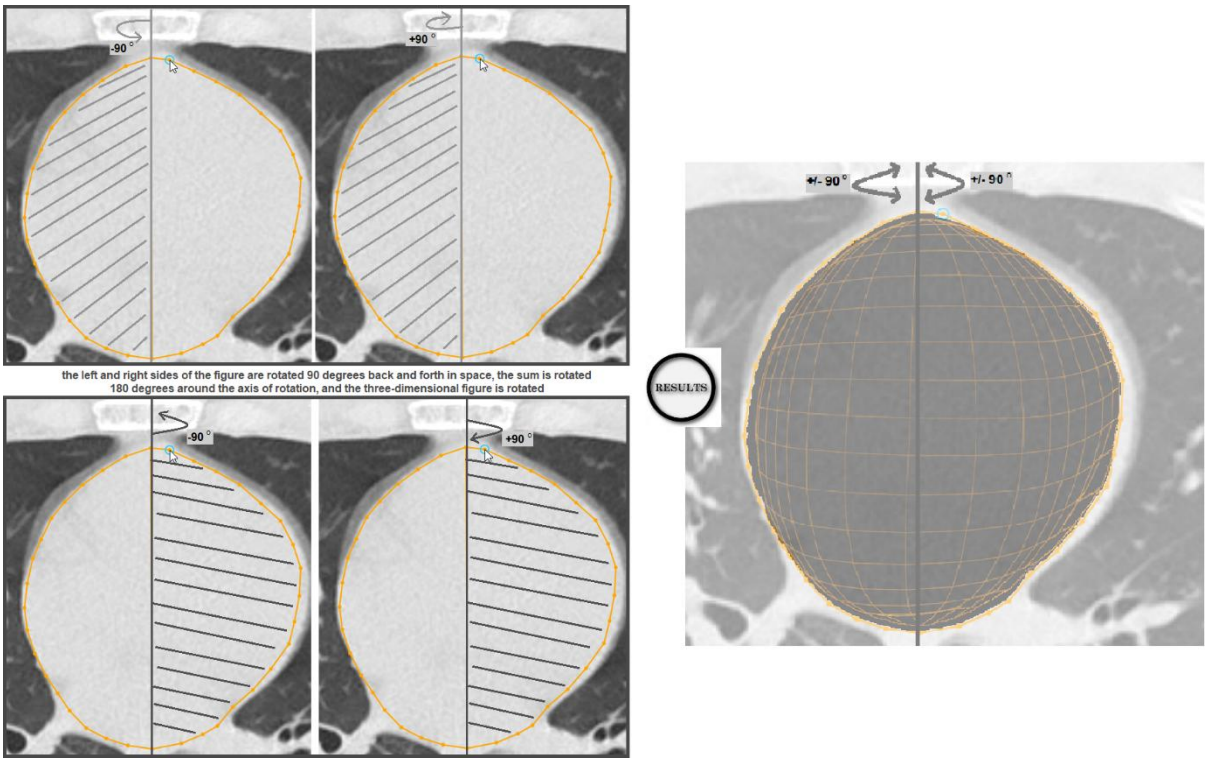


Figure 165. The three-dimensional shape formation

- when calculating the volume, the three-dimensional figure is divided into 20 equally spaced cross-sections; the result is a vertical section showing the transverse lines of the section;

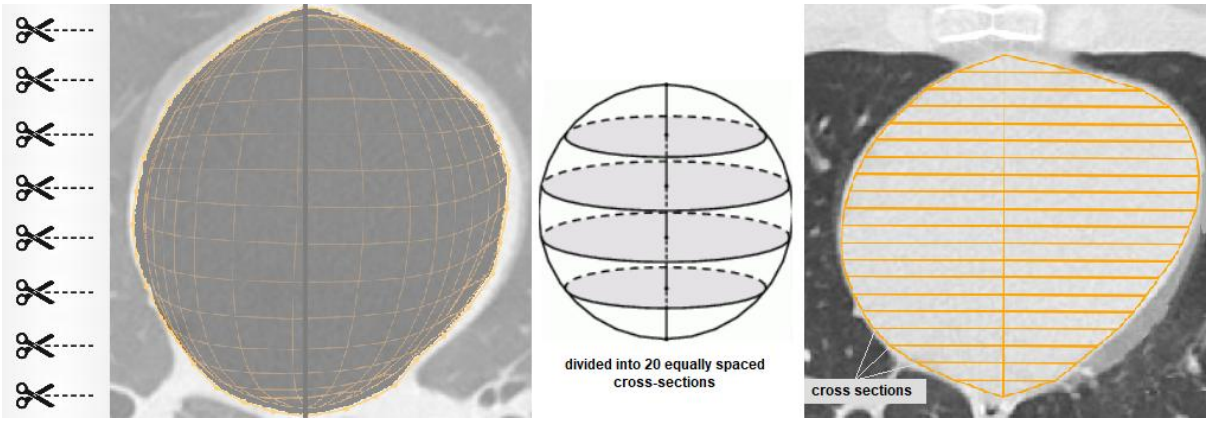


Figure 166. The Area calculation

- The result shows the perimeter (mm), area (mm2), and volume (mm3) of the resulting 3D three-dimensional shape.

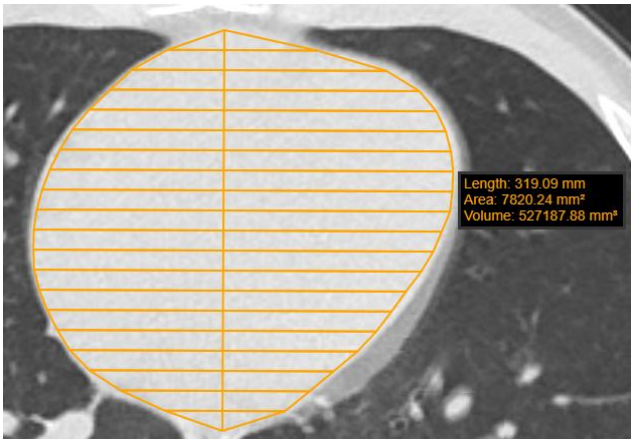


Figure 167. The result of volume calculation

The user can mark the area to be measured with different shapes, as needed, from which different three-dimensional shapes will be obtained.

For example, if the user defines two triangles, the result will be a cone:

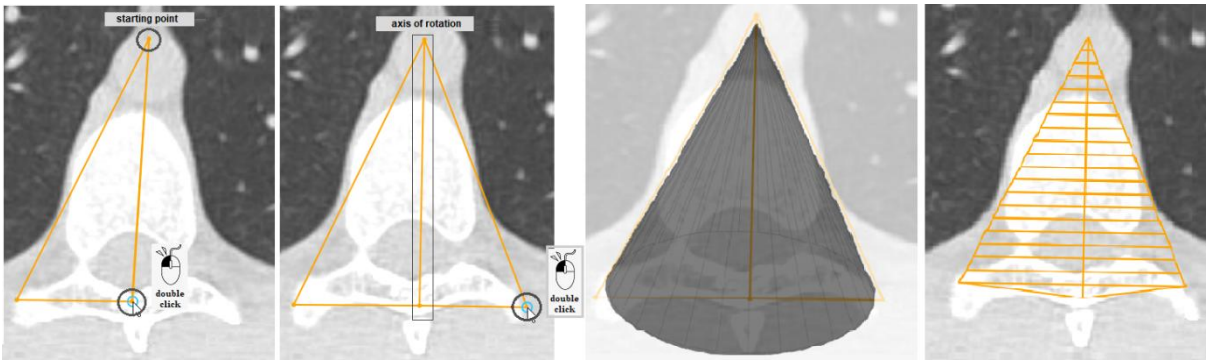


Figure 168. The cone volume

For example, if the user defines two rectangles, the result will be a cylinder.

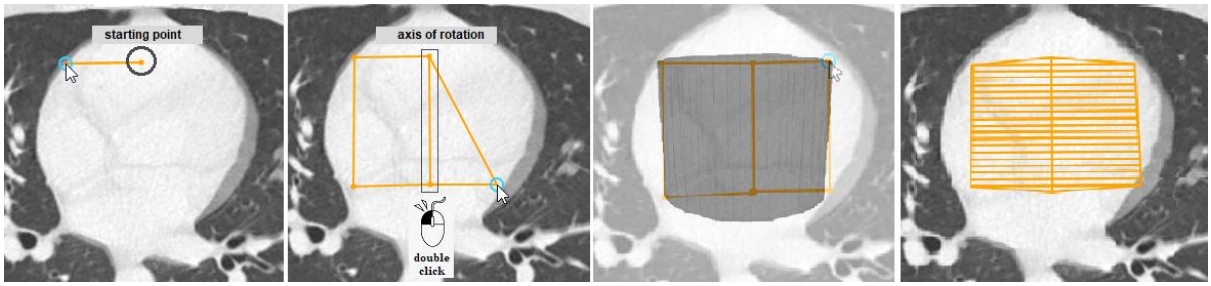


Figure 169. The volume of a cylinder

As the user draws more complex, irregular shapes, the three-dimensional shape becomes correspondingly more complex.

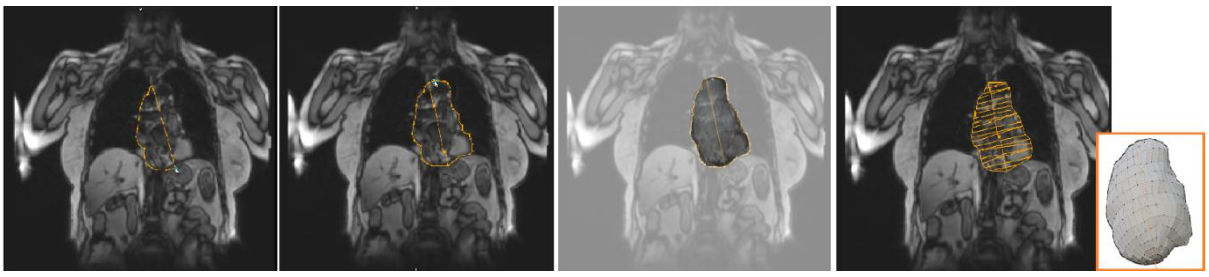


Figure 170. The volume of an irregular figure

⚠ **NOTE!** When calculating volume for three-dimensional shape, the system transforms the spatial shape by discarding the area behind the perpendicular lines drawn through the start and end points.

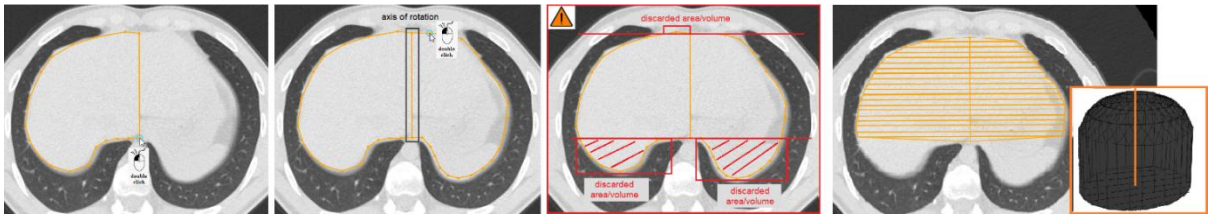


Figure 171. The area / volume outside the axis of rotation is rejected

⚠ **NOTE!** If, when the lower point of the axis of rotation is reached, the following points are marked on the same side of the axis of rotation, a hollow rotation is obtained.

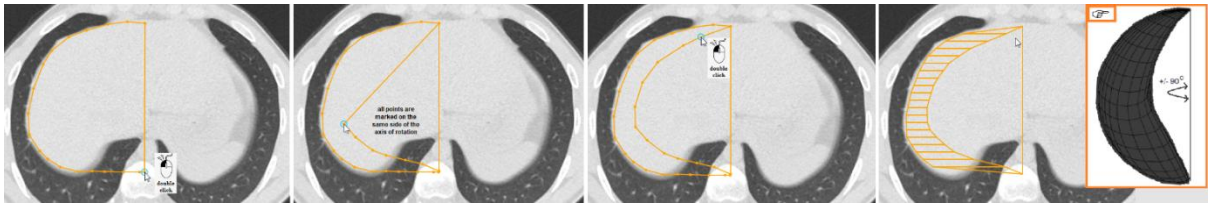
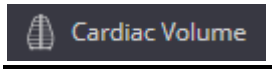


Figure 172. The hollow three-dimensional shape

Cardiac volume



The **Cardiac volume** button is used to measure the volume of the polyline rotation body.

The volume is calculated from a three-dimensional shape, which is obtained by rotating the left and right side of the polyline around the axis of rotation by 180 degrees.

⚠ **NOTE**! The system connects the ends of the polyline with a straight line (basis of the rotation body) and automatically draws the rotation axe from the midpoint of the basis line to the most remote user placed point on the polyline.

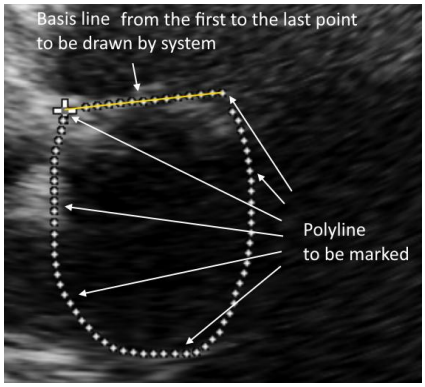


Figure 173. Cardiac volume measurement planning

In the **Measure** menu, select the **Cardiac volume** tool:

- position the mouse pointer on the point from which you want to start drawing polyline, click and release the selected mouse button;
- then move the cursor to the second, third, fourth, etc. points that mark the area of interest and each time click the selected mouse button once and release it;

⚠ **NOTE**! For proper calculation of measurement values the polyline should not intersect itself.

- when the cursor is moved to the which needs to be joint with the first point and form the basis line, double click the selected mouse button;
- the system draws the basis line and shows the length of sides (mm or cm, depending on image data) and the area (mm2 or cm2) of the closed polygon, that is formed from polyline and basis line. The system also draws the rotation axe from the midpoint of the basis line to the most remote user placed point on the polyline and shows the length of sides, the area, and the volume (in mm3 or cm3) of the body rotated 180 degrees around this axe. You can see more detailed explanation how the rotation body volume is measured in section “Volume”.

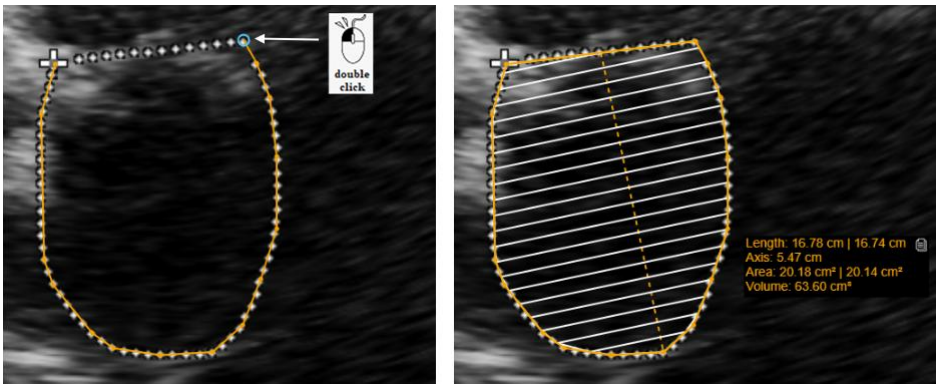


Figure 174. Cardiac volume measurement steps: polyline drawing (left picture) and finished measurement (right picture)

The volume of the rotation is calculated only for figures of triangle or right trapezoid. The system automatically straightens the edge of the polyline between the cross-section lines of the rotation body and marks the edge of the rotation body with white line (see green arrow in image A below). Therefore, the length of the sides and the area of the rotation body (second number) will usually be slightly smaller than of the drawn polygon (first number). A significant difference can occur if the automatically selected axis of rotation does not correctly fill the drawn figure. For example, if the figure between the base line and the cross-section line of the rotation body is not a triangle, the system does not straighten it and does not include it into rotation body (see red arrow in images A and B below). In such cases, you can correct the axis of rotation by dragging the end of the axis onto the polyline, or correct the excluded polygon to the triangle by dragging the points of the polyline:

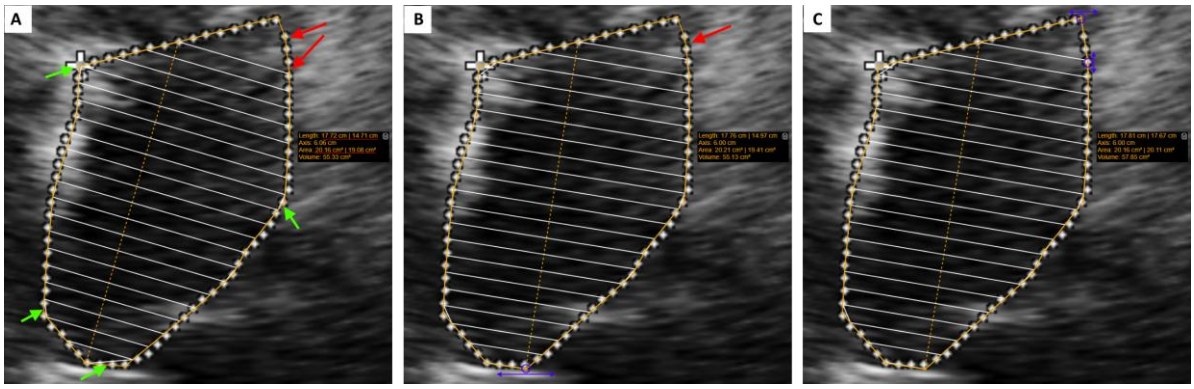


Figure 175. Cardiac volume adjustment steps: (A) Initial volume with major difference in original polygon and rotation polygon length and area (B) Rotation axis adjusted (C) Top right polygon changed to best filling triangle

Height Difference



The **Height Difference** measures the vertical distance between two points and the angle between the horizontal line and the line connecting the points, and may be used for measuring the shoulder balance, for example. To perform a height difference measurement:

- open the radiograph image,
- select Height Difference tool in Measure menu,
- place the mouse cursor on the first point, for example at the highest point of the right clavicle, and click the selected mouse button,
- move the cursor to the highest point of the left clavicle and click the selected mouse button again,
- the system draws the connected horizontal lines, and measures the vertical distance and angle between the horizontal line and the line connecting the points.

⚠ **NOTE!** The height difference measurement is performed in image coordinate system. Vertical distance is measured in absolute value. Angle is measured in range from -90 degrees to +90 degrees.

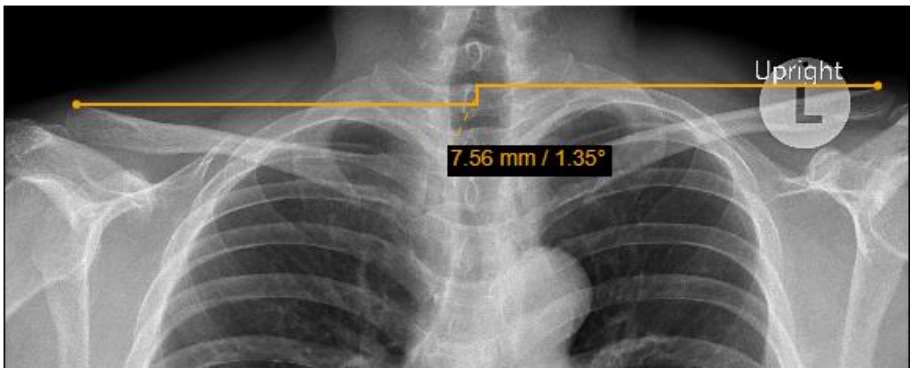


Figure 176. Height difference measurement

You can adjust the measurement according to your needs by dragging the points or the whole measurement.

Velocity Time Integral (VTI)



The **VTI** *(Velocity Time Integral)* button is used to measure the distance over which the blood was ejected per interval of time:

- select **VTI** tool in **Measure** menu;
- place the mouse cursor on the point from which you want to measure the velocity time integral, click and release the selected mouse button;
- then move the cursor to the second, third, fourth, etc. points of measured blood velocity profile and each time click the selected mouse button once and release it;
- when you reach the last point, double click the selected mouse button, and measurements of marked velocity profile are displayed:

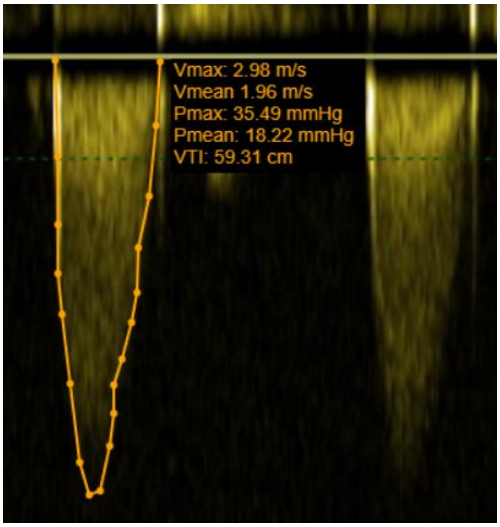
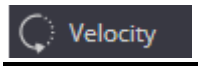


Figure 177. VTI measurement

⚠ **NOTE! VTI** measuring tool is applicable only for the images of "US" modality with visible blood velocity profile.

Velocity



The **Velocity** button is used to measure the blood ejection velocity at the point:

- select **Velocity** tool in **Measure** menu;
- place the mouse cursor on the point, click and release the selected mouse button;
- velocity value is displayed:

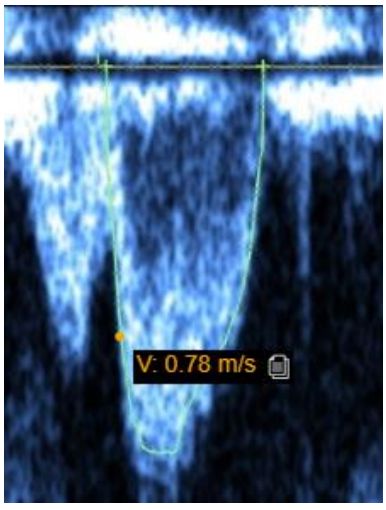


Figure 178. Velocity measurement

⚠ **NOTE! Velocity** measuring tool is applicable only for the images of "US" modality with visible blood velocity profile.

Tibial Plateau Angle



The **TPA** button is used to measure angle between two lines: the tibial plateau slope line and the line that is perpendicular to tibia axis line.

To measure angle:

- select **TPA** tool in **Measure** menu;
- draw the tibia axis line (A):

start from the ankle. Point the mouse cursor on the edge of the talus, click the selected mouse button, move the mouse to the center of talus, and click the mouse button - the system automatically draws the circle for better location of the talus center when moving the mouse;

then move the mouse to the other side of the tibia and click the mouse button – the system automatically draws the line while moving the mouse;

- draw the tibial plateau slope line (B) by clicking mouse button on one and the other end of the line;
- through lines intersection point the program draws the line (dashed line C), that is perpendicular to the tibia axis line A, and displays the angle between the line C and tibial plateau slope line B:

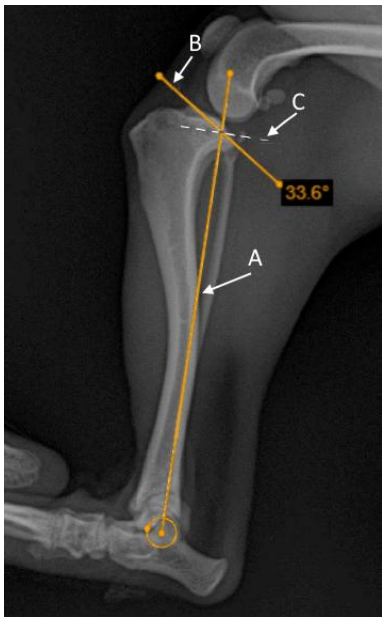


Figure 179. Tibial Plateau Angle (TPA) measurement

- you can adjust the circle size by dragging the dot on the circle, drag the line points, or the whole measurement object simultaneously.

⚠ **NOTE! TPA**, **Norberg Angle**, **VHS, Hip DI,** and **TTA** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.

Norberg Angle



The **Norberg Angle** button is used to evaluate canine hips. To measure the angle:

- zoom in the selected image and select **Norberg Angle** tool in **Measure** menu;
- point the mouse cursor on the surface of femoral head, click the selected mouse button, and draw the circle, fitting the femoral head - the first circle of the Norberg angle:

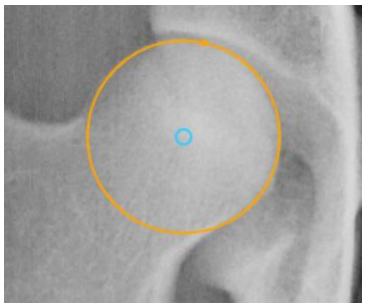


Figure 180. Norberg angle circle with the center in femoral head

- repeat the same process on other femoral head – draw the second circle of the Norberg angle;
- the program joins the circle centers with a line and draws a line from each center at 105.0 degrees - the Norberg angle for good hip:

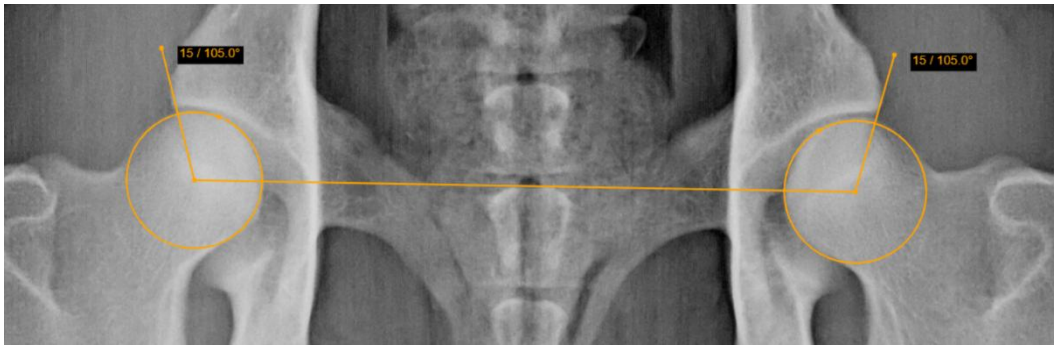


Figure 181. Norberg angle measurement

- drag the upper points of lines to fit the cranial acetabular rim for measuring the actual Norberg angle:

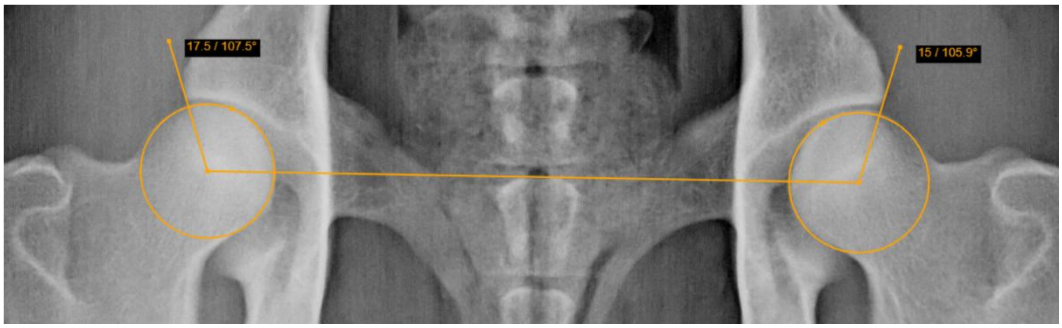


Figure 182. Adjusted Norberg angle measurement

- you can adjust the circle size by dragging the dot on the circle, or adjust circle position by dragging the circle center, or the whole measurement object by dragging the center line.

⚠ **NOTE! TPA**, **Norberg Angle**, **VHS, Hip DI,** and **TTA** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.

Vertebral Heart Scale



The **VHS** (Vertebral Heart Scale) button is used to measure heart size and provide an accurate assessment of true cardiac enlargement. To perform a VHS measurement:

- select **VHS** tool in **Measure** menu;
- place the mouse cursor and click the selected mouse button on the point from which you want to start measuring Long Axis (L),
- move the cursor to the end point of long axis and click the selected mouse button again - the Long Axis line will appear:

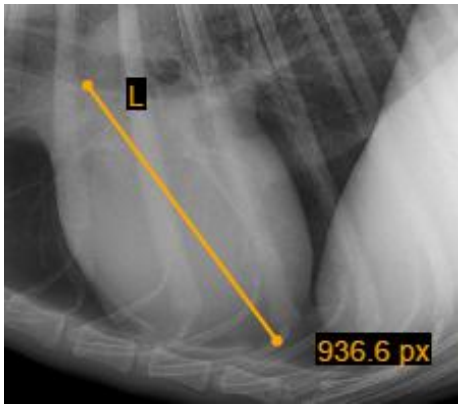


Figure 183. Long axis of VHS measurement

- place the mouse cursor and click the selected mouse button on the point from which you want to start measuring Short Axis (S);
- move the cursor to the end point of short axis and click the selected mouse button again – the Short Axis line will appear:

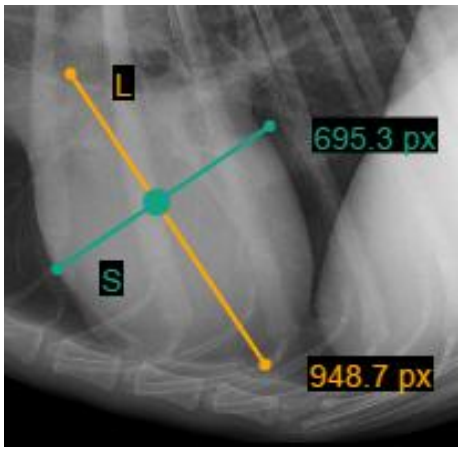


Figure 184. Short Axis of VHS measurement

- In order to define SL point, place your mouse cursor and click the left mouse button on the point from which you want to measure S and L lines - S and L lines will appear:

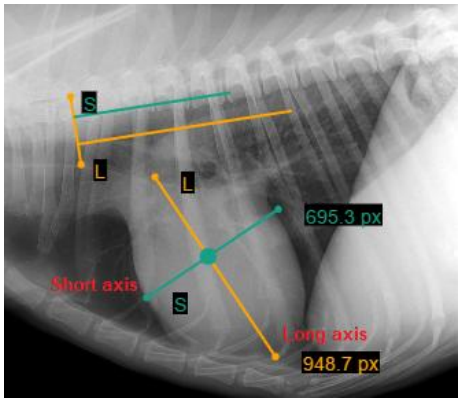


Figure 185. VHS measurement

You can rotate lines by dragging the ends of the line (dots) according to your needs. Click the left mouse button on the yellow dot (highlighted in red) and drag the line into a position where you want it to be. Middle vertical line (S and L line intersection point) allows to move S and L lines at the same time:

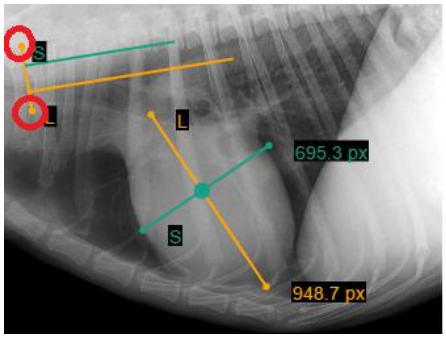


Figure 186. S and L lines rotation

⚠ **NOTE! TPA**, **Norberg Angle**, **VHS, Hip DI,** and **TTA** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.

Hip distraction index

Hip DI

The **Hip distraction index (DI)** measurement allows evaluating the laxity of hip joint. The DI is calculated as ratio of distance between centers of acetabulum and femoral head, and radius of femoral head. To measure the hip distraction index:

- zoom in the selected image and select **Hip DI** tool in **Measure** menu;
- point the mouse cursor on the surface of acetabulum socket, click the selected mouse button, and draw the circle, fitting the acetabulum socket;
- point the mouse cursor on the surface of femoral head, click the selected mouse button, and draw the next circle, fitting the femoral head;
- the program draws and measures the distance between centers of circles, the radio of the second circle (femoral head), and calculates the distraction index from the measured values:

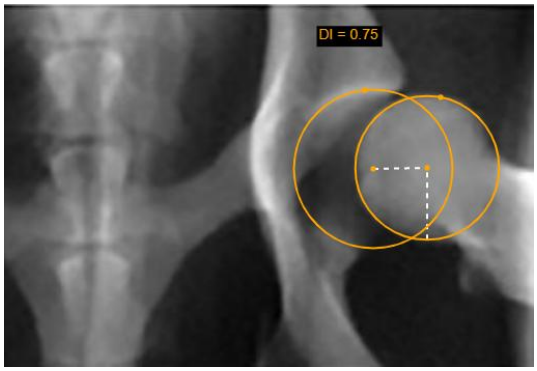


Figure 187. Hip distraction index measurement

- you can adjust the circle size by dragging the dot on the circle, or position of individual circle by dragging the circle center, or move the whole measurement object by dragging the distance or radius lines.

⚠ **NOTE! TPA**, **Norberg Angle**, **VHS, Hip DI,** and **TTA** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.

Tibial tuberosity advancement



The **TTA** measurement allows estimating the cage width of tibial tuberosity advancement (TTA) in the surgical stabilization of the dog's knee joint. Common tangent parallel lines method is applied for measuring. To measure the cage width:

- zoom in the selected image and select **TTA** tool in **Measure** menu;
- point the mouse cursor on the surface of tibial plateau, click the selected mouse button, and draw the circle, fitting the area of contact of the tibial plateau;
- point the mouse cursor on the surface of femoral condyle, click the selected mouse button, and draw the next circle, fitting the joint surface of the femoral condyle;
- point the mouse cursor on the most proximal point of the tibial crest and click the selected mouse button;
- the program joins the circle centers with a line, draws two parallel ruler lines with measured distance between them, and the guideline, perpendicular to all the three lines:

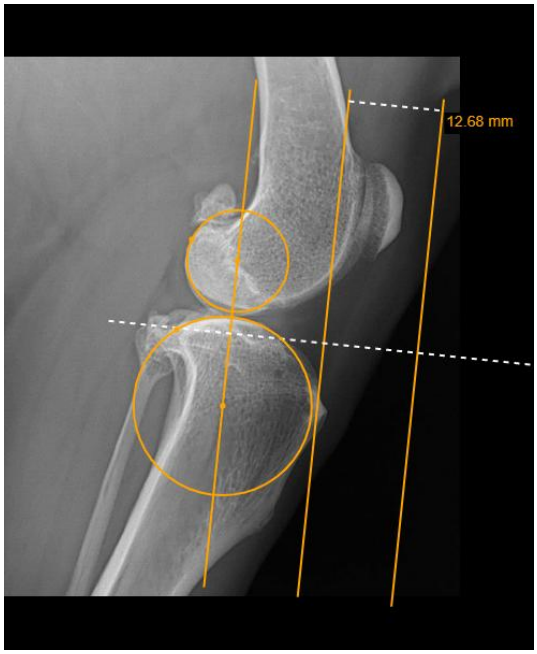


Figure 188. TTA ruler lines displayed by the program

- drag the outer ruler line to touch the distal patellar pole at the origin of the patellar ligament - the system measures the distance between ruler lines, that corresponds to the TTA cage width:

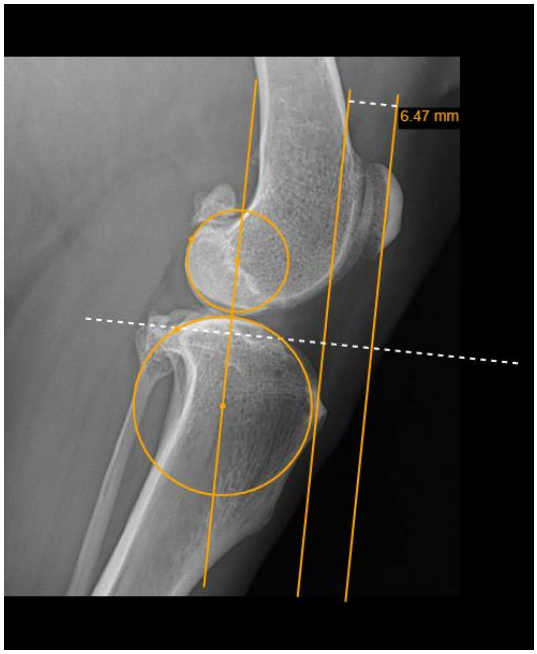


Figure 189. Adjusted TTA cave width measurement

- you can adjust the position of ruler lines by dragging the lines, or circle size by dragging the dot on the circle, position of individual circle by dragging the circle center, or the whole measurement object by dragging the perpendicular guideline.

⚠ **NOTE! TPA**, **Norberg Angle**, **VHS, Hip DI,** and **TTA** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.

Cardiothoracic ratio

CTR

The **CTR** (Cardiothoracic ratio) button is used to measure the ratio of maximal horizontal cardiac diameter to maximal horizontal thoracic diameter and aids in the detection of enlargement of the cardiac silhouette. To perform a CTR measurement:

- select **CTR** tool in **Measure** menu,
- place the mouse cursor and click the selected mouse button on the point at the inner border of rib in the widest place of thoracic cavity to start measuring thoracic diameter,
- move the cursor to the inner border of the same rib on the other side of thoracic cavity and click the selected mouse button again - the thoracic diameter line and measurement description with length of the line will appear while drawing:



Figure 190. Drawing the maximal inner thoracic diameter line of CTR measurement

- place the mouse cursor and click the selected mouse button at the most left point of the cardiac shadow,
- move the cursor towards the right edge of the cardiac shadow - the cardiac shadow transverse line and processing note in measurement description will appear while drawing:

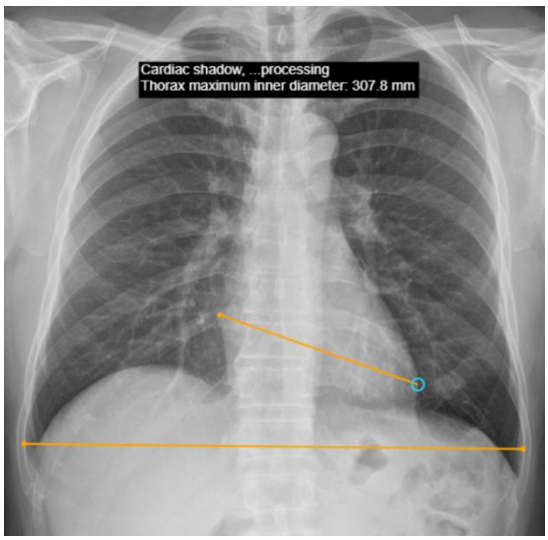


Figure 191. Drawing cardiac shadow transverse line of CTR measurement

- click the selected mouse button at the most right point of the cardiac shadow to finish the cardiac shadow transverse line to finish the CTR measurement,
- the system draws the midline of the thorax, and cardiac shadow diameter as two perpendiculars from the ends of the cardiac shadow transverse line to the midline. The cardiothoracic ratio is calculated as the percentage ratio of cardiac shadow diameter to maximal inner thoracic diameter, and displayed in the measurement description:

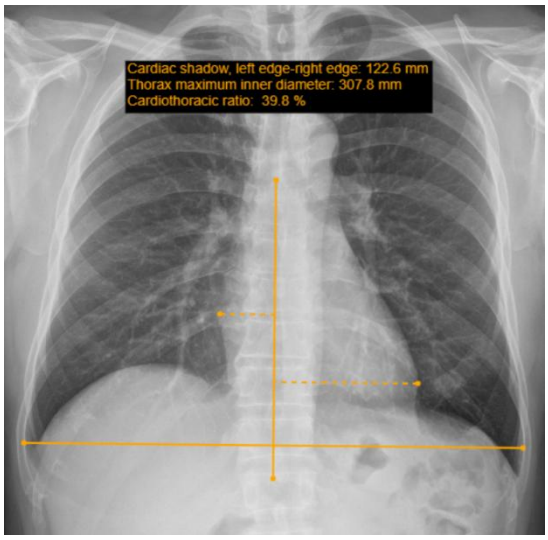
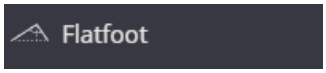


Figure 192. CTR measurement

You can adjust the measurement according to your needs by dragging the ends of the lines, or the whole thoracic diameter line, or the midline.

Flatfoot



The **Flatfoot** button is used to measure the angle and height of the foot medial longitudinal arch and aids in the detection of the longitudinal flatfoot. To perform a foot medial longitudinal arch measurement:

- open the foot radiograph image,
- select Flatfoot tool in Measure menu,
- place the mouse cursor on the point at the lower margin of calcaneus and click the selected mouse button,
- move the cursor to the lowest margin of cuneonavicular join and click the selected mouse button again – the line connecting the point and cursor will appear while moving the cursor,
- move the cursor to the lowest margin of the first metatarsal and click the selected mouse button to finish the foot medial longitudinal arch measurement - the line connecting the second and third points will appear,
- the system measures and displays arch angle on the image,
- the system draws the line through the angle’s end points and measures the distance from the angle vertex to this line.



Figure 193. Flatfoot measurement

You can adjust the measurement according to your needs by dragging the vertices of the angle.

Goniometry



The **Goniometry** button is used to measure the lengths of femur and tibia, and the femoral-tibial angular deformities (genu varum and genu valgum). To perform a goniometry measurement:

- open the lower limb radiograph image;
- select Goniometry tool in Measure menu;
- draw the circle around femoral head to define the center of the femoral head:

point the mouse cursor on the edge of femoral head, and click the selected mouse button to start drawing,

move the cursor towards the center of the femoral head to draw the circle around the femoral head, and click the selected mouse button when done;



Figure 194. Drawing the femoral head circle of Goniometry measurement

- draw the knee transverse line to define the center of knee:

point the mouse on the most lateral point of the knee joint, and click the selected mouse button to start drawing,

move the cursor towards the most medial point of the knee joint to draw the knee transverse line, and click the selected mouse button when done;

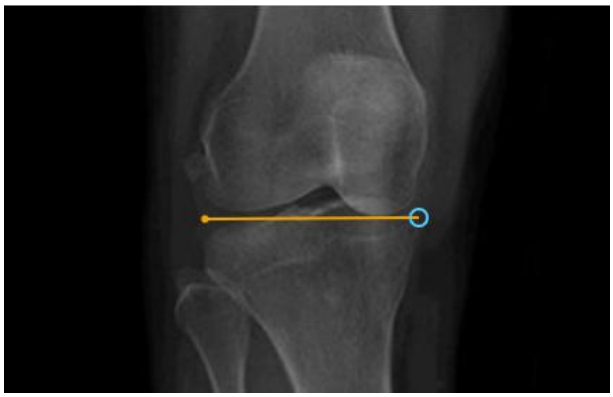


Figure 195. Drawing the knee transverse line of Goniometry measurement

- draw the talus and tibia contact line to define ankle center:

point the mouse on the most lateral point of the talus and tibia line, and click the selected mouse button to start drawing,

move the cursor towards the most medial point of the talus and tibia line, and click the selected mouse button when done;

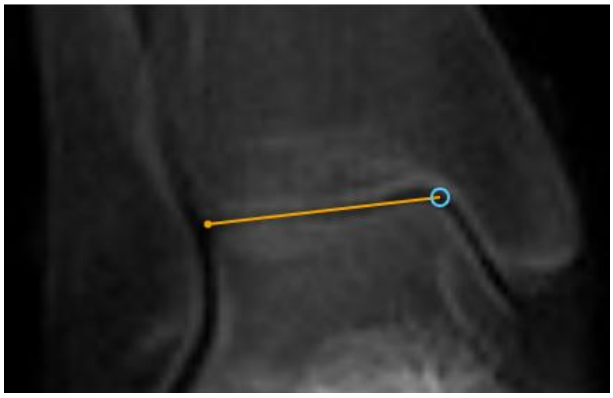


Figure 196. Drawing the talus and tibia contact line of Goniometry measurement

- the system draws the femur axis from the center of the femoral head to the center of the knee transverse line, and measures its length;
- the system draws the tibia axis from the center of the knee transverse line to the center of talus and tibia contact line, and measures its length;
- the system shows the sum of measured leg segments (femur and tibia) length;
- the system measures and shows angle between femur axis and tibia axis.

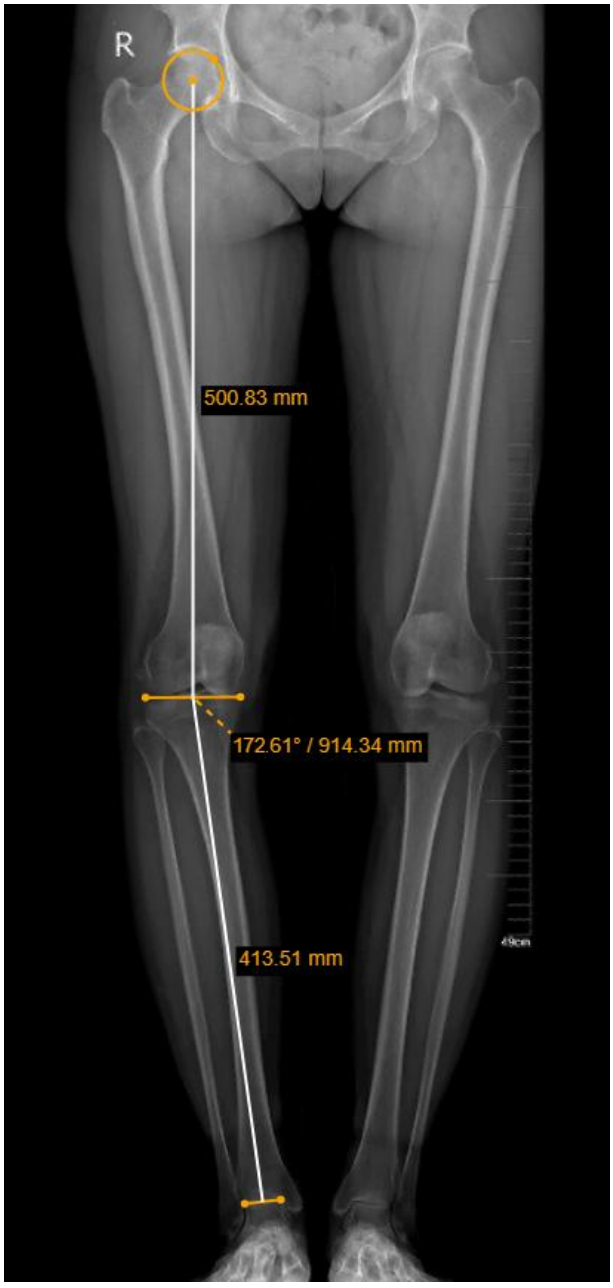
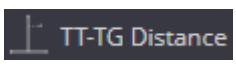


Figure 197. Goniometry measurement

You can adjust the measurement by dragging the and points of the knee or ankle lines, or the whole lines. The center of the femoral head may be adjusted by dragging the dot on the circle, or dragging the circle center.

TT-TG Distance



The **TT-TG Distance** button is used to measure the tibial tuberosity to trochlear groove distance for quantifying of the knee patellar instability. To perform a TT-TG distance measurement, the series should have the axial images of the femoral condyles, and the tibial tuberosity:

- open the image with the clearly visible femoral condyles and trochlear groove;
- select **TT-TG Distance** tool in Measure menu;
- draw the line along the posterior femoral condyles:

point the mouse cursor on the edge of one femoral condyle, and click the selected mouse button to start drawing, move the cursor towards the edge of other femoral condyle to draw the line along the femoral condyles, and click the selected mouse button when done:

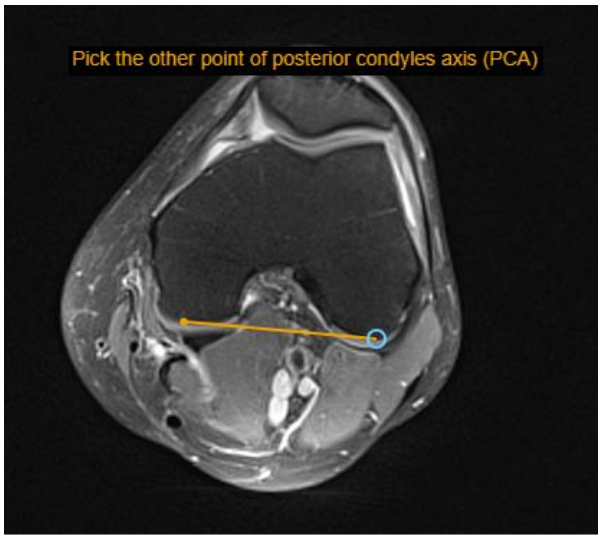


Figure 198. Drawing the line along the posterior femoral condyles of TT-TG Distance measurement

- the system finishes the femoral condyles line and displays the guidance for the next step;
- move the mouse to the deepest point of the trochlear groove, and click the selected mouse button to finish the TG line:

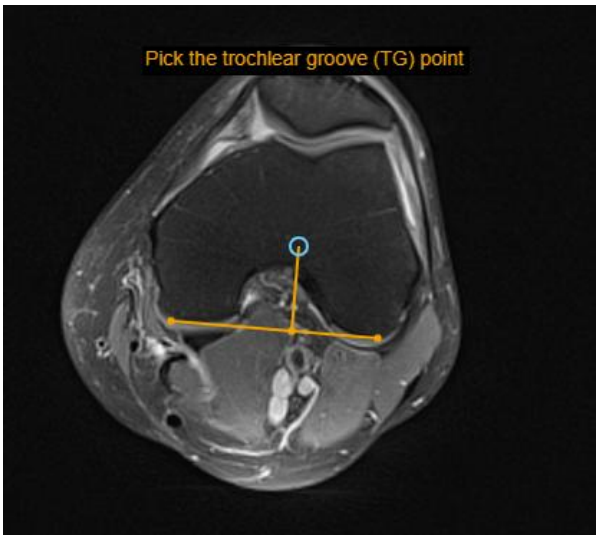


Figure 199. Drawing the TG line of TT-TG Distance measurement

- the system finishes the TG line, that is perpendicular to femoral condyles line, and displays the guidance for the next step;
- scroll the series to find the image with the clearly visible tibial tuberosity, and the system displays the already performed drawings and guidance while scrolling;

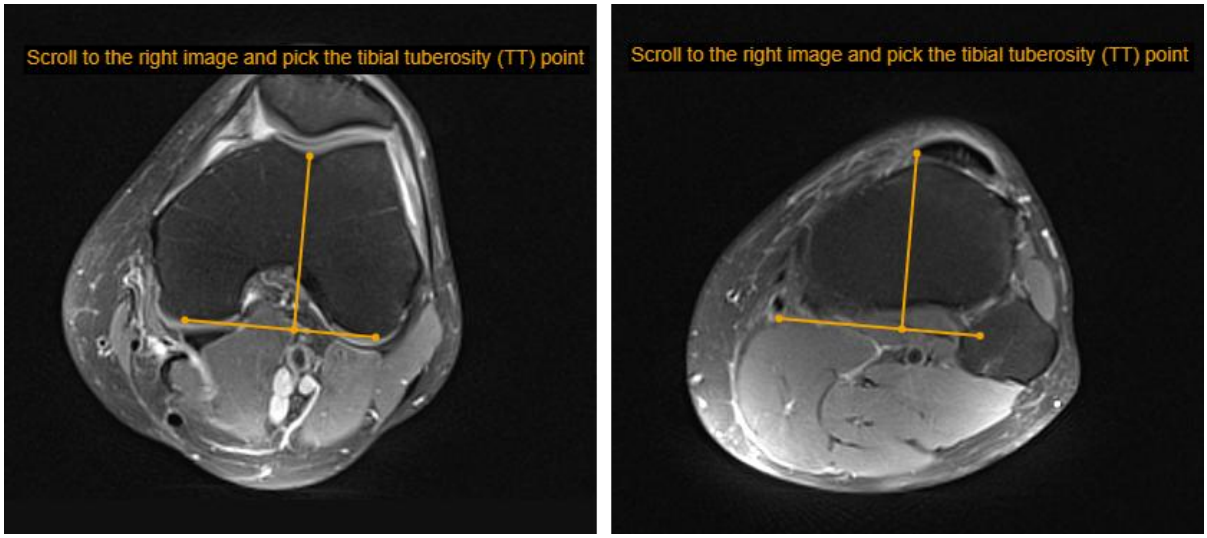


Figure 200. Finding the tibial tuberosity image in TT-TG Distance measurement

- when the right image is found, point the mouse on the most anterior point of the tibial tuberosity, and click the selected mouse button to draw the TT line;
- the system finishes TT-TG distance measurement:

the system finishes the TT line, that is perpendicular to femoral condyles line,

the system measures and shows the distance between parallel TT and TG lines,

the system fuses the femoral condyles and the tibial tuberosity images, on which the drawings were performed, and displays the opacity slider in the viewport:

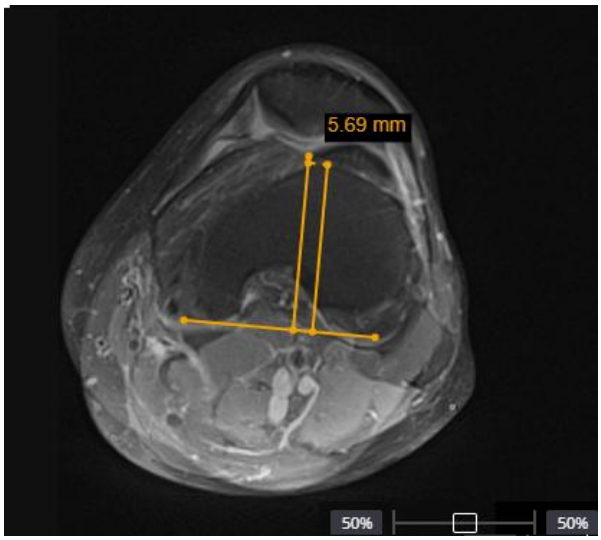


Figure 201. TT-TG Distance measurement

You can adjust the measurement by dragging the end points of the lines, or the whole measurement. By default, the 50% to 50% image fusion ration is applied. You can change the ratio with opacity slider, if better viewing of the one or the other image is needed for measurement adjustment.

⚠ **NOTE!** If saved as presentations state, the TT-TG distance measurement is related only to the one image, for which the saving is performed. The editing and image fusion options are not available for saved presentation state.

Vertebra angle



The **Vertebra Angle** tool measures the angle between user drawn vertebra axis and horizontal axis of the image:

- Select the **Vertebra Angle** tool in **Measure** menu;
- place the mouse cursor on the starting point, click and release the selected mouse button;
- move the cursor to the end point, click the selected mouse button and release it;
- the angle between the line and the horizontal axis of the image will be displayed:

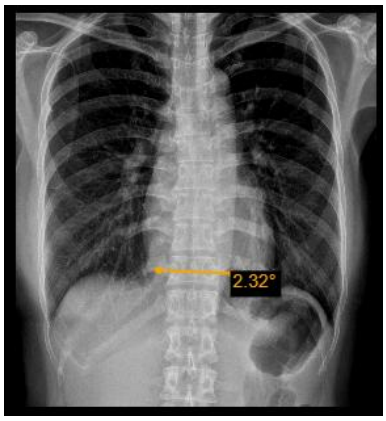


Figure 202. Vertebra angle measurement

Spine Labeling



The **Spinal Labeling** measurement is used to annotate the vertebrae of the spine. To perform the **Spine Labeling** measurement:

- open the image that shows the vertebrae of the spine;
- select the **Spine Labeling** tool in Measure menu;
- place the mouse cursor on the middle of the selected first vertebra and press the left mouse button;



Figure 203. The first vertebrae labeling

- in the action definition window, select the vertebrae that you clicked in the previous step, from which you want to start marking;

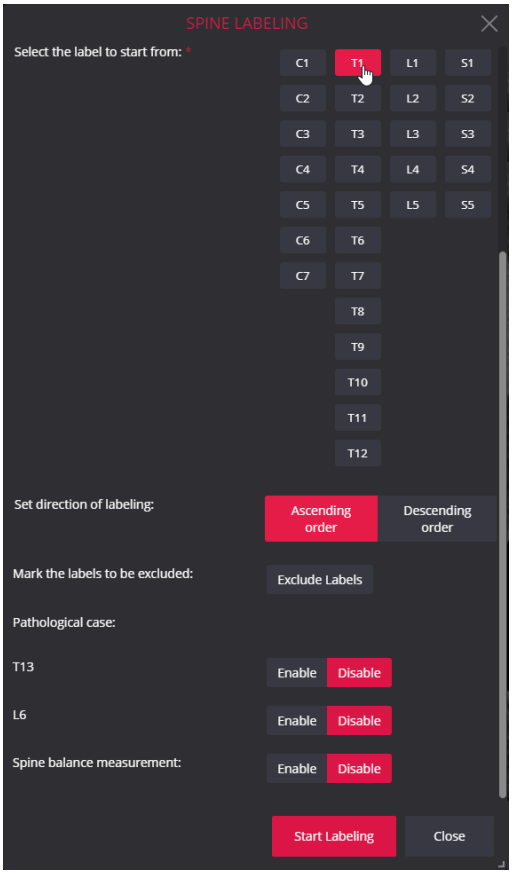


Figure 204. Spine Labeling Action Definition Window

- if the marking intended to perform from the last vertebra, on the image must be marked the relevant vertebral and changed the direction of labeling from the default “Ascending order” to “Descending order”;

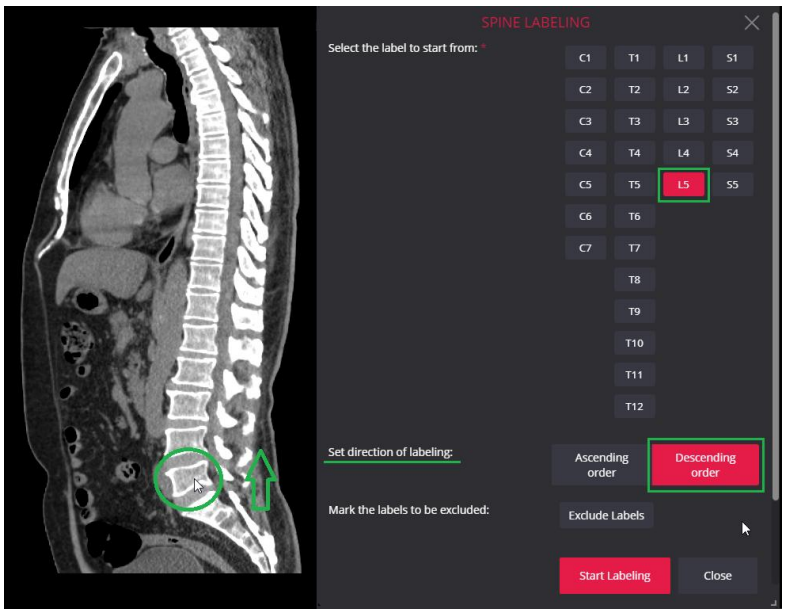


Figure 205. Spine Labeling action in descending order

- if some vertebrae do not need to be marked, select "Mark the labels to be excluded" → "Exclude labels" (1) in the action definition window, then in the list of labels use the mouse to highlight each unnecessary label (2) and confirm “Save labels” (3), the result - the marked labels will be skipped;

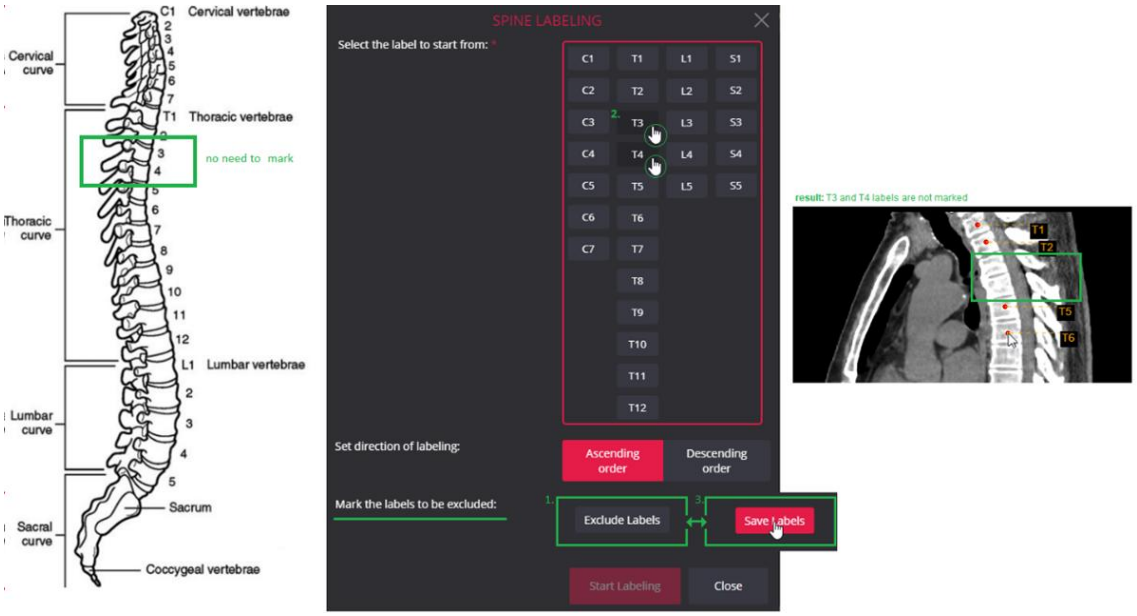


Figure 206. Definition of labels to be excluded in the Spinal Labeling action

- if the patient needs to mark pathological T13 and/or L6 vertebrae, activate the vertebrae in the lower part of the action window by selecting Enable, T13 and/or L6 vertebrae become visible in the list of vertebrae;

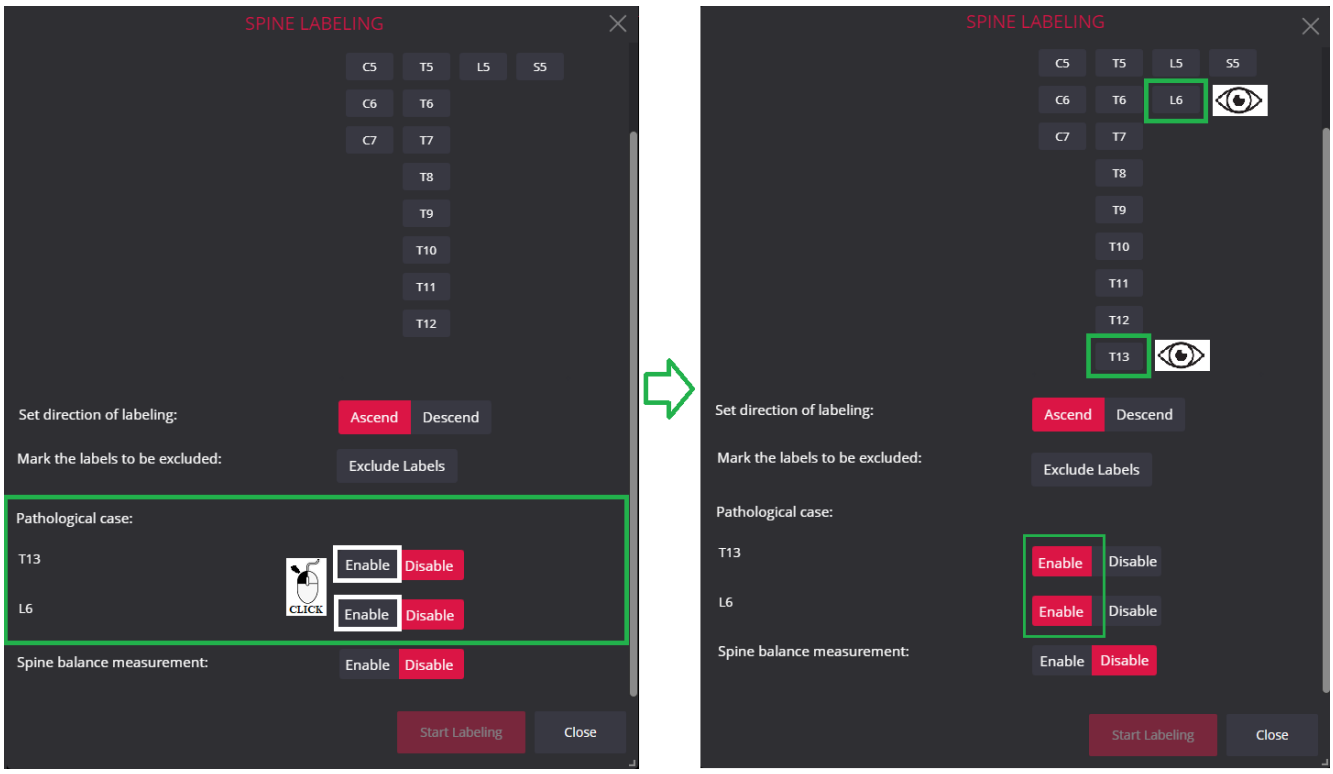


Figure 207. Spinal labeling pathological vertebrae T13 and L6

- to see the estimated spine balance between the C7 and S1 vertebrae at the end of the measurement, activate the measurement in the lower part of the action window by selecting Enable;

⚠ **NOTE!** Information on how the measurement is performed, what results are presented, is described in detail in the subsection of this chapter “Spine balance measurement”.

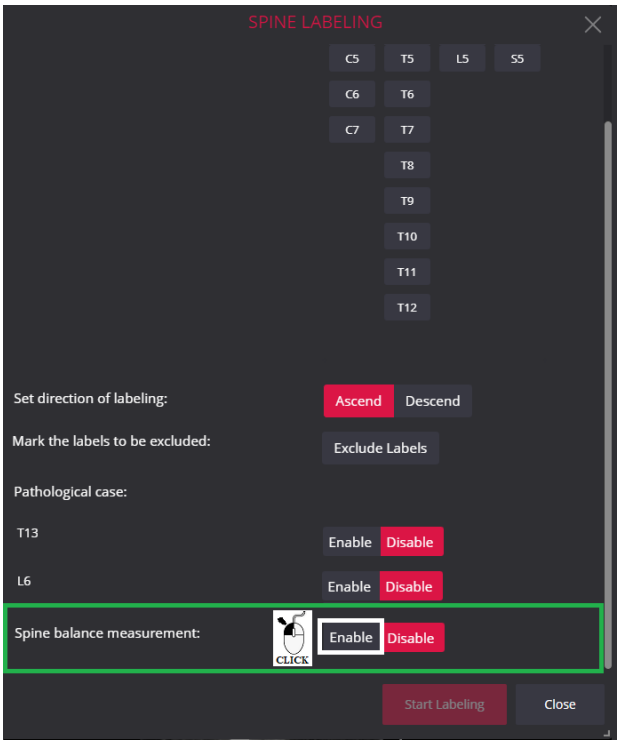


Figure 208. Enabling spinal balance measurement

⚠ **NOTE!** Selected values will be provided by default during the following step.

- to start the measurement, select “Start Labeling” in the action definition window or press the “Enter” button;

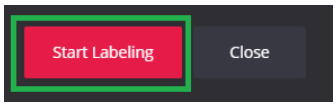


Figure 209. Beginning of the Spinal Labeling action

- the program closes the action definition window, marks the first vertebra in the image with a dot, nearby the dot includes labels and activates the next marking point with the label (the next dot is shown in a blue circle, the next label is shown in white);

⚠ **NOTE!** Vertebra mark points are automatically displayed and may be adjusted in all derived and/or primary series that are spatially related. See section "Spine labeling in related series" for details.

- move the mouse cursor in the chosen direction and click the left mouse button on the middle of the next vertebra - the second vertebra is marked with a dot and a label is displayed nearby;

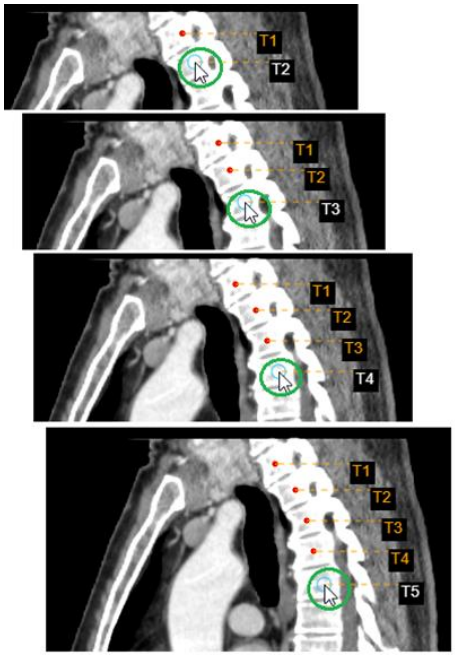


Figure 210. The course of the Spinal Labeling action

- repeat the action until you reach the last vertebra you want to mark, double-click the last point with the left mouse button;

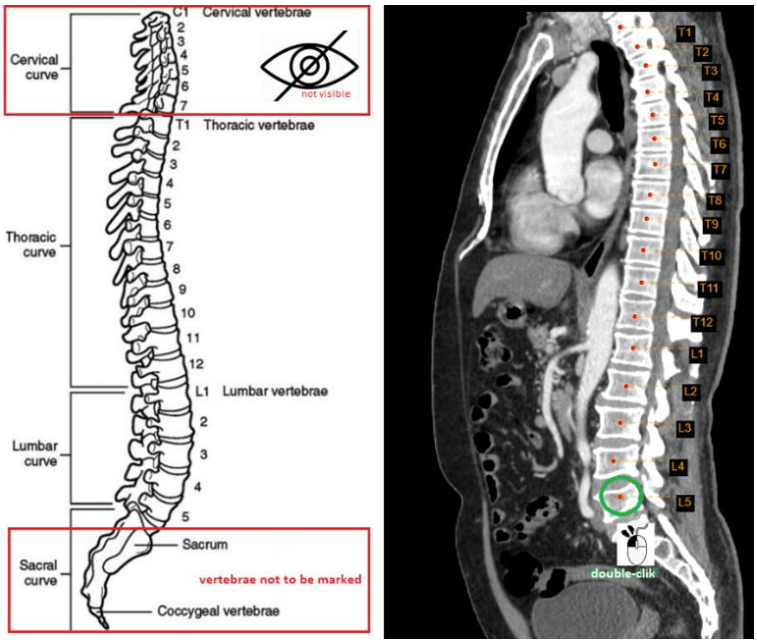


Figure 211. End of the Spinal Labeling action by double-clicking

- if there is no double-click with the left mouse button, the measurement ends with the dot with the last label;

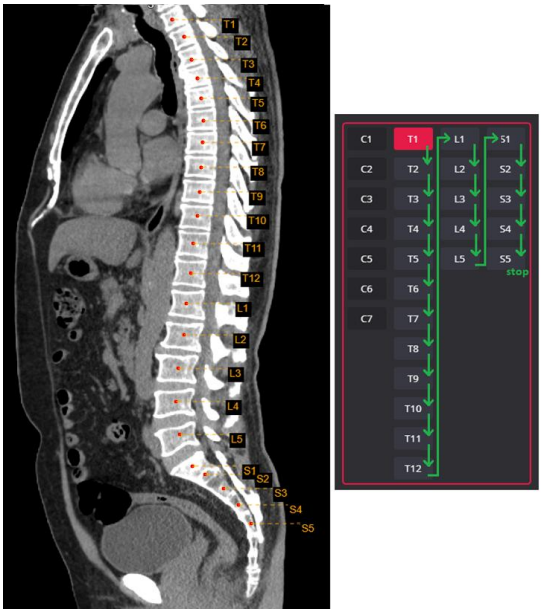


Figure 212. End of the Spinal Labeling action

- until the measurement is saved, the position of each point with the label can be changed:

  ⚠ **NOTE!** If the measurement points are placed on several images, see section "Spine labeling in related series" for measurement editing detailed description.

  - place the mouse cursor over any of the measurement point to mark it with blue circle, then press and hold the left mouse button (1);
  - and without releasing the button move the cursor to any desired location on the image (2), then release the left mouse button;

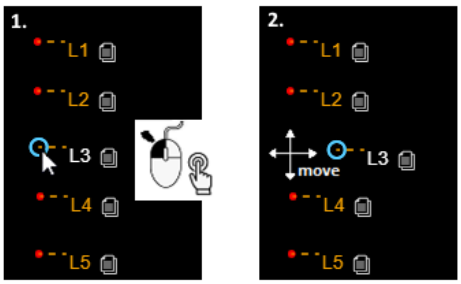


Figure 213. Changing the position of points in the Spinal Labeling action

- until the measurement is saved, the position of each label can be changed:
  - place the mouse cursor over the label which position you want to change until the corresponding point is marked with blue circle and the label text turns white, then press and hold the left mouse button (1);
  - without releasing the button move the cursor to any desired location on the image (2), then release the left mouse button;

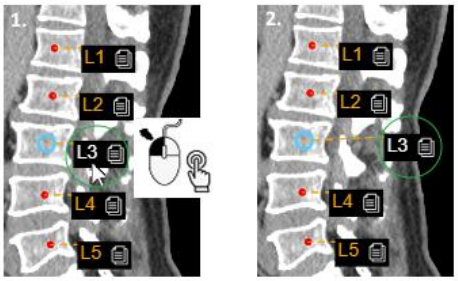


Figure 214. Changing the position of one label

- if you want to change the position of all labels in one step, place the mouse cursor over any label, and press the left mouse button - all labels will turn white (1), then again press left mouse button and without releasing button move the cursor to any desired location (2), then releasing the left mouse button (3);

⚠ **NOTE!** Moving all the labels in one step is allowed only in sagittal images.

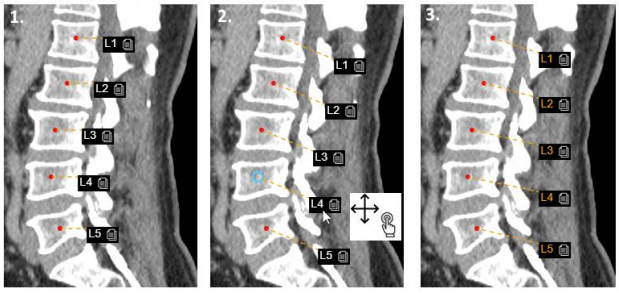


Figure 215. Changing the position of labels in the Spinal Labeling action

- until the measurement is saved, the position of the entire measurement can be changed:

⚠ **NOTE!** Moving all the points in one step is allowed only in sagittal images.

- place the mouse cursor over any of the measurement points until it is marked with blue circle, then click the left mouse button - all points are marked with blue circles, all labels will turn white (1),
- then again press left mouse button and without releasing button move the entire measurement to any desired location (2),
- then release the left mouse button (3);

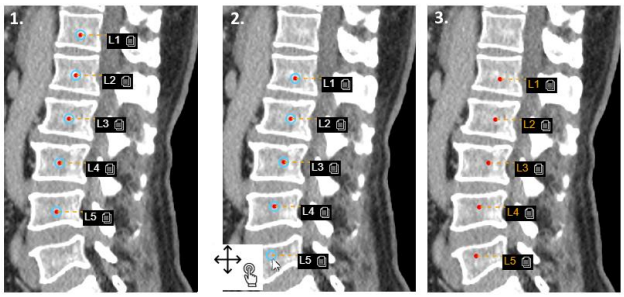


Figure 216. Changing the position of entire measurement in the Spinal Labeling action

Spine balance measurement

To perform a spinal balance measurement, enable the setting in the dialog at the beginning of the action.

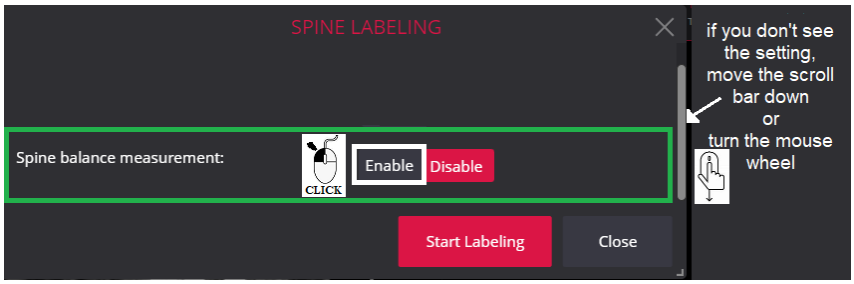


Figure 217. Setting of spinal balance measurement

After the user marks the C7 and S1 vertebrae, the system returns the result at the end of the spine labeling action

- calculated horizontal distance between C7 and S1 vertebrae,
- visually marked projection of vertebra C7  at the height of the S1 vertebra,
- provides qualification based on the calculated distance:
    - Positive (if C7 is more than -2 cm to the left);
    - Neutral (if C7 is less than or exactly 2 cm to any side);
    - Negative (if C7 is more than 2 cm to the right of S1).

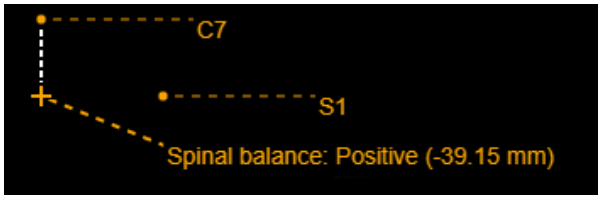


Figure 218. Measurement of spinal balance

⚠ **NOTE!** C7 and S1 vertebrae must be marked for the measurement to be performed. If at least one of these vertebrae is not marked, the measurement is not performed.

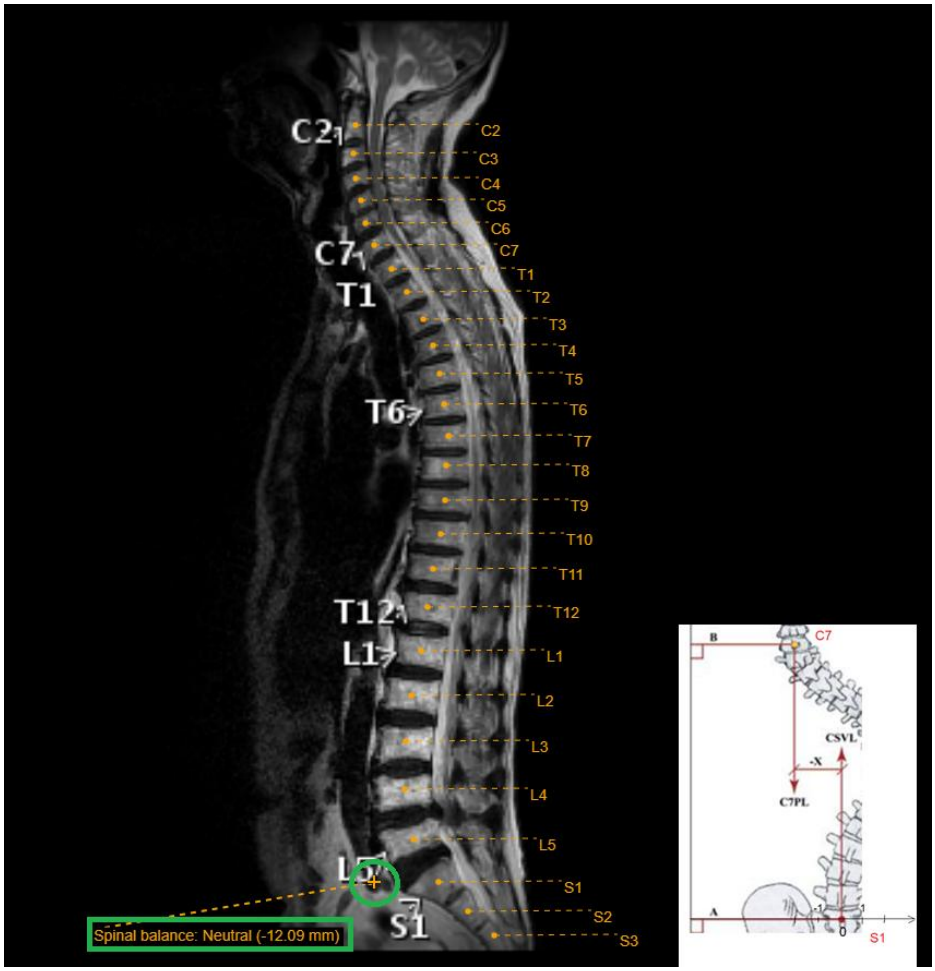


Figure 219. The result of spine balance measurement

After completing the marking of the vertebrae, the user has the option to change the position of the marking point. When changing the position of C7 and/or S1, the system recalculates the measurement result.

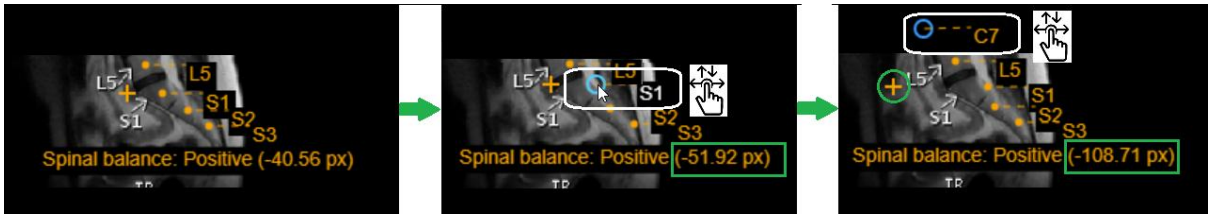


Figure 220. Recalculation of spinal balance measurement when replacing C7 and S1

Spine labeling in related series

If 3D coordinates data is available, the system places the vertebra marking point in 3D space and displays it in any primary or reconstructed series or image that share the same coordinates. You can navigate between the related series while performing the Spine labeling, viewing or editing the not saved measurement.

⚠ **NOTE!** The Spine labeling measurement is displayed in the reconstructed series but may not be saved for such series that only temporary are created in the Viewer.

⚠ **NOTE!** The Spine labeling measurement is saved for one series and may be activated only in the viewport of this series, however if activated it is displayed on other related series as well.

⚠ **NOTE!** If the unsaved Spine labeling measurement is deleted, the measurement is removed from 3D space and all corresponding viewports.

The following example describes the spine labeling using sagittal and axial series:

- open the related sagittal and axial series and locate the needed vertebra, for example L1, in both series using cross hair tool or reference line tool (1);
- select the **Spine Labeling** tool in Measure menu, point the mouse button to the center of the vertebra L1 on the axial image, and press the left mouse button;
- set the corresponding labeling parameters in the opened Spine labeling window to continue labeling. The system shows the already placed L1 point in axial and sagittal images. The red color of the point indicates that this point is located exactly on the currently viewed images. The next L2 vertebra point moves when moving the mouse cursor (2);
- in case you need to locate the exact vertebra center in axial projection, you can scroll the axial series till the reference line in sagittal view indicates the next L2 vertebra, point the mouse cursor to the center of the L2 vertebra on the axial image, and press the left mouse button.
- the system automatically locates and opens the sagittal image, that contains the L2 point and displays the red L2 point on it. The previous L1 point color changes to the blue, indicating that this point is not on the current sagittal image but near it (3);
- in case you need quick spine labeling, you can move the mouse cursor with next L3 vertebra label point to the sagittal image (3) and continue marking on this image. After placing each point on the sagittal image, the system automatically opens the corresponding axial image and displays the red mark point on it (4).

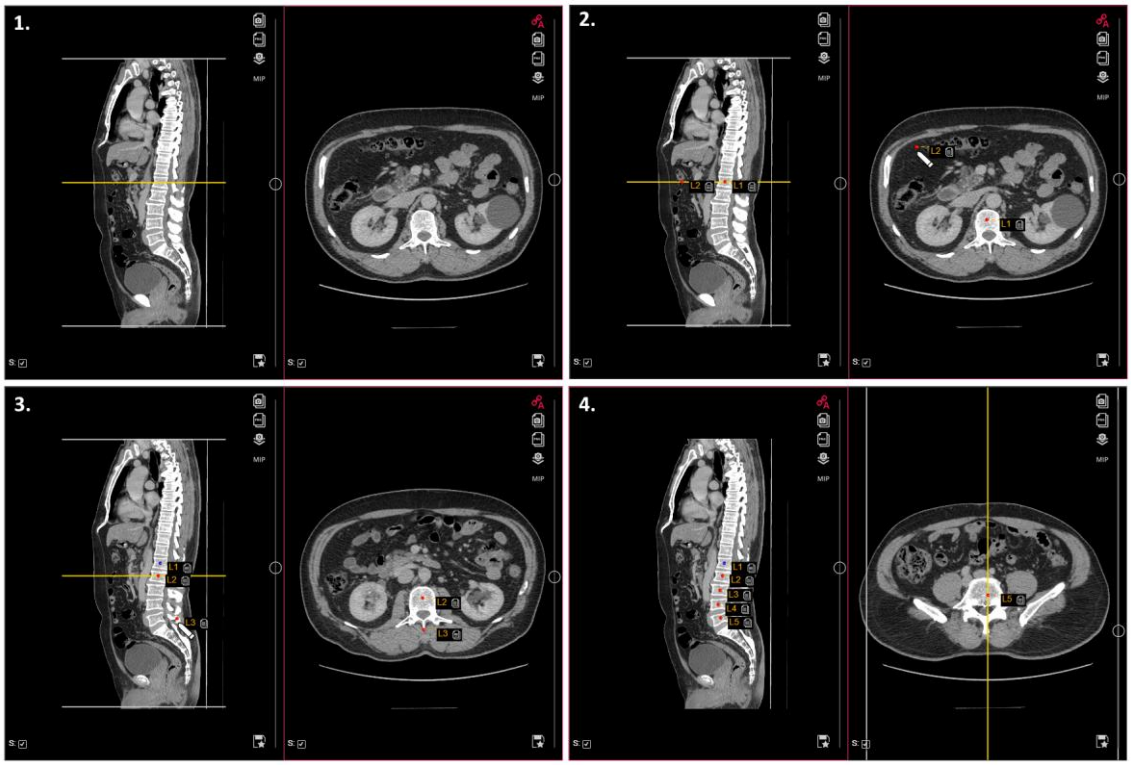


Figure 221. Spine labeling in related sagittal and axial series

If vertebra label point is placed in 3D space, you can see it in all the series having the same coordinate system. For example, if you scroll the coronal series with the spine already labeled in the related sagittal series, the label and green dots or blue dots, depending on what side you approach the spine, are visible at smaller than 10 mm distance from the current image (1). When the viewed coronal image is crosses the labeled lumbar part of the spine, all 5 points are inside 10mm distance and become visible on the coronal image: the red L2 and L5 points are located exactly at this image, the L3 and L4 green points are shifted towards the anterior side, and the L1 blue point is shifted towards the posterior side from the current image (2):

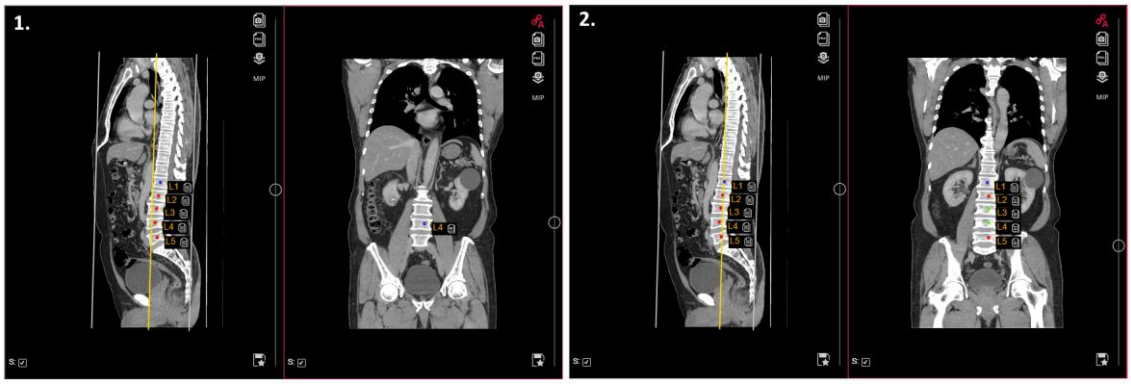


Figure 222. Viewing 3D Spine labeling in related sagittal and coronal series

If vertebra label points are placed in 3D space, you can move the points or labels at any image, where they are visible, as described in parent section.

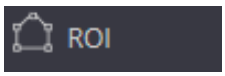
⚠ **NOTE!** Moving all the points or all the labels in one step is allowed only in sagittal images.

Moving labels affect only the label position in the current viewport, neither other series, nor the same series in another viewport are affected.

Moving the point affects its placing in 3D space and representation in all related series. Take attention to the following behavior if editing the placement of the point in 3D spine labeling measurement:

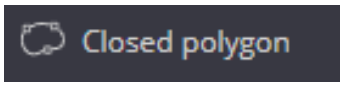
- editing the point automatically places it to the currently viewed image. If you want to avoid this behavior, you should scroll to the image where point is red and move it in this image.
- editing the point automatically opens the image with this point in all viewports with spatially related series, in the same way as cross hair tool does.

Region Of Interest



The **ROI** (Region Of Interest) is the same as area measurement only without measurements.

Closed polygon and Repulsor



Repulsor

The **Closed polygon** is used to mark the region of interest. As in case of ROI, the area is marked by placing the points around it, but the points are connected with curved lines. To perform the closed polygon measurement:

- select **Closed polygon** tool in **Measure** menu;
- mark points around the area of interest by clicking the selected mouse button;
- the system connects the points as you place them;
- double click the selected mouse button at the last point to finish the measurement:

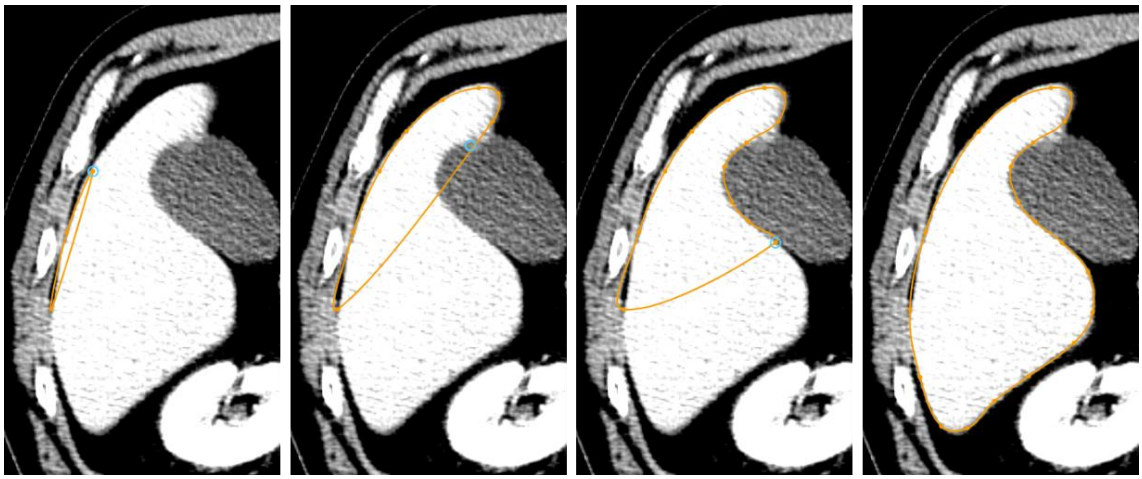


Figure 223. Marking region of interest with closed polygon tool

Until the **Closed polygon** is saved, you can move the whole measurement or adjusts its contour as described:

- change the line by dragging any of the points;
- change the line by double-clicking any of the points and removing it;
- change the line by moving, adding, or removing points with Repulsor tool.

Select the closed polygon measurement you want to edit with Repulsor tool:

- select **Repulsor** tool in **Measure** menu;
- adjust the image scale and position, and click the selected mouse button near the line from the side you want to push;
- the system places the Repulsor tool on the image;

  ⚠ **NOTE!** The system automatically adjusts the Repulsor radius according to the distance from the line. You can change the radius by holding the CTRL button and scrolling mouse wheel. The minimum and maximum allowed Repulsor radius is calculated depending on image width.

- hold the selected mouse button pressed and drag the Repulsor tool towards the line;
- the system adjusts the closed polygon line when the Repulsor tool touches it;
- release the mouse button if you need to cross the polygon and push with Repulsor from the other side.

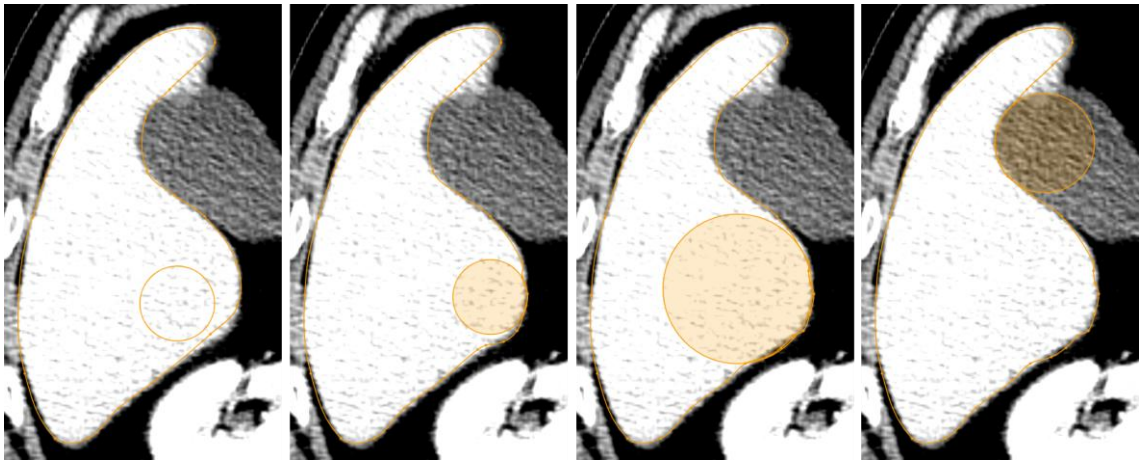


Figure 224. Adjusting closed polygon with Repulsor tool

The system can be configured to measure area and intensity values: mean brightness (labeled as *Mean*), standard deviation (labeled as *SD*), which indicates the dispersion of random variables around the mean, sum value, as well as minimum and maximum values. The measurement units depend on the study type. For more details, see the System Settings section.

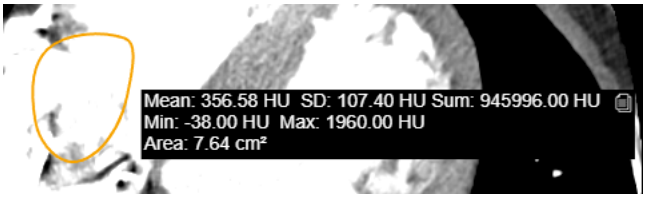


Figure 225. Measured parameters of a closed polygon: area and pixel intensity information

Flexpoly



The **Flexpoly** is used to freely mark the region of the image for which the area is calculated at the end of the measurement. To perform a flexpoly measurement:

- select **Flexpoly** tool in **Measure** menu or press **N** on the keyboard;
- place the mouse cursor over the image, press the left mouse button and move the area without releasing the left mouse button;
- release the left mouse button after circling the desired image region;
- the program connects the start and end points in a straight line and calculates the area of the selected region;

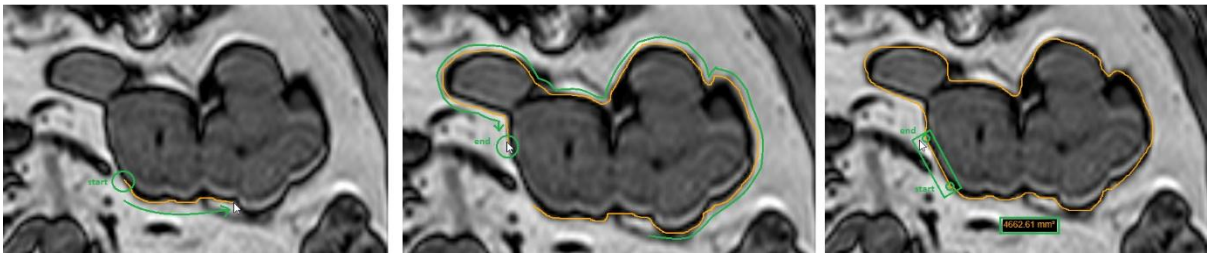


Figure 226. The Measure Flexpoly

- until the measurement is saved, the position of the flexpoly can be changed: place the mouse cursor, press the left mouse button without releasing the left mouse button, move it to the desired location, then release the left mouse button.

The system can be configured to display additional intensity values: medium brightness (marked Mean), the standard deviation (marked SD), which gives the variance of the random variables about the mean, sum value and minimum, maximum values. The units of measurement depend on the type of study.

⚠ **NOTE!** If the intensity values may not be calculated, only the area value will be displayed.

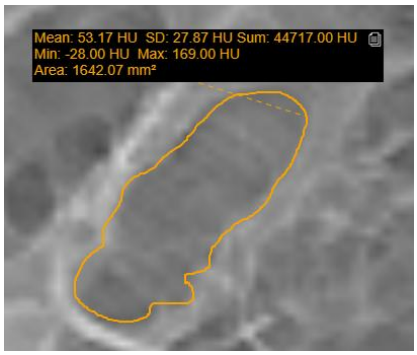


Figure 227. The Measure Flexpoly with brightness values

Pencil



The P**encil** is used to mark the area of the image with a free drawing:

- select **Pencil** tool in **Measure** menu or press **B** on the keyboard;
- place the mouse cursor over the image, press the left mouse button and encircle the area without releasing the left mouse button;
- release the left mouse button after circling the desired image area;
- if you only want to place a point, place the mouse cursor over the image, press the left mouse button and release it; the result will show a point slightly larger than the line drawn with the **Pencil**;
- measuring Pencil lines or points can be displayed in different colors and different thicknesses than other measurements (how to change pencil color and thickness, see the “Settings” section);
- when you encircle an area or place a point, the measurement remains active, you can immediately encircle another area or place another point;

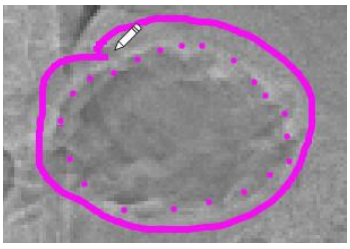


Figure 228. The Measure Pencil

- until the measurement is saved, the position of the encircle an area or place a point can be changed: place the mouse cursor, press the left mouse button without releasing the left mouse button, move it to the desired location, then release the left mouse button.

⚠ **NOTE!** The **Pencil** tool, unlike the other measurement tools, is not automatically deactivated. Click the mouse button on active **Pencil** measurement in toolbar to deactivate it.

Arrow



The **Arrow** intended for mark an area of interest in an image, a multi-frame, and a video viewports:

- select **Arrow** tool in **Measure** menu;
- place the mouse cursor over an image point or area of interest;
- click the left mouse button, the program will make a point with an arrow;
- without pressing the mouse button, move the cursor in the selected direction until the arrow line is the correct length, then click the left mouse button.

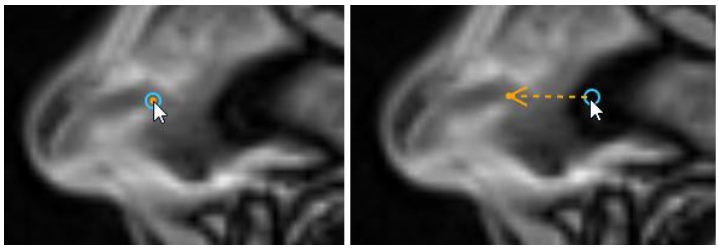
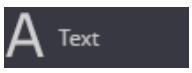


Figure 229. The Measure Arrow

- until the measurement is saved, the position of the arrow be changed: place the mouse cursor, press the left mouse button without releasing the left mouse button, move it to the desired location, then release the left mouse button.

⚠ **NOTE!** Measurement **Arrow** does not have the ability to add a text comment. If you need an arrow with a comment, use the Measurement **Text**.

Text



The **Text** tool allows you to add notes or comments to specific areas of the image or to other measurement annotations. It can be used either with an arrow or without one.

- select **Text** tool in **Measure** menu;
- to insert text box
  - **with arrow** pointing to an object or image location, click the mouse button at the arrow end and drag the mouse to the place of text box;
  - to insert **only text box**, simply click at the desired image place;
- a text window with an arrow (if selected) will appear on the selected image place and the text entry field (white field) will appear at the bottom of the image;
- enter the text in the text entry field and press **Enter** button;
- the entered text will appear in the text box and the box will be resized accordingly;

- yellow arrow can be pointed to any place of the image by dragging its end point;
- yellow–border text window can be placed with a drag and drop motion anywhere on the image, for example, next to the measurement you want to add text to;
- double-click the text box for opening the text entry field and changing the entered text.

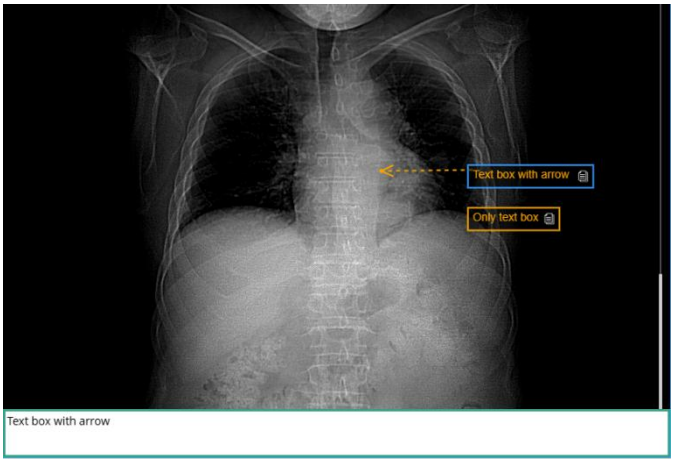


Figure 230. Text entry field

The measurement can be configured to display text **with** or **without a background**, **with** or **without a border**. Please contact your system administrator for configuration.

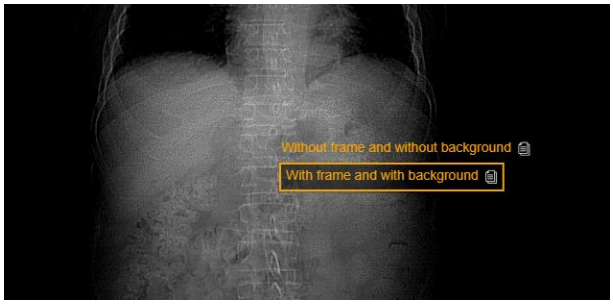


Figure 231. Text with/without background and with/without frame

Time-Intensity Curve



The time-intensity curve measurement allows for visualization of the lesions' behavior by plotting the ROI intensity values over time after the administration of contrast material.

⚠ **NOTE!** Measurement is most informative in studies that have phases.

To perform the **Time-Intensity Curve** (TIC) measurement:

- select **Time-Intensity Curve** tool in **Measure** menu;
- in the dialog window select
  a)  if it is needed to circle (or ellipse) the area of interest;
  b)  if the area of interest is to be outlined with flex poly;

- the system creates the first line of the ROI record;
- in case "a" the cursor in the active viewport changes to a circled cursor  hover the cursor over the area of interest and click the left mouse button;
- in case "b" the cursor changes to pencil  draw a flex poly around the area of interest;
- the system immediately determines the intensity values in all phases at the point where the ROI point is located and displays it on a graph: intensity values on the Y axis, phase number on the X axis;



Figure 232. Time-Intensity Curve. The first ROI point

- if there are more regions of interest, repeat the steps: click  or  , move the cursor to the region of interest and click the right mouse button or draw around the area of interest;
- the system assigns a unique color to each new point and provides the name "ROI *x*";
- if the area of interest is poorly visible or not visible at all, it is possible to move to the next image in the series or to the next phase and then perform the ROI placement action;

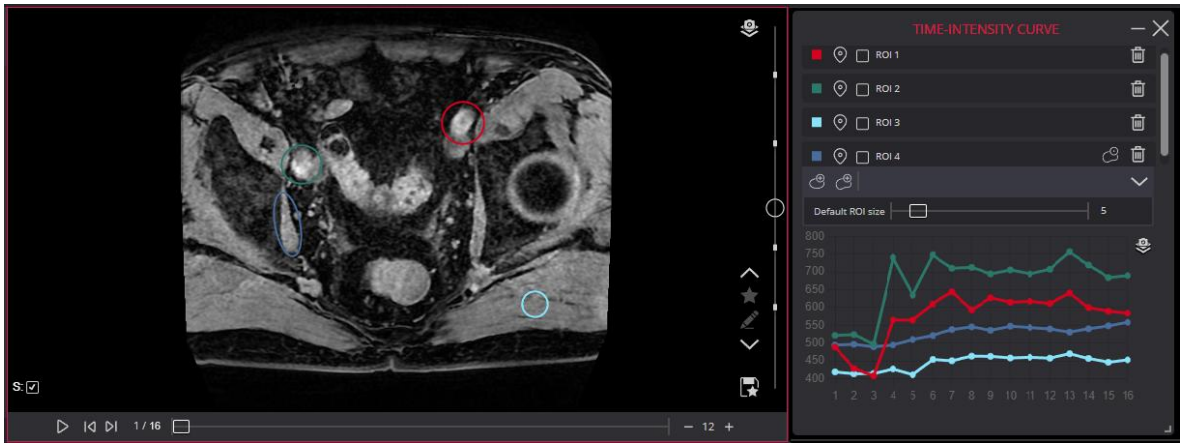


Figure 233. Time-Intensity Curve. With several ROIs

- if the **circle's** ROI is not the required size, move the mouse until four corner points appear, select an outline or corner point and drag the cursor in either direction without releasing the left mouse button until the ROI is reduced or increased;

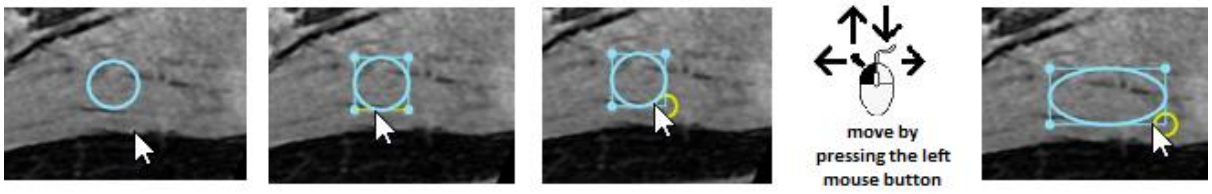


Figure 234. TIC. Changing the circle/ellipse ROI size

- each new point has a default size that can be changed; the changed value is stored in local storage;

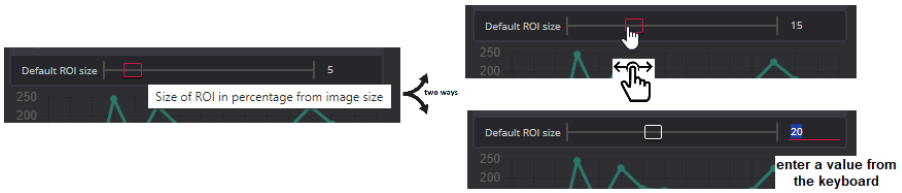


Figure 235. TIC. The default circle/ellipse ROI size

- to change the position of the ROI, move the mouse cursor to the middle of the ROI until the circles appear, hold down the left mouse button, and move the mouse to the correct position without releasing the mouse button;

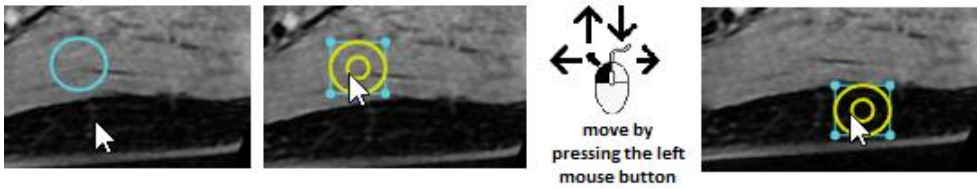


Figure 236. TIC. Change the circle/ellipse ROI position

- the ROI can be rotated: hover the mouse, click on the corner point, press Alt and rotate without releasing the left mouse button;

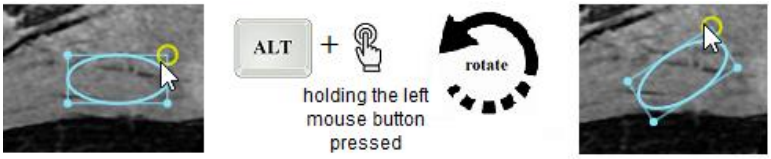


Figure 237. TIC. Rotate the circle/ellipse ROI

- to change the shape of the **flex poly** ROI, activate the Repulsor tool  on the right of the row; the active repulsor icon becomes highlighted  ;
- move the cursor to the place to be edited and press the left mouse button; a circle appears at the cursor - the repulsor;
- grasp the circle from the inside or outside of the outline and, without releasing the left mouse button, move the repulsor along the contour until you reach the required ROI shape;

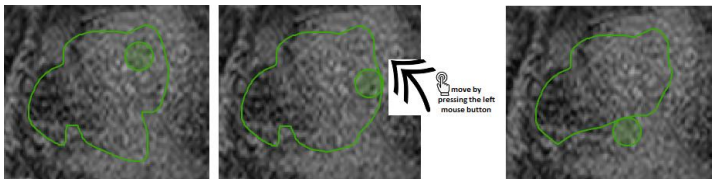


Figure 238. TIC. Flex poly ROI editing with repulsor

- when the repulsor tool is activated, the radius size is displayed at the bottom of the ROI list, which can be changed by scrolling the scroll bar or by typing a value;

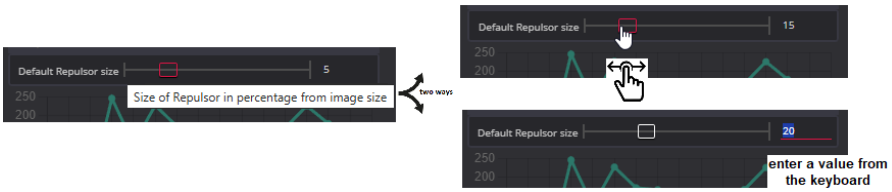


Figure 239. TIC. The default repulsor size

- to change the position of the flex poly ROI, hover the cursor over the outline, press the left mouse button and drag the complete ROI to the required position without releasing the mouse button;

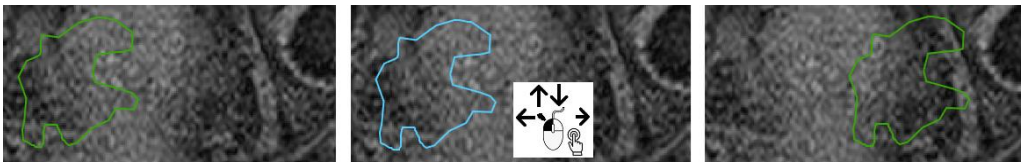


Figure 240. TIC. Change the flex poly ROI position

⚠ **NOTE!** The graph shows the average intensity calculated for the pixels that fall within the ROI. If the size of the ROI is changed or the position of the ROI is changed, the graph is immediately redrawn according to the current values.

- to change the position or size of an ROI that you don't see in the open image, click  and the system will open the phase and the image in which the ROI is located;
- to see the change from the ROI control point instead of the absolute intensity values, mark the control point;

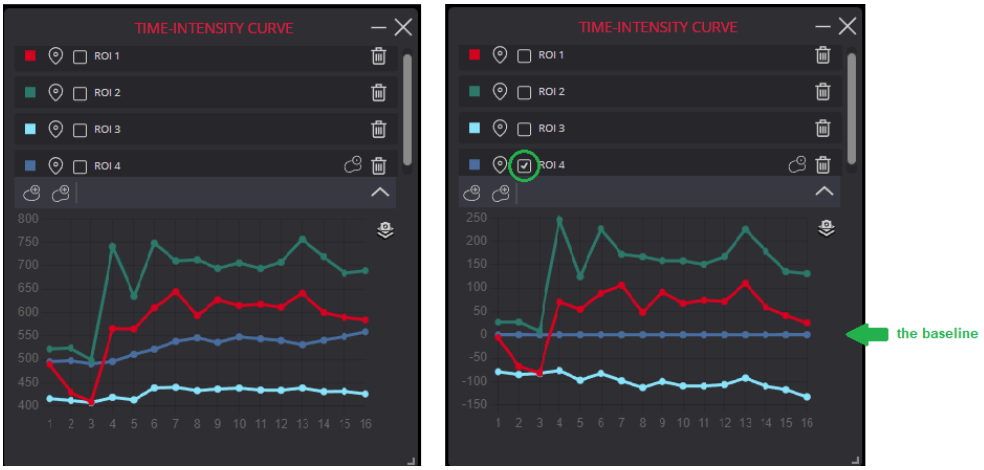


Figure 241. TIC. Change from control point

- the possibility to change the color, name or delete the ROI;

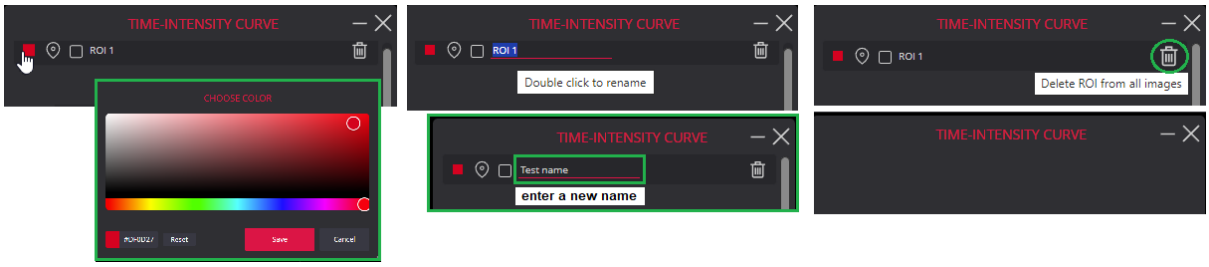


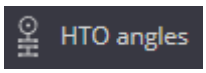
Figure 242. TIC. Change color, name, delete

- to save the graph as a secondary capture, click  near the top right corner of the chart.
- use the 4D slider controls to move to the next time point, or to start auto-play (see details in "4D tools. Show 4D slider").

⚠ **NOTE!** The Time-Intensity Curve ROIs and their information are not stored.

⚠ **NOTE! Time-Intensity Curve** does not work with video data type, with color images (RGBA or RGB data types) and JPEG transfer syntax encoded data. Samples_Per_Pixel attribute (0028,0002) is required to equal 1 for the measurement to work.

HTO Angles



Provide the ability to measure High Tibial Osteotomy (HTO) angles.

The user should select the HTO angles in the measurement menu. By default, the left measurement is created first Left Right. To first create the right measurement, the user must navigate to the “Right” tab Left Right. The user has to click at the point in the image where the measurement's high point should be placed.

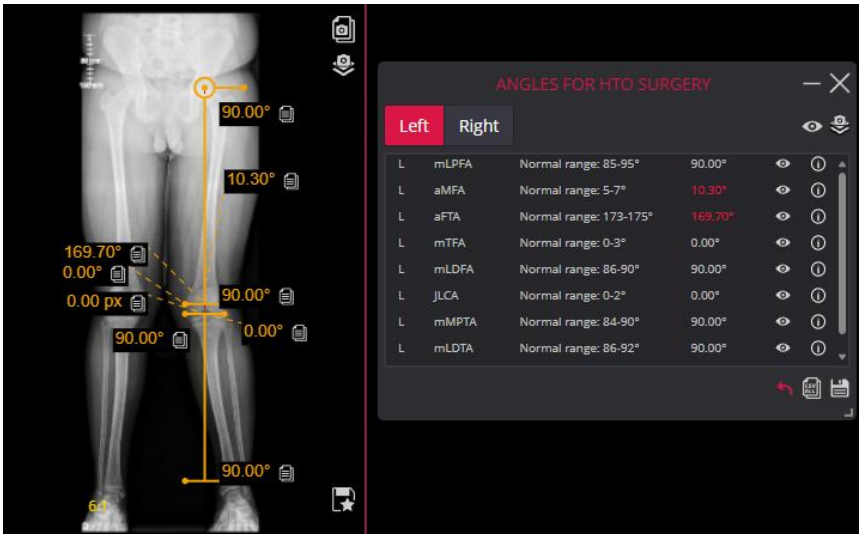


Figure 243. HTO Angles measure

To perform a two-sided measurement on one image, the user has to switch to another tab („Left“ or „Right“, depending on the first measurement to be performed) and select , then click on the image where the top of the measurement should be placed.

The measurement dialogue provides a list of the angles to be measured: side L or R, the abbreviation of the angle/distance name, the range, the values of the angles or the distance in units of survey data. If the value does not correspond to the normal range, it is highlighted in red Normal range: 5-7° 10.30°. The full name of the measured angle is shown in the tooltips line next to the icon .

The user can hide labels for angles that are not relevant by selecting in the angle row, or hide all angles by selecting the icon at the top of the list.

The measurement is placed as a template for the user to move one element at a time to the right place.

Hovering the mouse cursor highlights the measurement element, then click on the left mouse button to drop-down the element to the correct physiological location.

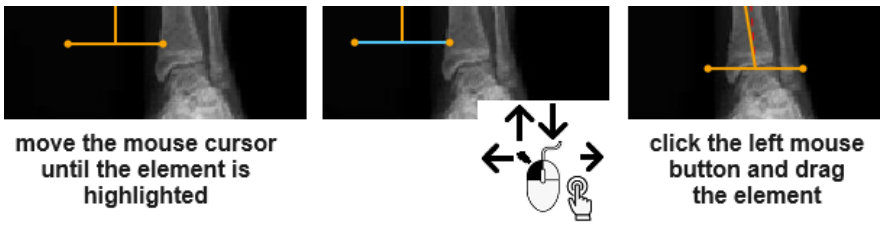


Figure 244. HTO Angles. Moving an element

At the end of the element-lines, there is a point at which the line is shortened or lengthened by drag-drop it.



Figure 245. HTO Angles. Shortening the element

After a measurement change action, a click allows you to undo the changes up to 5 steps back. When actions can not be undone the icon is gray .

Selecting any item and pressing the "Delete" button on the keyboard deletes the entire measurement. It is not possible to delete part of a measurement. The deletion action can be undone by selecting .

When the cursor is placed on the label, the lines between which the angle or distance is measured are highlighted, an arch is drawn on the angle .

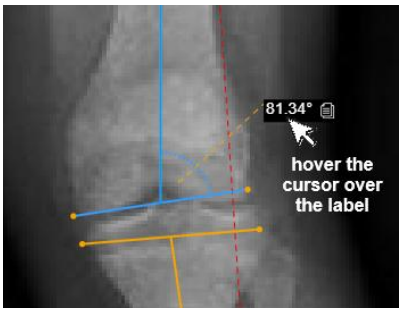


Figure 246. HTO Angles. Highlight lines

Measuring angles and single distance:

Nr.	Abbreviation	Name
1.	mTFA	Mechanical tibio-femoral angle
2.	mLPFA	Mechanical lateral proximal femoral angle
3.	mLDFA	Mechanical lateral distal femoral angle
4.	mMPTA	Mechanical medial proximal tibia angle
5.	mLDTA	Mechanical lateral distal tibial angle
6.	JLCA	Joint line convergence angle
7.	aFTA	Anatomical femoro-tibial angle
8.	aMFA	Angle between the anatomical and the mechanical femoral axis
9.	MAD	Mechanical axis deviation

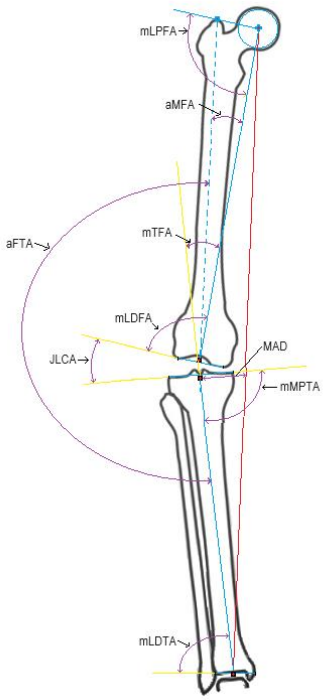
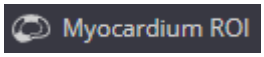


Figure 247. HTO Angles. All measured angles and distance

After the measurement, you can save a secondary capture  or save an annotation  . For more convenience, the action buttons are available from the measurement dialog.

The measurement values can be copied in CSV format - click on  . All measurement values are copied, even if the value is not visually displayed  .

Myocardium ROI



The **Myocardium ROI** is used to indicate the region of interest. As with the ROI, the region is marked by arranging points around it, but the points are connected by curved lines as in the case of a closed polygon. To measure a **Myocardium ROI**:

- select **Myocardium ROI** tool in **Measure** menu;
- mark points around the area of interest by clicking the selected mouse button;
- the system connects the points as you place them;
- double click the selected mouse button at the last point to finish the measurement.

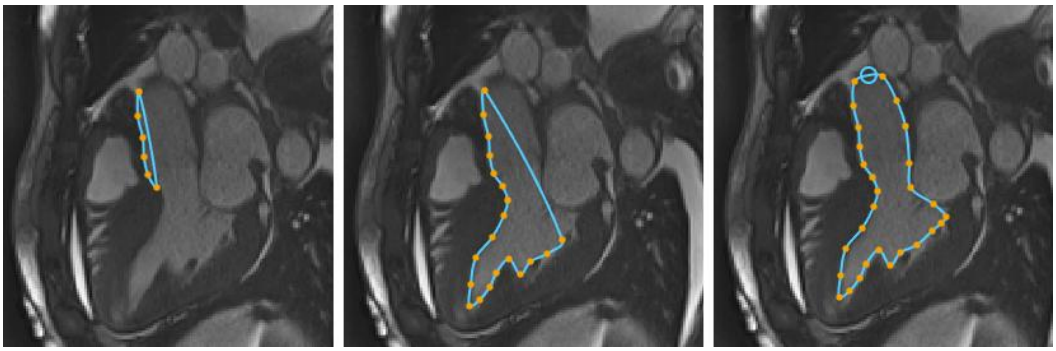


Figure 248. Myocardium ROI

When the initial drawing is complete, the ROI is selected and the editing mode is kept activated. Editing mode can be enabled/disabled by selecting “**Edit myocardium ROI**”.

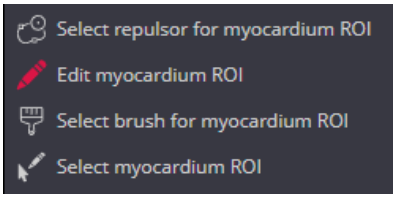


Figure 249. Myocardium ROI. All editing tools

In edit mode, you can move one point at a time: hovering the cursor highlights a point  and allows you to drop-down to another location. Double-clicking on a selected point deletes the point.

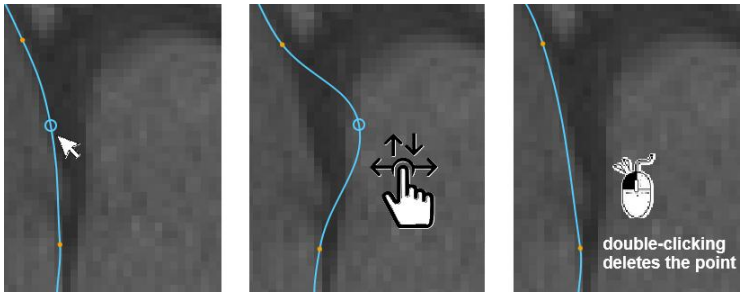


Figure 250. Myocardium ROI. Changing the position of a point

To move the entire outline, hover over the outline so that it is highlighted but no points are selected, then drag-drop the entire ROI.

To activate the repulsor, select the menu item "**Select myocardium ROI**", then select the contour and choose the menu item "**Selecte repulsor for myocardium ROI**". The repulsor tool allows you to adjust the contour by pushing the contour curve from the outside or inside. To decrease/increase the repulsor radius, press Alt and turn the mouse wheel. To finish editing with the repulsor, double-click or select the repulsor tool menu item again.

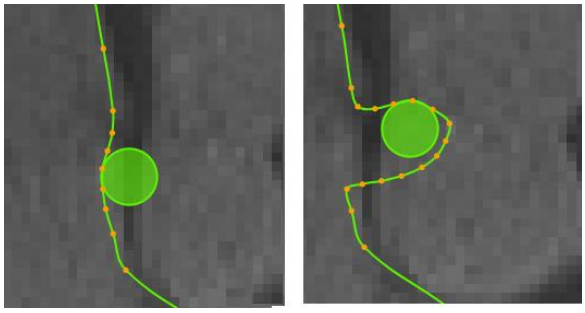


Figure 251. Myocardium ROI. Editing with repulsor

The Myocardium ROI can be built up from multiple contours that are processed as a single measurement object. The contours are represented in different colors.

⚠ **NOTE!** To have a single measurement with multiple contours, when the user finishes drawing the first contour after the double-click, draw the next contour immediately. If other actions have been performed and then you want to add the next contour, edit mode must be selected. If the Moycardium ROI action is re-selected, the contour to be drawn will be a separate measurement.

When drawing, editing, or moving a contour, overlapping of contours is not allowed. If the user draws, moves, or pushes a contour beyond the boundaries of another contour using the repulsor, the system automatically corrects the contour by clipping it to ensure that the contours do not overlap.

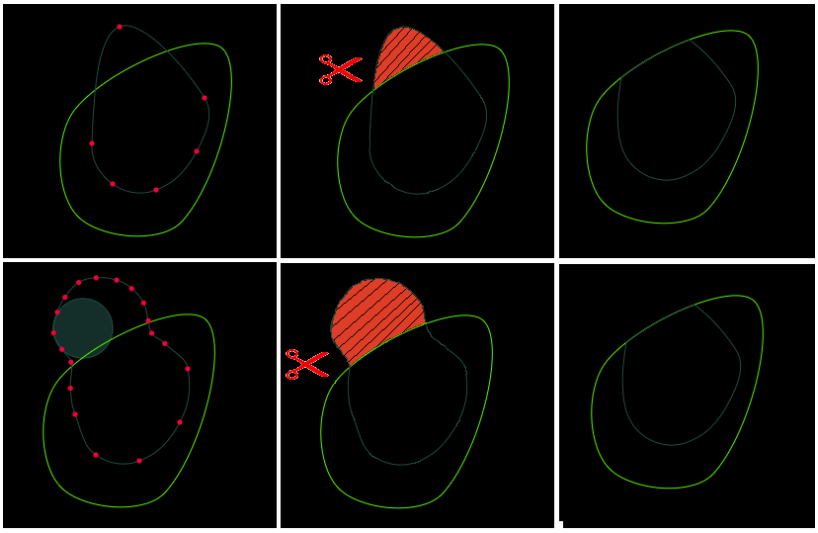


Figure 252. Myocardium ROI. Automatic clipping of overlapping contours

⚠ **NOTE!** The result of the contour correction depends on the proportion of the overlapping area of the contours to the total area and the proportion of the areas between the contours. For example, if more than half of an internal contour is moved to the outside of another contour, the moved contour will become the external contour and will be clipped to the external contour.

When drawing or editing, the contour shall not be allowed to cross itself. If the user draws an outline with a loop, the system automatically corrects the contour. The result may be a separate contour that can be selected and edited individually.

⚠ **NOTE!** Even if only one contour is selected out of two or more contours on an object, selecting the **Delete** function deletes the entire object, it means all contours.

If you want to remove only one contour out of several existing ones, you can do so by selecting a point in edit mode and double-clicking the mouse, which removes the specific point. This must be repeated until the minimum number of two points is reached, after which the system automatically deletes the contour.

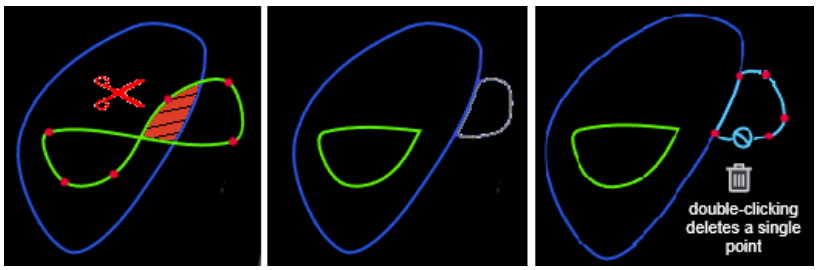


Figure 253. Myocardium ROI. Automatic deletion of loops

To fill a color, select “**Select brush for myocardium ROI**”. Move the cursor while holding down the left mouse button until you fill the area with color.

The tool fills the color inside the outline, without crossing over another outline of the same object. To remove a color, perform the action with the **Alt** button pressed.

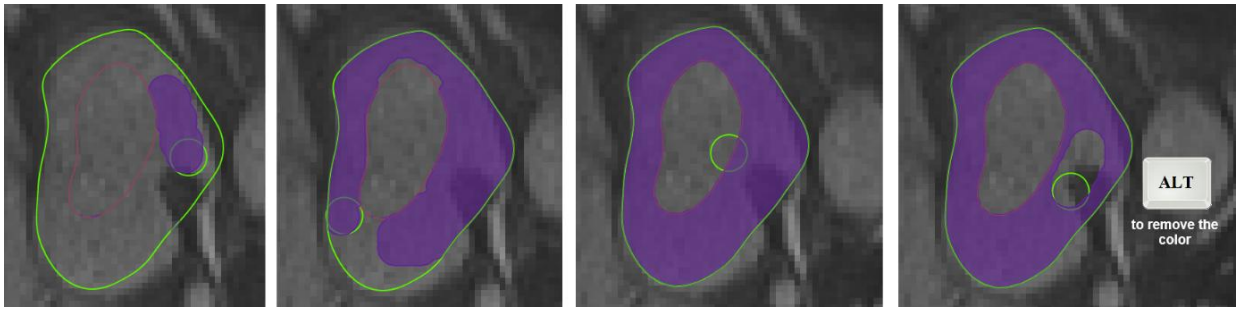
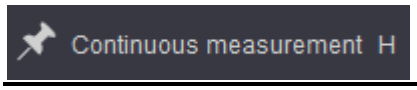


Figure 254. Myocardium ROI. Fill color with Brush

⚠ NOTE! Measurement of myocardial markers is not saved to presentation states.

Continuous measurement



The **Continuous measurement** button is used to repeat measurements several times in succession:

- select one measurement in the menu list and click on "Continuous measurement";
- in viewport make the selected measurement as usual;
- after action the selected measurement remains active and the action can be repeated in viewport.

To turn off should press the **Continuous measurement** button one more time.

Continuous measurements have the possibility to turn on/off using a shortcut. By system value by default, the shortcut is “H”. This value of shortcut can be change. For more information see in chapter "Shortcuts".

If the user turns on **Continuous measurement** it is saved in the browser's local storage and is applied the next time the dialog is opened.

Intensity



The **Intensity** button is used to measure the density of a CT image. To measure the density:

- select **Intensity** tool in **Measure** menu to activate the function: the highlighted icon indicates that function is activated 

.
- move the mouse cursor over the point you want;
- the density of the point (in Hounsfield units, HU) and its coordinates are displayed at the bottom left corner:

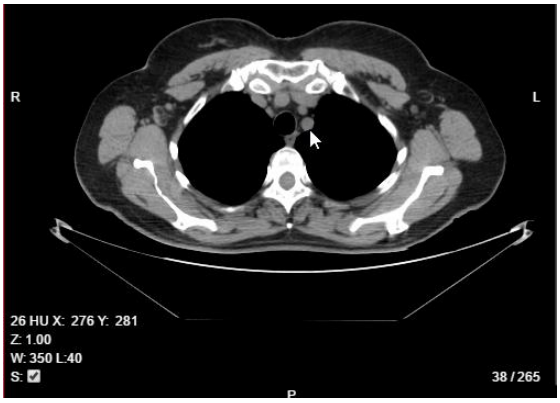
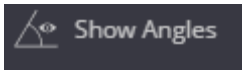


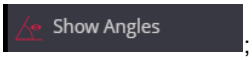
Figure 255. Intensity measurement

- click the activated **Intensity** menu once more to deactivate the function.

Show Angles



Use the **Show Angles** function to see the angles between any intersecting lines. To display the angle measurements:

- select **Show Angles** tool in **Measure** menu to activate the function: the highlighted icon indicates that function is activated 

;
- if **Show Angles** function is active, the angles between intersecting lines are displayed:

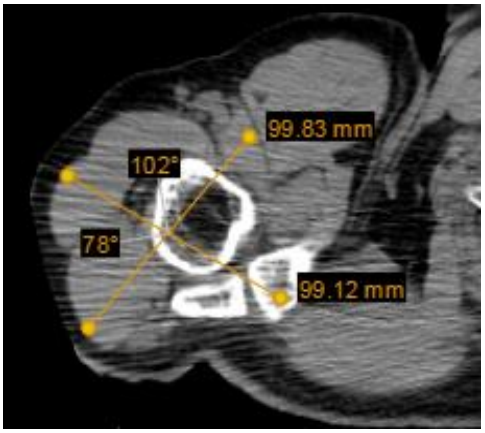
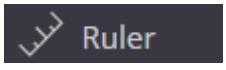


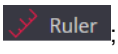
Figure 256. Angle measurement between intersecting lines

- Click the activated **Show Angles** menu once more to deactivate the function.

Ruler



Use the **Ruler** function to see the ruler in the viewport. To see the ruler:

- select **Ruler** tool in **Measure** menu to display the ruler: the highlighted icon indicates that ruler is activated 

;

- if **Ruler** is active, the rulers are displayed at the bottom and on the left of the viewport with images of the configured modalities:

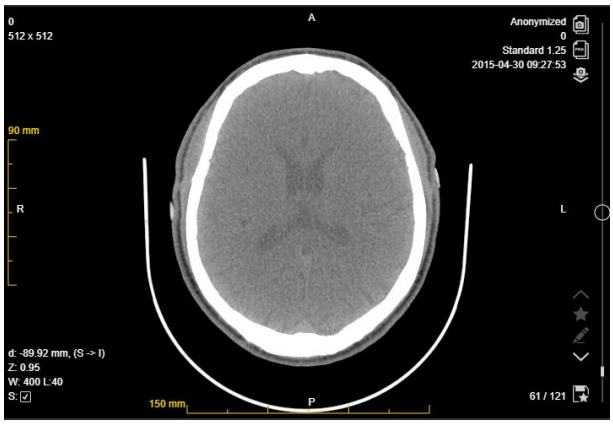


Figure 257. Ruler displayed in the viewport

⚠ **NOTE!** By default settings the Ruler is configured for CT and MR modalities. You can change the configuration in Settings.

- Click the activated **Ruler** menu once more to deactivate the function.

Horizontal Line

Horizontal Line

The tool is used to display a horizontal line in the viewport that remains visible at the same position on the screen when scrolling through images. The tool is most useful for analysing Nuclear Medicine studies. To see the **Horizontal Line**:

- select **Horizontal Line** tool in **Measure** menu to display: the highlighted icon indicates that tool is activated Horizontal Line;
- when the tool is activated, the initial horizontal line is activated in all viewports that contain studies of the modality defined in the settings;

⚠ **NOTE!** By default settings the **Horizontal Line** is configured for NM, PT and SC modalities. You can change the configuration in Settings.

- the starting line is displayed in the middle of the viewport and the user can change the position in each viewport by moving the line higher or lower;

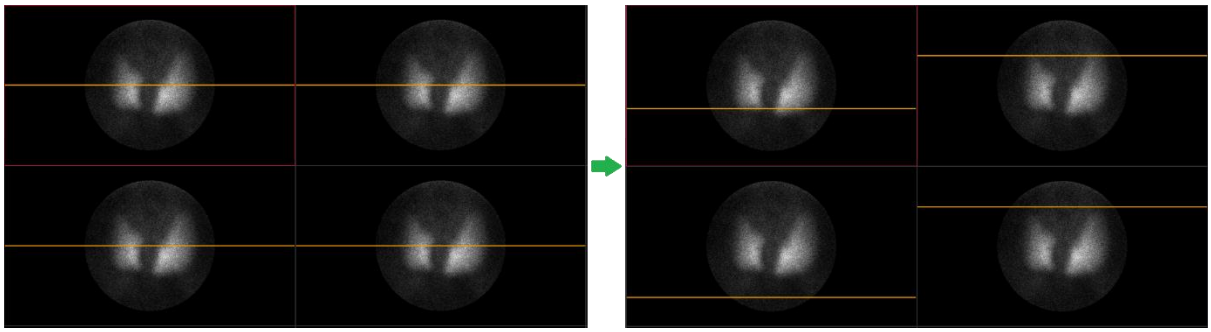
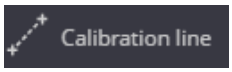


Figure 258. Horizontal Line displayed in the viewports

- the horizontal line remains in the same position when manipulating the viewport (e.g. zooming, pan etc.).

⚠ **NOTE!** The **Horizontal Line** is not stored in the presentation state (PR) and is not represented in MIST MPR projections.

Calibration line



The **Calibration line** button is used to change the scale of measurement:

- select Calibration line tool in Measure menu;
- draw a line between two points at a known distance:

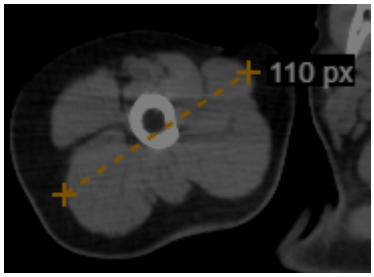


Figure 259. Calibration line

- indicate line length in millimeters in a pop-up window:

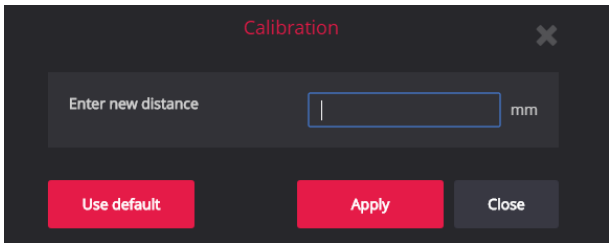


Figure 260. Entering the Calibration line length

- once the data is entered, click Apply button– data will appear on the left bottom corner of the screen:

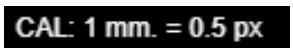
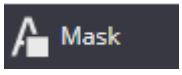


Figure 261. Calibration ratio result

⚠ **NOTE! Use default** button resets to default calibration settings.

Mask



Use the **Mask** to temporarily hide the sensitive information on the image. You can draw the mask in two ways:

- press the assigned mouse button at the corner of the area to be hidden, and immediately release the mouse button; then move the mouse cursor to the opposite corner of the area to be hidden and click the assigned mouse button again to draw the filled rectangular over the area, or

- press the assigned mouse button at the corner of the area to be hidden, and without releasing the mouse button, drag the cursor to the opposite corner of the area to be hidden, then release the mouse button to draw the filled rectangular over the area.

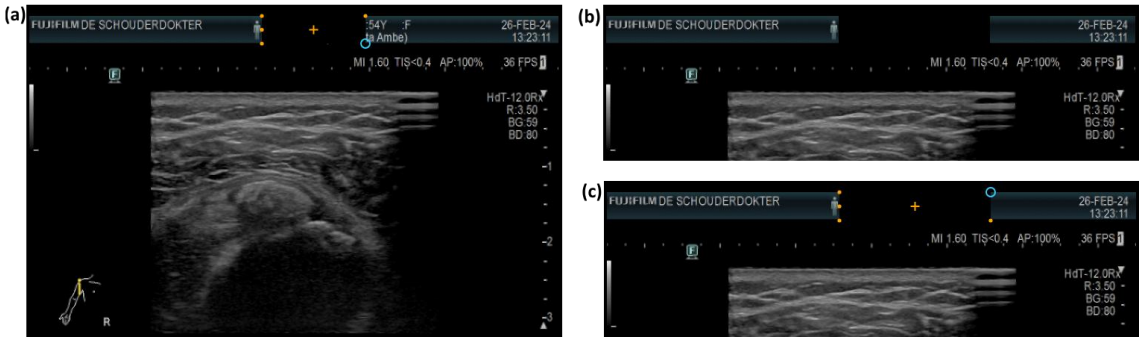


Figure 262. The Mask placed to hide the patient's information in the image: mask drawing, (b) mask drawing finished, (c) mask selected for editing

You can change the size and place of the **Mask** rectangular. See section "Ellipse and Rectangle" for detailed description of the editing possibilities. Note, that Mask does not have border and editing points expressed when its drawing is finished. To see the points and edit the Mask, point the mouse cursor to the corner point or middle point.

⚠ **NOTE!** The **Mask**, unlike the other measurements, is not saved when saving presentation state.

Delete measurements

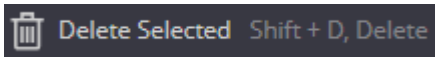
⚠ **NOTE!** The delete actions apply only to the active measurements, and do not apply to the measurements displayed as part of the saved presentation state. See section Presentation states for information on how to view or hide presentation states.



The **Delete All** menu is used to remove all measurements from the active series at once.

To remove the measurements:

- select the viewport with series from which you want to remove all measurements;
- select **Delete All** in **Measure** menu – all measurements will be deleted from the active series.



The **Delete Selected** menu is used to remove only selected measurement:

- select the image from which you want to remove some measurement;
- select the measurement on the image;
- select **Delete Selected** in **Measure** menu – the selected measurement will be deleted.

Save Presentation state

Save Annotation

The **Save Presentation state** menu allows to save the measurements for later usage and sharing. All measurements including text can be saved as presentation state. See description how to save and to review saved presentation states in section “Presentation states”.

Copy and paste measurement

Copy and paste measurement actions allows you to have the same measurement displayed in the same place on the different images, and so compare and analyze the difference among the images.

⚠ **NOTE!** Copy and paste is only available on the ellipse measurement and only with CT modality. For other measurements or other modalities, the copy button is not displayed.

The copy and paste measurement actions sequence is as follows:

1. The Copy measurement button is displayed in measurement’s label, if the copy and paste actions are available for this measurement. The measurements, that may by copied and pasted, are listed in subsections of this section.

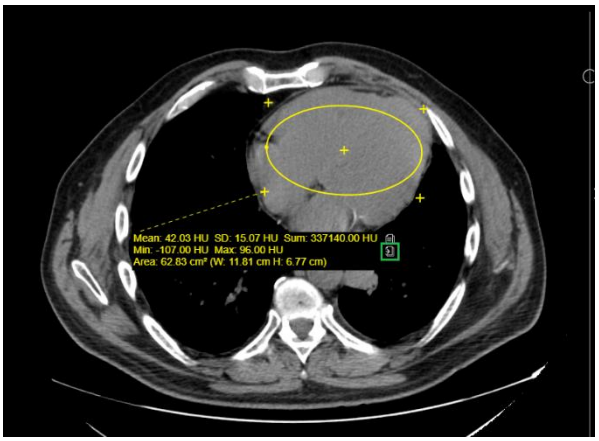


Figure 263. Copy measurement button

2. Clicking the Copy measurement button starts the copy and paste measurement actions sequence, and system performs the following actions:

- The copied measurement is highlighted;
- The Stop actions button is displayed in label of the copied measurement instead of the Copy measurement button;
- The Paste measurement button is displayed in all viewports with images, on which the measurement can be pasted.

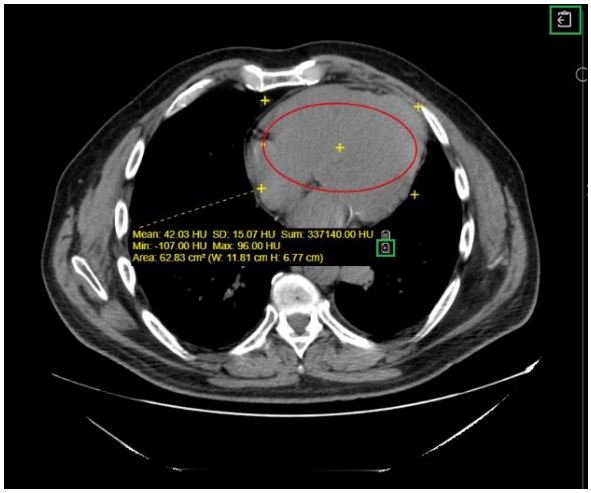


Figure 264. Stop and Paste buttons

⚠ **NOTE!** Only one Copy and paste measurement actions sequence is allowed at a time.

3. Clicking the Paste measurement button draws the copied measurement on the image:

- The pasted measurement is displayed exactly at the same place of the image where the copied measurement is displayed;
- The Stop actions button is displayed in the pasted measurement description.

4. You can locate the image for pasting the measurement in following ways:

- Locate the required image in the viewport with Paste measurement button by scrolling the series;
- Open image or series, and the system automatically displays the Paste measurement button in the viewport, if the measurement may be pasted on this image.

When done with pasting measurement, you can stop the copy and paste measurement actions sequence in following ways:

- By clicking the Stop actions button in the label of the pasted measurement;
- By starting a new copy and paste actions sequence;
- The system automatically stops the copy and paste measurement actions sequence when the last Paste measurement button is removed either because of changing Viewer layout, or because of opening another image in the viewport.

⚠ **NOTE!** Stopping the copy and paste measurement action sequence does not delete the pasted measurements.

When the copying sequence is stopped, the copy button is no longer displayed either on the ellipse being copied or on the ellipses that were placed before the action started.

To repeat the copying sequence for an ellipse created before the copying sequence was stopped, you need to select the ellipse and then the copy button will become visible again.

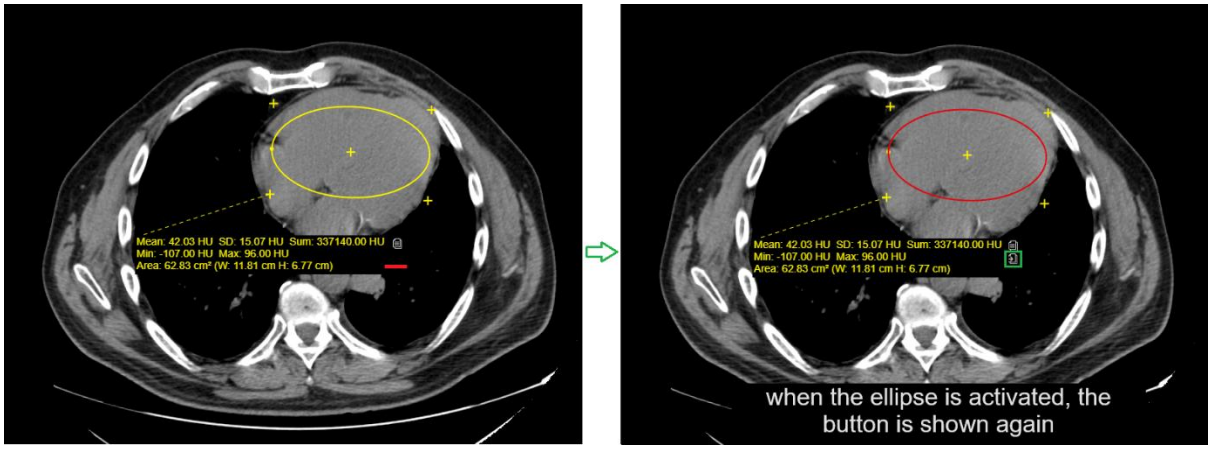


Figure 265. Repeating copying actions

Copy and paste ellipse

Copy and paste ellipse actions allows comparing the image statistics in different computer tomography series and images. The copied ellipse may be pasted on CT images, that have the same frame of reference identifier, patient orientation and scan direction.

The ellipse may be copied and pasted on CT images with fusions. In case of fused series, the PET image statistics is displayed in pasted ellipse label as well.

Copy measurement values to clipboard

The ability to **copy the value of measurements to the clipboard** allows you to work faster and prevent errors when manually writing down data.

Create a measurement and select the copy to clipboard icon.

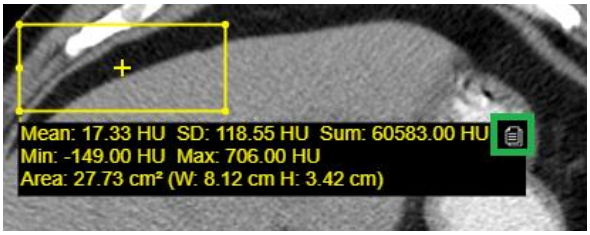


Figure 266. Copy measurement values to clipboard

When copied, the clipboard content may be pasted to any source.

If a measurement has more than one label, the copy icon will appear on each label.

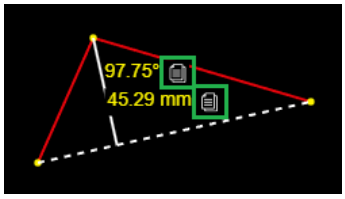


Figure 267. Copy measurement values to clipboard. More than one label

⚠ **NOTE!** If you do not see the copy to clipboard icon in measurement label, please contact your system administrator. The functionality may be disabled in configuration.

Presentation states

Presentation states can be created, saved, and viewed.

⚠ **CAUTION!** Presentation states functionality may be disabled. Contact the system administrator to verify the configuration, if presentation state functionality is missing.

To **create** and **save** presentation state:

- Open the image for which you want to save presentation state. In case of multiframe image, pause the playing and select the frame, for which you want to save presentation state.
- Do the required manipulations: change windowing, rotate, pan, zoom etc.
- Add the measurements, enter text.
- Save actual presentation state either with **Save Presentation state** menu, or with **Quick save of key object, presentation state** button, as described below:

1) select Save Presentation state in Measure menu - save presentation state window will appear:

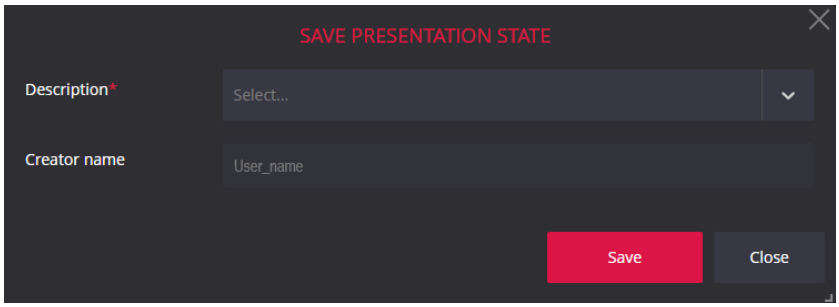


Figure 268. Save presentation state window

It is mandatory to enter a description, the value (or multiple values) of which can be selected from a list (list values are entered in the settings, see Settings chapter) or can be entered from the keyboard.

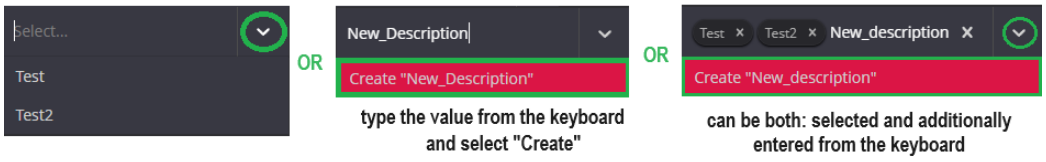


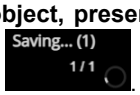
Figure 269. Save presentation state window. Description

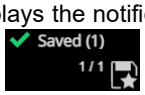
The username is filled in by the system, if the system was not able to retrieve the username, it can be filled in from the keyboard. Click **Save** button.

2) Click the **Quick save of key object, presentation state** button  at the bottom right side of the image. The current date and time are used as description of presentation state.

⚠ **NOTE!** A setting can be activated that on the **Quick save of key object, presentation state** button calls the **Save Presentation State** dialog as from the save from measurements menu. The description and user information fields can then be filled in. For details on activating the setting, see the settings chapter.

⚠ **NOTE!** Please notice, that **Quick save of key object, presentation state** button initiates double action: saves the presentation state and saves key objects.

⚠ **NOTE!** To prevent the repeated clicks, system deactivates the **Quick save of key object, presentation state** button and displays the notification about ongoing saving process on top of the button 

. Saving success notification 

is displayed on successful saving process completion. The number in parentheses is the serial number of the image in the series.

System saves presentation state with the following information:

- the date and time of presentation state saving;
- the presentation state description, creator name, if entered;
- any drawn measurements;
- written text;
- manipulation actions performed.

⚠ **NOTE!** Presentation state saving is implemented according to DICOM standard. The function is available only if the used study storage provides DICOM saving functionality.

⚠ **NOTE!** Several presentation states may be saved for the same image or the same frame of the multiframe image. Each presentation state is saved as separate series of PR modality.

⚠ **CAUTION!** Be cautious and verify the content before saving presentation state. All the measurements and text, including the zoomed outside of the currently viewed area, are saved and shared with other users viewing the study.

⚠ **CAUTION!** Be aware that system automatically opens the presentation state after saving, as well as maintains the active measurement and text objects, that overlap with opened presentation state.

⚠ **NOTE!** Active measurement is displayed on a single image, but on all the frames of the multiframe image. When saving, the presentation state is assigned to the frame of the multiframe image on which the saving is performed.

Once the presentation state has been saved, the presentation state icon (pencil) will appear on image thumbnail:



Figure 270. Presentation state icon on image thumbnail

⚠ **NOTE!** You should change the default Auto open saved presentation state setting, if you want the system to automatically open the last saved presentation state when opening the image.

⚠ **NOTE!** Contact your system administrator, if You want to not auto open the presentation states, that were generated and saved by the algorithms.

By default settings the presentation state for the image should be opened manually. To **view** saved presentation state:

- if thumbnails of the all series are displayed, drag and drop the image with saved presentation state (the one that has the presentation state icon) to the viewport
- or use quick access controls (see section “Viewport toolbar”). - the active presentation state button is displayed on the image in quick access controls group:

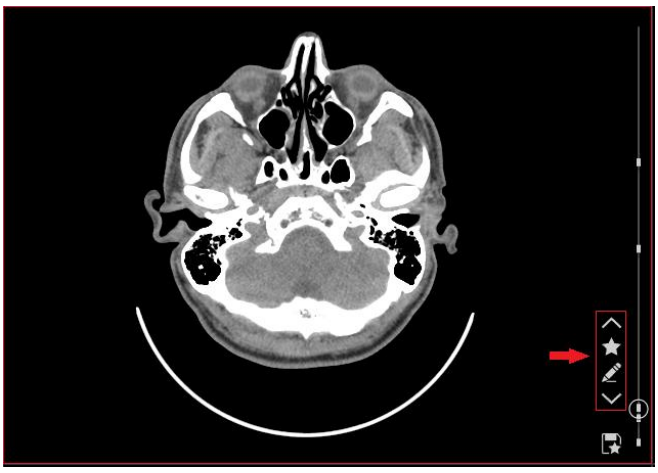


Figure 271. Presentation state button on image

- move your mouse cursor to the Presentation state button and click it. If there are several presentation states, you can choose one or more to review from the list manually, or to open / hide all at once by selecting All/None option. Hold the cursor over the menu item to see the tooltip with presentation state description, creator name, saving date and time, and information about saving, either through menu (PRESENTATION), or quick save button (KO_ PRESENTATION):

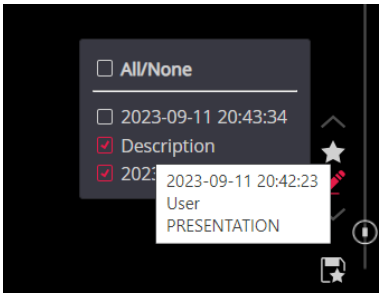


Figure 272. List of presentation states and presentation state description

⚠ **NOTE!** "YYYY-MM-DD hh-mm-ss" indicates anotations saved with **Quick save of key object, presentation state** button. When saved with **Save Presentation state** from the menu it shows description.

- click the check near the presentation state you have chosen to view and the saved presentation state will appear on the screen with an information that has been saved previously:

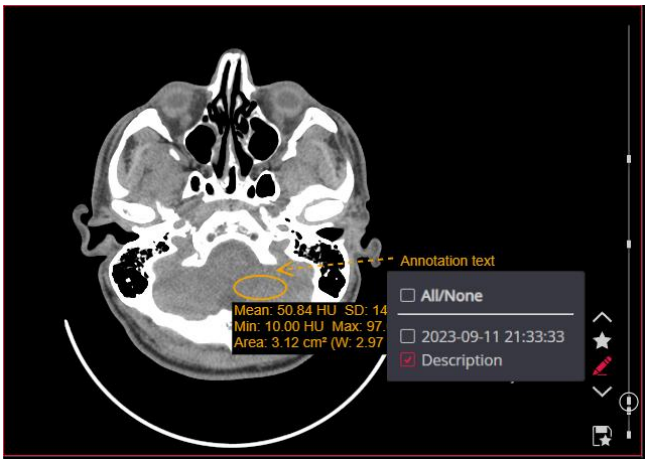


Figure 273. View presentation state

⚠ **NOTE!** Saved presentation states can only be viewed.

⚠ **NOTE!** If multiple presentation states are viewed, the system applies the visual and spatial transformations from the first selected presentation state, or the last saved presentation state in case all presentation states are opened at once.

⚠ **NOTE!** The measurements of all viewed presentation states are displayed.

⚠ **NOTE!** For multiframe images, the presentation states may be viewed only if playing is paused. The list displays all presentation states with a corresponding frame number, but presentation state of only one frame may be viewed at a time.

⚠ **NOTE!** If presentation state for multiframe image is saved without the frame number, it will be displayed on all frames.

⚠ **NOTE!** If the presentation state is opened, the check box is highlighted. Click the highlighted check box to hide the presentation state. Or select option **None** to hide all viewed presentation states and return to the image.

Key Objects



Key Objects concept is used in order to mark most interesting instances and save them for later review. Images, or frames of multi-frame images, marked as Key Objects, are stored in DICOM file of KO modality. Instances from different series of the same study can be stored in one Key Object selection. All instances marked as key objects are annotated with small star symbol.

⚠ **NOTE!** Key objects functionality may be disabled in configuration or by user rights.

To **create** key object:

- Open the image or frame that you want to include in key object.
- Expand the **Key objects** menu and select **"Mark image as Key Object"** from the list.
- The image marking as key object window will appear:

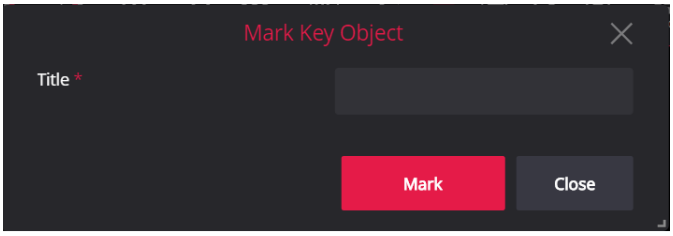


Figure 274. Mark image as key object window

- Enter the key object title or select the one from dropdown list of not saved key objects in the **Title** field, and click the **Mark** button.
- System adds the active image into selected key object. The unsaved key object (star filled with gray background) button is displayed on the active image in viewport and thumbnail. The key object title is displayed in extendable menu of **Key Objects** tool.

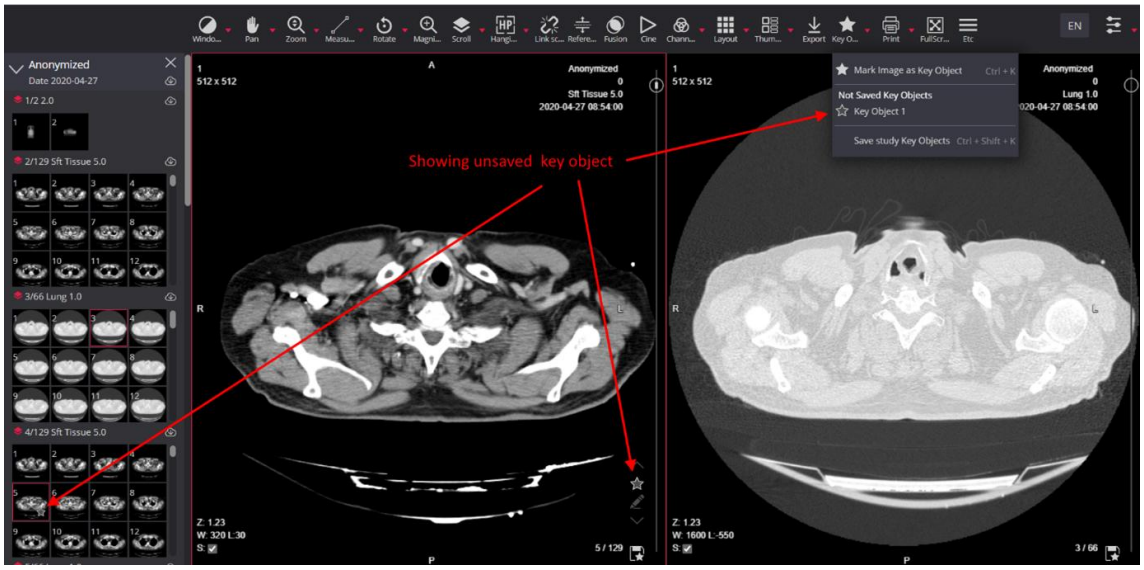


Figure 275. Not saved Key Object

⚠ **NOTE!** You can have several unsaved key objects at a time.

To **save** created (marked) key object:

- Expand the **Key objects** menu and select **"Save study key objects"** from the list. The key object saving window with all unsaved key objects listed will appear:

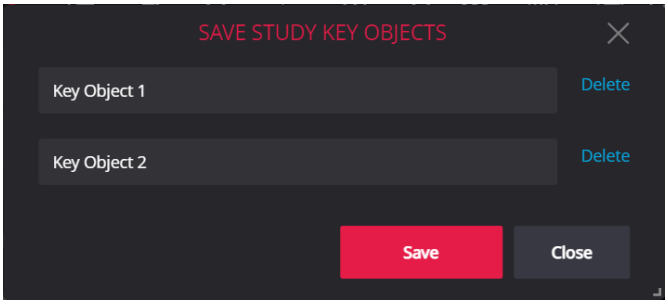


Figure 276. Save study key object window

- You can do the following actions in the window:

change the name of Key object by clicking the entry field and editing text in it,

delete the not needed Key object clicking **Delete** button on the right of the key object title,

After making the desired changes, save the Key objects by clicking the **Save** button.

- System saves the key objects with all the marked images and frames in it. The saved key object icon (star filled with white background) is displayed on the image in viewport and thumbnail. The key object title is displayed in Saved key objects group of extendable **Key Objects** button's menu.

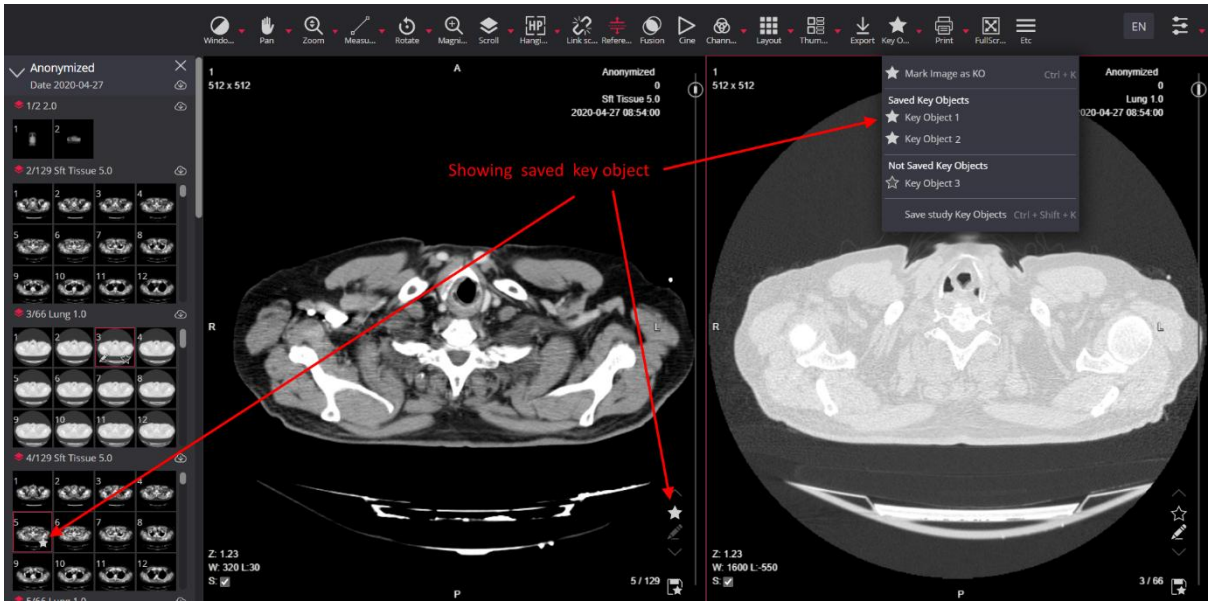


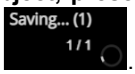
Figure 277. Saved Key Object

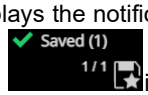
⚠ **NOTE!** Key object saving is implemented according to DICOM standard. The DICOM storage must accept C-STORE operations from MedDream. Alternatively, when using the DICOMweb integration, the STOW-RS method can be used.

You can use **Quick save of key object, presentation state** button  at the bottom right of the image to save the current image or frame as key object. In this case, the current date and time are used as title of key object.

⚠ **NOTE!** Please notice, that **Quick save of key object, presentation state** button initiates double action: saves the presentation state and saves key objects.

⚠ **NOTE!** Quick save can be used only one time per image or frame and saves key object only if the image or frame is not included in any other saved or unsaved key object.

⚠ **NOTE!** To prevent the repeated clicks, system deactivates the **Quick save of key object, presentation state** button and displays the notification about ongoing saving process on top of the button 

. Saving success notification 

is displayed on successful saving process completion. The number in parentheses is the serial number of the image in the series.

To **view** not saved key object or saved key object:

- Open the key object's image in viewport. You can do this either by selecting the title of the Key object from the drop-down menu of the **Key Objects** tool, or by dragging a key object image, that is marked with star icon, from thumbnail bar to viewport, or with quick access controls (see section "Viewport toolbar**"**).

  ⚠ **NOTE!** Use the drop-down menu of the **Key Objects** tool, to see the key object's images from several series of the study. If Key object, that contains images from several series, is opened from menu, each series is opened in a separate viewport, starting from the first viewport. Key object filter is automatically activated in each viewport. If the number of series exceeds the maximum possible number of viewports, the warning is displayed.

  ⚠ **NOTE!** If Key object image is opened from thumbnail or with quick access controls, Key object filter is not activated. To activate the filter, expand the key objects filter menu by clicking the key object icon on the right of the image, and click the Key object title in filter menu.

- Scroll through the images of the activated key object with mouse as described in section "Scroll".

⚠ **NOTE!** The scroll is performed only in one series.

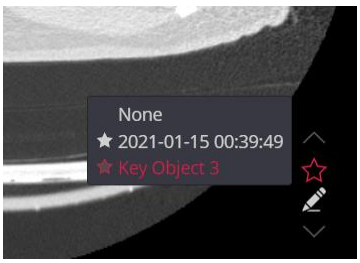


Figure 278. Selection of Key object filter in context menu

⚠ **NOTE!** Key object filter displays all key objects that contain the active image. The star with transparent background indicates that image is included in both, saved and unsaved, key objects. If filter is applied, the title of active key object and the star icon are highlighted.

Key Objects with presentation state

The possibility to save an **key object with a link to the presentation state**. This functionality provides that when the user performs a transformation on the image (for example, rotating the image or changing the windowing), saving the key object will be associated with saving a presentation state which will be automatically opened when the saved key object is displayed.

⚠ **NOTE!** Functionality is activated in the settings.

The step flow is the same as described in the previous section, but when the system setting is activated, a additional check box is displayed in the windows.

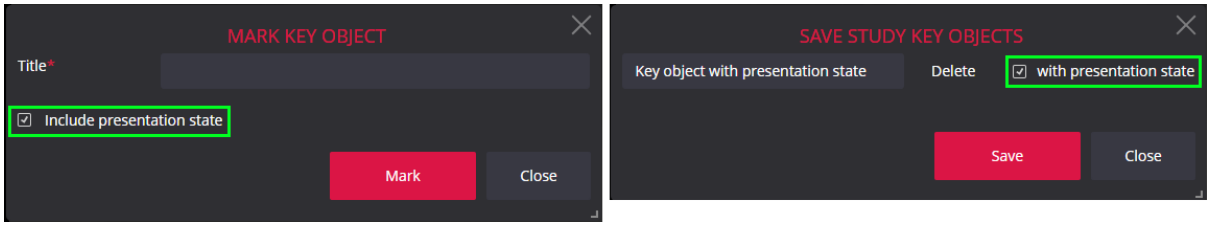


Figure 279. Key object with presentation state

If the check box is unmarked, the key object will be stored without a presentation state.

If the Quick KO, PR storage button  is selected, the key object will always be stored with a presentation state.

Opening a key object that has been saved with a presentation state automatically opens the linked presentation states.

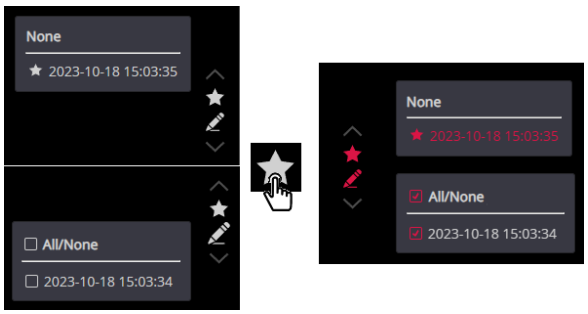


Figure 280. Opening a key object with presentation state

A presentation state that is saved with a key object is displayed in the list in the same way as normally saved presentation states, and can be opened normally - without the key object.

Segmentation



Segmentation provides tools for marking regions of interest in medical images, saving them as RTSTRUCT, and sharing them with other stakeholders or using them in AI modules. The system also allows the user to measure segment data and copy it to the clipboard.

To start working with the segmentation tools, expand the **Segmentation** menu in the toolbar and select the desired tool from the list:

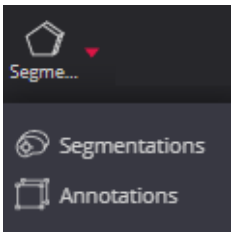


Figure 281. Segmentation menu

The system opens the Segmentation window with the selected segmentation tool tab active:

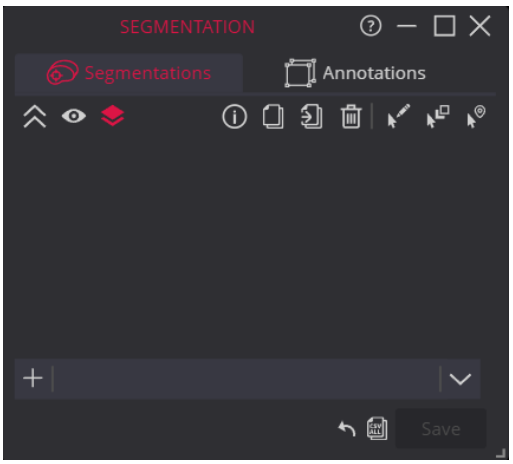


Figure 282. Segmentation. Segmentation tab

⚠ **NOTE!** If you do not see the segmentation tool, please contact your system administrator. Any or all segmentation tools may be disabled in configuration, or by user rights.

⚠ **NOTE!** Segmentation can be performed only on supported modalities and SOP classes. By default, supported modalities are MR, CT, PT, NM, MG, CR, DX, and US. The list of supported modalities and SOP classes can be extended or reduced if needed. More detailed information is provided in the installation documentation.

⚠ **NOTE!** The segmentation tool is not supported for multiframe studies.

⚠ **NOTE!** In studies where the volume cannot be calculated (for example, DX and MG modalities), only 2D tools are available for use.

⚠ **CAUTION!** Until not saved, the created, deleted or edited segments are held in program temporary storage and will be lost, if closing the Viewer or closing the study, that has segmentations with unsaved changes.

Segmentations



Segmentation tools allow you to mark the region of interest. Two types of tools can be used: free-draw tools and smart tools (Smart Paint).

To start working, open the *Segmentation* menu and select the *Segmentation* submenu from the list.

The system opens the segmentation window and activates the selected segmentation tool tab.

Create a new Segmentation

If you want to create a segmentation, select 

on the left side of the window.
The system creates a new segmentation with an empty contour (until a contour is created, a warning icon is shown in the color field ...). The result appears in the list of segmentations, and the system assigns it a unique name and a unique color, which the user can change. How to change the name and the color is described in the section below.

⚠ **NOTE!** When creating segments via the Communication API, it is possible to define the segment name, color, and default tool. Detailed information is provided in the technical documentation.

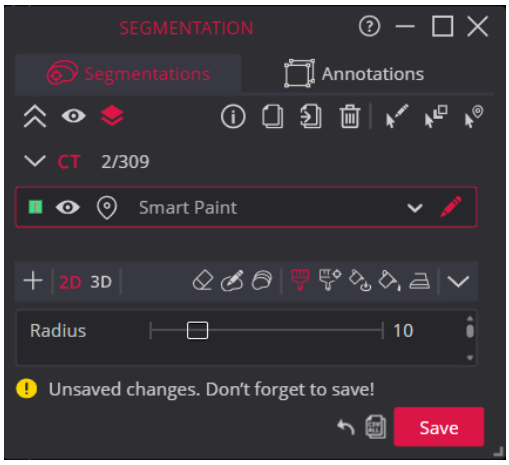


Figure 283. Segmentation creation

Free draw tools

The **free draw tools**  allow you to mark the area of interest by drawing a contour on the image. The area inside the contour is assigned to the segment. A single segment may contain multiple contours. If a contour is drawn inside another contour, the overlapping area is removed from the segment. By drawing contours on several adjacent images of the series, you can define a three-dimensional segment.

⚠ **NOTE!** A segment may consist of multiple contours drawn on the same or on different images within the same series.

⚠ **NOTE!** Free drawing tools are used only for 2D, single-image work.

Contour



- Draw the contour:
  - place the mouse cursor on the edge of the contour to be drawn,
  - press and hold the left mouse button,
  - draw the contour around the region of interest by holding the button pressed and dragging the mouse,
  - release the mouse button when the drawing is finished.

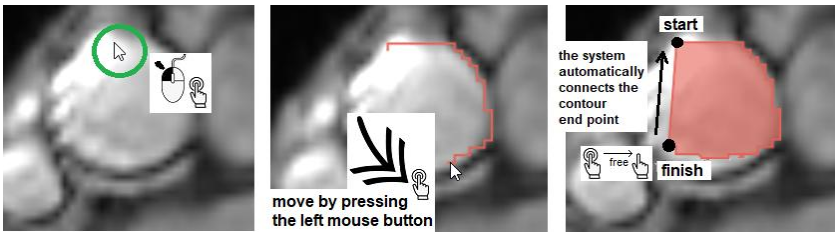


Figure 284. Draw the contour

Parameters: *Transparency*.

NOTE! The system automatically connects the start and end points of the contour.

NOTE! You can use viewer tools, like zoom, pan, and windowing so that the contour can be drawn as accurately as possible.

Remove an inner area from a segment

To remove the inner area from the segment, draw the contour inside the existing contour:

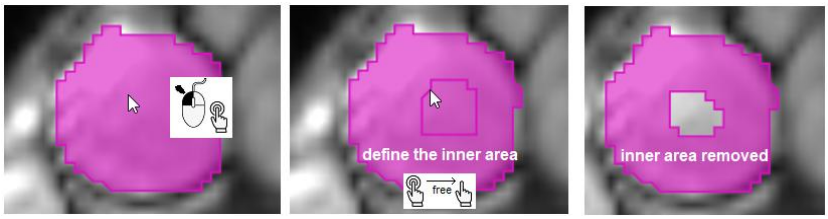


Figure 285. Removing the inner area

NOTE! The same result is achieved by drawing the inner contour first, then the outer contour around it.

Remove the area from the side

To remove an area from the side of the segmented region, press and hold the ALT key and draw the contour intersecting the segment border.

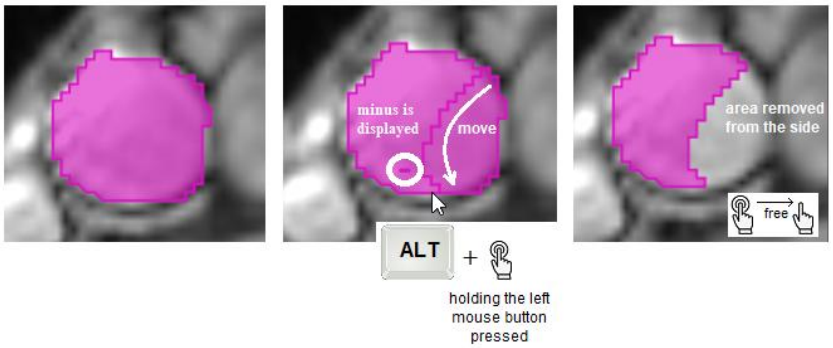


Figure 286. The area removed from the side of segment

Add additional area to the side

To add area to the side of a segmented region, press and hold the SHIFT key and draw the contour that intersects the segment border.

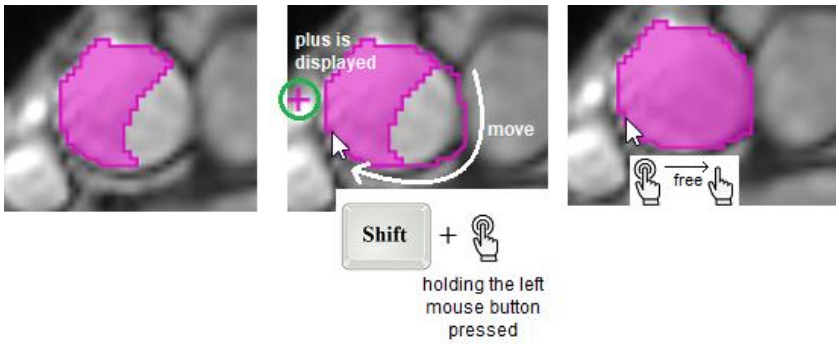


Figure 287. The area added to a side of the Free Draw

Add an additional region

To add a region to an active **Free Draw** segment, simply draw a new contour. You can draw a new contour either on the same image, or scroll in the series and use another image.

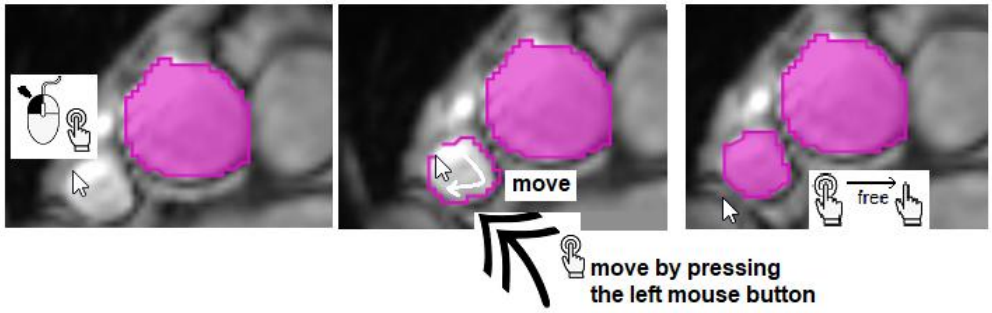


Figure 288. Adding a new Free Draw region

Erase tool

It is possible to erase the contour from **Free Draw** segment or to delete the whole segment. You can remove the contour with the contour erase tool  :

- Place the mouse cursor on the outline, until it is marked,
- Press the left mouse button,
- The marked contour will be removed.

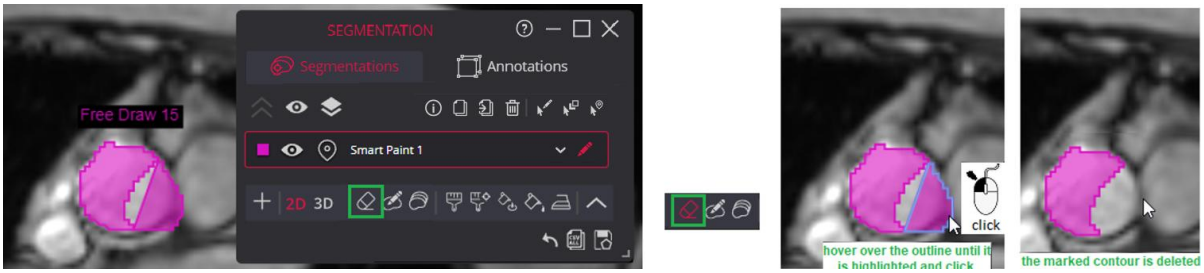


Figure 289. Removal of a section of a **Free Draw** segment

When the undesired contours are deleted, press the active Contour to erase icon to deactivate contour erasing. The icon highlighting is switched off.

Parameters: *Transparency*.

Interpolation tool

The tool provides the ability to automatically fill intermediate images with segments between two, three or more user segmented images.

The user must first segment the images starting and ending with the region of interests (ROI) using the . For example, ROI starts to be visible on slice 10 and the last fragment is visible on slice 30.

If the shape of the area of interest changes, then the intermediate slices must also be outlined using **Contour**.

The segmentation can be either a single area or, for example, a pair of areas. Segments with holes can also be available.

In the example below, the area of interest is outlined with the **Contour** tool in images 181, 185 (+4), 196 (+11), 201 (+5), 221 (+20). In these slices the shape of the ROI starts to change from the previous image.

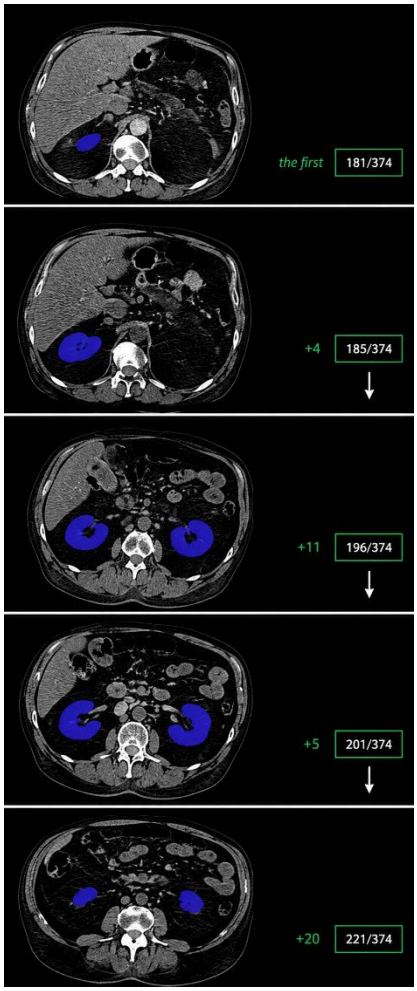


Figure 290. Preparing images for interpolation

After outlined the ROI in the first, last and if necessary, intermediate images, the user must select interpolation action button  . The system fills with segments intermediate images that have not been manually segmented.

The user must review the result of the interpolation and accept or reject it.

Visually, the segments created by the user and those generated through interpolation look different: system-generated segments are more transparent and do not have a bold outline.

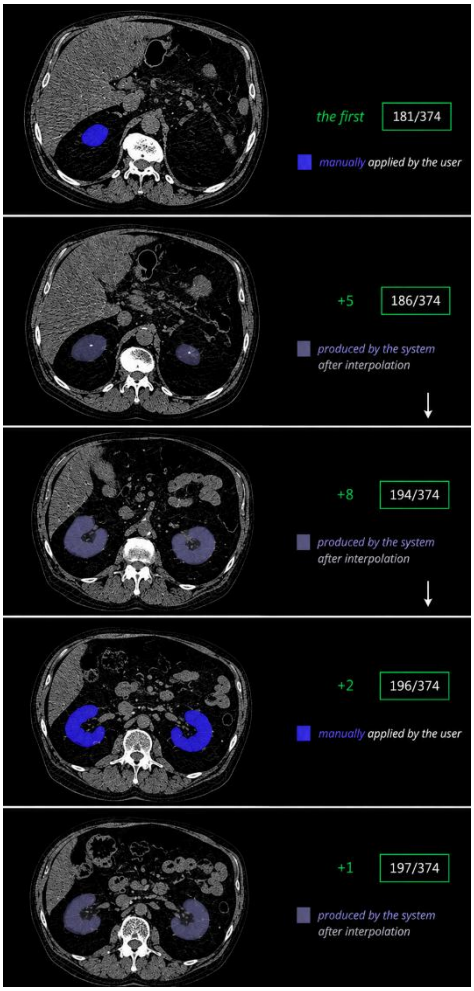


Figure 291. Unconfirmed interpolation result

If the result is not correct, the user must select the "Discard" button and additionally add segments in the intermediate slices.

If the result is correct, select the confirmation button to complete the action. The system aligns the automatically created segments and displays them on a vertical scroll slider.

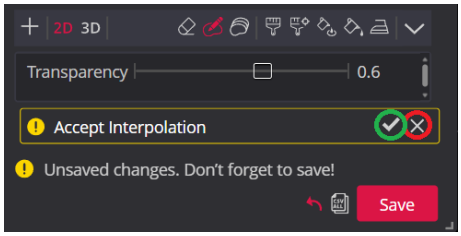
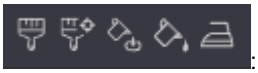


Figure 292. Rejection or Accept of the interpolation result

If, after confirming the interpolation result, the user notices inaccuracies, the user is given the option to undo the interpolation step with  or the user can correct specific areas of the segment using other segmentation tools.

Smart tools

The user can segment - fill color or remove color - by selecting one of 5 tools  :

- Paintbrush;
- Paintbrush with Reference Pixel;
- Fill color;
- Fill Paintbrush;
- Smooth Edges.

⚠ **NOTE!** When you activate a tool, its color changes to make it stand out visually in the toolbar.



⚠ **NOTE!** All **Smart Paint** tools can be used in 3D and 2D modes.



Selecting any of the five tools activates the segmentation cursor - a circle of the variable radius with a marked center.



*Figure 293. The **Smart Paint** segmentation cursor*

⚠ **NOTE!** When switching between 3D and 2D modes, the visual cursor is displayed in the same way, but the operation is different.

3D and 2D mode

When 3D 

is selected, segmentation is done from within a ball. The result of the horizontal section of the ball is a circle. When cutting the ball horizontally, the result of each cut away from the center is a smaller and smaller circle. As a result, the farthest images in the series will be colored less and less when colored.

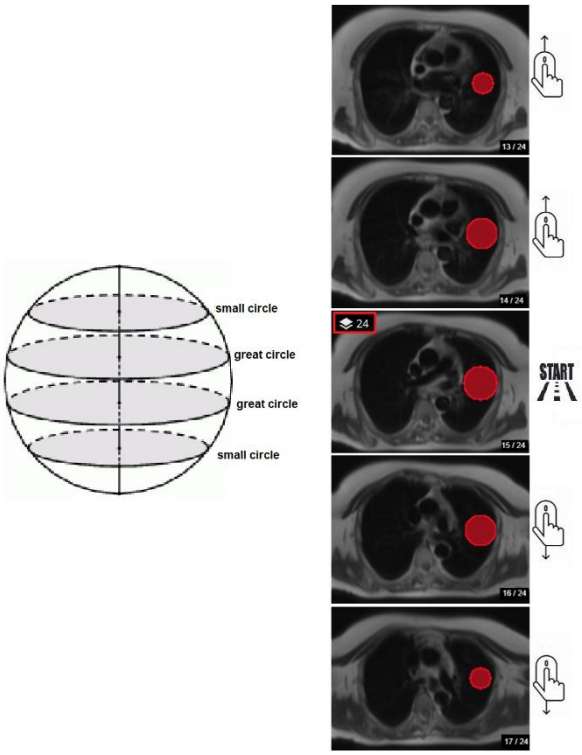


Figure 294. The Smart Paint 3D mode

When selected 

, only the active image in the series is segmented, the tool acts as a circle.

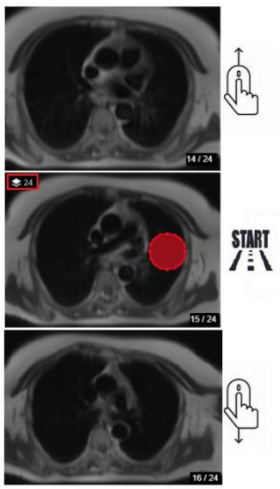


Figure 295. The Smart Paint 2D mode

Paintbrush



Select the **Paintbrush** tool, place the cursor on the area you want to fill, click the left mouse button, and without releasing, swipe with the cursor, similar to using a brush.



Figure 296. The Paintbrush

The tool analyzes each volume (3D) / image (2D) element that falls into the ball/circle. Calculates the inclusion probability based on:

- The distance of the element to the center of the brush
- The intensity similarity of the element to the center point.

When the calculated probability reaches a threshold defined by the calculation methodology, the area is included.

If you want to remove a volume/are, press the **Alt** key and repeat the process as you would when painting.

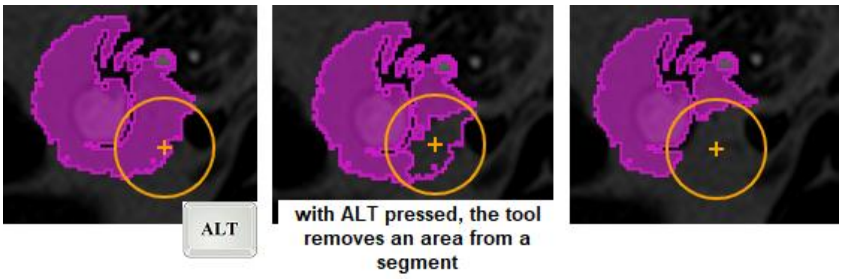


Figure 297. Removing an area with the Paintbrush tool

Parameters: *Radius, Sensitivity, Transparency.*

The parameters are common to all tools, described in a section below.

Paintbrush with reference pixel



Before using the tool, it needs to place a referent point:

- hover the cursor over the area where the fabric is most appropriate;
- increase or decrease the cursor radius to accurately select the pixels to align;
- press ALT and left mouse button;
- the system takes all the pixels that fall within the specified radius and calculates the average value;
- when a probability is calculated, it is based on the similarity to the calculated average intensity of the pixels (or voxels).

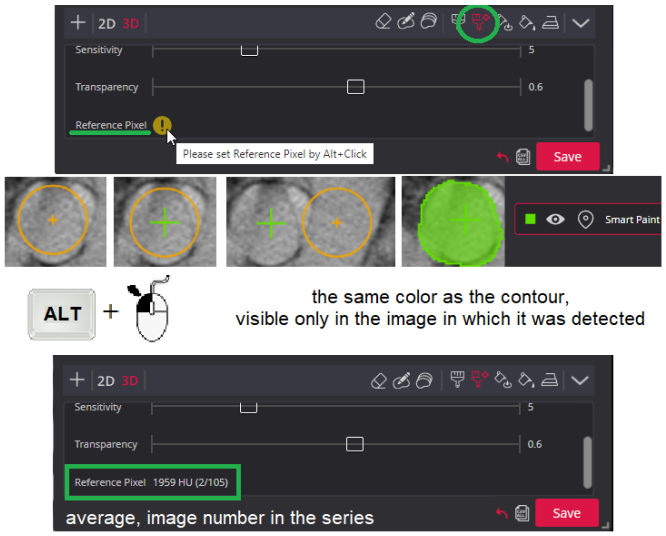


Figure 298. The Paintbrush with reference pixel

The probability is calculated and the result of which depends on:

- The distance of the element to the center of the brush (as well as using a Paintbrush tool);
- The similarity of the voxels to the calculated average (using a Paintbrush, compared to how similar the voxels are to the center point that moves with the Paintbrush).

Parameters: *Radius, Sensitivity, Transparency.*

Fill color



Select the **Fill color** tool, hover over the area/volume in the image you want to include:

click he left mouse button

or press the left mouse button and without releasing, drag the area you want to fill.

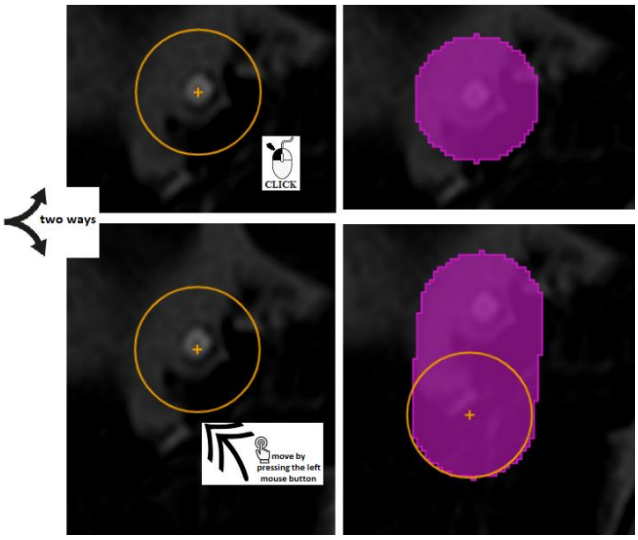


Figure 299. The Fill color

The tool does not analyze the image and includes the entire volume/area the cursor covers.

⚠ **NOTE**! The Fill Color tool does not apply a calculation methodology. The result of the tool is completely dependent on the user.

If you want to remove the segmentation, press the **Alt** key and repeat the process as you would when painting.

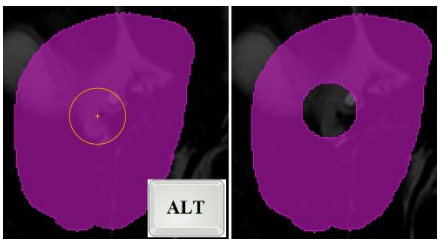


Figure 300. Removing an area with the Fill color

Parameters: *Radius, Sensitivity, Transparency*.

Fill Paintbrush



Select the **Fill Paintbrush** tool, hover over it, and click the left mouse button. If necessary, move the cursor to the next area and click the left mouse button again.

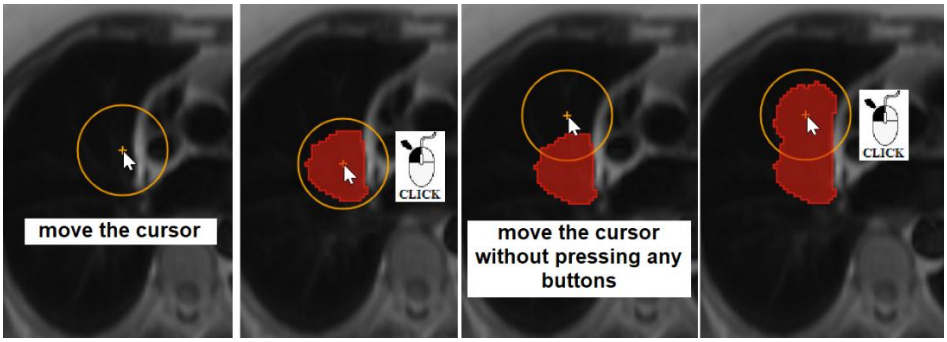


Figure 301. The Fill Paintbrush

Compared to the Paintbrush tool, the user does not need to swipe the mouse cursor, just one mouse click. The operation algorithm is the same as for “Brush”: a probability is calculated, and the result depends on distance and similarity to the center point.

If you want to remove the included voxels, press the **Alt** key on your keyboard and repeat the process as you would when painting.

Parameters: *Radius, Sensitivity, Transparency*.

Smooth Edges



When segmenting noisy images, using the brush tool alone tends to produce segmentation results with jagged boundaries. Therefore, a smoothing operation is provided.

Select the tool, hover over it, and click the left mouse button.

If the result is still with jagged boundaries, then click the left mouse button again or move the cursor, then click the left mouse button.

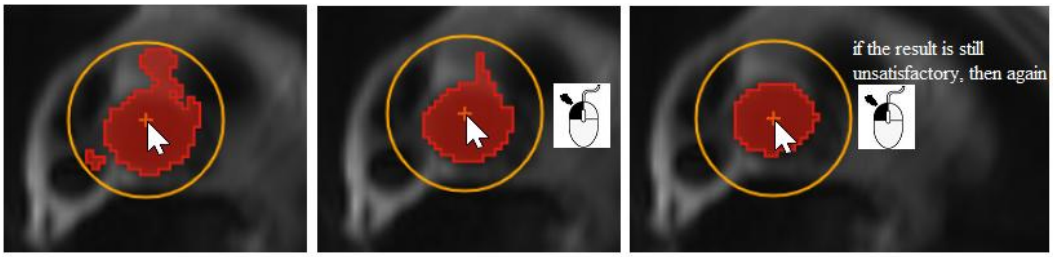


Figure 302. The Smooth Edges

⚠ **NOTE!** The tool does not function when pressing the left button and dragging the cursor without releasing a button.

Parameters: *Radius, Sensitivity, Transparency*.

Parameters of smart tools

The operation of all tools depends on the values of the parameters "Radius" and "Sensitivity". Improved visualization can be achieved by controlling "Transparency".

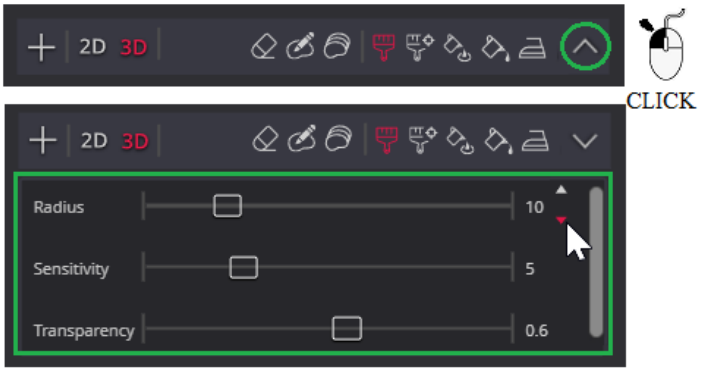


Figure 303. Parameters of tools

⚠ **NOTE**! If you do not see the parameters, then press the expand button right on the panels of tools.

⚠ **NOTE**! When editing multiple segments at the same time, you can set different parameters for each of them.

Radius

By increasing the operating **radius**, the segmentation algorithm processes a large amount of data, resulting in a larger volume/area segmentation. Reducing the radius also reduces the amount of data processed, but the user can target the tool more accurately.

Radius can be changed:

a) by pressing ALT and rotating the mouse wheel: rotating forward will increase the radius, back - will be smaller;

b) in the tool parameter area changing the value by scrolling with the mouse;

c) by increasing/decreasing the value with the arrows  (the arrows become visible when you move the cursor to the right of the numeric values).

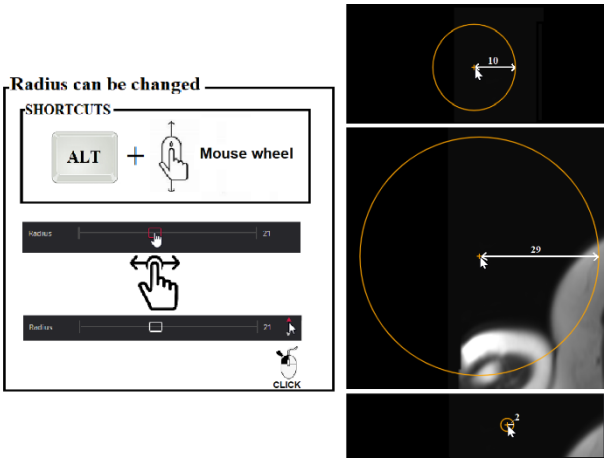


Figure 304. Radius

d) Other shortcuts, if such were assigned by the administrator or user; you can find out the values by choosing  .

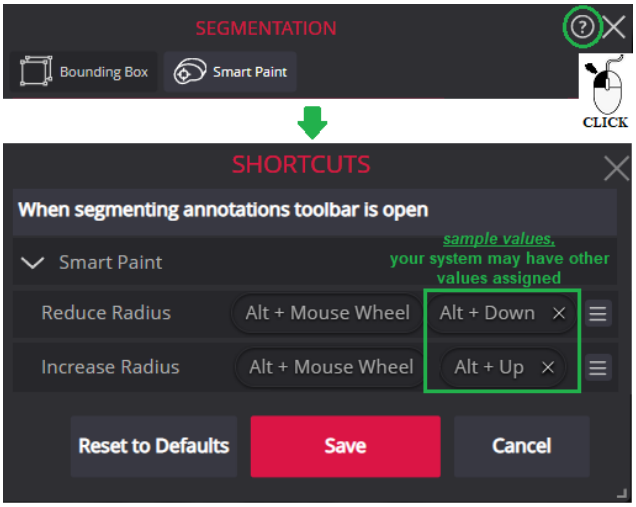


Figure 305. Changing radius with assigned shortcut

Sensitivity

The **sensitivity** parameter for the operation algorithm indicates how much the analyzed volume/area element must be “similar” to the center or reference point. If the parameter value is high, only practically overlapping elements are segmented in the result, and if reduced to 0, all volume/area elements will be colored, even if they are not similar.

When you change the sensitivity parameter, a second circle is visually displayed in the cursor circle. The smaller the inner radius of the inner circle, the higher the sensitivity. When the minimum or maximum sensitivity value is reached, one circle is visually visible.

Sensitivity can be changed:

a) by pressing Shift and rotating the mouse wheel: rotating forward will increase the sensitivity, back - will be smaller;

b) In the tool parameter area changing the value by scrolling with the mouse;

c) By increasing/decreasing the value with the arrows  (the arrows become visible when you move the cursor to the right of the numeric values).

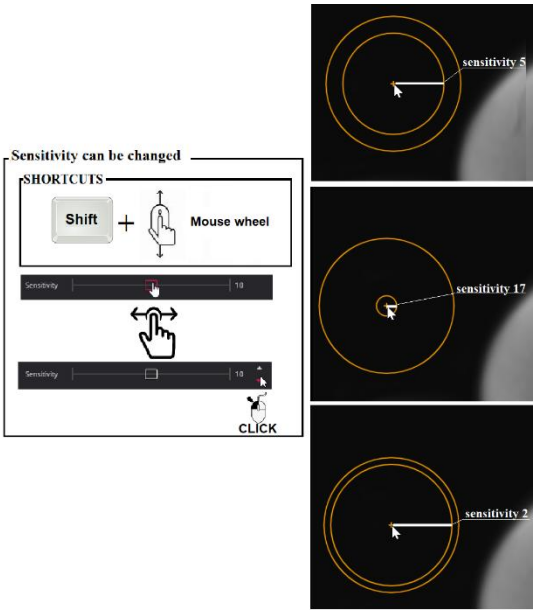


Figure 306. Sensitivity

d) Other shortcuts, if such were assigned by the administrator or user; you can find out the values by choosing  .

Transparency

Controls the transparency of the segmentation fill color. If it is difficult to see the edges of the organ through the paint layer, you can change the color transparency:

a) Fully transparent **ALT + H**;

b) In the tool parameter area by changing the value by scrolling with the mouse;

c) By increasing/decreasing the value with the arrows  (the arrows become visible when you move the cursor to the right of the numeric values).

Reducing the transparency of segmentation color is useful for judging the correctness of current segmentation.

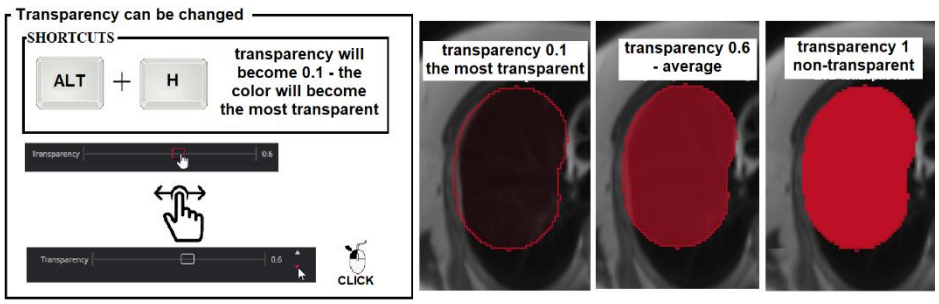


Figure 307. Transparency

Contour drawing with the smart tools

The **contour** of the segmented area is always highlighted. When a new fill color or color deletion iteration is performed, the area processed during the operation is temporarily highlighted by a separate outline. Releasing

the left mouse button updates the outline of the segmented area: either the previous and new action outlines are merged or remove a colorless outline.

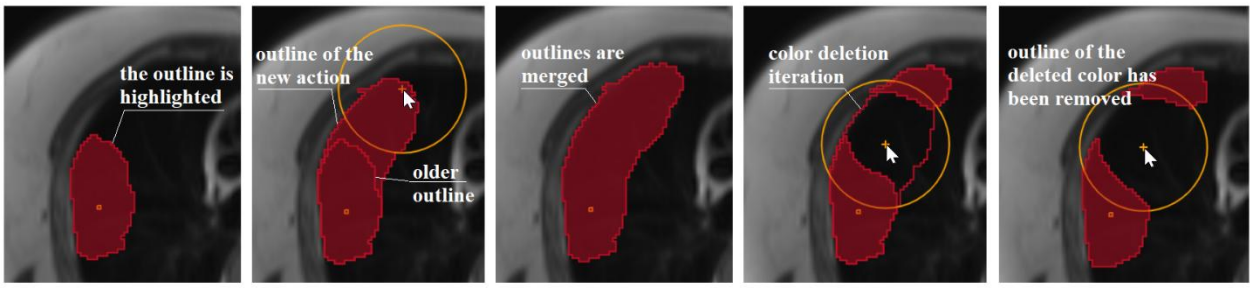


Figure 308. The outline of the segmented area

Edit Smart Paint

⚠ **NOTE!** The saved Smart Paint is linked to the original series where the segment is created. Editing is allowed **only in the original series**. The saved segment is linked to the original series in which it was created. The segment is visible in overlapping series and MPR reconstructions.

⚠ **NOTE!** Visibility in MPR reconstructions may be limited by the condition that the action window must be open. Please contact your system administrator.

To work with an existing **Smart Paint** segment, activate it by clicking:

1) edit segment icon on the row;
2) or first mark the row then press the edit segment icon in the tools bar at the bottom of the Segmentation window;
3) or press on the keyboard “Alt + E” or click icon , the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and edit icon are highlighted .

If a prohibition sign is displayed when the cursor is placed or a prohibition sign is displayed when the cursor is placed , when activate "**Point-and-click**" mode, it means that the active series is not the original series, it is not the series in which the segment was created; first press and go to the original series.

The segmentation name Bounding box 1 and color can be changed without editing mode.

It is possible actions before or after editing: to move the segment to the background , duplicate , delete , and undo the last action . When you have finished editing, select **Save** .

Also are possibilities to view measures , hide/show one or all segments , and hover to select or open the image with selected segmentation .

These actions are common to Segmentations and Annotations are described in separate sections below.

Recommendations

There are no general recommendations on how to segment an organ/area as the result is highly dependent on e.g. the user experience and skills, image quality, resolution and size of the area to be segmented.

To start segmenting move the cursor to the center of the region of interest and select  . Start segmenting by left-clicking and dragging in the image, similar to how a brush is used.

If there is a lot of noise in the image, it is recommended to use the  .

Large areas can be segmented starting at the edges using or  , or  , and the inner area can be filled with the tool  .

Small areas can be segmented to cover the entire area and select a tool  , then the result will be obtained with a single click.

If the paint covers an area that the user did not intend to segment, the paint can be removed with Alt + any of  tools and repeat the action as painted.

When you reach the desired result in the image, move to the next image in the series.

If the shape of the organ is very irregular, you can switch to the 2D mode. This mode is also useful when you want to adjust the segmentation of only one image in a series.

At the end of segmentation, if the result has sharp corners, it can be smoothed using  .

The resulting 3D Smart Paint segmentation result can be seen in three orthogonal views.

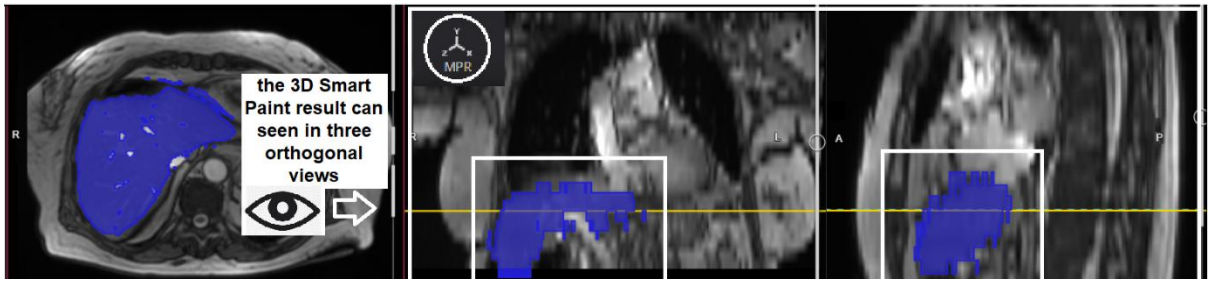


Figure 309. Smart Paint results in three orthogonal views

Annotations

The annotation tab provides tools to mark an area of interest, draw a line, polyline, curve, or mark a point. All these objects are saved in an **RTSTRUCT** file, just like the segmentation contours.

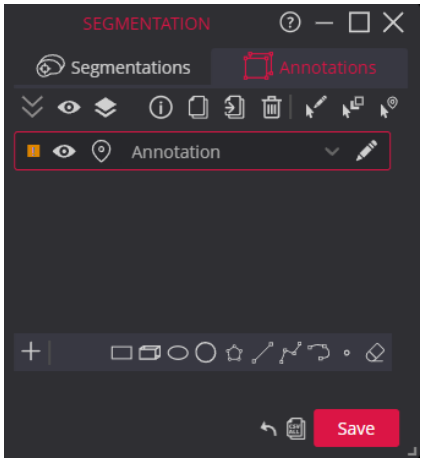


Figure 310. Segmentation: Annotation Tab

To create an annotation, select the corresponding button 

on the left side of the window.

Choose the desired annotation tool  . When a tool is selected, it is highlighted  .

⚠ **NOTE!** Annotations can be saved as a group: for example, a single entry can contain a rectangle, circle, curve, and point, all sharing one name and one color. If you want each annotation to have a separate entry with its own name, color, and navigation function, click the "+" button for each annotation.

Bounding Box



The **Bounding Box** tool allows you to mark an area of interest by drawing a bounding rectangle. A **2D Bounding Box** can be used to mark a rectangular area on a single image. A **3D Bounding Box** can be used to mark a three-dimensional area across a series of images.

Create a new Bounding Box

2D Bounding Box

To **create** a new 2D bounding box segment:

- Open the image, in which you are going to mark the region.
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **New 2D Bounding Box** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the 2D Bounding Box segment will be part of the group, there is no need to click the **New** button  ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer at the center of the area of interest. There are two drawing methods:
  - Place the mouse pointer at the desired location and click the left mouse button (do not hold it down). Drag the mouse pointer, which will "snap" to the contour, until the shape reaches the desired size. Click the left mouse button again to complete the drawing of the shape.

- Click and hold the left mouse button, then drag the mouse pointer until the shape reaches the desired size. Release the left mouse button.

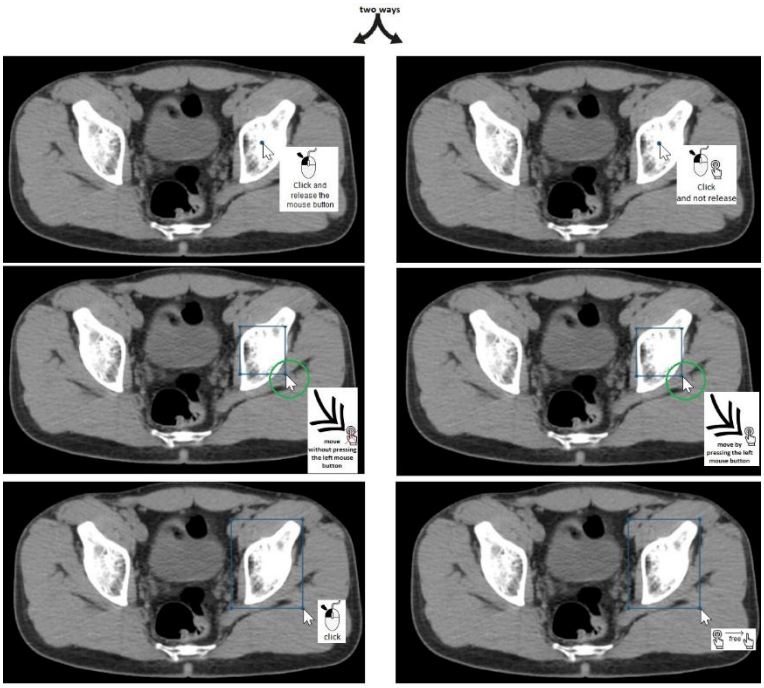


Figure 311. Creating a new 2D Bounding Box

3D Bounding Box

To mark the volumetric region using the 3D **Bounding Box** tool, it is recommended to have the intersecting original or reconstructed series displayed in the viewports of the Viewer window for locating the region of interest:

- Select the orthogonal reconstructions from the MPR tool menu, if MPR reconstructions have not yet been developed.
- Adjust the Viewer layout and open the intersecting series in the viewports.
- Use reference lines or crosshair tools to locate the region of interest in the intersecting series.

⚠ **NOTE! 3D Bounding Box** segmentation does not work with MG and DX. There should be more than two images in the series.

To **create** a new 3D **Bounding Box** segment:

- Open the series in which you want to segment a region. Navigate to the desired image and place the crosshair at the center of the area of interest. The system will automatically expand the box on both sides from the current image.
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **New 3D Bounding Box** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the 3D Bounding Box segment will be part of the group, there is no need to click the **New** button  ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Draw a **3D Bounding Box** by placing the mouse pointer at the center of the area of interest. You can create the shape either by clicking the left mouse button once, dragging the pointer, and clicking again

to finish, or by clicking and holding the left mouse button, dragging the pointer to the desired size, and then releasing the button.

- The system creates a **3D Bounding Box** based on the drawn rectangle. The 3D Frame extends perpendicularly in both directions from the current image, and its width is calculated by dividing the perimeter of the rectangle by 4.
- The 3D Bounding Box and image plane intersection contours are displayed on all the images in the original or reconstructed series that intersect the 3D Bounding Box.

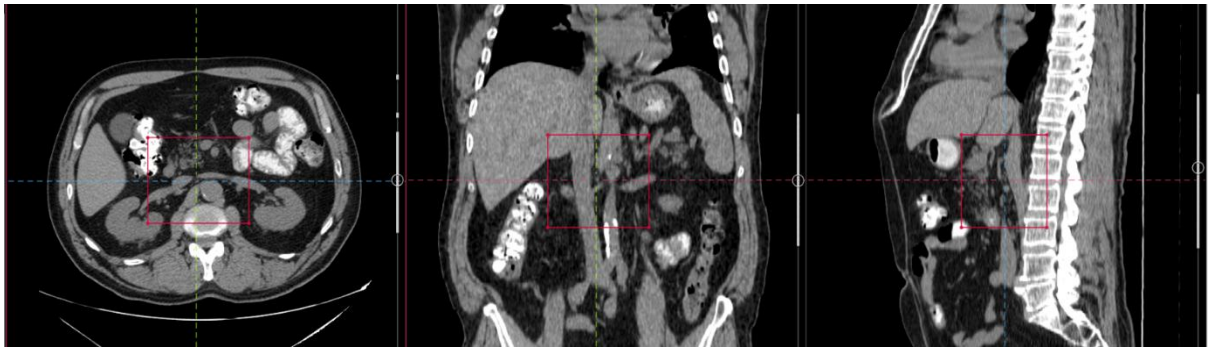


Figure 312. 3D Bounding Box

⚠ **NOTE!** The saved 3D **Bounding Box** is linked to the images of the original series on which the 3D **Bounding Box** segment is created. If the 3D B**ounding Box** is created in the reconstructed series, the original series, that was used to create the reconstructed series, is used.

Edit Bounding Box

Activating editing mode

To work with an existing 2D/3D **Bounding Box** segment activate it by clicking

1) edit segment icon on the row;
2) or press on the keyboard “Alt + E” or click icon, the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and edit icon are highlighted .

When done with Bounding Box editing, press the active edit icon once more to stop the editing. The icon highlighting is switched off .

⚠ **NOTE.** The **Bounding Box** is linked to the original series; however, it is possible to edit the segment in all related images where it is displayed, including all intersecting original and reconstructed images.

The segmentation name and color can be changed without editing mode.

It is possible actions before or after editing: to move the segment to the background , duplicate , delete , and undo the last action . When you have finished editing, select **Save** .

Also are possibilities to view measures , hide/show one or all segments , and hover to select or open the image with selected segmentation .

These actions are common to Bounding Box and Smart Paint segmentation and are described in separate sections below.

Position change

To move the **Bounding Box**, hover the mouse cursor over the center of the rectangle until the light blue circle appears indicating that the segment is selected, then press the left mouse button, drag the box to the desired position, and release the mouse button.

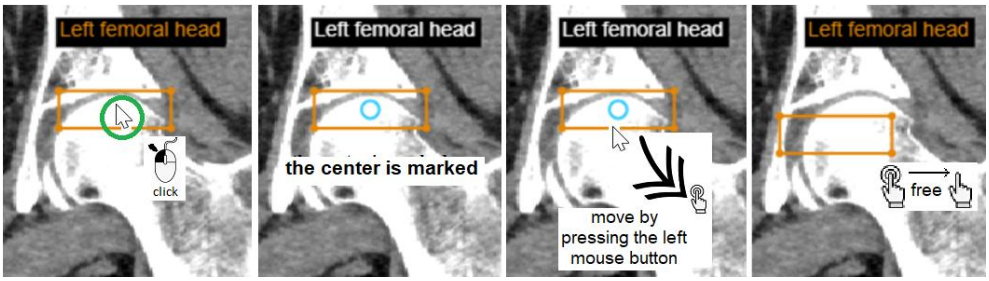


Figure 313. The Bounding Box moved to the center of the femoral head

Resize the Bounding Box

The **Bounding Box** may be resized by dragging the corner of the box, or by dragging the edge of the box. To resize the **Bounding Box**, hover the mouse cursor over the corner or the edge until the object is marked, then press the left mouse button, and, holding the button pressed, drag the corner or the edge. Release the mouse button when the box reaches the desired size.

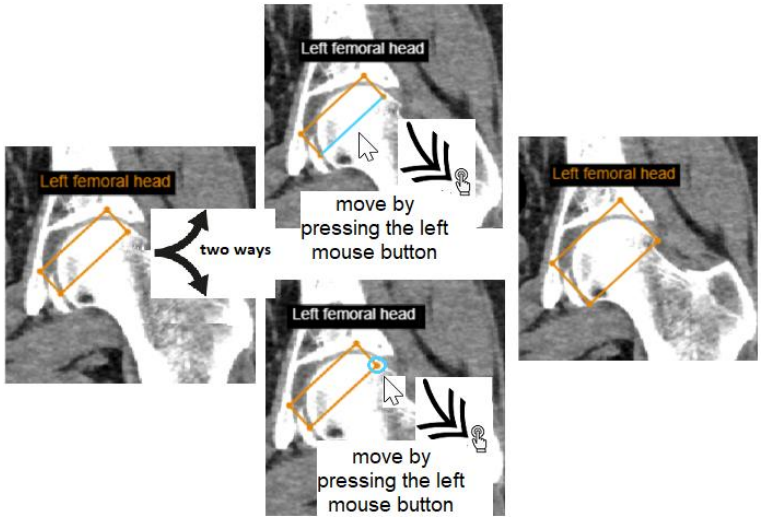


Figure 314. The Bounding Box is resized to fit the femoral head

Rotate the Bounding Box

To rotate the **Bounding Box**, hover the mouse cursor over the corner of the rectangle until the corner is marked, then press the ALT key and the left mouse button, and, holding the keys pressed, drag the corner. Release the mouse button when the box is rotated to the desired position.

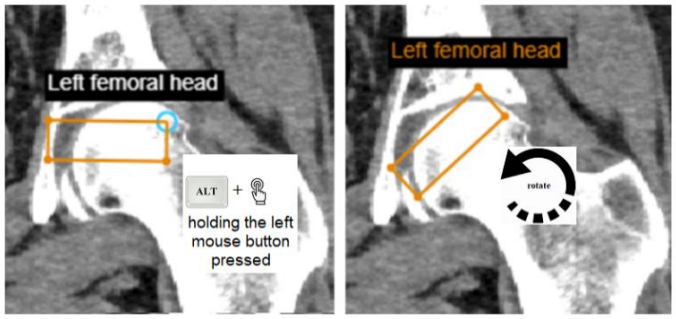


Figure 315. The Bounding Box rotated to better match the femoral head

⚠ **NOTE!** You can edit the 3D **Bounding Box** on any image in the original or reconstructed series, that intersects the box and has the tetragonal intersection contour. The changes apply to the whole box and all the contours of the 3D **Bounding Box** on the other images are automatically updated.

⚠ **NOTE!** The shape of the image and 3D **Bounding Box** intersection contour may vary from triangle to hexagon if a 3D **Bounding Box** is rotated in more than one plane.

⚠ **NOTE!** The 3D **Bounding Box** editing actions (move, rotate, resize) are not allowed in have other than tetragonal intersection contours.

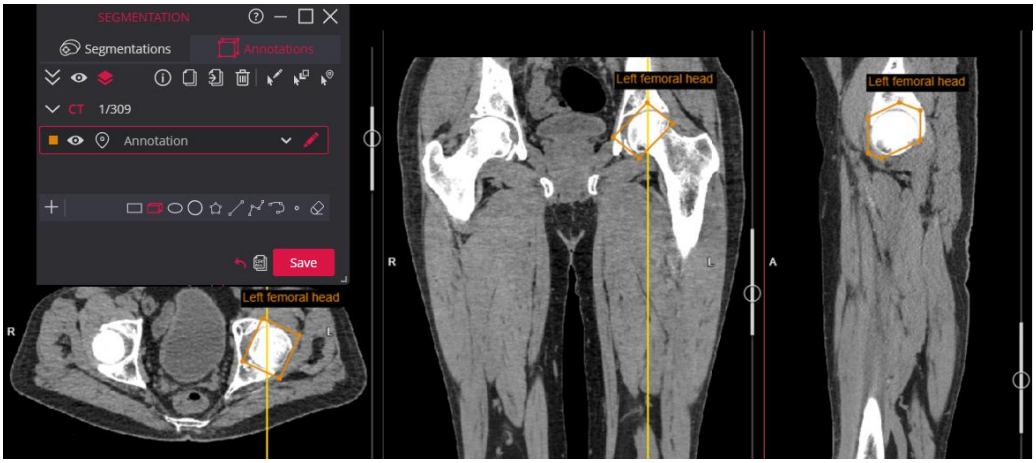


Figure 316. Rotated Bounding Box

Ellipse



The tool allows you to mark an area of interest by drawing a bounding ellipse.

Create a New Ellipse

To create a new Ellipse annotation:

- Open the image in which you want to mark the region;
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **Ellipse** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.

- If the user has already created an annotation and the **Ellipse** segment will be part of the group, there is no need to click the **New** button ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer at the center of the area of interest. You can draw the shape either by clicking the left mouse button once, dragging the pointer, and clicking again to finish, or by clicking and holding the left mouse button, dragging the pointer to the desired size, and then releasing the button.

Edit Ellipse

Activate Edit Mode

To edit an existing Ellipse annotation, activate it by clicking:

1) edit segment icon on the row;

2) or press on the keyboard “Alt + E” or click icon , the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and the edit icon become highlighted .

Position change

To move an Ellipse, place the mouse pointer over the center of the rectangle until a light blue circle appears, indicating that the segment is selected. Then click the left mouse button, drag the box to the desired position, and release the mouse button.

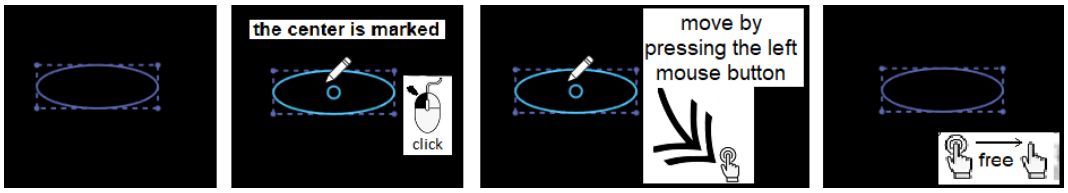


Figure 317. Move Ellipse

Resize

You can resize an Ellipse by dragging the corners or edges of the bounding rectangle. Place the mouse pointer over a corner or edge until the object is highlighted, then click and hold the left mouse button while dragging the corner or edge. Release the mouse button when the box reaches the desired size.

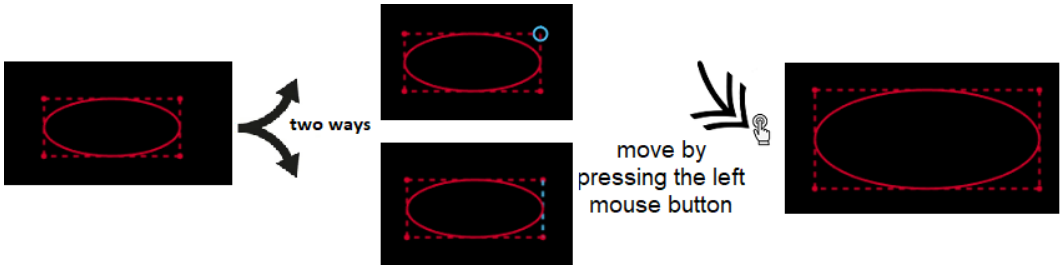


Figure 318. Resize Ellipse

Rotate Ellipse

To rotate an Ellipse, place the mouse pointer over a corner of the bounding rectangle until the corner is highlighted. Then press the **ALT** key and the left mouse button, and while holding both, drag the corner. Release the mouse button when the box is rotated to the desired position.

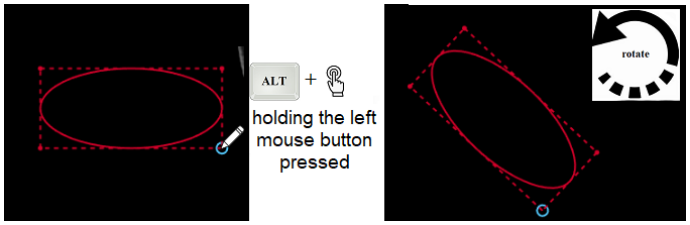


Figure 319. Rotate Ellipse

After finishing the edits, click the active edit icon again to exit edit mode. The icon highlighting will be turned off .

Circle

The tool allows you to mark an area of interest by drawing a bounding circle.

Creating a New Circle
To create a new Circle annotation:

- Open the image in which you want to mark the region;
- To create an annotation as a separate entry (or if it is the first annotation), click and the **Circle** icon in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the **Circle** segment will be part of the group, there is no need to click the **New** button ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer at the center of the area of interest. You can draw the shape by clicking and holding the left mouse button, dragging to the desired size, and then releasing the button.

Edit Circle

Activate Edit Mode

To edit an existing Circle annotation, activate it by clicking:

1) edit segment icon on the row;
2) or press on the keyboard “Alt + E” or click icon , the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and the edit icon become highlighted .

Position change
To move a Circle, place the mouse pointer over the center until a light blue inner circle appears, indicating that the segment is selected. Then click the left mouse button, drag the box to the desired position, and release the mouse button.

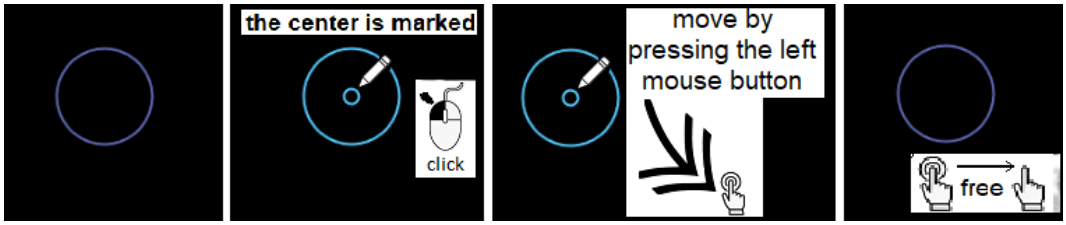


Figure 320. Move the Circle

Resize the Circle

You can resize a **Circle** by dragging its contour. Place the mouse pointer over the contour until the object is highlighted, then click and hold the left mouse button while dragging the contour. Release the mouse button when the circle reaches the desired size.

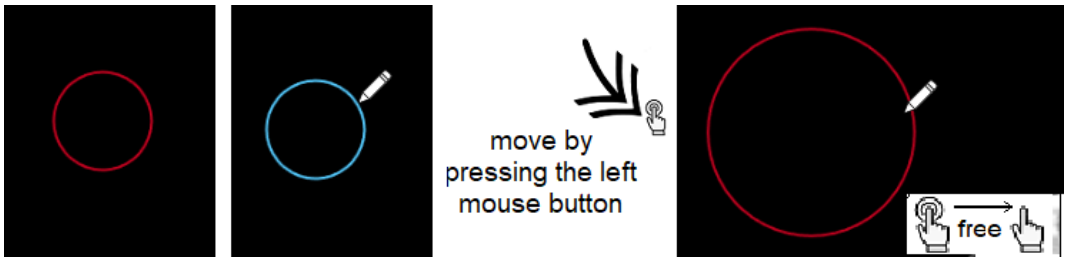


Figure 321. Resize the Circle

Polygon

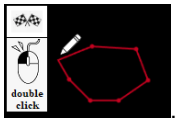


The Polygon annotation allows you to mark an area of interest by placing points, which the system connects with straight lines to form a closed contour.

Creating a New Polygon

To create a new Polygon annotation:

- Open the image in which you want to mark the region.
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **Polygon** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the **Polygon** segment will be part of the group, there is no need to click the **New** button  ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer on a point of the area of interest and click the left mouse button. The system displays the first point  . Move the mouse pointer to another location within the area and click the left mouse button again. The system connects the two points with a straight line  . As you continue moving the mouse pointer, a line is displayed connecting the first and the last points  . When you reach the next edge of the area of interest, click the left mouse button. Continue this process until you

have marked the entire contour of the area with points. Complete the polygon by double-clicking the left mouse button 

.

Edit Polygon

Activate Edit Mode

To edit an existing Polygon annotation, activate it by clicking:

1) edit segment icon on the row;

2) or press on the keyboard “Alt + E” or click icon , the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and the edit icon become highlighted .

Position change

To move the **Polygon**, hover the mouse cursor over any edge of the polygon until the outline turns light blue, then press the left mouse button, drag the polygon to the desired position, and release the mouse button.

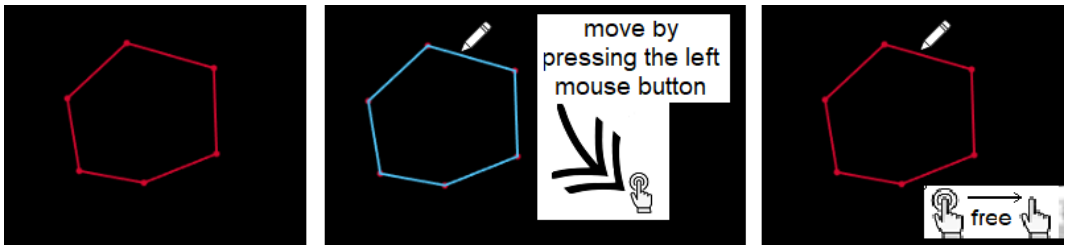


Figure 322. Move the Polygon

Changing point positions

To move a **Polygon** point, hover the mouse pointer over the point until a light blue outer circle appears around it, then press the left mouse button, drag the point to the desired position, and release the mouse button.

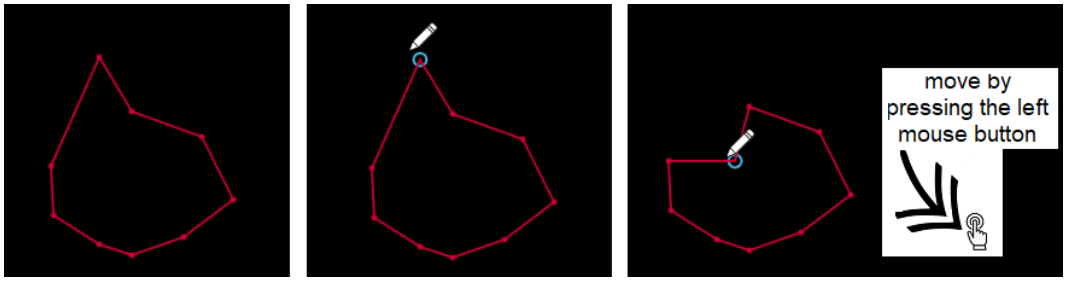


Figure 323. Polygon point position change

Adding an extra point to the polygon outline

To add an extra point to the **Polygon** outline, press ALT — a plus sign will appear next to the cursor . Move the cursor over the polygon edge where you want to insert the additional point, then click the left mouse button. The system will add a new point on the selected edge.

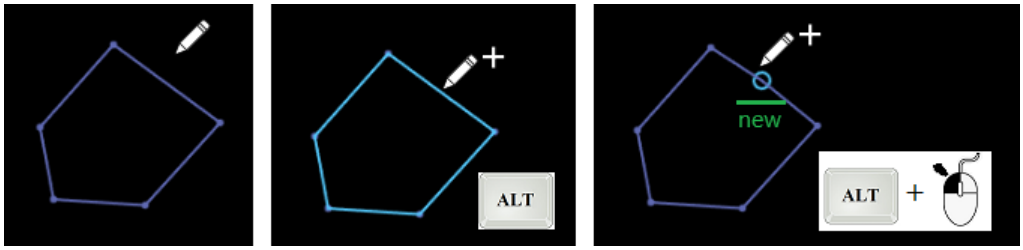


Figure 324. Adding an Additional Point to the Polygon Outline

Deleting Points from an Existing Outline

To delete excess points from a **Polygon** outline, hover the mouse pointer over the point you want to remove until a light blue outer circle appears around it, then double-click the left mouse button.

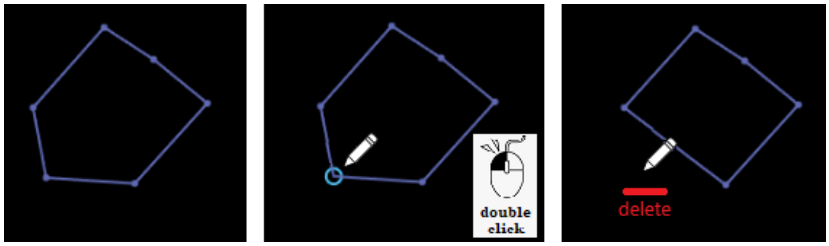


Figure 325. Deleting a Point from a Polygon Outline

Ruler



The user can take a **Ruler** measure and save it in the RTSRTUCT file.

Creating a Ruler

To create a new Ruler annotation:

- Open the image in which you want to mark the region.
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **Ruler** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the **Ruler** segment will be part of the group, there is no need to click the **New** button  ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Once activated, the user must set the start point by clicking the left mouse button, and then click again to set the end point.

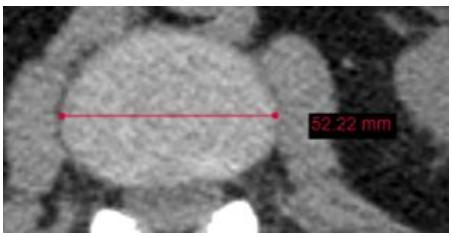
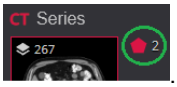


Figure 326. Ruler annotation

Measure the distance between the start and end points. The result is displayed in the viewport and can be seen by selecting .

The Ruler is visible in MPR projections and a related series.

The Ruler can also be created in the MPR projection. When the line has been created in the MPR projection, a segmentation marker is made on the thumbnail bar next to the original series 

.

Edit Ruler

To change a line, activate edit mode . Or press on the keyboard “Alt + E” or click icon , the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

When both points of the line are on the same plane, the start and end points are visible  . In this case, the whole line can be moved to another location.

Start and end points can be moved.

If the line crosses a plane, a point is shown at the crossing point. A point which is not at the start or the end but, for example, in the middle  , cannot be moved .

Editing is possible in the original series and in the MPR projection in case the start or end points of the line cross the plane of the MPR projection.

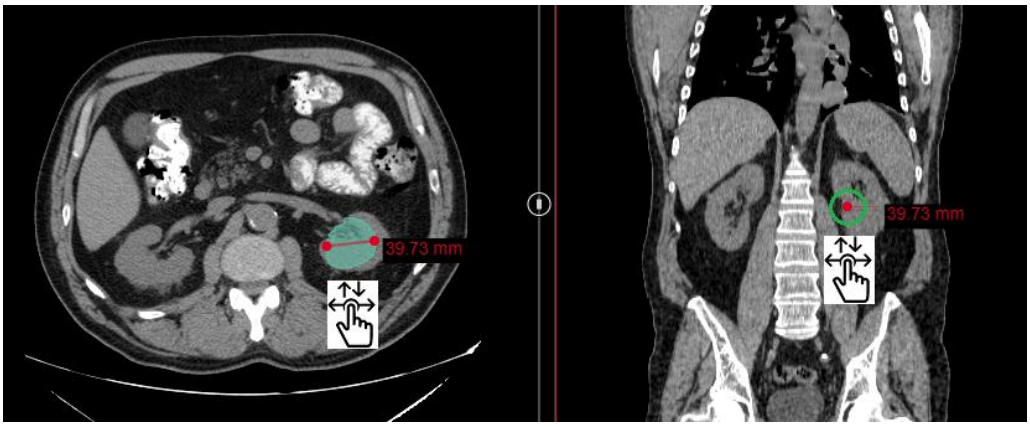


Figure 327. Editing a Ruler

Polyline



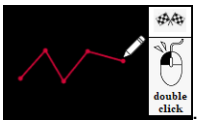
The **Polyline** annotation tool allows you to mark an area of interest with points connected by a series of straight segments, forming an open contour. Only the length is measured; the area is not measured.

Creating a Polyline

To create a new Polyline annotation:

- Open the image in which you want to mark the region.

- To create an annotation as a separate entry (or if it is the first annotation), click and the **Polyline** icon in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the **Polyline** segment will be part of the group, there is no need to click the **New** button; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer on a point of the area of interest and click the left mouse button. The system displays the first point. Move the mouse pointer to another location within the area and click the left mouse button again. The system connects the two points with a straight line. As you continue moving the mouse pointer, a line is displayed connecting the last point to the cursor. When you reach the next location in the area of interest, click the left mouse button. Continue this process until you have marked the entire area with points. Complete the polyline by double-clicking the left mouse button



Edit Polyline

Activate Edit Mode

To edit an existing **Polyline** annotation, activate it by clicking:

1) edit segment icon on the row;

2) or press on the keyboard “Alt + E” or click icon, the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and the edit icon become highlighted.

Position change

To move a **Polyline**, hover the mouse pointer over any connecting line until the shape is highlighted in light blue. Then click the left mouse button, drag the polyline to the desired position, and release the mouse button.

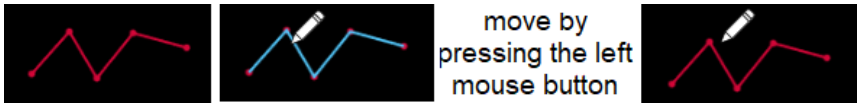


Figure 328. Polyline Position Change

Changing Point Positions

To move a **Polyline** point, hover the mouse pointer over the point until a light blue outer circle appears around it. Then click the left mouse button, drag the point to the desired position, and release the mouse button.

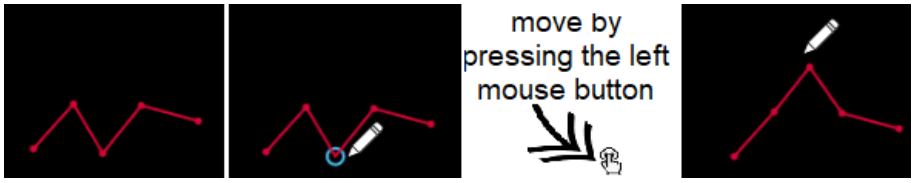


Figure 329. Polyline Point Position Change

Adding an Additional Point

To add an additional point to a **Polyline**, press **ALT** — a plus sign will appear next to the mouse pointer  . Move the pointer over the segment connecting the points where you want to add the new point, then click the left mouse button. The system will insert a new point on the selected segment.



Figure 330. Adding an Additional Point to a Polyline

Deleting Points

To delete excess points from a **Polyline**, hover the mouse pointer over the point you want to remove until a light blue outer circle appears around it, then double-click the left mouse button.

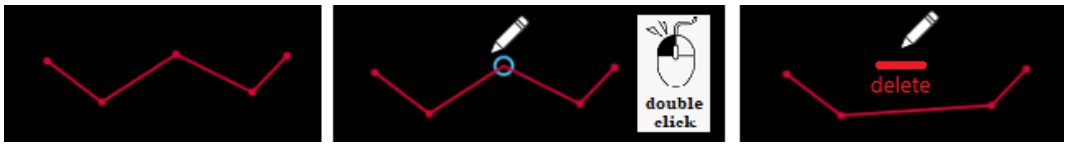


Figure 331. Deleting a Point from a Polyline

Spline



The **Spline** annotation tool allows you to mark an area of interest by placing points connected with a smooth curve. The curve is not closed, so the first and last points are not connected, and the area is not measured.

Creating a Spline
To create a new Spline annotation

- Open the image in which you want to mark the region.
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **Spline** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the **Spline** segment will be part of the group, there is no need to click the **New** button  ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer on a point of the area of interest and click the left mouse button. The system displays the first point  . Move the mouse pointer to another location within the area and click the left mouse button again. The system connects the two points with a straight line  , which will later be curved according to the next point's position. As you continue moving the mouse pointer, a curve is displayed connecting the last point to the cursor  , and the previous line/curve is also adjusted according to the cursor position. When you reach the next location in the area of interest, click the left mouse button. Continue this process until you have marked the entire area with points. Complete the spline by double-clicking the left mouse button 

.

Edit Spline

Activate Edit Mode

To edit an existing **Spline** annotation, activate it by clicking:

1) edit segment icon on the row;

2) or press on the keyboard “Alt + E” or click icon , the cursor icon changes from to in the viewport, hover over the segment you want to edit, the outline becomes highlighted, click the left mouse button.

The active row and the edit icon become highlighted .

Position change

To move a **Spline**, hover the mouse pointer over any connecting curve until the entire curve is highlighted in light blue. Then click the left mouse button, drag it to the desired position, and release the mouse button.

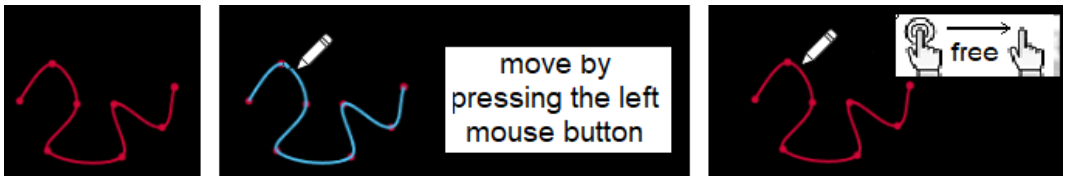


Figure 332. Spline Position Change

Changing Point Positions

To move a **Spline** point, hover the mouse pointer over the point until a light blue outer circle appears around it. Then click the left mouse button, drag the point to the desired position, and release the mouse button.

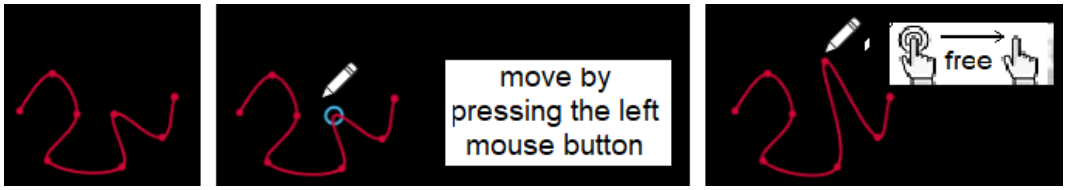


Figure 333. Spline Point Position Change

Adding an Additional Point

To add an additional point to a Spline, press **ALT** — a plus sign will appear next to the mouse pointer . Move the pointer over the curve connecting the points where you want to add the new point, then click the left mouse button. The system will insert a new point on the selected segment.

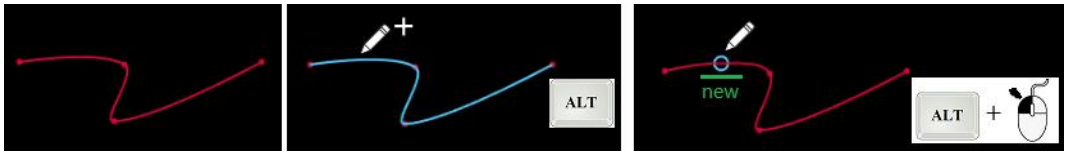


Figure 334. Adding an Additional Point to a Spline

Deleting Points

To delete excess points from a **Spline**, hover the mouse pointer over the point you want to remove until a light blue outer circle appears around it, then double-click the left mouse button.

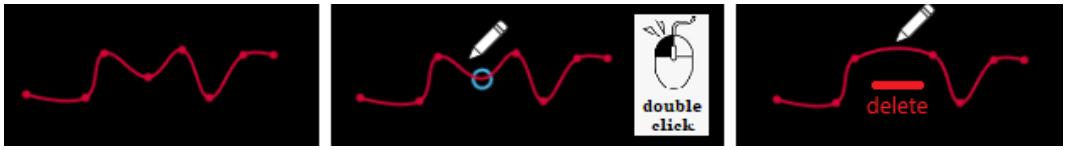


Figure 335. Deleting a Point from a Spline

Point



The **Point** annotation allows you to mark an area of interest with a point. Only the intensity is measured.

Creating a Point
To create a new **Point** annotation

- Open the image in which you want to mark the region.
- To create an annotation as a separate entry (or if it is the first annotation), click  and the **Point** icon  in the toolbar on the left. The system adds a new entry in the **Annotations** segmentation tab, assigning a default name and color.
- If the user has already created an annotation and the **Point** segment will be part of the group, there is no need to click the **New** button  ; simply select the tool icon.
- The icon is highlighted, and drawing is enabled.
- Place the mouse pointer on the point of interest and click the left mouse button.

Edit Point
When the annotation mode is active, the only available action is to move the point. Hover the mouse pointer until the point is highlighted, click and hold the mouse button, drag the point annotation to the desired location, and then release the mouse button.

Annotation Eraser



The Eraser tool is used to delete annotation(s) from a group.

Activate the tool  in the annotation toolbar. The icon will be highlighted  , and a minus sign will appear next to the mouse pointer  .

Hover the cursor over any element of the annotation you want to delete (this can be a point, edge, connecting curve, or midpoint) until it is highlighted. Then click the left mouse button once — the system will delete the entire annotation containing the highlighted element.

After completing the deletion, deactivate the Eraser tool to avoid accidentally removing other annotations.

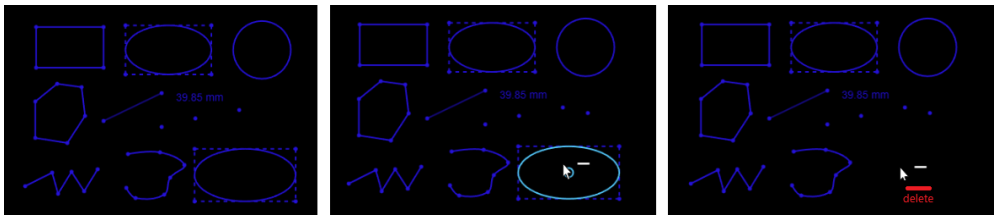


Figure 336. Annotation Eraser

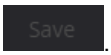
Common actions of segmentations

Most actions work the same in both the Segmentations and Annotations tabs. This chapter describes the common actions.

Save

To **save** the created or edited segments, press the save button 

in the right bottom corner of the Segmentation window. The system converts segments data to RTSTRUCT DICOM format and sends it to PACS.

If successfully saved, the notification is displayed, and the save button becomes inactive 

.

While storage is in progress, actions to create a new segment or modify existing segments are forbidden.



Figure 337. Actions forbidden in save progress

If the saving icon shows an empty segment, indicating that changes have not been saved.

If the user tries to close the segmentation window without saving, a warning message is displayed.

⚠ **NOTE!** Pressing the save button saves the segments of all tabs of the Segmentation window.

⚠ **NOTE!** Segments are saved in RTSTRUCT DICOM format. The function is available only if the used study storage provides DICOM saving functionality.

⚠ **CAUTION!** Until saved, the created, deleted or edited segments are held in program temporary storage and will be lost if closing the Viewer or closing the study, that has segmentations with unsaved changes.

⚠ **NOTE!** A shortcut key combination can be assigned to the save action. More information about shortcut keys is provided in the “System Menu. Shortcut Keys” section.

Change color



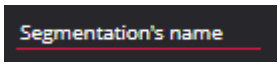
To change the color of the segmentation, hover over the color box and click with the left mouse button. A color selection dialog will open:

- Select the desired color from the color bar
- Adjust the intensity from the intensity selection area above.



Figure 338. Modifying the color of a segmentation

Change name



To change the segment name, hover the mouse cursor over the name and click with the left mouse button.

⚠ **NOTE!** A list of names can be provided via the Communication API. The list is displayed in the order it was received; additional sorting or filtering is not supported (detailed information is available in the technical documentation).

Regardless of the provided name list, the user can manually enter a new value or paste it from the clipboard.

Show/Hide

If viewing or editing segments is difficult due to overlapping contours, use the segment hiding function:

- click the eye icon of the segment whose contours you want to hide;
- the system hides the contours and label of the selected segment. A crossed-out eye icon indicates that the segment contours are hidden.

If there are many segments, you can hide all segments in the tab (except the active one) by selecting the function located at the top of the tab.

Navigate

To quickly navigate to a segmentation then you can select the navigation button . When selected, the system will move to the center of mass of segmentation in series with the contour of this segment.

If segmented in another study or in a series that is not open, the system will automatically open the required one.

⚠ **NOTE!** If more than one series is open in the viewport, the system navigates through all related series. **Exception,** if several images of the same series are open in the viewport, then the system navigates only in one.

When a segmentation item is selected in the list, the segmentation icon is highlighted in the thumbnail bar next to the series where the segmentation was created. If the series is not visible, the system automatically scrolls the thumbnail bar until the series becomes visible.

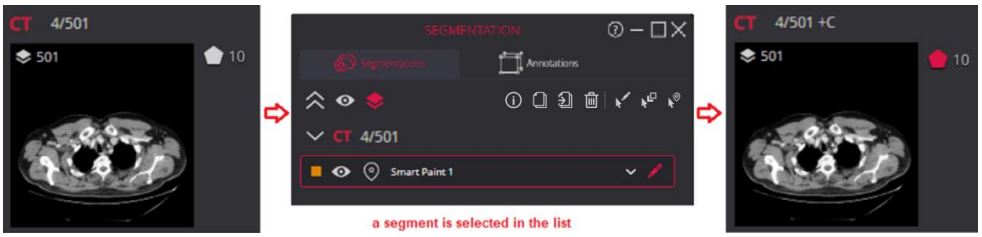


Figure 339. Highlighting a segment icon in the thumbnail bar

The segmented location/organ can be found manually:

- Open the series in the viewport and preload the series data , if not preloaded automatically. When series data is preloaded, the marks on the scrollbar indicate the place of images with segment contours. If there are more segments, you will see more highlighted areas in the scrollbars.
- Press the mark on the scrollbar to navigate to the image. The image is displayed in the viewport, and the segment contours are displayed on the image.
- Use the mouse wheel to scroll to the image one by one and see the segments on nearby images.

⚠ **NOTE!** If Crosshair has been switched on , Crosshair is automatically switched off when a navigation action is selected in the segmentation dialogue. If the user needs to use Crosshair in further actions, the user has to switch it on again in the menu toolbar.

Measurements

The system provides the possibility to measure the area, volume, and pixel intensity statistics for a chosen segment. The measurement values are calculated for the whole segment and per image. The user can view the segment measurements or copy the measurements to the clipboard.

The Sum, Mean, SD, Min, Max, Count, and Volume for each segment is calculated. To view the measurements, select the information icon in the upper right corner of the window  .

The system calculates the area, the number of volume units, for each image in the series that contains the segmented area or volume.

For example, if the segmentation is in five images in a series, the information groups will be 5, the first number “Index” indicating the sequence number of the image in the series.

To collapse the info card, press the icon  again.

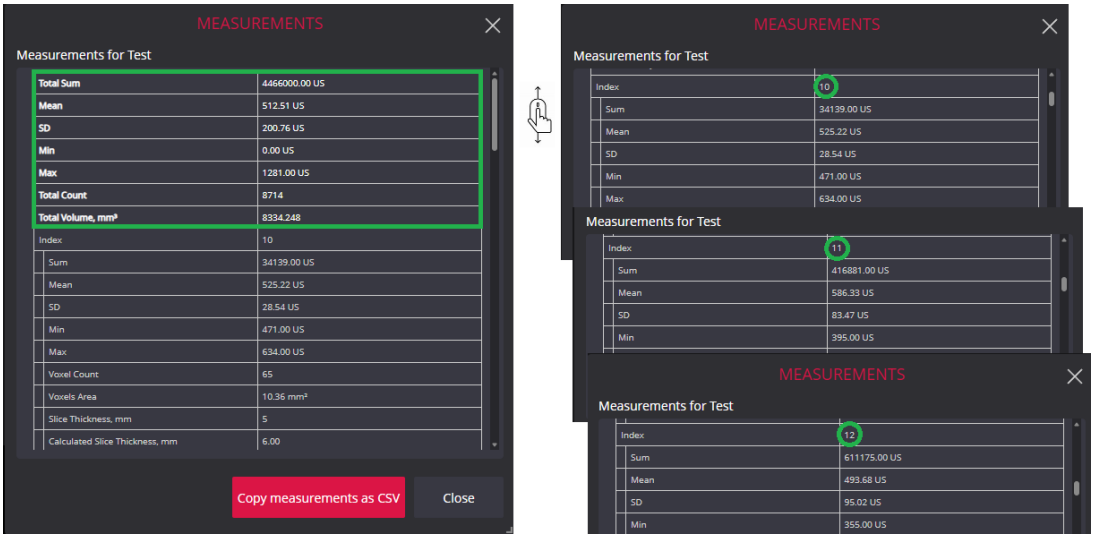


Figure 340. Measurements information for each image

To copy the measured values to the clipboard, press the button Copy measurements as CSV.

To copy the measured values of all segments that are currently displayed in all tabs of the Segmentation window, press the Copy measurements as CSV icon  , which is displayed in the bottom right corner of the Segmentation window. The system calculates the values for all segments and copies the values to the clipboard.

The CSV file headers are fixed and always visible, even if the corresponding segmentation or annotation object does not exist. For example, the “Spline” column will appear even when no such object was created. The CSV file entries are filled in according to the increasing image order: segmentation data is listed first, followed by annotation data.

Type	Label														
			Total Sum	Mean	SD	Min	Max	Total Count	Voxels Volume, mm³						
Image UID	Index	Slice Thickness, mm	Calculated Slice Thickness, mm	Voxel Width, mm	Voxel height, mm	Voxel Count	Min	Max	Mean	SD	Units	Sum	Area	Area Units	Voxels Volume, mm³
	Point	Center	Sum	Min	Max	Units									
	Ruler	Length	Length Units												
	Polyline	Length	Length Units												
	Spline	Length	Length Units												
	2D Bounding Box	Center	Edges	Sum	Mean	SD	Min	Max	Units	Pixel Count	Area	Area Units			
	Circle	Center		Sum	Mean	SD	Min	Max	Units	Pixel Count	Area	Area Units			
	Ellipse	Center		Sum	Mean	SD	Min	Max	Units	Pixel Count	Area	Area Units			
	Polygon	Center		Sum	Mean	SD	Min	Max	Units	Pixel Count	Area	Area Units			
	3D Bounding Box	Edges	Total Sum	Mean	SD	Min	Max	Total Count	Voxels Volume, mm³						

Figure 341. Segment/Annotation Information in the CSV File

⚠ **NOTE!** The segment is measured, and values are calculated on request and are not saved in DICOM when saving segments.

⚠ **WARNING!** Note, that measuring functions in MedDream is approximate.

The following values are measured and displayed per image, that contains the region of the segment:

- The Slice thickness value from the DICOM file is displayed for the image, if available.
- The Calculated slice thickness is measured based on the position and orientation of the image itself and neighboring images. The value is calculated for parallel slices, and only if the image position and orientation in patient coordinate system data are available in DICOM.

⚠ **NOTE!** The Slice thickness value and Calculated slice thickness measurement are applicable for CT, MR, and PET modalities, and not applicable for MG and DX modality.

⚠ **NOTE!** The Slice thickness value and Calculated slice thickness measurement are applicable for **Free Draw** segments, and not applicable for **Bounding Box** segments.

- Voxel count is the number of voxels that are counted as belonging to a segment on this image. A voxel belongs to the segment if the center of the voxel (pixel in the 2D image) is in the contour or inside the segmented region.
- Intensity values for the voxels that belong to a segment on the image: minimum intensity, maximum intensity, mean intensity, standard deviation, and sum.

⚠ **NOTE!** The radiodensity in Hounsfield units (HU) is calculated for images of CT modality. The Body Weight standard uptake value (SUVBW) in g/ml is calculated for images of PT modality. For other modalities, or in case the data required for HU or SUVBW calculation is not available in the DICOM file, the pixel intensity values are used.

- Voxels area is calculated by multiplying the row spacing, the column spacing, and the voxel count. The value is calculated only if the pixel spacing information is available in the DICOM file.

⚠ **NOTE!** Voxels' area may not be equal to the geometric area inside the contours of the segment.

- Voxel volume is calculated by multiplying the voxels area and calculated slice thickness if these were measured.

⚠ **NOTE!** The Voxel volume measurement is applicable for **Free Draw** segments, and not applicable for **Bounding Box** segments.

If total segment measurement values are calculated, they are shown in bold at the top of the measurement window:

- **Total Sum** - the sum of the values of all pixels belonging to the segmentation (calculated over all images);
- **Mean** - the Total Sum divided by the Total Count;
- **SD** - deviation calculated

$$\sqrt{\frac{1}{N}\sum_{i=1}^{N}(pixel\ value - \mathbf{Mean})^2}$$

*where N – **Total Count***

- **Min** is the smallest value of all pixels in the segment (counted over all images);
- **Max** - the maximum value of all pixels in the segment (calculated over all images);
- **Total Count** - the total number of pixels in a segment (counted over all images);
- **Total Volume**:
  - The total volume for the **Free Draw** segment is calculated as the sum of the volume of the voxel per each image that contains the regions of this segment.
  - The total volume of the 3D **Bounding Box** segment is calculated as the geometric volume of a 3D cube, by calculating the length of the three cube edges (length, width, and height) from the coordinates of the corner points in the patient coordinates system, and then multiplying these lengths.

⚠ **NOTE!** The total volume measurement is not applicable for the 2D **Bounding Box** segment.

⚠ **NOTE!** The volume is not measured, if the data, that is required for calculations, is not available in the DICOM files.

⚠ **NOTE!** The 3D **Bounding Box** measurement values are always calculated for the referred series.

Duplicate

To create a new segmentation as a copy of the existing:

- Open the Segmentation dialog and select the segment from the list that you want to duplicate.
- Press the Duplicate icon  .
- The system creates a copy of the selected segment, assigns a label and a color to it, and displays the contours on the image. The new segment is added to the tab of the Segmentation window.

⚠ **NOTE!** The newly created copy is displayed on the original segment, so the old contours are not visually visible. The system activates the newly created copy for editing.

The Bounding Box segment can change the position: move the mouse cursor to the middle of the segment until a blue circle appears. Click the left mouse button and without releasing bring a copy to the right place.

⚠ **Note.** The Smart Paint segment cannot be moved but can be hidden. After the original segment is changed, this duplicate can be used to evaluate the change.

Copy to another series

Action: copy the segment to another series. Annotations can be copied to a series within the same study or to a different study.

Activate the annotation to be copied and click the action button  .

The system displays a dialog with a list of series, which consists of all open studies. Select the series (or multiple series) to which the annotation is intended to be copied, then click the "Copy" button.

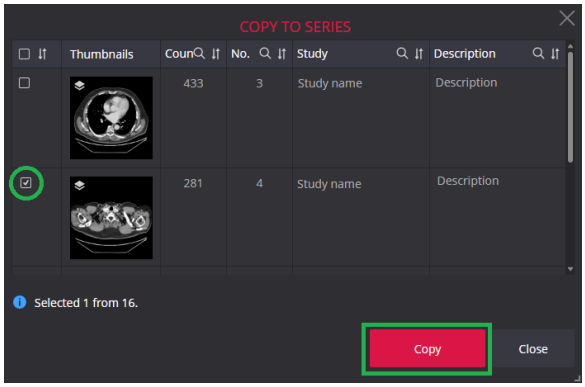


Figure 342. Copy to another series. Series list dialogue

The system creates a copy of the segment in the selected series (or multiple series if more than one is selected) and closes the dialog.

If the series to which the segment is copied is not open in the viewport, it will not be opened automatically.

If the copying operation fails to at least one of the selected series, the system displays an informative error message in the dialog. In this case, the user should select another series and attempt the copying operation again or close the action window.

⚠ **WARNING!** When copying a segment to another study series, the copy operation may fail if the 3D coordinate systems between the studies are completely incompatible.

The risk of a failed operation increases when copying segments between studies from different manufacturers.

⚠ **WARNING!** Copying a segment from one series to another may lead to shape distortion if the series have different distances between images or if they have different orientation parameters. The probability of this increases when the segment area is small.

⚠ **WARNING!** If the localization of a segment does not fully overlap in another series, the segment will be clipped during copying to the next series, which may result in shape distortions.

⚠ **Note!** Copying segments between series is not available for 2D segments, such as those in mammographic studies.

⚠ **Note! Lines** cannot be copied to other series.

⚠ **Note!** The system does not allow the copying of a segment that has no data (e.g., a newly created annotation without any content).

⚠ **Note! Undo the last action** does not reverse the copy action.

Delete

To delete a segment: select the entire row and click the icon .

The system will ask you to confirm the delete action and will remove the segment contours from all images and the row from the list.

⚠ **Note.** The delete action cannot be undone.

Grouping

The information in the actions window will be automatically grouped by study if more than one study is open and there is more than one segment. The header displays the patient's name and the date of the study.

The user can indicate that he/she wants additional grouping by series  . When selected, the icon changes to red  and the list records are additionally grouped by series in which they were created, with the series information in the group header.

To view group content, press  . To collapse press  . To expand all groups, press  . To collapse all groups, press  .

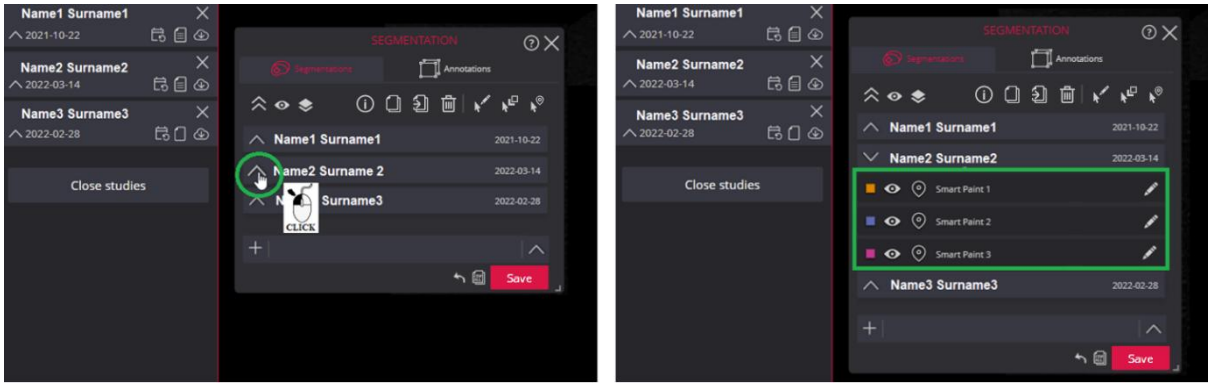


Figure 343. The groups by study

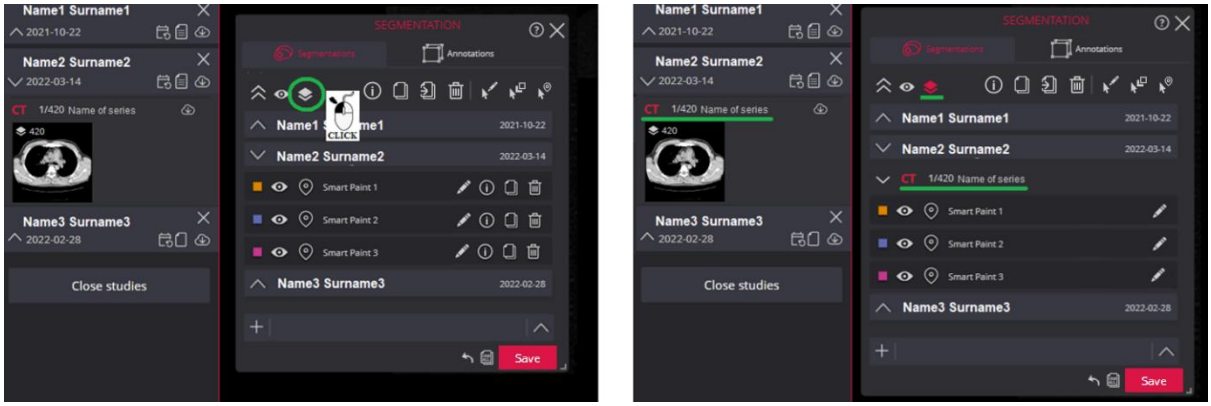


Figure 344. The groups by series

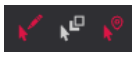
Send to background

If the segment you want to edit is covered by another segment, the interfering segment can be moved to the background:

- press on the keyboard “**Alt + B**” or click icon  ;
- the cursor icon changes from  to  ;
- in the viewport, hover over the segment you want to move to the background;
- the outline becomes highlighted;
- click the left mouse button, the system moves the interfering segment to the background.

Hover to select

The option to enable a mode **Hover to select**  that changes the mouse cursor from  to  , and when hovering over a segment in the viewport, to see the system open the appropriate segmentation tab **Segmentations** or **Annotations** and mark the item in the list on which the cursor was hovering.

This mode can work in combination with **Click to Edit**  or Click to Send to Background  modes. In this case, the system not only marks the item in the list, but also performs the corresponding action.

Can also operate without additional modes  .

Annotation Names in the Viewport

If there is only one annotation in the group, its name is displayed next to the contour.

A single annotation may consist of one or multiple contours created using the same or different tools. If the “+” button is not pressed when creating a new contour, the new contour is assigned to the same annotation.

If there is more than one annotation in the group, the name is displayed only when the  “Hover to select” function is enabled and the mouse cursor is placed over any contour of the group annotation.



Figure 345. Annotation Name Display in the Viewport

⚠ **Note.** The names of segments displayed in the “Segmentations” panel are not shown in the viewing area, even if the segment consists of only one contour.

Undo the last action

The Undo button  is available to all tabs of the Segmentation window.

The system provides the ability to undo one last action. Select  .

After undoing the last action or saving changes the button then becomes inactive  .

Note! Undo the last action does not reverse the copy to another series or delete actions.

Shortcuts, closing, resizing, and moving windows

Users can view segmentation action shortcuts, close the action window by performing actions on any segmentation tab, minimize and resize the window.

Shortcut

To recall the segmentation shortcut combinations, you can find them by selecting the help icon  in the upper right corner of the window.

Close the segmentation window

If you have finished the segmentation actions or do not want to continue it, close the window by pressing  .

If the last segmentation actions performed were not saved, the system will display a message.

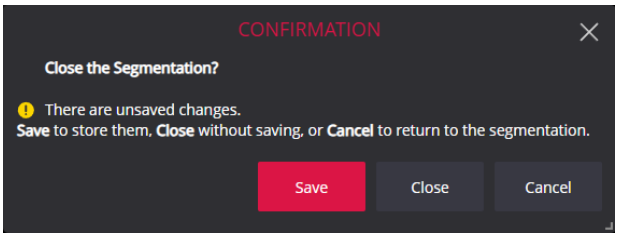
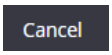
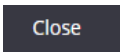


Figure 346. Message attempting to close a window without saving

To keep the action taken, select  . Once you select  option, the message will close and you will return to the action window, where you can choose the Save action.

Note! Then selecting  the window will close without saving changes.

If the changes have been saved, the message is not displayed, and the Save button at the bottom of the window is disabled  .

Resize the window

To reduce or enlarge the window, select the triangle  in the bottom-right corner of the window. The cursor changes to a double-headed arrow. Press and hold the left mouse button, then move the cursor in any direction.

Move the window

If the action window covers the study, you can change its position: hover the mouse cursor over the top area of the window (to the right of the title, on the right side, or directly over the “SEGMENTATION” title) until the cursor changes to a four-directional arrow. Then press and hold the left mouse button and move the cursor in any direction.

Minimize the window

If segmentation actions are temporarily not needed, the window can be minimized by clicking the button  . To restore the previous window size, click the same button again.

CAD marks



CAD marks tool allows viewing the findings, which computer aided detection (CAD) algorithm detected and saved in Mammography CAD SR document. The system provides the user the possibility to show or hide the CAD findings on the mammography images, and also to view findings either as CAD marks, or as detailed regions.

The mammography CAD SR, if available in the study, may be viewed as text SR document, and also as findings rendered on the mammography image. To view the mammography CAD SR findings rendered as marks on the mammography images, the CAD functionality should be enabled for the system, and showing the CAD marks should be switched on in the Viewer window.

⚠ **NOTE!** By default system configuration, the mammography CAD functionality is switched on, and the findings, that are marked as required to present, may be presented for the user.

⚠ **NOTE!** By default Viewer settings, showing of the CAD marks is switched on, and the CAD marks icon is highlighted in the Viewer toolbar 

.

If the CAD algorithm checked the mammographic image and identified potential problem areas, the CAD findings data is displayed on the image and in the viewport labels:

- The CAD label with number of findings in current image and total number of findings in all the mammography CAD SRs of the study is displayed in the bottom left corner of the viewport.
- If current image has findings, the label with numbers of mass and calcification of findings in current image is also displayed in the bottom left corner of the viewport.
- The marks for mass ✱ and calcification ▲ findings are displayed on the image, at the center of the particular finding. If available in the CAD SR, the certainty of the finding, and the number of individual calcifications (applicable for calcification cluster) is displayed in the label below the mark.
- The hint is displayed when mouse cursor is pointed to the mark. The hint contains the information about the applied CAD algorithm and finding details.

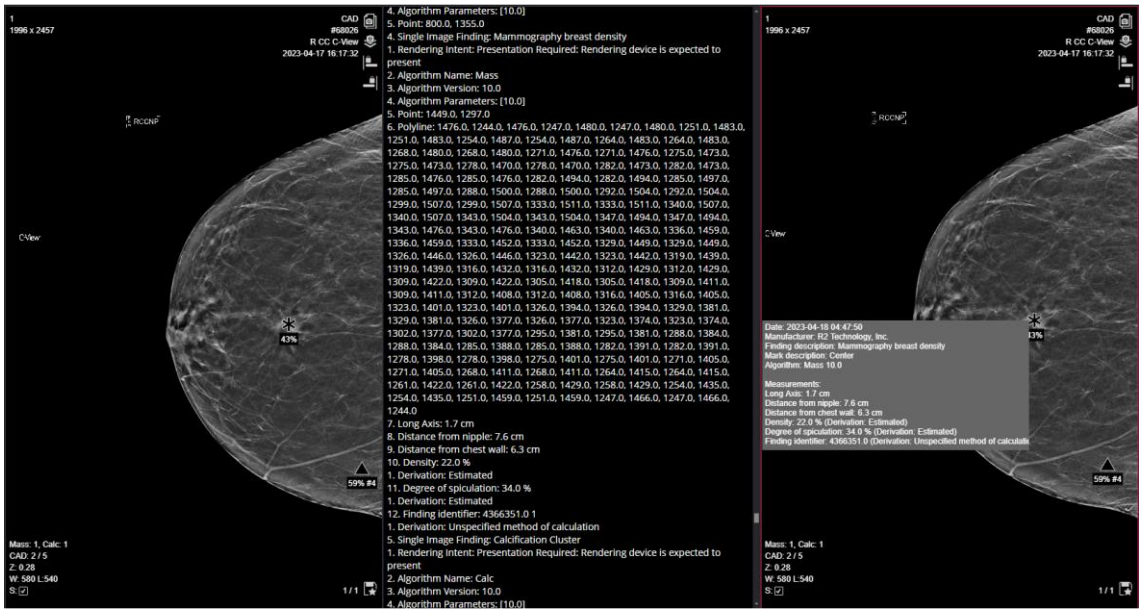


Figure 347. Mammography study having CAD SR with 5 findings in total and 2 findings in currently viewed image

If the multiframe mammography image is viewed, the CAD marks for the whole multiframe image are displayed in the viewport. Marks of the currently viewed frame are brighter and may be distinguished from the grayer marks of the other frames. Clicking on the grayer mark, the system automatically opens the frame in which the mark is found. Note, that the above-described behavior is also applicable when the system is configures to display the mammography multiframe as series of images.

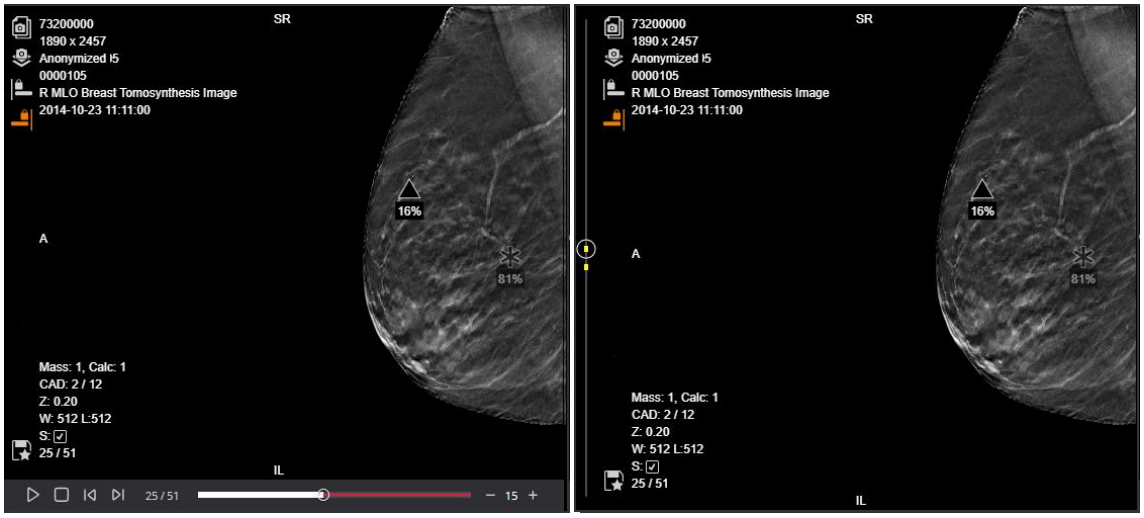


Figure 348. Mammography multiframe image with CAD marks viewed as multiframe image and as series of images

The user can hide the CAD marks by clicking the highlighted CAD tool icon 

in the Viewer toolbar. The system turns the icon highlighting off 

and hides the CAD marks.

The user can select the CAD regions view instead of CAD marks by expanding the CAD marks tool menu and clicking the Show CAD regions option. The system highlights the Show CAD regions option icon 

and displays the findings contour and center point instead of mark symbol on the image:

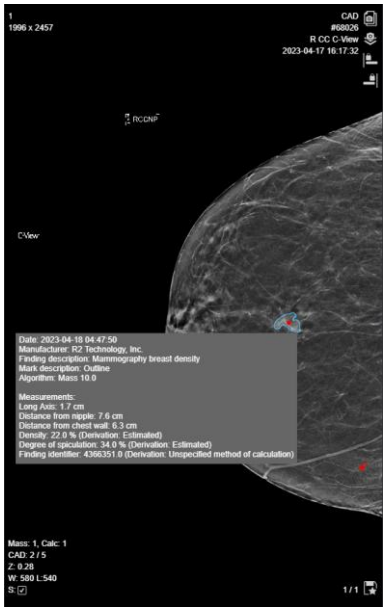
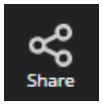


Figure 349. Mammography CAD SR findings viewed as regions

⚠ **NOTE!** To view the CAD SR findings, either as CAD marks, or as CAD regions, the CAD marks tool should be switched on (highlighted) in the Viewer toolbar.

Tools for study exchange

Share files via DICOM Library



Share via DICOM Library tool is used to send files to DICOM Library.

⚠ **NOTE!** DICOM Library is an external service. MedDream product includes the integration functionality only. **The actual service is provided under MedDream SLA (Service Level Agreement), for educational or scientific purposes only, not for diagnostic use.**

Select the images you want to share:

- To send several images from different series or studies:

select the layout to fit the images you want to send,

and open the required images in separate viewports;

- To send one image, or series of images, or the whole study

open the required image, or any image of the required series/study in the viewport,

or activate the viewport with such an image.

Press **Share via DICOM Library** button, and dialog window will appear on the screen. Please indicate, what are you going to send in expandable list of available **Scope** selection:

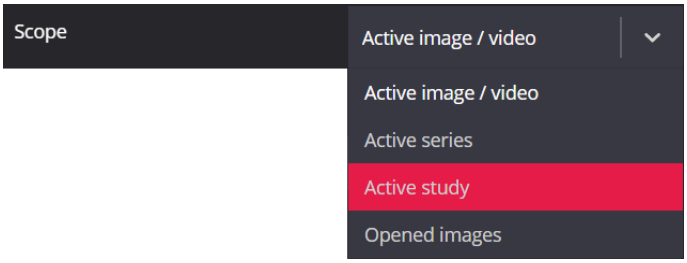


Figure 350. Selecting scope for sharing via DICOM Library

Please enter e-mail of the sender and recipient, subject, and message for recipient. If needed, change the e-mail template language in the expandable languages list above the message entry field. When done with data entry, click **Send** button.

⚠ **NOTE!** The sender's email address and subject field may have default values, if entered in system configuration.

⚠ **NOTE!** You can resize the message entry field to fit the message by dragging the bottom right corner of the field.

⚠ **CAUTION!** The system does not anonymize the content of shared images and entered message. You take responsibility for sensitive data in shared information.

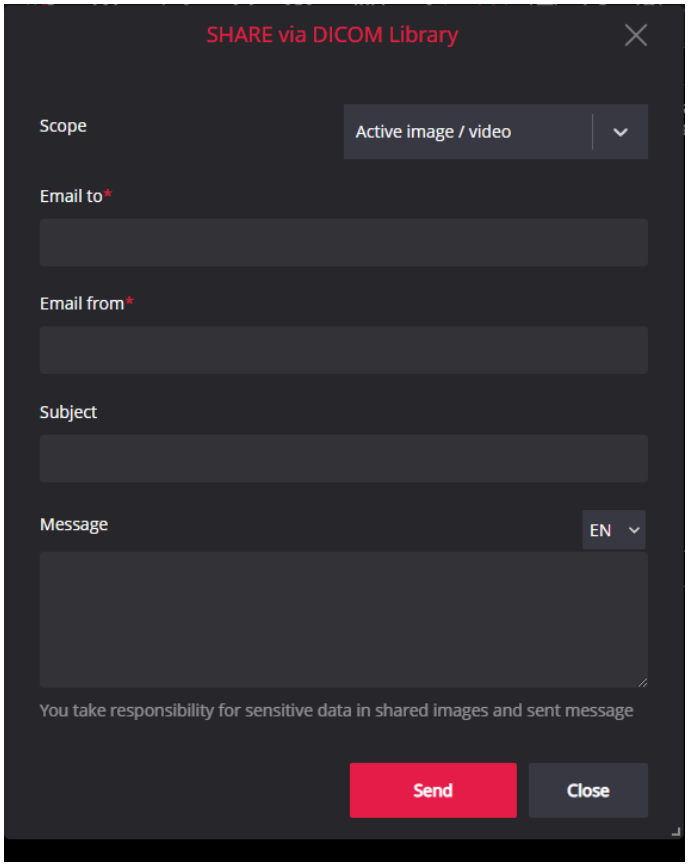


Figure 351. Share via DICOM Library dialog window

⚠ **NOTE! Share files via DICOM Library** function should be enabled and the required parameters should be set in configuration.

Forward



The **Forward** tool allows you to forward studies, study series, and/or individual series images that are open in the viewing window to another workstation.

When you click the **Forward** button, the Forward dialog opens, displaying a list of studies currently open for viewing.

The study selection in the list is performed automatically:

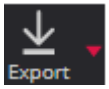
- if an image of a study is displayed in the active viewing area, that study is selected;
- if the active viewing area is empty, all studies are selected.

You can modify the study selection manually in the Forward dialog.

For a detailed description of the Forward dialog, see the section **“**Export and Forward**”**.

⚠ **NOTE! Forward** function should be enabled, and the required parameters (list of forward destination machines) should be set in configuration.

Export



The **Export** tool lets you save an active image, series, or entire study as an archive or as an ISO image for recording on CD / DVD media.

⚠ **NOTE! Export** function should be enabled and the required parameters (path to DICOMDIR viewer and size of ISO archive) should be set in configuration.

Please, select the studies for export:

- To export one currently viewed image, series, or study, activate the viewport with series/studies image and click Export tool's button;
- To export all the studies, that are currently opened in viewer, activate the empty viewport and click Export tool's button.

Clicking the **Export** button opens the export window with the list of studies selected for export in it. You can start a new export in the export window, or to open the previous export jobs list. You can use the Export menu for opening the export jobs list directly:

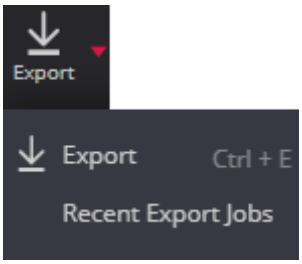


Figure 352. Recent Export Jobs option in Export menu

See detail export window and recent export jobs window description in section "Export and Forward".

Upload



The "Upload" tool allows users to upload DICOM files to the PACS system from their computer or another storage location accessible to them.

⚠ **NOTE!** To use the Upload tool, it must be enabled in the system configuration, the PACS system path must be defined, limiting parameters must be configured, and the user must be granted upload permissions (described in more detail in the installation documentation).

When selecting the Upload function  , a dialog box opens where you need to choose a file or a folder containing the data files.

For a detailed description of the upload process, see the section "Export and Forward."

LiveShare



LiveShare tool is used to share the content of user's (further named as host) Viewer window with one or more other users (further named as guests).

First, prepare the Viewer window for content live sharing:

- Open the studies you are going to share in the Viewer window, and close the studies, that are not supposed to be shared.

⚠ **CAUTION!** The system grants to the guests the access to all the studies, that are opened in host's Viewer window when starting live sharing, and these studies will be displayed in the thumbnail panel of the guests' Viewer window. Opening or closing the studies, while sharing is on, is not supported.

- Select preferred layout and open images in viewports.

⚠ **NOTE!** Live sharing is dedicated for images. Multiframe, video, ECG, PDF, SR documents is not supposed to be live shared.

To start live sharing, do the following:

- Press the **LiveShare** button to open the LiveShare host window:

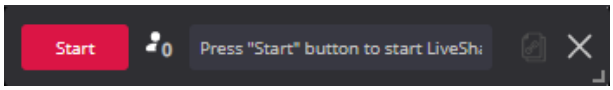


Figure 353. LiveShare host window when live sharing not started

⚠ **NOTE!** You can change the shared studies list, while liveShare session is not started and guest URL is not generated by system.

- Press the **Start** button in the LiveShare host window to start live sharing session. The system warns about limited live share functionality, and you should confirm the action. The system generates the guest URL and shows it in the LiveShare host window.
- Deliver the guest URL to session attendees:

Copy the guest URL to the clipboard by clicking Copy LiveShare link button  , or using keyboard shortcuts in URL field: CTRL+A for selecting the link text, and CTRL+C for copying the selected text to clipboard;

Paste the copied link and send it to session attendees.

- When remote attendee launches the guest URL, the guest Viewer window with the live shared studies is opened and connected to your liveShare session, and the Viewers count is updated in the LiveShare host window:

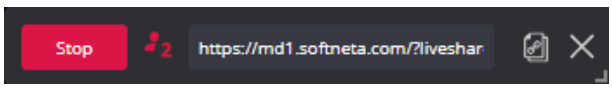


Figure 354. LiveShare host window with liveShare session running and two guests connected

⚠ **NOTE!** The non-modal LiveShare host window should not be closed, while liveShare session is running. Closing the window ends the liveShare session.

⚠ **NOTE!** The system informs the host user in case the liveShare session is destroyed due to network problems.

The guest URL may by copied, send to guest user, and guest may connect at any time during the session. The number of guests is not limited.

⚠ **NOTE!** Separate license connection is used per host, and per each connected guest.

Do the work you want to share with session attendees, after guests are connected. The live sharing of the following actions is supported:

- Changing the appearance of the Viewer window (layout, thumbnail panel position, multi-image, and multi-series);
- Opening images and SR documents in viewports;

  ⚠ **NOTE!** To share SR documents, the liveShare guest should have the rights to view documents configured.

  ⚠ **NOTE!** Multiframe, video, ECG, and PDF documents is not supposed to be live shared

- Image visual transformation: changing windowing values, changing image smooth;
- Image spatial transformations (pan, scale, rotate, flip);
- Image scrolling (scroll menu actions, scrollbar actions);
- Location functions (reference line, crosshair);
- Measurements (except the calibration line and time intensity curve measurement);
- Resetting changes in viewport (applied measurements, spatial transformations);
- Multiplanar reconstruction.

The guest Viewer window repeats the host Viewer window content and host’s actions:

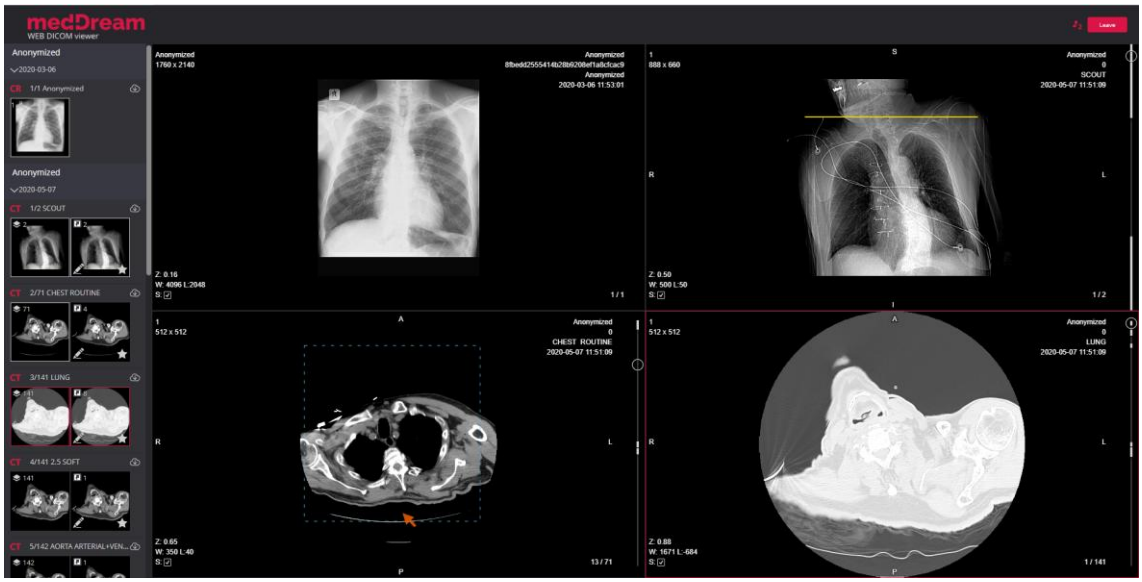


Figure 355. Guest Viewer window

LiveShare session guest is not allowed to perform any action with studies and images in the guest Viewer window.

Guest may leave the liveShare session by pressing the Leave session button in Guest Viewer window. If guest has left the session, the Viewers count is automatically updated in the LiveShare host window.

Stop the liveShare session, when done:

- Press the Stop button in the LiveShare host window, or
- Close the LiveShare host window with Close button  , and the liveShare session will be stopped.

⚠ **NOTE! LiveShare** function should be enabled in configuration, and sockets connection to MedDream server from host's and guests' workplace should be allowed.

Fusion function



The **Fusion** function allows you to combine the series: overlay the selected for fusion series on the already displayed series. For example, link the PET series representing the sites of radioactive drug concentrations with the anatomical patient structure. The series fusion function can be selected only after loading the series into the active window. The **Fusion** function is achieved by selecting the Fusion icon in the main toolbar.

⚠ **NOTE!** The **Fusion** function by default provided of CT, MR, and PET modalities. The list of modalities and/or SOP classes can be extended or reduced. For more information, see the install manual.

To start fusion:

- Select or open the image the CT, MR or PET series that you want to combine with other series.
- Click **Fusion** button and open the Fusion window:

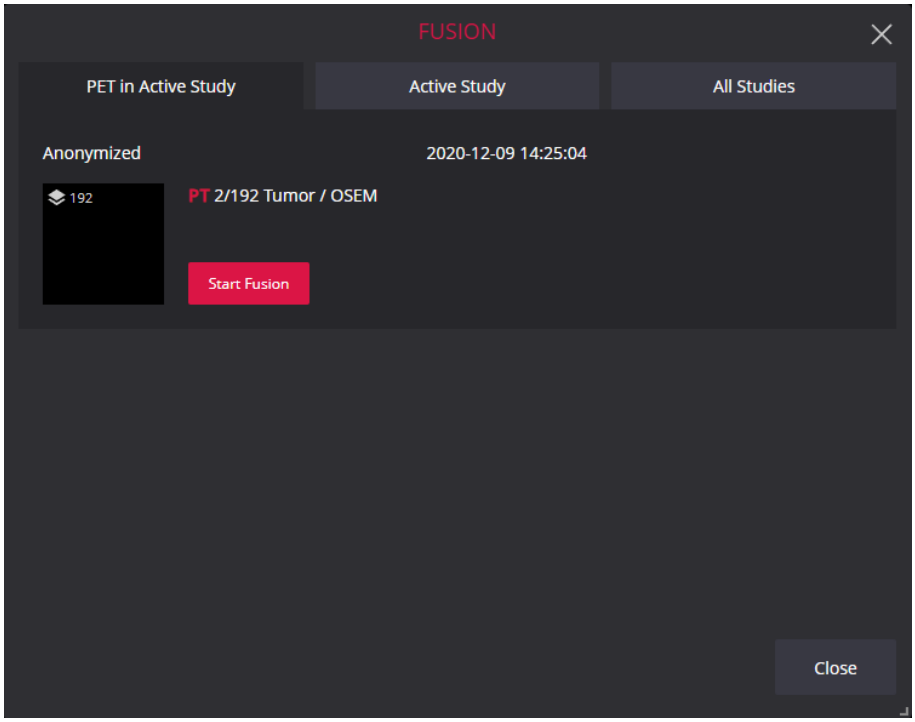


Figure 356. Fusion window

- In the Fusion window the user can select the series from the active study or from the other studies, that are opened in the Viewer. The system finds and displays all series that contain *one* or more images. Select the series you want to overlay with the already viewed active series, and click the **Start Fusion** button.

⚠ **NOTE!** If the active study has PET series, they are displayed in the separate tab, and this tab is selected by default on Fusion window opening.

⚠ **NOTE!** CT, MR, or PET series from any study, that is opened in the Viewer window, may be selected in All studies tab. This allows the user to combine series of different studies.

- The program preloads viewed active series, and the selected series, if not loaded earlier, and then fuses them. The preload process progress is seen on the screen.

⚠ **NOTE!** The time of series preload process depends on the size of series and the connection speed.

- Once the fusion process is finished, the fusion series and the toolbar of fusion series are displayed in the active viewport:

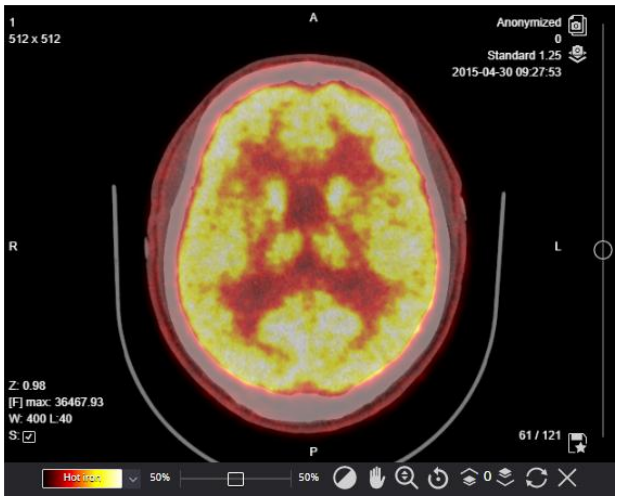


Figure 357. Fusion series

- If the fusion is performed on MIST MPR projections, there are less control buttons, but their functionality is identical:

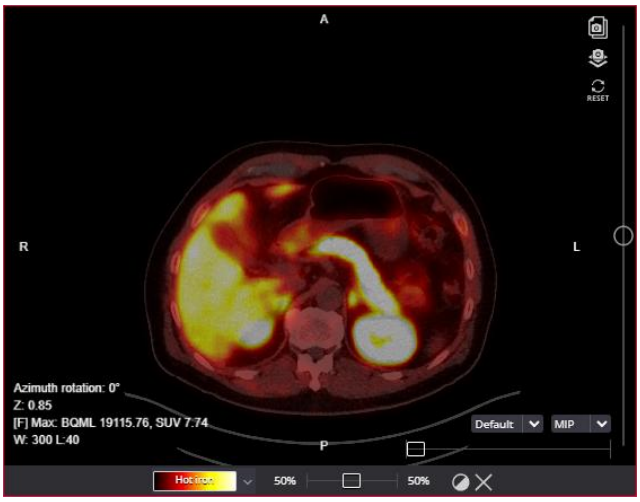


Figure 358. Fusion. MIST MPR

Manipulating fusion series

The functionality of the fusion series toolbar is described below.

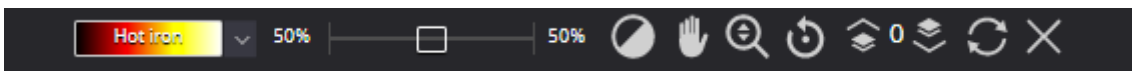


Figure 359. The toolbar of the fusion series

⚠ **NOTE!** If there is not enough space for the buttons to be displayed, the More button 

is displayed. Click it to see the missing buttons.

1. **Changing the color range**

By default, the **Hot iron** color range is applied to the PET or other top image of fusion series. However, according to the specificities of the anatomical body sections analyzed, different color range can be used. The choice of the color selection is performed by expanding the list of color schemes and choosing the desired color range. **None** option displays overlayed image pixels in grayscale. The selected color range is automatically applied for the fusion top series immediately after selection.

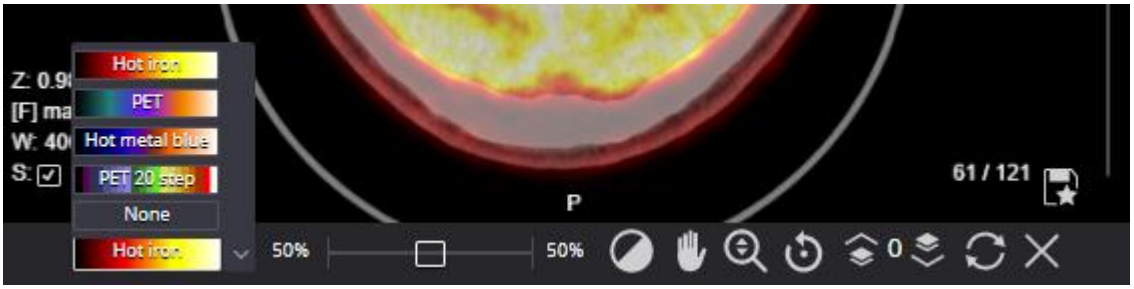


Figure 360. Changing color range of the fusion top series

2. Changing the fusion ratio

In the analysis of fusion series, it is important to have the ability to change the fusion ratio, what affect better visibility of bottom or top series. You can change the ratio in fusion ration bar by dragging the marker to the right or the left, exposing the top or the bottom series. In this way, one or the other series is highlighted and a clearer view is provided. By default, the 50% to 50% ration is applied.



Figure 361. Fusion ratio bar in fusion series toolbar

3. Upper layer data adjustment

If the fusion of the series is not completely symmetrical, then the **Pan** tool in the fusion series toolbar can be used. This tool allows you to change position of the top fusion series and visually anatomically link the fusion series.

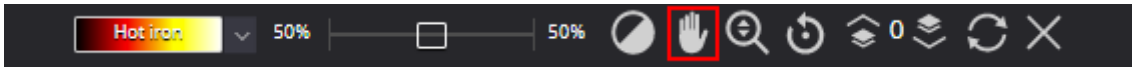


Figure 362. Pan tool in fusion series toolbar

⚠ **NOTE!** To change the position of the whole fusion images, use the **Pan** tool located on the main Viewer's toolbar.

4. Adjust the contrast and brightness of the upper layer

By choosing the **Windowing** tool in the fusion toolbar, the user can change the contrast and brightness of the top fusion series. If the **Windowing** tool is selected from the Viewer's main toolbar, then the brightness level of the bottom series is changed. Note, that brightness of top or bottom series may be changed from the other viewport, if synchronize windowing for the same series is switched on.

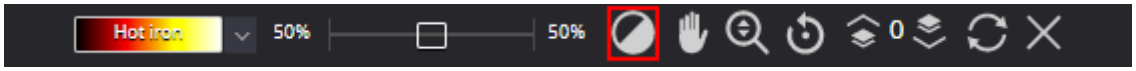


Figure 363. Pan tool in fusion series toolbar

5. Upper layer zoom function

By choosing the **Zoom** tool in the fusion toolbar, the user can change the scale of the top fusion series. If the Zoom tool is selected from the Viewer's main toolbar, in this case the overall (top and bottom series) scaling is changed.

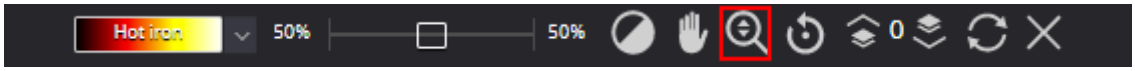


Figure 364. Zoom tool in fusion series toolbar

6. Upper layer rotation

By choosing the **Rotate** tool in the fusion toolbar, the user can rotate the image of the top fusion series. If the **Rotate** tool is selected from the Viewer's main toolbar, in this case the whole fusion image (top and bottom series) is rotated.

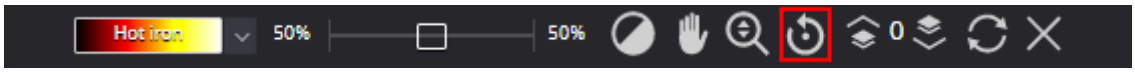


Figure 365. Rotate tool in fusion series toolbar

7. Upper layer image overlay

If there is a mismatch between the fusion series, the series images can be shifted with the **Manual Adjustment** tool in the fusion series toolbar. Clicking the down-pointing chevron button shifts the image of the top fusion series to the next, and clicking the up-pointing chevron button shifts the image of the top fusion series to previous one.

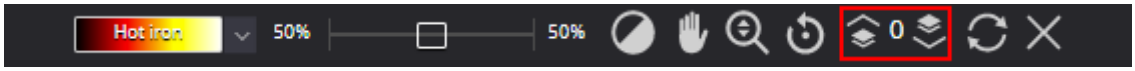


Figure 366. Upper layer Manual Adjustment tool in fusion series toolbar

8. Standard Uptake Value (SUV)

The main measurement used in the fusion series is the standard uptake value (**SUV**). The standard uptake value is calculated according to the formula:

$$SUV_{bw} = \frac{weight\ in\ grams}{injected\ dose}$$

The **Standard Uptake Value** is calculated by choosing **Ellipse** measurement (see description in section "Ellipse") from the **Measure** expandable menu in the Viewer's main toolbar and marking the location in the fused image. Three standard uptake values (average, minimum and maximum) are calculated:

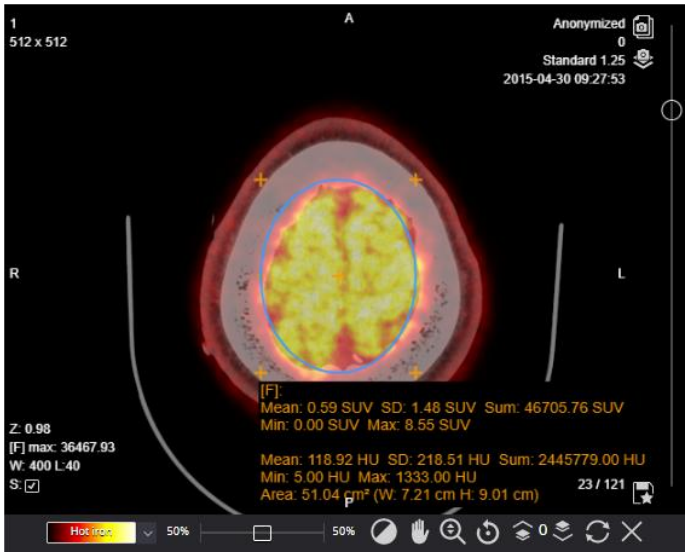


Figure 367. Standard uptake value measurement in fusion series

9. Reset top series manipulations

Reset button in fusion series toolbar cancels all the manual adjustments that were done with the top fusion series and restores the fused series to the original state.

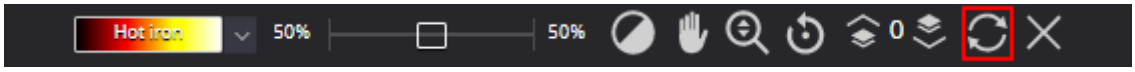


Figure 368. Reset button in fusion series toolbar

10. Closing fusion series

To close the fusion series, click on **Close** button (**X** icon) at the end of the fusion series toolbar.

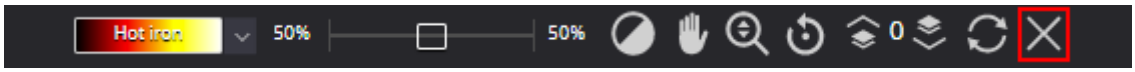


Figure 369. Close button in fusion series toolbar

Cine mode



Using **Cine mode**, you may put all series images into one movie. Click on the **Cine mode** tool in Viewer's main toolbar wait until the series images preload is done, if not loaded earlier:

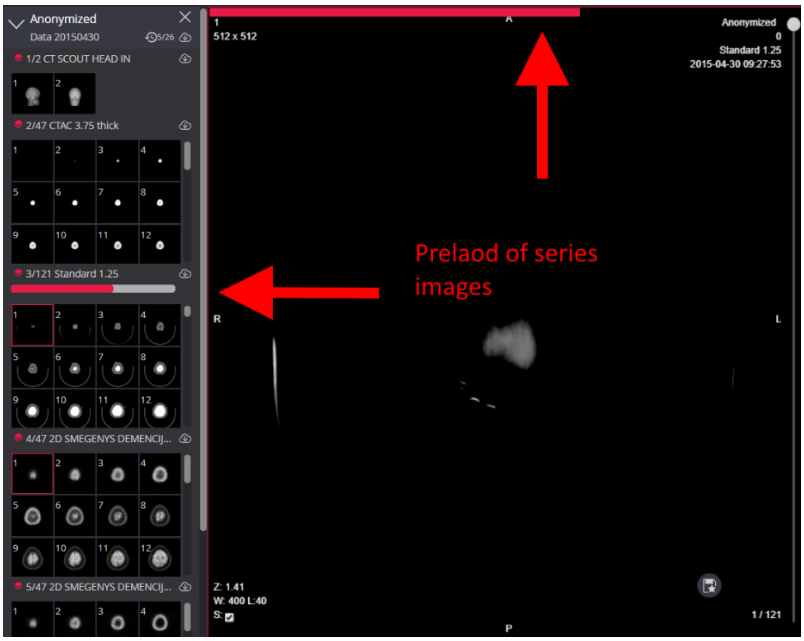


Figure 370. Preload of series data for cine mode

When images are preloaded, the function allows you to play series images as movie (one image corresponds to one frame):

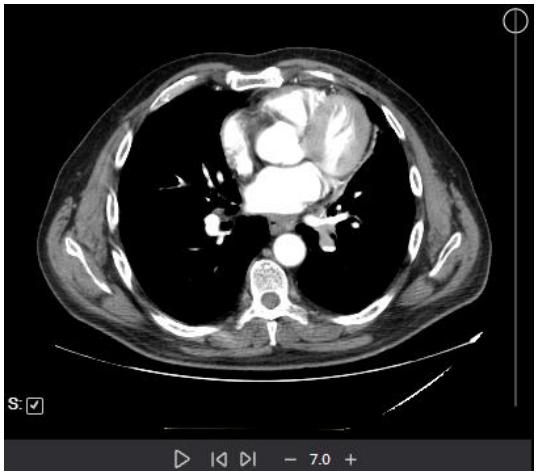


Figure 371. Cine mode movie playing

Toolbar for controlling the movie playing is displayed at the bottom of the viewport:

- To switch the movie playing off or on, click Pause or Play button. The button icon changes correspondingly to the current play status;
- To increase or decrease the movie frame rate, click '+' or '-' button correspondingly. The changed number of frames per second is displayed in toolbar , and immediately applied;
- To view the movie frame by frame, use the Previous Instance and Next Instance buttons. If movie was playing, clicking the Previous Instance or Next instance button pause movie and then navigates to the previous or next frame from the stopped frame until movie beginning or end is reached.

NOTE! If there is not enough space for the buttons to be displayed, the More button is displayed. Click it to see the missing buttons.

NOTE! An automatic cine toolbar hiding may be configured in settings (see Settings).

To turn the Cine mode off, just open an image from a different series in the same viewport, or click the **Cine** button once more time.

NOTE! Windowing, **Pan** and **Zoom** functions are available during cine mode (see Manipulating and analyzing images).

Other Viewer tools

Thumbnails for mobile

Thumbnails for mobile button shows or hides the thumbnails zone in split mobile device display or desktop with mobile display mode enabled. See section Viewer window in mobile mode for detail description of the thumbnails for mobile zone.

Plugins



Plugins button extendable menu holds links to external systems and services. The plugins are displayed in expandable menu of **Plugins** button, if configured by system administrator. You can run the external plugin by clicking the appropriate menu action.

⚠ **NOTE!** The system may automatically run external plugin, if automatic start is configured.

⚠ **NOTE!** Third party plugin for DICOM print may be integrated for some PACS. For details, contact to MedDream support at this email: support@meddream.com.

⚠ **NOTE!** The image sharpening and edge filters may be configured and accessed in Plugins tool menu

Image Processing Filters

Image processing filters can be configured in the plug-ins (detailed configuration information is provided in the installation documentation).

Filters can be opened in three ways: in the image viewing window (iframe), in a modal window, or in a separate window. The visibility, order, and names of the menu items depend on the configuration.

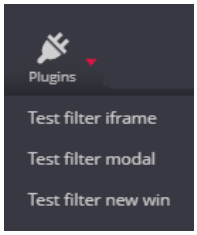


Figure 372. Processing Filters Menu in Plugins

Regardless of the chosen method of opening, the filters operate in the same way. The images and examples below are from a filter opened in a modal window.



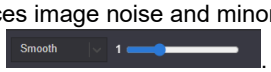
Figure 373. Image Processing Filters

The filter window opens empty. First, select the image opened in the preview area and choose **Reload**. The image is then loaded into the filter window with applied changes (e.g., **zoom**).

By default, the image is **stretched**, but you have the option to view it at its original size.

Select the desired filter:

- **Smooth**

This filter reduces image noise and minor irregularities, making the image smoother. The value can be adjusted using the slider 

.

Purpose: It is used to improve image quality when the image is grainy or visually "noisy," providing a clearer overall perception.

- **Edge**

This filter enhances the edges and boundaries of objects in the image.

Purpose: It is used to highlight structures, contours, and boundaries between different objects or tissues.

- **Sharpen**

This filter increases the contrast between adjacent pixels and enhances image details. The value can be adjusted using the slider.

Purpose: It is intended to emphasize fine structures and contours, making details more clearly visible.

- **Emboss**

This filter creates a relief effect by emphasizing the transitions between light and shadow in the image.

Purpose: It is intended for additional visual analysis, to better assess changes in shapes and structures.

After finishing image processing with the filters, close the dialog or window, or load the image into the preview area from the thumbnail bar.

Full Screen



Full Screen button is used to turn on the full screen mode. Move mouse cursor on **Full Screen** icon and click it - the Full Screen mode will be enabled and icon will be highlighted  . Click either the icon once again or ESC button in the keyboard in order to exit the Full Screen Mode.

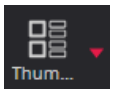
Theme



Theme changes MedDream default color (red color in standard product version) to the blue color that is clearly visible on black and white monitors.

⚠ **NOTE!** The default color may be different if the product is used in an integrated solution and rebranded to meet the colors of the integrating system.

Thumbnails



Thumbnails button enables changing the thumbnail place in viewer window. You can select the desired place from dropdown menu: Left; Top; Bottom; Right; Quick menu.

The auto hide may be switched on for the thumbnail bar that is displayed at the Left, Right, Top or Bottom of the Viewer window. If the auto hide is on, the system automatically collapses the thumbnail bar and displays the narrow bar with chevron icon instead, when the user moves the mouse cursor outside the thumbnail panel zone. Click the chevron icon to expand and view the thumbnail panel again. Note, that thumbnail bar is displayed on top of the viewed image, if auto hide is on.

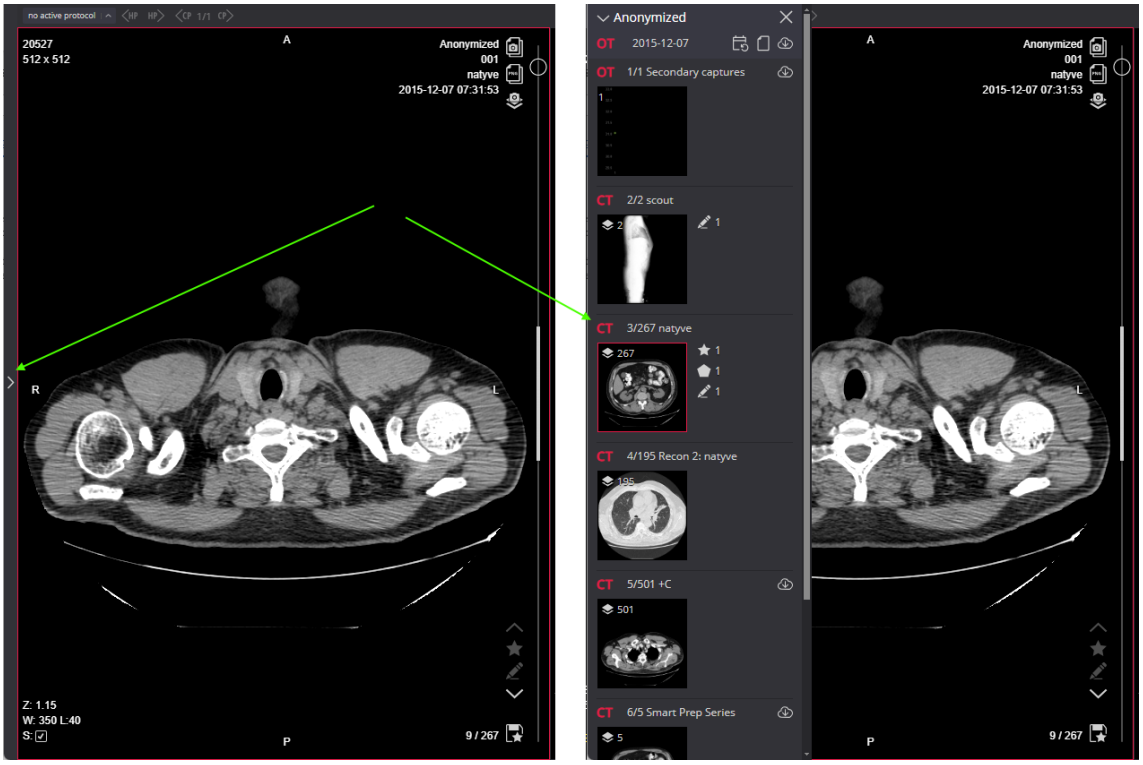


Figure 374. Auto hiding the thumbnails bar

To change the auto hide mode, expand the **Thumbnail** button menu and click the Auto hide menu option 

- the menu icon is highlighted  , if the auto hide is on.

⚠ **NOTE!** The user selection is saved in browser's local storage and used when starting the viewer. If local storage does not contain the thumbnail position value, the position is set according the system settings.

⚠ **NOTE!** The default thumbnail place is configured in Settings.

Preload Series



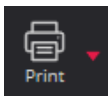
The **Preload Series** button preloads the series images, so scrolling the images with mouse wheel works much faster. Once you click the preload icon, preloading starts and preload progress bar appears in the viewport:



Figure 375. Series preload process progress bar

⚠ **NOTE!** The **Preload series** button is not displayed if the series data is already loaded.

Print



To print, select the **Print** menu option:

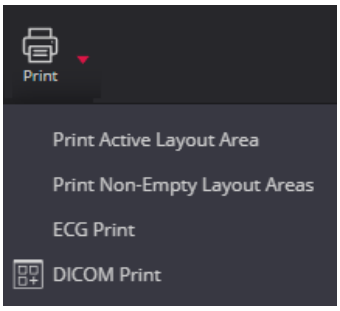


Figure 376. Print options

⚠ **NOTE!** The menu items **Print Active Layout Area** and **Print Non-Empty Layout Areas** are not displayed for SR and PDF cases. The ECG printing menu item is shown only for ECG studies.

Select one of the printing options:

- **Print active layout area** – prints the image from the active viewer window;
- **Print non-empty layout areas** – prints the viewer windows that contain images;

- **ECG printing** – prints electrocardiogram (ECG) data (a detailed description is provided in the corresponding subsection).
- **DICOM printing** – printing of medical images using the DICOM printing function (a detailed description is provided in the corresponding subsection).

ECG Print

ECG print is intended for printing electrocardiogram (ECG) data. The ECG image is printed in A4 format (210 × 297 mm), in landscape orientation, and is arranged to maximize fill the page width while maintaining a scale suitable for diagnostics.

The following data are included in the ECG printout:

- patient's name and surname;
- patient's date of birth;
- patient's sex (if available);
- study date and time;
- main ECG parameters (e.g., heart rate, intervals), if available in the data.

The data used for ECG printing are obtained from the ECG data structure *(ecgData)*, which is generated from the DICOM study data. The availability of additional ECG data may depend on the structure of the received data.

⚠ **NOTE!** The printing template can be configured – printed fields can be added or removed. Detailed information is provided in the installation documentation.

Printing includes several parameters configurable in the system settings:

- **Background grid size** – by default, the grid displayed in the viewer (1 × 1 mm) is used. An option is available to select a larger grid size (5 × 5 mm).
- **Printing mode** – by default, printing does not take into account actions performed in the viewer (such as zooming, panning, etc.), and the ECG image is arranged to maximize the page width. An option is available to enable a printing mode that preserves user-defined zoom and position parameters ("as shown").
- **Print quality** – by default, 300 DPI (dots per inch) resolution is used. An option is available to increase the print quality to 600 DPI.
- **Date and time format** – not filled in by default. If the value is not filled in, the system uses the default format YYYY-MM-DD HH:mm:ss; the format can be changed, e.g. by entering dd-MM-yyyy HH:mm:ss.
- **Month abbreviation** – the parameter is required when the date format is dd-MMM-yyyy, where „MMM" is the month name abbreviation. The abbreviations must be entered in the required language, e.g. Dutch: jan, feb, mrt, apr, mei, jun, jul, aug, sep, okt, nov, dec. If no values are entered but the date format is set to dd-MMM-yyyy, the system will use the default English abbreviations: Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec.

A detailed description of changing the settings is provided in the **System Settings** section.

DICOM Print



DICOM printing is intended for printing medical images using the DICOM printing function. The user can select images from the viewer, arrange them on the print sheet, and adjust their position. The print layout can be modified by changing the image arrangement and page orientation.

In the Print menu, select **DICOM Print**.

In the opened window, the system automatically includes the image from the active viewport.

The user must select a printer from the list of configured printers. The system automatically suggests the last used printer.

It is also possible to search the printer list by printer name or part of the printer's name.

A film size must be selected (the list of available values depends on the parameters of the selected printer). If needed, the page orientation can be changed, the number of print copies can be set, and a higher print priority than the default (**"Low"**) can be selected.

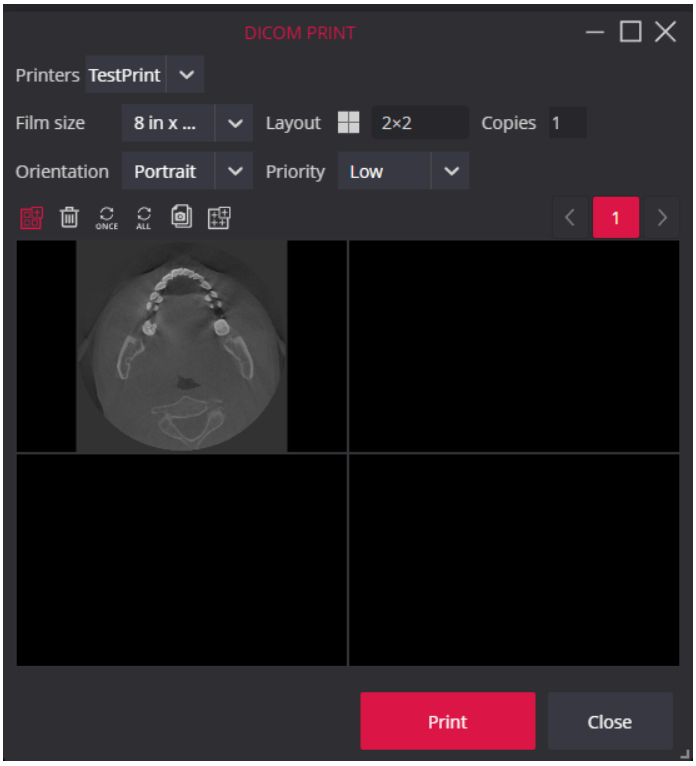


Figure 377. DICOM Print

The page layout is opened using the last layout used by the user. If the action is performed for the first time or the browser local storage data is cleared, the default layout defined in the system settings is used.

The user may change the DICOM Print page layout by selecting the required number of rows and columns.

The maximum allowed number of rows and columns is defined in the system settings.

The layout selection window visually displays layouts up to 6x6. If the printer supports a larger layout, the user may increase the number of rows and columns using the arrow buttons or by entering numeric values. In such cases, the layout icon is displayed with a "+" symbol.

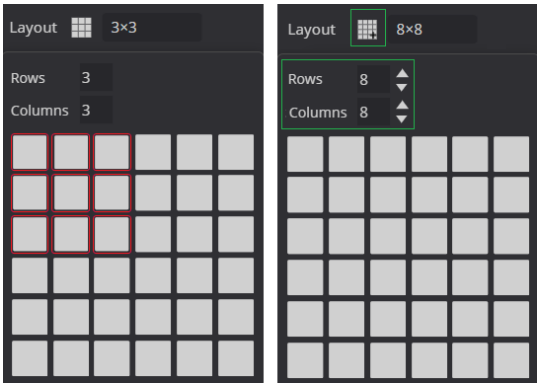


Figure 378. DICOM Print. Layout Change

In the opened window, the **Add images** button is active by default: 

⚠ **NOTE!** The button may become inactive after certain mouse actions – before adding an image, make sure it is active.

Click an image in the viewer to add it to the last available cell in the print layout.

When the first page is filled, a new page is automatically created, and images continue to be added to it.

The print window also provides additional image management options: 

 **Delete image**. Select the function and click the layout cell containing the image you want to remove. The remaining images automatically shift to fill the empty space. This is a one-time action – after use, the button becomes inactive.

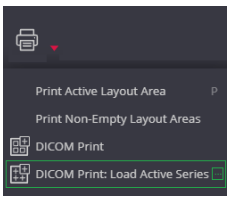
 **Replace image**. Select the function, click the layout cell with the image to be replaced, then click an image in the viewer. The selected image is inserted into the chosen cell in place of the existing image.

 **Reset**. Remove all images and restore the first empty page with the selected layout.

 **Copy to Clipboard**. The system copies the active DICOM Print page layout and the images displayed in it to the clipboard. The user may paste the copied image into another file, for example, a report, image file, or another document.

 **Add active series to printing**. When the action is selected, the system removes all previously loaded images and loads images from the active series into printing. The number of loaded images cannot exceed the maximum allowed value defined in the system settings. If the maximum allowed image count is smaller than the total number of images in the series, the system loads images starting from the currently viewed image. If the currently viewed image is near the end of the series, all remaining images until the end of the series are loaded.

⚠ **NOTE! Add active series to printing** action is also available through the menu item, therefore a keyboard shortcut combination may be assigned to it.



Hanging protocols

NOTE! Hanging protocol is automatically applied only to the first study that is opened in the viewer.

NOTE! The hanging protocol execution and reapply may be configured on first study close or studies change in the Viewer in the Hanging protocols version v2 settings.

NOTE! Other hanging protocol may be manually selected only from applicable Hanging protocols groups and protocols.



Clicking the **Hanging protocol** button opens Hanging protocol options window.

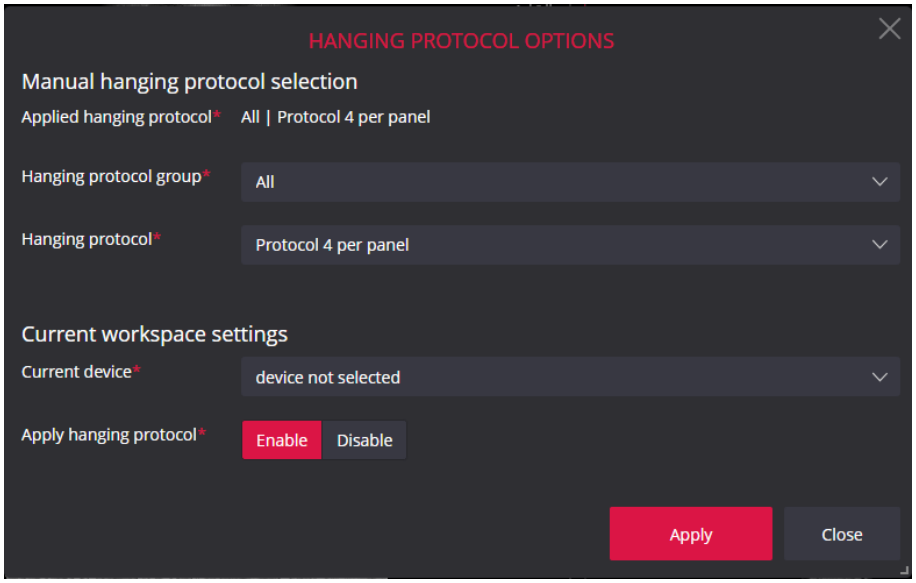


Figure 379. Hanging protocol options window

You can see the currently applied hanging protocol and apply the other hanging protocol in **Manual hanging protocol selection** section.

To apply other hanging protocol:

- select the hanging protocol group from **Hanging protocol group** drop-down list;
- select the hanging protocol from **Hanging protocol** drop-down list;
- click **Apply** button.

In **Current workspace settings** section, you can see and change the setting of automatic apply in workspace:

- to change device setting select the device from **Current device** drop-down list;
- to change the **Automatically apply hanging protocol** setting select **Enable** or **Disable** button;
- click **Apply** button to save the settings.

NOTE! The workspace settings are saved in browser's storage and are applicable only for the same browser.

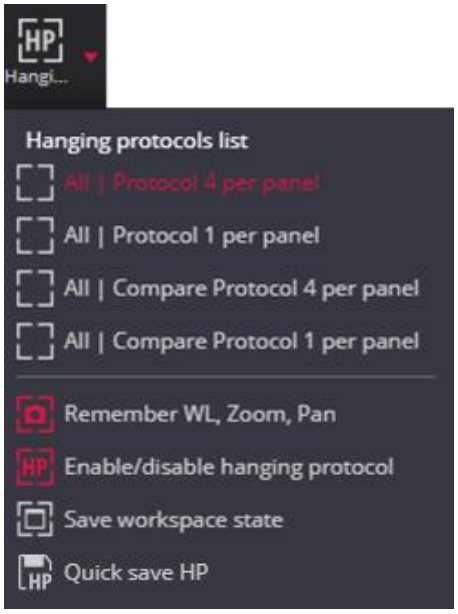


Figure 380. Hanging protocol menu options

Hanging protocol button's pop-up menu provides quicker access to some information and functions of Hanging protocol options window:

- menu **Enable/disable hanging protocol** shows the current property value – highlighted icon means that that hanging protocols execution and apply is enabled. Clicking the menu inverts the value and highlighting;

- menu **Remember WL, Zoom, Pan** shows the current property value – highlighted icon means that that hanging protocol visual state is automatically saved and loaded on the quick navigation actions, that are described below. The state icon in the protocols list indicates the saved or displayed state, as described below.

  The state saves the displayed images, measurements and text, visual and spatial transformations, that the user has applied to the images. In general, one state is saved for a hanging protocol. In case the hanging protocol has multiple multi series pages or comparison studies to show, the separate state is saved per each multi series page and/or comparison study. If previously saved state exists for the protocol, it is automatically displayed.

  ⚠ **NOTE!** The state saving is available only in Hanging protocols version v2.

  ⚠ **NOTE!** All the saved states are deleted, if the hanging protocol execution is repeated and new list of applicable protocols is set.

  ⚠ **NOTE!** All automatically save states are deleted if the window is closed. The permanent saving may be made with **Save workspace state** menu.

- menu **Save workspace state** saves the visual state of the current window and stores it on the server. The system links the saved workspace state with the currently logged user and the first study which is opened in the Viewer window. Next time the same user opens the same study in an empty Viewer window, the system by default displays the saved workspace state.

  ⚠ **NOTE!** To use workspace saving functionality, the cache should be configured and workspace saving enabled in the system. Contact your system administrator for details.

⚠ **NOTE!** One workspace state may be saved per study. The previous saved state is overwritten, if saved once more. Removing the saved state is not available and system does it automatically when cleaning the study cache.

⚠ **NOTE!** Hanging protocol is of lower priority than saved workspace state. If saved workspace state exists for the study, it will be loaded automatically and the notification about displayed saved workspace appears. The applicable hanging protocols may be selected manually from the list by the user.

⚠ **NOTE!** Instances of other studies may be used in saved workspace state. System tries to open the studies and instances that are referred in the saved workspace state, and displays the error, if user does not have access to these images.

- menu **Quick save HP** allows the user to quickly create the hanging protocol from the layout and images in the Viewer window. Note that system allows the user to quickly save HP only if the primary study is not closed in the Viewer window and the modality of the primary study may be defined. In addition, the Viewer window should display the images of primary study, or the images of one comparison study, or the images of primary and one comparison study.

  ⚠ **NOTE!** The Quick save HP function is available only if the Hanging protocols version v2 is used, the quick save HP functionality is enabled, and the user has rights to create hanging protocol. Contact your system administrator for details.

  ⚠ **NOTE!** Quick save hanging protocols are saved together with manually created hanging protocols but are assigned to automatically created quick save HP group for the modality. The user may view and modify the quick save hanging protocols (see Hanging protocols v2 setup manual for details).

  ⚠ **NOTE!** If Quick save HP feature is disabled, the system will not apply the quick save HP groups protocols however the user can still view and delete these protocols in Hanging protocols v2 settings page.

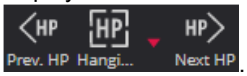
- menu group **Hanging protocols list** lists all the applicable protocol groups and protocols. Currently applied protocol is highlighted.

  The icon  near the hanging protocol name in Hanging protocols list indicates, that at least one state is saved for this hanging protocol. The icon  near the highlighted hanging protocol name in Hanging protocols list indicates, that the previously saved state is displayed.

  Clicking the hanging protocol menu clears all the states, if saved previously, and opens the initial hanging protocol. Use the quick navigation actions, that are described below, to keep and display the saved states.

  Hanging protocols list with the functions described is also available in panel toolbar.

The other way to quickly navigate through the protocols of the applied hanging protocol group, or applied protocol is using the toolbar buttons and shortcuts:

- The buttons for applying previous Hanging protocol and next Hanging Protocol buttons may be displayed in Viewer toolbar on the left and the right side of the Hanging Protocol button correspondingly:
  

  The navigation is cyclic and is done through all the applicable protocol groups and protocols.

  Hanging protocols list navigation button is also available in panel toolbar.

  ⚠ **NOTE!** By default configuration, the Prev. HP button, and Next HP button are disabled in system settings.

- Shortcuts **ALT+V** and **ALT+C** can be used to apply correspondingly the next and the previous hanging protocol from current hanging protocol group.

  ⚠ **NOTE!** The ALT+V and ALT+C shortcuts may be used even if Prev. HP and Next HP are disabled in system settings.

  ⚠ **NOTE!** By default, ALT+V and ALT+C shortcuts are also configured for quadrant navigation in quadrant zoom (see section “Quadrant zoom for mammography” for details).

- The Next CP (Comparison study) 

button may be displayed in toolbar, if the Hanging protocol foresees the iteration trough comparison studies. Clicking the button displays the next comparison studies images in the viewports, that displays the comparison study. Shortcuts **Backspace** is assigned to the Next CP button by default.

  Next comparison study button is available in panel toolbar. Besides, the panel toolbar also has previous comparison study button, the total number of comparison studies pages and the current page displayed.

  ⚠ **NOTE!** The Next CP (Comparison study) functionality is available only in Hanging protocols version v2.

  ⚠ **NOTE!** The maximum number of displayed comparison studies may be limited in hanging protocol.

- If the multi series protocol is applied, the system automatically creates multi series viewports for the study and, if specified in the protocol, comparison study. Multi series layout shortcuts **PageUp**, **PageDown**, **Alt+PageUp**, and **Alt+PageDown** may be used to quickly navigate through all the series of the study and/or comparison study. See section “Panels, Layout, and Multi image/series” for details.

  ⚠ **NOTE!** The Multi series protocol is available only in Hanging protocols version v2.

- If scroll between matched series function is set for the viewport, the scroll with mouse or keyboard shortcuts automatically opens the first image of the next series or previous series, that matches the series selection criteria of the hanging protocol, when correspondingly the end or beginning of the current series is reached. The keyboard shortcuts for opening the next series or previous series, opens the next or previous matched series correspondingly. If viewing the matched series is set, the number of the currently viewed series, and the total number of the matched series is displayed in the bottom left corner of the viewport.

When hanging protocol is opened in an empty Viewer window, and further navigated, the Viewer thumbnails bar is filled as follows:

- The first study in the thumbnails bar is the study for which the hanging protocols rules are executed, and this study is expanded and has a focus.
- All the comparison studies, which images are currently opened in the Viewer, are also expanded in the thumbnails bar.
- If all the comparison study images are closed due to navigation inside the HP, for example to next comparison study, or next page in multi series protocol, the study is not closed, but is automatically collapsed in the thumbnails bar.

Report



Clicking the **Report** button opens the report form. See detail requirements for report module accessibility and report form description in section “Report module”.

Info Labels



Info Labels allow the user to hide the viewport labels for image, multi-frame, or video. By default, the info labels are displayed and the **Info Labels** button is highlighted, when the Viewer window is opened. Clicking the button hides all the labels in all viewports and removes highlighting from the **Info Labels** button  . Click the **Info Labels** button to show the labels again.

4D Tools



4D tools menu unites the tools for working with studies that have not only space but also time parameters.

Construct 4D series



The tool is used to create a virtual series from the study series, where the data are sorted in space and then in time. The tool can be used for both multi-series merging and single-series processing.

⚠ **NOTE!** The tools are available for all studies that consist of images. Unsupported formats: video, ECG, SR (text format), PDF and multiframe. Does not work with reconstructions.

The user should select the required series in the thumbnail bar. If the virtual series will be created by merging more than one series, it can be select the first, or the second, or the following series.

Then the user has to open the menu **4D tools** and the sub-menu **Construct 4D series**.

⚠ **NOTE!** After click menu **Construct 4D series**, the system first preloads all study's series (if it has not already done so). If the study large, this may take some time.

The system opens a virtual series creation dialog where the user can mark or unmark series.

The dialogue shows a list of study’s series with:

- the same modality
- the same orientation in 3D
- the same tag "Frame of Reference UID"
- as the series on which the action is selected (this series is highlighted in the list in the dialogue window).

The dialog allows sorting by marking status, and sorting or searching by instance number, by serial number in the study (the same number is visible in the thumbnail bar), acquisition time and by description (DICOM tag (0008,103E)).

The thumbnail column displays thumbnails with the number of instances (thumbnail size is the same as in the thumbnail bar; can be changed in settings).

Number of series selected and number of filter results is shown at the bottom of the window.

If there are not enough series selected by default, it is possible to click unmark  in the table header (unmark also series that are not included in the filtering result), perform the filtering according to the required attributes and then click on the mark  in the table header (only records that are included in the filtering result are marked) or to manually mark the records one by one.

The option to check the checkbox at the bottom of the table "Mark/Unmark series with matching secription" has been provided to mark/unmark all the series with the same description as the one selected in the thumbnail bar at the beginning of the action (the series is highlighted in the table).

Provides the ability to filter by a full match of the value entered in the description filter. To do this, select  . When full match filtering is activated, the icon is highlighted  .

Normally, when the filter  , only the beginning matching check is performed. For example: if the list contains series with the descriptions "*Test*", "*Test_1*", "*Test_0002*", entering "***Test***" in the filter and selecting  it will filter out only one series with the description "*Test*", while selecting  will filter out all series "*Test*", "*Test_1*", "*Test_0002*".

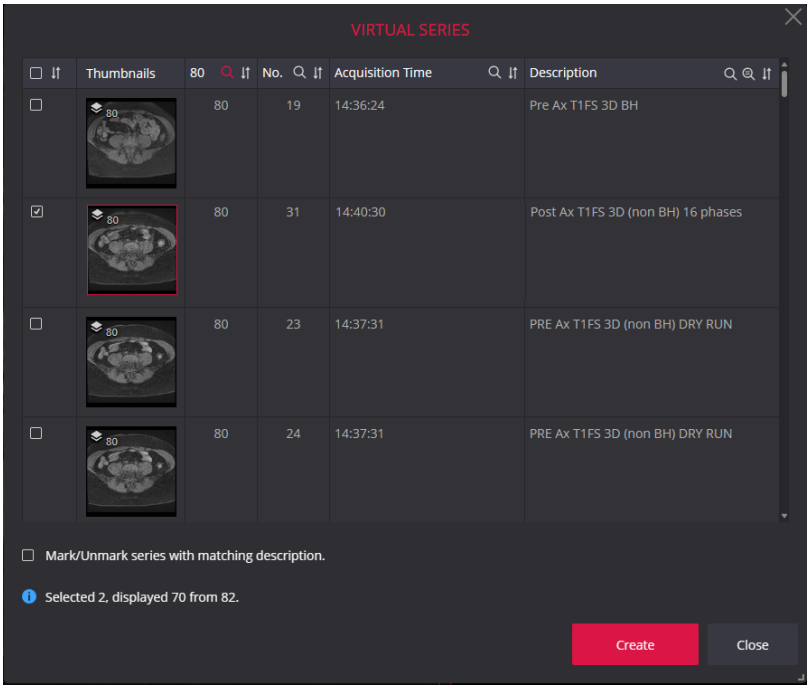


Figure 381. Creation of a virtual series. Series selection dialogue

To create a virtual series, the user must select the "Create" action button.

A thumbnail is created for the virtual series and displayed at the bottom of the thumbnail list of the study, with the virtual series icon and the name "Virtual". The virtual series exists until the end of the session.

There is no limit to the number of virtual series, and the uniqueness of a virtual series is not explored.

The virtual series opens in the active viewport.

When constructing virtual series, the system rearranged instances from one or more series so that they are sorted by space and time. If there is more than one time point, a horizontal slider is displayed.

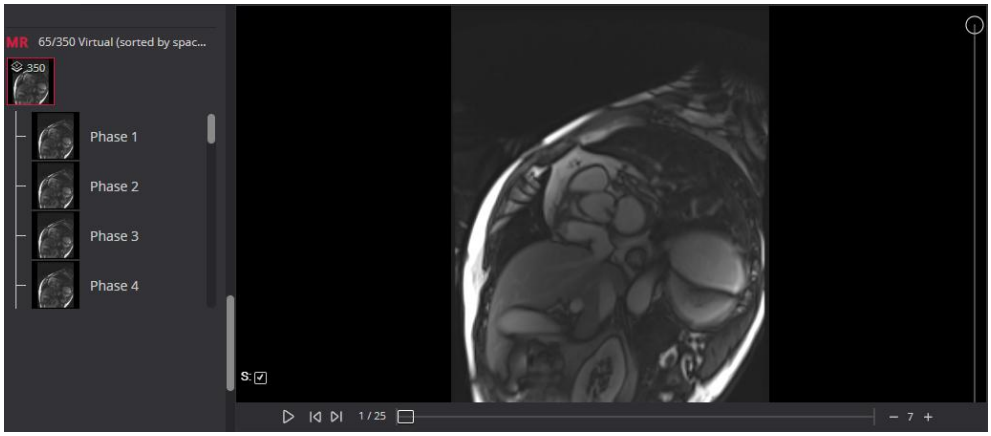


Figure 382. Creation of a virtual series. Horizontal slider

The horizontal slider is also known as the **4D slider**.

As the **4D slider** is moved, the system represents a different point in time. Meanwhile, the vertical slider shows another instance in space.

See more information about **4D slider** in the next chapter.

⚠ **NOTE!** If an action is repeated, at the start of each action, the user must select the required series in the thumbnail bar. A virtual series cannot be selected. If a virtual series is activated/selected, the Construct 4D Series action button is not available for menu.

Show 4D slider bar

Show 4D slider bar

The **4D slider** is for steering time points in studies that have time parameters.

If studies have identified phases, but it does not make sense to have a phase controller, users can disable the controller by selecting the **4D tools** menu and the sub-menu **Show 4D slider bar**. When disable, the setting is saved in local storage.

By default, the functionality is activated and the menu is highlighted.

⚠ **NOTE!** If there are time points in the Virtual Series, the **4D slider bar** is always displayed, even if "Show 4D slider bar" is disabled.

4D slider bar has the ability to play automatically through time points (or phases): the user shall click ▷. When the button changes to a pause button ⏸, which can be used to stop playing.

It is possible to assign a Shortcuts value to a play/pause action: open the shortcut window, find "Play/Pause timeline" and assign a value. For more detailed information, please see “System meniu function. Shortcuts”.

⚠ **NOTE!** The shortcut value must be unique. For example, the value "c" is assigned by default to the **Cine** function. If the value "c" is reused for the **4D slider** play/pause function, pressing "c" will still only work for the **Cine** function.

⚠ **NOTE!** When **Cine** is activated, the **4D slider** is hidden. Only one mode at a time can operate: either **Cine** or **4D slider**.

It is possible to go to the next time point by selecting  , or to the previous time point with  .

It is possible to assign a Shortcuts value to next/previous actions: open the shortcut window, find "Go to *next* (or *previous*) image on timeline" and assign a value. For more detailed information, please see “System meniu function. Shortcuts”.

Shows at which time point the review is currently in progress and how many time points are available. For example: the 7th point in time (or 7th phase) out of twenty-four  .

It is possible to reduce or increase play speed  .

Presenter tool



The presentation tool helps the user to temporarily mark an area of interest in a viewport to share knowledge with colleagues or students. The user can link one of the mouse buttons by selecting from several options:

- Fading line,
- Fading arrow,
- Draw,
- Arrows.

The first two certificates expire automatically after a set period of time. Selecting “Draw” and “Arrow” keeps the highlight drawn by the user until the user selects “Clear All” or “Reset Selected”/“Reset All” from the main menu.

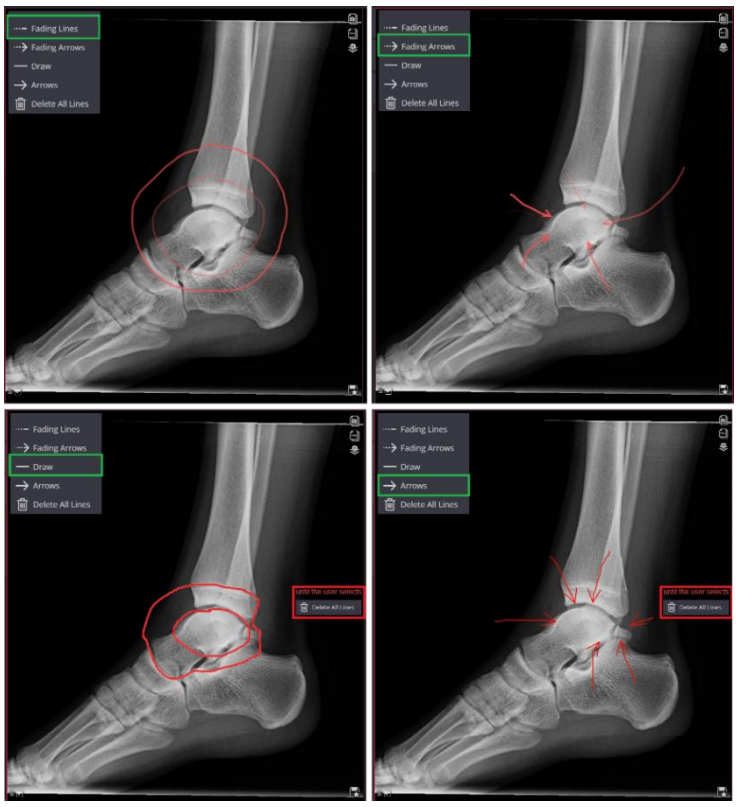


Figure 383. Presenter tool

⚠ **NOTE!** Lines, arrows or curves drawn by the user are not redrawn when the layout is changed and remain on the screen where the user drew them.

Laser pointer



The user can enable **Laser pointer**, which adds a dot to the cursor to help focus attention on the cursor position  .

Whiteboard



When a menu item is selected, a separate white-background window opens across the entire viewport, allowing the user to draw or write notes with a pencil as if on a regular whiteboard.

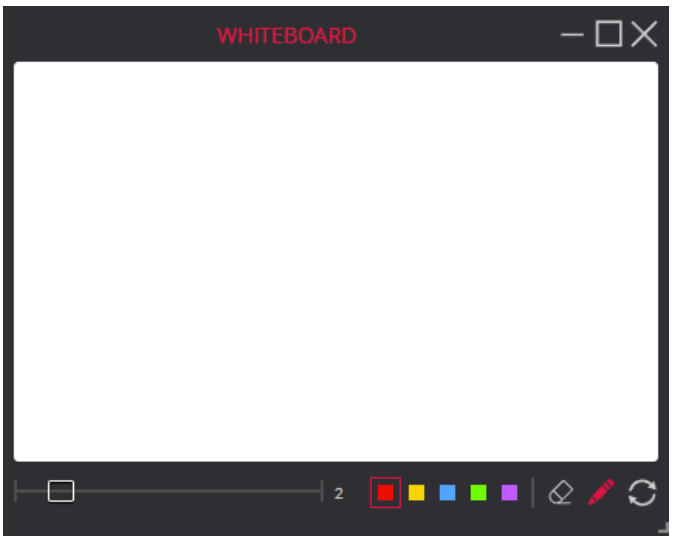


Figure 384. Whiteboard

By default, the window opens in full viewport mode, but it can be resized, minimized, and manipulated like any standard dialog window.

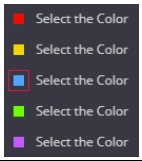
The user can select one of five available drawing colors, identical to those used in the presenter tool (see section below for details). Pencil thickness can be adjusted via the slider in the bottom-left corner. By default, the thickness matches that of the presenter tool and can be changed in the system settings.

The eraser tool can be selected. Once activated, the eraser icon is highlighted  , and the slider in the bottom-left corner allows adjusting the eraser size. By default, the eraser is five times thicker than the default pencil thickness.

The entire whiteboard can be cleared by clicking the button  or using the assigned shortcut. By default, the shortcut key is set to "Escape," but it can be customized. For details on assigning shortcuts, see the relevant section.

⚠ **NOTE!** Whiteboard content is not stored in the system, all information will be lost when the window is closed.

Colors of Presenter tool



The user can choose from 5 colors.

The colors that are selected from the menu are configured in the settings. It is also possible to change the fading time and the thickness of the line/arrow.

Swap



Swap tool allows you to swap the two viewports in the Viewer window.

To enable the Swap tool, click with the left mouse button on it  . Then you can use the left mouse button to drag and drop the selected viewport on top of the other viewport. The viewports are swapped after dropping.

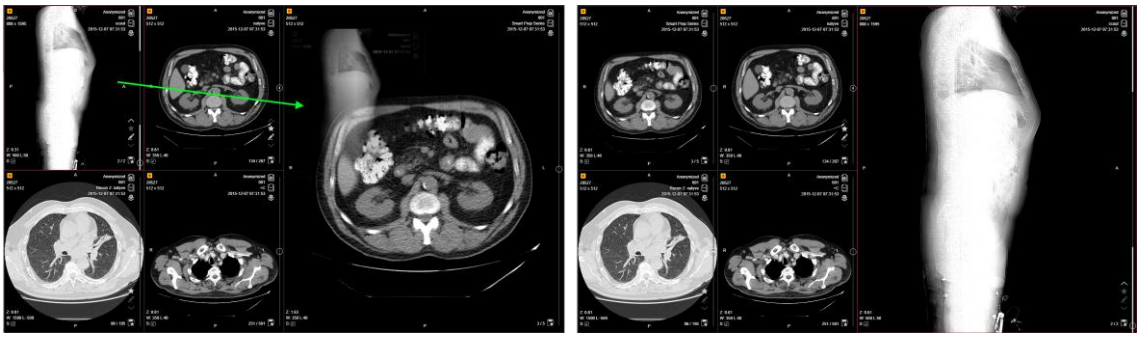


Figure 385. Steps of viewports swap

⚠ **NOTE!** Swap tool is not available on mobile devices.

Interpolation type

Interpolation type is used to improve image rendering quality when scaling the image. Different interpolation algorithms allow selecting between sharper, smoother, or more detailed image rendering.

The interpolation algorithm is applied only when the “S” (Smooth) function is enabled in the viewport. If the “S” function is not enabled, no additional interpolation algorithm is applied, and image scaling is handled by the browser.

The user may select one of the following interpolation types:

- Linear;
- Bicubic;
- Bicubic spline;
- Linear (WebGL API);

- Lanczos.

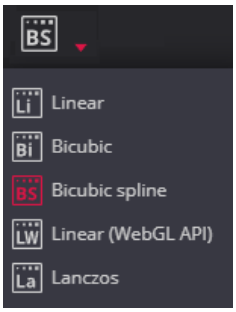


Figure 386. Interpolation types

By default, the “Bicubic spline” interpolation type is used.

When the user selects a different interpolation type, it is automatically applied to the image and saved in the user browser. When the Viewer window is opened again, the last user selected interpolation type is automatically used.

Special views

The section describes the image types that may be included in DICOM file and that needs the special handling when opened in viewer’s window.

ECG module

This module allows you to view DICOM ECG wave data.

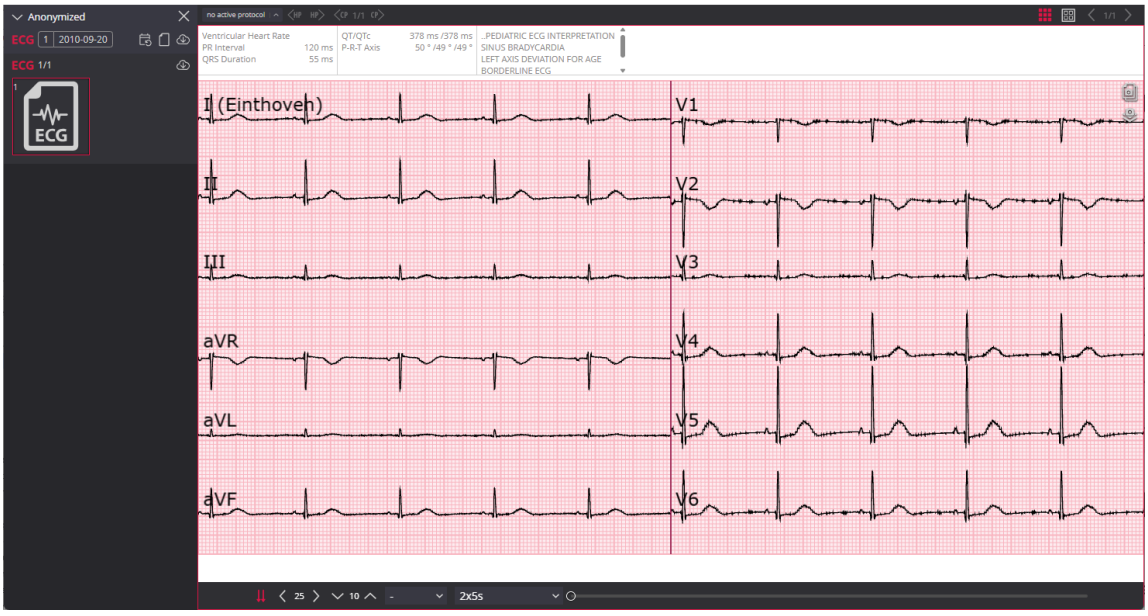


Figure 387. ECG viewer window

The section describes ECG annotation, ECG measurements and ECG viewport toolbar. See the description of the main Viewer window toolbar for other tools.

The annotation section is displayed either at the top or at the right, depending on the height to width ratio of the viewport.

By default, the following data is provided for opened ECG file: Ventricular Heart Rate, PR Interval, QRS Duration, QT Interval, QTc Interval, P Axis, R Axis, T Axis, diagnosis. Contact your system administrator to change the configuration.

ECG Viewer window has different **Measure** menu:

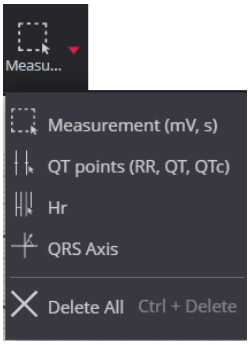


Figure 388. ECG measure tools

Measurement (mV, s)

The **Measurement** button is used to measure the duration (first number, 0.75 s in the example) and amplitude (second number, in this case 1.18 mV) of the selected ECG segment, and to calculate the heart rate per minute (third number in the example, 80 bpm). To measure the values:

- select **Measurement** tool,
- hover the mouse cursor on the point where you want to start the measuring,
- press the selected mouse button and drag the cursor to desired possition,
- release the mouse button when the cursor is on the point where you want to end measuring.



Figure 389. Using Measurement (mV, s) tool

QT points (RR, QT, QTc)

The **QT points** tool (duration of the electrical systole) is used to measure the QT intervals (RR, QT, QTc) of a selected ECG fragment. To measure the intervals:

- select **QT points** tool,
- hover the mouse cursor over the start-point of the Q wave and click the selected mouse button,
- hover the mouse cursor over the end-point of the T wave and click the selected mouse button,

- hover the mouse cursor over the start-point of the next Q wave and click the selected mouse button.

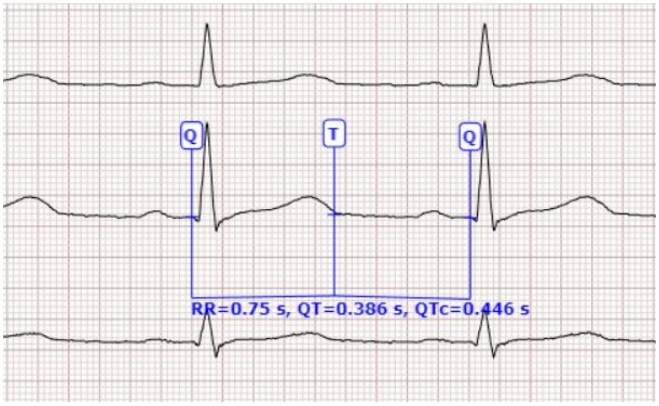


Figure 390. Using QT points tool



The button **HR** is designated to measure heart rate and visually estimate its irregularity. To measure:

- select **HR** measurement tool;
- hover the mouse cursor over the peak of the R wave and click the selected mouse button,
- hover the mouse cursor over the peak of next R wave and click the selected mouse button,
- now you can compare given interval with other R waves.



Figure 391. Using HR measurement tool



The **QRS Axis** is used to measure cardiac interventricular partition and ventricular depolarization spreading. Measurement is performed on one or more complete segments of lead I and aVF lead. To measure:

- select **QRS axis** measurement tool,
- hover the mouse cursor over the isoelectric line before P wave and click the selected mouse button,
- hover the mouse cursor over the isoelectric line after T wave and click the selected mouse button.

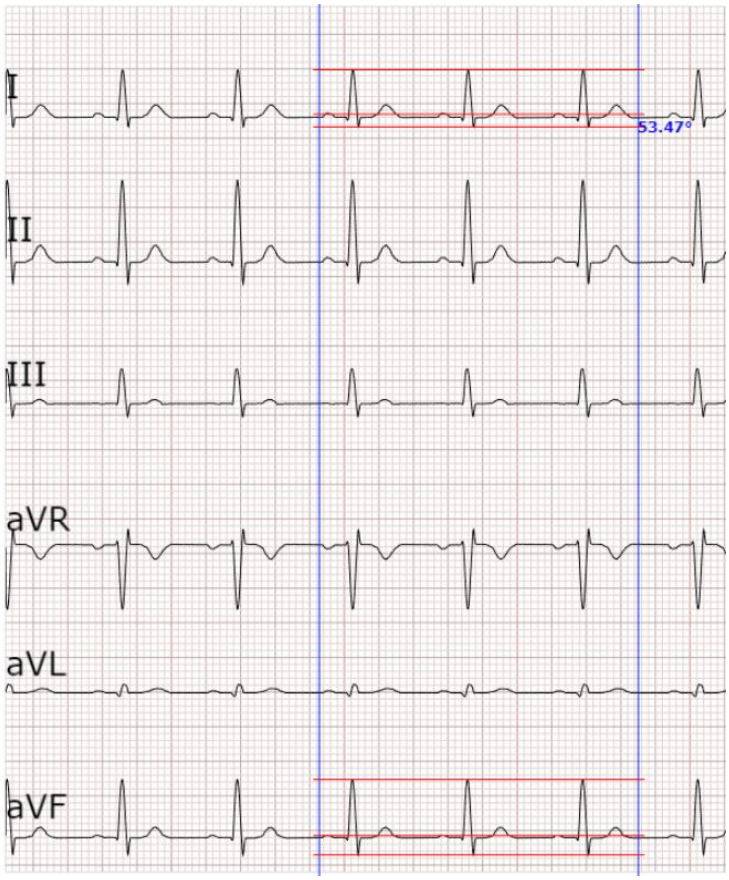
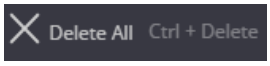


Figure 392. Using QRS Axis tool



The **Delete All** menu is used to remove all measurements.

Description of ECG viewport toolbar's tools:

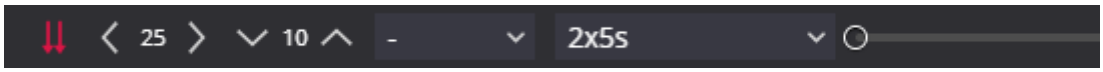


Figure 393. ECG viewport toolbar



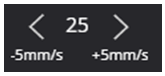
Filter function is used for the following:

to trim the edges of unnecessary points (points to the first spike that has no importance);

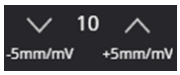
to trim high and low frequency signals applying low–pass and high–pass frequency filters under the "Filter Low Frequency" (003A,0220) and "Filter High Frequency" (003A,0221) tags;

to eliminate baseline wandering interference;

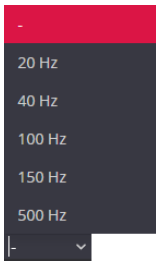
filters out specified frequency signals adjusting band-stop filter by **Notch Filter Frequency** (003A, 0222) tag.



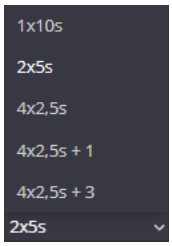
Change horizontal scale (mm per second).



Change vertical scale (mm per mV).



Select ECG frequency filter. By default ECG is not filtered (selection “-“).



Select ECG output layout. The default layout may be configured in Settings. 2x5s layout is selected by default configuration.



ECG view scrollbar.

SR view

SR view enables to view structured reports.

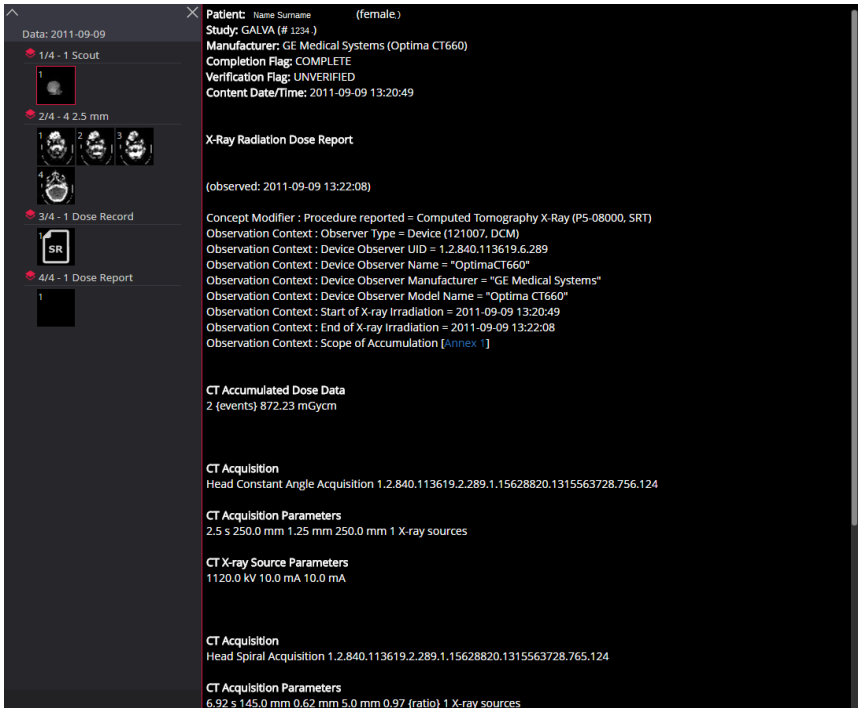


Figure 394. SR viewer window

SR window displays standard DICOM Structured Reports.

⚠ **NOTE!** The SR document is displayed only if the user has rights to view documents.

⚠ **NOTE!** The SR viewport does not support the html formatting. Converting the html content to text may be configured in system properties.

⚠ **NOTE!** Contact your system administrator, if there are SR documents included in series of other modality, and you need these SR documents to be displayed in a separate series.

The system also provides possibility to view Keratometry Measurements, Ophthalmic Axial Measurements, and Intraocular Lens Calculations data in text format:

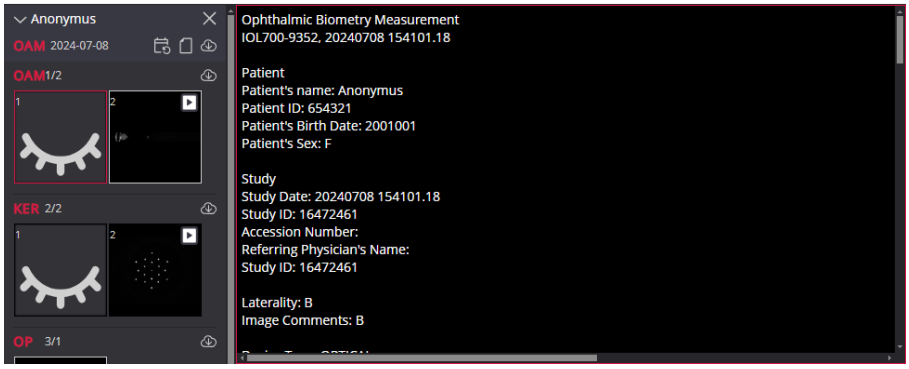


Figure 395. SR window with Ophthalmic measurement data in text format

PDF view

PDF view enables to view PDF files encapsulated in DICOM format.

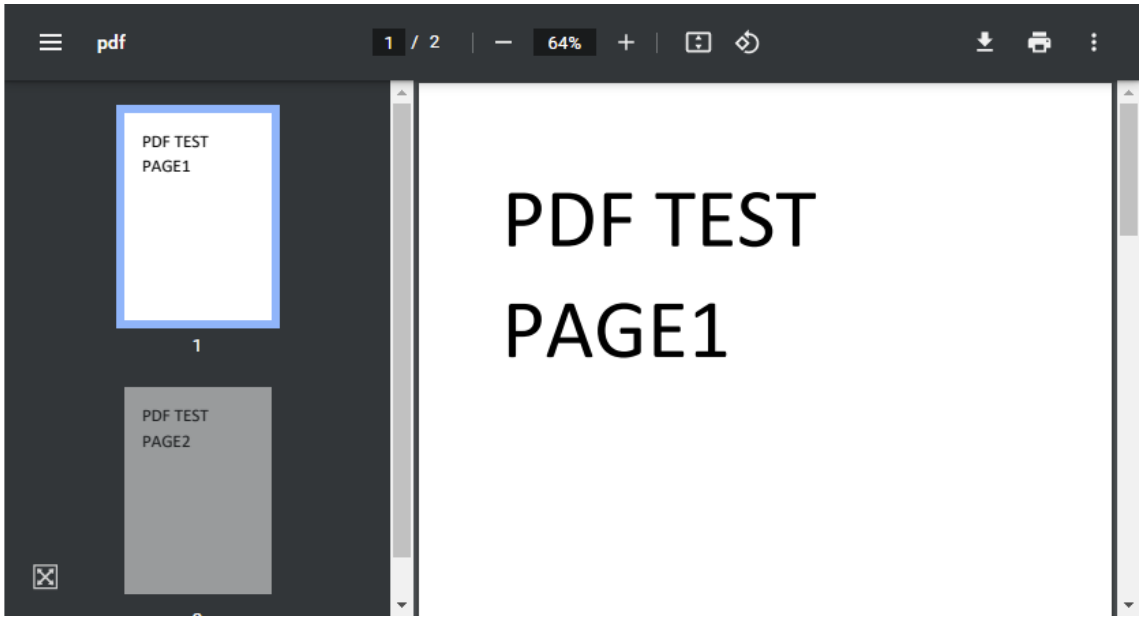


Figure 396. PDF display

NOTE! The PDF document is displayed only if the user has rights to view documents.

CAUTION! PDF file is opened with default PDF reader. Some Web browsers have built-in readers. In other cases, the additional software for pdf reading and displaying, like Adobe Acrobat Reader, should be deployed in user workplace.

NOTE! Use the full screen button at the bottom left corner of the pdf viewport to maximize and minimize the viewport, as the double click maximize does not work in the pdf viewport.

Video view

Software enables to view video files, MPEG2 and MPEG4 (H.264), encapsulated in DICOM format.

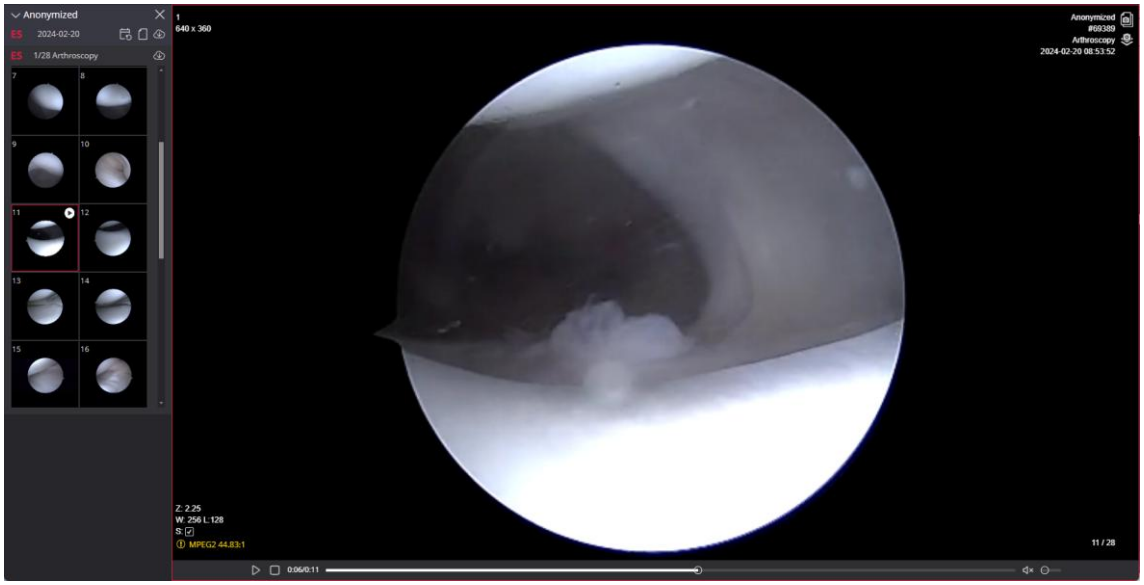


Figure 397. Video player

The play icon is displayed on the thumbnail of video image. The standard video player is used for opening and playing video.

Toolbar for controlling the video playing is displayed at the bottom of the viewport:

- To switch the vidoe playing off or on, click Pause or Play button. The button icon changes correspondingly to the current play status;
- To navigate quickly to the particular place in the video file, click on timeline, or drag the timeline cursor , or hover the mouse pointer over the timeline and scroll the mouse wheel. If timeline is used to view video by instance, the video playing is paused, if it was switched on. After finishing the actions with timeline, the video playing is automatically switched on. The time played from the beginning of the video and full time of video is displayed on the right of the timeline 0:06/0:11;
- To stop playing and set the player to the beginning of video file, click the Stop playback button;
- To switch the volume Off , or On , click the volume icon. To change the volume of the played video, drag the volume bar cursor or click on the volume bar .

NOTE! If there is not enough space for the buttons to be displayed, the More button is displayed. Click it to see the missing buttons.

By default, the visual and spatial transformations may be applied for the video instance using the tools in Viewer toolbar.

NOTE! Video visual and spatial transformation are not allowed if video is configured to run in browsers video player. Contact your system administrator if Windowing, Zoom, Pan tools are not available for video.

Multi-frame view

Software enables to view multi-frame images, encapsulated in DICOM format.

NOTE! By default, the system displays enhanced multi-frame image of CT, MR, NM, MG, or OPT modality as a series of images, and system is configured to not show the image thumbnails for the multiframe that is displayed as series of images.

NOTE! By default configuration, the system retrieves data and calculates the windowing values for each frame. If such behavior is not desired, contact the system administrator to change the configuration.

CAUTION! Depending on application configuration, in case of corrupted frame the system may either show warning, or ignore the corrupted frame and show the last not corrupted frame instead. Contact your system administrator for system configuration.

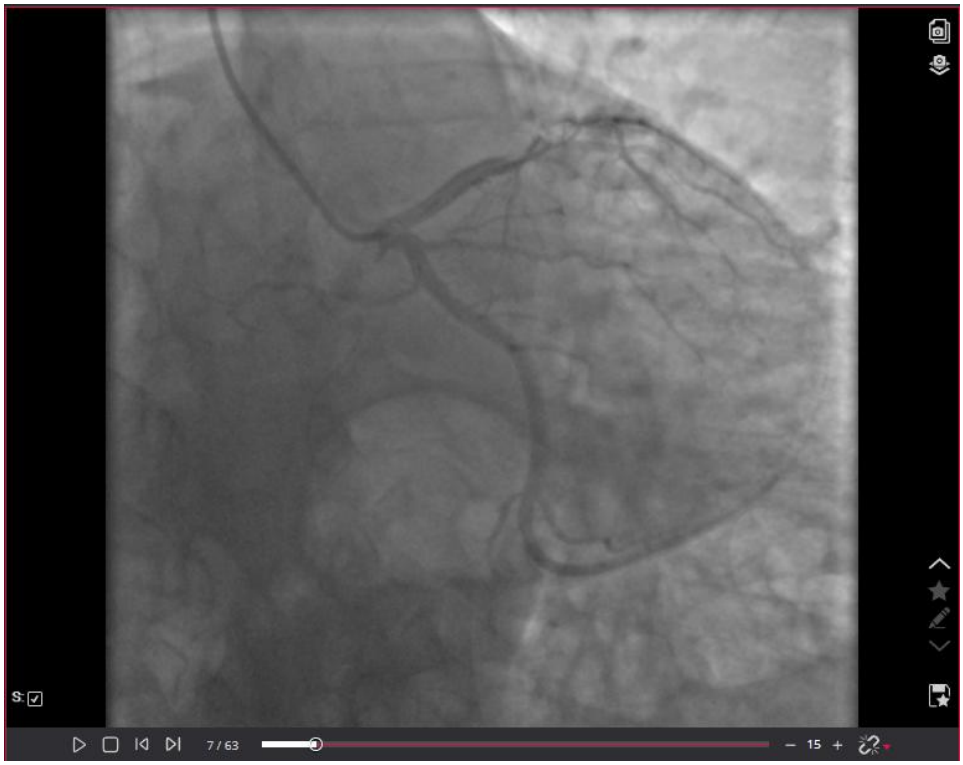


Figure 398. Viewing multi-frame image

The play icon is displayed on the thumbnail of multi-frame image.

System automatically starts loading of instances, when the multi-frame image is opened in the viewport.

System automatically starts playing multi-frame instance when loaded, if multi-frame AutoStart is configured in settings.

Toolbar for controlling the multi-frame playing is displayed at the bottom of the viewport:

- To switch the multi-frame playing off or on, click Pause , or Play buttons. The button icon changes correspondingly to the current play status;
- To navigate through the multi-frame image by instance, use the Previous Instance , or Next Instance buttons;
- The frame number and the total number of frames in the image are displayed before the timeline, e.g., 7 of 63 7 / 63;
- To navigate quickly to the particular place in the video file, click on timeline, or drag the timeline cursor , or hover the mouse pointer over the timeline and scroll the mouse wheel. If timeline is used to view multi-frame image instances, the multi-frame playing is automatically switched off;
- The values from DICOM file, if available, are used to set the initial frame rate. To increase or decrease the frame rate, click '+' or '-' button correspondingly. The changed number of frames per second is displayed in toolbar − 15 +, and immediately applied.
- A mode is available that allows synchronized start and stop of playback in all viewports . More detailed information is provided in the following section.

⚠ **NOTE!** If there is not enough space for the buttons to be displayed, the More button More is displayed. Click it to see the missing buttons.

⚠ **CAUTION!** System tries to achieve the requested fps when playing multi-frame. If achieving the requested fps is not possible due to hardware or software limits, some frames may be skipped and not displayed to the user while playing. To see all frames, reduce the fps or use instance by instance navigation.

Synchronized multi-frame image playback

A mode is available that allows synchronized start and stop of playback in all viewports containing multi-frame images. When the mode is disabled, the icon is displayed .

Two synchronization modes are available:

- “Play sync start”;
- “Sync playback”.

Play sync start – in all viewports containing multi-frame images, playback occurs at the same speed and is synchronized with the active viewport. Playback starts from the same frame.

If all images start from frame 1, they will be played from the beginning to the last frame. If some images contain more frames, shorter images will wait until the longer ones are fully played to the end.

If, for example, the active viewport is currently showing frame 20 of 30, and other viewports are showing frame 10 of 20, when the **Play sync start** mode is started, the active image will first be played to the end (from frame 20 to 30). Then it will continue from frame 1 up to frame 9 – from this point, all multi-frame images will be played synchronously, starting from frame 10.

Sync playback – playback in all viewports starts at the same time, but occurs at individual speeds (i.e., unsynchronized) and begins from the frame where the play button was pressed.



Figure 399. Synchronized multi-frame image playback

By clicking the icon, the modes are switched in the following order: unsynchronized → **Play sync start** → **Sync playback** → unsynchronized. The modes can also be activated from the **“Synchronize actions”** menu item , and keyboard shortcuts can be assigned.

Slide microscopy view

Software enables viewing digital pathology images that are captured from microscopes and saved in DICOM Slide Microscopy format.

The thumbnail image shows the whole slide image, if it is available for the series in the DICOM file. The whole slide image is opened in the viewport by default. The overview window in the bottom left corner of the viewport displays the boundaries of the whole slide image and red rectangular marking the slide region that is currently visible in the viewport, further called viewed region.

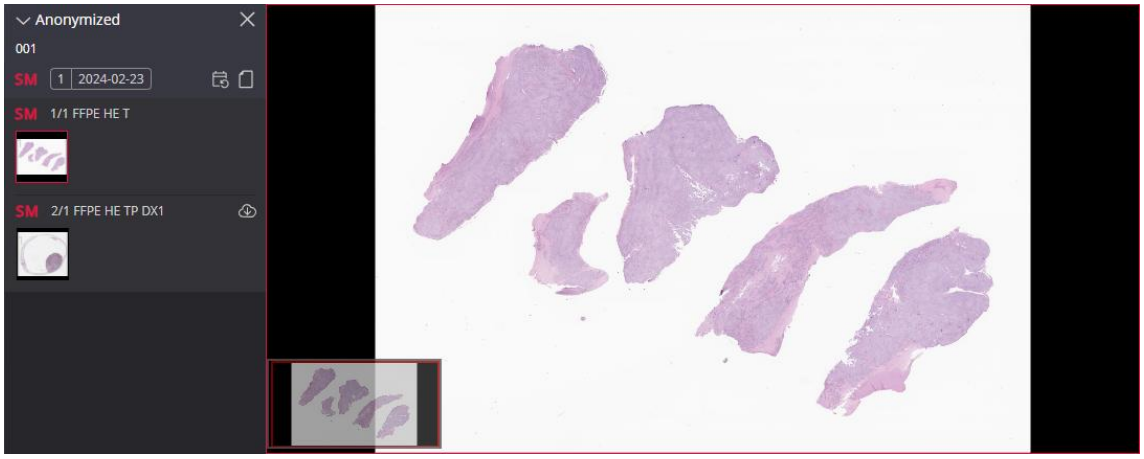


Figure 400. Displaying the whole slide image of the slide microscopy modality

⚠ **NOTE!** The overview window fades in few seconds. Point the mouse cursor to the viewport with slide microscopy image for system to display the overview window again.

In case the whole slide image is not available in the DICOM file, the system shows default slide microscopy thumbnail image. When opening such series, the system displays white image in the overview window to represent the boundaries of the whole slide image, and the middle slide region from the volume with lowest resolution is opened in the viewport by default:

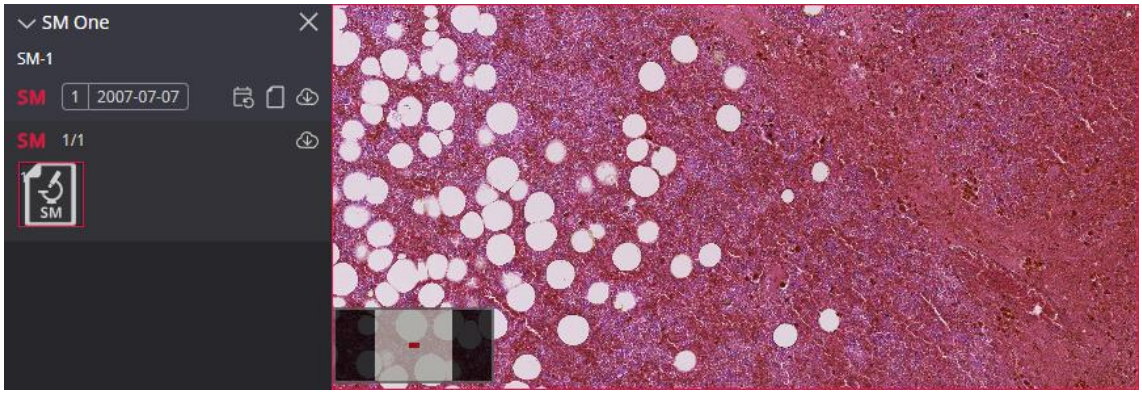


Figure 401. Displaying the slide microscopy series if whole image is not available

The following tools may be used to view the slide microscopy images:

- Zoom with mouse zoom to change the scale of the displayed slide microscopy image. While zooming the red rectangular that marks the viewed region is automatically resized in the overview window. In case the slide microscopy series has volumes of different resolution, the appropriate higher resolution volume or lower resolution volume is automatically selected while zooming:

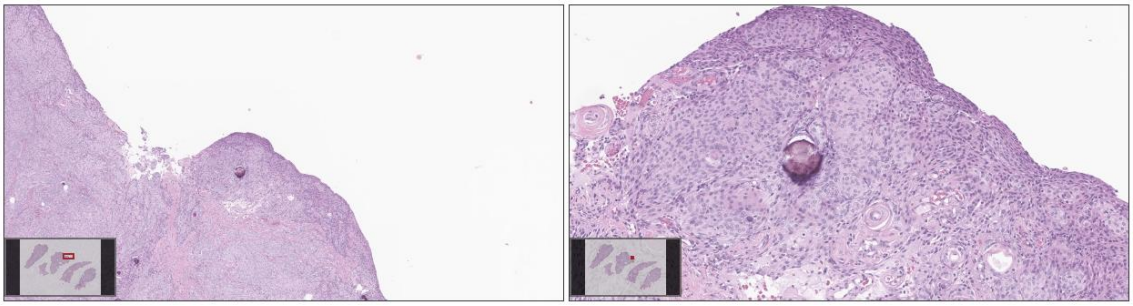


Figure 402. Slide microscopy images of different resolution

- Move the image with mouse pan tool to change the viewed region. While moving the image the red rectangular that marks the viewed region is automatically moved in the overview window.
- Quickly change the viewed region to the required part of the slide by double clicking with the left mouse button on the desired place in the overview window. The center of the rectangular red that marks the viewed region is automatically placed at the click point.

MedDream DICOM Viewer Chrome browser extension for multi-monitors

Requirements

- MedDream DICOM Viewer multi display browser extension requires Google Chrome browser version 52 or newer.
- The multi display functionality supported only with https protocol.
- Multi display requires more than one display.
- Recommended to have monitors with the same resolution (and Windows PC - the same scale), to expand browser content to correct size and position.

Extension installation

1. Extension can be found here:
- Open Google Chrome Properties -> More tools -> Extensions:

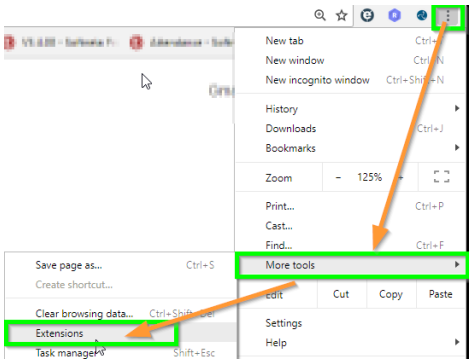


Figure 403. Chrome properties

In opened window select Extensions (in the left upper corner) -> Open Chrome Web Store

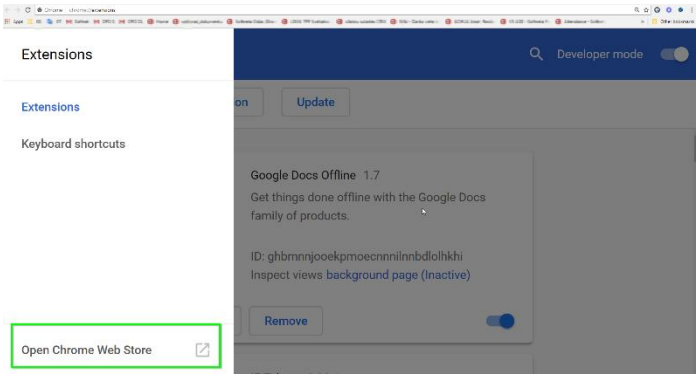


Figure 404. Chrome web store

- Go directly to Google Chrome extensions website -> https://chrome.google.com/webstore/category/extensions

2. Search for MedDream browser extension: type “meddream” or “multi-monitors” in the search field.

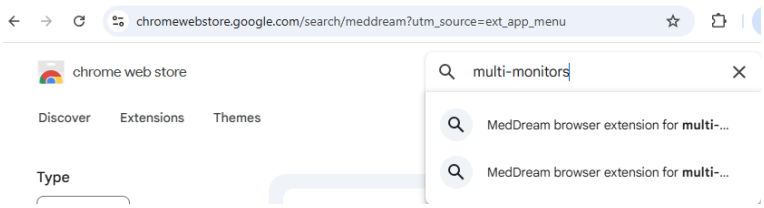


Figure 405. Filtering MedDream extension

3. Find the “MedDream browser extension for multi-monitors” in Extensions list, select to add the extension by pressing the Add to Chrome button, and confirm the installation.

⚠ **NOTE!** The beta version of new MedDream browser extension for multi-monitors is available. For new features and configuration contact to MedDream support at this email: support@meddream.com.beta.

4. The extension is added to the Chrome browser:

- the extension icon is displayed in the browser’s extensions toolbar,
- the notification about possibility to manage the extension by clicking on the icon, or by finding the extension in the extensions list under Extensions menu, is displayed.

Extension configuration

1. Open the extension options window by clicking the extension icon the In Google Chrome browser`s extension toolbar in the right upper corner, or by opening the extension from extensions list, and selecting the extension options.

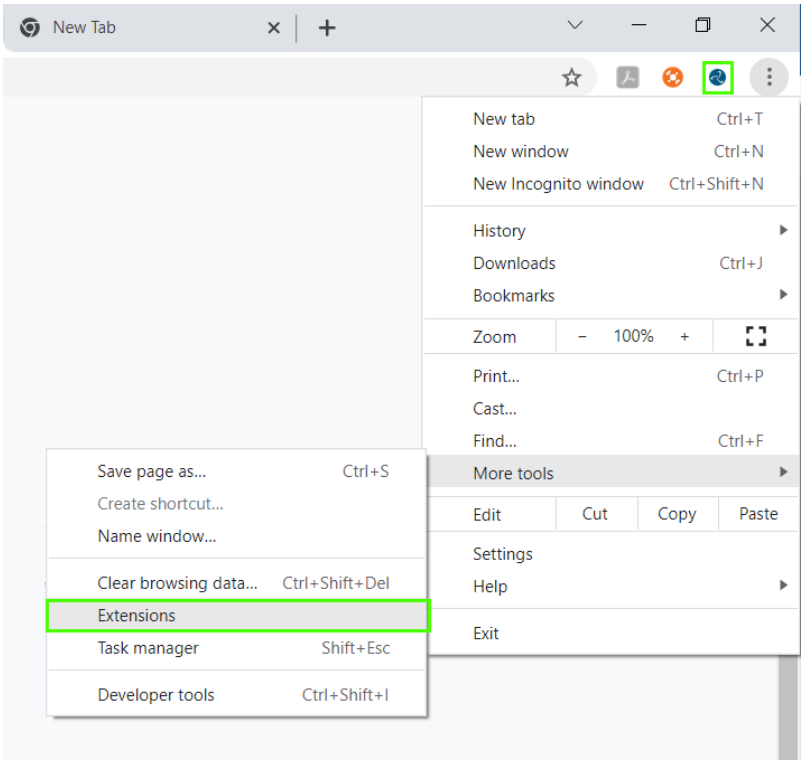


Figure 406. Accessing the options of the added MedDream extension

⚠ **NOTE!** Please note, that parameters are stored in browser local storage, thus after deleting temporary files should be set up again.

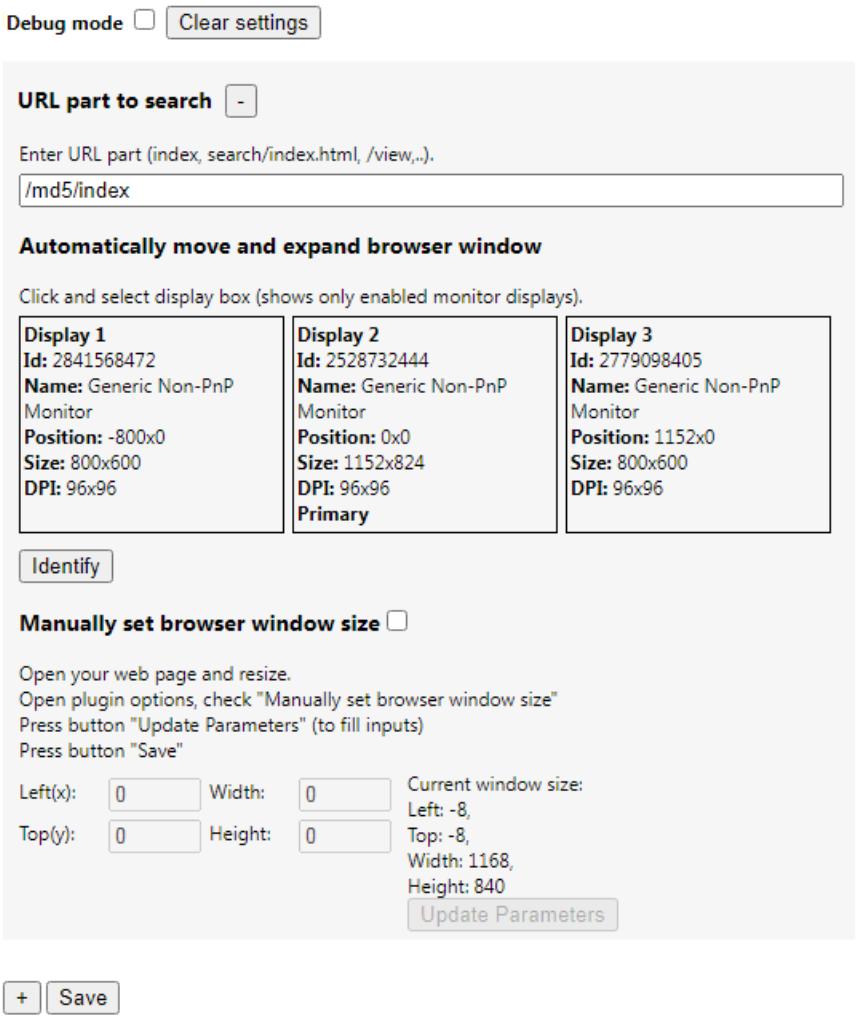


Figure 407. MedDream extension options window with 3 monitors

2. The user can change the following options:

- Debug mode:

Check the **Debug mode** check box to inspect extension logic (find URL) and calculations (set window position and size). In console window, will display information about founded window and options that will try to apply.

Pressing the **Clear settings** button resets options and clears all saved settings. Extension is using chrome.storage.local to save all data.

- URL part to search:

Write appropriate URL context path or part in entry field. This will be used to find matching URL in new opened or refreshed windows.

> Example: for MedDream DICOMViewer 7.5 version or newer -"/view", "IP/view", for older versions- "md5/index", "index.html".
>
> ⚠ **NOTE!** Settings will not be savded, if URL context path is empty.

Pressing the **Remove** - button removes your created options for URL part for search.

- Automatically move and expand browser window:

Select displays (PC monitors) to automatically adjust matching window position and size. Selected display will be marked with green color and word “Selected”:

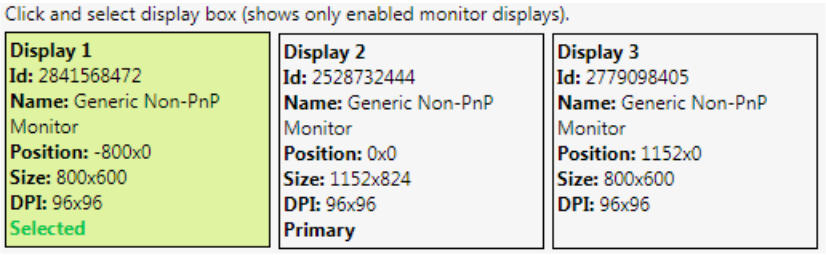


Figure 408. Display 1 monitor selected

Pressing the **Identify** button shows display numbers in each display (PC monitor) left bottom corner. It allows to identify, in what order extension sees displays.

- Manually set browser window size:

Check the **Manually set browser window size** check box to set matching window position (Left, and Top inputs) and size (Width, and Height inputs).It is useful to set custom position and size if displays (PC monitors) are not the same size or different DPI.

Pressing the **Update Parameters** button quickly fills **Left**, **Top**, **Width** and **Height** inputs with values of current active window. If the user opens a new window, position and reseize this window, and then in the same window opens extension option window, the calculated current window size and position should be displayed.

⚠ **NOTE!** Settings will not be savded, if position or size inputs are empty.

- Pressing the Add [+] button adds another **URL part for search block** options. This allows different URL have different window size and positions.
- Pressing the **Save** button saves all options.

3. Option setting workflows:

- Set to automatically move and expand browser window:

Open MedDream extension option window.

Fill **URL part for search** input with matching URL part.

Click on desired displays in **Automatically move and expand browser window**.

Press button **Save** and try open or refresh your window.

- Manually set browsers window size:

Open your MedDream viewer window which you want to expand on more than one display.

Move to desired position and resize browser window.

Open MedDream extension’s option windows.

Select checkbox **Manually set browser window size.**

Press button **Update Parameters** to fill inputs(top, left, width and height)with current window size or fill manually.

Press button **Save** and try open or refresh your window.

- **Examples**. When MedDream DICOM Viewer will be opened, the extension detects context path and automatically seizes web browser window in specified displays. It is recommended to use appropriate thumbnail layout like Thumbnail Top or Thumbnail Down.

⚠ **NOTE!** If using multiple viewports layout with several monitors in Chrome browser and with window placement allowed, the system displays the whole viewport inside one monitor, and maximize the viewport inside one monitor.

⚠ **NOTE!** For proper viewports placement in several monitors, the monitor resolution and window scale must be the same.

⚠ **NOTE!** When opening MedDream for the first time on a particular browser, you should get a prompt that the website wants “manage windows on all your displays”, and then click “Allow”. If not prompted, or previously blocked, this can be adjusted by clicking the “lock” icon near the URL, choosing “Site settings” and looking for “Window management” there.

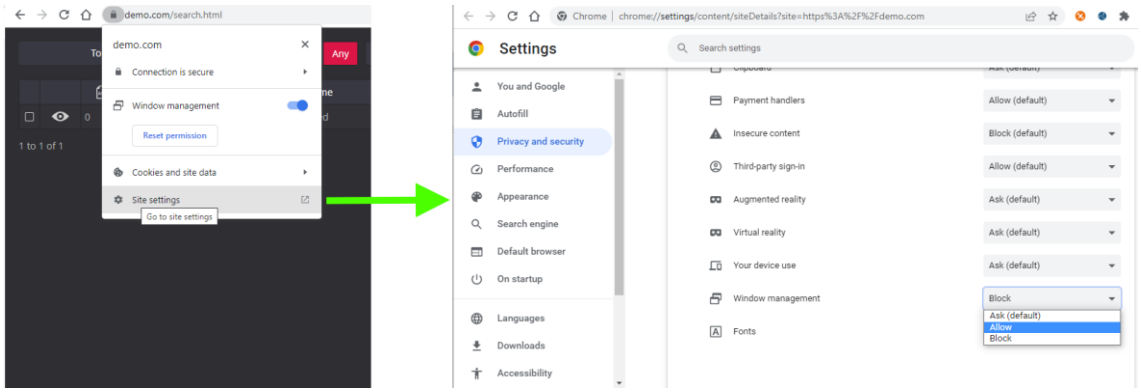


Figure 409. Configuring window management

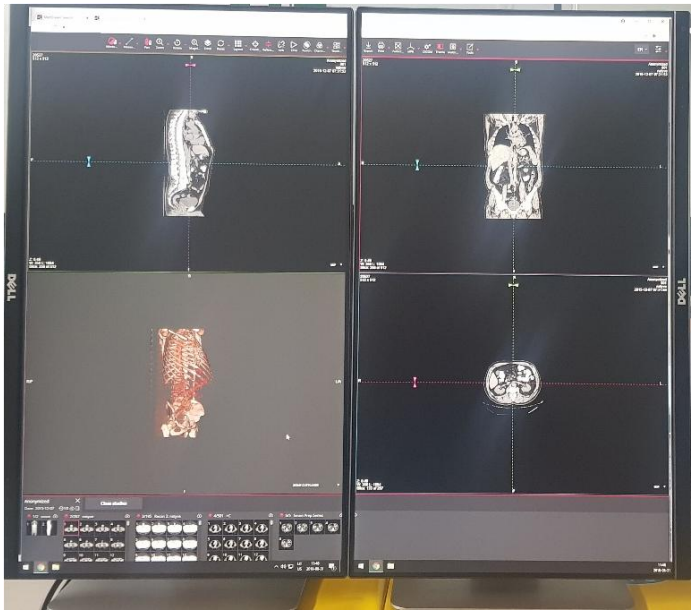


Figure 410. MedDream DICOM Viewer on 2 displays



Figure 411. MedDream DICOM Viewer on 3 displays

Size and position of window

Modal dialog

Each modal dialog in the system is designed to fit one of the width groups:

- narrow dialog with a width of 570 pixels,
- medium dialog with a width of 750 pixels,
- wide medium dialog with a width of 850 pixels,
- wide dialog with a width of 1200 pixels.

⚠ **NOTE!** The default width of each width group may be changed in configuration.

By default, system opens the dialog in designed or configured width for this group and aligns it horizontally in the center of the parent window, and vertically at the top of the parent window. If the default dialog size or position is inconvenient, for example in large monitors, or when multiple monitors are used, the user can change it.

To change the width of the dialog window, perform the following:

- hover the mouse pointer over the gray triangle at the bottom right corner of the dialog window (the cursor should obtain the resize cursor look),
- press the left mouse button, and drag the mouse right or left to change the size of the dialog window,
- release the mouse button when the dialog has the preferred size.

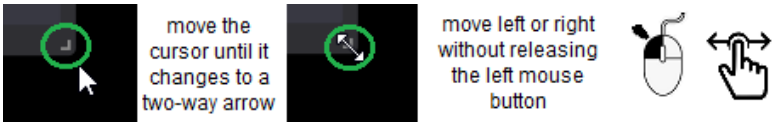


Figure 412. Modal window resizing

⚠ **NOTE!** The dialog height may be changed only for dialogs with dynamic content resize. If needed, the separate heigth may be set for any dialog window in system configuration.

⚠ **NOTE!** By default, the width is changed for all the dialogs, that belong to the same width group. If needed, the separate width may be set for any dialog window in system configuration.

⚠ **NOTE!** The new size of the dialog is saved in browser local storage at the dialog close and is applied next time the dialog is opened.

To change the place of the dialog window in the parent window, perform the following:

- hover the mouse pointer over the title of the dialog window (the cursor should obtain the move cursor look),
- press the left mouse button, and drag the dialog window,
- release the mouse button when the dialog is in the preferred position.



Figure 413. Changing the modal window position

⚠ **NOTE!** The system saves the distance from the top left corner of the parent window in browser local storage on dialog close and opens modal dialog at this place of the parent window next time.

Non-modal windows

Non-modal windows do not disable the main content and the user can continue interacting with the viewport.

The size depends on the features available in the window, and by default it is displayed in the top right corner of the viewer. If the user changes the size and/or position of the window, the next time the window will be based on the saved parameters.

The user can move, resize, minimize, or close the non-modal window.

To reduce or enlarge the window, select the triangle  in the lower right corner of the window. Then the cursor changes to a two-way arrow, press the left mouse button, and move in any direction without releasing the button.

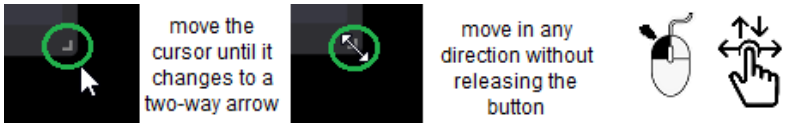


Figure 414. Resizing the non-modal window

If the non-modal window covers the view, you can change the position of the window: hover over the top of the window until the cursor changes to a four-way arrow, then press the left mouse button and move in any direction without releasing the left button.



Figure 415. Changing the non-modal window position

If you are temporarily not working in a non-modal window, you can minimize it by clicking . Or you can maximize a non-modal window by clicking . To restore the previous non-modal window size, click .

To resume the action, click again to maximize the window.

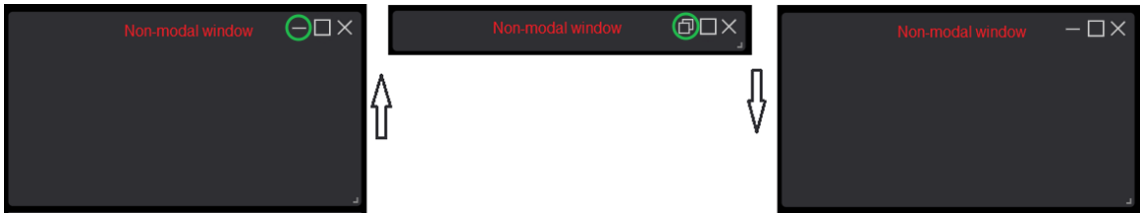


Figure 416. Minimizing the non-modal window

To close the non-modal window, press .

Export and Forward

Clicking the export menu in Search window or Viewer window opens the Export window. Clicking the forward menu in Search window or Viewer window opens the Forward window.

NOTE! Forward and Export functions are not available in Search results window if working in mobile mode.

CAUTION! Export, and Forward functionality may be disabled. Contact the system administrator to verify the configuration, if export or forward is missing.

You should select the studies that you are going to export or forward in advance. The study selection in Search window is done by marking the tick-box as described in section “Search of studies”. The study selection in Viewer window is done by activating the required viewport as described in sections “Forward” and “Export”. The selected studies are displayed in export or forward window. The studies list contains the following information about the study:

- **ID** - patient's identification number,
- **Name** - patient's name and surname,
- **Modality** - the method which was used to obtain the study images (modality),
- **Description** – the study description,
- **Date Time** – study date and time,
- **Source AE** – device from where the study was sent to the PACS.

Forward window

The **Forward** dialog can be opened from the viewer or from the search results list. In both cases, studies can be forwarded. When the Forward dialog is opened from the viewer, it also provides the option to forward study series and/or individual series images.

Click the **Forward** button. The Forward dialog is displayed:

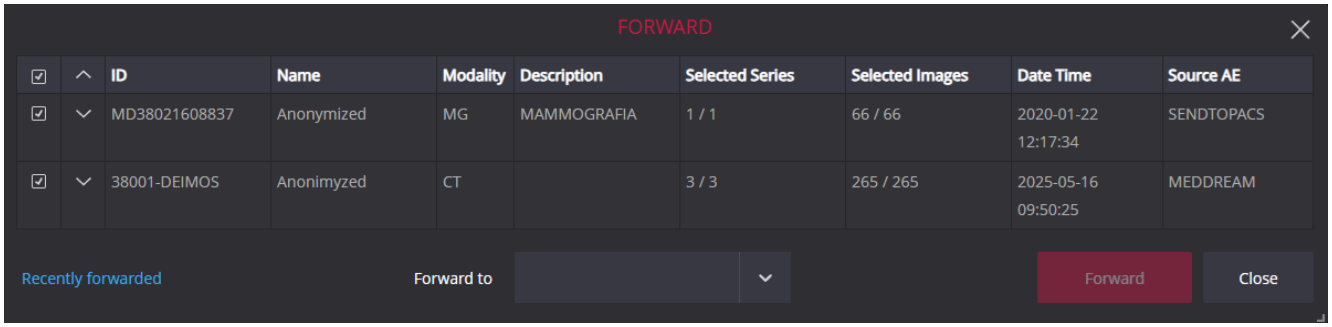


Figure 417. Forward window

When the Forward dialog is opened from the search results list, its layout is the same; however, it is not possible to expand a study into a list of series, and the informational columns for selected series and images are not displayed. In addition, all studies in the list are selected by default.

If there are no studies open in the viewer or no study is selected in the search results list, the message “The list is empty” is displayed.

When opened from the study viewer, study selection in the list is performed automatically:

- if the active viewing area displays a study image, the corresponding study is selected;
- if the active viewing area is empty, all studies are selected.

To expand a study into the series list, click the expand button  .

The list expands to the series level—each row displays the series thumbnail, number, type, description, and information about selected images.

Automatic selection can be modified manually:

- To select all studies, check the checkbox in the header row.
- To select an entire study, check the checkbox in the study-level row or in the series header row.
- To select all images in a series, check the checkbox in the series row.

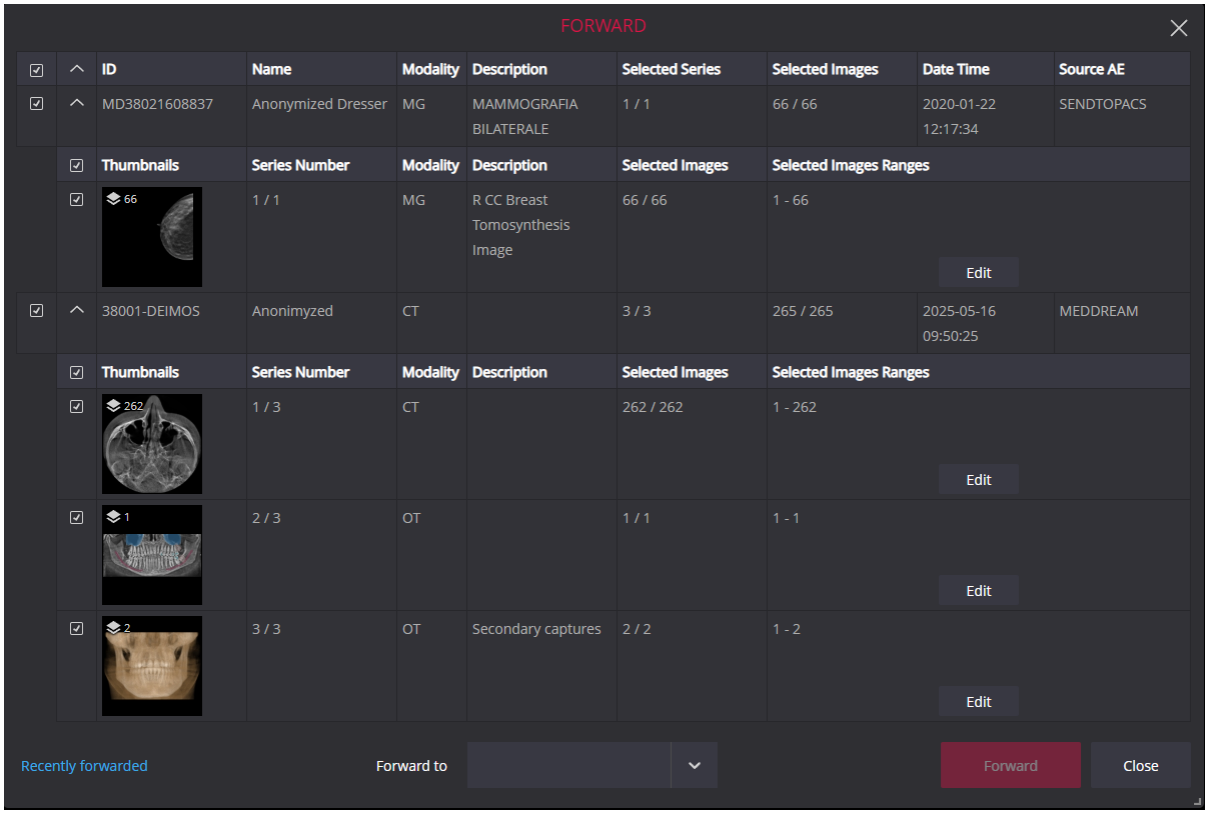


Figure 418. Forward window. Series level

The checkbox has three states: unchecked, checked, and partially checked  . The partially checked state indicates that not all study series and/or not all images within a series are selected.

To select specific series images for forwarding, click the “Edit” button in the “Selected Image Ranges” column.

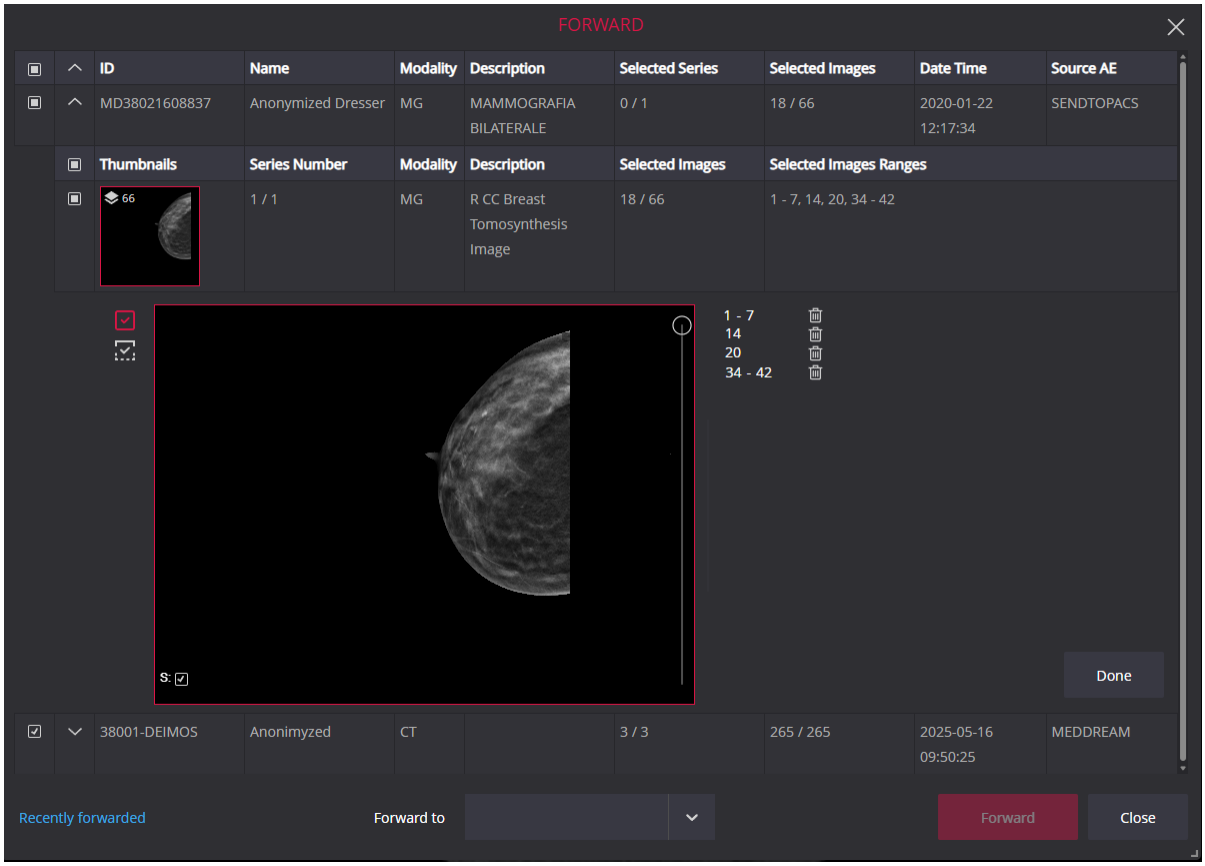


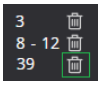
Figure 419. Forward window. Images level

The system opens the series image preview area, where the user can scroll through the images using the slider or mouse wheel and select a single image, a range of images, or all images in the series.

Action buttons:



To mark a single image, scroll to it in the list and click the marking button on the left side of the Viewer window.
After the image is marked, the action button becomes highlighted.
To unmark the image, press the marking button again – it will become unhighlighted.
An image or image range can also be removed by selecting it in the list and pressing the remove button. For example:





To start selecting a range, click the range start selection button.
Once selected, the button changes to the range end selection button.
Scroll through the images using the slider or mouse wheel until you reach the last image you want to select, then click the end button.

To finish the action, click the “Done” button.

After selecting one or more studies, series, or images, choose a device from the **Forward to** dropdown list. Only devices defined in the system configuration are displayed in the list.

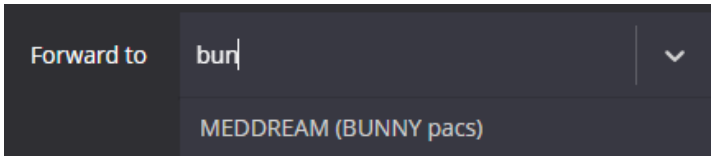


Figure 420. Searching for the forward destination

⚠ **NOTE!** Each PACS device may have different forward destinations configured. If studies from different PACS are marked for forward, only the forward destinations, that are common for all the PACS, are displayed in the forward destinations list.

⚠ **NOTE!** For proper forward functioning the forward destination should be properly configured and the device should support DICOM saving functionality.

To start forwarding, click the “Forward” button in the Forward dialog:

- if the list of studies or devices is empty, an error message is displayed and forwarding is not performed;
- once forwarding is initiated, an informational message is shown and the “Forward” button is temporarily disabled.

To view the status of requested forwarding processes, click the **Recently forwarded** link in the Forward dialog:

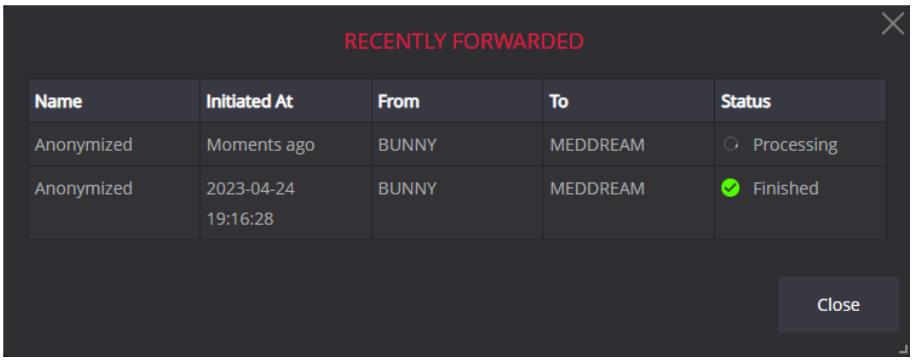
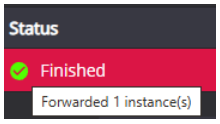


Figure 421. Forward processes list in Recently forwarded window

The forward processes list contains the following information about each forward process:

- **Name** - patient's name. Multiple commas separated names are displayed, if several studies for different patients are forwarded;
- **Initiated at** - date time, when the forward process was initiated. For processes, that are initiated less than 1 minute ago, the value *Moments ago* is displayed;
- **From** – the name of storage from which the study is forwarded. Multiple commas separated names are displayed, if several studies from different storages are forwarded;
- **To** – forward destination;
- **Status** – status of the forward process. The possible values:
  - *Waiting to be picked up* – waiting for response from forward service;
  - *Preparing* - forward process initialization, that might take a long time in some cases, is in progress;
  - *Processing* - forward process is in progress;
  - *Finished* – forward process is finished;
  - *Error* - error occurred during forward process.

The additional information about the number of forwarded studies is displayed in the hint of the completed forward process status



Click the **Close** button to close the **Recently forwarded** window and return to the **Forward** dialog.

Click the **Close** button in the **Forward** dialog once you have initiated all required forwarding tasks.

⚠ **NOTE!** The Recently forwarded window shows the last ten forward processes that were initiated from the current browser window. You can access the forward processes list from the Forward window until the browser window is not closed.

⚠ **NOTE!** The Viewer windows don't share the forward processes list, and each browser window or tab has separate list in Recently forwarded window.

Export / Burn to CD/DVD window

To export the selected studies, click the **Export** button. The system displays the Export window:

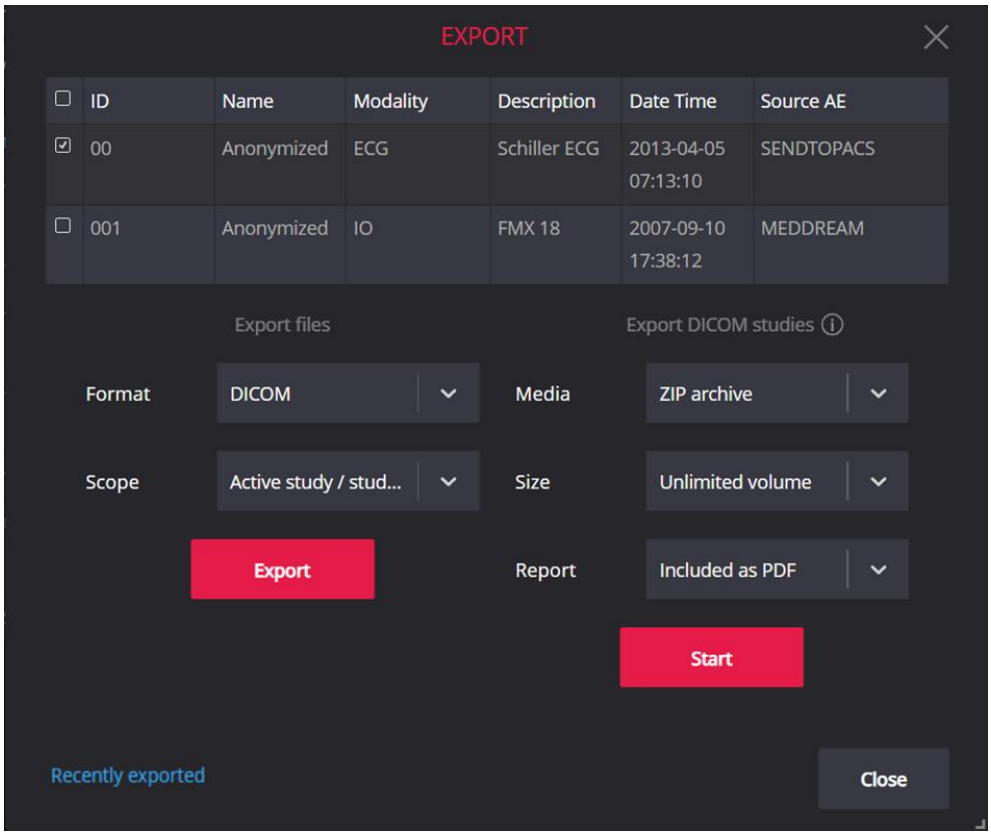


Figure 422. Export window

Studies list at the top of the window contains the studies that you have selected for export. If no studies were selected, the "Empty list" message is displayed.

⚠ **NOTE!** The studies list may include DICOM studies as well as non DICOM files. Only **Export files** option is applicable for non DICOM files.

If export in the Viewer window is selected for the currently viewed image, series, or study, only this study is marked at the Export window opening. Otherwise, all the studies in the list are marked. To change the selection, press and mark the tick-box next to the study.

⚠ **NOTE! Report** options field is available only if report exporting is enabled in report settings.

I. Export files

To save the selected for export studies in the archive file on the local disk, do the following:

1. Select the file saving format in the **Format** field:

if **DICOM** format is selected, the output archive contains DICOM files;

if **JPEG/MP4/pdf** format is selected, the output archive contains jpg, mp4(mpg) or pdf files, depending on image format;

if **TIFF/MP4/pdf** format is selected, the output archive contains tiff, mp4(mpg) or pdf files, depending on image format;

if **PNG/MP4/pdf** format is selected, the output archive contains png, mp4(mpg) or pdf files, depending on image format;

if **BMP/MP4/pdf** format is selected, the output archive contains bmp, mp4(mpg) or pdf files, depending on image format.

⚠ **NOTE!** The non DICOM files are included into archive in the original format. The Format selection will be disabled, if only non DICOM files are selected for export.

⚠ **NOTE! JPEG/MP4/pdf**, **TIFF/MP4/pdf**, **PNG/MP4/pdf**, and **BMP/MP4/pdf** formats are disabled in the following conditions:

- At least one study contains object of SR or ECG type, if study export (Active study / studies) is selected.
- The active series contains object of SR or ECG type, if series export (Active series) is selected.
- The active image is SR or ECG type, if image export (**Active image / video**) is selected.

⚠ **NOTE!** If DICOM file format is selected, the archive will include additonal data. The presentation states for series images are included in active series archive. All the related data, like presentation states, key object, segmentation data, secondary captures, are included in study archive.

2. Select the export scope in the Scope field:

selecting the Active image / video, exports the image from the active viewport;

selecting the Active series, exports the series of the active image;

selecting Active study / studies, exports all the selected studies.

⚠ **NOTE! Active image / video** and **Active series** scopes are enabled only for active study export from Viewer window.

3. Click the **Export** button.

The system launches export process and disables the Export button, while the export process is ongoing. If you do not close the export window until the export to file is successfully ended, you can download the created archive from the export window:

The button 

for saving the created archive is displayed bellow Export button.

The Export button color is changed to gray, indicating that archive with currently selected export options is already created.

⚠ **NOTE!** You can close the Export window after initiating the export. You will be notified about the finished export in Viewer window, and will be able to download the created archives in the Recent Export Jobs window.

II. Export DICOM studies and portable viewer

The system provides possibility to export the one or more studies in DICOM file format, and save it as ZIP or ISO archive, together with portable viewer software. All the study related data, like presentation states, key object, segmentation data, secondary captures, are included in study archive.

⚠ **NOTE!** The viewer may be included in archive, if the appropriate viewer software is provided and system administrator configures to enclose it in export archive.

⚠ **NOTE!** The system may be configured to generate and include into the archive web content and index page for previewing the study images in the web browser. Be aware that web content images are not of diagnostic quality, and not generated by default configuration.

To export the selected studies, do the following:

1. Select output archive type in **Media** field:

by default, **ZIP archive** option is selected;

select **ISO disk image** option, if you need the archive of ISO format or to burn the CD/DVD disk.

2. Select archive size in **Size** field.

⚠ **NOTE!** For ZIP archive Size selection is disabled, and Unlimited volume is selected by default.

The following media sizes are provided for ISO disk image in default system configuration:

Unlimited volume format for image saving in a single file;

CD format for image split to 650 MB volumes;

DVD format for image split to 4.7 GB volumes;

Dual-Layer DVD format for image split to 8.5 GB volumes.

⚠ **NOTE!** The media sizes may be supplemented or replaced with other values by system administrator.

⚠ **NOTE!** Only Unlimited volume size option is allowed, if web content is configured and included into archive.

3. Select either you need to include the study's **Report** in archive:

⚠ **NOTE! Report** options field is available only if report exporting is enabled in report settings.

You can select the following options:

Included as PDF, if you need the study's report to be included in study's archive;

None, if you do not need report to be included into archive.

⚠ **NOTE! Included as PDF** option is not displayed, if no one of the studies, that were selected for export, has the saved report.

4. Click the **Start** button.

The system launches export process and disables the Start button, while the export process is ongoing. If you do not close the export window until the process is successfully ended, you can download the created archive from the export window:

The list of created volumes and controls for saving them are displayed in Export window:

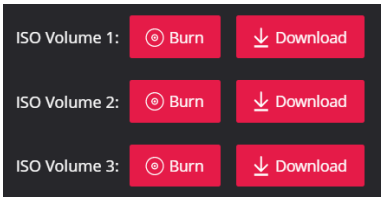


Figure 423. ISO volumes list and saving buttons

The **Start** button color is changed to gray, indicating that archive with currently selected export options is already created.

⚠ **NOTE!** You can close the Export window after initiating the export. You will be notified about the finished export in Viewer window, and will be able to download the created archives in the Recent Export Jobs window.

⚠ **NOTE!** The **Burn** option is not displayed for ZIP archive.

⚠ **NOTE!** For Burn functionality, the burning software must be installed and the automatic burning software launch must be configured on user's machine.

Recent Export Jobs window

You can open the Recent Export Jobs window in such ways:

- By clicking the **Recently exported** link in Export window;
- By clicking the **Recently exported** link in notification about finished export:

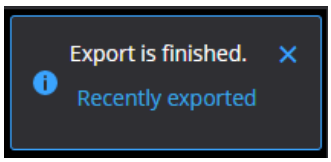


Figure 424. Notification about finished export

- By clicking the **Recent Export Jobs** item in Export drop-down menu.

The Recent Export Jobs window displays the list of export jobs:



Figure 425. Recent Export Jobs window

The list contains the information for easier identification of the export job:

- **Patient Name** - patient's name. Multiple commas separated names are displayed, if several studies for different patients are exported;
- **Initiated at** - date time, when the export process was initiated. For processes, that are initiated less than 1 minute ago, the value *Moments ago* is displayed;
- **Contents** describes what was included into archive. It could be one instance, series, study or multiple studies. If portable viewer or report is included, this information is provided in content field;
- **Format** details either the format of exported instances for files export, or output archive format for DICOM studies export;
- **Media** provides the size of output media and is applicable only for DICOM studies export;
- **Download** displays the links for archive download. The **Download** link is displayed for ZIP archive. The **Burn**, and **Download** links are displayed for each volume of ISO archive. In case of error in export process, the error information is displayed in Download field instead of download links.

Click **Close** button to close the Recent Export Jobs window.

⚠ **NOTE!** The storage time of created archive depends on the system configuration. If the archive was deleted, such export job is not displayed in the Recent Export Jobs window.

⚠ **NOTE!** The Viewer windows don't share the export processes list, and each browser window or tab has separate list in Recent Export jobs.

Upload



The "Upload" tool allows users to upload DICOM files to the PACS system from their computer or another storage location accessible to them.

⚠ **NOTE!** To use the Upload tool, it must be enabled in the system configuration, the PACS system path must be defined, limiting parameters must be configured, and the user must be granted upload permissions (described in more detail in the installation documentation).

When selecting the Upload function  , a dialog box opens where you need to choose a file or a folder containing the data files.

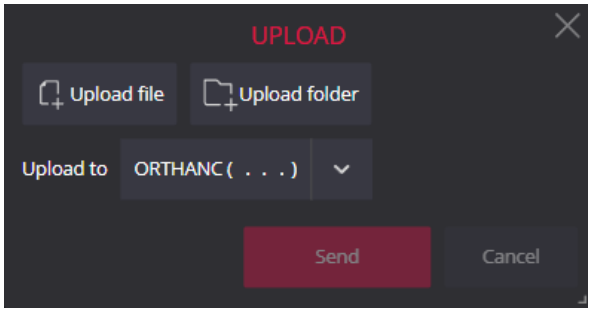
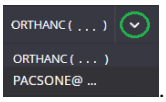
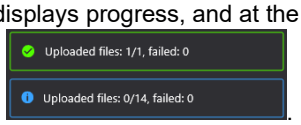


Figure 426. Upload functionality dialog

After selecting files, the system displays the number of files, for example: 

You need to select the appropriate PACS system if more than one is specified in the configuration, by expanding the list: 
.

To start the upload, click "Send."

During the upload, the system displays progress, and at the end, it shows a message indicating whether the upload was successful or failed 
.

Report module

The Report window of the system report module is opened by clicking the displayed report icon in the results list of the Search window, or in thumbnail zone, Study modal, or toolbar of the Viewer window:

- Create report  icon is displayed, if the study does not have saved report and the user has right to edit reports.
- Edit report  icon is displayed, if the study has saved report and the user has right to edit reports.
- Open report  icon is displayed, if the study has saved report and the user has right to view reports.

  ⚠ **NOTE!** If integration with third-party reports is configured, instead of the report, that is created in the system, the third-party generated PDF report may be displayed.

⚠ **NOTE!** The **Report** icon is visible only if the Report module is allowed by license, system configuration, and the user has right to view or edit reports.

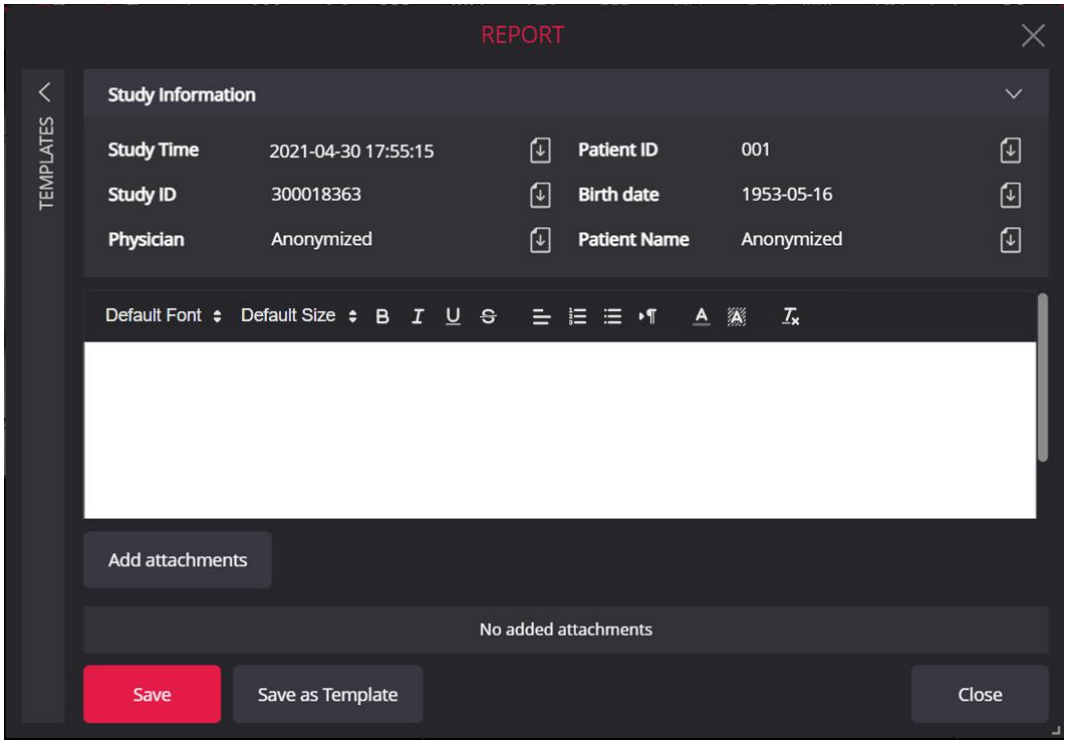


Figure 427. Report window in edit mode is opened after clicking the Create report icon

⚠ **NOTE!** By default, the Report window is opened as modal window. Opening Report window in separate browser tab may be configured in Reports settings (see Settings).

⚠ **NOTE!** The fields in the Study information may not be displayed, if the corresponding data is not obtained from the DICOM file.

⚠ **NOTE!** The default report template may be automatically loaded for a new empty report, if such template is configured in the system.

By default, the Report window size is adjusted to the screen size, Sdudy information is expanded, and Templates group is collapsed and displayed either on top, or at the left of the main report fields. You can adjust the report's window view and size.

⚠ **NOTE!** The changes in report window size, expand/collapse status of Templates, template group, and Study information are saved in browser local storage and are restored next time the report window is opened by the user.

You can perform the following in the Report window:

- To use and manage the report templates:

To expand or collapse Templates section, click the chevron icon above the Template label;

To open the Template window with the content of current report to be saved as template, click the Save as Template button.

- To view or collapse the study information by clicking the chevron icon on the right of the field.
- To enter and save the report for the study.
- To view and restore the previous report version.

- To print the saved report.

Creating or editing the report content:

- You can enter the report content in editor field. The text and image copy (Ctrl+C), cut (Ctrl+X), and paste (Ctrl+V) is allowed. Use the toolbar above the editor to format text.
- You can use the text direction tool to change from the default left-to-right text writing to the right-to-left text writing, that is used in languages like Arabic or Hebrew.
- You can copy the Study Time, Study ID, Patient ID, Patient name, Birthday, and Physician data from the Study information to report content:
  - place the cursor in the text editor at the position where the data should be copied,
  - click the Paste to report icon on the right of the appropriate field,
  - and the system copies the field value to the specified place.
- You can copy the content from the selected report template to the report:
  - place the cursor in the text editor at the end of the line bellow which you want the template content to be copied,
  - find the template in the templates list, and click the Load template to report icon on the left of the template name,
  - and the system copies the content of the template in a new line.
- To save the report content, click the **Save** button at the bottom of the Report window. The system saves the report content – the notification about saved report is displayed above the editor, and report saving time is displayed in the first row of Study information:

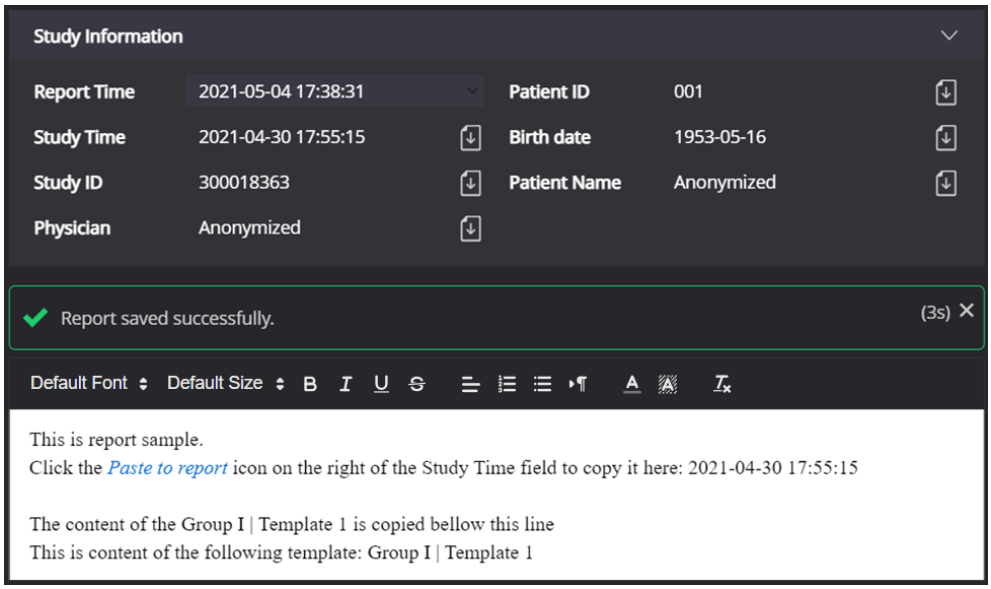


Figure 428. Report content successfully saved

NOTE! The report content size is limited and may be exceeded if images are inserted. Contant your system administrator to check the system logs and configuration, if the error is prompted when saving the report.

- You can apply all the above-described action to edit the content of the saved report either directly after saving, or if opening the previously saved report window with Edit report button. Each time you save the report content by clicking the **Save** button, the system creates a new report version and updates the

saving time in the Report time field. All the attachments that were added to the previous report version are automatically added to the new report version.

⚠ **NOTE!** All the unsaved report content changes are discarded if the Report window is closed with **Close** button.

Managing report attachments:

⚠ **NOTE!** Attachment can be added only to the saved report, and only to the last report version.

- You can add attachments to the saved report:
  - click the **Add attachments** button,
  - select one or more files in the displayed file open dialog and close the dialog with Open button,
  - system saves attachments, and adds to the last saved report version – the notification about saved attachments is displayed above the editor, and added attachments are listed below the Add attachment button:

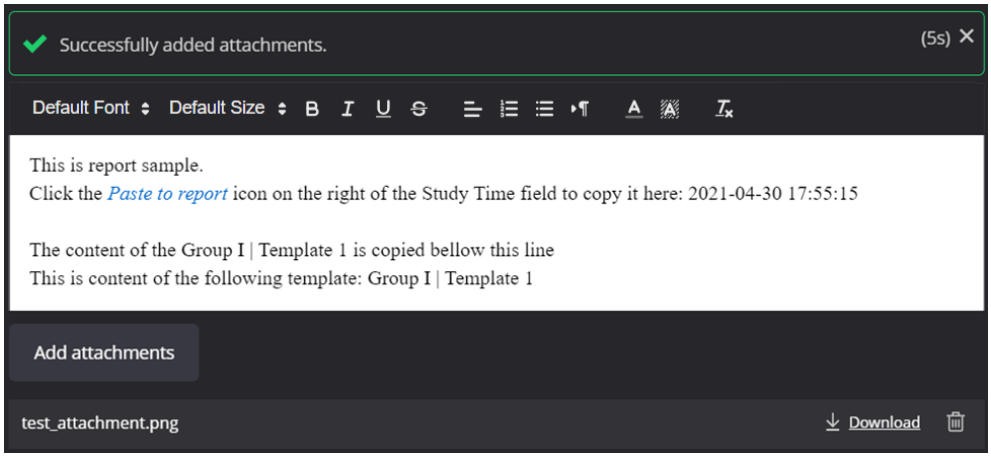


Figure 429. Report attachments successfully added

⚠ **CAUTION!** The size limits for one attachment file and one-time upload package, that are defined in system configuration, cannot be exceeded.

- You can remove the report attachment by clicking the Remove buton on the right of the attachment – system removes the attachment and displays notification above the editor.
- You can download the attachment to your computer by clicking the Download link on the right of the attachment.

Viewing and restoring the previous report version:

- You can view the previous report version, if more than one report version is saved. Click the chevron icon at the right of the Report Time field and select the report version that you want to view from the report versions drop-down list:

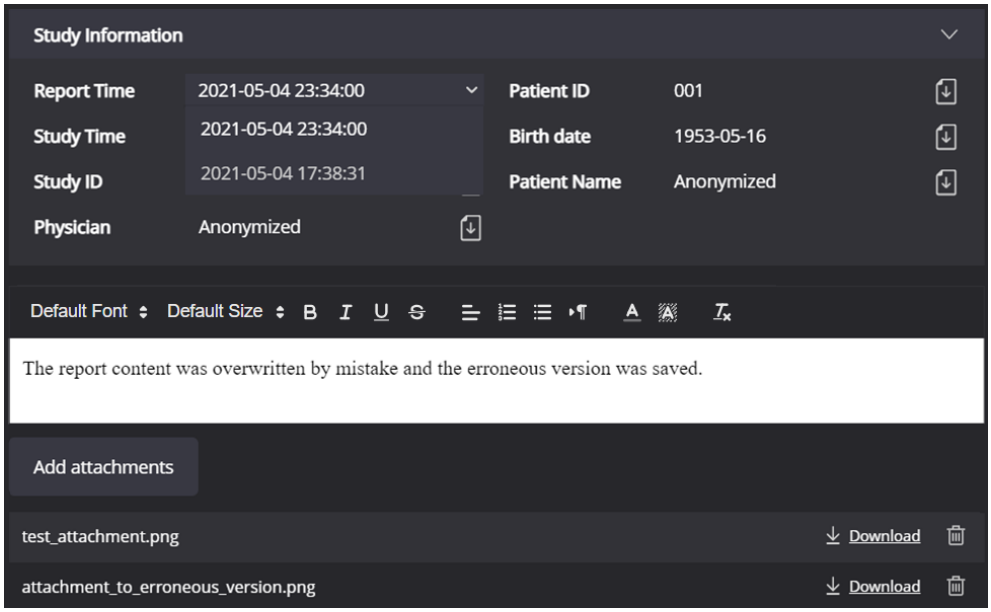


Figure 430. Selecting the report version

- System loads and shows the content of the selected report version. The attachment list displays all the attachments, that were either automatically attached when saving the version, or added to the version by the user after saving.
- You can download the attachments of the report version, view and print the report version. It is not allowed to change the content and attachments of the historical report version.

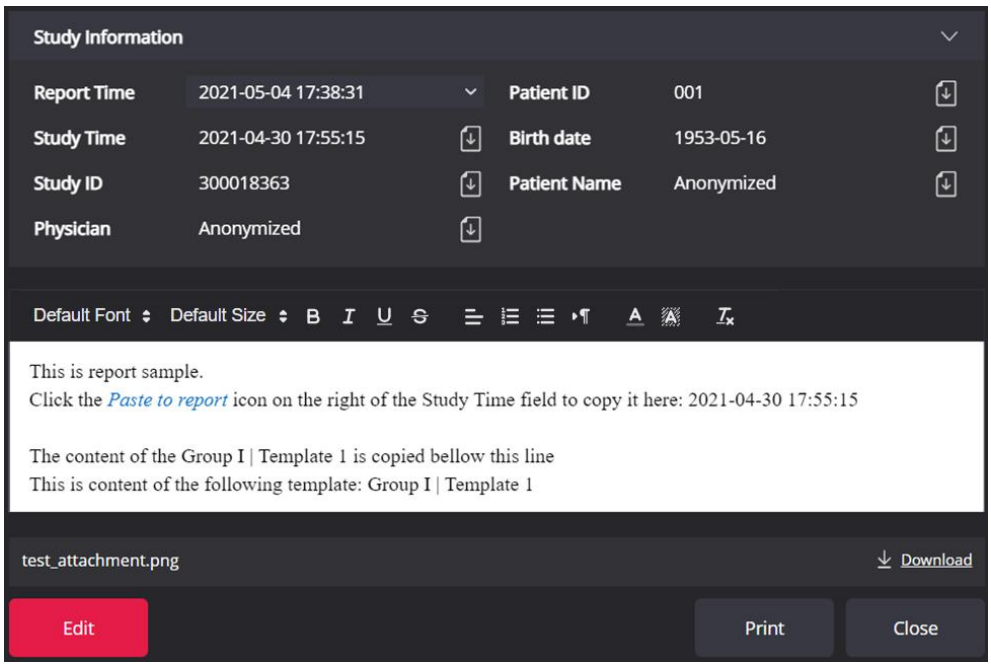


Figure 431. Viewing historical report version

- You can restore the historical report version by clicking the **Edit** button. If action is confirmed, the historical report versions is be saved as the latest.

⚠ **NOTE!** Attachment of the historical report version will be attached to the latest report version, if the historical report version is saved as the latest.

Printing report:

⚠ **NOTE!** The system prints the historical or latest saved report version. You should save the changes you have done, if you want to print them.

To print the report content, click the **Print** button at the bottom of the Report window. The system opens the report print preview in a new browser tab with the report content wrapped in the print template. The print template may include the additional data, such as company logo, users' signature, data from studies DICOM file.

⚠ **NOTE!** Report print template is configured by system administrator. The separate template may be configured for modality, user or user group.

Viewing report:
If the user does not have right to edit report, but has right to view reports, the system opens Report window in view mode:

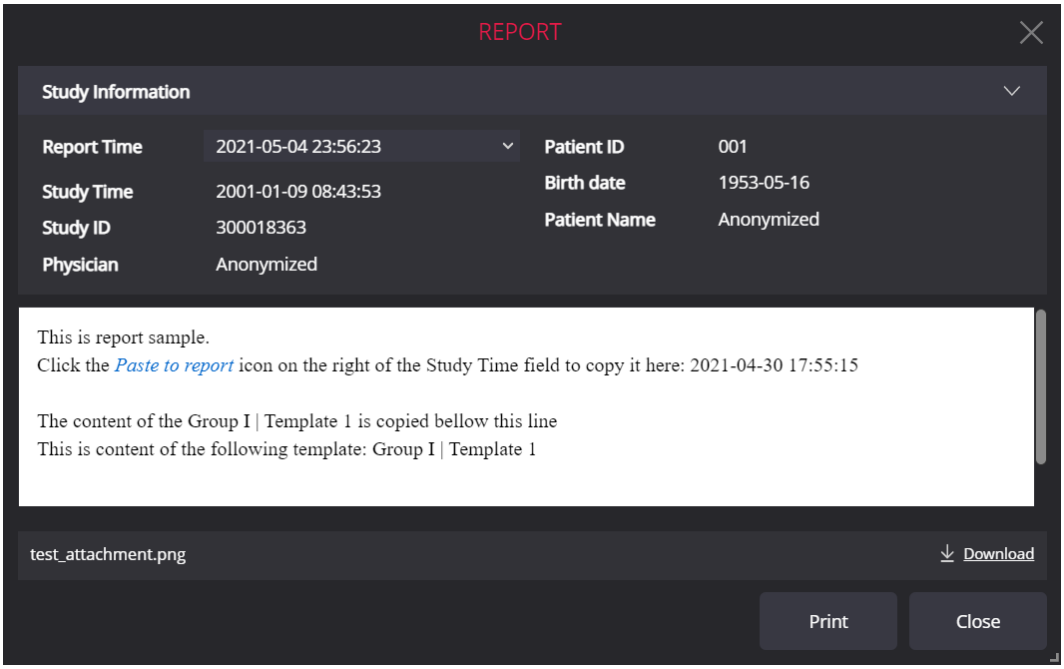


Figure 432. Report window in view mode

The user with report viewing rights can perform the following in the Report window:

- View the content of the historical or latest report version;
- Print the content of the viewed report version;
- Save attachments of the viewed report version in users computer.

Managing report templates

⚠ **NOTE!** The report templates are assigned to the system user and are visible only for this user.

⚠ **NOTE!** The default report template may be configured in the system. The default template is not visible in templates window, but is automatically loaded for a new empty report, if configured.

⚠ **NOTE!** The report templates section in Report window is visible only if the user has rights to edit reports.

User's report templates are displayed in Templates section of the Report window. You should expand the Templates section to view the list of available templates:

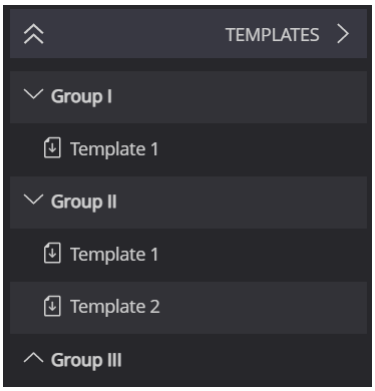


Figure 433. Templates section of the Report window

The templates are grouped by group name, and sorted in a group alphabetically by template name. You can expand and collapse the template group by clicking the chevron icon on the left of the group name. You can expand or collapse all template groups at once by clicking double chevron icon in the templates' header row.

Hover mouse cursor over the group row to see the group management buttons 

. You can do the following actions:

- Press the Edit button, or double-click group name to turn the group name to entry field and edit it directly in templates list;
- Press the Remove buton, and confirm the action to remove the templates group with all the templates in this group.

Hover mouse cursor over the template row to see the template management buttons 

. You can do the following actions:

- Double-click template name to turn the template name to entry field and edit it directly in templates list;
- Press the Remove buton to delete the template. The system shows action confirmation message and deletes the template, if confirmed.

⚠ **NOTE!** The template group will not be displayed, if the last template with this group name is deleted.

- Press the Edit button to view and edit the template's data in Template window:

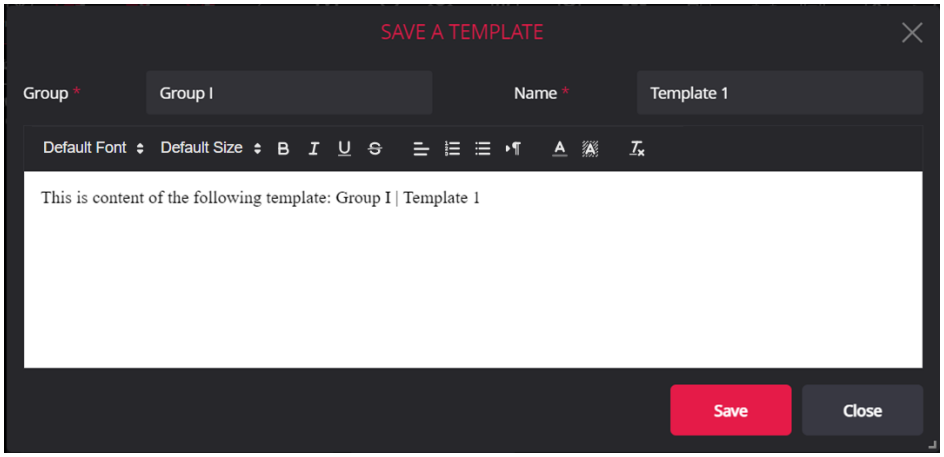


Figure 434. Report template window

NOTE! To create a new template, click the **Save as Template** button at the bottom of the Report window. The system opens Report template window and copies the text displayed in the Report window to it.

You can perform the following in the Report template window:

- To enter or edit group name in Group entry field. If the entered group name equals to the already existing group name, the saved template is displayed in this group. Otherwise, a new group is displayed in template list.
- To enter or edit template name in Name entry field.
- To save the template by clicking the **Save** button. The system saves the template, closes the Template window, and displays the new or updated template in templates list.

NOTE! The report template content size is limited and may be exceeded if images are inserted. Contant your system administrator to check the system logs and configuration, if the error is prompted when saving the template.

NOTE! The changes are not saved, if the Template window is closed with **Close** button.

System menu functions

The section describes all the options that may be displayed under expandable **System** menu  .

The system menu in the Search window contains options: **About, License Agreement, Help, Settings** and **Log Off**. The system menu in the Viewer window contains options: **About, License Agreement, Help**, **Shortcuts, Clear cache**, **Settings** and **Log Off**. Read the conditions, under which the one or more options are not shown, in the Search window and the Viewer window description.

About

Clicking **About** meniu opens the information window:

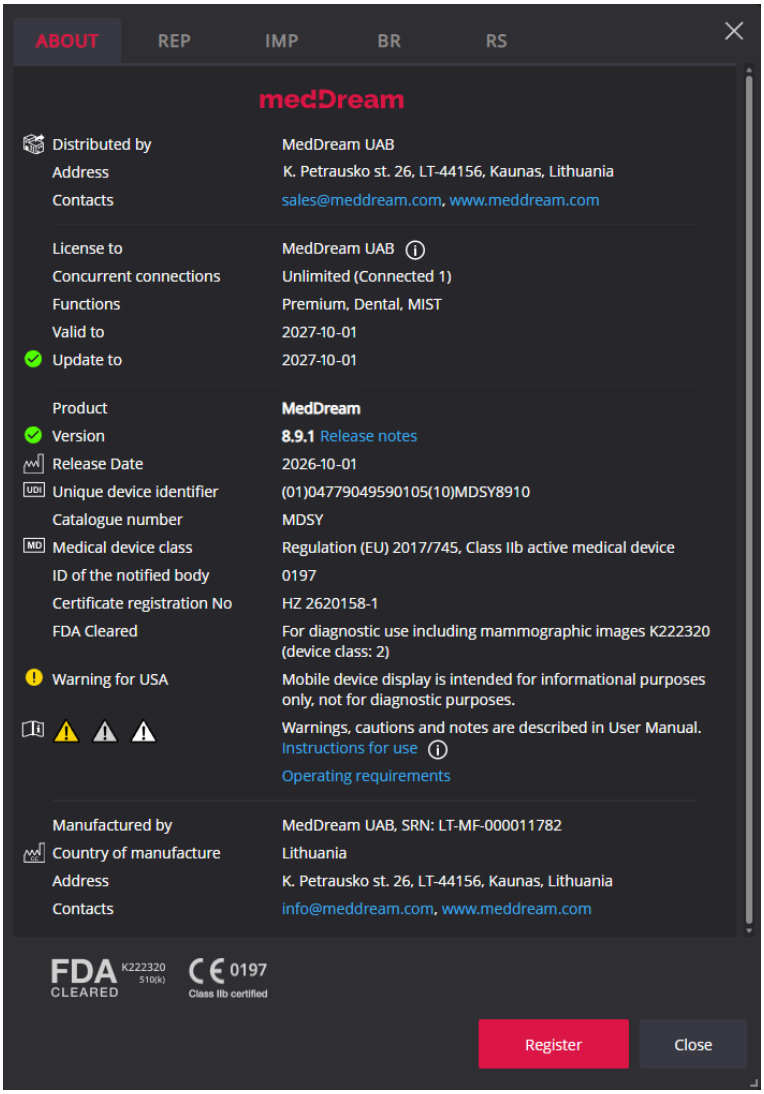


Figure 435. Information window

The information about the product identity is displayed in the following groups, and in the listed order:

- The distributor group contains Distributed by, Address, and Contacts fields, that show name and contacts of product distributor.
- The license group provides the following information about the product license:
  - **License to** contains the information about organization that owns the license of current product installation. If available, the name and contacts of the end user are displayed in the hint of the information icon ⓘ;
  - **Concurrent connections** describe the number of concurrent connections that is issued for the license and the number of currently used connections. The text ‘unlimited’ indicates that number of connections is unlimited;
  - Field **Functions** shows the software edition (Premium, Enterprise or Lite) and modules (for example, Dental module) that are granted by the license;
  - Fields **Valid to** and **Updates to** indicates dates, until the current license is valid and will receive updates;
  - License update status is also provided as a status icon ✓ near the **Update to** field, and the additional information about the update is displayed in the hint of the status icon.

- The product group provides the following information about the product and certification:
  - **Product** provides the official product name;
  - Fields **Version**, and **Release date** holds information about the installed version;
  - The versions' release notes are accessible by clicking the **Release notes** link;
  - Version update status is also provided as a status icon near the **Version** field, and the additional information about the update is displayed in the hint of the status icon;
  - **Unique device identifier**;

Fields **Catalogue number**, **Medical device class**, **ID of the notified body**, **Certificate registration number** and **FDA cleared mark** holds the products' certification data. Warning regarding not using mobile display for diagnostic of mammographic images is available. In addition, the CE and FDA certification logos are displayed at the bottom of the about window, and designated agents contacts are available in REP (representatives), IMP (importers), BR (Brazil) or RS (Serbia) tabs.

NOTE! The certification information is not applicable for VET installation.

Explanation of safety signs is included, with **Instructions for use** link, which opens the user manual of MedDream viewing functionalities, and **Operating requirements** link.

- The manufacturer group contains **Manufactured by**, **Country of manufacture**, **Address**, and **Contacts** fields, that show name and contacts of product manufacturer.

You can open the release notes modal by clicking the **Release notes** link near the version number.

You can initiate the license registration or update by clicking the **Register** button (see description in section "License registration").

NOTE! The **Register** button is visible only if user has administrator right granted by user rights and Settings menu is enabled in system settings.

License Agreement

License Agreement menu opens the **Software License Agreement (EULA)** modal:

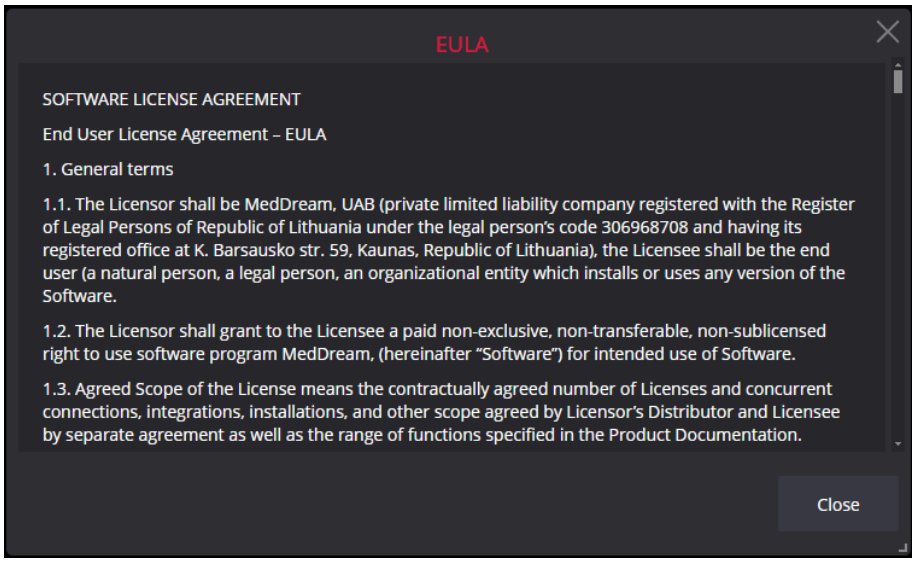
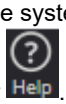


Figure 436. EULA window

Help

Help menu forwards you to the user manual of MedDream viewing functionalities. The user manual also may be accessed from the About window by clicking the **Instructions for use** link.

In addition, the system provides short description of actions for mobile, that may be accessed through the Help tool in toolbar 

. See section “Panel toolbar settings” for toolbar button configuration.

Shortcuts

Shortcuts menu will display modal with keyboard shortcuts and mouse shortcuts tabs.

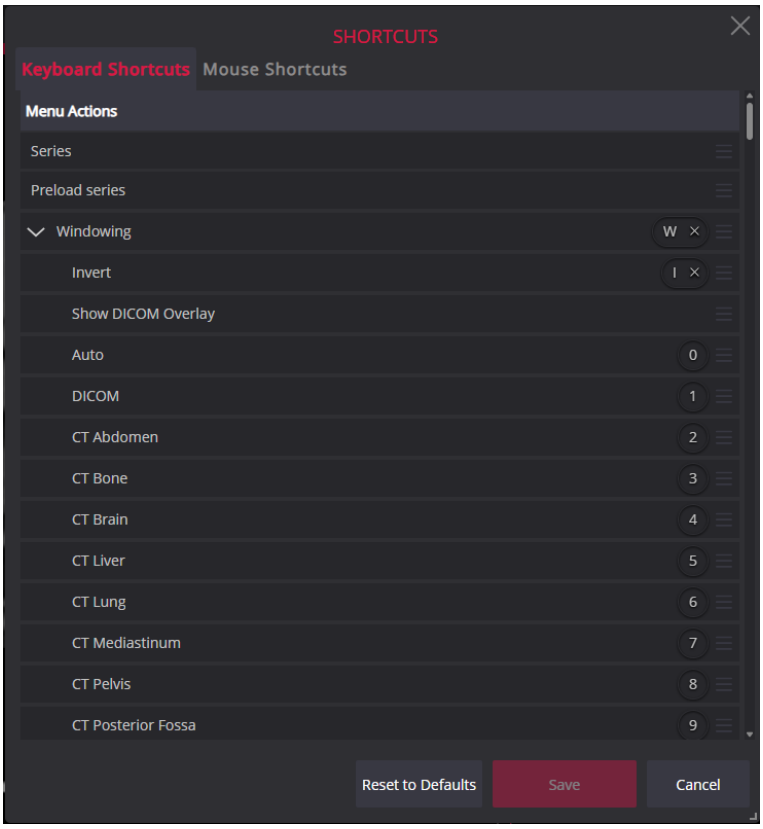


Figure 437. Keyboard shortcuts tab

A *keyboard shortcut* is a sequence or combination of keystrokes on a computer keyboard which invokes commands in a software. The keyboard shortcuts tab displays the commands, that have or may have the assigned shortcuts:

- If the command has shortcut assigned, the keystrokes combination is displayed for the command;
- If the shortcut may be assigned or changed for the command, the shortcut editing notification icon is displayed on the right.

The user can configure the shortcuts.

To remove the shortcut, that is assigned to the command, press “x” near the shortcut.

To assign the shortcut to the command:

- press the icon , the system opens the shortcut assignment window,
- press a keyboard key or a combination of two keys with special keys such as “Ctrl”, “Alt”, or “Shift”,

⚠ **NOTE!** Shortcut combinations may differ depending on the operating system used. In macOS environment, most actions use the “Command (⌘)” key instead of the “Ctrl” key.

The system automatically adapts the default shortcut combinations according to the user operating system.

- the system displays pressed shortcut in the Create keyboard shortcut window,
- if the selected value is already used by another command, a warning notification is displayed,

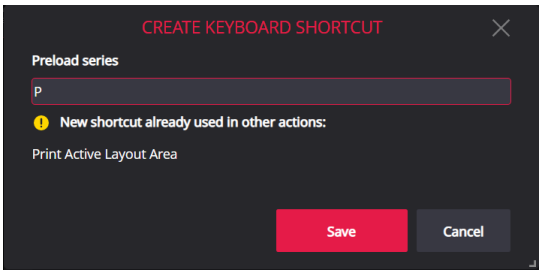


Figure 438. Warning notification about already used shortcut

⚠ **NOTE!** The system displays a notification if the shortcut is already assigned to another command. The notification does not prevent saving duplicated shortcuts. For example, if you decide to assign the “P” shortcut to the “Preload series” command, you should manually remove the shortcut from the “Print active layout area” command before or after the assignment.

⚠ **NOTE!** Some shortcut combinations may not work if they are reserved by the browser or operating system. Especially in macOS environment, combinations using “Alt (Option)”, “Ctrl”, or “Command (⌘)” keys may be reserved for system functions or character input.

- press Save button,
- the system closes the Create keyboard shortcut window and displays the new shortcut for the command in the Shortcuts window.

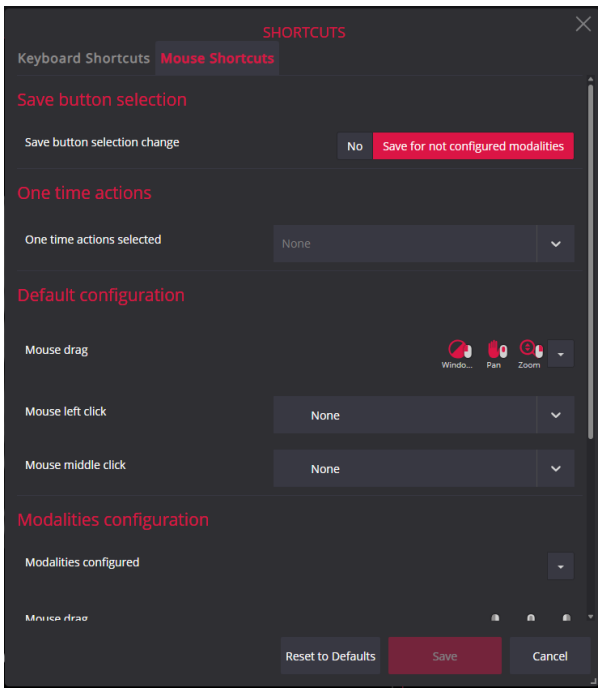


Figure 439. Mouse shortcuts tab

⚠ **NOTE!** The mouse shortcuts configuration is used only in Desktop display mode.

⚠ **NOTE!** Some mouse shortcut combinations using “Ctrl”, “Alt (Option)”, or mouse wheel actions may behave differently depending on the operating system and browser used. In macOS environment, some combinations may be reserved for operating system functions and may not behave the same as in Windows environment.

In the mouse shortcuts tab, the user may configure the actions that are assigned to the mouse buttons:

- **Save button selection change** defines if the user made changes of the mouse button assignments are stored in browsers local storage and used the next time, when opening the Viewer window. This option is available only for the system administrator and is set for the system. The default value is “Safe for not configured modalities”, and this option is recommended, if the shortcuts editing is not allowed for the users.
- **One time actions selected** field lists the functions that are configured to be assigned to the mouse button temporarily, for one time use and then to return the mouse button assignment to the previous function. By default, the list is empty. The user may add to the list one or more of the functions: Pan, Measure, Swap.

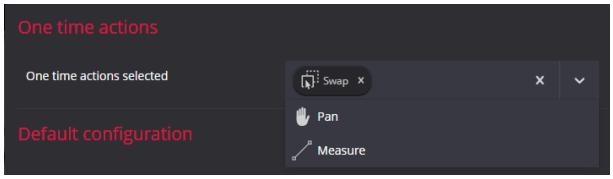


Figure 440. Swap function configured as one time action

The following example explains the one-time action. Let’s the Swap function be configured as one time action, and the left mouse button In the Viewer window be assigned to the Windowing function  . Clicking with the left mouse button on the Swap tool in Viewer toolbar removes the assignment from Windowing function and sets it to the Swap function for one time using  (the mouse button icon is gray). After the user swaps the desired viewports, the system automatically returns the left mouse button assignment to the Windowing function  .

Note that the mouse button is assigned for one time only if it is currently used by the other function. Otherwise, the button will be assigned permanently (the red mouse button icon will be displayed).

- Default configuration is applied for all the modalities that do not have separate configuration entered.

  By default, the left mouse button is assigned to the Windowing function, the middle mouse button is assigned to the Pan function, and the right mouse button is assigned to the Zoom function. The user can change the assignment by extending the drop-down list and clicking with the desired mouse button on the desired function. The list has all the Viewer tools that may be applied using mouse.

  As most tools require only mouse drag action, the user can configure additional functions to be assigned to the Mouse left click and Mouse middle click by selecting the one function from the extendable functions list: Montage, Zoom selection, Invert.

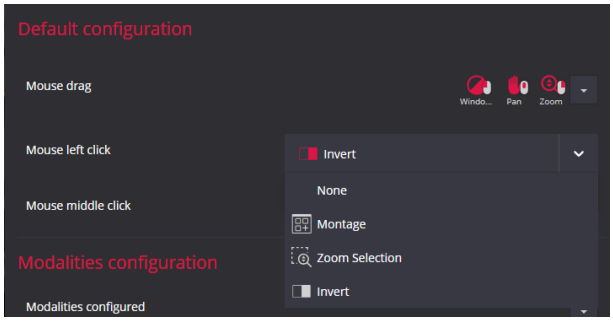


Figure 441. Invert function assigned to mouse left click action

For example, if the left mouse button in the Viewer window is assigned to the Windowing function 

, and the Invert function is assigned to the mouse left click, dragging the mouse with the left button pressed change windowing, and clicking the left mouse button inverts the image.

Note that Measure, Magnifier, Croshair and Montage tools take the mouse button click action. If these tools are currently assigned to the left or middle mouse button, the mouse button click action will be reserved for this tool, but not for the configured Mouse left click or Mouse middle click function.

- The **Modalities configuration** allows the user to assign the different function to the mouse for a particular modality. By default, the **Modalities configured** list is empty. The user can select the modalities from the extendable list and then define what function should be assigned to the mouse button for the selected modalities.

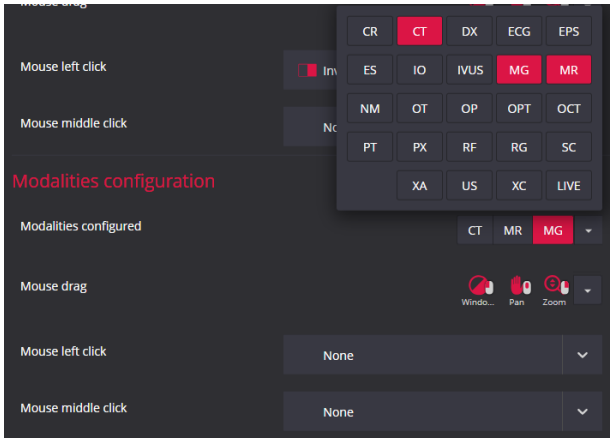


Figure 442. CT, MR and MG modalities selected to have different mouse button assignments

Note that mouse button assignments should be set for each selected modality separately in the same way as described above for Default configuration. The values are displayed and may be edited for the modality, that is currently highlighted in the **Modalities configured** list, in the figure above it would be the MG modality.

If done with changes in Keyboard shortcuts or Mouse shortcuts tabs, the user may apply the changes:

- To restore the default shortcuts values, press the Reset to Defaults button, and the system updates all the shortcut values in the Shortcuts window from the default shortcuts configuration;
- The Save button in Shortcuts window is activated, if there are any changes in the previously assigned shortcuts. To save the shortcut changes, press the Save button. The system permanently saves the shortcuts in the user settings.

⚠ **NOTE!** To modify personal user shortcuts, the user should have the right to modify shortcuts, do not have the administrator right, and should be logged in with his login name.

⚠ **NOTE!** If the user has administrator right and saves the shortcuts changes, the system shortcuts settings are modified and further used as default shortcuts for all the users. See install manual for description how to restore the system shortcuts settings to default values or to configure the shortcuts per user group.

⚠ **NOTE!** User-assigned shortcuts, as well as default shortcuts, may not work if the same key combination is already used by the browser or operating system. In macOS environment, some combinations using “Command (⌘)”, “Ctrl”, or “Alt (Option)” keys may be reserved for system functions and cannot be used to activate MedDream actions.

⚠ **NOTE!** Only actions related to visible menu items or windows are included in the shortcuts list. If an action is hidden through system settings (for example, by hiding a menu item), it will not be displayed in the list and its assigned shortcut combination will not work. When the action becomes visible again, the shortcut combination will work as expected.

⚠ **NOTE!** When restoring default shortcuts, the system applies default values according to the operating system used. For example, Windows environment commonly uses “Ctrl” key combinations, while macOS environment may automatically use “Command (⌘)” key combinations for the same actions.

⚠ **NOTE!** Not all shortcuts can be modified by the user. Some mouse and keyboard combinations used for specific MedDream functionality are fixed by the system and are not displayed in the shortcuts configuration list.

Impact of Operating System Differences on Shortcuts

The system supports different shortcut combinations depending on the operating system used.

In Windows environment, most actions are performed using “Ctrl” key combinations, while in macOS environment the same actions may use “Command (⌘)” key combinations.

The system automatically adapts and displays default shortcut combinations according to the user operating system.

Some shortcut combinations may not work or may be limited due to browser or operating system reserved functionality. Especially in macOS environment, combinations using “Alt (Option)”, “Ctrl”, or “Command (⌘)” keys may be reserved for system functions or character input.

⚠ **NOTE!** When restoring default shortcuts, the system applies default values according to the operating system used.

Clear cache

⚠ **NOTE!** The **Clear cache** menu is visible only if user has right granted and cache clearing is enabled in system settings.

⚠ **NOTE!** The Clear Cache function is intended to be used when you know the data has been changed on the PACS, yet MedDream still shows the old data. If Clear Caches doesn't help, you'll need to contact the administrator for troubleshooting and adjusting the configuration, as multiple places in the configuration might cause this effect.

To remove the cached data of the currently viewed study, click option **Clear cache** and it will lead you to the Clear Cache window:

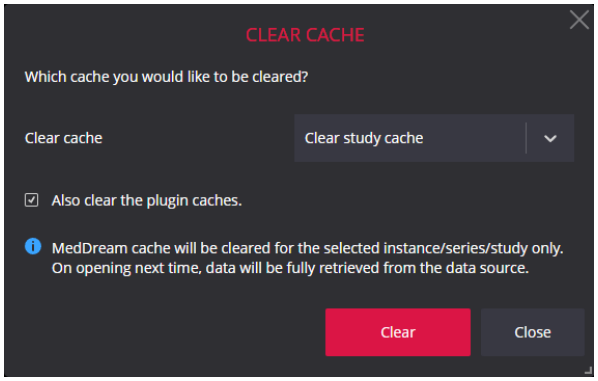


Figure 443. Clear cache window

The clear cache scope options are listed in **Clear cache** expandable list. By default, the system suggests to remove the whole study from the cache. You can clear the active instance cache, or active series cache by expanding the list and selecting the appropriate item from the list:

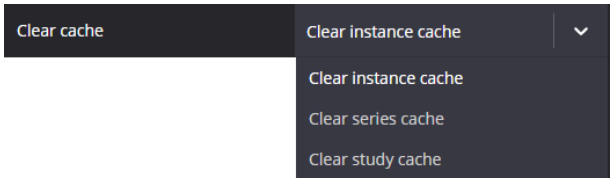


Figure 444. Cache clearing scope selection

Checking "**Also clear the plugin caches**" will also clear the plugin caches (if working through plugins).

Click the **Clear** button in Clear Cache window to initiate the removing of the selected content from the system cache.

⚠ **NOTE!** The cache clearing removes all the study data, that was previously preloaded to the Viewer. And only the currently viewed instances are loaded automatically.

⚠ **NOTE!** If study changes tracking is supported by studies storage and is configured, the study structure may be updated without removing the previously preloaded data (see the Thumbnails bar section for details).

Click **Close** button to close the Clear Cache window.

Settings

To change MedDream viewer's settings, click button **Settings** and it will lead you to the settings window. For more information see Settings.

⚠ **NOTE!** The **Settings** menu is visible only if user has administrator right, or right to view personal settings, granted by user rights and Settings menu is enabled in system settings.

Log Off

Use **Log Off** option, if you finished working with the program. Logging off from the Search window, closes all the Viewer windows that were opened from Search window and destroys the browser session.

In case the integrated solution is used and the Search window is disabled, **Log Off** is available under the System menu in Viewer window.

⚠ **NOTE!** If after login the error about forbidden functionality is displayed instead of Search window, press the Log Off button, in case it is displayed on the error page, and contact your system administrator to verify the system configuration and user rights.

⚠ **CAUTION!** Please notice, that closing the program without Log Off (using browser window close 'x' button) is not safe and may lead to unauthorized access to medical data.

License registration

⚠ **NOTE!** License registration is required for legal software use. The license registration function is accessible only for users having administrator rights.

You can open the license registration window in such ways:

- By clicking the **Register** button in demo notification window. The demo notification window is displayed, if the system runs without registered license (in demo mode):

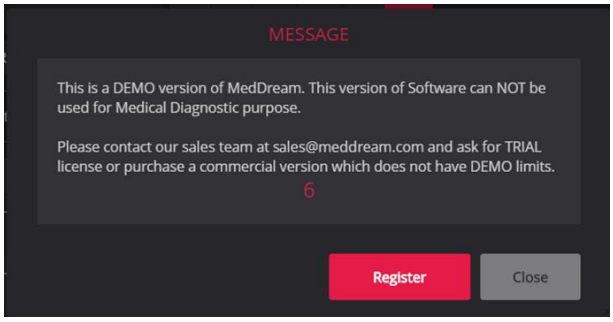


Figure 445. Demo version notification

- By click the **Register** button in About window (see description in section "About").

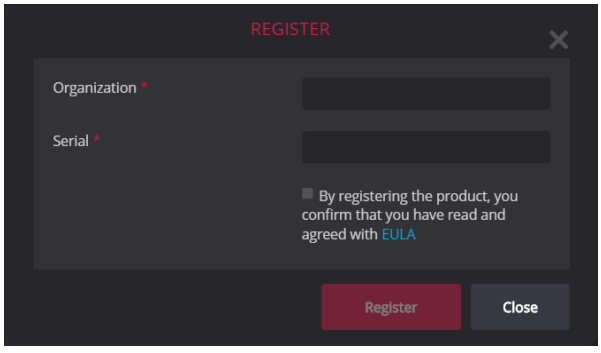


Figure 446. Registration window, if EULA is not read

You should enter the organization and license number that you were given by system administrator or system provider in license registration window. To start registration, you should read the end user license agreement. Click EULA link to open and read the end user license agreement, and check the confirmation box after the reading - the **Register** button is activated:

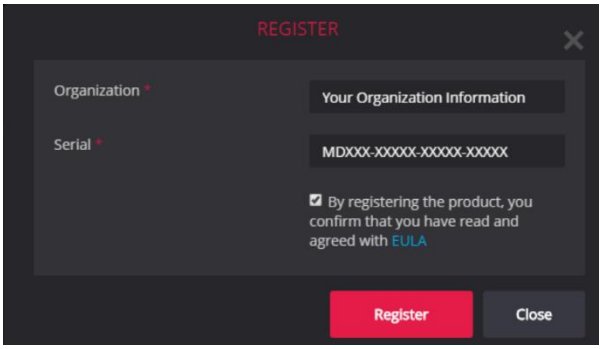


Figure 447. Registration window – registration activated

After the **Register** button is clicked, the system connects to the license server, verifies the entered license data, and registers the license. You can view the registered license data in About window.

⚠ **NOTE!** The internet connection and access to license server should be ensured for successful license registration.

⚠ **NOTE!** The system automatically renews the license, if license update is purchased and data is renewed in license server.

Settings

System settings allow you to customize the appearance and functionality of the system according the user's needs. To change your MedDream settings, select **Settings** from the system drop-down menu. The **Settings** menu is displayed for the user, that either has right to modify his settings, or has administrator right.

⚠ **NOTE!** Note that the user with the administrator right can modify only the global settings or global hanging protocols, which, after saving, are shared by all users. See the install manual how to configure the settings per user group or user manually.

⚠ **NOTE!** To modify particular user settings, the user should have the right to modify user settings or hanging protocols, do not have the administrator right, and should be logged in with his login name.

⚠ **NOTE!** If the setting related data is cached per system, the global setting configuration is always used and setting configuration for the particular user is ignored. The warning icon is displayed near the label of such setting, if the user settings are viewed.

You can do the following using the buttons in the top right corner of the search window:

- **Language** menu enables language change by picking language code in expandable list.
- Clicking **Notifications** button opens the notification window. The notifications functionality is explained in the section “Displaying notifications”.

System settings are grouped by system windows and / or functions. Each set of settings is in a separate tab, which is opened by clicking on the tab name.

If the tab content does not fit to the window, the scrollbar is displayed. You can scroll the page with the scrollbar, or with the mouse wheel while hovering over scrollable tab content.

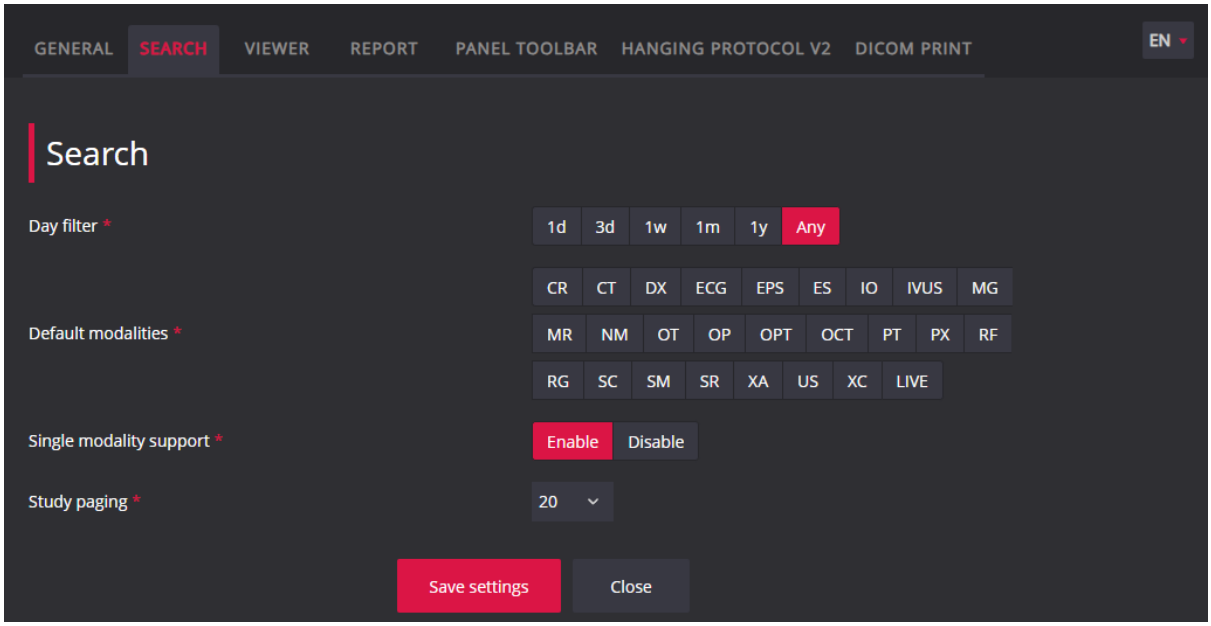


Figure 448. Settings window

The **Save settings** button at the bottom of each tab saves the settings' values into the settings storage. The saved settings are applied after the system restart.

⚠ **NOTE!** You will lose the changes that you've made if you exit the tab or close the settings window without clicking Save Settings at the bottom of the tab.

⚠ **NOTE!** If the user settings are saved at least once, the global settings are no longer used for this user. Contact your system administrator, if you need the user settings to be removed and return to the global settings.

⚠ **NOTE!** User settings and user hanging protocols are stored separately, so it is possible, for example, to save and use user's hanging protocols, but still have the global system settings.

⚠ **NOTE!** Note that user can change some of settings and these changes are saved in browser's local storage. If the browser's local storage contains setting values, the system used these values instead of settings file. To use the settings file, you should clean the browser's local storage on user machine.

A detailed description of each tab is provided in the subsections of this section.

General settings

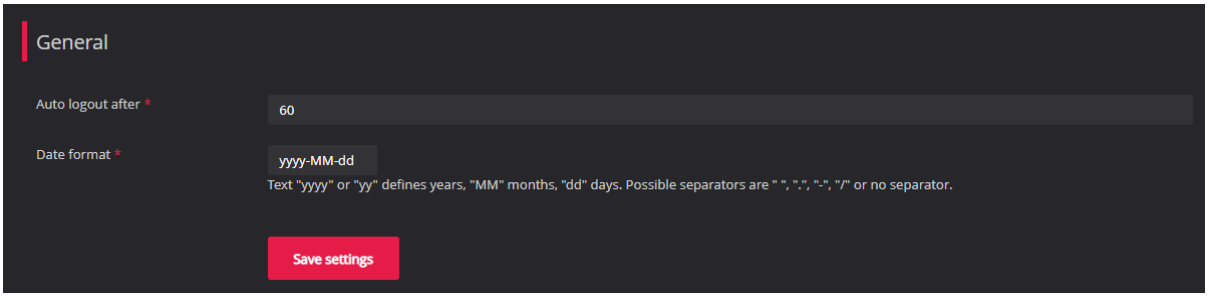


Figure 449. Settings window: general settings

On **General** tab you can modify the following settings:

- **Auto logout after** – you can enter the time frame in minutes when the system will logout automatically in case you forget to logout and close the system window. The default value is 60 minutes.
- **Date format** – you can specify the date display format. The default value is yyyy-mm-dd.

Search window settings

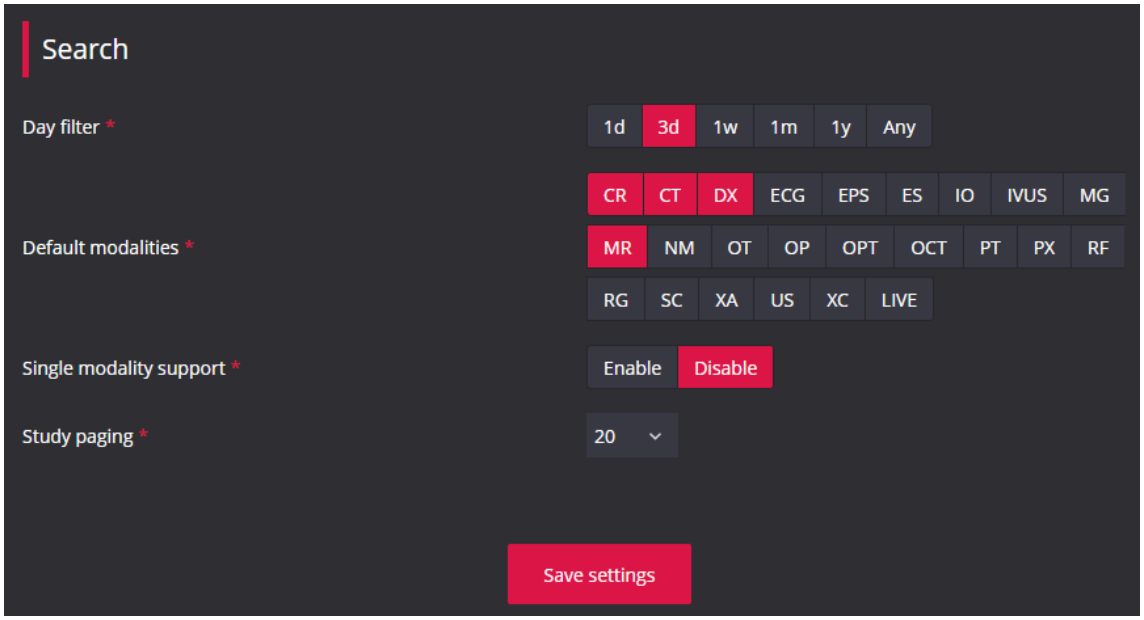


Figure 450. Settings window: search setting

On **Search tab** you can modify the following settings:

- **Day Filter** – you can create day filter that will be applied by default when Search window opens. The filter options are: **any, 1d, 3d, 1w, 1m, 1y**. The default day filter is **3d**.

⚠ **NOTE!** This filter is for compatibility with some PACSes (in MedDream "DICOM" PACS integration mode) that require a date range in all queries. It can also be used in direct integration modes if the database is too slow and accidental activation of the "Any" date choice results in unexpectedly long response times that disrupt the ordinary workflow.

- **Default modalities** – you can select modalities which buttons will be shown on the main search window for quick access. Click the modality button and it is highlighted. To change the selections status, click the modality button once more. The default selection is: CR; CT; DX; MR.

⚠ **NOTE!** The user can change the default modalities in Search window. The changes are saved in browser's local storage and will be applied when the user opens the Search window in the same browser.

⚠ **NOTE!** The default modalities setting is not applicable in mobile mode. In list all modalities are displayed in Search criteria window and this list cannot be configured.

- **Single modality support** – if enabled, the system allows the user to pick only one modality in modalities component in Search window. It should be used if the storage supports search only by one modality at a time. The default value is **Disabled**.

- **Study paging** – this setting allows you to set the number of studies shown on the page of the main search window. Select the studies per page that you wish to be shown as a default setting from the drop-down list values: 10, 20, 30, 40, 50, 100. The default value is 20 records per page.

Viewer window settings

In **Viewer tab** you can edit general Viewer settings, info label settings, toolbar settings and custom windowing settings.

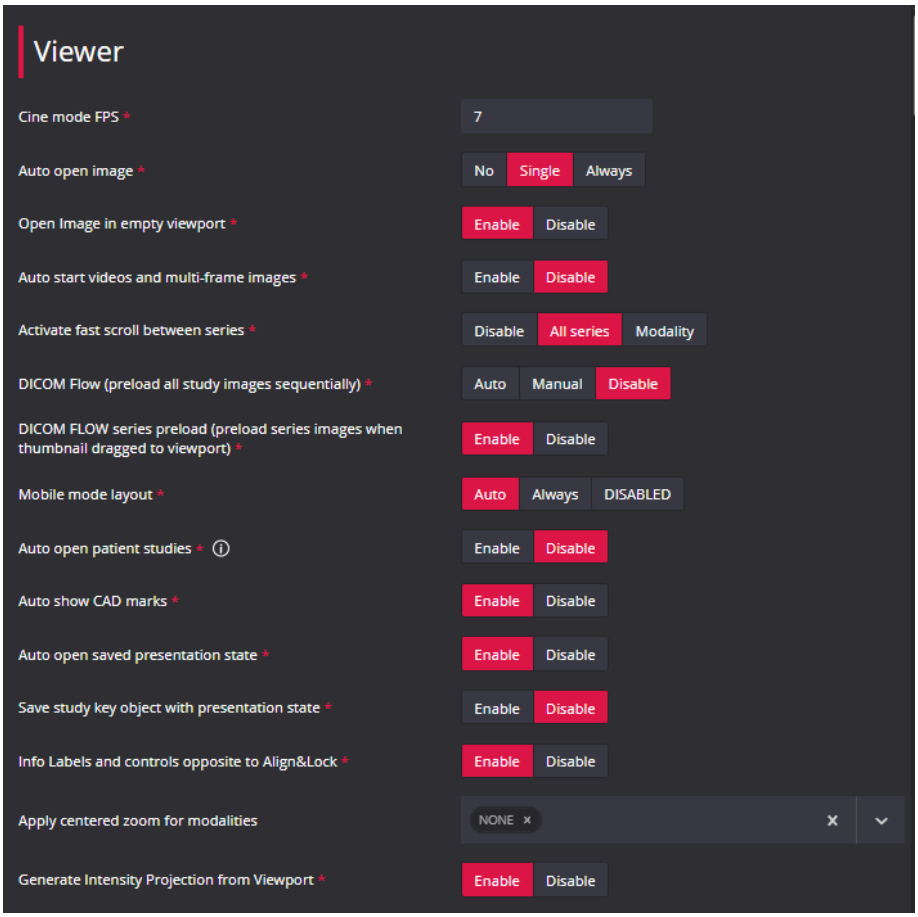


Figure 451. Settings window: general Viewer window settings

In Viewer tab of the Settings window, you can change the following Viewer settings:

- **Cine mode FPS** – number of frames per second when playing multi-frame images. The default value is 7 fps.
- **AutoOpen Image** – automatically opens the first image of the first series in the first viewport according to your choices:

  No The image does not open automatically when the study is opened in Viewer.

  Single The image is opened automatically only if the study consists of one image.

  Always The image is always opened automatically.

  The default selection is **Single**.

⚠ **NOTE!** Automatic image opening is applied only if opening study in new Viewer window and in desktop mode.

- **Open image in an empty viewport** - if option is enabled, right mouse button click on the image in thumbnail bar is activated, which opens the image in an empty viewport. The default selection is **Disabled**.
- **Autostart videos and multi-frame images** - automatically start playing multi-frame images, if enabled. The default selection is **Disabled**.
- **Activate fast scroll between series** – if option is enabled, the fast scroll function scrols throughout all the series of the study, that is the first image of the next series is opened when the end of the current series is reached. The default selection is **Disabled**.
- **Activate fast scroll between series** – if **All series** or **Modality** option is selected, the fast scroll function scrolls throughout all the series of the study, or the series of a particular modality, that is the first image of the next series is opened when the end of the current series is reached. The default selection is **Disabled**. If **Modality** option is selected, the modalities list is displayed, and modalities should be selected by clicking and highlighting the desired modalities:

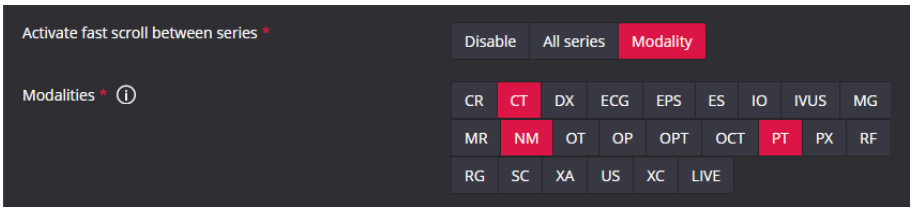


Figure 452. Settings window: modalities selection for Activate fast scroll between series setting

NOTE! The user can activate or deactivate the fast scroll between series in Viewer window, and the scroll will be allowed even if **Activate fast scroll between series** is set to **Disabled**. Hide the Scroll button option “Activate the first scroll between series” in toolbar properties, if you do not want the user to be able to activate the scroll between series.

- **DICOM flow (preload all study images sequentially)** – preload all images in advance. If the **Auto** option is selected, the system automatically starts loading all the images on study open, and scrolling through adjacent images takes very little time, but the entire study must fit into browser's memory. The default selection is **Manual**., what means that series or whole study images if the user clicks preload button. If the **Disable** option is selected, the system performs progressive image preload around the viewed image, but manual preload of the series or the whole study images is also possible.
- **DICOM FLOW series preload (preload series images when thumbnail dragged to viewport)** – if enabled, the preload of all series images starts after opening the image of the series. The default selection is **Disable**.
- **Mobile mode layout** forces mobile view used in desktop mode. The **Auto** option applies the mobile layout if working in mobile mode. The software automatically switches to mobile mode, if detects the mobile devise on startup or desktop window resolution is resized to less than 992 pixels. If you need the Viewer’s window mobile layout in desktop mode, use **Always** option. If you do not want to use mobile layout for desktop, use **Disabled** option. The default selection is **Auto**.
- **Auto open patient studies** – if option is enabled, the system automatically opens patient’s studies in thumbnail panel. The default selection is **Disabled**.
- **Auto show CAD marks** – if option is enabled, the CAD marks are displayed on mammography images.
- **Auto open saved presentation state** – if option is enabled, the last saved presentation state is automatically selected and displayed, when opening the image. The default selection is **Disabled**.

NOTE! See installation documentation for configuring to not auto open the presentation states, that were generated and saved by the algorithms.

- **Save study key object with presentation state** – if option is enabled, when a KO object is saved, the PR is also save and a linking reference is created; when a KO with a link to a PR is opened, the PR is also opened.

- **Info Labels and controls opposite to Align&Lock** - if enabled, when '**Align&Lock**' is activated in the viewport, all labels are displayed on the opposite side to the alignment. Be default is **Enabled** and allows the specification of labels that must be displayed (see under "**Mandatory visible labels for Align&Lock"**").
- **Apply centered zoom for modalities** – specifies for which images the zoom with mouse is done to or from viewport center instead of mouse cursor initial position.
- **Generate Intensity Projection from Viewport** – the setting is used to activate the visibility of the MIP button in the viewing area. This functionality allows generating the appropriate Intensity Projection (*Maximum Intensity Projection*, MIP) based on the orientation of the opened view plane, where the user can adjust the Intensity Projection value (MIP/MinIP/AVG). The default value is **Enable.**

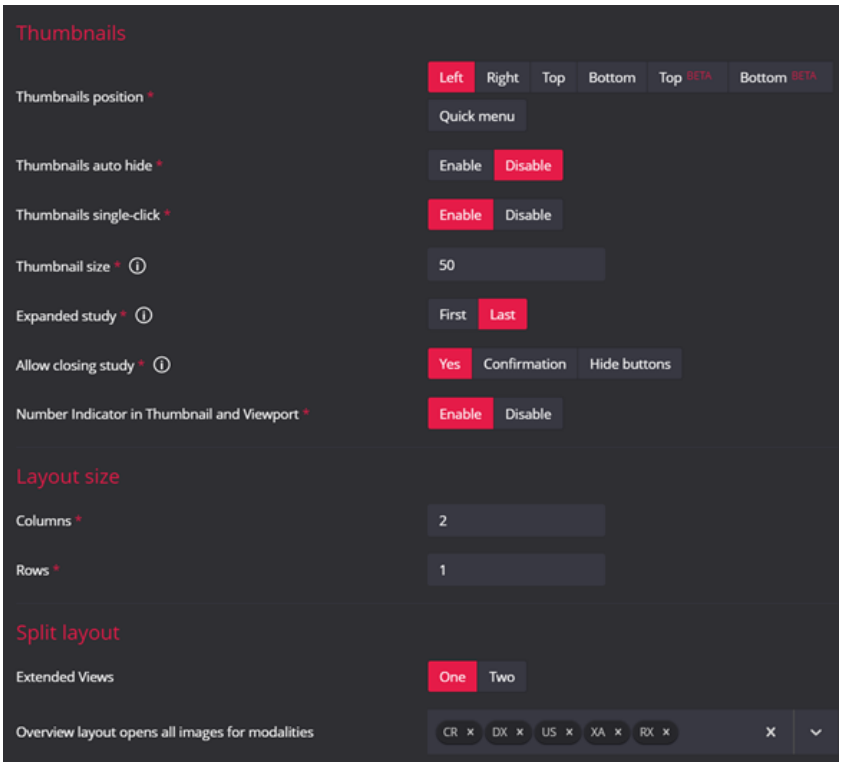


Figure 453. Settings window: Viewer thumbnails and layout window settings

The **Thumbnails** section of Viewer tab of the Settings window, you can change the following settings:

- **Thumbnails position** – allows to modify position of thumbnails with five possible options: Left, Right, Top, Bottom, Quick menu. The default selection is **Left**.
- **Thumbnails Single-Click** - once the option is enabled, a single click on an image icon will open the image (otherwise a double click is required). The default selection is **Enable**.
- **Thumbnail size** - indicates the size of the thumbnail image from minimum size equal to 50px to maximum size equal to 150px. The default value is 50 px.
- **Expanded study** - indicates which study, the firs or the last, is expanded by default, when multiple studies are opened at once in the empty Viewer window. The default selection is **Last**.
- **Allow closing study -** indicates whether the user is allowed to close a single study or all studies from the thumbnail bar, or to display a confirmation dialogue before the closing action, or to hide the studies' close buttons at all.
- **Number indicator in thumbnail and viewport** – when this setting is enabled, a number indicator is shown in both the thumbnail and the viewport, helping the user to easily identify which study is opened in each viewport. If header highlighting is configured for a comparison study, the number in the viewport is displayed in the highlighted header row. If headers are not highlighted, the number is shown in the first right-hand header row. Studies are numbered from 1 to 99. The numbering remains stable during

the session – opened studies are not renumbered, even if one of them is closed. When all studies are closed using the **Close studies** button in the thumbnail bar, numbering of newly opened studies starts again from 1.

The **Layout Size** indicates the number of viewports in the Viewer window:

- **Columns** - indicates the layout`s number of columns. The values from 1 to 8 are allowed. The default value is 2.
- **Rows** - indicates the layout`s number of rows. The values from 1 to 4 are allowed. The default value is 1.

⚠ **NOTE!** The user can change the layout size in Viewer window. The changes are saved in browser's local storage and will be applied when the user opens the Viewer window in the same browser next time.

- **Split layout. Extended views** - specifies into how many parts - **one or two** - the viewer view zone is split for image enlargment; this setting is used to construct the different functionality of the image enlargement on a mouse double-click.
- **Split layout. Multi-series opens all images for modalities** – specifies for which studies all the images of all the series are sequentially opened in multi-series layout, instead of opening one image per each series.

Measurements settings

In the Settings window, in the Viewer tab, the **Measurements** group allows users to configure measurements:

- to change the colors and thicknesses of the measurements,
- and, separately, to change the colors and thicknesses of the pencil measurements,
- to change the modalities for the **Auto-Ruler** to be displayed,
- to change the modalities for the **Horizontal Line** to be displayed

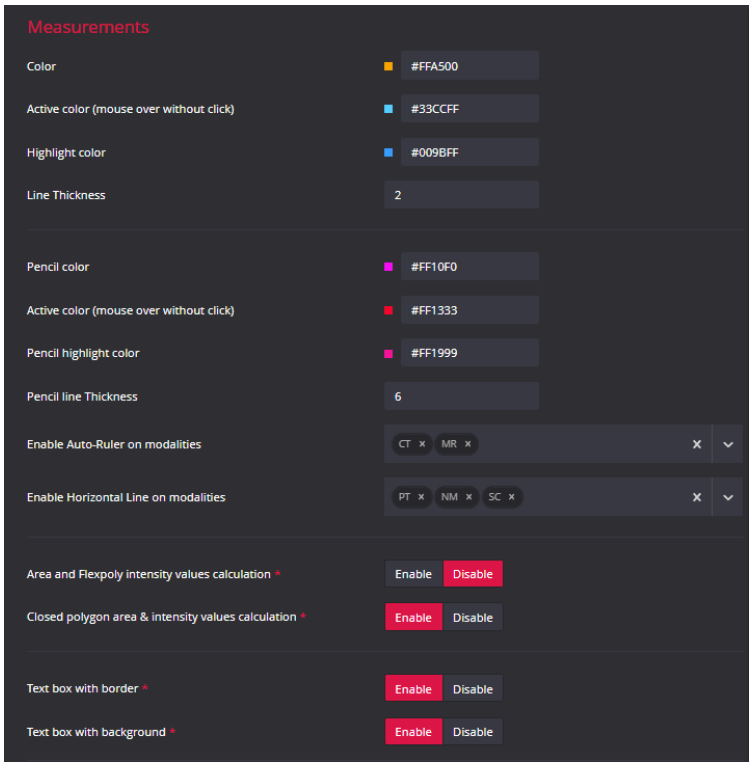


Figure 454. Settings window: measurements' settings

Specify three colors and line thicknesses for measurements, and separately for the pencil tool:

- **Color / Pencil Color** - which is used to represent the measurement when an action is performed;
- **Active color (mouse over without click)** - the color that highlights the measurement when the mouse cursor hovers over the measurement but the left mouse button is not pressed and editing is not activated;
- **Highlight color / Pencil highlight color** is used to highlight the measurement when editing mode is activated.
- **Line Thickness / Pencil line Thickness** - defines the line thickness.

Enable Auto-Ruler on modalities setting shows the list of modalities, for which the **Ruler** is displayed, if enabled by the user. By default, the "CT" and "MR" modalities are in the list.

Enable Horizontal Line on modalities setting shows the list of modalities, for which the **Horizontal Line** is displayed, if enabled by the user. By default, the "NM", "PT" and "SC modalities are in the list.

Select the modalities from the expandable list, or enter the modality directly at the end of the list to show the **Ruler** / **Horizontal Line** for this modality. Click the icon "x" near the modality to delete it from the list.

When **Area and Flexpoly intensity values calculation** is activated, intensity values will be calculated in the above measurements. If not activated, only the area is measured in Area and Flexpoly measurements.

When **Closed polygon area & intensity values calculation** is enabled, area and intensity values are calculated for the **Closed polygon** measurement. If not enabled, the measurement is used only to mark the region of interest, and no metrics are calculated.

The settings **Text box with border** and **Text box with background** are used to define whether the measurement text box has a border and background. Both options are enabled by default.

Synchronization Settings

In the Settings window, in the Viewer tab, in the **Synchronization Settings** the user can configure the default properties for automatic synchronization.

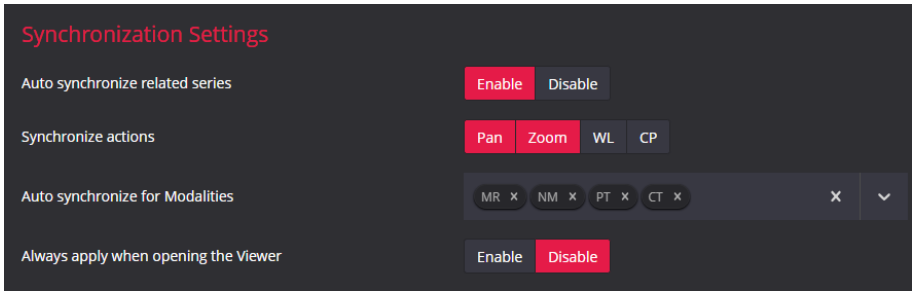


Figure 455. Setting window: Info Synchronization settings in Viewer tab

By default, **Auto synchronize related series** is **Enabled**, the other setting fields of the group are displayed, and the related series synchronization is applied when the user opens the Viewer window:

By default, the **Link scrolled series button** in the Viewer toolbar is set to **Auto synchronize** mode, and the Auto synchronize icon in viewport is automatically set as active for MR, NM, PT, and CT series. You can add or remove the modalities in the **Auto synchronize for Modalities** list.

By default, the **Pan Sync in linked series** and **Zoom Sync in linked series options** are marked in the **Sync actions** button's menu. You can change the actions you want to synchronize by selecting or deselecting the corresponding options in the **Synchronize actions** field.

The user can select to switch off the **Default auto synchronize** mode for the **Link scrolled series** button, or to set the **WL Sync for same series option** on in **Sync action**s button's menu directly in the Viewer window.

These selections are saved in browser's local storage and further used as default when the user opens the Viewer window on that machine. You can configure to ignore the values of the local storage by changing the **Always apply when opening the Viewer** to **Enabled**.

Label Properties

The **Info Label properties** section of Viewer tab in Settings window is used to indicate DICOM tags containing the information that should be displayed over the image, and configure another label related functionality.

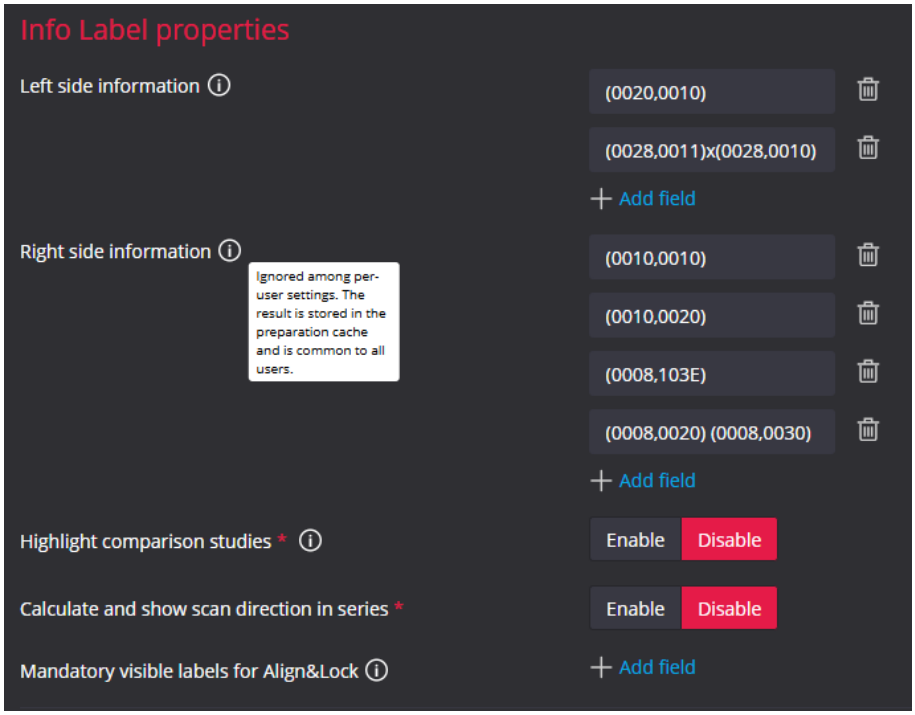


Figure 456. Setting window: Info Label properties in Viewer tab

Info labels on image

⚠ **NOTE!** The metadata of the Left side information and the Right side information is cached in the system, so the global settings configuration is always used. The particular user settings configuration is ignored, and a warning icon will be displayed , if the user settings are viewed.

Left side information and **Right side information** settings describe the info labes displayed on image. In order to add new info label:

- Select the label place (**Left Side Information** or **Right Side Information**) and click **Add Field** in the appropriate section. The system shows the entry field:

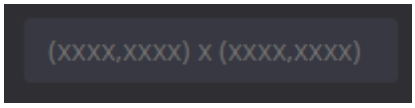


Figure 457. Info Label entry field

- Enter the label. The DICOM tag should be enclosed in parentheses using format (xxxx,xxxx). Label example: Patient position (0018,5100): (0020,1040).
- Save settings.

⚠ **NOTE!** Only first level DICOM tags may be used in labels.

⚠ **NOTE!** If DICOM tags with time are used in Info label, the system displays the data in the format it is stored, including millisecond.

After restart the system loads the new settings and shows the label on the image:

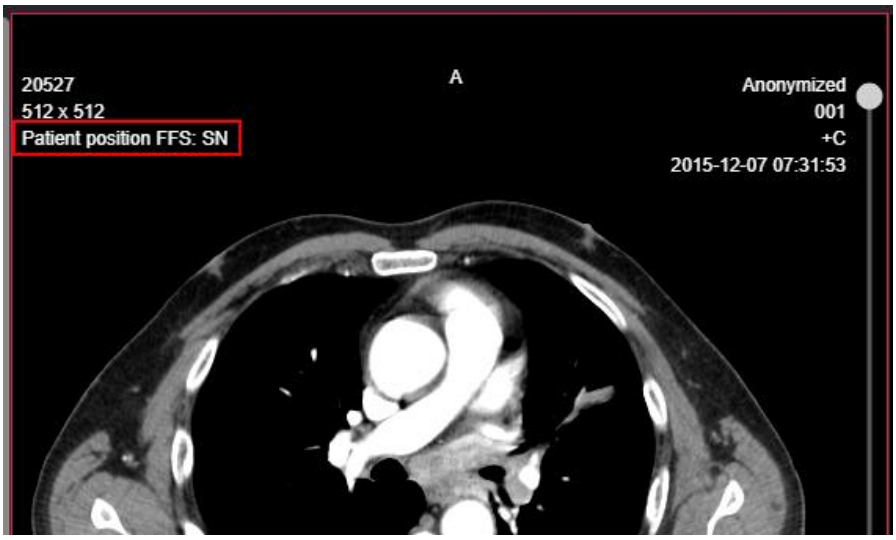


Figure 458. Showing Info Label on image

The default info labels are (see labels' view in the picture above):

- Left Side Information

(0020,0010)	Study ID
(0028,0011) x (0028,0010)	Image size in pixels Columns x Rows

- Right Side Information

(0010,0010)	Patient's name
(0010,0020)	Patient's ID
(0008,103E)	Series Description
(0008,0020) (0008,0030)	Study date Study time

To remove the label:

- click **Remove** on the right side of the label entry field,
- confirm the action,
- save settings

Calculate and show scan direction in series setting enables calculation and display of the Series scan direction and slice distance (position) in scan axis. The default value is **Disable**. Note, that the calculations require additional data and may cause the delay in image display.

Highlight comparison studies

The **Highlight comparison studies** setting allows to distinguish more easily the first opened study from all other studies, that are opened in the Viewer window for comparison. By default, the **Highlight comparison studies** option is disabled. If **Highlight comparison studies** option is enabled, the study date is highlighted in the thumbnail bar, and the last Right side information label is highlighted in the viewport for comparison study instance. You can select other Right side information label for highlighting by clicking the **Select comparison label**.

If the settings **Highlight comparison studies** and **Number indicator in thumbnails and viewport** are enabled, the number is displayed at the beginning of the highlighted header. For more details, refer to the description of the **Number indicator in thumbnails and viewport** setting.

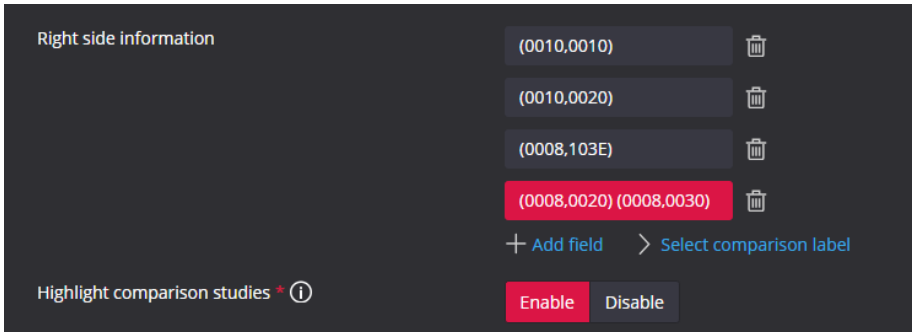


Figure 459. Setting window: Highlight comparison studies settings

Mandatory visible labels for Align&Lock

The setting **Mandatory visible labels for Align&Lock** allows user to add labels that will remain visible even when the height of the viewport is reduced to the size where all the labels cannot fit. The setting is only valid if "**Align&Lock** " is enabled and the setting **Info Labels and controls opposite to Align&Lock** is activated.

Custom study label properties

The **Custom study label properties** section of Viewer tab in Settings window is used to configure additional label in study header section of thumbnail bar. By default, the **Enable custom study label** option is **Disabled**. If **Enable custom study label** option is enabled, the additional label is inserted between the patient's name and study date in thumbnail bar. The label value may be selected from the **Value for custom study label** drop down list. The "none" value inserts the empty row, which may be filled with custom data by integrating system.

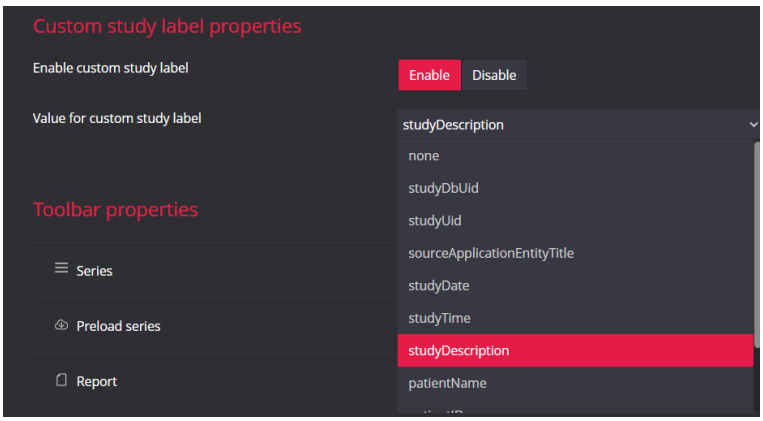


Figure 460. Setting window: Custom study label properties

Presentation state properties

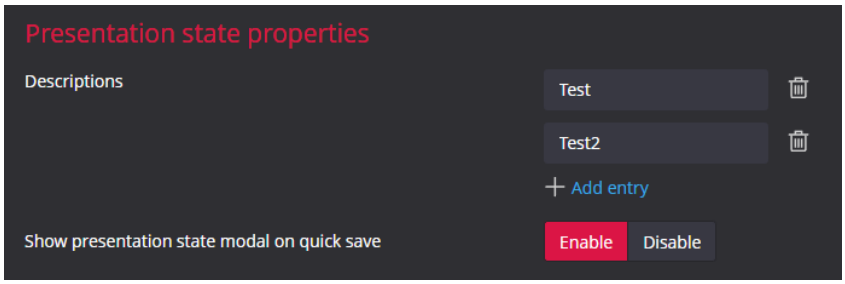


Figure 461. Setting window: Presentation state properties

The **Descriptions** group of fields adds the most commonly used PR description options, which the user will be able to select from a list when the PR is stored.

Show presentation state modal on quick save activates a call to the storage dialogue, which is not normally called during quick save, and allows a description to be added, e.g. by selecting from the list of values added above.

Presenter Settings

In the Settings window, in the Viewer tab, the **Presenter Settings** group allows users to configure:

- Line Thickness;
- Fade Out Time (in seconds);
- Values of the 5 colors visible in the tool menu.

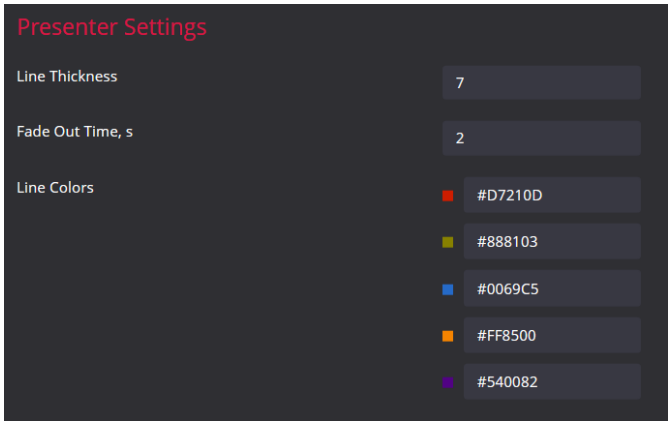


Figure 462. Settings window. Presenter settings

Montage Settings

In the Settings window, in the Viewer tab, in the **Montage Settings** the user can configure the background color for the saved montage image.



Figure 463. Settings window. Montage settings

ECG Settings

In the Settings window, in the Viewer tab, in the **ECG Settings** the user can configure the default ECG output by selecting it from the list of available outputs.

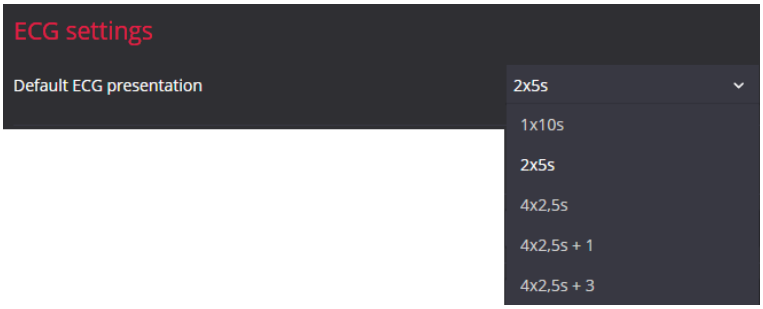


Figure 464. Settings window. ECG settings

ECG print settings

In the **Settings window**, under the **Viewer** tab, within the **ECG Printing Settings** group, the user can configure the default ECG printing parameters:

- **Large grid** – disabled by default, meaning a **1 × 1 mm grid** is used; when enabled, a **5 × 5 mm grid** is applied;
- **Print viewport as shown** – disabled by default, meaning that printing does not take into account actions performed in the viewer (such as zooming, panning, etc.); when enabled, the viewer settings are applied during printing (user-defined image parameters are preserved);
- **High quality** – disabled by default, resulting in **300 DPI (dots per inch)** resolution; when enabled, **600 DPI** resolution is used.
- **Date and time format** – not filled in by default. If the value is not filled in, the system uses the default format yyyy-MM-dd HH:mm:ss; the format can be changed, e.g. by entering dd-MM-yyyy HH:mm:ss.
- **Month abbreviation** – the parameter is required when the date format is dd-MMM-yyyy, where „MMM" is the month name abbreviation. The abbreviations must be entered in the required language, e.g. Dutch: jan, feb, mrt, apr, mei, jun, jul, aug, sep, okt, nov, dec (twelve values separated by a comma). If no values are entered but the date format is set to dd-MMM-yyyy, the system will use the default English abbreviations: Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec.

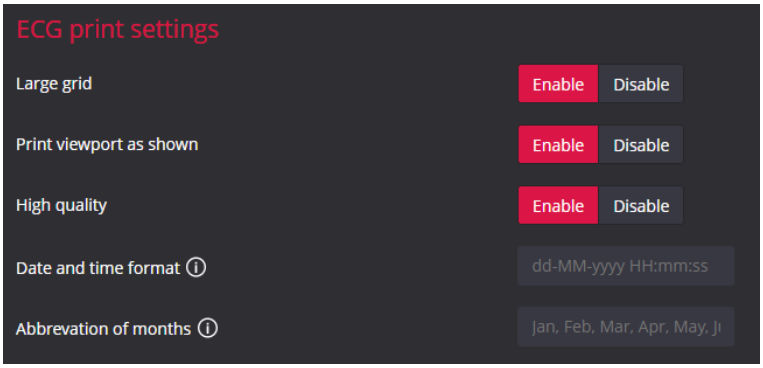


Figure 465. Settings window. ECG print settings

Toolbar Properties

In the **Toolbar properties** section of the Viewer tab in the Settings window, you can customize the Viewer toolbar tools, define the order in which they are displayed, tools placed in main toolbar or under extendable additional tools list and specify whether to show labels for the main toolbar buttons.

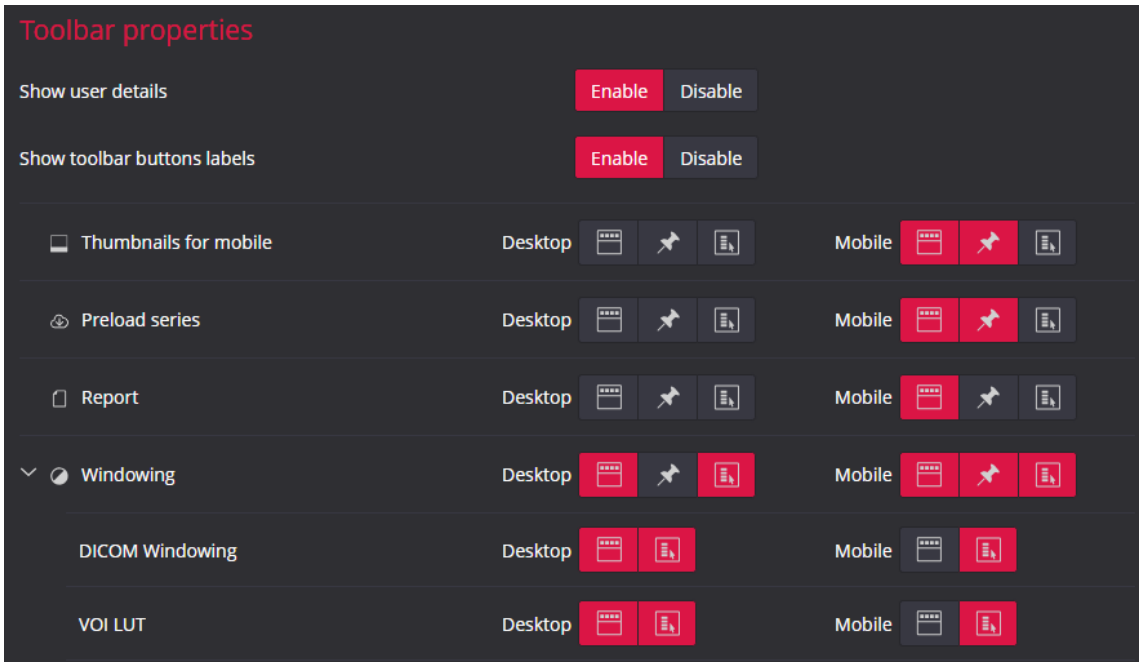


Figure 466. Setting window: Toolbar properties in Viewer tab

Use toolbar properties for:

- You can configure user and session information access in Viewer. The user details icon will be removed from toolbar, if option **Show user details** is set to **Disable**.
- You can enable or disable the display of button labels in the main toolbar: either show only the icon or show both the icon and the label.
- Changing the order of toolbar's tools.
- Showing or hiding the tool.
- Placing the tool in main toolbar or additional tools list.
- Customizing the quick menu.

To change the place of tool (or tools group) in toolbar, press the right mouse button on the tool and drag the tool on top of the desired place (line). After releasing the mouse button, the tool will be inserted above the line.

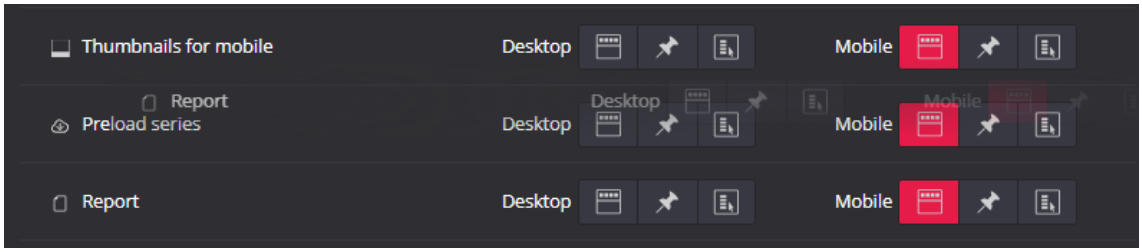


Figure 467. Changing the tool's position in toolbar

NOTE! You can change the tool (or tools group) place in toolbar. You cannot change the item place in tool group (tool's expandable menu).

To customize the toolbar view for different modes, press the use tool button  near the mode for which the tool should be available in toolbar – the selected button is highlighted:

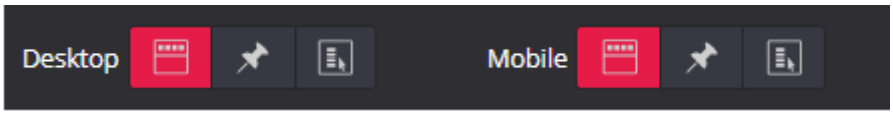


Figure 468. Selecting the tool's showing mode

NOTE! You can change the display mode selection for all levels: the toolbar's tool, options group and menu option in tool's expandable menu. Verify the visibility of higher hierarchy items (like tool's group, or tool's) when changing the item's visibility mode: the option in expandable menu is displayed only if the tool group and tool are visible in the selected mode.

To customize tools to be displayed directly in toolbar or in expandable other tools list, use the pin button  near the tool. Select the button for the Desktop or Mobile display mode to highlight it  and to have the tool displayed in toolbar. The other not pinned tools will be displayed in the additional expandable list.

NOTE! In default settings no tools are selected to be pinned, and such configuration is treated as disabled pin. If pin is disabled, all the buttons that are marked available for the mode, will be displayed directly in toolbar, and only the buttons that not fit to the window are placed under the additional expandable list.

NOTE! Pin button is available only for the main tools and not available for tool's menu items.

NOTE! Pin option for the display mode may be selected only if the tool is marked as available for this display mode.

To include the item in quick menu, use the include in quick menu button  . Select the button for the Desktop or Mobile display mode to highlight it  and add the item in quick menu for the corresponding mode. You can include in quick menu the following:

- the menu option from expandable tool's menu, for example the **Line** option from **Measure** tool's menu;
- the group of generated menu options – all the generated menu options will be included in quick menu. For example, the **DICOM Windowing** menu group from **Windowing** tool's menu.

NOTE! The system generates two-level quick menu, if you specify to include the tool itself (for example, **Measure**) in the quick menu in the settings. If the tool (for example, **Measure**) include in quick menu is disabled, and its menu option (for example, **Line**) include in quick menu is enabled in the settings, the **Line** option is included in first level quick menu.

⚠ **NOTE!** Quick menu button for the display mode may be selected only if the tool or menu item is marked as available for this display mode.

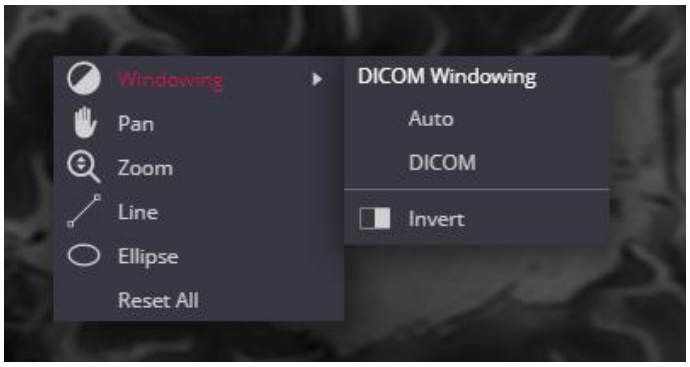


Figure 469. Quick menu: measurement in the first menu level by default

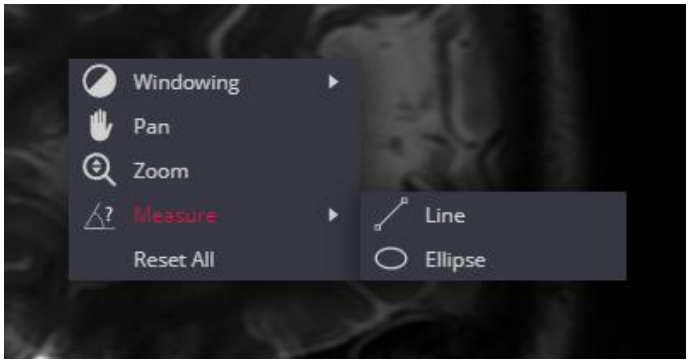


Figure 470. Quick menu: Measure tool included in quick menu and measure option moved to the second menu level

Windowing settings

In the Windowing settings of Viewer tab in Settings window the option **Increase Window Center while dragging the mouse** may be set to Up or Down. The default selection is **Down**.

MPR MIST 3D presets setting defines the list of programmed Windowing level presets that can be selected in the MIST Oblique 3D projection. By default a complete list of programmed values is provided. By selecting the delete button next to a certain value ⊗, the list can be reduced or it can be added by selecting it from the list. The list is displayed by selecting ⌄. The default list is filled when selected ✕ or the system automatically fills if all values are deleted.

Default MPR MIST 3D presets setting defines what 3d preset value is selected by default. The default value is Surface.

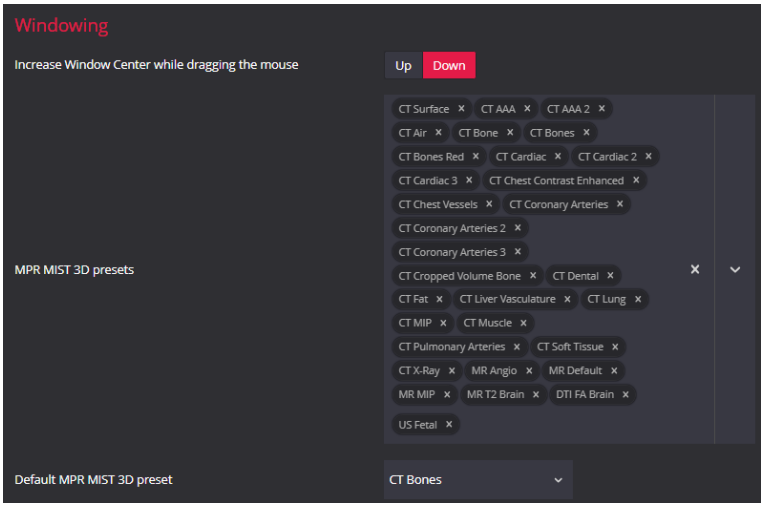


Figure 471. Windowing settings

The Windowing settings of Viewer tab in Settings window allows users to create a custom window level preset for a selected modality list. The custom windowing options will be shown in expandable **Windowing** menu under **Custom Windowing** group.

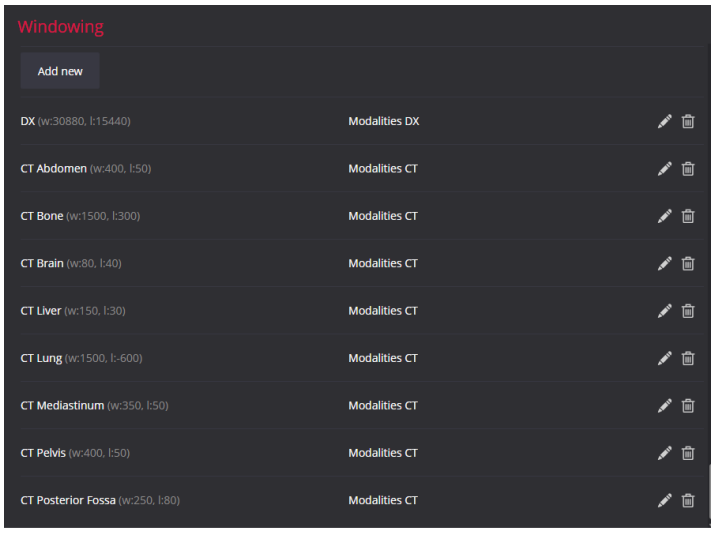


Figure 472. Custom windowing options: default values

The default settings after system deployment contain the following options for CT modality:

- **CT Abdomen** – a preset setting for abdomen studies.
- **CT Bone** – a preset setting for bone studies.
- **CT Brain** – a preset setting for cerebrum studies.
- **CT Liver** - a preset setting for the liver studies.
- **CT Lung** – a preset setting used for studying the images of the lungs.
- **CT Mediastinum** - a preset setting for mediastinum studies.
- **CT Pelvis** – a preset setting for pelvis studies.
- **CT Posterior Fossa** - a preset setting for Posterior Fossa studies.

The Edit, and Delete icons-buttons at the end of each windowing line provides access to windowing data review and edit.

To create custom windowing option:

- click **Add new**;
- enter values for the custom windowing option: **Label**, **Width**,and **Center**. Select modalities of your choice in order to assign the new window level function to certain modality (-ies). All four fields are mandatory:

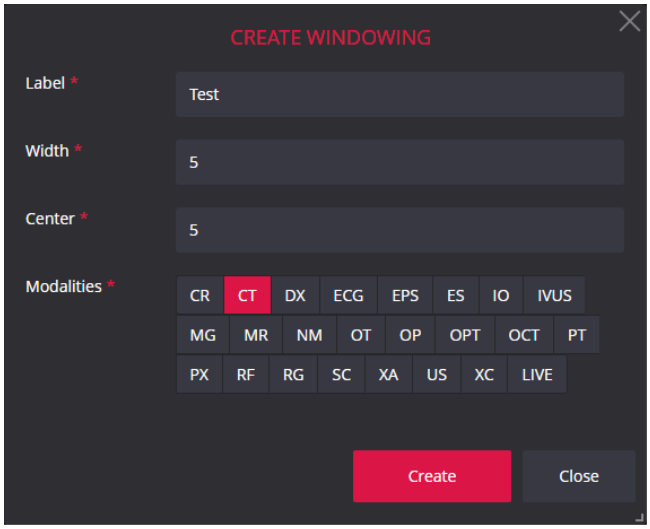
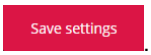


Figure 473. Custom Windowing creation window

- once done that, click on **Create** button;
- make sure to save the settings changes 

.

If a window level preset is created for a PT modality study, additional input fields for width and center values in SUV (Standardized Uptake Value) units are displayed in the window.

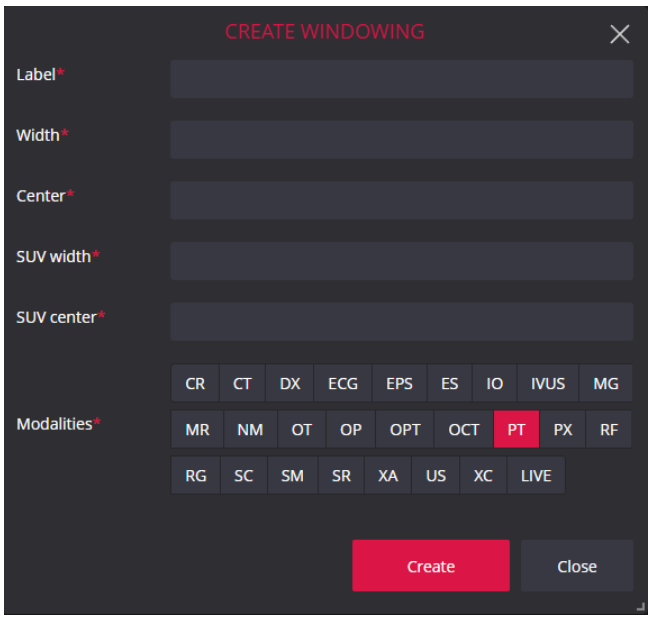


Figure 474. Custom Windowing creation window for PT studies

New predefined Windowing level will appear on the Windowing menu, if the modality of the active image corresponds to the custom windowing modalities. To apply the custom windowing, click its title in drop-down menu.

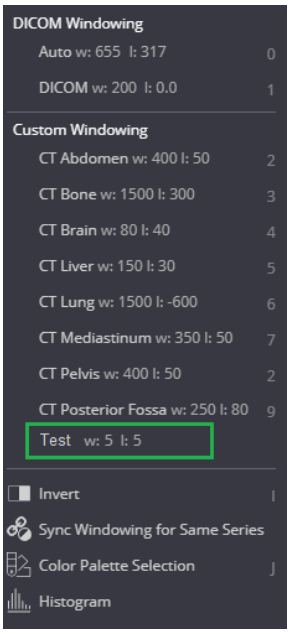


Figure 475. Custom windowing in the drop-down Windowing menu

For PT studies, if the study contains sufficient data for SUV calculation, predefined window level values in SUV units are displayed and applied in the menu. If there is insufficient data for SUV calculation, for example if the study is anonymized, values in the study units are displayed and applied instead. Units are not explicitly indicated in the menu.

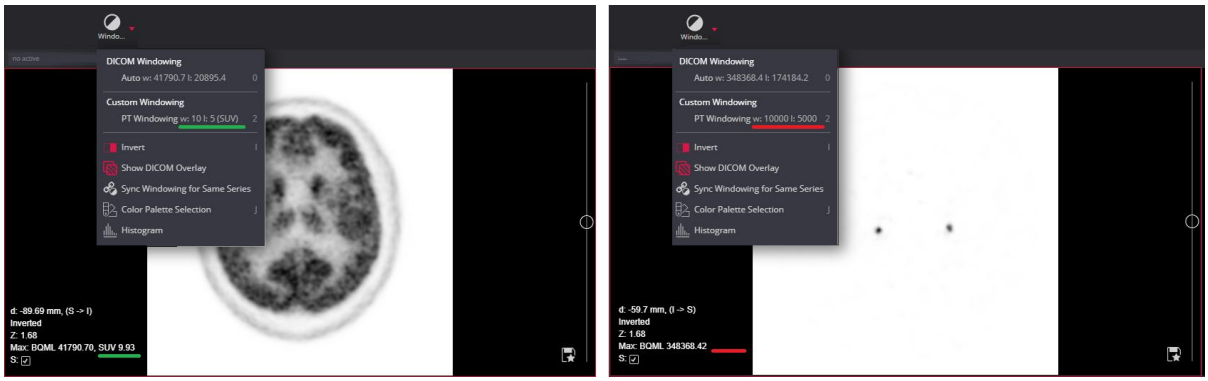


Figure 476. Custom PT Study Window Level in SUV Units

You can remove the custom windowing by clicking the **Remove** button on the right of the record. You can **Edit** the custom windowing values, if desired.

⚠ **NOTE!** It is possible to change the order of the values. The same order in which the Windowing are sorted in the Settings window is used to sort the values in the Windowing menu item, and the same order is used to create the dynamic values for the shortcuts.

Report settings



Figure 477. Settings window: report settings

On **Report** tab you can modify the following settings:

- **Open in new window** – selecting the **Enable** option opens the study Report in a new browser tab. The default selection is **Disable** and the Report is opened in modal window.
- **Allow export to PDF** – selecting the **Disable** option eliminates the possibility to include the study report in study archive. The default selection is **Enable**, and in the Export window the user has possibility to select either include the report into study archive, or not include.

Panel toolbar settings

In **Panel toolbar tab** you can edit the look of panel toolbar and tools in it.

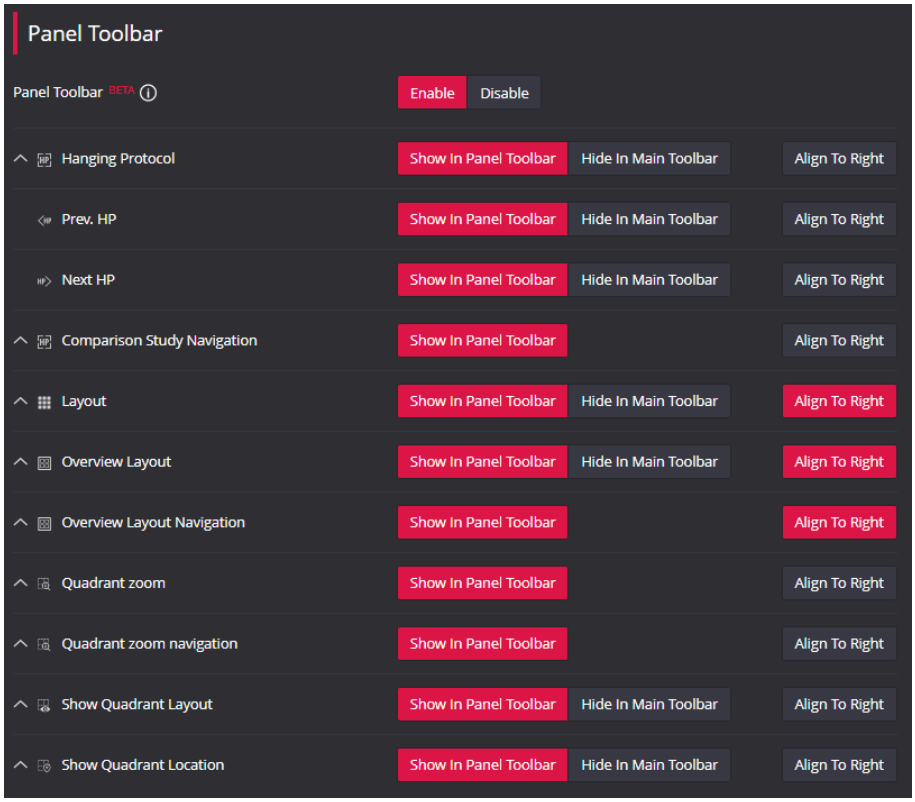


Figure 478. Settings window: Panel toolbar settings

In Panel toolbar tab of the Settings window, you can change the following settings:

- **Panel toolbar** – by default the option is enabled and panel toolbar is displayed in panel. Select **Disable** to not display panel toolbar.

- In the panel **Tools list,** you can customize the panel toolbar's tools and the order in which they are displayed.

  Use tools list for:

Changing the order and alignment of toolbar's tools.

Showing or hiding the tool.

Automatically hide the same tool in Viewer toolbar.

To change the place of tool (or tools group) in panel toolbar, press the right mouse button on the tool and drag the tool on top of the desired place (line). After releasing the mouse button, the tool will be inserted above the line.

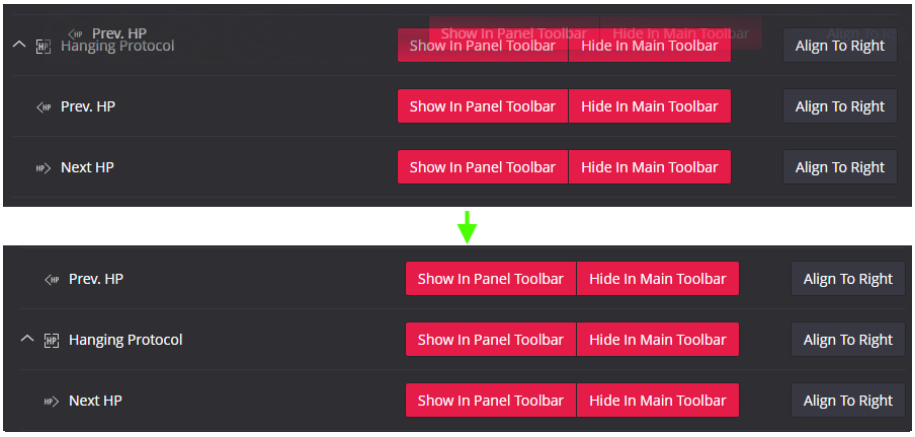


Figure 479. Changing the tool's position in panel toolbar

The tool may be aligned to the left or to the right side of the panel toolbar by changing the **Align to Right** option. The tool is aligned to the right, if the **Align to Right** option is highlighted.

⚠ **NOTE!** You can change the tool (or tools group) place and alignment in toolbar. You cannot change the item place or alignment inside the tool group (tool's expandable menu).

By default all the tool groups with all the tools or menu items inside the group are displayed in panel toolbar, and the **Show in panel toolbar** option is highlighted. You can hide the whole group or inner item, that may be found in the expandable menu, by disabling option **Show in panel toolbar**:

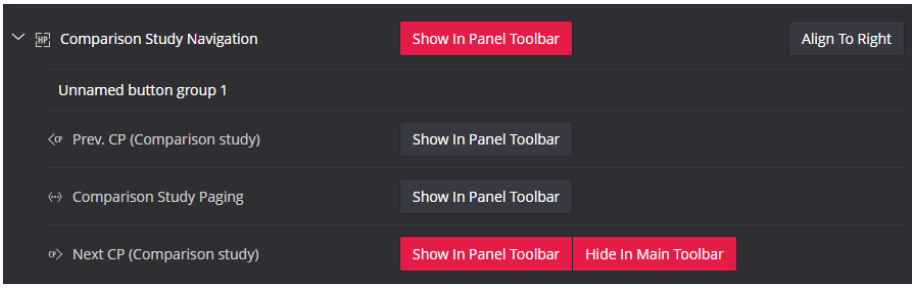


Figure 480. Hiding Prev. CP and comparison study paging elements in panel toolbar

⚠ **NOTE!** Verify the visibility of higher hierarchy items (like tools group, or tool with expandable menu) when changing the item's visibility mode: the inner element is displayed only if the **Show in panel toolbar** is enabled for the group.

If the tool group or the tool in the group may also be displayed in the Viewer toolbar, the option **Hide in Main Toolbar** is available for such element. By default, the **Hide in Main Toolbar** option is highlighted for all the elements, and they are automatically hidden in Viewer toolbar, if panel toolbar is enabled. Disable the **Hide in Main Toolbar** option for the tool, if you want it to be displayed in both the Viewer and the panel toolbars:

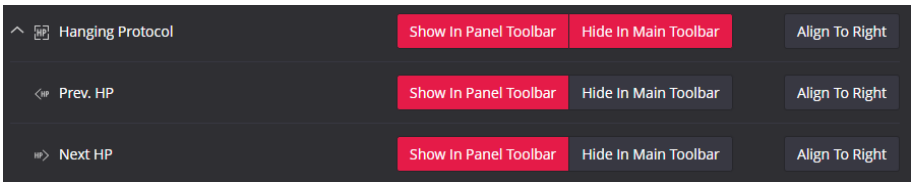


Figure 481. Prev. HP and Next HP tools will be displayed in the Viewer toolbar

Hanging protocol settings

⚠ **NOTE!** The hanging protocols version v2 is available for usage. For details, contact to MedDream support at this email: support@meddream.com.

On **Hanging protocol** tab, you can create new hanging protocols, review and modify existing hanging protocols. The window below lists the hanging protocols, which are provided in default hanging protocols.

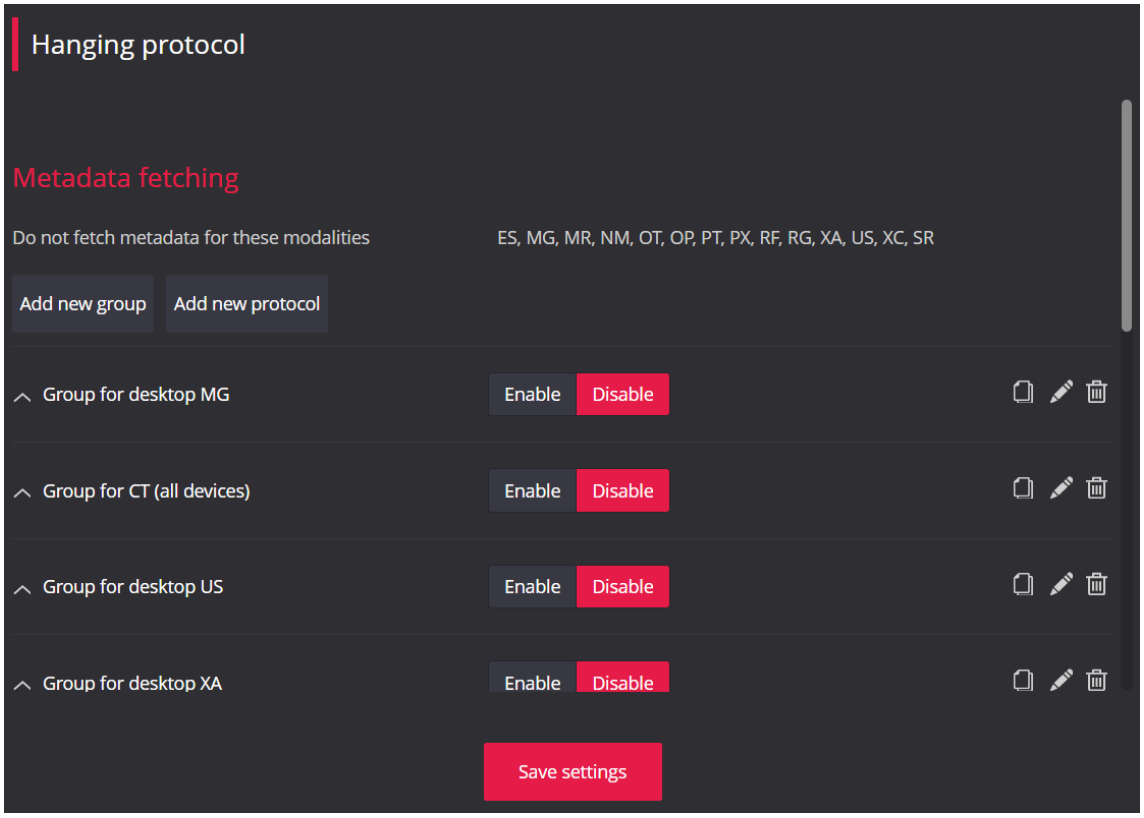


Figure 482. Hanging protocol settings

⚠ **NOTE!** All the data changes that are done in Hanging protocol list, group and protocol child windows (like create group window, create protocol window) are saved in the temporary storage. That means the changes are not accessible to the other users and would be lost in case of program accidental close. The permanent data saving is done only when the **Save settings** is done.

⚠ **NOTE!** The hanging protocols are stored separately from the other system settings.

⚠ **NOTE!** Note that the user with the administrator right can modify only the global hanging protocols, which, after saving, are shared by all users. See the install manual on how to configure the hanging protocols per user group or user.

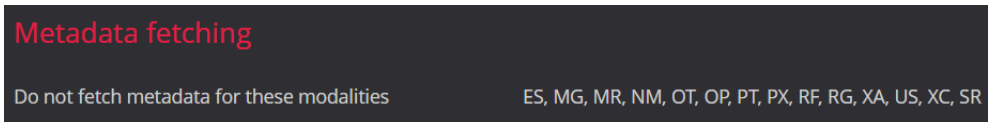


Figure 483. Modality filter for metadata fetching

By default, “Do not *fetch metadata for these modalities*” are set for modalities CT, ES, MR, NM, OT, OP, PT, PX, RF,RG,XA, US, XC, SR. If metadata is not used, only the conditions with following tags are executed:

- Special tags: series_count, instances_count, no.
- DICOM tags: (0008,0016) SOPClassUID, (0002,0010) TransferSyntaxUid, (0008,0060) Modality, (0010,0010) PatientName, (0008,1030) StudyDescription, (0008,103E) SeriesDescription.
- In conditions with DICOM tags (0020,0011) SeriesNumber and (0020,0013) InstanceNumber, the system correspondingly uses the series or image serial number, starting from 0, instead of the tag’s value from DICOM file.

If the Hanging protocol includes conditions with tags other than those listed above, such conditions are ignored.

⚠ **NOTE!** In Hanging protocol, the setting **Do not fetch metadata for these modalities** can only be modified in settings file. Note that for large-scale studies (for example CT, MRI) it is recommended not to use metadata due to long loading time.

Clicking the **Add new group** button on Hanging protocol tab opens the **Create group** window:

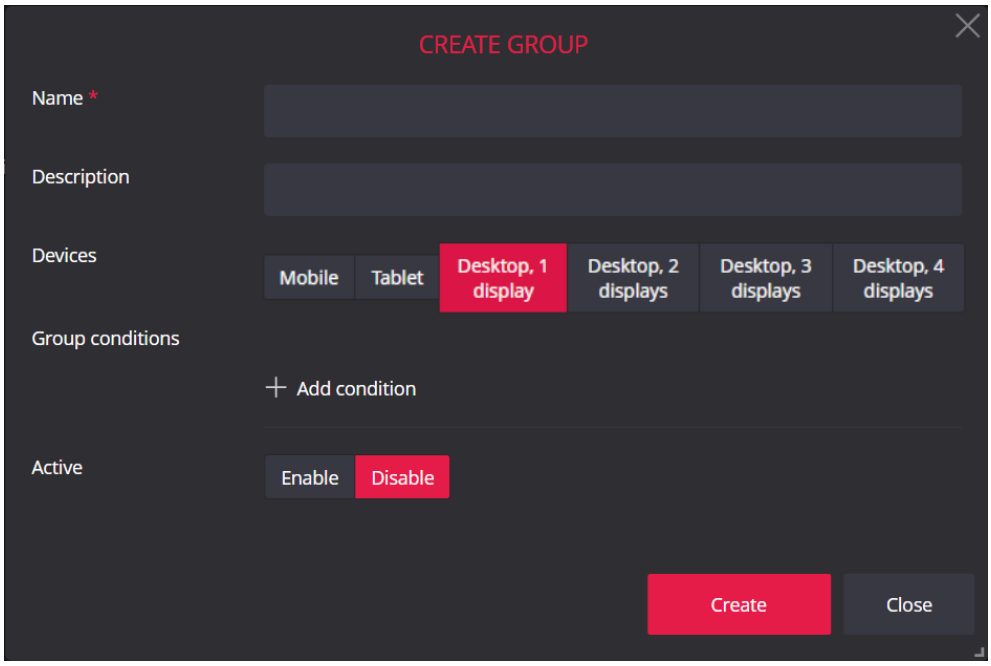


Figure 484. Create hanging protocol group window

To create a new hanging protocol group:

- Enter the required group name in **Name** field. The group name is used for protocol identification and is shown to the users in MedDream viewer.
- If you need, enter the group description in **Description** field. The group description is only visible in settings.
- Select the **Devices** for which the group's protocols should be applied. Clicking the button with device name enables or disables selection.

⚠ **NOTE!** The device settings may be used only by web browsers based on Chromium. And Window management should be allowed in the MedDream site Privacy and security settings for getting access to device information.

⚠ **NOTE!** If no one device is enabled, or device information may not be received from the browser, the protocol group is treated as applicable for any devices.

- Specify the Group conditions.

Entering the Hanging protocl condition

Condition is an expression that could be evaluated as true or false and is used for automatic applying of Hanging Protocol. Condition consist of special tag or DICOM tag that is evaluated against static value according the specified 'operand. An example of condition: 'Modality equals to 'XA''. Several conditions are joined using AND operand, that means all conditions in the group should be met.

A **Tag**, **Operand** and **Value** fields for new condition entry is displayed if "+" icon near the **Add condition** field is clicked:

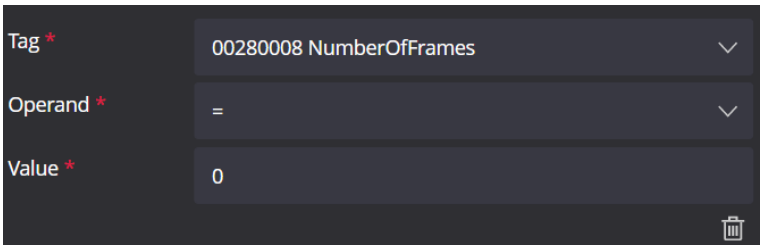


Figure 485. Hanging protocol condition's entry fields

To enter the condition:

- select DICOM or special tag in Tag drop-down list. In group conditions the special tags series_count (number of series in study) and instances_count (number of images in study) can be used;
- select the evaluation operand in Operand drop-down list. The operands list is automatically adjusted to the type of selected tag. The operands list for numeric tags: "=", ">", "<", ">=", "<=", "!=". The operands list for string tags: "match", "not_match", "begins_with", "end_with", "contain";
- enter the value in Value field. The string value should be entered for string tag, and the numeric value should be entered for numeric tag.

⚠ **NOTE!** If the user enters more than one condition with Modality tag and the identical operand in all the conditions, the protocol group is applied only for the studies having the series of all the requested modalities.

To remove the entered condition, click the **Remove** icon below the condition entry fields.

- Activate hanging protocol group by selecting Enable or Disable buttons in the **Active** field. The disabled groups and its protocols are not used for automatic or manual apply.
- Click the **Create** button when all the group data is entered. The **Create group** window is closed, the entered group data is saved in temporary storage and is shown at the end of hanging protocol list on Hanging protocol setting tab.

Clicking the **Add new protocol** button on Hanging protocol tab opens the **Create protocol** window:

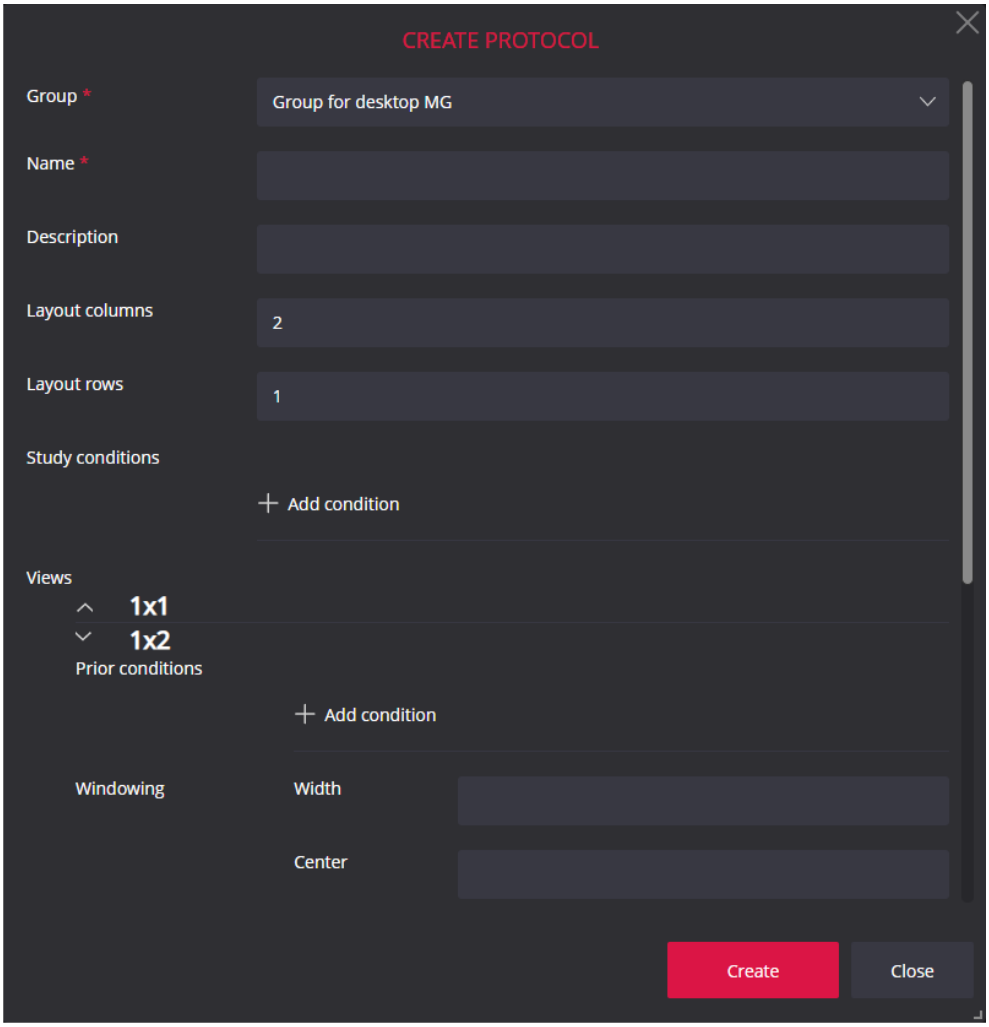


Figure 486. Create protocol window

To create a new hanging protocol:

- Select the group of the hanging protocol in **Group** drop-down list.
- Enter the required protocol name in **Name** field. The protocol name is used for protocol identification and is shown to the users in MedDream viewer.
- If needed, enter the protocol description in **Description** field.
- Define the layout by entering the number of columns in **Layout columns** field and the number of rows in **Layout rows** field.
- Specify the **Study conditions**, that will be used to select whether the protocol should be applied to the study. See description of condition entering on page 318.
- Specify the image selection and display data for each view:

  ⚠ **NOTE!** The view is identified by number [row number]x[column number], that is identifier “1x2” indicates the view in the first row and second column. The arrow near the view indicator can be used to expand or collapse the data entry fields for the view.

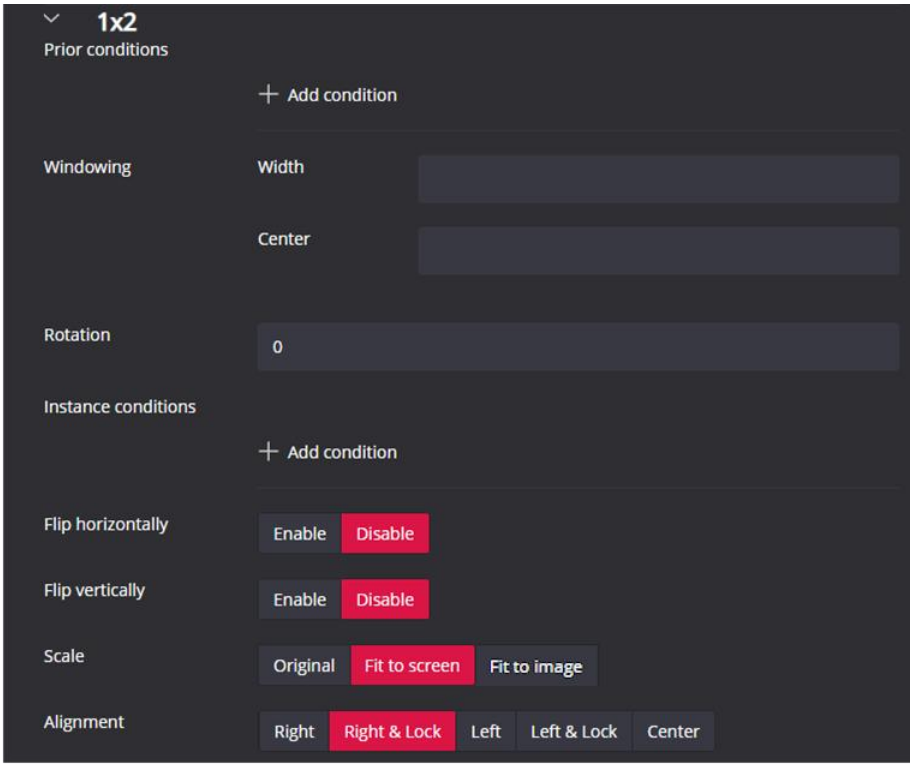


Figure 487. Entering View settings in hanging protocol

specify the **Prior conditions** if you want the image from other study in patient history to be loaded in the view. The special tag **no** (the number of prior study from patient's history, starting from the most recent as "1") can be used. If **no** not specified, the most recent prior study that meats the other conditions is taken. See description of condition entering on page 318;

specify the **Instance condition** for selecting the image from the study, that you are opening (or prior study, if prior study conditions are entered), to display in the view. See detail description of condition entering on page 318;

enter the values for image display: windowing, rotation, scale, alignment.

- Click the **Create** button when all the protocol and views data is entered. The Create protocol window is closed, a new protocol is saved in temporary storage and is shown as the last protocol of selected group in protocols list on Hanging protocol setting tab.

The Hanging protocol list is two level expandable list with the hanging protocol group in the first level and the hanging protocols of the group in the second level.

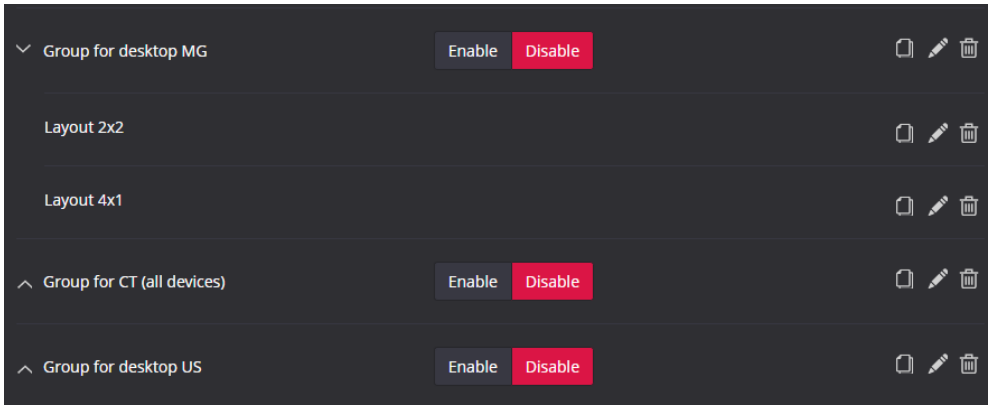


Figure 488. Hanging protocols list

You can perform the following in the hanging protocols list:

- To expands or collapse the list of group's protocols with chevron icon at the left of group's name.
- To enable the group's protocols by selecting the Enable/Disable buttons. The disabled groups and its protocols are not used for automatic or manual apply.
- The Copy, Edit, and Delete icons-buttons at the end of each group's and protocol's line provides access to group's or protocol's data review and edit:

clicking the **Copy** icon makes the copy of hanging protocol or group of protocols. The protocol is placed at the end of the group protocols list and postfix "-copy" is added to the name of the copied protocol. The group is placed at the at the end of the group list and postfix "-copy" is added to the name of the copied group and all its protocols;

Clicking the **Edit** icon at the end of group line opens the **Edit group** window with group data filled in the entry fields. You can review and edit the group's data. See detail fields description on page 317;

Clicking the **Edit** icon at the end of protocol line opens the **Edit protocol** window with protocol data filled in the entry fields. You can review and edit the protocol's data. See detail fields description on page 319;

Clicking the **Remove** icon at the end of group or protocol line deletes the item. If the group is removed, all the protocols of this group are also deleted.

- The drag-and-drop functionality for changing the order of group in the list and for changing the order of protocols in the group. To change the place of the group or protocol item, press the right mouse button on the item and drag the item to the desired place. The items order is important in automatic hanging protocol apply: the first group, that meets the group conditions, is chosen and the first protocol of this group, that meets the study conditions, is applied.

DICOM Print settings

DICOM Print settings are used for configuration of DICOM printers and management of printing parameters.

DICOM Print settings are available in the Settings window, in the DICOM Print tab. The tab is displayed only when the DICOM Print functionality is enabled in the system configuration.

DICOM Print settings are stored in a separate configuration file.

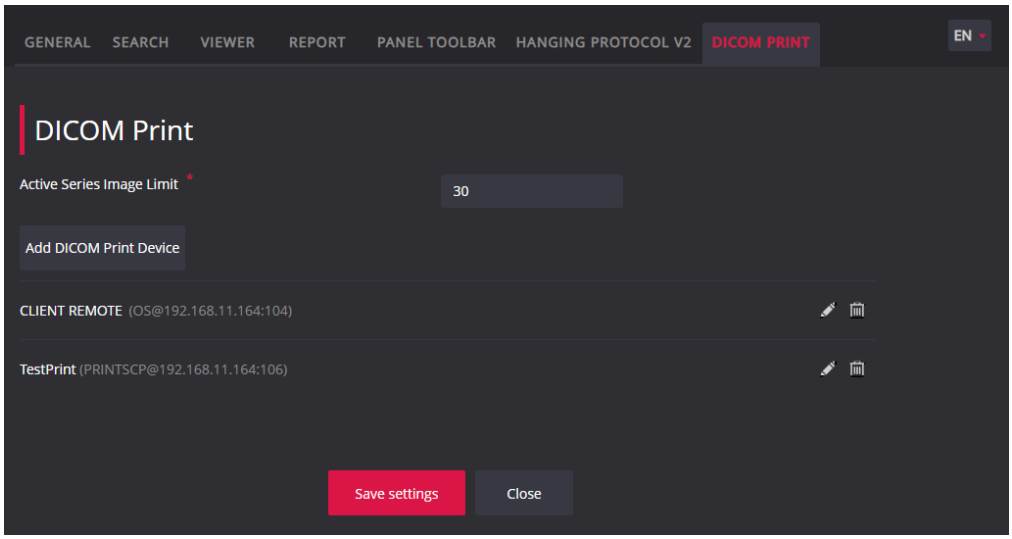


Figure 489. DICOM Print

In the tab, it is possible to specify the Active Series Image Limit value, which is used in the related printing action. The field is mandatory. Allowed values are from 1 to 999.

It is possible to add a new DICOM print device, edit existing printer settings, or remove a printer from the list.

To add a new printer, press the button Add DICOM Print Device. The system opens a separate printer settings window.

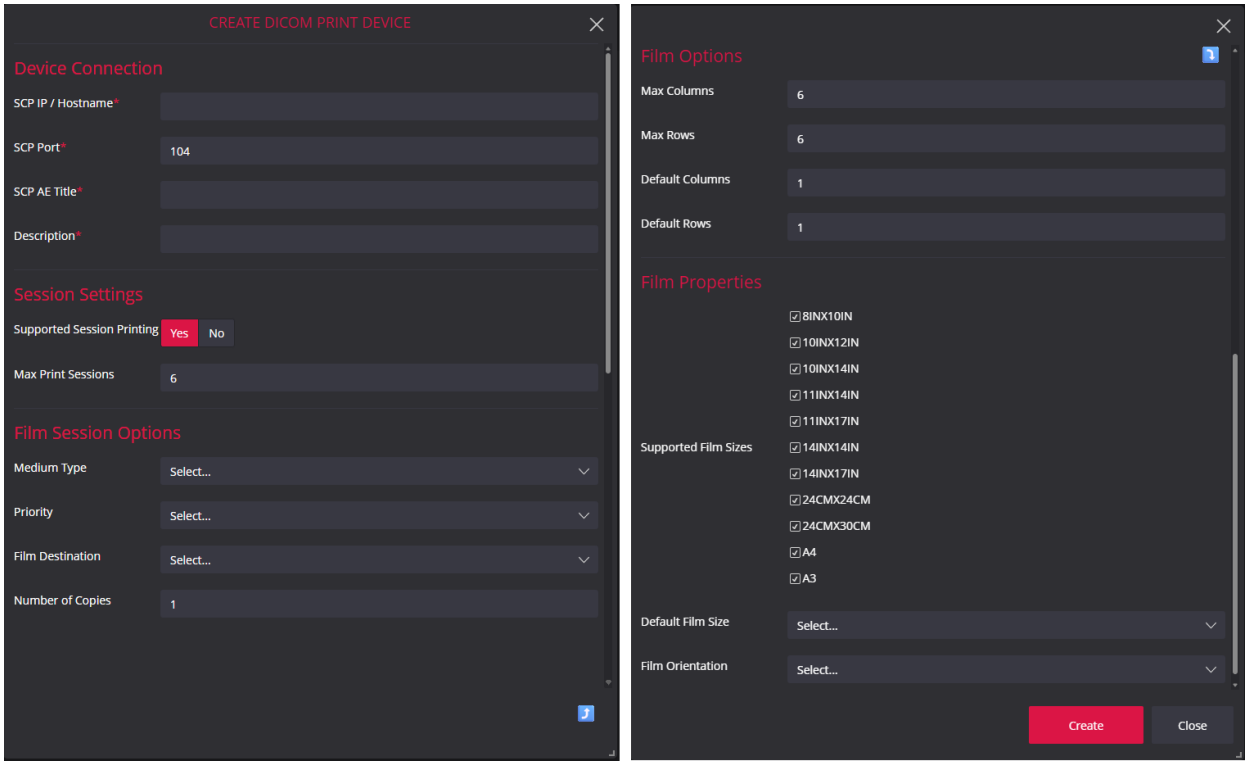


Figure 490. DICOM Print Device Entry

Device Connection

- Field **SCP IP / Hostname** is used to specify the DICOM printer IP address or server name. Field type – text value. The field is mandatory.
- Field **SCP Port** is used to specify the DICOM printer communication port. Field type – numeric value. The field is mandatory.
- Field **SCP AE Title** is used to specify the DICOM printer AE Title value. Field type – text value. The field is mandatory.
- Field **Description** is used to enter the printer name or short description. Field type – text value. The field is mandatory.

Session Settings

- Field **Supported Session Printing** specifies whether the printer supports session printing. Field type – logical value (Yes / No).
- Field **Max Print Sessions** is used to specify the maximum allowed number of print sessions. Field type – numeric value.

Film Session Options

- Field **Medium Type** is used to select the printing media type. Field type – selection from list. Available values:
  - PAPER;
  - CLEAR FILM;
  - BLUE FILM;
  - MAMMO CLEAR FILM;
  - MAMMO BLUE FILM.
- Field **Priority** is used to select the print job priority. Field type – selection from list. Available values:

  - HIGH;
  - MED;
  - LOW.
- Field **Film Destination** is used to select the print destination type. Field type – selection from list. Available values:
  - MAGAZINE;
  - PROCESSOR.
- Field **Number of Copies** is used to specify the number of printed copies. Field type – numeric value.

Film Options

- Field **Max Columns** is used to specify the maximum allowed number of image columns on the page. Field type – numeric value.
- Field **Max Rows** is used to specify the maximum allowed number of image rows on the page. Field type – numeric value.
- Field **Default Columns** is used to specify the default number of image columns on the page. Field type – numeric value.
- Field **Default Rows** is used to specify the default number of image rows on the page. Field type – numeric value.

Film Properties

- Field **Supported Film Sizes** is used to select the allowed film sizes. Field type – selection from list. Available values:
  - 8INX10IN;
  - 10INX12IN;
  - 10INX14IN;
  - 11INX14IN;
  - 11INX17IN;
  - 14INX14IN;
  - 14INX17IN;
  - 24CMX24CM;
  - 24CMX30CM;
  - A4;
  - A3.
- Field **Default Film Size** is used to select the default film size. Field type – selection from list.
- Field **Film Orientation** is used to select the film orientation for printing. Field type – selection from list. Available values:
  - PORTRAIT;
  - LANDSCAPE.

MedDream Mobile mode

You do not need a separate MedDream software version to use it on mobile devices. MedDream software automatically switches to mobile mode, if detects the mobile devise on startup or desktop window resolution is resized to less than 992 pixels.

⚠ **NOTE!** Note, that browser's zoom function changes resolution and the software may automatically switch to mobile mode.

Features of MedDream mobile mode:

- Adjusted Search window layout;
- Adjusted Viewer window layout;
- Adjusted Settings window menu;
- Some functional limitations.

Further subsections describe Search window, Viewer window, and Settings window mobile layout and mobile mode functional limitations. For detail functionality and usage description see "Minimum hardware requirements for client-side MedDream viewing functions", "Displaying notifications", "MedDream DICOM Viewer", and "Settings" sections of this manual.

Search of studies in mobile mode

Search for studies mobile layout consist of two windows:

- Search criteria window;
- Search results window.

If successfully logged in, the **Search criteria** window opens:

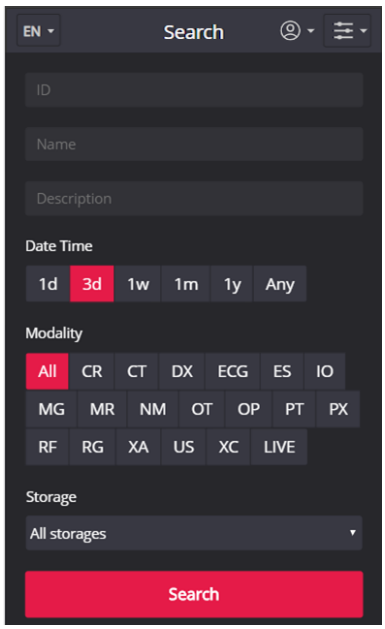


Figure 491. Search criteria window in mobile mode

The following search criteria are supported in mobile mode:

- **ID** – patient's ID,
- **Name -** patient's name and/or surname,
- **Description** –study description,
- **Date Time** - date interval, selected in pick list,
- **Modality** – modalities selected in pick list,
- **Storage** – the PACS or other configured storage, selected in drop-down list.

See the detail description of search criteria in section “Displaying notifications”.

⚠ **NOTE!** The mobile mode has the following search limitations comparing to desktop version:

search according accession number and source AE title is not allowed;

search according custom date interval is not allowed;

the customization of modalities pick list and search according custom modality is not allowed.

To find the study, enter **search criteria** and press the **Search** button. System displays the studies list in the **Search results** window:

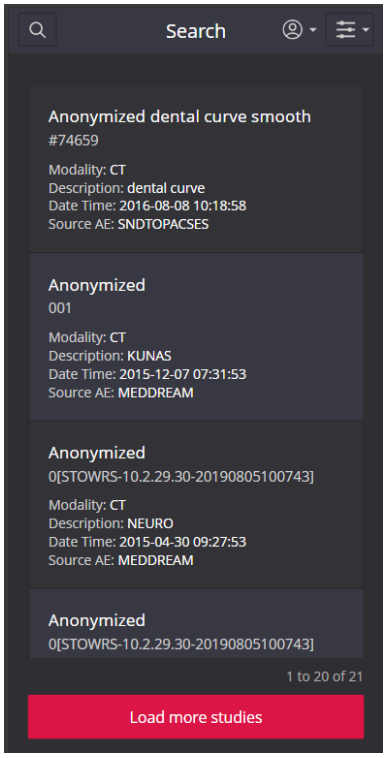


Figure 492. Search results window in mobile mode

The results list displays the following study information:

- Patient's name and surname in the first line.
- Patient's ID number in next line.

- **Modality** – field shows method which was used to obtain the study images (modality).
- **Description** – field shows study description
- **Date Time** – field shows study date and time
- **Source AE** – field shows title of the device from where the study was sent to the PACS.

⚠ **NOTE!** The field is empty if the DICOM file or PACS does not have the particular data.

In the search results window, you can do the following*:*

1. To navigate through the result list, use the scroll bar or drag up and down whit one finger (or fingers) on the result list. The number of currently loaded studies and total number of search results are displayed at the bottom of the window:

2. To load more studies, press **Load more studies** button – next page is loaded.

⚠ **NOTE!** The number of studies per page is defined in system settings.

⚠ **NOTE!** The **Load more studies** button is not displayed if all the studies are loaded.

3. To open the study in viewer, press at any place of study description. The selected study opens in Viewer (see Opening studies in MedDream Mobile mode section for detail description).

4. To return to the Search criteria window, press the search button  at the top left corner of the search results window.

The description of the other buttons in the **Search criteria** window and **Search results** window:

1. To change the language, press the **Language** button 

at the top left corner of the **Search criteria** window and press the language option in drop-down menu.

2. **System** menu  at the top left corner of the **Search criteria** window and **Search results** enables access detailed system information and functionality description (see System menu functions section for detail description).

3. **User details** menu  allows to see the login name and time. If provided, the user name is also displayed.

⚠ **NOTE!** System menu options and User details may be disabled in Settings. The Settings options may also be not allowed by user rights.

⚠ **NOTE!** The Forward and Export functions in search results list are not available in mobile mode.

Viewer window in mobile mode

The Viewer window mobile layout contains the following zones:

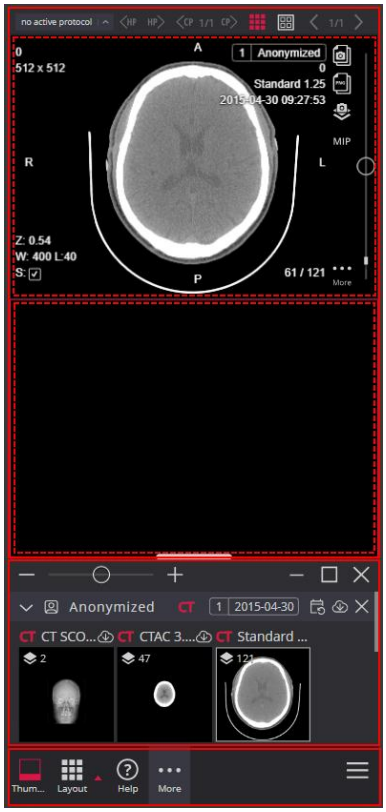


Figure 493. Viewer window zones in mobile mode

1. Image manipulation tools zone is shown at the bottom left side of the window. What buttons and in what order are shown in toolbar is described in system settings (see section Toolbar Properties).

⚠ **NOTE!** The tools set may vary depending on content of the active viewport.

If there is not enough space for the buttons to be displayed, or there are pinned tools configured in settings (see section Toolbar Properties), the system automatically displays button **More** and places the other tools under this button. Tap the More button to view and select the tools:

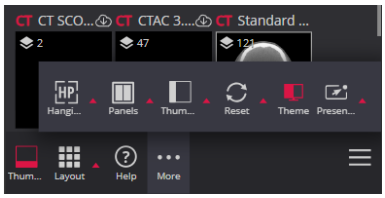
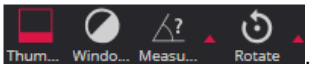


Figure 494. More tools list opened in mobile mode.

In toolbar or More tools list you can activate tool usage, if the tool can be operated on the touch screen. To activate the tool, follow these steps:

- Tap the icon of inactive tool 

.
- The tool is activated and tool icon is highlighted  . In the example, the activated Windowing tool can be used on the touch screen: dragging upwards or downwards changes Level values, and dragging right or left changes Window values.

The tool activation is deleted by pressing the tool icon once more or by activating another tool.

NOTE! Mobile mode does not support middle and right mouse button actions and only the tool, that is associated with the left mouse button (indicated by mouse icon), is activated.

For a description of image manipulation tools in mobile mode, see the section Manipulating images in MedDream Mobile .

Press the triangle on the left of tool icon or long press tool icon to open the modal with tool's menu:

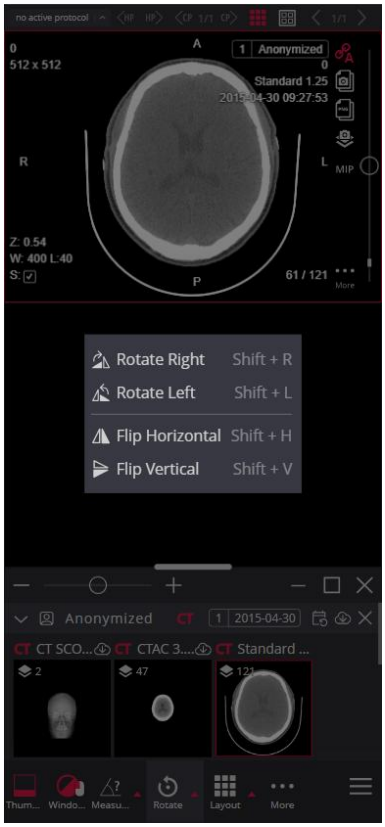


Figure 495. Tool's menu in Viewer window in mobile mode

You can activate the menu option by pressing it. If the option has an assigned shortcut, the key combination is written on the right: pressing 'SHIFT' and 'R' keys rotates the active image right.

Grouped system tools button is shown at the bottom right side of the window. Long press the tool icon to open the list of the system tools, that function identically as in desktop mode (see description on page 20):

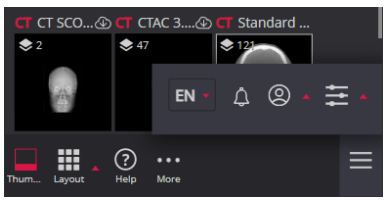


Figure 496. Expanded system tools in Mobile display mode

2. By default, Thumbnails for mobile icon is highlighted  and the thumbnails zone is displayed between the tools zone and the view zone:

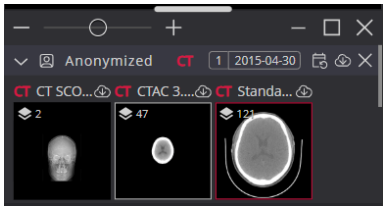
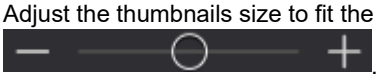


Figure 497. Thumbnails for mobile in Mobile display mode

In thumbnail zone you can perform the following (see section Thumbnails bar for details):

- Expand or collapse the thumbnails of the study by tapping the chevron icon  at the top left corner of the study description.
- Remove the study from Viewer window by tapping the close study icon  at the top right corner of the study description.
- Open patients' studies modal by tapping the patient's history icon  .
- Preload the data by tapping the preload icon  . Taping the preload icon in the study description, preloads the whole study. Taping the preload icon in the series description, preloads the series.
- Open the image or series by tapping the corresponding thumbnail.

You can adjust the look of the Thumbnails for mobile:

- Adjust the thumbnails size to fit the mobile display with the thumbnail size slider  . Drag the slider or tap the "-" or '+' icons. The thumbnail zone height automatically adjusts to fit one row of thumbnails. This height is treated as minimal zone height.

  ⚠ **NOTE**! The adjusted thumbnail size is saved in browsers local storage and used for thumbnails for mobile next time.

- Manually adjust the thumbnails zone height by dragging the separation bar  up or down. Note that automatic adjustment based on thumbnail size is no longer available after the user adjusts the height manually. You will need to minimize the Thumbnails for mobile zone to restore the default adjusting feature.
- Minimize or maximize the height of the Thumbnails for mobile zone by tapping the icons  or  respectively.
- Hide the Thumbnails for mobile zone by tapping the highlighted Thumbnails for mobile icon  . The icon highlighting is removed, and the thumbnails zone is no longer available. To view the thumbnails again tap the not highlighted Thumbnails for mobile icon  .

3. The view zone takes the largest part of the Viewer window and is designated to view and analyze the images. The view zone may be divided to several sections, each section (dashed line in figure) working as separate viewport for image viewing. The manipulation is allowed in one active viewport at a time. To activate the viewport, press on the viewport area – the active viewport is highlighted. The image manipulation toolbar is automatically adjusted according the content of the active viewport.

At the right side of the viewport the scroll bar with the scroll cursor, that is scrolled respectively to the position of the active image in the series, is shown. At the bottom of the scroll bar is the total number of images in the series and the number of the active image. Dragging the cursor along the scroll bar or pressing on the desired scroll bar position changes the image.

⚠ **NOTE!** Separate tools may be configured to be included in quick menu for Desktop display mode and for Mobile display mode.

Opening studies in MedDream Mobile mode

⚠ **NOTE!** See section “Patient studies list in mobile mode” for detail description how to open the studies from the Patient studies list.

To open the study from MedDream Search window, please do the following:

1. Find the required study in Search results window and press on the study description area:

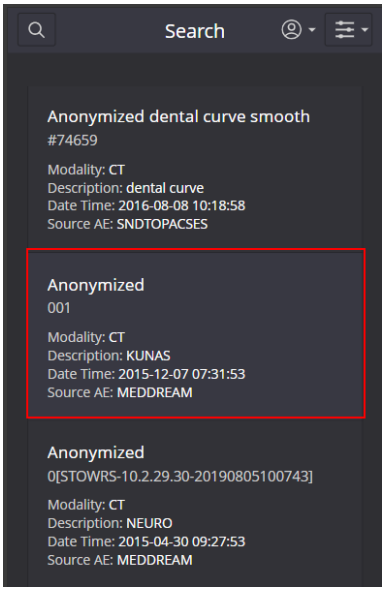


Figure 498. Study description area in Search results window in mobile mode

2. A new browser tab with a Viewer window will pop up with Thumbnails for mobile zone opened by default and the study displayed in it. You can adjust the thumbnail and thumbnails zone size for better navigation as described in parent section:

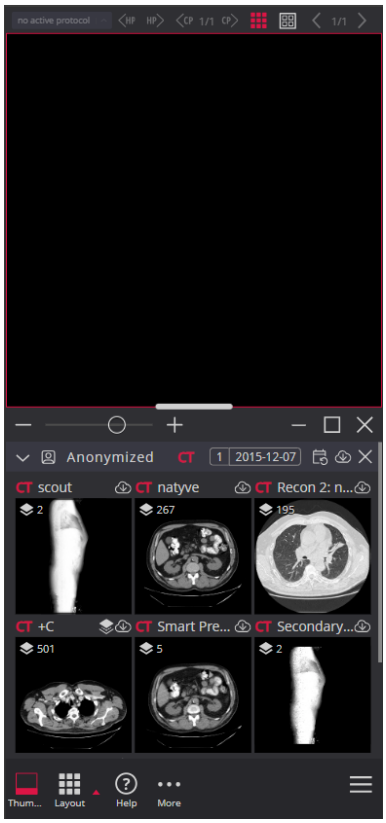


Figure 499. Selecting the study image in mobile mode

⚠ **NOTE!** The first image automatically opens, if the first image opening conditions are met (see description in Settings).

⚠ **NOTE!** The progress bar appears at the top of the window if the study preload process is ongoing.

3. Find and tap the image thumbnail to open the image or series in Viewer.

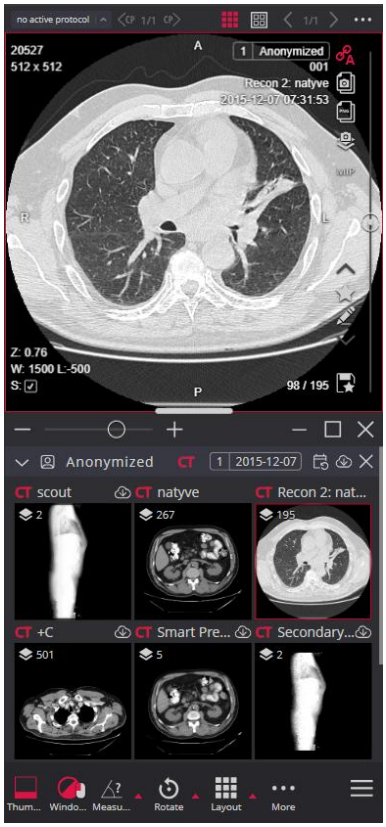


Figure 500. Viewing selected image in mobile mode

4. If you need to open more than one study (e.g. to compare the images from different studies) in the same Viewer window, please do the following:

- Change the Viewer window layout (see description in section “Panels, Layout, and Multi image/series”) and press on the viewport in which you want to open other study. The viewport is activated:

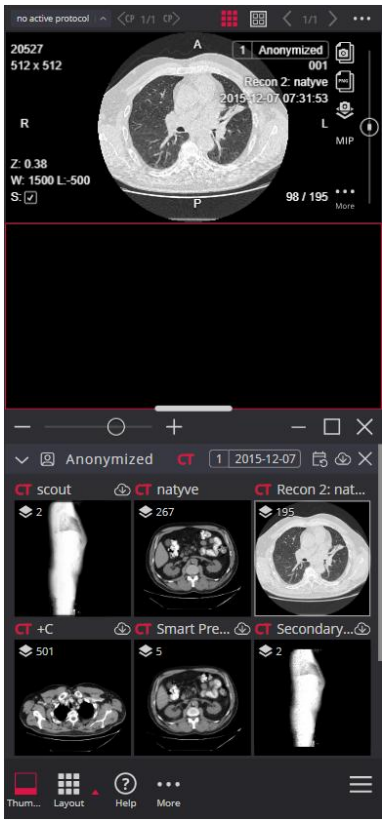


Figure 501. 2x1 Screen layout with active bottom viewport in Viewer window mobile mode

- Go back to the search results window by pressing MedDream search browser's tab.
- Find and select the study in search results, as described in step 1.
- The program navigates to MedDream viewer browser's tab. The study is added to the end of the studies list for the same patient in Thumbnails for mobile zone and automatically expanded. The thumbnails for the other studies automatically collapsed:

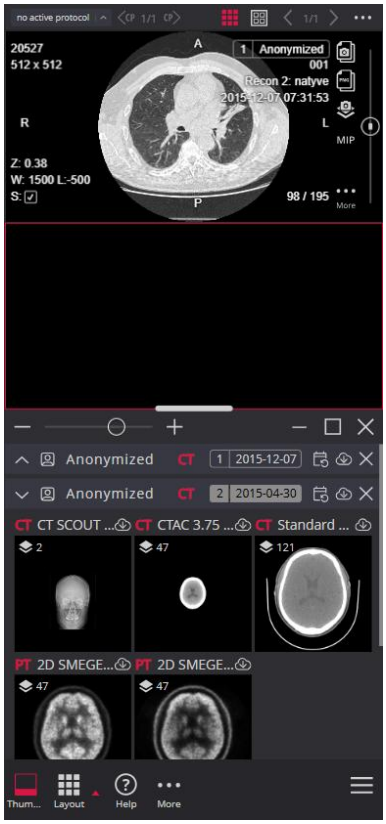


Figure 502. New study added at the top of the studies list of the viewer window

⚠ **NOTE!** The opened studies are automatically grouped by patient, ant patient icon and info is displayed only at the beginning of the studies list for the patient.

⚠ **NOTE!** Use Thumbnails for mobile icon to show the thumbnails zone, if it is hidden.

⚠ **NOTE!** Use patient history button in Study description to open the study from patient historical studies list.

- Find and press the image thumbnail to open the image in an active viewport. To use the whole mobile device display space for image viewing, tap the highlighted Thumbnails for mobile icon to hide the thumbnails zone:

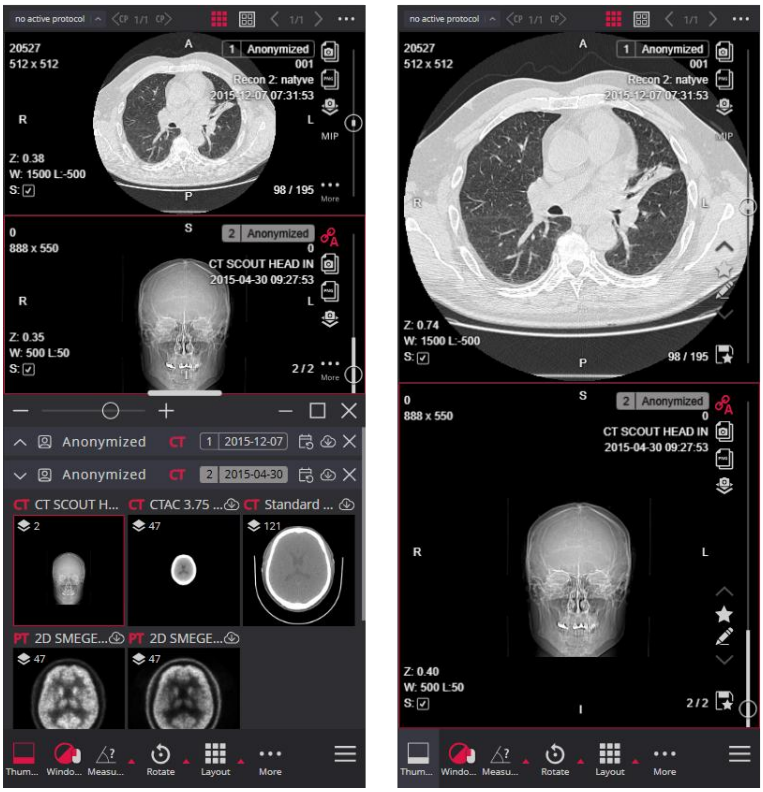


Figure 503. Multiple images opened in mobile mode

Patient studies list in mobile mode

The **Patient studies list** may be viewed in Patient studies window, and Patient history window. See sections "Patient studies window" and "Patient history" for detail conditions when and how these windows may be opened.

In mobile mode the list view is used for patient studies list:

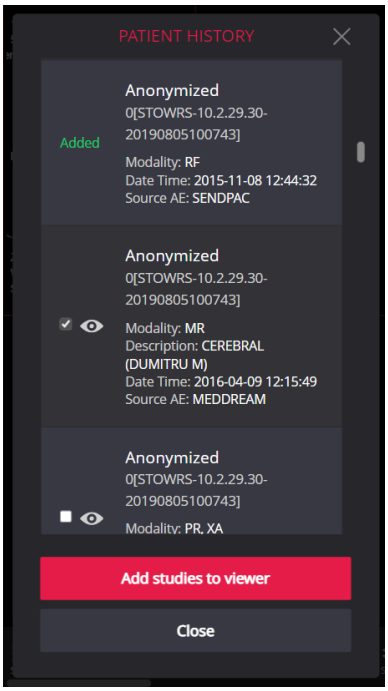


Figure 504. Patient studies list in mobile mode

You can scroll the list and open the patient studies for viewing:

- To open one study, press on the eye icon at the left of the study description;
- To open multiple studies at once, press and mark the tick-box next to the studies description and press the **Add studies to viewer** button, when all the required studies are marked;
- All the studies, that are already opened in Viewer, are highlighted as **Added** and haven't controls for opening.

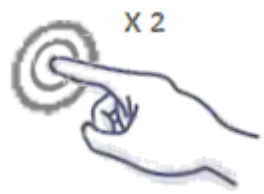
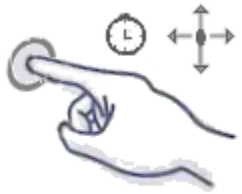
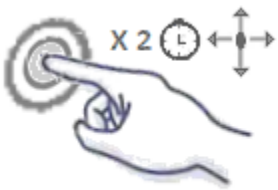
Manipulating images in MedDream Mobile mode

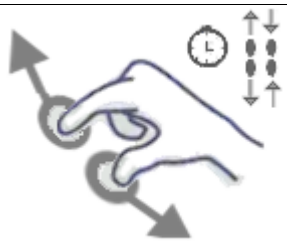
The section describes the specifics of using the image manipulation tools with touch screens. See detail description of particular tool in the following sections:

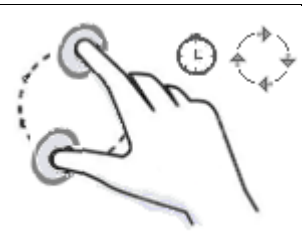
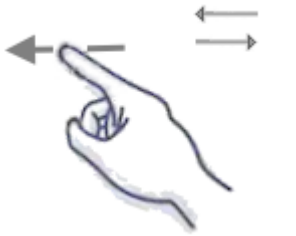
- "Tools for image manipulation and analysis" section describes tools: Windowing, Pan, Zoom, Channels, Scroll, Magnifier, Layout, Multi image, Reset, MPR, Reference Line, Crosshair, Rotate, DICOM, and Link;
- "Tools for measuring, and presentation state saving" section describes Presentation states, Key Objects, Segmentation, and measure menu tools: Line, Angle, Polyline, Area, Volume, Velocity Time Integral (VTI), Ellipse, Cobb Angle, Tibial Plateau Angle, Norberg Angle, Vertebral Heart Scale, Hip distraction index, Tibial tuberosity advancement, Cardiothoracic ratio, Text comments, Region Of Interest, Spine labeling, Flexpoly, Pencil, Arrow, Flatfoot, Calibration line, Show Angles, Intensity, Delete measurements, Save Presentation state;
- "Tools for study exchange" section describes Share files via DICOM Library, Forward, Export, and LiveShare tools;
- "Fusion function" section describes the fusion tool;
- "Cine mode" section describes the playing as video tool;
- "Other Viewer tools" for tools Thumbnails for mobile, Plugins, Full Screen, Theme, Preload Series, Print, and Hanging protocols;
- "ECG module" for ECD manipulation toolbar and measure tools.

The table below describes what finger actions should be used on touch screens instead of mouse actions.

Touch / Touch description	Action description
One finger tap - briefly touch the screen with a finger. Corresponding the mouse left button click action.	
	Selecting actions from the menu, selecting the active viewieport and other selection actions.
One finger double tap - tap the screen quickly with your finger twice. Corresponding the mouse left button double click action.	

Touch / Touch description	Action description
	If the layout is not 1x1, double-tap on the image temporarily viewing it on top of the layout. Repeated double tap returns to the previous layout.
⚠ **NOTE**! One finger double tap drag is not working if any of tools is activated.	
One finger tap and hold (may also be called **long press**) - touch the screen with a finger and hold down until you perform the action. Does not have a direct correspondence to a mouse action. Used only in mobile.	
	To open the tool's expandable menu, tap and hold one finger on the menu item. One finger tap on the menu item also works. To open the quick menu, tap and hold one finger on the viewport area without any active component below the finger.
One finger tap and drag - touch the screen with a finger and move finger towards required direction without losing contact. Corresponding mouse drag when the tool is activated.	
	When the someone tool is activated (is icon is highlighted, e.g. the activated Windowing tool ) one finger tap and drag perform an activated action (e.g. change WL properties). Also can be "Pan", "Zoom", "Rotate", "Measure", "Scroll" and another. When no tool is activated, the image pan is performed on one finger tap and drag in viewport with image.
One finger double tap and drag - tap the screen quickly with your finger twice, do not release the finger after the second press, hold it down and drag without losing contact. Does not have a direct correspondence to a mouse action. Used only in mobile.	
⚠ **Note!** For double tap (both one and two fingers) to be activated, the interval between taps must be no more than 300 ms. Double tapping will only work if approximately the same area of the screen is touched. It is recommended to hold the finger for at least 300 ms after the second press, then start moving.	
	To change images contrast and brightness (Level and Width values) settings use one finger double tap and drag in either direction. Up-down changes the L value, side-to-side changes the W value. Moving diagonally - both values.

Touch / Touch description	Action description
⚠ **Note!** Finger movements are not precise, so the position relative to the X-axis may also change slightly as you move up and down. This results in changes in both L and W values.	
Two fingers tap - briefly touch the screen with two fingers. Does not have a direct correspondence to a mouse action. Used only in mobile.	
	Selecting the active viewieport, in the same way as tapping with one finger.
Two fingers double tap and drag vertically to scroll - tap the screen quickly twice with two fingers, do not release your fingers after the second press and drag your fingers up or down.	
	To scroll between series instances, use two fingers double tap and drag to scroll.
Two fingers tap and move them closer or further - touch the screen with two fingers, hold them down and then move them closer or further; when you reach the maximum or minimum distance between your fingers, you can release your fingers and repeat the action again. Does not have a direct correspondence to a mouse action. Used only in mobile.	
	To increase or decrease the size of the image (commonly known as zoom), tap with two fingers and move them closer or further away.
Two fingers tap and drag - tap the screen with two fingers, hold them down, and drag an object to a different location.	
	To move an image (commonly known as Pan), touch the screen with two fingers and drag in any direction without releasing.

Touch / Touch description	Action description
⚠ **NOTE!** Pan with two fingers tap and drag is not working if any of tools is activated (is icon is highlighted, e.g. the activated Windowing tool ).	
Two fingers hold and rotate - touch the screen with two fingers, leaving space between the fingers, hold them down, and make a circular movement; if necessary, the action can be repeated until the object is rotated to the required angle. Does not have a direct correspondence to a mouse action. Used only in mobile.	
	To rotate the image, use two fingers to hold and rotate.
One finger swipe vertically - swipe the screen briefly with one finger vertically, either up or down. Does not have direct correspondence to a mouse action. Used only in mobile.	
	To scroll between series instances, use one finger swipe in vertical direction, up or down.
One finger swipe horizontally - swipe the screen briefly with one finger horizontally, either right or left. Does not have direct correspondence to a mouse action. Used only in mobile.	
	To change to the next or previous series of the study, use one finger swipe in horizontal direction, right or left.

⚠ **NOTE!** The description of actions for mobile, that may be accessed through the Help tool in toolbar  .

Setting window in mobile mode

The Settings in mobile mode are grouped by system windows and / or functions as in desktop mode.

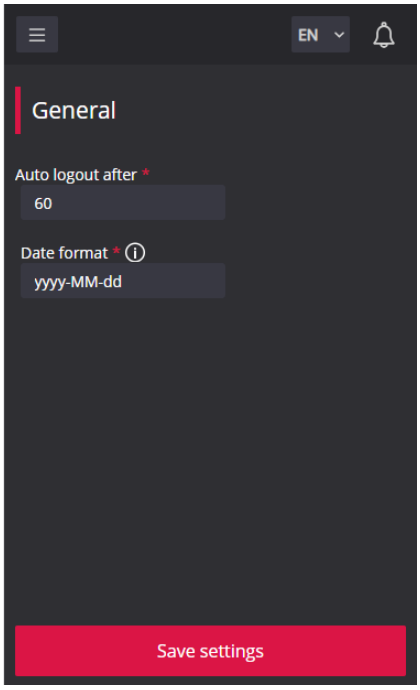


Figure 505. Settings window in mobile mode: General settings

To open the required setting group, do the following:

- Press the menu button ☰ on the top left corner of the Settings window. The system displays the settings window menu:

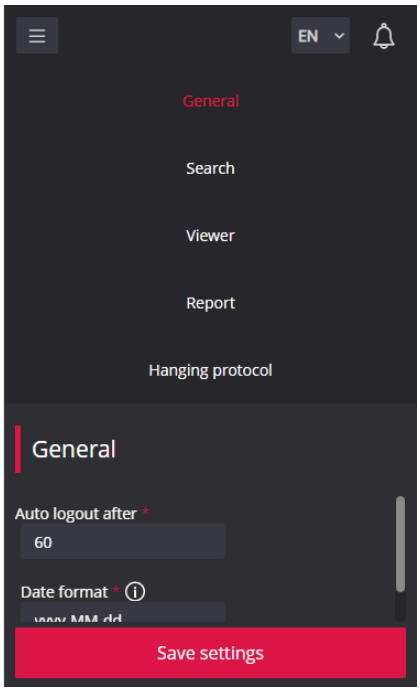


Figure 506. Settings window menu in mobile mode

- Press the menu item. The selected settings tab is opened:

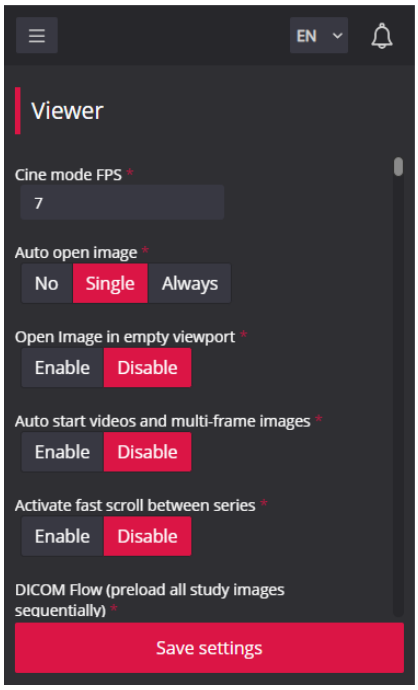


Figure 507. Settings window in mobile mode: Viewer settings

See detail settings groups and fields description in section “Settings”.

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