MedStation®

The complete solution for diagnostic images management

User's Manual

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Intended Use

The MedStation system[1] is a free-standing, image, waveforms and clinical documents processing device that is a component of a Picture Archiving and Communication System (PACS) for Radiology, Cardiology, Endoscopy and other diagnostic departments designed to be networked with a PACS Image Archive, a Radiological Information System (RIS) and a wide variety of diagnostic imaging devices (e.g. X-ray, Nuclear Medicine, Magnetic Resonance (MR), Computed Axial Tomography (CAT), Ultrasound and electrocardiographs). It does not contain controls for the direct operation of a diagnostic imaging system and it is designed to retrieve, receive, archive and transmit data both on-line and off-line. It is configured to provide capabilities to create, manipulate and/or view patient images, waveforms and information collected from diagnostic imaging systems, diagnostic waveform systems, and clinical documents repositories, following the Dicom and IHE XDS international standards.

The system consists of the MedStation software and a Personal Computer with a monitor, keyboard and mouse. Optionally one or more of the following components may be added: a RIS client program (the eRis web client or other RIS supplied by a third party), one or more specialized imaging software components (e.g. for viewing 3D or cardiological images), up to four additional Radiological monitors, a smartcard reader, a barcode/magnetic card reader, a voice reporting software package with microphone, a local paper printer, and a CD production robot.

The system interfaces with diagnostic techniques exclusively via a data network. The system is not connected to patients or installed near them.

The system is made up of the MedStation Express software and a Personal Computer with a monitor, keyboard and mouse.
The system is not connected to the patient or placed close to him/her.

[1] In the particular **MedStation Express** configuration, the system is a device for viewing images, tracings and clinical documents, a component of a PACS system for Radiology, Cardiology, Endoscopy and other diagnostic services. It does not include devices for testing the operation of the diagnostic equipment and is designed to search for and display off-line data stored on CDs and DVDs. It has some functions for creating, manipulating and displaying images, tracings and the patient's clinical data coming from diagnostic systems that produce images or tracings and clinical data archives, on the basis of the DICOM international protocols.
The system is made up of the MedStation Express software and a Personal Computer with a monitor, keyboard and mouse.
The system is not connected to the patient or even used close to him/her.

GMDN Classification

40943 – PICTURE ARCHIVING AND COMMUNICATION SYSTEM WORKSTATION

GENERAL WARNING





RC-07

Unauthorized changes to configuration files of MedStation may cause the application to malfunction. Contact Exprivia S.p.A. support before making any changes.



RC-07

MedStation should be used by persons qualified to perform radiological analysis, such as medical radiographers or radiologists. If the results of analysis are used to obtain a diagnosis, these results should be interpreted by a medical radiologist.



RC-11

The use of MedStation for diagnostic purposes requires the use of a suitable configuration and workstations equipped with medical monitors suitable for the types of images displayed. MedStation should not be used for purposes other than those specified in the *Intended Use* section.



RC-07

Users should read this manual in order to be able to use the software properly and conduct reliable analyses with it.



RC-08

Exprivia advises to install antivirus products and to periodically update systems in order to ensure security against computer viruses.



The images displayed reflect the contents of the DICOM files read. Exprivia declines all liability for the compliance of the files read with the originals generated by the diagnostic device.



Exprivia shall not be held responsible for any disputes that may arise with patients of the users regarding medical decisions concerning the prevention, diagnosis and treatment made by the doctor.

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If you contact the Exprivia call center by e-mail, please indicate the software name and version of the entire version number in the subject or in the body text. To find the version number of your software, select the item **eM | Help | Info.**

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Soup

Supported Operating System

Operating System	Build Service Pack	Platform	Build
Windows 10		32, 64 bit	All
Windows 8.1		32, 64 bit	All
Windows 7	SP1	32, 64 bit	All
Windows Vista	SP2	32, 64 bit	All
Windows Server 2003	SP1	32, 64 bit	All
Windows XP	SP3	32, 64 bit	All

External Software System

Title	Manufacturer	Designator / Build	Note
3DNet Suite	Biotronics 3D Ltd http://www.biotronics3d.com/	2.2.6.9.0	Professional 3D visualizer
Alma 3D	Alma IT Systems http://www.alma3d.com	4.1.2.0033	Professional 3D visualizer
Agfa Impax	https://global.agfahealthcare.com	6.6.1.3004	Professional 3D visualizer
BarcoMed DLL	www.barco.com	1.2.70.RC01	Monitor 10 bit
EliEdit	http://www.mortara.com	1.3	DICOM ECG Library
FFmpeg	http://www.ffmpeg.org/	0.6.3	Video decoder library
GE Centricity PACS System	GE http://www3.gehealthcare.com	4.0.3	Centricity PACS System
Medis QAngio XA	Medis medical imaging systems bv http://www.medis.nl/products/qangioxa.htm	7.2.20.0	Angiographic XA images visualizer
Medis Qflow	Medis medical imaging systems bv http://www.medis.nl/products/QFlow.htm	5.1.78.0	Emodynamic MR images visualizer
Medis QMass CT	Medis medical imaging systems bv http://www.medis.nl/products/QMassCT.htm	7.2.76.0	Cardiac CT images visualizer
Medis QMass MR	Medis medical imaging systems bv http://www.medis.nl/products/QMassMR.htm	7.2.76.0	Cardiac MR images visualizer
Nero Burning ROM 7	Ahead http://www.nero.com/	7.0.1.4	Burning CD/DVD tool
Terarecon iNtuition	http://www.terarecon.com/	4.4.11	Professional 3D visualizer

Vitrea Enterprise Suite	Vital Images Inc. http://www.vitalimages.com/Solutions/Vitrea_Enterprise_Suite.aspx/	5.1.1559.1696s	Professional 3D visualizer
Voxar 3D Workstation	Toshiba Medical Systems Co. http://www.tmvse.com/Products-and-Services/Voxar-3D-Workstation/	6.3	Professional 3D visualizer



RC-09

Consult this list to help minimize the risks of using unsuitable SOUP components.



RC-04

Some external products (integrated with MedStation) for processing specialized images maintain a local archive for recent examinations. After a patient-examination reconciliation, the local archive could therefore contain data that is not up to date, without MedStation being able to update it.

MedStation

Diagnostic images, waveforms and clinical documents visualization and processing software

REF MST

LOT Version 5.2.3

SN Build 228

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Introduction

MedStation is a family of medical software products for the integrated management of departmental activities (RIS system) and diagnostic images (PACS system).

All the **MedStation** products are designed for use on Windows XP/Vista/7, in a Client/Server environment. The modular design enables flexibility in configuration definition: each component can be considered independently from other components, which in so doing allows for easy updating of equipment and software, thereby protecting the investment made.

The **MedStation** *PACS* system incorporates a multi-server structure which is able to simultaneously manage several local or remote storage nodes, a simple user interface, flexible configuration tools, and quick and efficient display functions. **MedStation** allows connection to the various diagnostic tools, image capture, storage on optical media, distribution on a network of consultation terminals, post-processing and printing.

The **eRis/eVisit** department management system is made up of modules for examination appointments, patient admission, electronic distribution of worklist, conventional reporting, or reporting using pre-defined phrases or assisted by voice recognition systems, and structured.

Complete integration between the two *RIS* and *PACS* systems enables the necessary exchange of information to guarantee security and maximize automation of electronic capture and distribution procedures for information and images. The system has obtained authorization for marketing in the USA from the Food and Drug Administration (FDA Clearance).

MedStation software is able to access one or more file servers, and select and display any saved diagnostic image. All the standard tools for display, window/level processing, zoom, and open definition of the display matrix are available in an intuitive, easy-to-use environment.

MedStation is the ideal tool for electronic distribution of images to the hospital wards or remote access to studies, which are of interest (remote radiology).

MedStation is a multi-mode display station that can display diagnostic images from TAC, RMN, Computer Radiography, SPECT, Echography, PET, film scanners, Endoscopy, and Digital Angiography, Mammography (MG), Ultra Sound (US). **MedStation** has been designed for rapid selection and display of diagnostic images. The diagnostic images are loaded immediately as soon as they are received from the communication network. This function allows a drastic reduction in waiting times and optimization of utilization of communication devices. The series of images in the study are displayed by means of icons, which assist the user in the rapid identification of images of interest and to browse through the study images. **MedStation** is able to manage several x-ray monitors connected up to the same display workstation.

The modular structure of **MedStation** systems enables flexibility in configuration definition: these can be used as display terminals in a PACS system, as non-standard mode data capture stations (for example, it is possible to capture images from echo graphs), as stand-alone storage and reporting stations or terminals in a remote radiology system.

MedStation systems are expandable: besides a **print module**, an elaboration module **MPR** (Multi-Planar Reformatting) can be installed on the base version. By means of MPR module, it is possible to reconstruct two-dimensional sections from a three-dimensional tomographic study along fundamental planes (axial, coronal and sagittal plane) and to generate sections on free planes interactively defined by the user.

MedStation systems essentially use standard hardware and software components, and no graphics card or dedicated accelerator is required for rapid display of images. Dedicated graphics cards are only used to drive the high-resolution monitor.

MedStation can be integrated with any RIS departmental management system. Integration with **eRis/eVisit** enhances the capacity for information exchange between the two subsystems. This integration gives maximum automation of procedures and cross-checking of data to ensure that the diagnostic images are associated with the right patients.

MedStation Express is a "light" version of **MedStation** that provides the main functions for viewing the examinations saved in DICOMDIR on a CD.

Non-exhaustive list of **MedStation** *functions (some of these functions are not available in MedStation Express*)

1. Display of diagnostic images in color and grayscales from TAC, RM, SPECT, DSA, CR, DR, US, RX, MG,…
2. Display of image series preview in the study selection window.
3. Loading and display of images in any bit per pixel depth (256, 4096, 32768 and several grayscales).
4. Real time adjustment of window and level range, automatic calculation of the optimal window/level based on image sub-areas defined by the user.
5. Prompt display of grayscale values (density); histograms and profiles.
6. Possibility to use several monitors connected to the same display station; support of very high resolution and brightness x-ray monitors
7. Open definition of the number of images to be represented on the screen.
8. Immediate display of the images as soon as they are received from the communication network.
9. Representation on the localizer of the position of the tomographic images currently displayed.
10. Cine/loop environment for display of video clips and series of images directly integrated into the area of work.
11. Display of DICOM images encapsulating videos in MPEG format
12. Selection of the studies of interest by means of multiple queries, with the option of selecting only the most significant or "key images".
13. Possibility of simple and guided access to different file servers.
14. Zooming functions: enlargement, reduction, 1:1 zoom, zoom lenses, true size. Image pan-

ning.

15. Possibility of applying window/level, zoom and other functions to a specific image, all images in a series, all images in a study, or a set of selected images.
16. Possibility to send to print or export a specific image, all images in a series, all images in a study, or a set of selected images.
17. Horizontal and vertical mirroring.
18. Image rotation.
19. Calibration of x-ray images to compensate scale factors.
20. Measurement of distances, angles and areas.
21. Echocardiographic measures.
22. Entering of free text and graphic symbols.
23. Interactive definition of transformation curves of images grayscales.
24. Capture of diagnostic images from standard and non-standard video sources and manual scanners.
25. Functions for image processing, filters, representation in false colors, etc.
26. Manual or semi-automatic definition of regions of interest, measurement of their area and volume.
27. Management of a structured report: manual entry of the report connected to the study or by means of reporting graphical trees or voice recognition systems. Report send and/or print.
28. Presence of an integrated calculation that can use values of measurements made on the images viewed in order to apply complex formulae.
29. Studies printing on x-ray film or paper.
30. Scope for expansion with additional modules, including those of third parties.
31. Display of information relating to individual images, the series or the study.
32. Integration with the most widely-used negative editing and production systems.
33. Capturing ultrasound and endoscopic images by means of A/D conversion.
34. Integrated DICOM interface functionality. The system is therefore able to access any DICOM server.
35. Read/write management of the DICOMDIR format.
36. Possibility of copying a study to any archive node connected to local or geographic network. Local saving of studies or images of interest.
37. Configuration and automatic application of study display protocols.

Additional functions of the **Print module**

1. Printing of all the images of a study.
2. Selective printing of single images and/or parts of images.
3. Personalization of print format (number and layout of images on the page …).

Additional functions of the **MPR** *and* **3D** *modules*

1. Generation and display of MPR views along the three main planes.
2. Generation and display of images in different planes defined interactively by the user.
3. Studies reformatting along a defined plane with the possibility of selecting the number and distance of the slices to be generated. The new series generated is associated as a new series of the original study.
4. Surfing along a polygonal curve drawn on one of the main views and re-formatting of the oblique that follow the curve.
5. Three-dimensional reconstruction of CT studies. Display of the working area and simple interaction with the volume by the user.

New functions

Compared with MedStation 5.1, **MedStation 5.2** has:

- Specific new features for managing and displaying Digital Breast Tomosynthesis (DBT) images according to IHE.

Compared with MedStation 5.0, **MedStation 5.1** has:

- Specific new features for managing and displaying mammographic images according to IHE, including the interpretation and visualization of CAD SR content.
- Support of profile IHE "Key Image Notes": resque and store of KO with additional notes, and possibility to choose which KO to apply.
- Search Query Evidence Document (to DICOM server admitting image-level query).
- Support of Storage Commitment.
- Support of ATNA logging.
- Ability to automatically create virtual series (starting from actual series) based on a configurable DICOM tags.
- Position link between series in MPR mode.

Compared with MedStation 4.9, **MedStation 5.0** has:

- A completely renewed graphic user interface with easy access to the tools of interest, optimization of space for image display, smart panels anchored to the main windows.
- New color theme with shades grayscale for a more comfortable visual into low light environment reporting.
- Allow customize toolbars and context menu with the user's preferred shares.
- New system shortcuts based on the IHE standard Basic Image Review (BIR).
- New tool to fast search system actions applicable to the current view.
- New multimonitor configuration management with the availabilithy to exclude any secondary monitors.
- A simplified environment for reports consultation and writing, for bookmarks management and series navigation.
- A revised CINE environment for the display of DICOM multiframe and MPEG videos.
- Full internationalization with Unicode data management of DICOM communications and user interface.
- Support of DICOM attributes Pixel Padding Value and Pixel Padding Range Limit for

automatic suppression of air into monochrome images.

- Advanced management of external examinations imported with Exprivia eCDImport.
- New optimized protocol to access images on Exprivia eArchive server.
- Review of the interpolation algorithms and image processing to achieve higher performance using SSE2, SSE4 technology and hardware acceleration.
- Renewed centralized management of end user licences with Exprivia License Manager.

Compared with MedStation 4.8 version, **MedStation 4.9** has improved new functions such as:

- the possibility to search and display reports from RIS Exprivia eRis sources(version 1.8 or subsequent).
- New tool for folder management, publication and connections with preferred exams.
    - Saving of references to exams/series of interest with links for their quick retrieval.
    - Possibility to customize publication per single user and/or per user groups.
- New tool for 2D measurement for the semi-automatic marking of the spine.
- New 2D tool for measuring scoliosis deviation (Cobb angle).
- Query/Retrieve from XDS registry
    - Query/retrieve of DICOM documents KOS manifest from registry/repository (IHE ITI-16, ITI-17)
    - Query of PDQ IHE registry (IHE ITI-22).
- Print nodes DWAM and DICOM3:
    - DICOM print towards print gateway DWAM (DWAM 4.4 and superiors).
    - Print towards DICOM printer without the use of MedStation Printer Server module.
- 3D environment for three-dimensional rendering of DICOM CT and MR series:
    - Algorithms of drawing Ray-Cast (CPU) and GPU (with graphic cards which support graphic libraries OpenGL).
    - Volume Rendering and MIP, Surface Rendering, Cine Rendering.
    - Volume of interest definition (VOI) through six orthogonal planes.
    - Management of window/level, color palette and transparency.
    - Functionality of bones segmentation/removal.
    - Creation of 3D snapshot in DICOM OT format.
    - Generation of a 3D sub-volume from 2D images and selection of ROI.
    - Introduction of 3D Window/Level concept with the possibility to manage in a unique way W/L values, opacity curve, configurable by the user.
    - Function of 3D preset distribution created by other users.
    - Tree-organization of W/L 3D selection menu.
    - Improvement of multi-monitor surfing functions.
- New environment of analyses CINE:
    - New layout CINE multi-study.
    - Possibility to effect measures during CINE display.
    - Possibility to display measure only on few film frames.
- Support of MPEG videos encapsulated in DICOM images.

- Evolution of MPR and MPR-Curvilinear environments:
    - Zoom, Stack-View, MIP, MinIP, AverageIP on every MPR planes (sagittal, coronal, transverse and oblique).
    - 3D display of MPR planes.
    - Generation of MPR images configurable with CT, MR modality in accordance with DICOM standard.
    - Curvilinear surfing along a polygon drawn on an MPR plane.
    - Creation of MPR snapshots in DICOM OT format.
    - Improvement of memory management during MPR/CMPR analysis.
    - Real-time surfing along a curve on a predefined projection.
    - Re-formatting along a curve on a predefined projection
- New MPR-Curvilinear 2D environment
    - Real-time re-formatting along a curve on one image of the study.
    - Re-formatting along a curve of panoramic views (parallel or concentric) on one image of the study.
- Support for region calibration of DICOM Ultra Sound images.
- New group of measures for Echocardiography
    - Distance in M-Mode
    - M-Mode (Diastole and Systole)
    - Area/Volume
    - Pressure gradients
    - Velocity
    - Time
    - Deceleration time
    - Acceleration time
    - Pressure Half Time (PHT)
    - Ventricular volume with Simpson Biplane algorithm
- Calculator for the definition of calculations that involves measurements performed on displayed images.
- New synchronization link among box for Automatic Positioning.
- Functions of change/re-compilation of DICOM Structured Report.
- Possibility to inhibit application of a Presentation State DICOM associated with a study.
- Unified LOG functions.
- New menu for the application of W/L Min/Max.
- WADO display of images with references on DICOM Structured Report.
- Possibility to include IHE web content to export DICOMDIR on PC directory.
- Capture of images with measures through Copy/Paste commands.
- Simplification of function application level, with only three levels (Image /Series / Views).
- Improvement of performance in studies loading from DICOM standard nodes.
- Improvement of Hanging Protocol selection during study opening.
- Support of DICOM ECG studies with 2D display of layouts.
- ECG display interface with the possibility not to visualize automatic interpretation and to personalize the display layout.
- SR IHE compatibility as in test MESA for Connectathon 2008.

- Possibility to calibrate CT images with Secondary Capture (SC) modality.
- Possibility to view 16 bit images with Photometric-Interpretation PALETTE – COLOR.
- Support of DICOM Overlay.
- Support of tag DICOM Pixel Aspect Ratio (0028, 0034) for multi-frame images.
- Support of tag DICOM Additional Patient History (0010, 21B0).
- Improvement of large size films (IVUS) surfing through video-streaming towards SCP DicomWare 4.4.x or superiors.
- Possibility to export films in video-streaming in AVI format.
- Reading of studies from CD-ROM in MedWeb with DICOMDIR or MedStation format.

Compared with MedStation 4.7 version, **MedStation 4.8** has improved many features and offers several new functionalities:

- New module for 3D reconstruction and display
- MPR module completely renewed
- Curve cuts: from images acquired form a series or in MPR environment
- Management of lookup table DICOM
- Improvement of overlay DICOM support
- Optimization of multi-frame image management
- Support of studies in ECG modality
- Improvement DICOM structured reports support both in creation and in recovery and reading.

Compared with MedStation 4.0 version, **MedStation 4.7** has improved many features and offers several new functionalities:

- Increase of studies opening speed.
- Improve the performance of display and operation.
- Renew user interface.
- Possibility to customize a tab so that it contains all and only the most often used features
- Strengthen the possibility of the Hanging Protocol configuration. You can now create "virtual" series by choosing to display DICOM images that have certain attributes.
- Saving and search for Hanging Protocol may also consider multiple anatomic parts present in the same study
- Organization of Window / Level mode for examination.
- Presence of a "Dashboard." A moving window that allows you to manage the opening of studies and print operations and where the HTML browser is integrated. Using the Drag & Drop functionality.

- New features for storing on digital support: anonymization of CD and generation of CD in IHE format.
- Possibility to select certain images of different series of the study for the export and printing operations
- Possibility to perform operations on a set of selected images, as well as on a single image, on a sequence or on all displayed images.
- New reporting environment. Support for reading and writing of reports in Structured Report format with the possibility to define the templates.
- Support of JPEG2000 compression.
- Support of Key Object and Presentation State according to DICOM standards.

Compared with version MedStation 3.5, **MedStation 4.0** has completely new structure and functionalities.

- Management and display of multiple studies of the same patient or different patients.
- Possibility to define complex layouts at monitor level.
- Depending on the type of open studies, it applies the disposition of series / studies and workplace based on rules configurable by individual user (Hanging protocol).
- Increased speed of studies opening.
- Improved display and operability performance
- Loading of the study in the background to allow the immediate operation
- New user interface
- Opening from within each display box.
- Adding new filters for processing images with depth greater than 8 bits per pixel.
- Synchronized navigation of series or studies (scrolling links).
- Displaying a study on multiple pages (links per page - continued).
- Spatial navigation of the study (3D cursor).
- Navigation among slices on localizer view
- Changing window-/level on localizer view.
- Possibility to choose whether to display the localizer view in the view panels.
- Possibility of having a dedicated box for displaying localizer images of an opened study in another box (link to localizer).
- Display of spatial reference lines of current image on the rest of the study.
- Display Mode cine in place.
- Tool for vertebral morphometry.
- Possibility to select a rectangle of interest of images to be sent to print or copied to the clipboard.

- New interface for COM integration with bidirectional support.
- New ActiveX object to simplify integration with third-party applications.
- Study research on multiple sources into a single request (Metanode)
- Pre-defined researches at user level.
- Integrated HTML browser (Web Link).
- Integration with video-conference environments and application sharing.
- Integration with ActiveX components (Word, Excel, etc.)
- New libraries of image compression.

Layout of this manual

This manual is made up of nine chapters and seven appendices.

- Chapter 1, *Running the application*, describes how to execute the program, the application window functions and the main menu.
- Chapter 2, *Managing studies*, contains all the study search, opening, management and organization functions, their import/export procedures and the reporting module.
- Chapter 3, *Managing images*, describes the main image manager window and the utility functions associated with it: window/level setting, zoom, measurements, annotation manager options, processing, capture and general information on the images. Moreover, it describes the links that allow correlating different view frames.
- Chapter 4, *Hanging Protocols*, describes how to manage the automatic disposition of studies view at the opening.
- Chapter 5, *Printing studies*, contains the description of the image print functions.
- Chapter 6, *MPR display mode*, describes the functions of the MPR add-on module (*Multi-Planar Reformatting*) and generation of oblique sections of tomographic studies MPR Curved.
- Chapter 7, *3D display mode*, describes the functions of the 3D add-on module for 3D reconstruction of volumetric studies.
- Chapter 8, *Cine/Loop Manager*, deals with the film/loop module functions, which enable you to view series of studies and DICOM Multi-frame, MPEG and AVI files in video format.
- Chapter 9, *The "Options" Menu*, describes the configuration functions of the transformations applied to the images and the program operating parameters.
- Appendix A, *Using the keyboard*, contains a list of keyboard shortcuts for performing commonly used functions.
- Appendix B, *User Manager*, describes the application user administration program.
- Appendix C, *MedStation Configuration*, describes the MedStation configuration program.

- Appendix D, *Operating parameters*, describes the parameters for running MedStation from the command line.
- Appendix E, *COM Interface.*
- Appendix F, *Using measures, measurements and calculations on eRis/eVisit forms*, provides a description of the advanced functions that can be performed using the measures, measurements and calculations in MedStation integrated with eRis/eVisit

Conventions

The various types of characters used in this manual have the following significance:

Italics These are used for emphasis and to introduce new terms.

KEY This type of character indicates a key on the keyboard. It is often used to indicate depression of a key, for example, "Press RETURN to confirm the operation".

Note Notes give additional information of the subject covered, as an exception to the general rule or technical information for expert users.

Warning! These are warning messages for critical situations or of potential loss of information.

 All situations with significant impact on clinical risk are preceded by this symbol. The code entered next to the symbol is for internal use of Exprivia.

When commands are displayed separated by a vertical line (|), this indicates a complete sequence of menu options. For example, "**File | Print**" refers to the command selected by opening the **File** menu and selecting the **Print** option.

The following terms indicate specific mouse functions:

- *Point* means moving the mouse cursor over a specific object. For example, pointing to one of the keys on the scroll bar, means moving the mouse cursor over the key indicated. In certain situations, the cursor will change shape to indicate that the mouse is carrying out certain actions. For example, by positioning the cursor over the edge of a window, the cursor changes into a double arrow. The direction of the arrow indicates the direction of movement that can be carried out.
- *Click* means pressing the left mouse button when pointing to an object. For example, clicking the Close button (corresponding to the 'X' in the upper right of any window) means pressing the left mouse button after having positioned the cursor over the button.
- *Double-click* means quickly pressing the left mouse button twice after placing the cursor over a specific object. For example, to activate a specific file from a list, point to the file name and then double click.
- *Drag* means moving the cursor over an object, pressing the left mouse button and dragging it while continuing to press the button.
- *Right-click* means pressing the right mouse button when pointing to an object.

- *Shift-click* means simultaneously pressing the shift key and the right mouse button when pointing to an object.
- *Control-click* means simultaneously pressing the CTRL key and the left mouse button when pointing to an object.

Note: This manual assumes reasonable familiarity with the basic functions of Windows. You must, for example, know how to use a mouse and to open, close and maximize windows. Reference can be made to the Microsoft Windows *User's Manual* and online help for this purpose.

Chapter

1

Running the application

The methods for running **MedStation** program, application windows and main menu will be described here.

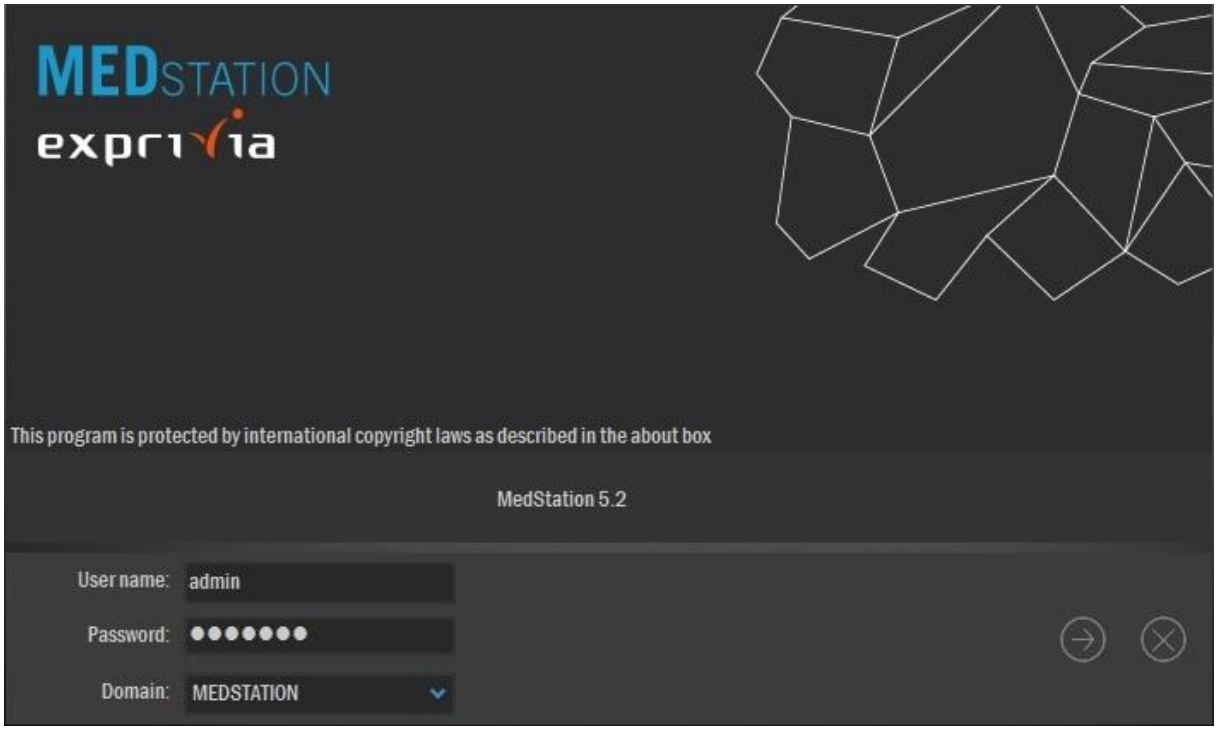
*To run the **MedStation** application*

1. Click on the **Start** button on the task bar
2. Select the **Programs** menu (Windows English version)
3. Select the **Exprivia | MedStation® 5** menu
4. Select **MedStation 5**

An alternative way of starting the program is to double-click on the **MedStation 5** icon on the Windows Desktop.

The Login window will be displayed (Figure 1), in which you are to identify yourself by entering your user name and password. The data input into the "Password" field is hidden by asterisks. To move the cursor between the two fields either the mouse button or the TAB key can be used. The OK key confirms the data entered.

Figure 1. MedStation 5 access window



RC-07

The system implements users' authentication

- *to set users' access rights (called privileges) for the system functions (See Appendix B "User Manager")*
- *to allow customization option for using the program and to adapt the interface and some tools to user's needs*
- *to ensure conformance with the Italian Legislative Decree n. 196 " Codice in materia di protezione dei dati personali" about the processing of sensitive and clinical data of patients whose studies are being analysed. (See the section "Authentication Sheet "Appendix C "Configuration"). This conformance is ensured by the presence of an external application that MedStation uses to validate credentials and to manage procedures of authentication. This external application is managed by the customer or a party designated by the latter, who will ensure that the authentication system conforms to the Italian Legislative Decree no. 196, by implementing at least the minimum safety measures concerning the management of passwords for systems that control sensitive data.*

*To run **MedStation Express***

- **MedStation Express** starts automatically when the CD is inserted in the drive on the computer without you having to enter the user name or password.

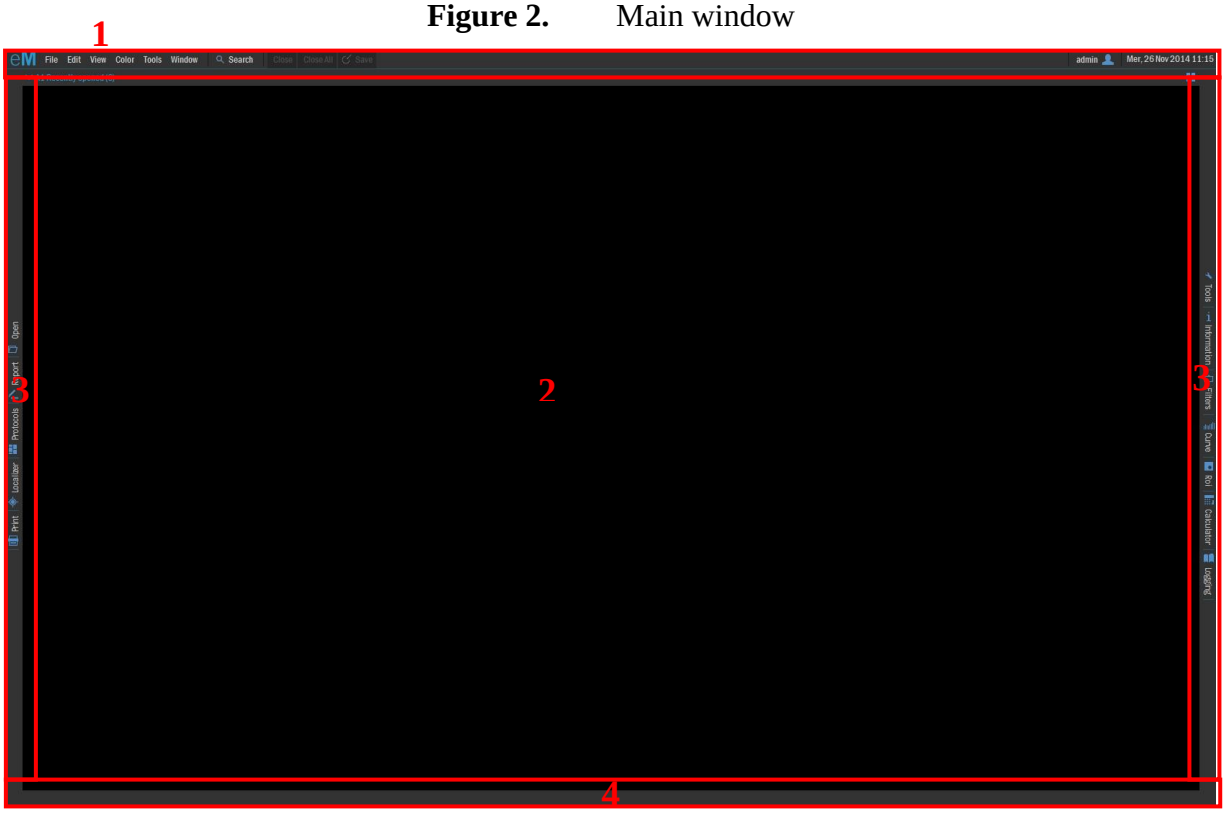
- ***Note:*** *If the system has the autorun function disabled, select "Explorer" or "Computer", according to the version of Windows, and then the letter assigned to the CD-ROM drive. Double click on the* Express *folder, then on the* bin *folder and, finally, on the executable file* Express.exe*; or, having selected the letter assigned to the CD-ROM drive, click the right mouse button and then click on "AutoPlay".*

The application window

Once you have been identified, the main **MedStation** window will be displayed (Figure 2).

Note: *With **MedStation Express**, by pressing the* Original *button in the User preferences configuration window (eM | Options | Preferences… menu), you can request all the updated configuration files from the folder in which Express was started (normally the CD). The files currently present on the client will be saved to a backup folder.*

Figure 2. Main window



The main window is divided into areas, which include, from top to bottom:

1. The ***main menu***, which is used to access all the functions provided by MedStation via the submenus **File**, **Edit**, **View**, **Color**, **Tools**, and **Window**. The main menu area also includes a **Search** box for searching for the functions that may be activated in the program, the <**User name**> box from which you can access a personalized toolbar that you want to keep close at hand. See the following section for a detailed explanation.
2. The ***study graphic display area*** (alphanumeric data and images) and dialog boxes. The

graphic area is subdivided into boxes in which you can view the studies opened, that is their diagnostic images. When at least one study is open, the *series/study navigation panel* appears so that you can quickly select the series or study to be shown in the current box. In each study display box, the diagnostic images are shown in a layout (that is, a display matrix) that can be modified interactively by the user.

3. The ***side panels (left and right)***, which are used to
   a) *find and open* studies
   b) *read* and *write*[2] *reports* and documents of the studies displayed
   c) *print* images
   d) view *scanograms* of the current study
   e) access the *log* of the application
   f) access the *tools*, which are normally (but may change according to the study display mode) the following:
      i) choice of the *favourite* tools (tools that you can add if there are operations that you perform more frequently, so that you can have them all together in the same position without having to move from one set to another)
      ii) *cursor* selection (left mouse button interaction mode)
      iii) *alignment* options for displayed images
      iv) *zoom* tools
      v) *measuring tools for X-ray images*
      vi) *measuring tools for echocardiographic images*
      vii) tools for *advanced operations*[2]
      viii) *geometrical transformations*
   g) manage the automatic study *display protocols*; save a new user-created Hanging Protocol, enable/disable functions, view the list of protocols available and select one of them
   h) access the *information* about the study (format, size and position of images) and view the *DICOM data of the image* selected
   i) use the image *processing filters*[2]
   j) to manage and apply *correction curves*[2] to images
   k) to manage *ROIs* (Region Of Interest)[2]: to select and propagate polygonal ROIs for statistical analysis of 2D regions or for 3D reconstructions of subregions of interest on 3D images
   l) to use the *calculator*[2]
4. The ***status bar***, which is used to display short operator prompts, the status of the study and the progress of copies in progress.

[2] Function available only in MedStation but not in MedStation Express.

Main menu

MedStation main menu comprises the following items:

1) eM

a) **Expand main menu** (**Show Menu Bar**) Used to choose whether to show the items of the main menu on the bar or to group them all here with their submenus. If the non-expanded option is chosen, the main menu bar will only contain the **Search** box in which to enter the first few letters of an enabled function to find and activate it.

b) **Show menu description** Shows or hides an explanatory string under each menu item

c) **(any items)** corresponding to the submenus **File**, **Edit**, **View**, **Color**, **Tools**, **Windows**

d) **Options** to access the configuration of the application. It comprises the following items:

i) **Information on images…** opens the panel for establishing the information to be laid on top of the images

ii) **Preferences…** to change some of the program's settings

iii) **Configuration…** to gain access to the MedConf.exe program

e) **Help**

i) **User's manual** opens this user's manual in pdf format

ii) **Shortcut** shows keyboards shortcuts list

iii) **Info…** shows the details of the current version of the application and the modules installed

f) **Exit** exits from the application

2) File

a) **Operations on files**: Used to view list of previous studies associated with the study currently open (**Previous Studies**), open studies (**Open…**), reopen the most recently viewed studies (**Reopen**), set to "reported" (**Reported**), view information about the patient and the study (**Information…**), save changes (**Save**), save Key Object with possibility to insert a code and notes to the corrisponding KO (**Save Key Image Note**), remove the current study from the display (**Close**) and close all open studies (**Close all**)

b) **Print**: Used to set up the print page (**Page setup …**), add the image to the print job (**Add to print**), view a print preview (**Print preview …**), print (**Print…**), and quickly print key images (**Print key images…**)

c) **Import/Export**: Used to import*Errore. Il segnalibro non è definito.*/export studies (**Import…/Export**), create a CD*Errore. Il segnalibro non è definito.* (**Create CD…**)

3) Edit

a) **Edit operations** Used to assign the key image attribute to an image (**Tag as Key Image**), remove the key image attribute from all images (**Clear all key images**), assign

the localizer image attribute (**Localizer image**), create a virtual series (**Set Virtual Series …**), select sets of images and deselect all the images displayed (**Select** with the various options and **Deselect all**), copy the current image to the clipboard (**Copy**), paste the image from the clipboard (**Paste**), refresh all the controls and the work area (**Update all**) and restore the view of the images to their status before any changes after the last save operation were made (**Reset view**).

b) **Apply** Used to establish the range of application of the graphical operations: to the current image only (**Apply to image**), to the series of the current image (**Apply to series**) and to all views present in the box (**Apply to views**). You can also choose to propagate (**Propagate**) the transformations made in one display box to the views present in the other boxes or not to propagate them, so that each box is independent of the others (even if the same images are shown in them)

4) View

a) **View** Used to set the operating mode (**Mode**), it enables you to choose, according to the modality of the study and the configuration of the program, between **2D**, **MPR/MIP**, **2D curved MPR**, **3D**[3] and **external 3D**[3]. Function for starting a video with the images in the static series displayed or the current multiframe image or MPEG video (**Play series** or **Play video**). Possibility of *showing/hiding* the status bar (**Status bar**). Possibility of anchoring the series/study navigation panel to the monitors (**Studies bar**). Possibility of overlaying the shortcut menu button on the current image or having this menu opened by double clicking (**Shortcut menu button**).

b) **Protocols** Used to access the list of protocols that can be applied to the studies currently open on the display (**Protocols**), apply the protocol before the one applied on the list of available protocols (**Previous protocol**), apply the protocol after the one applied on the list of available protocols (**Next protocol**).

c) **Image** Used to apply interpolation to the images when enlarged or reduced (**Show interpolation**), text on top of them (**Show text on image**), a representative scale of the color palette applied to the image (**Color lookup bar**). The **Localizer** item gives access to a submenu on which you can choose the position in which mini localizers can be displayed on each image and, using the **Box localizer** item, you can choose whether to show/hide a box inside the panel displaying a single series of a study with localizer images. The item **Key Image Notes** allows you to choose the application of one (or none) of the KO files in the current study.

d) **Presentation** MedStation instance settings for applying to the images DICOM Presentation States if present in the DICOM study (**Presentation State**), choice between all the Presentation State of the study (**Available Presentation States**), DICOM overlays if present in the DICOM files of the images or the presentation states (**Overlay**), choice between available overlay planes of the study (**Overlay Planes**), DICOM shutters if present in the DICOM files of the images or presentation states (**Shutter**). The possibility of viewing the intersection lines of the current image with images of the same study shown in other boxes and the lines of intersection with the series to which the current image belongs (**Reference lines**), the intersection lines of all the images in the series to which the current image belongs (**Intersection lines**) (you can choose, ac-

[3] Function available only in MedStation but not in MedStation Express.

cording to the previous flag, to see **None, All** or **First and last** on the basis of the DICOM numbering of the images). You can align the images within the view (**Alignment**) to the left, right, top or bottom, or not align them at all. You can also set the order of presentation of the images in the series (**Sort**):

- by image number (**Number**)
- by image increasing position (**Increasing Position**)
- by image decreasing position (**Decreasing Position**)
- by image acquisition time, using DICOM TAG "***Acquisition Time***" (**Acquisition Time**)
- by image time, using DICOM TAG "***Image Time***" (**Image Time**)
- by DICOM image number, using DICOM TAG "***Image Number***" (**DICOM Image Number**)
- (for MR image series only), by "***Echo Number***"
- (for MR image series only), by "***Echo Time***"
- (for MR image series only), by "***Echo Effective Time***"
- (for MR image series only), by "***Temporal Position ID***"

5) Color

a) **Window/Level** used to add the current window/level to the favourites[4] (**Add to favourites …**) and to manage favourite window/levels[5] (**Organize favourites …**)

b) **LUT** used to choose from a palette of colours to be applied to the images displayed (**Color palette**), apply a sigmoid curve (**VOI LUT Sigmoid**), invert the grey tones of a picture (**Negative**), optimize window/level values (**Contrast stretch**), apply window/levels saved in DICOM Presentation States (**Reset original window/level**), apply all the window/levels saved to the DICOM file when the images were acquired (**DICOM window/level**). Finally, a list of window/level values and correction curves appears for the current image.

c) **Favourites** List of preset window/level values present in the MedStation installation and values set by the user, shown on the basis of the current study DICOM modality.

6) Tools comprises the various submenus providing access to all the tools available

a) **Favourite** tool menu, as chosen by the user

b) **Cursor** to return to the default cursor if measuring and image processing tools are used or to choose the method by which the user interacts with the images displayed using the mouse

c) **Zoom** to select the zoom scale to be applied to images

d) **Measure** to select a tool for making measurements and modifying the properties of figures and measurements

[4] Function available only in MedStation but not in MedStation Express.

e) **Cardiac echo** to select a measuring tool for echocardiographic images and modifying the properties of figures and measurements

f) **Geometry** to select geometrical transformations to be applied to images or to return to the original image after making measurements, applying geometrical transformations or new window/level values, … (**Original**)

g) **Advanced**[5] to delete images or entire series of the study (**Delete image**, **Delete series**, **Delete study**), to add image acquisition tools (**Add**). Used to create new images starting from a rectangular area of the current image (**Cut**).

h) **Tasks Activity…**[5] Opens a window for managing copies of studies currently in progress

7) Window

a) **Panels** Used to open and close the panels to the left and right of the work area and to return them to their position when they have been closed by clicking on the X button and have thus disappeared from the side bars

b) **Layout** Enables you to choose whether to use the entire display area for a single study without closing any other studies open and retaining the possibility of accessing them by clicking on tabs at the bottom of the window (**Tabbed view**). You can personalize the main window with a full-screen view (**Full screen**), or minimize the application (**Minimize**). You can choose where to show the current view on a multi-monitor workstation, that is, shift it from the current monitor onto another screen. It is used, for example, to transfer colour images (such as 3D reconstructions) from a grey-tone X-ray monitor onto a colour service monitor (**Monitor**).

On the main menu bar there is a **Search** box in which you can enter the first few letters of a function to find and activate it.

The name of the user that started the current MedStation instance appears on the right-hand side of the menu bar. By clicking on this button (**Personalize toolbar**), you can set up your own personalized toolbar (made up of a set of buttons that appear on the same menu bar) or log out (**Logout <user name>...**).

*To set up the **personalized toolbar***

To set up the **personalized toolbar** containing buttons with the functions you use most frequently, click on the item **<UserName> | Personalize toolbar**. The part of the bar containing the function shortcuts you have chosen will be highlighted.

1) Search the menus for the item corresponding to the desired function (that is, for which you want a button to appear on the menu bar)

2) Select this item and, with the left mouse button held down, drag it onto the highlighted part of the bar and release the mouse button

3) To remove an item from the personalized bar, click on the corresponding button and drag

[5] Function available only in MedStation but not in MedStation Express.

it off the bar

4) Repeat for all desired functions

5) Press the **Done** button to finish setting up the personalized menu bar.

Shortcut menus Some menu options of the application are also present on the shortcut menu of the current image, which is opened by clicking on the button that appears on top of the current image or – if it is not present - by clicking the right mouse button. Other operations can only be performed from a shortcut menu.

Chapter

2
Managing studies

In conformance with the DICOM standard, **MedStation** organizes information into three hierarchical levels:

- *patients'* archive
- *study* archives
- *image* data, grouped together in *series.*

The patients' archive is at the top of the hierarchy. A patient refers to one or more studies. The studies are organized into series, made up of one or more images or other DICOM objects such as, for example, structured reports and presentation state.

The functions of study management allow to search and insert descriptive data relative to patients' archives and studies.

Nodes

In the **MedStation** structure, study and patient data are contained in nodes, which can be of different types:

- *DICOM node*: allows you to connect to an external DICOM server that contains the archive. Studies are searched according to the most common DICOM query keys.
- *DWAM node*: it is a DICOM node, whose server is DWAM 4.x of Exprivia. You can configure this node in different ways depending on whether the node is *local* or *remote* or *http*.
- *XDS-I node*: is a type of DWAM node that acts as gateway for searching and displaying XDS documents (Cross enterprise Document Sharing).
- *DICOMDIR node*: allows you to read and write archives according to the DICOMDIR standard. This is useful for study sharing among applications of different producers.
- *Path node*: used only to export studies and to compress or change image format. Some available formats are JPEG, BMP, TIF. Exported studies are saved in a directory on

disk.

- *Metanode*: allows you to group a certain number of nodes. Each search performed on this node queries all nodes in the group.

RIS service connection

Every node can be configured to be linked to an external **eRis/eVisit** reporting service. If this connection is established, beside the name of the type of node, in the study search and open dialog box, an icon will appear indicating whether there is a connection or not.

Note: *MedStation Express accesses the studies via a DICOMDIR node.*

Searching for and opening a study

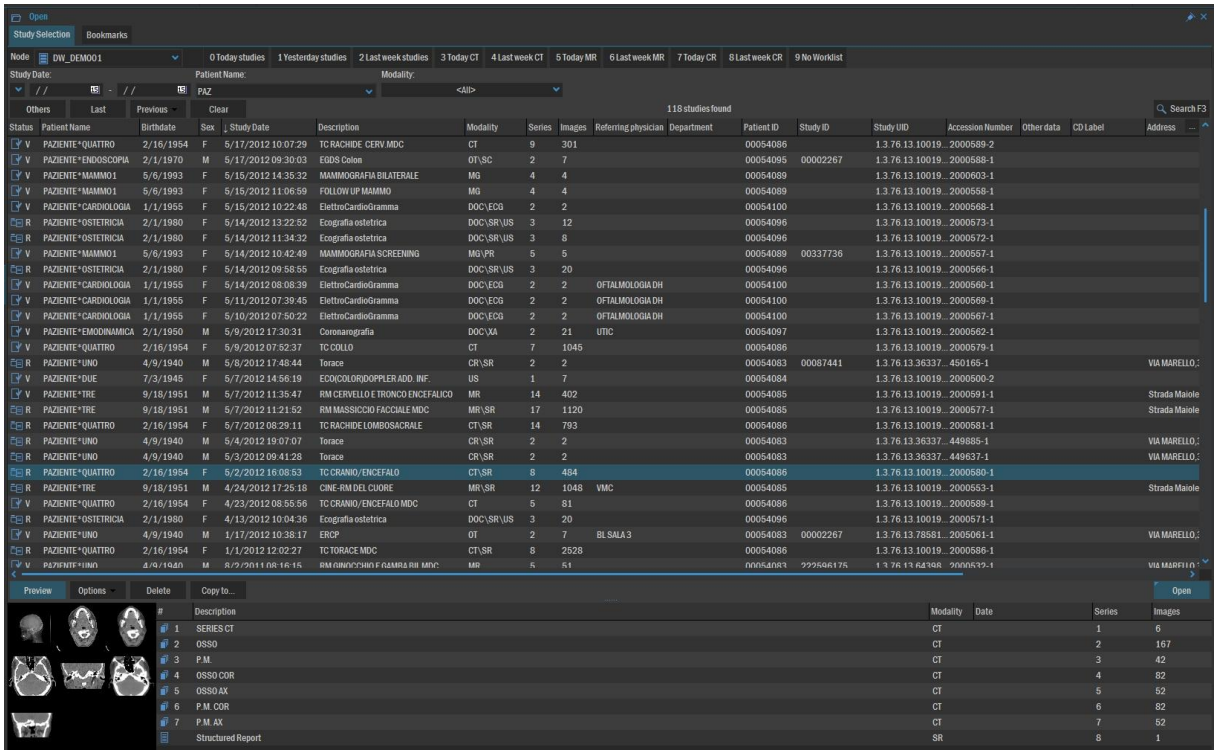
To search for and open a study, select **File | Open** or **Window | Open** from the main menu or click on the **Open** button on the vertical bar on one side of the work area. The program will display a window with a drop-down menu from which you can choose one of the storage nodes (enabled in the configuration) connected to the station. There are several fields in which you can enter data for searching for studies of interest. In general, having set some of these fields (as described later on), when you press the **Search** button or F3, the corresponding query will be made to the storage server and a list of the studies returned in response will appear in the central area of the window. If you select one of these results, you will see a preview of the first image of each series of the study and a list of all the series that make it up at the bottom of the window.

Note: *The part displaying the results of the queries made to the nodes where the studies and their documents are stored is divided into columns. Each of these columns contains data referring to the studies and patients.*

*You can choose which columns to show by choosing them from the menu that appears when you click on the "**…**" button that appears after the label of the last column that can be seen.*

A single click on the label of the column will sort the list of studies in ascending or descending order on the basis of the values that each study has in the column concerned.

Figure 3. Searching for and opening a study



To search for a study

1. Open the **Open** panel.
2. Choose the node to be searched for the studies.
3. Specify the selection criteria *(this is not necessary for DICOMDIR nodes for which all the studies present on the node are shown automatically).*

We shall describe in particular how to open studies from *non* XDS-I nodes, because they require a more detailed explanation.

Some search fields are always visible. If necessary, use the **Others** button to specify other search criteria, and **Documents** button to specify search criteria for DICOM query at image-level according to IHE profile *Document Imaging Consumer*.

Note: *The number of search criteria will depend upon the type of storage node.*

Search methods[6]

- An initial filter of studies to be selected can be performed by means of *pre-defined queries* (configurable by user), which are numbered starting from zero and allow you to search all the studies from a certain period or a specific diagnostic technique. These queries can be made using buttons that appear beside the name of the node to be searched.
- The last query can be repeated by pressing the **Last** button, or one of the last ten queries

[6] Function available only in MedStation but not in MedStation Express.

can be repeated by selecting it from the **Recent** menu.

- The **Clear** button clears all the values from the fields for making the query.
- To search for a patient's study, simply enter the first few characters of his/her name.
- If you know exactly the value to be searched for, simply enter it in the corresponding field. Alternatively, the following methods can be used:
  - for *alphanumeric fields*, the wildcard characters '_' e '*'. The '_' character refers to any one character in the position indicated while the '*' character refers to a sequence of zero, one or more characters. These characters can be inserted in any position of the sequence of characters specified. For example: entering '*HIP*' the description will list all the studies containing the text 'HIP' in any position, whilst entering '_IP' will list all studies containing any letter in the description followed by the letters 'IP'.
  - For *numerical fields* use can be made of the common comparison operators: < (less than), > (greater than), = (equal to), <= (less than or equal to), >= (greater than or equal to), <>(different from). These operators are to be indicated before the value to be indicated, that is, they must be the first characters entered.
  - For date-type fields, you can indicate a range of dates in which to search. This range is indicated by entering the start and end dates separated by the '@' character without any other separator character between them. The range is intended to be inclusive of the start and end dates indicted.
- For non-DICOMDIR nodes, press the **Run** button or **F3** on the keyboard to activate a search with the parameters entered. On the contrary, *for DICOMDIR nodes, all studies present are always listed.*
- Use the scroll arrows or the mouse to select the study of interest. Use the CTRL or SHIFT keys to make multiple selections.
- Use **Open** button or **double-click** to open the studies or series selected.
- By clicking on the **Options**[6] button, you can create or delete local storage nodes or modify their properties (for both local and DICOMDIR nodes).

Note: *When you open an exam, in the navigation panel of series/exams you will find the list of any related previous exams present in the same archive. You may open and view previous exams by selecting the icon that represents them and dragging it to a display box with the left mouse button or by double clicking on it. When you open an exam by dragging it to a display a box, you don't apply any hanging protocol: it will be displayed in the box of your choice, both when it is empty and when it is already displaying something else. If you use the double-click to open an exam related to the present one, this will apply a display protocol (if any HP exist and are active).*

Note[7]***:*** *If you use the settings on the* ***General*** *sheet of the window that appears and you select* ***eM | Options | Preferences*** *from the main window, you can set automatic repetition of the search at regular intervals.*

[7] Function available only in MedStation but not in MedStation Express.

To delete a study[8]

1. Select the study or studies to be deleted

2. Press the **Delete** button to permanently delete the study



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This operation will remove the study from the archive and it will not be possible to retrieve it so perform this operation with caution.

To copy a study[8]

1. Select the study or studies to be copied
2. Press the **Copy to…** button
3. Specify the destination node into which the file is to be copied.

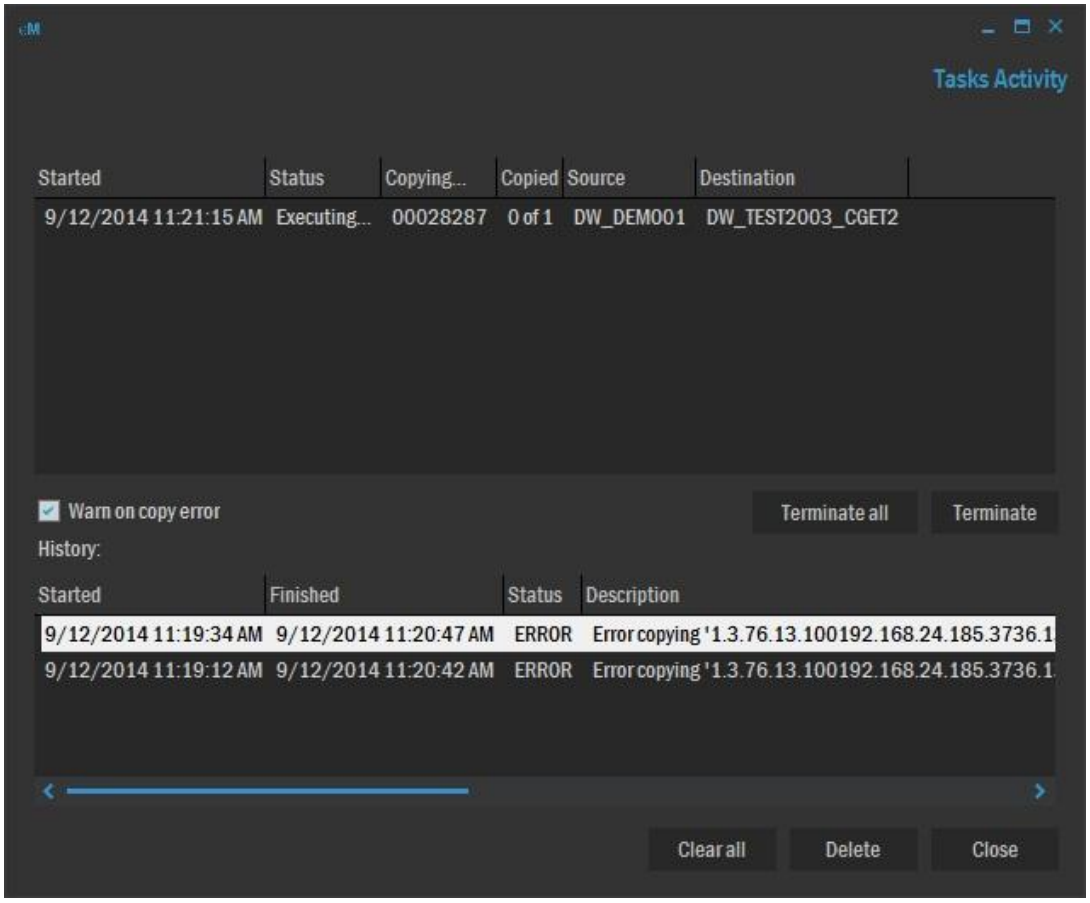
Note 1: *For studies in DWAM nodes, the node in which the file is to be copied can be chosen from those of two lists. The first one contains all nodes configured in the client workstation. The second one contains the nodes of DWAM server to which the node is pointing.*

Note 2: *The copy procedure generates a new study number on the basis of the numbering on the destination node. In some cases, the original study number will be recorded as a study note.*

While studies are being copied from one node to another, an icon indicating that a copy is in progress appears on the status bar. If you click on this icon, activate the keyboard shortcut CTRL+SHIFT+F1 or select the menu item **Tools | Activity…** a window for managing the copies currently in progress will appear. The information about the studies being copied appear in the *copies in standby* area while the information about the studies already copied (that have completed the process) will be summarized in the *History* area. The *Terminate* button can be used to cancel the copy in progress selected. The *Terminate all* button cancels all copies: the one in progress and those in standby. The *Clear all* button situated in the *History* area removes all the studies that have been copied from the list while the *Delete* button removes the study selected from the list of those already copied. If you enable the *Warn on copy error* option you will be warned of copying errors by a graphic message.

[8] Function available only in MedStation but not in MedStation Express.

Figure 4. Window for managing copies currently in progress



BatchBurn

If a node named **BATCHBURN** was configured into the system, a button with the same name will appear. It's behavior is the same of **Copy to…** , with the difference that the system will copy directly to that node without asking any questions.

Se nel sistema è stato configurato un nodo col nome **BATCHBURN** .comparirà un tasto con la medesima etichetta. Il suo funzionamento è analogo al **Copia in…** con la differenza che il sistema andrà ad effettuare la copia direttamente su tale nodo senza fare alcuna domanda.

Storage node options [9]

From the **Options** button, you can access some node management functions.

The **Options | Connect node** item is used to create a local or DICOMDIR node, specifying the directory that contains the studies. For example, to access the contents of a CD of studies (in MedStation format, in the particular case of studies contained on a CD, the format could also be DICOMDIR), you will select the driver path.

The item **Options | Disconnect node** (only enabled for local or DICOMDIR nodes) is used to delete the currently selected node permanently.

Note: *This operation does not actually eliminate the studies, just the node that referred to*

[9] Function available only in MedStation but not in MedStation Express.

them.

The item **Option | Node properties** shows some node configuration parameters. For local or DICOMDIR nodes, you can select a different path containing the studies.

Image preview of the selected study

Having pressed the **Preview** button, you can select a study from a list (of some nodes) and view some significant images and the list of its series. To hide the preview, click the **Preview** button again**.**

Study management functions on the "File" menu

Reopening a study

The **File | Reopen** option allows you to open one of the last 10 studies displayed. Studies are numbered from 0 (most recent) to 9 (least recent).

You can find the same list under the "*Recently opened studies*" item, which appears to the left on the bar of each display box, when no study is open.

Favourite studies (Bookmark)[10]

If the favourite studiesmanagement function has been enabled from *MedConf* (see Appendix C of this manual) and a connection with bookmarks server has been established, in MedStation, a **Bookmark** sheet with all the bookmarks for the favourite studies already saved will appear in the study search/open screen. In searching for a bookmark, you can use the following filters, indicating:

- the date or a range of dates in which the bookmark was added
- the description of the bookmark
- the type of permission assigned for the use of the bookmark

By pressing the **Modify** button in the same window, you can manage the set of favourite studies. The following functions are available:

OK Saves the changes made to the bookmark tree to the server

Cancel Cancels the changes made after the last save operation

Down Moves the bookmark selected down the favourite study structure

Up Moves the bookmark selected up the favourite study structure

[10] Function available only in MedStation but not in MedStation Express.

Add Having loaded a study from a remote note, you can add it to the list of favourites by pressing this button. A child node of the node selected on the favourites management tree structure will be added automatically with the description <Patient name: Study description >, the current date as the date of entry, and, as the *Node*, the storage node created in the MedStation configuration for gaining access to the archive containing the study and, as permissions, those of the user connected.

You can modify the *description* of the bookmark selected by clicking on it and then making the desired changes.

The *date of entry* and the AE Title of the storage server containing the study identified by the bookmark cannot be changed.

The *permissions* represent the users or group that can see and modify the links. You can assign the permission for one user only or, using the **GROUP** option, for all the groups to which the user belongs, or, using the **PUBLIC** option, share the selected bookmark with all users.

New folder Creates a new branch on the favourites management tree. The permissions of the folder will be inherited automatically by the child bookmarks of this node.

Modify or **F2** Enables you to edit the description of a connection, a folder or the permissions of the item selected

Public Makes public all the connections belonging to the folder selected

Delete Removes the connection to the favourite study or empty folder selected

Reload Reloads the lists from the server

In the window for research and study selection you can enable the column "Bookmarked" in which the symbol of a bookmark appears to indicate that the study is in the tree of favourite studies. If the study is not a favorite, in the same column appears a star. By clicking on this icon, it will open the Bookmarks tab and will automatically create an entry corresponding to the study chosen.

Patient/study information

The dialog box containing the description of a study is opened by clicking on the patient's name on the bar of the display box. The information includes data concerning the patient (including the date on which the study concerned was conducted) and data concerning the study itself.



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Users with the relevant privileges[11] can change some information about the patient and the study from this dialog box. These changes may lead to studies being associated with the wrong patients and therefore incorrect clinical analyses. To make sure this does not happen, you exercise great caution in making the changes. The system will prompt you for your credentials before saving the data in the archive containing the study and your user name and the time at which the changes were made will be recorded in DicomWare archives.

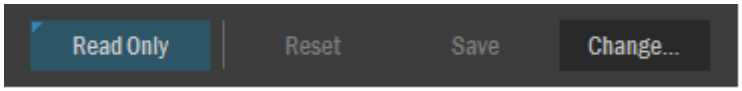
[11] Function available only in MedStation but not in MedStation Express.

Figure 5. Current study information panel



The **Modify**[12] button enables you to move out of read-only mode data and modify some of these (if you have the necessary privileges) while the **Print**[12] button shows the print preview of the patient's data sheet and the study, and then enables it to be printed.
In modify mode, the following buttons are available:

[12] Function available only in MedStation but not in MedStation Express.



Read only[13] enables you to return to the mode in which the data can be read but not edited

Reset[13] restores the data modified to its status at the last save operation

Save[13] saves the changes made to the archive and applies the changes to all places where the information is displayed

Change[13] enables you to access a worklist server interface screen from which you can obtain information required to change the patient's personal data

Description of the data shown in the panel

PATIENT

Name	Patient's name coded in DICOM format (obligatory data)
Birth date	Patient's date of birth
Age at study date	Patient's age when the study was conducted (calculated automatically by the application)
Sex	Patient's sex
Height (m)	Patient's height in metres when the study was conducted
Weight (kg)	Patient's weight in kilograms when the study was conducted
Identification code	Patient's ID code (generated by the system)
Alternative code	Alternative patient ID code

STUDY

Date/time	Date and time of the study
Accession	Appointment/reception number
Description	Description of the study
Modality	List of the DICOM diagnostic modalities of the study images
Type	String identifying the type of study
Origin	String identifying the patient's place of origin or hospital department
Refer. physician	String identifying the doctor that ordered the study
Date last modify	⚠ RC-03 RC-04 Date on which the last change was made (Security information to identify studies that have undergone modifications).
Label	Indicates the label of the optical disk or CD-ROM on which the images

[13] Function available only in MedStation but not in MedStation Express.

	are stored
Node	Name of the archive containing the study
ID	(MedStation) code identifying the study (generated automatically by the application)
UID	Unique DICOM ID of the study or unique ID generated by the acquisition system

Status *(Study Status)*

Archived: this is the initial status. It identifies studies archived (data and images), but which have not yet been opened or reported. Set automatically by the system.

Viewed: identifies archived studies that have been opened at least once. It is automatically set by the system.

Reported: identifies studies of which a report has been produced.

Locked: identifies studies to be locked (because they are awaiting approval or correction). They are ignored by automatic storing procedures. No anagraphic changes will be allowed, while the exam remains in this state.

Stored: identifies studies whose images have been transferred to secondary long-term storage media such as optical disk or CD-ROM juke-boxes.

Offline: the study will be saved on a CD which will have to be inserted into the CD recorder drive

Nearline: the study lies on a CD in the CD recorder driver and will be loaded at the request to open the study

Reporting

From version 4.5 on, MedStation supports the reading and writing of reports in *Structured Report (SR)* format with the possibility of defining templates.

If MedStation is properly configured, you will be able to access the reporting environment by clicking on the lateral **Report** button, by opening the **Window | Report** menu or by clicking on the icon that represents the series of reports in the study/series navigation panel.

Depending on the configuration of MedStation (see Appendix C of this manual), one of the following three methods of work can be activated[14]:

- you can use the internal viewing and reporting environment of MedStation

- you can connect to an external third-party reporting environment

- (if MedStation is properly configured, see Appendix C in this manual) you can render a study status "reported", simply by selecting the **File | Report** menu item in the MedStation in-

[14] Function available only in MedStation but not in MedStation Express.

terface. In this configuration, the **Report** side panel can simply be used to view documents and reports, but not to create SR reports.

Internal reporting environment

The reporting environment is accessed by clicking on the lateral **Report** button, from the **Window | Report** menu or by clicking on the icon that represents the series of reports on the study/series navigation panel. A side panel thus appears and can be kept permanently open by clicking on the dock symbol in the top right-hand corner.

The work environment is divided into tree work sheets:

- *Archive*: for viewing documents associated with the current study in descending order from the most recent to the least recent. Different types of documents are managed and can be displayed:
    - DICOM SR reports
    - pdf documents encapsulated in a DICOM SR file
    - reports **signed in eRis/eVisit** (version 1.8 or later), if the node from which the study is opened is configured appropriately – see appendix C of this manual.
    - pdf documents present in the REPORTS folder on a CD or DVD in DICOM-DIR format.
- *New Report:* for creating new DICOM SR reports, with manual input mode or through speech recognition engine.
- *Templates*[15]: for writing new DICOM SR reports and defining templates for writing structured reports.

At the top of the panel *Report* there is a bar with the following tools:

New... creates a new structured report or start the external reporting system.

Edit...[15] (*key that is only present for a user with the "Edit report" (E) privilege on the node from which the study whose report is on the display was opened*). The *Edit* key gives access to the writing environment in order to create a new report starting from a screen precompiled with the contents of the report currently being read.

Print… opens a menu with the following items:

Print prints the report currently displayed on the default printer

Print to … opens a window for choosing a printer and related options

Page setup… opens a window for making the settings for the page printed by the printer selected (Size of page, margins, …)

Print preview … to see how the report will appear when printed.

Send…[15] opens a menu from which you can choose to send the report displayed in the body of

[15] Function available only in MedStation but not in MedStation Express.

an e-mail or as a DICOM SR file to one of the DICOM servers configured in MedStation as storage nodes.

Send to RIS[15] if MedStation was started via COM from eRis/eVisit and a structured report is being written on a form, the *Send to RIS* button can be pressed to send the contents of the DICOM SR report displayed to the form in eRis/eVisit; this form can use the data to set some of its components.

Import…[15] used to display DICOM SR reports saved to a local folder (normally the user's *Documents* | *Reports* folder) following an unsuccessful save operation.

Tempaltes…[15] access environment definition of report templates.

To the left, below the toolbar described above, there is a list of the *documents associated with the current study* (this list is hidden if the study has one document only, but it can be shown by pressing on the ▶ symbol on the left side of the window. To close the panel containing the list of study documents, press the ◀ symbol).
On the right-hand side of the window, there is the area in which the report selected is displayed. If the report is a DICOM SR file (not pdf), it will be displayed in html format, whose style can be configured.

New Report[16]

Note *In order to ensure the traceability of all versions of a report and eliminate the risk of inconsistency between the report delivered to the patient and the reports associated with a study, as laid down by the DICOM standard, a previously stored report cannot be edited. Every modification creates a new report. As a result, whenever an edited report is saved, printed or sent, it is added to the list of reports associated with the study.*

You access the environment for writing a new report by clicking on the **New** button. The environment for writing a new report has a bar with the following tools at the top:

Save the report written is saved to the server (if the latter supports the storage of DICOM SR files) on which the study under examination is stored. The document produced is stored in *Structured Report* format as laid down by the DICOM standard (DICOM file with SR mode), irrespective of the node containing the study; and a legible version will be shown in the report display area.

> ***Note*** *If, for any reason, a structured report is not saved successfully, two files will be saved in your* Documents/Reports *folder. One of these files will be in DICOM format and will contain a copy of the report that the user was trying to save while the other will contain a version of the report in XML format, from which some of the data entered can be copied to write a new report. The DICOM version can be retrieved using the* import *function to display it and save it to the archive subsequently.*

Phonema starts the voice reporting module. This mode is only present after configuring the application appropriately (see appendix C of this manual).

Add key active when a template for a structured report is being defined, it is used to add a

[16] Function available only in MedStation but not in MedStation Express.

node with references to all key images of the study being analysed to the structured report being written.

Delete node active when a template for a structured report is being defined, it is used to remove the selected node and all its child nodes from the template.

Delete report closes draft document, prompting user to save changes if available.

Below the tool bar is the work area in which new reports can be written.

- On the left-hand side, the *decision tree* on which all the *templates* configured for writing reports are catalogued.

  The first item on this tree is *Text report*. If you click on it, you will be able to write free text in the right-hand area of the window and this is entered in a specific tag of a DICOM SR file. At the moment, this mode does not support text formatting.

  Other branches of this tree are only present if, for the storage node containing the current study, *templates for writing structured reports* have been configured; these guide you in entering the data and enable them to be catalogued using standard or personalized dictionaries.

  If any of these templates were catalogued by grouping them under labels that indicate their use, you will be able to select them by browsing through the tree until you find the branch with the label. All the templates not grouped in this way will be placed on a list on the "Other SR templates" branch.

  By double clicking on the item corresponding to the template or the *Add Structure* button, the template will be loaded into the area on the left. All the fields on the screen are to be set and, if any of the field are not used, they should be deleted (using the *Delete node* button) before saving the report.

  The data will be entered in each visual component of the template according to the type of data used by the component concerned.

  - CODE type field: you can choose an item from a drop-down menu using a dictionary of options
  - NUMBER type field: only numerical data can be entered and you shall insert a unit of measure
  - IMAGE type field: it is set by selecting an image on the display (using the small selection rectangle in the bottom right-hand corner of the image) and dragging it onto the component of the screen
  - PNAME type field: three fields in which you are to enter (using DICOM coding for forenames) the forename, surname and "middle name", where applicable
  - DATE type field: will present a calendar from which you can select a date
  - TIME type field: when you click on the corresponding box the current system time will be entered but can be edited
  - DATETIME type field: two boxes like the ones described above will appear

- TEXT type field: enables you to write unformatted text or use preset texts as described in the following note
- #MEASURE# type field: double clicking on this component prepares for making a measurement on an image displayed and creating a node in the structured report so as to write all the measurement data in conformance with the DICOM standard (numerical data, units of measurement, references to the image on which the measurement was made, …). The measurements supported by these components are distance, angle, area and perimeter of a polygon, area and perimeter of a circle, and vertebral morphometry.

Entering other templates in addition to the one being written or using preset texts to write a text only report or fill in text fields on structured report templates. [17]

Between the area for selecting templates and the area for writing reports there is a third area, which can be opened and closed by pressing the ►/◄ buttons, respectively. Having selected a template from the template selection tree, the structure of the template will appear in this panel.

If you are writing a text only report or a text component of a structured report screen, preset texts can be entered by selecting a template that has TEXT type nodes in which preset texts were entered during the configuration phase. These texts can be found at the bottom of the latter area when you select the nodes to which they belong. *To add the text after the text of the component being written, press the **Add phrase** button. To add text from the node selected and any parent nodes (if the latter are also text nodes containing predefined phrases), click on **Add chain**.*

If you are writing a structured report, you can add another template or part of it by selecting the parent node of the template to be added to the one being written from the area showing the structure of the template and then pressing the **Add structure** button.

Templates section[17]

By pressing the ***Templates*** button on the right of the toolbar of the main enviroment (of reports reading), you can proceed to configure structured report templates and catalogue.

This section describes the environment for configuring templates and cataloguing them on a decision tree.

This environment is essentially divided into two parts each with its own toolbar. On the left side is the decision tree (as configured previously) and the tools for modifying it. On the right side is the work area for modifying and creating structured report templates.

***Note:** The templates and lists of templates managed here converge in the configuration of the node from which the displayed study was opened.*

Managing the decision tree for cataloguing structured report templates

Items of this tree are only present if templates for writing structured reports have been config-

[17] Function available only in MedStation but not in MedStation Express.

ured for the storage node containing the current study.

If some of these templates have been catalogued, grouping them under labels indicating their use, the tree will have a branch for each label and items with the names of the templates below the labels.

All the templates not grouped in this way will be on a list on the "Other SR templates" branch.

The tools available can be accessed using the buttons on the toolbar above the tree.

Add node adds a branch to the tree (child of the branch selected). The new node is to be selected and renamed with a label indicating the group of templates that it will contain.

Delete node removes the selected branch from the tree and the templates that were catalogued under this label will reappear on the "Other SR templates" list. The "Text report" and "Other SR templates" branches cannot be removed.

Rename node used to rename the label of a branch.

Add template used to add a template to the branch selected. When this button is pressed, a window with a drop-down menu will appear enabling you to choose the templates present in the configuration of the node from which the current study was opened. After this operation, the item corresponding to the template disappears from the "Other SR templates" list. Templates cannot be added to the "Text report" or "Other SR templates" branches.

Delete template used to delete a template from the branch selected if this branch is not the "Text report" or "Other SR templates" branch. After this operation, the item corresponding to the template reappears on the "Other SR templates" list.

Save decision tree saves the changes to the tree cataloguing the report templates in the configuration of the node to which the current study belongs

Reset cancels all changes made to the configuration of the tree and restores the situation when the last save operation was performed.

Creating and modifying a report template

On the right-hand side is the work area for creating and modifying structured report templates.

Below the toolbar you will see the structure of the template selected on the tree to the left and the data of each node of the template can be seen in a small panel on the right.

We will describe here the tools used to configure a report template.

It should, first of all, be considered that, in accordance with the DICOM standard (for details see http://www.dclunie.com/pixelmed/DICOMSR.book.pdf and the DICOM standard, which can be downloaded from http://www.dclunie.com/dicom-status/status.html), a structured report has a tree structure, normally with a main branch that contains everything. Each branch and leaf (which will refer to as nodes) of this tree has properties that characterize the value that it will have in the report written. These properties comprise the type of data, a code taken from a dictionary (standard or private) and a relation with the parent node. Through the classification of each element of the structured report on the basis of an internationally recognized nomenclature, it will subsequently be possible to make statistical queries that can be used for qualitative and quantitative analyses of the provided services.

The following types of nodes can be configured in MedStation:

CONTAINER for a node that will contain others.

TEXT for nodes that are to be set with text. You can insert a text that will appear as preset in the writing phase and can be used as it is or edited.

DATE for nodes that will contain a date.

TIME for values that represent a moment in time.

DATETIME for values that comprise a date and a moment in time.

NUM for numerical values. In this case, the code of the unit of measurement of this numerical value must also be indicated.

CODE for coded values that are to be chosen from the items in a preconfigured dictionary.

PNAME to enter a person's name.

IMAGE to enter references to DICOM images of the study in the report.

#MEASURE# to enter, as laid down with the DICOM standard, the values of a measurement made with MedStation on a DICOM image displayed (the measurements available are distance, angle, area or perimeter of a polygon, area or perimeter of a circle, and vertebral morphometry).

New template creates a blank template. You will be prompted to enter a name for the tree that will represent the structured template.

Remove template removes the template from the configuration of the storage node from which the current study was opened. The template will thus be irretrievable.

Rename template used to change the name of the template.

Add node adds a node to the template (the node will be a child of the node selected). The node added is to be configured using the panel on the right, indicating the title of the node, the type of value that it will contain in the report (the number of section to be configured will depend on the type), the relationship with the parent node, the three values that represent the code, any necessary data according to the type of node. ***Note:*** *the "Clear" button below the panel for configuring the single node is used to clear all the node configuration fields.*

Remove node removes the node selected from the tree structure of the template.

Move up moves the node selected up to the higher branches of the tree.

Move down moves the node selected down to the lower branches of the tree.

Save salves all changes made to the template.

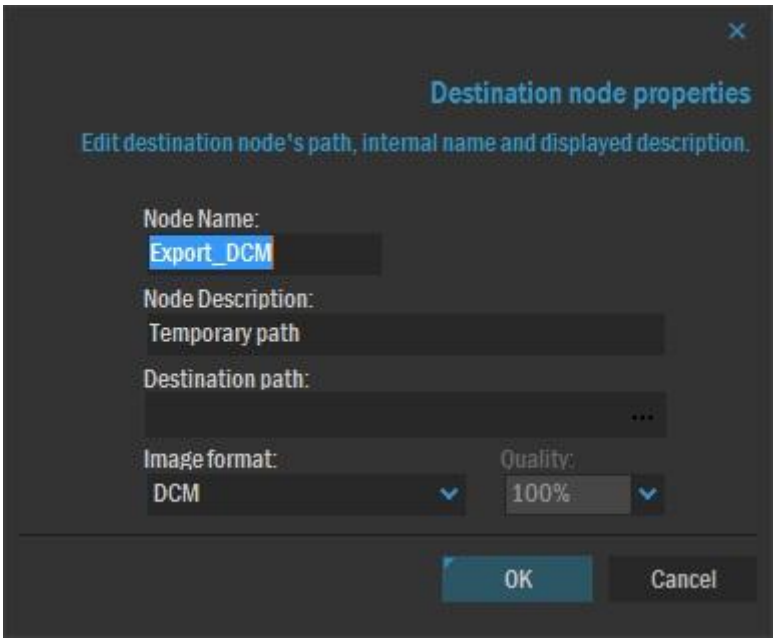
Import / Export

The **Export/Import**[18] functions allow you to store the images of the current study in a folder and subsequently to load them from it, respectively. They can be used to transfer data on a local or geographical network (via file and/or internet) or to process images format.

To export a study

1. Select the **File | Export** option**.** The program will show a window in which you can choose the destination node. If you press the **Options…** button, the **Preferences** window will appear. Here, from the "*Import/Export*" sheet (if you have the relevant privileges) you can add/modify the destination nodes and choose the format in which the current image, series or study is to be exported. Pressing the **Edit** button gives access to the screen containing the properties of the Export node selected. You can choose not only the destination name and path of the node but also the format in which the images are to be exported: NATIVE (original format of the image), BMP, TIF, JPG or DCM (DICOM format).

Figure 6. Export node properties



2. If you press **Next** button, you will enter another screen where you can indicate the images to be exported: the currently displayed image, the current series, the current study, the key images or the images selected (*Export: Current image, Current series, Current study, Study's key images, Selected views*).
3. On the same screen, you must indicate if the export is to maintain the original structure of the study files *(COMPLETE study structure)*, for example when you export a study in "MedStation format" (as in a local node), when you generate a single compressed file (*COMPRESSED export file*) that will be faster to send, when you export images in their

[18] Function available only in MedStation but not in MedStation Express.

original format *(Images only)* or if the export operation is to generate a DICOMDIR structure from the images selected *(DICOMDIR structure).*

Note *When you choose DICOMDIR export mode: the images of the study will be exported in raw format or lossless Jpeg compressed format according to the flag that can be set on the screen. You can also create the IHE web content of the study exported*

4. You can create a CD[19] with the exported study *(Create CD after export)*

Note *You can only select this option[19] if the Nero Burning ROM 7 program is installed on the workstation on which MedStation is installed*

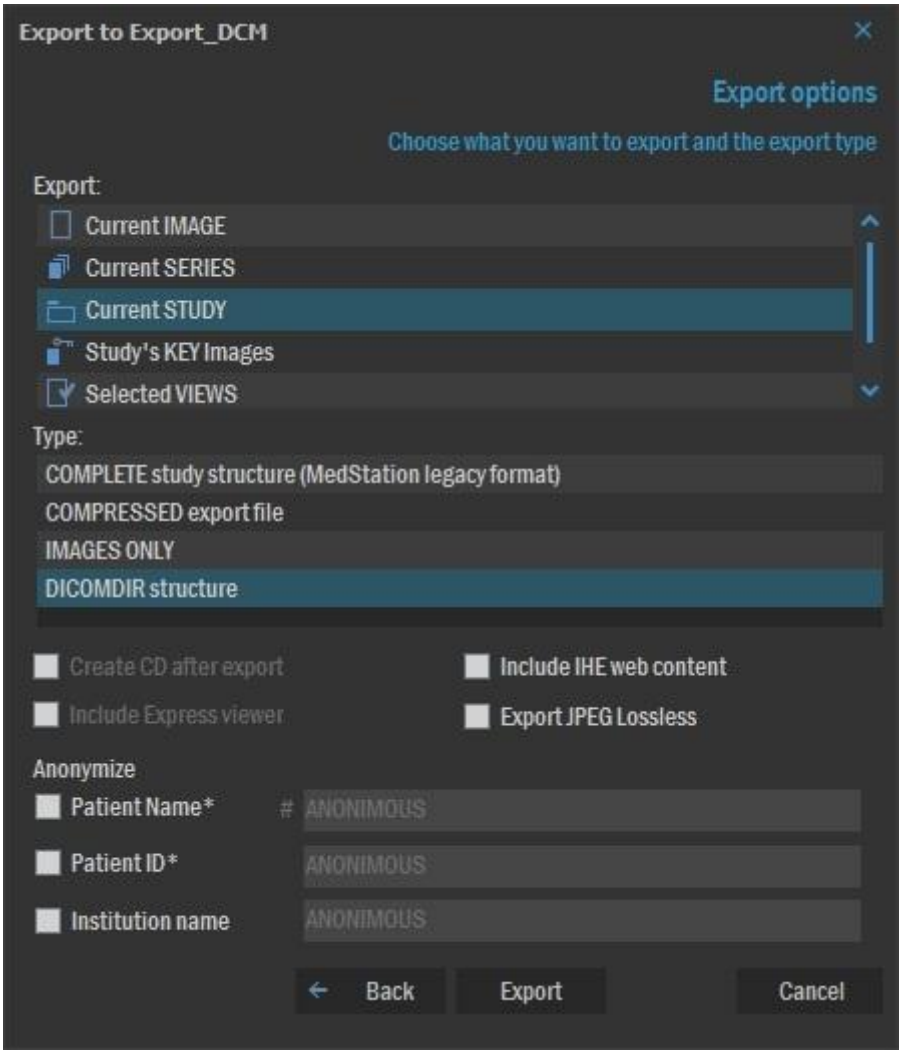
5. It is also possible to include[19] in the export files the **MedStation Express** module (if previously installed on the MedStation client), which allows you to view the exported studies *(Include Express viewer)*

6. The study can be anonymized during the export operation by selecting *Patient Name, Patient ID* and/or *Institute Name* in the *Anonymize* section. You can choose an additional string to fill in the corresponding fields of the exported images

Now you can press the **Export** button to start transferring the files. If you have selected the *COMPLETE study structure* option, before starting the writing operations, the application will check that there is a sufficient amount of space on the destination disk (this applies to *PATH* nodes).

[19] Function available only in MedStation but not in MedStation Express.

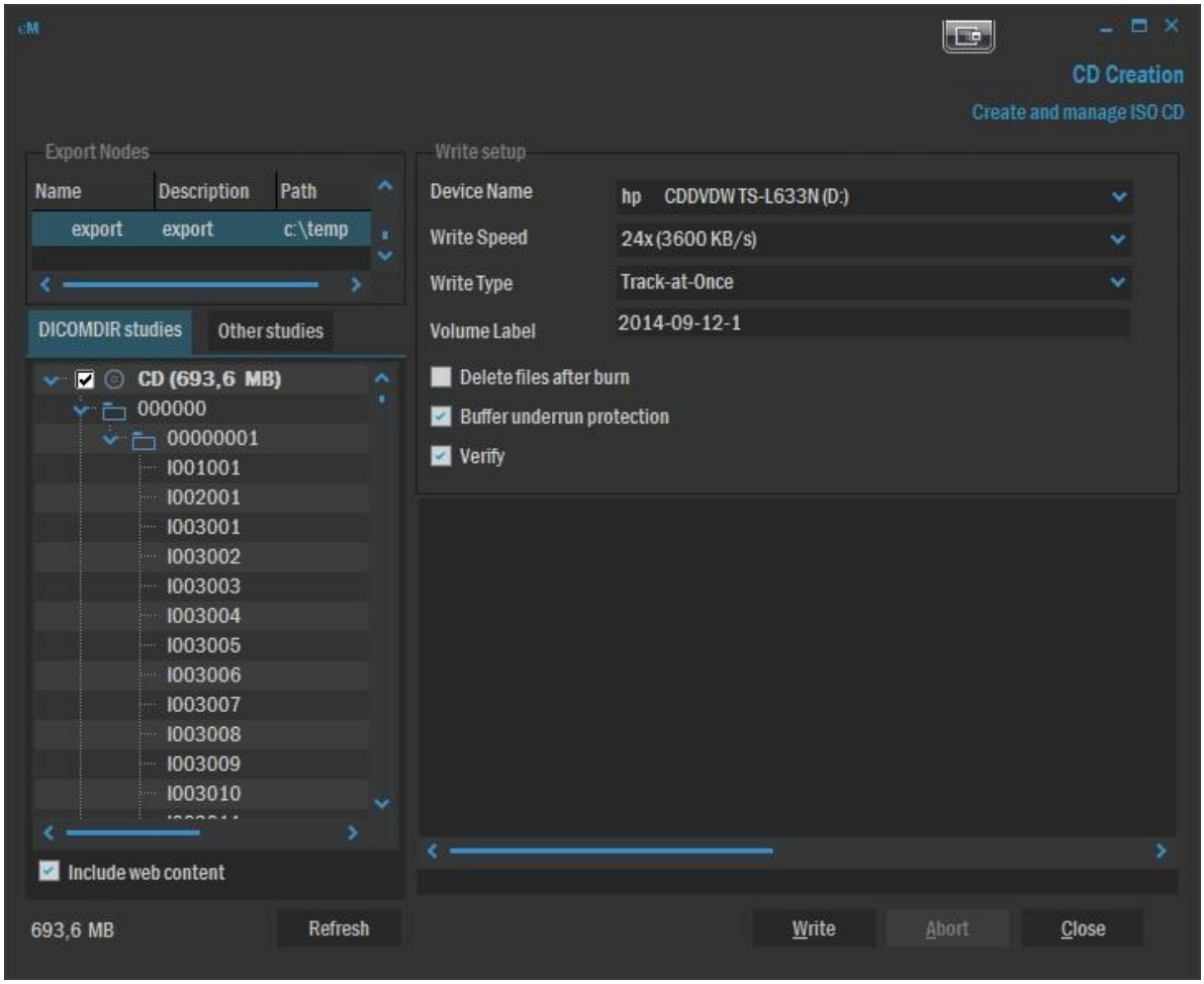
Figure 7. Choosing the export options



If you have chosen to create an ISO CD after export or by clicking the **File | Create CD** item[20], the program will display a window for managing the CD creation options. In addition, the list of export nodes as configured in MedStation appears in the *Export Nodes* section. If you select one of them, all the studies exported in DICOMDIR or different formats will appear in the section below. From this list, you can choose studies to be saved to the CD. The option *Include web content* allows you to add to the CD the study in a format viewable by a navigation web. In the right part of the window, in the section *Write setup*, you can set burning parameters. The *buffer underrun protection* option, if enabled, will enable safe burning mode, trying to avoid failing the burning process. The *Write* button starts the CD writing process. During this operation, a bar indicates the progress of the process and a window shows a log of activities in progress. If the *Verify* option is selected, at the end of the burning process, the data written will then be checked.

[20] Function available only in MedStation but not in MedStation Express.

Figure 8. CD creation management window



To import a study20[20]

1. Select the **File | Import** option
2. Select the file to be imported from a folder. This file must have been created by the MedStation export function.

Note: *The import function always creates a new study.*

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The operations of imports of images in examinations are to be carried out carefully to avoid wrong associations of images with patients. When you try to add DICOM images or DICOM files to an exam with patient data such as patient name and / or date of birth different from the examination itself, the operation is not allowed and an error message is shown.

Chapter

3
Managing images

This chapter deals with functions for displaying exams and associated diagnostic images.

The 2D environment for managing images can be accessed immediately after selecting and opening a study from the study search and selection screen, from the list of previous studies on the Patient/study information panel or from the list of the studies most recently opened from the **File | Reopen** menu.

From the **View** menu you can select some work area options for managing images: display the status bar, apply interpolation to images, display text on the image, apply any overlays, presentation states and shutters set and SR CAD marks, display the colour bar for each image, set the display mode of any localizers set, sort the images in the display box and display modes other than 2D, manage the alignment of the images in the views, set lines that represent the intersections between the images of a study.

From the **Window** menu you can open the side panels when they are closed or when the corresponding label is no longer present on the bars beside the work area (if the panels were closed using the "X" button in the top right-hand corner of each panel). The open panels are shown on this menu.

From this menu you can activate *Sheet view* mode when there are several studies open in a grid of boxes, they are arranged in sheets and each one occupies the entire work area. You can also choose to switch to *full-screen mode*, which displays images in the largest available area. In this mode, the menus, accessory panels and toolbars are hidden but can be shown by moving the cursor close to the edges of the screen. On a multi-monitor workstation, the *Monitor*[21] item, displays a submenu with functions for shifting the current screen onto another monitor. It is used, for example, to shift colour images (such as 3D reconstructions) from a grey-tone X-ray monitor to a colour service monitor.

Note *It should be noticed that all screens have the same layout - which includes a main menu bar and a status bar - and can be split into display boxes (or image views) as described.*

[21] Function available only in MedStation but not in MedStation Express.

Box view bar

First, we will describe the bar located at the top of every image view.

Note *By clicking on this label, a window appears with information about study and patient (see the section "Patient/exam information" in the previous chapter).*

Figure 9. Sample image view bar



- On the left of the image view bar is a label bearing the view name. This consists of a letter which indicates the screen containing the view (A for the first screen, B for the second, and so on) and the number of the image view inside the screen (numbering follows the order of the views from left to right and from top to bottom). Left clicking on this label gives access to:
    - a menu with a *list of open studies*, by clicking on one of these items you can display the study selected in the current box
    - a possible menu with a list of any *links* between this view and other views:
        - a list of any views of which a subsequent page can be seen (**Continue viewing from**)
        - a list of any views whose position can be synchronized (**Synchronize position with**)
        - a list of any views whose scrolling can be synchronized (**Synchronize scroll with**)
        - it will also be possible to link two views by means of a *localizer link* (**Linked scanograms**); so that all and only the localizer images related to the current image shown in the linked view are loaded into the current view
        - a list of the links with the current view, which can be *destroyed*, thus making the views independent of one another again
    - a menu for changing visualization mode, selecting from 2D, MPR, 2D Curved MPR, 3D[22], external 3D[22] (if configured).

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- *To reduce the risk of a user viewing studies different from those he wishes to analyse*, the image view bar indicates
    - - if there are opened studies of different patients - the name of the patient to which the study displayed refers, his sex, date of birth and age on the current date
    - the study modality, the study execution date and the time that has passed since the study was conducted
    - The index, the description and the number of images of the series

[22] Function available only in MedStation but not in MedStation Express.

displayed in the current box.

Note: *If the study displayed is the first opened of the group of studies, a bullet will precede the caption.*

- If page, scroll or position links have been enabled with other image views, a symbol representing the link will appear on the bar beside the name of the view.
- The  button is used to access the panel for configuring the splitting of the screen into image views and the splitting of the current view into a grid of images
- The  button is used to switch from the subdivision of the work area into image views to display a single view occupying the entire work area, managing the other views that were previously on the grid as sheets. To return to grid mode from sheet mode, press the  button.
- The last button  present in the image view bar is used to close the study displayed in it.

  Note: *This operation closes the display, but the exam remains loaded. In order to actually close the study, click on the* **File | Close** *menu item or use the* CTRL+F4 *shortcut. The study will also be closed, together with all other open studies, if you select the* **File | Close all** *menu item (or the* F9 *shortcut).*

Image view

On the current image view, the window that contains the *current image* is highlighed by a bright border at its four corners, while all the other images have a thin grey border. To make an image become the *current* one, simply click on it. If you double click on the current image it will be shown in full-screen mode and, to return to the previous mode, simply double click again.

The image view of each image shows the following information:

- In the bottom right-hand corner the window/level values displayed. 'W' indicates the window value and 'L' the level value.
- For images whose window/level values are processed on a sigmoid curve, the "SIGMOID-LUT" string will appear above the W and L values.
- For images without window/level values but with a VOI LUT indicated among the DICOM tags, the window/level values are replaced on the image by the string "VOI-LUT" followed by the name of the VOI LUT, if one has been assigned.
- If a correction curve has been applied to the image, the message: "CORRECTION CURVE: curve name" will appear at the bottom of the view.
- In the bottom right-hand corner a solid square will appear coloured if the image is

selected, otherwise it will appear transparent. By clicking on this square you can change the selection status of the image from selected to unselected and vice versa.

- If the DICOM image has the Positioner Primary Angle (0018,1510) and Positioner Secondary Angle (0018,1511) tags set, the values will be shown in the bottom right-hand area.
- If the image is calibrated, the "CAL" indication will appear together with a ruler on the right whose length (in the patient's reference) is always indicated below it.
- In the bottom right-hand area there is an indication, in square brackets, of the scale of the image displayed with respect to its actual size. For example [75%]. Also, if the system has been set with the information about the size in mm pixel monitor, you will also see the zoom percentage from the actual sizes, as [n% - True].
- If the image is DBT, for each tomosynthesis frame is shown the thickness in mm based on the value of the DICOM Slice Thickness tag. In addition - according to the IHE indications for DBT profile - is shown the frame position in the stack obtained by measuring the distance along the normal to the image. It is also shown, if different from the previous one, the distance between the positions of the frames in the stack, without considering the projection on the normal to the plane of the frame.
- If the image is of the multiframe type, the indication "Fr" and the number of the current frame in relation to the total number of frames present will appear in the bottom right-hand corner.
- If the image is a localizer, the indication "LOC" will appear in the bottom right-hand corner.
- The bottom right-hand area also contains the ID of the image, which consists of the series number (actual series to which the image belongs, even if it is displayed within a virtual series) and the number of the image (within the series to which it actually belongs). For example, the first image in the second series will be labelled as "2.1".
- If the image was reformatted using the MPR modes, the letter "R" will appear in round brackets to the right of the image ID.



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- If the image displayed was compressed in JPEG LOSSY or JPEG2000 LOSSY format, the "JPEG Compressed" indication will be shown at the bottom of the screen. In addition, if the image is DICOM, the *compression ratio* (that is, the ratio between the number of bits necessary to save the original image and that required to save the compressed image) and the compression percentage will appear in brackets. For example, if the size of the compressed imge in bits is 10 and that of the uncompressed image is 100, the compression ratio will be 10:1, while the compression percentage will be 90%.

- For CT and MR and MG images, beside the image appear letters (or combinations of letters) that, in accordance with the DICOM standard, indicate the position of the image in the patient. A=anterior, P=posterior, H= head, F=foot, L=left, R=right

Information that can be defined during configuration is shown in the top left, top right and bottom left corners.

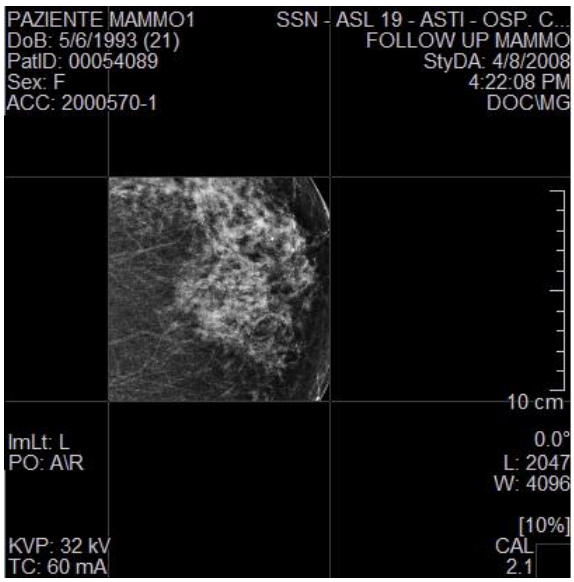
In addition to this information laid on top of the images, you can display in one corner of the image (if it has localizers) a small square that shows the current localizer and the slice corresponding to the image.

Information on mammography images

The mammographic images are exceptions to what is written above. To adhere to the IHE directives, all annotations overlayed on the displayed image shall not be annotated on the edge that contains the chest wall, so as to avoid covering breast tissue. The system locatee the annotations on the opposite side to that corresponding to the chest wall, to minimize the overlapping area of the breast and of information symbols (ie. Calibration ruler, selection rectangle, ...). The side of the image where is chest wall is automatically recognized by the system and the image is so positioned with the rib part aligned to an edge of the view and oriented so that the armpit is in the high part of the view, then on mammographic images it is superimposed on the string encoding (according to IHE) laterality and location.
Also if the study has CAD SR applicable to study images, on each image is shown the information about the presence of CAD SR. If one is applied there will be the annotation "CAD SR applied n / tot", or "CAD SR available ignored in view." To view the details of each CAD mark drawn on the images you must select the mark of interest and click. You will see a mask, here select the *Text* option and press OK. The applied SR CAD information are in the corresponding entry in the submenu under *View* | *CAD SR applicable*.

To simulate the curtains of the diaphanoscope

When the mouse cursor is moved close to the borders of the image selected, it turns into a two-tipped arrow ↔ or ↕. If you then drag the mouse in the directions indicated by the arrows, you can darken part of the image in order to limit the view to a rectangular area of interest as shown in the figure below.



Navigating through the images displayed

The images of the studies displayed are arranged in grids in the image view boxes dividing up the work area of each screen used by MedStation. Depending on the number of images present in the series displayed in the image view and on the views contained in a chosen grid, not all images can be displayed simultaneously. A variety of methods can be used to browse through all the images in the study.

Use the arrow keys to move between images one at a time. The Home and End keys display the first image and last image of a displayed series (or entire study if *All images loaded* are displayed), respectively.

Note: *The buttons Page Down, Page Up change the series in the current display box, by choosing the next or previous series in the list of exams/series (see next paragraph), without changing the study if there are several open studies, navigating between the series of the study in the current box.*

Instead of using the keyboard, you can interact directly with the scrollbar in the lower part of the work area of the current monitor, or with the mouse. If the mouse is equipped with a central scroll wheel, this can be used to bring to the foreground all the images previous or subsequent to the current images.

By clicking the left mouse button on the **Stack** item among the **Cursors** and moving within the display area of an image you will enter ***stack view*** display mode. In this mode, you will see all the images in the series to which the current image appear one after another in the same image view. For movements down navigation proceeds from the first to the last frame of the movie, for upward movements navigation will be the opposite. All the images in the series or all frames of the current video (whatever their number) will scroll by dragging the mouse in an area having a height equal to one-fifth of the monitor. The navigation step will therefore be proportional to the number of images in the series or frame of the movie. The navigation step remains unchanged if you hold down the CTRL key while the drag action.

Study/series navigation panel

In the work area in each monitor used by the application, there is a panel containing a list of loaded studies, according to the patient, with details of the series they contain and any of studies referring to the same patient present in the same archive as the current study.


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Note *In the panel there is a detailed grouping of studies based on patient data to highlight the patient's studies of different patients even if they are homonyms.*

Below patient data, for each open study there are several icons with the following information:

- An icon provides information about the study. If you click on this first icon, *all the im-*

ages loaded in the memory that make up the study will be displayed in the box.

- Below the first icon that represents the entire study there are other icons that indicate whether and how many *DICOM SR reports* and DICOM DOC documents are present. Similarly, there is an icon that indicates the presence[23] of *reports signed in eRis/eVisit* in pdf format. They can be read in the "Reports" side panel that appears when you click on the reports icon.
- The icons mentioned above are followed by icons representing the *series of images that make up the study*. The information given beside the icon consists of the number of the series, the modality of the images, a description, where entered, and the number of images present in the series. If any of the images in the series are ***videos*** (multi-frame images or an MPEG video), below the icon of the entire series appears a list with an icon for each video image and, finally, an icon that represents all and only the ***static images***. If you double-click on the icon of a video, the video will be played in the image view containing it and, in this view, all the commands for managing the "Cine" display options will be activated and, if you double-click on the same icon again, the video will be stopped and the image layout will be restored in the view. If you click on the icon representing the group of static images, only the non-video images in the series will be shown in the image view.
- Finally, there will be some icons for additional series that group the images according to their characteristic properties. If you click on one of these icons in the current view, the group of images with these characteristics in common will be loaded and displayed as though they formed an independent series. The additional series may be of the following types:
    - Series of *key images* (KO)
    - Series of *localizer images*
    - series of *images selected by the user* when displayed (by clicking on the small square in the bottom right-hand corner of the images)
    - any *virtual series* created by applying the display protocol.

Note *The series represented by the icon with the colored background is the one currently displayed.*

Note *The series not yet loaded are represented by a symbolic icon.*

Note *The images of another series are loaded into the box by selecting it from this panel as described above. Having loaded a single series, you can add other series of the study in the same box by selecting them from the menu, holding down the CTRL key (the series displayed will be indicated by a name consisting of the numbers and descriptions of the series they contain).*

Note *The panel can be hidden so as to broaden the image viewing area. The panel can be made invisible and visible again by clicking the button at the bottom left of the workspace*

[23] Function available only in MedStation but not in MedStation Express.

next to the panel just described, or by clicking the shortcut '\'.

Previous exams

If the patient, in addition to current study, has other exams in the same storage node, this panel will also display a list containing these exams in chronological order from most to least recent, included current exam. In the list, each exam has an icon that shows the main diagnostic modalities of its images, and, if the study is open, next to this icon, there is a small arrow that lets you expand or collapse the detail of the series that make up the study. Each of these studies can be displayed in a box in the work area by double clicking on the icon (the corresponding images will appear in the first box available or the HPs available will be applied (if enabled)), or by dragging the icon into the desired box (in this case, the corresponding HPs will not be applied). Each item on the list of the patient's studies includes information such as the date on which the study was conducted and the difference in time with respect to the current study, the modes of the DICOM files that make up the study, a description of the study itself and the number of series and images.

Note: *The list of* previous *studies (all the patient's studies are shown even if they were conducted after the current study), is created on the basis of the search criteria set on the window that can be accessed in* **eM | Options… | Preferences** *on the "Other" sheet, in the "Previous search criteria" section*.

Search filters

In the box that appears above the list of patients and their studies, you can enter alphanumeric strings to search exams in the list with a same string in the date, in the modalities list or in the description. Studies that matches this search are highlighted and brought to the top of the list.

Links

This section describes the modes (which we will also call *links*) that can be used to link together a number of image views.

Page links (continuation of a study)

If a study or one of its series is present in an image view, and its images are not all already displayed (because the grid has fewer views than the total number of images), it can be continued in other image views. In other words, subsequent images can be seen in other image views arranged with the same layout.

Note: *Pages created in this way behave as though they all belonged to one and the same image view.*

If an image view has a subsequent page in another view, the former will have the indication

"Continues in <name of box containing next page>", and the first image in the second box will have the indication "Continued from <name of box containing the previous page >".

The total number of images displayed in linked pages will determine whether it is possible or not to continue displaying a study.

Once the link has been activated, a chain symbol will appear on the bar above the image views.

To activate a page link in a view currently displaying images, click on the name of the view on the bar over it to open a menu and choose the desired option. Once the links have been created, they can be destroyed from the same menu, which will include an item for breaking links between image views.

Scroll Links (synchronization)

You can create a link between two studies displayed in different views in such a way as to make them move in a synchronized manner.

If two views display images of studies (even different ones), an image in each view is made current by clicking the left mouse button. On the drop-down menu on the bar above one of the two views concerned, if you click on the name of the box, the "*Synchronize scroll with <name of the boxes available for this type of link>*" item will be present. The link is activated by clicking on the string with the name of the view with which it is to be created. Having created the link, the items necessary to destroy it will appear on the same menu. If there are two or more scroll links enabled, you can destroy them all from the shortcut menu of one of the images in these views by choosing the "Disconnect all" item.

From the moment when the link was created until it is destroyed, the images in the two views will be linked. They will be displayed with the same layout and any movements made in one of the images using the arrow keys or the scroll bars will be replicated in other linked views, in such a way that the images which were current in the given views at the time of creation of the link will always be found in corresponding positions. This rule means in practice that 'empty' images can appear because a linked image may not have a corresponding visible area within another image view.

Localizer links

If views display studies that support scanograms (CT or MRI diagnostics), you can use other views to display these images alone.

A link of this type can be *activated* by choosing from the drop-down menu on the name of the box the **Localizer Link** submenu item with the name of the image view whose localizers are to be displayed. Once the link has been created, this menu will contain an item for destroying it.

Images displayed in the localizer image view are always linked to the current image in another image view in accordance with the options chosen when creating the link. When changes are made to the current image in the first view, therefore, the images in the localizer view are simultaneously and correspondingly updated in such a way as to show all (and only) the rele-

vant scanograms (where available). The segment corresponding to the intersection of the plane of the linked image will always be drawn on each localizer image.

Anatomical position links

If an image view contains an exam or an exam's series and its images have an anatomical position reference, (CT or MRI or Breast Tomosynthesis diagnostics) it is possible to synchronize the images of another view in such a way that both contain the same anatomical position.

A position link can be activated for an image view currently displaying images by clicking on the name in the bar over the image view and choosing the desired menu option. Once the link has been created, this menu will contain an item for destroying it.

Note: *Links of different types may not always simultaneously coexist for a given image view. For example, an image view with a scroll link cannot also contain a page link or localizer link. An image view may have only one previous page and one next page, and similarly it may have a scroll link with only two other image views.*

Display of Digital Breast Tomosynthesis images

The Digital Breast Tomosynthesis (DBT) images constitutes an exception to what is written above. As for the conventional 2D mammography images, to adhere to the directions IHE, all information relating to an image of the breast must be located on the opposite side to that corresponding to the chest wall, to minimize the breast area of the overlap of the strings and the information symbols (eg. calibration ruler, bounding box, ...).

The side of the image on which is located the chest wall is automatically recognized by the system. Also on mammographic images it is superimposed on the string encoding (according to IHE) laterality and location.

The DBT images are generally multi-frame and many DICOM information varies from frame to frame, as for example the position and orientation data, but also those of calibration, of Modality LUT and VOI LUT, the thickness of the slice corresponding to the reconstructed frame, ... the system updates all the information at each change of frame.

In the configuration of the information to be superimposed on the images, all the values indicated by DICOM IHE directions are made available, these are partly different from those indicated for conventional mammography images. For this reason, in the configuration mask for information on images it is given opportunity to indicate the modality and the DICOM SOP Class of images (see this manual in chapter 9 "The Options menu", section "Information on images").

The system presents the tomosynthesis images in views in a manner similar to the display of conventional 2D mammograms. For multi-frame tomosynthesis images, the system provides the user with some methods of navigation between frames. Two scrolling methods are available, one manual and one automatic (CINE).

For the automatic navigation in CINE mode, the user can control the playback speed (during movie playback move the mouse wheel) and configure the initial speed of the cinema (with the button settings in the cine toolbar).

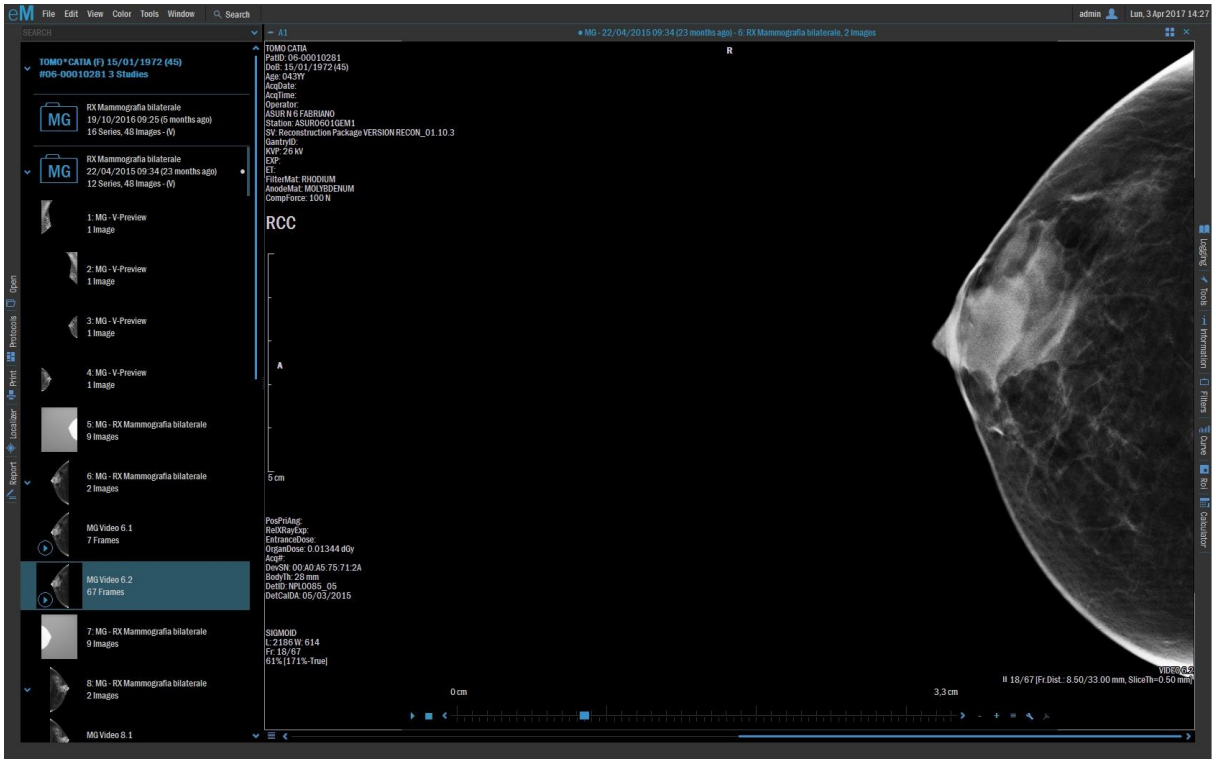
The scroll is set to manual (no need to start the cine and then pause) when selecting from the side panel studies /series an icon corresponding to a multi-frame DBT and positioning on the current image, thereby the scroll with mouse wheel will move between frames and will not change image.

You can navigate the frames even with the stack view mode.

In manual navigation mode, on the view it will appear a navigation bar that contains the indication in cm of the total thickness consisting of the entire reconstructed frame package, the ticks representing a subdivision in cm and in millimeters. Also ticks appear corresponding to the location of the image frame.

For each frame, on the view an annotation appears that shows the frame number of the current image frame and the total number of frames in the lower right corner of the view, in the format "Fr: F / N" where F is the index corresponding to the frame, and N is the total number of frames contained in the video. For multi-frame images DBT, the frames may be reordered, for example, based on mutual position within the reconstructed volume, and therefore the numbers may not be ordered according to the order of the same frame in the encoding of the pixel data.

According to the indications for the IHE DBT profile, for tomosynthesis frames the thickness in mm and the position in the stack frame are shown. The position is calculated from the DICOM data in Image Position (Patient) (0020,0032), by measuring the distance along the normal to the image (the normal is obtained from the data in Image Orientation (Patient) (0020,0037)). Also the data of the distance between the positions of the frames in the stack is shown, without considering the projection on the normal to the plane of the frame.



If in a series there are at least two DBT multi-frame images acquired in the same reference system, and you navigate through the frames in 2D display box, choose another image, clicking on the corresponding icon of the study panel / series, so this second image will be displayed showing the closest frame (in position within the reconstructed packet) to the current frame of the previous image previously displayed in the same box.

If the two images are displayed in different boxes you can link them by position (from the drop-down menu in correspondence of one of the two boxes). So that the navigation (both automatic and manual) between frames in one of the images triggers the navigation in the other, in such a way that the frame of the positions of the two images are the closest possible in the patient's reference system in which they are acquired.

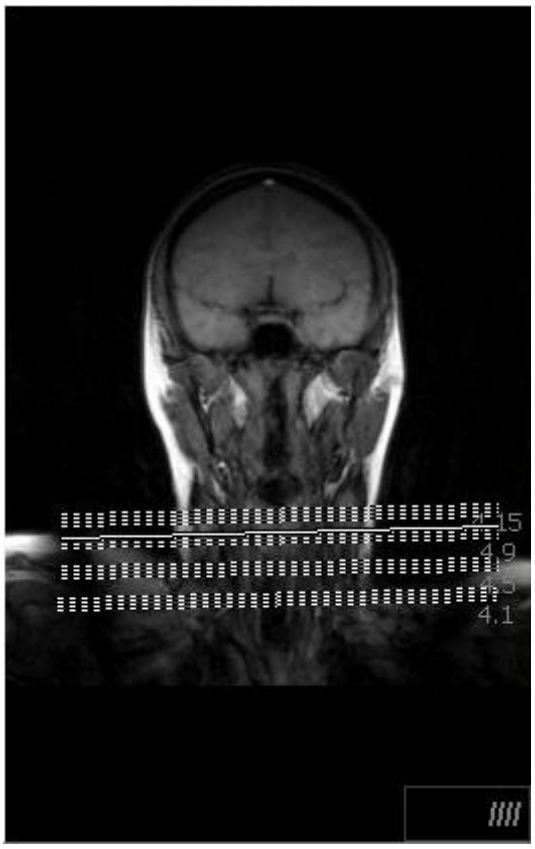
As with conventional mammography images, you can use the zoom tools, in particular those dedicated “Fit breast” and “Same size”, that will be applied at the frame level.

Viewing Localizer images

The panel for viewing localizer images is opened by clicking on the label on one side of the work area or selecting the **Window | Localizer** menu item. The localizer shown is one of the scanograms associated with the image displayed in the current image view.

If an exam contains two or more scanograms you can switch from one to another using the < > buttons present at the bottom right of the panel. Next to these is another button for drawing scout lines for *all*  or only *the first and last*  images of the series to which the current image belongs.

Figure 10. Scanogram panel



A similar panel appears in the image views if they are displaying (in an image layout other than 1x1) a series of a study with localizers. This panel when integrated in the display box, allows the user additional interactions to those described above. In fact, it is possible to modify the window/level values of the localizer image contained in it by right clicking and dragging. Left click and drag to update the display of images from the series, bringing to the front the image corresponding to the point at which the cursor is located. In other words, if the cursor is located at a specific point in the localizer corresponding to the line of intersection of the scanogram in an image, this image is displayed (if it was hidden), generally as the first image in the view.

- This panel can toggle between hidden and shown modes by activating or deactivating the **View | Localizer | Localizer in box** menu item.

Note: *The **Edit | Localizer Image** menu item (active for images of MRI or CT studies) allows the images to be set as reference scanograms for the other images of the study.*

Scanograms relating to CT or MRI images can be displayed overlaid on the image that has these scanograms. From version 4.7 on, MedStation can be configured by the user in such a way as display a mini localizer in a corner of the image being analysed, with only the intersection corresponding to the image drawn on the scanogram. To set this configuration, choose the position of the mini localizer from the **View | Localizer | Localizer on image** submenu.

Note: *Left click inside the view containing the mini localizer to display the next scanogram of the same image, if it has more than one localizer.*

Similarly, a corresponding mini localizer can be overlaid on printed images. Configuration for printed images is performed using the *Settings* panel of the print settings window.

Detailed description of the menus

This section provides a detailed description of some of the functions for viewing, processing, managing the images of the studies, which can be activated from the menus and/or the panels with the tools.

Range of application

The **Edit | Apply…** menu can be used to define the range of application of the graphic functions and, with certain conditions, printing. Depending on the option selected, the functions will affect only the current image (**Apply to image**), to the series of the current image (**Apply to series**), or to all of the images of the exam currently displayed (**Apply to views**).
If the range of application is the *Series*, in general the function will affect all of the images of the actual series to which the current image belongs. However if the current image is displayed inside a virtual series, the function will affect only images in this virtual series.

Note: *Regardless of the range of application, if you drag an image (having clicked on the selection square at the bottom right) onto the print preview panel and use the left mouse button with the CTRL key, all (and only) the images marked as selected will be added to the print job.*

Regardless of the range of application, if you drag an image (having clicked on the selection square at the bottom right) onto the print previous panel and use left click only the dragged image will be printed to the print job.

Window/level

To change the window/level of the grayscale values of images, right click inside the image views or left click if the window/level tool has been selected from the shortcut bar of the image. The current window/level values are always shown in the bottom right-hand corner of the images.

Note: *If the propagation parameter* is not active, *window/level changes affect only the image view for the current exam; thus if the same images are contained in different views, they may be displayed with different window/level values. If on the other hand the propagation parameter* is active, *the change in window/level affects all image views contained in the same exam, always in accordance with the chosen range of application (Apply to …)*

Favourite window/level values can be saved to a menu for rapid recall when required[24]. There are different menus for the different modalities of exams, in addition to a *General* menu, which always appears in addition to the menus with specific values.

[24] Function available only in MedStation but not in MedStation Express.

To change the level value

1. Select the image
2. Right click and hold or left click if you have chosen the window/level modifying tool (from the shortcut bar on the image) and drag to the right to increase the level or left to decrease it. You can also use the following key combinations: CTRL+ right arrow to increase level, CTRL+left arrow to decrease level.

To change window value

3. Select the image
4. Right click and hold or left click if you have chosen the window/level tool (from the shortcut bar on the image) and drag downwards to increase the window or upwards to decrease it. You can also use the following key combinations: CTRL+ down arrow to increase the size of the window, CTRL+ up arrow to decrease the size of the window.

Note: *To increase by a factor of 10 the modification increment of the window/level value, while moving the mouse or using the arrow buttons, press and hold down the CTRL+SHIFT keys.*

To optimize window/level in a particular area of the image

1. Select the image
2. Right click holding down ALT and drag to define the rectangular area to be used as a basis for calculating the optimized *window/level* of the image.

To add the current window/level values to the favourites menu

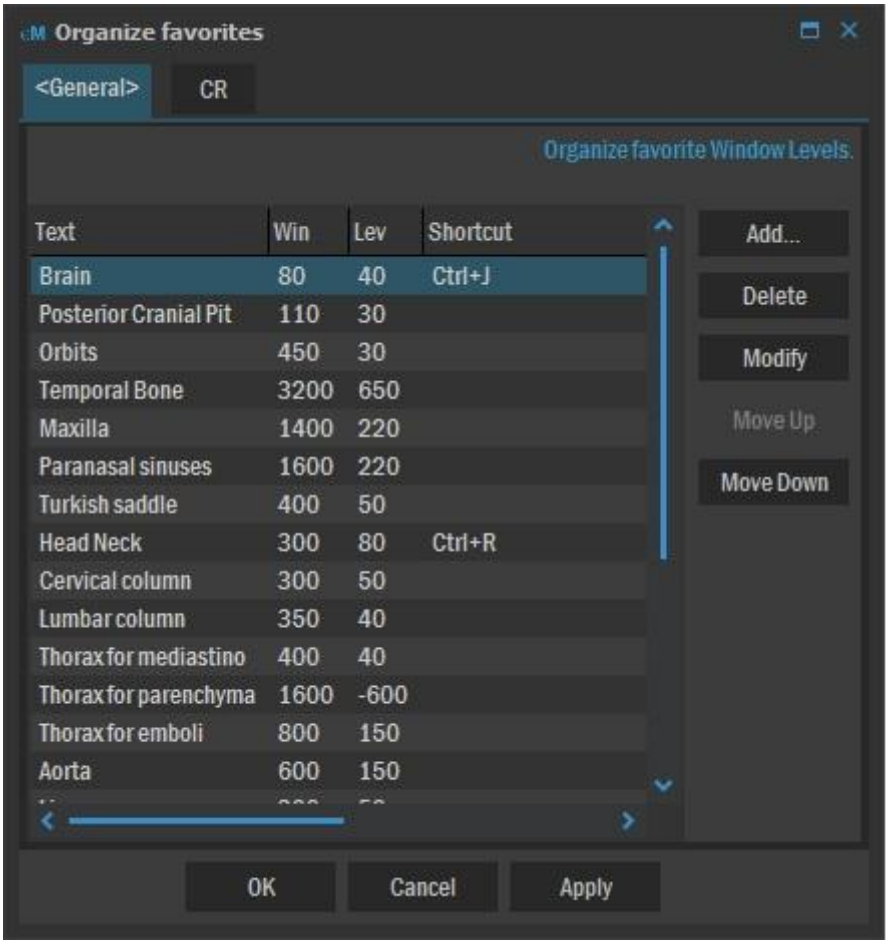
1. Select the desired window/level value.
2. Select the **Colour | Add to favourites** option or press CTRL+F6.
3. In the recording window, choose the study modality to which the window/level values to be saved refer, choose a combination of keystrokes with which to create a shortcut to apply the values, type a name and change the suggested values if so desired.

To change the favourites menu[25]

Use the **Colour | Organize Favourites…** option to recall, rename, move and add stored window/level values (see Figure 11). Values thus defined are displayed in the **Colour** menu.

[25] Function available only in MedStation but not in MedStation Express.

Figure 11. Window for managing window/level values



To recall a stored window/level

Select the name given to the window/level on the **Color** menu, which can also be opened from the shortcut bar on the current image.

Correction curves[26]

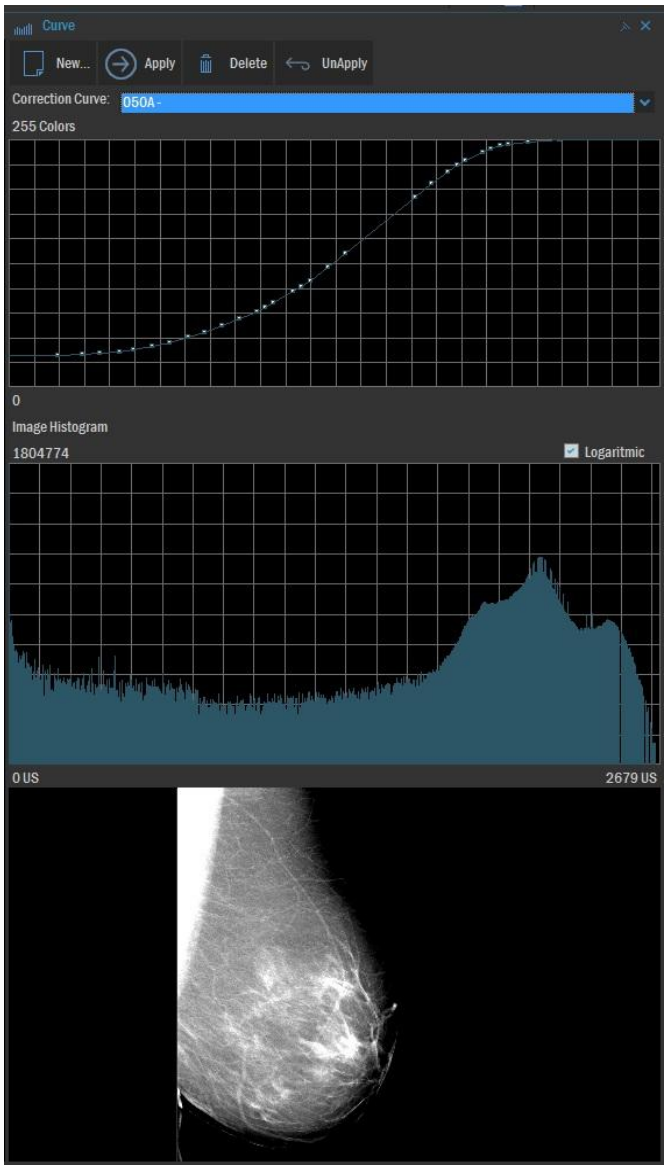
The environment for curve correction management allows selection and interactive generation of functions for changing image pixel values.

Management of correction curves

Correction curve management is activated using the **Window | Correction Curve** option or from the side panel with the **Curve** label.

When the image is displayed, the correction curve will be applied first, followed by changes in the window/level values.

Figure 12. Window for managing correction curves



[26] Function available only in MedStation but not in MedStation Express.

The window for managing correction curves is divided into three areas:

- The curve display area
- The image histogram display area
- The area in which the current image is displayed. This will contain a preview in real time of the application of the curve chosen or being modified to the image.

The **New…** button opens a dialog box for entering the name and description of a new correction curve. By dragging the mouse cursor into the correction curve display area, you can interactively modify its shape by clicking at significant points of the curve.

The **Apply** button enables you to apply the correction curve chosen from the **Correction curve** drop–down menu containing a list of all the curves configured in the system to the current image and the range of images set according to the **Modify | Apply to…** value.

The **Unapply** button removes the curve applied to the current image.

The **Delete** button removes the currently displayed correction curve from the list.

Sigmoid function

The **Color | VOI LUT Sigmoid** menu option is displayed if the image has window/level values and allows application to/removal from the images of a given correction curve, on the basis of the range of application of the changes (to the current image, to the series to which the current image belongs, to all of the views displayed in the current box), but independently of propagation settings. This correction curve is a sigmoid function of the grayscale values of the images and the window/level values interactively defined by the user or contained in the DICOM (0028,1050) and (0028,1051) tags:

$$OUT = \frac{Output_Range}{1 + \exp(-4\frac{IN - WC}{WW})}$$

Where *IN* is the input value of the LUT, *WC* is the level value, *WW* is the window value, *Output_Range* is the maximum value for the image pixel values (a value which depends on the bit depth of the image itself).

This curve is automatically applied (and cannot be removed) for images with the DICOM *VOI LUT Function* tag (0028,1056) with a string “SIGMOID-LUT” and particular mammographies for which the curve is known to be applied by default in all cases.

Favourites

The **Tools | Favourites** submenu and the **Favourites** sheet of the **Tools** side panel can be configured by the user to contain the tools used most frequently in a single place that can be reached quickly. In fact, the favourite tools will appear on the shortcut toolbar (as shown in the figure below) that appears above the current image.



To create a set of favourite tools:

1. Open the **Favourites** sheet of the **Tools** side panel
2. Click on **Modify**, to enter configuration mode
3. Select a tool from one of the sheets of the **Tools** panel and drag it onto the **Favourites** sheet
4. Repeat step 3 to add all the desired tools
5. Drag buttons corresponding to functions that you do not want among the favourites off the sheet area
6. Press the **Done** button to save the changes and exit from configuration mode

Beside the **Modify/Done** button there is a menu on which you can choose whether to show the button labels on the shortcut bar of the image or not

- *Icon only*, the buttons on the shortcut bar will have an indicative symbol only and not the name of the tool
- *A label*, shows the label with the name of the tool when you move over the button, otherwise it shows the icon only
- *Show labels*, each button on the shortcut bar will have the icon and label with the name of the tool.

Cursor

The **Tools | Cursor** submenu and the **Cursor** sheet of the **Tools** side panel list the functions that may be performed on the images shown with the left mouse button held down

Colour Activates the function for changing the Window/Level values of the current image (and other images in the same series or in the entire study according to the range of application of the transformations) by moving the mouse with the left button pressed, as described in the "Window/Level" section above.
Pan Activates the function for panning the current image (and other images in the same series or the entire study according to the range of application of the transformations) maintaining the enlargement factor by moving the mouse with the left button pressed in the image view of the image concerned.
Zoom Activates the zoom in or zoom out function with the center at the initial point of application of the cursor of the current image (and other images in the same series or in the entire study according to the range of application of the transformations) by moving the mouse with the left button pressed upwards to enlarge the view or downwards to reduce it. The same function can

be performed using the + and – keys of the numeric keypad.

Stack Activates the possibility of viewing the images in *stack view* mode. In this mode, you see all the images of the series to which the current image belongs appear one at a time in the same view. By holding the Ctrl e Shift keys pressed in stack view, you can scroll the images more quickly.

Magnifying glass Used to view an enlargement window at a point of the image. You must hold the left mouse button pressed to display the enlargement window. The enlargement zone will change as the mouse is moved.

When the Magnifying glass *function is active, you can change the zoom factor using Up Arrow to increase it, Down arrow to reduce it, Left arrow to reduce the area and Right arrow to increase it.*

3D cursor sets the spatial navigation mode on the images of a study shown in more than one view and in the panels of the localizers situated in the top left-hand corner of the views.

The *3D cursor* function activates a special mode for browsing through the images of a study shown in at least two views. When you enter this mode, the mouse point turns into a small cross.

3D Cursor mode can be used to precisely identify the position of a specific anatomical point on images acquired from different points of view.

This function is based on the fact that when two images do not lie on the same plane, the planes on which they lie intersect along a line; so each point on this line belongs to both images and can be displayed.

When you move holding the left mouse button pressed on an image, in the other views, the image that intersects with it will be positioned as the first image in the view (according to the layout, normally in the top left-hand corner). A small cross-centered at the point of the line of intersection of the two images indicated by the mouse point will appear on the current image.

Select Having selected this cursor, by clicking the left mouse button you can select an image of the study to make it the current one and select the objects laid on top of the images to modify or delete them.

Note: *To select more than one measurement with this tool, press and hold SHIFT when you left click.*

In this mode, the significant points of the measurement selected will be highlighted and you can move them, thus modifying the measurement, by clicking on them and dragging the mouse as required.

In addition, in this mode, when you double click on a selected measurement (other than the selection rectangle) you can change its properties. The program will display a window; in the **Text** box, you will be able to write some text that is to appear beside the measurement. The boxes below are used to choose whether to view on the image the text associated with the measurement,

the numerical data of the measurement and an index that uniquely represents the measurement on the current image.

Note: *The measurements for which the indication of their unique index may appear are those with which values that appear written on the image are associated. These measurements include distance, angle, angle between lines, circle, ellipse, polygon and echocardiographic measurements*.

Clicking on the **Properties…** button gives access to a window in which you can set the colour, thickness, type, effects and font size of the object selected.

Selection shows a rectangular area of interest on the image.

Move to a point on the image that corresponds to the top left-hand corner of the rectangular area and drag the mouse (whose point will now correspond to the bottom right-hand corner of the area) to define the shape of the rectangular area. When you release the left mouse button, some buttons will appear in the area, allowing you to activate the following functions:

- Print the part of the image lying within the rectangular area
- Copy a bitmap image containing the part of the image lying within the rectangular area to the Windows clipboard
- Apply the optimized window/level value calculated on the selected area to the image
- Remove the selection of the rectangular area.

You can change the size of the rectangle, by moving the mouse to the small squares highlighted on the border of the rectangle, clicking on them and dragging the mouse with its left button pressed. By clicking on the area lying within the rectangular area you can drag it onto the print preview so as to print the part of the image lying within this area.

MPR cursor enables you to navigate through the volume of the study shown in MPR mode.

Curved MPR present when the study is shown in 3D curved MPR mode, enables you to navigate through the volume of the study in such a way that the oblique plane follows curves (whether they are open polygons, closed polygons or lines) selected on the current view, if it is one of the three fundamental sections.

3D (present only if the study is displayed in 3D mode) enables you to navigate through the volume of the study.

Zoom

The submenu **Tools | Zoom** and the **Zoom** sheet of the **Tools** side panel list functions for scaling images up and down.

Zoom in increases the display scale of the image by a single unit. Starting from a 1:1 scale factor (also called *pixel view* or *normal view*), the enlargement factors are 2:1, 3:1, 4:1 and 5:1. *This same function can be performed by pressing the '+' key on the numeric keypad, or by left-clicking on an image while pressing the CTRL key.*

Zoom out reduces the display of the image by a scale unit. *This function can also be performed by pressing the '-' key on the numeric keypad, or by left-clicking on an image while pressing the CTRL key.*

Normal displays the image at a scale of 1:1 *(pixel view:* where one image pixel occupies exactly one screen pixel). *This function can also be performed by pressing the '/' key on the numeric keypad.*

Fit increases or decreases the display scale in such a way as to display the entire image in the view. This is the default display setting when the exam is opened. *This function can also be obtained by pressing the '*' key on the numeric keypad.*

Lens allows a zooming window to be opened and displayed at a given point on the image. The user must left click and hold in order to display the zoom window. Moving the mouse changes the zoomed area. *This function can also be obtained by pressing CTRL and the '+' key on the numeric keypad.*

When the Lens *function is enabled, you can change the zoom factor using the Up Arrow to increase it, Down arrow to reduce it, Left arrow to reduce the area and Right arrow to increase it.*

True size arranges displayes images so that all of these are in their true size, regardless of the size of the pixels of the images involved, which may also have different values. "True Size" means that the images are displayed in such a way that an object on them if measured with a ruler on the monitor has the physical dimensions as close as possible to the real size. Therefore, after you choose this feature, the current image and the images in the "Applies to..." range will zoom in so that the image size on the screen corresponds to the real size.

To enable this feature, configure the system by setting the dot pitch value (or dot pixel) of monitor used by MedStation in the win.ini file, adding the following section that specifies the dimensioned it in millimeters of a pixel video:

```
[PROGRAM]
DIMPIXELMONITOR=0.28
```

where 0:28 is the size in millimeters of a pixel of an example generic monitor.

When it is configured DIMPIXELMONITOR parameter in the [PROGRAM] section of the win.ini file, and if the images are properly calibrated, among the annotations shown on displayed images, next to the zoom percentage of the image - Pixel Size Magnification- will appear the percentage corresponding the relationship with the true size zoom - true size Magnification-.

***Note** Currently, you can specify a single calibration factor used on all system monitors. Therefore, to use this feature in a multi workstation, MedStation shall use identical monitors.*

Same size allows to display several images that all of them are mutually the same physical size, regardless of the size of the pixels of the images involved, which may also have different values. Following this, the display scale will be calculated so that the pixels on the screen of the images involved correspond to the same physical dimension in patient current image.

Starting from the current image in a box, each image involved in the range specified by "apply to..." will be scaled to a zoom such that the physical relative sizes of the images are the same (that means that the dimension of the caliper on images involved is identical) of the current image.

If in other boxes there are other studies, the same operation is applied to the current of each of these boxes and to the images in the range " apply to ..." of the current of each box.

Fit breast This feature allows the arrangement of mammography images displayed in different boxes with FIT breast profile (excluding side air zones) and subsequent display in "Same size" taking as reference the spacing of the largest profile.

The image of the breast that occupies more space within the view will be scaled so that the part of the air above, below and to the contour of the breast side is minimized (fit excluding the surrounding air), and all other views will be rescaled so as to have the same physical-dimension of this image.



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When some zoom functions are applied, image data are usually rescaled by interpolation algorithms and thus represent a processing of original data on the diagnostic device.

Measurements



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Users must have followed a training course held by qualified personnel and read this manual to be able use these tools properly.



Note: *You can select a measurement to modify the position of its points even if the cursor is not the Select tool described below. If the active function is the drawing of a measurement and you actually want to draw a new measurement rather than select one that has already been drawn and the new measurement is to be close to another, hold down CTRL when you left click for the first time.*

The submenu **Tools | Measurements** and the **Measurements** sheet of the **Tools** side panel can be used to added measurements, notes and symbols to the image.

Select allows you to select an image of the study to make it the current one and to select the objects overlaid on the images in order to change or delete them.

Note: *To select more than one measurement with this tool, press SHIFT when you left click.*

In this mode, the key points of the measurement selected can be highlighted; they can be moved by clicking on them and dragging, thus changing the measurement.

Furthermore, in this mode, you can change the properties of the measurement (different from the selection rectangle) selected by double clicking on it and thus accessing the relevant window.

The **Text** field allows text to be entered to accompany the measurement. Ticking the boxes below allows optional display of the text associated with the measurement on the image, the numerical data of the measurement itself, and an index providing univocal representation of the measurement on the current view.

Note: *Measurements with associated values (which are displayed written on the image) appear with an indication of their univocal index. These measurements include distance, angle, angle between lines, circle, ellipse, polygon and echocardiographic measurements.*

Click on the **Properties** button**…** to open a window allowing definition of colour, thickness, type, effects and font size for the selected object.

Distance measures the distance between two points in Euclidean space, in the patient reference system if the image is calibrated. The result is a real number, with two digits displayed after the decimal point.

The unit of measurement is the linear one defined by the calibration of the DICOM region in which two end points of the segment are inserted. The units of measure is pixels (*px*) if the image is not calibrated or if points are in different regions. The units of measure is not defined (*No Units*) if the calibration is different for the two direction of the region containing the points.

The user must choose a position on the current image and click on two points.

Right click while drawing the measurement to cancel the operation.

Angle measures the angle in degrees between three points, the result of which is a real number in degrees, with two digits displayed after the decimal point.

The unit of measurement is the degree.

You must position the cursor over the current image, click on the vertex and then two reference points defining the legs of the angle.

Right click while drawing the measurement to cancel the operation.

Angle between lines measures the angle in degrees between two line segments, even if their point of intersection cannot be seen in the area of the image. The result is a real number in degrees, with two decimal digits displayed.

The unit of measurement is the degree.

You must position the cursor over the current image and click on the vertices of the two line segments.

Right click while drawing the measurement to cancel the operation.

Cobb Angle a measurement used to assess deviations in scoliosis. An angle is measured in degrees and expressed as a real number with two decimal digits shown on the screen.

The unit of measurement is the degree.

You must position the cursor over the current image and click on the vertices of the two segments tangential to the superior end plate of the first vertebra and to the inferior end plate of the last vertebra of the scoliotic curve. The system will automatically draw the lines perpendicular to these two segments and the angle formed by the two perpendicular lines.

Right click while drawing the measurement to cancel the operation.

Area enables you to drawing a closed polygon inside the area of the image. Having positioned the cursor over the current image, each click ‘anchors’ a point of the polygon, allowing accurate tracing of any area of the image. Double click to terminate the drawing of the polygon.

Right click while drawing the measurement to cancel the operation.

The following are measured:

- The area and the perimeter. The results are real numbers, with two digits displayed after the decimal point. The perimeter's unit of measurement is the linear one defined by the calibration data of the image or a part of it that contains all the vertices of the polygon. The perimeter will be expressed in pixels (*px*) if no calibration data is present or the points are in different regions. The units of measure is not defined (*No Units*) if the calibration is different for the two direction of the region containing the points. The area will be expressed in *No Units* if the linear unit of measurement of the region containing all the vertices of the polygon is *No Units*, otherwise is the square of it.
- The maximum, the minimum, the average and the standard deviation of the values (Hounsfield numbers for CT images, *No Units* otherwise) of the pixels contained inside the area represented on a grayscale image; for color images these data will have no value.



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Note: *The algorithm measures the right area only if the polygon is not autointersecting.*

Open Polygon allows drawing of an open polygon inside the area of the image. Each click 'anchors' a point of the polygon. Double click to terminate the drawing of the polygon.

Right click while drawing the measurement to cancel the operation.

The following are measured:

The length of the polygon is measured. The result is a real number with two decimal digits shown on the screen.

The unit of measurement is the linear one defined by the calibration data of the image or a part of it containing all the points of the polygon. The length will be expressed in pixels (*px*) if no calibration data is present or if the points are in different regions. The length with be expressed in undefined units of measurement (*No Units*) if the units of measurement are different in the two directions of the plane containing the points.

Circle enables you to draw a circumference on the current image. The following are measured:

- The area, the perimeter and the radius. The results are real numbers, with two digits displayed after the decimal point. The units of measurement of perimeter and radius are the linear one defined by the calibration of the DICOM region in which two end points of the radius are inserted. The units of measure is pixels (*px*) if the image is not calibrated or if points are in different regions. The units of measure is not defined (*No Units*) if the calibration is different for the two direction of the region containing the points. Area's units of measurements is *No Units*, if perimeter's units of measurements is *No Units*, otherwise is the square of it.
- The maximum, the minimum, the average and the standard deviation of the values (Hounsfield numbers for CT images, *No Units* otherwise) of the pixels contained inside the circular area represented represented on a grayscale image; for color images these data will have no value.

You must position the cursor over the current image and clicks on the center and any point on the circumference.

Right click while drawing the measurement to cancel the operation.

Ellipse draws an ellipse and measures:

- The *area* and the *perimeter*. The results are real numbers, with two digits displayed after the decimal point. Perimeter's units of measurement is the linear one defined by the calibration of the DICOM region in which all four end points of the ellipse's axes are. The units of measure is pixels (*px*) if the image is not calibrated or if points are in different regions. The units of measure is not defined (*No Units*) if the calibration is different for the two direction of the region containing the points. Area's units of measurements is *No Units,* if perimeter's units of measurements is *No Units,* otherwise is the square of it.

You must position the cursor over the current image and click first on the two end points of one axis and then on any point identifying the eccentricity. Right click while drawing the measurement to cancel the operation.



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Note: *Measurement of the perimeter is only accurate within a given range, which may vary slightly depending on the zoom factor*.

Text inserts a text annotation. You must position the cursor over the current image and click on the upper left point for entering annotations. This opens a window for inserting text annotations.

Value shows the coordinates and the pixel value (which corresponds to the Hounsfield number in the case of CT images).

You must click on the relevant pixel to be queried.

Arrow inserts a symbol (a pointing arrow). You choose a position on the current image and click twice: first for the point at which the symbol is to be inserted, and second to define the direction of the arrow. Right click to cancel the operation.

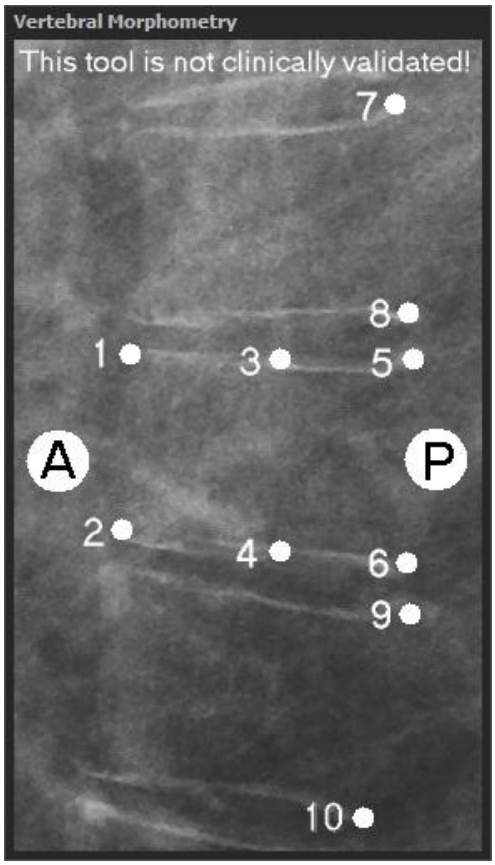
Ruler inserts a ruler.

You choose a position on the current image and click to define the end points of the ruler. Once the two end points have been set, a window appears enabling you to enter the value to be assigned to the two end points.

Right click to cancel the operation.

Vertebral Morphometry The purpose of this measurement is to identify vertebral fractures (in accordance with the definition of the Commissione Unica del Farmaco - Italian Pharmaceutical Commission). It implements a method used in clinical practice for establishing the anterior, middle and posterior measurements of the vertebral bodies of the thoracic and lumbar sections of the vertebral column in lateral projection.

When this measure is selected, a help window is opened (see below) to guide the physician in positioning the points of the vertebra under study.



The physician clicks on the points of the heights of the vertebrae under study and the posterior heights of the two adjacent vertebrae, inserting *in this order* the anterior height, middle height and posterior height of the vertebra in question, then the posterior heights of the two adjacent vertebrae above and below.

Note *The algorithm measures correctly the heights only if the user insert points in the right order as described.*

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Right click to cancel the operation.

After these ten points have been defined, the program will display a window in which you can choose the name of the vertebra under study.

Having selected the name of the vertebra, click OK and a window listing the data for the measurements performed will appear: the vertebral heights (*Ha* = anterior height, *Hm* = middle height, *Hp* = posterior height), the percentage ratio between the heights (*Ha/Hp, Hm/Hp, Hp/Hpp,* where *Hpp* is the average of the posterior heights of adjacent vertebrae). If one of these percentages is lower than 85%, the program signals the presence of a suspected vertebral fracture.

The units of measurement generally used for the vertebral heights taken are the linear one defined by the calibration of the DICOM region in which two end points of all segment are inserted. The units of measure is pixels (*px*) if the image is not calibrated or if points are in differ-

ent regions. The units of measure is not defined (*No Units*) if the units of measurement are different for the two direction of the region containing the points. The results are real numbers with two decimal digits shown on the screen.

To display the data regarding a given vertebra, select it and right click.

During use of this measurement, two buttons appear in the top left-hand corner of the view displaying the current image. The first of these can be used to copy (in text format) the information about all of the morphometric measurements performed on the image. The second clears the two buttons so that the measurement can be drawn.

Calibrate enables you to define the numerical ratio between the pixels and a real unit of measurement, that is, the distance that actually corresponds to a pixel of the image. For example, this ratio can be defined by positioning a ruler of a known length on the patient while the study is conducted.

Click on two control points (ends of the ruler) on the current image and enter in the field of the dialog box the distance between the two points indicated (length of the ruler) and the unit measurement that shall be *mm*.

Right click to cancel the operation.



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Note *This calibration is only correct for images that have pixels with the same distance and unit of measurement for height and length.*



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Calibration is fundamentally important to calculate the measurements correctly.

Spine Label *(labelling)* is a tool for assigning labels to points of an image in a semiautomatic way. This is particularly useful to highlight vertebral column segments.

Having images shown in the working area in 2D or MPR mode, select this tool and click on the first point in which you want to add a label. The program will display a window in which you can choose:

- the list of labels
- the first label on the list chosen
- the "forward" or "backward" order in which the following labels will be chosen
- the method of drawing the points corresponding to the labels

Click **Cancel** in this window to remove the labels. Otherwise, make your choices from this window and click on **OK** to initialize the figure and at each click a label will be assigned automatically to the point. Double click to terminate.

Right click while drawing to cancel the insertion of the figure.

You can modify lists of labels by editing configurations files installed with MedStation "<...>\Shared\Config\SpineLabelsList.xml" (which, by default, contains two lists, one with the names of the vertebral bodies from top to bottom and the other with the names of the intervertebral spaces) or the files of individual users that are created from this one. User files have names of the "SpineLabelsList_<username>.xml" type and are also located in the shared configura-

tion directory.
Show Shows the objects hidden by the Hide function.
Hide Hides objects.
Delete Removes all the objects of an image, having received confirmation from the user.
Options (Measurement preferences) *Independently for each type of measurement*, through the "Appearance" section, you can set the colour, thickness and font size of the new objects to be entered. Some measurements have extra fields that can be modified. For example, for some echocardiographic measurements in which the outlines of areas must be drawn precisely, you can choose the distance between one point and another entered by the program when the mouse is moved over the image and the precision with which the curve between one point the next is to be interpolated. For the "Cardiac Echo Area-Volume" measurement, there is another section for choosing the algorithm to be used to calculate the volume estimated on the basis of the area outlined by the user. If you want to *modify the properties shared by all measurements in a single operation*, press the "Preset" button in the bottom left-hand area. A window will be displayed, allowing you to set the colour, thickness, type, effects and font size of the new objects to be inserted. You can also choose whether to indicate a single value (on the image on which they have been drawn) beside each measurement for which associated values can be written on the image, so that the measurement and its values can always be distinguished from one another even if distant from one another. You can access the same window by double clicking on a selected measurement and then clicking on the **Properties…** button in the window that appears.
Send all simple measurements Function only available if MedStation is started through COM integration, used to send the caller a message with all the measurements made using the MedStation tools (present on the **Measurements** and **Cardiac Echo** menus) on the images of the study displayed.
Send all measurements Function only available if MedStation is started through COM integration, used to send the caller a message with all the measurements made using the MedStation tools (present on the **Measurements** and **Cardiac Echo** menus) on the images of the study displayed, and those made following a calculation performed using the *Calculator*.

Cardiac Echo



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Users must have followed a training course held by qualified personnel and read this manual to use these tools properly.



Note: *You can select a measurement to change the position of its points even if the cursor is not the Select tool described here below. If the active function is the drawing of a measurement and you actually want to draw a new measurement rather than select one that has already been drawn, when the new measurement must be close to another one, press and hold down the CTRL button when you left click.*

The submenu **Tools | Cardiac Echo** and the **Cardiac Echo** sheet on the **Tools** side panel enable you to make specific measurements for analysing echocardiographic images.

Select is used to select an image of the study to make it the current one and the objects overlaid on the images in order to change or delete them.

Note: *To select more than one measurement with this tool, press and hold down SHIFT when you left click.*

In this mode, the key points of the measurement selected will be highlighted. You can change the measurement by clicking on them and dragging them to different positions.

Furthermore, in this mode, you can change the properties of a measurement (other than the selection rectangle) selected by double clicking on it. The program will display a window with a **Text** field in which you can enter text to be placed alongside the measurement. The boxes below enable you to choose whether to display on the image the text associated with the measurement, the numerical data of the measurement and an index univocally representing the measurement on the current image.

Note: *The measurements for which the indication of the index may appear are those with associated values, which are displayed written on the image. These measurements include distance, angle, angle between lines, circle, ellipse, polygon and echocardiographic measurements.*

Click on the **Properties...** button to open a window that enables you to set the colour, thickness, type, effects and font size of the selected object.

Distance For 2D regions measures the distance between two points in Euclidean space, in the patient reference system if the image is calibrated. The result is a real number with two decimal digits shown on the screen.

The units of measurement is the linear one defined by the calibration of the DICOM region in which two end points of the segment are inserted. The units of measure is pixels (*px*) if the image is not calibrated or if points are in different regions. The units of measure is not defined (*No Units*) if the unit of measurement is different in the two direction of the region containing the points.

You must choose a position on the current image and click on two points.

Right clicking while drawing the measurement cancels the operation.

Distance in M-Mode. For MMode regions it draws a segment defined by two points selected on an echocardiographic (US) image, in an M-Mode region calibrated in seconds in the horizontal direction and in centimetres in the vertical direction. It measures:

- *Length*: the spatial distance between the ordinate of the two points. The units of measurement is the linear one in vertical direction (y) written DICOM in the calibration data of the region containing the points. The units is pixel (*px*) if the region is not calibrated

or if points are in different regions.

- *Time*: the temporal distance between abscissa of the two points. The units of measurement is the linear one in horizontal direction (x) written DICOM in the calibration data of the region containing the points. The units is pixel (*px*) if the region is not calibrated or if points are in different regions.
- *Slope*: the ratio between *Length* and *Time*. The units of measurement is that of *length* on that of *time* if different, *{ratio}* if they are the same.

M-Mode Diastole and **M-Mode Systole** For MMode regions: carry out M-Mode measurements for diastole and systole. Select one of these measurements and the cursor assumes the form of a large thin cross covering the entire image. Click once to insert the first measurement point and fix the vertical direction of the image along which the remaining points will be inserted successively (in all 5 for diastole and 4 for systole).

Diastole measurements:

- RVD (*Right Ventricular Internal Diastolic Dimension*): linear distance between the first two points inserted
- IVS (*Interventricular Septum Diastolic Thickness*): distance between the second and third points
- LVID (*Left Ventricle Internal End Diastolic Dimension*): distance between the third and fourth points
- LVPW (*Left Ventricle Posterior Wall Diastolic Thickness*): distance between the fourth and fifth points
- estimate of telediastolic volume: *Teicholz (Left Ventricular End Diastolic Volume)* using the formula derived from the Teicholz regression equation: $\frac{7}{2.4+LVID}\cdot LVID^3$. Units of measurement: millilitre (*ml*) if the region containing all points is calibrated in *s* in horizontal direction and *cm* in vertical direction, *No Units* otherwise
- estimate of mass of left ventricle *(Left Ventricle Mass by M-mode)* using the formula derived from the Devereux regression equation:

  $0.8\cdot 1.04\cdot[(LVID+LVPW+IVS)^3-LVID^3]+0.6$.

  Units of measurement: grams (*g*) if the region containing all points is calibrated in *s* in horizontal direction and *cm* in vertical direction, *No Units* otherwise

MMode *systole measurements*:

- IVS (*Interventricular Septum Systolic Thickness*): distance between the first and second points
- LVID (*Left Ventricle Internal Systolic Dimension*): distance between the second and third points
- LVPW (*Left Ventricle Posterior Wall Systolic Thickness*): distance between the third and fourth points
- estimate of volume: *Teicholz (Left Ventricular End Diastolic Volume)* using the formula

derived from the Teicholz regression equation: $\frac{7}{2{,}4 + LVID} \cdot LVID^3$. Units of measurement: millilitre (*ml*) if the region containing all points is calibrated in *s* in horizontal rection and *cm* in vertical direction, *No Units* otherwise

The measurement units for the linear measurements RVD, IVS, LVID, LVPW are defined by the linear calibration in vertical direction (y) of the DICOM region in which all points are inserted, or in pixel (*px*) if the image is not calibrated with *s* in x direction and *cm* in vertical direction or some points are in different regions.

The results are real numbers, with two decimal digits displayed accompanied by an indication of the unit of measurement.

Right clicking while drawing the measurement cancels the operation.

Area Volume For 2D regions, carry out monoplane measurements of the cardiac chambers.

Click to begin tracing the polygon outlining a cardiac chamber. The other points will be automatically inserted with cursor movement. Click to 'anchor' a point on the curve. This allows accurate tracing of any area of the image. Double click to close the outline with a segment.

Automatic insertion of points is achieved using a step and interpolation decided when setting the measurements up. The interpolation calculates a spline curve on the basis of the points inserted as the vertices of a polygon.

Right click while drawing the measurement to cancel the operation.

The measurements calculated are

- *Diameter* measures the length of the axis of the identified cardiac chamber in the patient reference system if the image is calibrated. The result is a real number, with two digits displayed after the decimal point. The units of measurement is the linear one defined by the calibration of the DICOM region in which all points of the shape are inserted. The units of measure is pixels (*px*) if the image is not calibrated or if points are in different regions. The units of measure is not defined (*No Units*) if the calibration is different for the two direction of the region containing the points.
- *Area* measures the area enclosed in the curve drawn on the image. The results are real numbers, with two digits displayed after the decimal point. Area's units of measurements is *No Units*, if perimeter's units of measurements is *No Units*, otherwise is the square of it.

⚠ ***Note:*** *The algorithm will only measures the area correctly if the polygon is not autointersecting*

- *Volume* estimates the volume (a real number, with two digits displayed after the decimal point) of the outlined cardiac chamber using one of the following methods
    - *Simpson monoplane:* a method that sums discs based on Simpson's rule. The overall volume is calculated as the sum of the volumes of about twenty superimposed and similarly shaped cylindrical sections: $\frac{\pi}{4}\sum_{i=1}^{20} d_i^2 \cdot \frac{Diameter}{20}$, where d_i = cylinders' diameters.

- *Area-Length:* a method which estimates the volume on the basis of the area (*A*) enclosed in the curved outline of the cardiac chamber and by the length of its axis (*L*) using the formula $\frac{8 \cdot A^2}{3\pi L}$

The unit of measurement of volume is millilitres (ml) if the region containing all the points is calibrated in *cm* as the linear unit of measurement, *No Units* otherwise.

Selecting the measurement, the axis of the cardiac chamber (the vertices are initially chosen by the program: the first at the mid-point of the closing segment and the second at the point of the curve furthest from this point) and the main points of the outline can be modified separately.

Biplane Volume For 2D regions enables you to transfer two polygons onto two 2D regions of one or two echocardiographic (US) images normally perpendicular to one another. These polygons create two "Area Volume" measurements using Simpson's Monoplane Rule with the configurations described in the previous section.

Then the global volume is calculated by the *Simpson's Biplane Rule*: the summation of 20 cylindrical sections perpendicular to the axis

$$\frac{\pi}{4} \sum_{i=1}^{20} a_i \cdot b_i \frac{\max(Diam_1, Diam_2)}{20}$$

a_i, bi = cylinder diameters

$Diam_1$, $Diam_2$ = long axes of the two polygons

The unit of measurement of the volume is that of the two volumes of the monoplane measurements. *No Units* otherwise.

PGrad Vel For Doppler images: draws a polygonal curve on an echocardiographic (US) image in a Doppler region calibrated in seconds (*s*) in the horizontal direction and centimetres per second (*cm/s*) in the vertical direction.

Click at a point of the image to begin tracing the outline polygon in the area of interest, and the remaining points are automatically inserted (with a pitch and interpolation set when the measurement was configured) with cursor movement. Another click 'anchors' a point of the curve. This allows accurate tracing of any area of the image. Double click to close the outline with a segment, the end points of which are then anchored on the baseline.

The measurements performed are:

- *Peak Velocity*. The maximum value of the vertical distance of the points of the curve from the baseline. The unit of measurement is not defined *(No Units)* if the region containing the points is not a Doppler region or has no baseline, otherwise the linear unit of measurement in the vertical direction (y) indicated by the calibration data of the image or a region of it containing the points.
- *Peak Gradient* indicates the pressure gradient corresponding to the peak velocity, calculated using the simplified Bernoulli equation: $4.V_{max}{}^2$. Unit of measurement: millimetres of mercury mmHg *(mm[Hg])*, if velocity is in cm/s, *No Units* otherwise.
- *Mean Velocity* The mean value of the velocities under the curve drawn. The unit of measurement is not defined *(No Units)* if the region containing the points is not a Doppler region or has no baseline, otherwise the linear unit of measurement in the vertical

direction (y) indicated by the calibration data of the image or a region of it containing the points.

- *Mean Gradient* calculates the mean of the pressure gradients corresponding to the velocity under the curve drawn, calculated using the simplified Bernoulli equation. Unit of measurement: millimetres of mercury mm[Hg] *(mm[Hg])*, if velocity is in cm/s, *No Units* otherwise.
- *VTI (Velocity Time Integral)* integral of the curve drawn. Unit of measurement: centimetres (*cm)* if the velocity is in *cm/s* and time is in *s. No Units* otherwise.

Velocity For Doppler regions: if the calibration region has, as units of measurement, seconds (s) on the x axis and centimetres per second (cm/s) on the y axis then, by inserting a point, this tool

- measures point velocity in a unit of measurement equal to the undefined unit of measurement (*No Units*) if the region is not a Doppler region or has no baseline, otherwise it is the linear unit of measurement in the vertical direction (y) indicated by the image calibration data or a region of it containing the point.
- measures the pressure gradients (for the point velocities) calculated using the simplified Bernoulli equation: $4.V^2$. The unit of measurement is millimetres of mercury mmHg *(mm[Hg])* if velocity is in *cm/s*, otherwise *No units*.

Time For Doppler regions: draws a segment identified by two points selected on an echocardiographic (US) image in a Doppler region calibrated in seconds in the horizontal direction and, by inserting two points, the tool measures

- *Time* as the interval between the times identified by the ends of the segment. Unit of measurement: not defined *(No Units)* if the region containing the point is not a Doppler region or has no baseline, otherwise it is the linear unit of measurement in the horizontal direction (x) indicated by the calibration data of the image or a region of it containing the points.
- *Peak Velocity* as the maximum distance of the two points from the baseline of the Doppler region. Unit of measurement: not defined *(No Units)* if the region containing the point is not a Doppler region or has no baseline, otherwise it is the linear unit of measurement one in vertical direction (y) indicated by the calibration data of the image or a region of it containing the points.
- *Slope* ratio between *velocity* and *time*. Units of measurement is given by the ratio between the unit of measurement of velocity and that of time, if different, *No Units* otherwise
- PHT (Pressure Half Time), calculated as the time necessary it takes for the maximum pressure gradient to drop to half its value. Unit of measurement: not defined *(No Units)* if the region containing the point is not a Doppler region or has no baseline, otherwise, it is the linear unit of measurement in the horizontal direction (x) indicated by the calibration data of the region containing the points.
- *MVA (Mitral Valve Area)*: Estimates the mitral valve area on the basis of the pressure half time: $220/(PHT[s]\cdot 1000)$. The units of measurement is cm^2 if PHT is in *s*, *No Units* otherwise.

Deceleration time For Doppler regions: click to begin tracing the outline polygon in the area of interest, and the remaining points are automatically inserted with cursor movement. Another click 'anchors' a point on the curve. This allows accurate tracing of any area of the image. Double click to close the outline with a segment, the end points of which are then anchored on the baseline. Automatic insertion of points is achieved using a step and interpolation decided when configuring the measurements. The interpolation calculates a spline curve on the basis of the points inserted as the vertices of a polygon.

The following flow curve measurements are made:

- All *PGrad Vel measurement values*
- *peak velocity E*: the maximum velocity measured along the highlighted outline (distance between the maximum peak of the curve and the baseline). The units of measurement is the linear one in vertical direction (y) written in the DICOM calibration data of the region containing the points. The units is not defined *(No Units)* if the region is not calibrated or is not a Doppler region or if hasn't the baseline or if points are in different regions
- *peak velocity A*: the velocity measured at the second peak on the curve (distance between the second peak and the baseline). The units of measurement is the linear one in vertical direction (y) written in the DICOM calibration data of the region containing the points. The units is not defined *(No Units)* if the region is not calibrated or is not a Doppler region or if hasn't the baseline or if points are in different regions
- *E/A* ratio between the two velocities measured at the peaks of the curve. The units of measurement is *{ratio}*
- *DecT* measures the deceleration time of the wave E; extrapolating the deceleration of the flow at the baseline and measuring the time between the peak of velocity E and the extrapolation at the baseline of the deceleration. The units of measurement is the linear one in horizontal direction (x) written in the DICOM calibration data of the region containing the points. The units is not defined *(No Units)* if the region is not calibrated or is not a Doppler region or if hasn't the baseline or if points are in different regions

Right click while drawing the measurement to cancel the operation.

Acceleration time For Doppler regions: click to begin tracing the outline polygon in the area of interest, and the remaining points are automatically inserted with cursor movement. Another click 'anchors' a point on the curve. This allows accurate tracing of any area of the image. Double click to close the outline with a segment, the end points of which are then anchored on the baseline. Automatic insertion of points is achieved using a step and interpolation decided when configuring the measurements. The interpolation calculates a spline curve on the basis of the points inserted as the vertices of a polygon.

The following flow curve measurements are made:

- All *PGrad Vel measurement values*
- *ET(Ejection Time):* Time from first to last points of the polygonal. The units of measurement is the linear one in horizontal direction (x) written in the DICOM calibration data of the region containing the points. The units is not defined *(No Units)* if the region is not calibrated or is not a Doppler region or if hasn't the baseline or if points are in dif-

ferent regions

- *AccT (Acceleration Time)* Time from the beginning to the apex of the flow. The units of measurement is the linear one in horizontal direction (x) written in the DICOM calibration data of the region containing the points. The units is not defined *(No Units)* if the region is not calibrated or is not a Doppler region or if hasn't the baseline or if points are in different regions
- *AccT/ET* ratio between the two times. The units of measurement is *{ratio}*

Right click while drawing the measurement to cancel the operation.

PHT (Pressure Half Time) For Doppler regions: click to begin tracing the outline polygon in the area of interest and the remaining points are automatically inserted with cursor movement. Another click 'anchors' a point on the curve. This allows accurate tracing of any area of the image. Double click to close the outline with a segment the end points of which are then anchored on the baseline. Automatic insertion of points is achieved using a step and interpolation decided when configuring the measurements. The interpolation calculates a spline curve on the basis of the points inserted as the vertices of a polygon.

The following PHT measurements are made:

- All *PGrad Vel measurement values*
- *half maximum pressure gradient*: $\frac{PGrad_{\max}}{2}$. Unit of measurement: millimetres of mercury mmHg *(mm[Hg])*, if the velocity is in cm/s (the unit of measurement in the vertical direction (y), *No Units* otherwise.
- *relative velocity at half pressure gradient* is estimated using the formula $v = 0.7\ v_{max.}$ Unit of measurement: not defined (*No Units*) if the region containing the points is not a Doppler region or has no baseline, otherwise it is the linear unit of measurement in the vertical direction (y) indicated by calibration data of the image or a region of it that contains the points
- PHT (Pressure Half Time) calculated as the time necessary it takes for the maximum pressure gradient to drop to half its value. Unit of measurement: not defined *(No Units)* if the region containing the point is not a Doppler region or has no baseline, otherwise, it is the linear unit of measurement in the horizontal direction (x) indicated by the calibration data of the image or a region of it containing the points
- MVA (Mitral Valve Area): Estimates the mitral valve area on the basis of the pressure half time: $220/(PHT[s]\cdot 1000)$. The units of measurement is cm^2 if PHT is in *s*, *No Units* otherwise

Right click while drawing the measurement to cancel the operation.

Show displays objects hidden using the Hide function.

Hide hides the objects.

Delete cancels all objects within the image having received confirmation from the user.

Options (Measurement preferences) *independently for each type of measurement*, using the "Appearance" section, you can set the colour, thickness and font size of new objects to be inserted.

Some measurements have some extra fields that can be modified. For example, for some echocardiograph measurements that require the outlines of areas to be traced accurately, the distance between one point and another inserted by the program can be chosen as the cursor moves over the image and the precision with which the curve is interpolated between one inserted point and the next one. In the case of the "Cardiac Echo Area-Volume" measurement, there is an additional field for the selection of the algorithm for calculating the estimated volume on the basis of the area outlined by the user.

If *the properties shared by all measurements are to be changed simultaneously,* press the "Preset" button in the bottom left-hand area. This displays a panel (similar to that shown below) that enables you to set the colour, thickness, type, effects and font size of new objects to be inserted. It is also possible to choose whether a univocal value is to be displayed next to each measurement (in the image on which it has been drawn) that may have associated values written on the image, in such a way that the measurement and its values are always distinguishable even if distant from each another.

Double click on the selected measurement in the same dialog box to display a new window and click the **Properties…**button.

Send all simple measurements Function only available if MedStation is started through COM integration, used to send the caller a message with all the measurements made using the MedStation tools (present on the **Measurements** and **Cardiac Echo** menus) on the images of the study displayed.

Send all measurements Function only available if MedStation is started through COM integration, used to send the caller a message with all the measurements made using the MedStation tools (present on the **Measurements** and **Cardiac Echo** menus) on the images of the study displayed, and those made following a calculation performed using the *Calculator*.

Derived measurements and calculations[27]



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Users must have followed a training course held by qualified personnel and read this manual to use these tools properly.



Calculator environment

The system has a *calculator* for performing mathematical operations of various kinds. It was designed, in particular, for use together with the measurements made on one or more images displayed, thus performing derived calculations.

Some preset lists of measurements and formulae are provided and the user can define new

[27] Function available only in MedStation but not in MedStation Express.

measurements and/or calculations.
The "calculator" environment has a user interface on the **Calculator** side panel. The user interface is divided into areas, one of which shows the trees containing the preset measurements and calculations and any user-defined tree created. Every formula is identified by

- a label
- a code
- the actual formula made up of numeric constants, mathematical operators and codes of other formulas
- the unit of measurement in which the value of the formula calculated will be returned.
  A second area of the window shows the log of the operations performed using the calculator. Below this area there is a list of the labels for the measurements that are being made and that are used in the formula, chosen by double clicking on an item on the tree structure. Finally, there is a command line. You can interact with the tree of definitions and instances of variables, measurements and calculations using a shortcut menu, which contains commands for cloning, deleting and removing the formulae.

Managing measurements and calculations using the calculator
The system manages lists of measurements and calculations.
We call ***measurement*** a label that recalls a measuring tool (of those described in previous sections) and obtains one of the possible return values with the unit of measurement.
We call a ***calculation*** a label with which is associated a mathematical formula that involves constants, measurement values and/or other calculations (measurements and calculations chosen from the same lists provided).
When the system is installed, a list of measurements and a list of calculations available to all users are provided in one or more configuration files.


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Note: *The definitions of preset measurements and calculations provided with the product installation have not yet been clinically validated and serve simply as examples of some possible definitions. This validation is to be performed by the user who, in each plant in which the system is to be installed, will reconfigure the definitions of the measurements and calculations that will be used.*

Each user can configure his own list, which will be saved to a file in the system's configuration.
The structure of these files will permit the classification of measurements and calculations in subsets (for example, according to the type of image on which the measurements are to be made: 2D, MMode, Doppler,...). When the program is started, the configuration files containing the definitions of measurements and calculations are read, interpreted and loaded from the folder containing the shared system configuration. When you open the "Calculator" panel, you will see that a part of this sheet contains the tree structures with the definitions. Two branches will be present, a "variables" branch with the definitions of the measurements and a "formulae" branch with the definitions of the calculations. There will be a third branch if the user logged on to the system has saved his own definitions of measurements and calculations.

Making measurements and performing calculations using the calculator
Having opened a study for viewing, on the "calculator" sheet, browse through the tree with the definitions of the measurements (*Variables*) and calculations (*Formulae*), select a measurement and a calculation and double click on the *label*.

Making a measurement

If you choose a *measurement*, the system automatically sets the mode for drawing the measurement corresponding to the one chosen and, in the calculator environment, clones the definition, thus creating the instance of the measurement that will receive the value. Having drawn the measurement, the value and the unit of measurement of the instance, they will appear in the calculator environment and then the cursor will be set in figure selection mode.

Performing a calculation

If a *calculation* is chosen, the system automatically sets the mode for drawing the measurements necessary to assess the formula corresponding to the calculation chosen and, in the calculator environment, clones the definitions of the calculation and each measurement required, thus creating the new instances that will receive the values. Once each measurement has been drawn, its value and unit of measurement will appear in the calculator environment and the cursor will be set in figure selection mode. All the values and units of measurement of the single measurements and the value of the calculation will be indicated if no errors occurred during the assessment of the measurements (any errors and related descriptions are recorded in the log section of the calculator). In particular, the assessment of the formula checks the units of measurement of its variables and will only return the correct result if all the units of measurement of the instances measured correspond to those declared in the definition of the formula.

Changes and deletions

All changes made to the measurements on the images are reflected on measurements / calculations in the calculator environment.

If the points of a measurement are moved, its values may change and so the instance of the measurement with which this value has been associated must also be changed. If this instance is used in the formula of a calculation, this calculation will also have to be reassessed and its value modified.

If a measurement is deleted, the instance of the measurement with which one of its values has been associated is also removed from the calculator environment. If this instance is used in a calculation, the latter will have to be reassessed and, as it no longer has all the elements necessary for the formula to be assessed correctly, the instance of the calculation is removed from the calculator environment.

Backing up and restoring calculator data

When a study on which measurements and/or calculations have been performed is saved, the presentation state will contain all the information necessary to restore the calculator environment, when the study is reopened. In this way, the next time the study is opened, the images will be loaded complete with all the measurements made and the calculator environment will restore all the links between measurements and calculations, indicating all the instances measured and assessing the formulae of which they may be variables. At this point, all the changes to measurements on the images (movement of the characteristic points of the figure, deletion) will be reflected in the measurements/calculations. If the study is saved subsequently, the current situation of the study and the calculation will be recorded in a new presentation state.

Warning! *All and only the formulae associated with a single study will be saved. Any measurements made involving more than one study will not be saved.*

Using the command line of the calculator

From the command line of the calculator you can write expressions in accordance with the rules described above and also invoke commands.

Variables

You can define *variables*, which are identified by a letter followed by alphanumeric characters, "_" or "::". These variables can be assigned expressions of all kinds and measurement/calculation labels. The expressions of the variables may contain a numerical value, a formula or one of the return values of a measurement or calculation. A variable may have more than one instance, each of which is defined by a uniquely generated number

Note: *The calculator is case-sensitive, so V1 and v1 are two different variables. Only measurements and their return values have been made independent of their case.*

Comparison between expressions

You can compare expressions, returning a different value according to a specific condition. The syntax is *if (exp1 op exp2) exp3 else exp4*, where *expN* are the various expressions and *op* is a comparative operation between them: >, >=, <, <=, *!*=.

For example, for the definition *L1 = Line.length* and *L2 = Line.length*, you can write

if (L1 > L2) L1 else L2.

Commands

From the command line or in some functions that can be activated from a shortcut menu, the following commands are available: assign, *-desc, remove, clear.*

- **Assign**

Used to assign a value to a variable. The value may be a constant, the return value of a MedStation measurement, or a formula.

Examples

- *a = 3.14*
- *L=Line.LENGTH*
- *A = 2*pi*R^2*

- **Desc**

Used to change the description (*description* attribute of the definition) of a label.

Examples

- *desc MedstMeasurement::LUNGMILZA = "Length of spleen "*

- **Remove**

Used to remove a variable from the calculator's memory. If a formula is removed, the values of the variables that use this calculation will also be removed.

Examples

- { R ← 8, A ← 2*pi*R^2} before

  remove A: { R ← 8} after

- **Clear**

Used to delete the value of a variable

Examples

- { R ← 8, A ← 2*pi*R^2} before

  clear A

  { R ← 8, A ← } after

Note: *The formulae inserted from the command line of the calculator are also saved when a study is backed up but they cannot be used to elaborate new calculations or measurements. To do this, you must define your own calculation model file.*

Composition of formulae and derived calculations

The formulae managed by the calculator follow the canonical infix notation involving, through the operators and functions listed below, constants, variables and labels of measurements and calculations preset in the configuration files.

The constants recognized are

pi	Pi
e	Euler's constant

The operators

+	sum
-	subtraction
*****	multiplication
/	division
^	exponential
||	absolute value

Single-parameter functions

sqrt(x)	Square root
sin(x)	Sine
cos(x)	Cosine
tan(x)	Tangent
round(x)	Rounding
ln(x)	Natural logarithm
log(x)	Common logarithm
abs(x)	Absolute value

Two-parameter functions

pow(x,y)	Exponentiation

N-parameter functions

min(a0,a1,a2,...,an)	Minimum
max(a0,a1,a2,...,an)	Maximum

Examples

- *ln(1+cos(pi))*

- *4/3*pi*(((MedstMeasurement::LUNGMILZA)/2)*((MedstMeasurement::LARGMILZA)/2)*((MedstMeasurement::ALTMILZA)/2))*
- *Log 10*

Unit of measurement

Using the assignment operation, you can set a unit of measurement for a given variable. In this way, if this unit is not respected in a calculation, it will be blocked and an error signalled.

Examples

- R[cm] = 8
- G[cm/s2] = 981
- G("Gravita")[cm/s2] = 981

In addition to assignments, you can use units of measurement within a formula, requesting that a given variable conforms to the unit chosen. To do this, simply follow the variable to be controlled with square brackets enclosing the chosen unit of measurement.

Examples

- A = 2*pi*R[cm]^2

List of all units of measurement supported

- **1** no unit
- **%** percentage
- **dB(A)** decibel
- **dB** decibel
- **m** meter
- **mm** millimetre
- **cm** centimetre
- **g** gram
- **s** second
- **Hz** Hertz
- **dB/s** decibel per second
- **cm/s** centimetre per second
- **cm2** square centimetre
- **cm2/s** square centimetre per second
- **cm3** cubic centimetre
- **cm3/s** cubic centimetre per second
- **cm/s2** centimetre per square second
- **°** degree
- **deg** degree
- **[hnsf´U]** Hounsfield unit
- **[hu]** Hounsfield unit
- **m/s** meter per second
- **m/s2** meter per square second
- **mm[Hg]** millimetre of mercury
- **mmHg** millimetre of mercury

- **mm2** square millimetre
- **mm3** cubic millimetre
- **ml** millilitre
- **ml/s** millilitre per second
- **ms** millisecond
- **{pixels}** pixel
- **px2** square pixel

Note: *When using derived variables and calculations, the units of measurement are not calculated. For example, 1000 millimetres will not be equivalent to 1 meter. Each formula will check the units of measurement of the variables involved in it and will return one, if specified manually. Consequently, if you declare "a[mm] = 1000", using "a[cm]" as in F = a[cm] * 10 an error will be signalled. If you declare the following variables "L= Line.Length" and "F[mm] = 4/3*pi * L" F will be expressed in millimetres even if the unit of measurement of L is not checked.*

Values that can be used in defining measurements

- *Distance*
  - Line.LENGTH (*Length*)
- *Angle*
  - Angle.ANGLE (*Angle*)
- *Angle between lines*
  - AngleLine.ANGLE (*Angle*)
- *Cobb angle*
  - CobbAngle.ANGLE (*Angle*)
- *Polygon*
  - Polygon.AREA (*Area*)
  - Polygon.PERIMETER (*Perimeter*)
  - Polygon.AVG (*Mean*)
  - Polygon.DEV (*Standard deviation*)
  - Polygon.MAX (*Maximum*)
  - Polygon.MIN (*Minimum*)
- *Circle*
  - Circle.RADIUS (*Radius*)
  - Circle.AREA (*Area*)
  - Circle.PERIMETER (*Perimeter*)
  - Circle.AVG (*Mean*)
  - Circle.DEV (*Standard deviation*)
  - Circle.MAX (*Maximum*)
  - Circle.MIN (*Minimum*)
- *Ellipse*
  - Ellipse.PERIMETER (*Perimeter*)
  - Ellipse.AREA (*Area*)
- *Morphometry*
  - Morphometry.HA (*Ha, Anterior vertebral height*)
  - Morphometry.HM (*Hm, Central vertebral height*)
  - Morphometry.HP (*Hp, Posterior vertebral height*)

    - Morphometry.HPP (*Hpp, Mean of two adjacent posterior vertebral heights*)
    - Morphometry.HA_HP (*Ha/Hp*)
    - Morphometry.HM_HP (*Hm/Hp*)
    - Morphometry.HP_HPP (*Hp/Hpp*)
- *Distance in MMode*
    - MModeLine.LENGTH (*Length*)
    - MModeLine.MMODETIME (*Time*)
    - MModeLine.DERIVATIVE (*Slope*)
- *MMode in diastole*
    - MModeDiastole.RVD (*Right Ventricular Internal Diastolic Dimension*)
    - MModeDiastole.IVS (*Interventricular Septum Diastolic Thickness*)
    - MModeDiastole.LVID (*Left Ventricle Internal End Diastolic Dimension*)
    - MModeDiastole.LVPW (*Left Ventricle Posterior Wall Diastolic Thickness*)
    - MModeDiastole.TEICHOLZ (*Left Ventricular End Diastolic Volume with Teicholz*)
    - MModeDiastole.MASS (*Left Ventricle Mass by M-mode*)
- *MMode in systole*
    - MModeSistole.IVS (*Interventricular Septum Systolic Thickness*)
    - MModeSistole.LVID (*Left Ventricle Internal Systolic Dimension*)
    - MModeSistole.LVPW (*Left Ventricle Posterior Wall Systolic Thickness*)
    - MModeSistole.TEICHOLZ (*Left Ventricular End Systolic Volume with Teicholz*)
- *Area Volume*
    - EcoCardioAreaVolume.AREA (*Area*)
    - EcoCardioAreaVolume.DIAMETER (*Diameter*)
    - EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO) (*Volume with Simpson's moneplane rule*)
    - EcoCardioAreaVolume.VOLUME(ELLIPSOIDSINGLEPLANE)(*Volume with "Area-Length"*)
- *Volume with Simpson's Biplane Rule*
    - EcoCardioBiplaneVolume.VOLUME (*Volume*)
- *Velocity*
    - EcoCardioVelocityMeasure.VELOCITY (*Velocity*)
    - EcoCardioVelocityMeasure.PRESSUREGRAD (*Pressure gradient*)
- *Time*
    - EcoCardioTimeMeasure.TIME (*Time*)
    - EcoCardioTimeMeasure.MAXVELOCITY (*Maximum velocity*)
    - EcoCardioTimeMeasure.PHT (*Pressure Half Time*)
    - EcoCardioTimeMeasure.MVA (*Mitral Valve Area (PHT)*)
    - EcoCardioTimeMeasure.DERIVATIVE (*Slope*)
- *Velocity and pressure gradients*
    - EcoCardioPressureGradient.PEAK_VEL (*Peak velocity*)
    - EcoCardioPressureGradient.PEAK_GRAD (*Peak gradient*)
    - EcoCardioPressureGradient.MEAN_VEL (*Mean velocity*)
    - EcoCardioPressureGradient.MEAN_GRAD (*Mean gradient*)
    - EcoCardioPressureGradient.VTI (*Time-Velocity integral*)
- *PHT (Pressure Half Time)*
    - EcoCardioPressureHalfTime.PEAK_VEL (*Peak velocity*)
    - EcoCardioPressureHalfTime.PEAK_GRAD (*Peak gradient*)

    - EcoCardioPressureHalfTime.MEAN_VEL (*Mean velocity*)
    - EcoCardioPressureHalfTime.MEAN_GRAD (*Mean gradient*)
    - EcoCardioPressureHalfTime.VTI (*Time-Velocity integral*)
    - EcoCardioPressureHalfTime.HALF_GRAD (*Half maximum pressure gradient*)
    - EcoCardioPressureHalfTime.HALFGRAD_VEL (*Velocity at half maximum pressure gradient*)
    - EcoCardioPressureHalfTime.PHT (*Pressure Half Time*)
    - EcoCardioPressureHalfTime.MVA (*Mitral Valve Area (PHT)*)
- *Deceleration time*
    - EcoCardioDecelerationTime.PEAK_VEL (*Peak velocity*)
    - EcoCardioDecelerationTime.PEAK_GRAD (*Peak gradient*)
    - EcoCardioDecelerationTime.MEAN_VEL (*Mean velocity*)
    - EcoCardioDecelerationTime.MEAN_GRAD (*Mean gradient*)
    - EcoCardioDecelerationTime.VTI (*Time-Velocity integral*)
    - EcoCardioDecelerationTime.PEAK_VEL_E (*Peak velocity E*)
    - EcoCardioDecelerationTime.PEAK_VEL_A (*Peak velocity A*)
    - EcoCardioDecelerationTime.RATIO_EA (*E/A*)
    - EcoCardioDecelerationTime.DECTIME (*Deceleration time*)
- *Acceleration time*
    - EcoCardioAccelerationTime.PEAK_VEL (*Peak velocity*)
    - EcoCardioAccelerationTime.PEAK_GRAD (*Peak gradient*)
    - EcoCardioAccelerationTime.MEAN_VEL (*Mean velocity*)
    - EcoCardioAccelerationTime.MEAN_GRAD (*Mean gradient*)
    - EcoCardioAccelerationTime.VTI (*Time-Velocity integral*)
    - EcoCardioAccelerationTime.ET (*Ejection time*)
    - EcoCardioAccelerationTime.ACCTIME (*Acceleration time*)
    - EcoCardioAccelerationTime.RATIO_ACCTET (*AccT/EjT*)

Most measuring tools have more than one return value. For the calculator to be able to access more than one return value when making a single measurement, you must declare a variable without attributes and then use it as an instance of the measurement followed by the return value that you wish to access.

Examples

- C=Circle
- C1=C->AREA
- C2=C->PERIMETER
- C1+C2

In this way, if you recall the formula C1+C2 you will be prompted to draw one circle only and the value of both the area and the circumference will be taken into consideration. *Note: Only recalling the C1 + C2 formula, the variables C1 and C2 are instantiated and only one measuring circle tool will give value to both of these variables. By directly invoking the variable C, the circle tool will be activated but will not add value to C1 and C2.*

Calculator error messages

The following errors may occur while making a measurement or a calculation.

- *Different size*: if one of the units of measurement have not been respected. For example, if

the return value of a measurement involved has any unit of measurement other than the one indicated in the definition of the formula being applied.

- *Unknown size*: if one of the units of measurement is unknown. For example, if the return value of a measurement involved has a unit of measurement not present on the list of units of measurement.
- *Null variable*: if you have tried to perform an operation with a variable that has no value. For example, if you request the execution of a formula but before starting to execute it you request a different one, or if you try to assess a formula whose variables have not yet been set.
- *Invalid operand*: if one of the operands has an invalid value.
- *Invalid left operand*: if the left operand is not valid.
- *Invalid right operand*: if the right operand is not valid.
- *Unknown operation*: Invalid operation.

User measurements

Each user can define a calculation model file of his own, it must be named *MedstUsers_<username>.xml* and must be located in the shared configuration folder. To create it you can start from one of the preset files, an example of which is given below:

```
<calculationsDictionary xmlns="MedstMeasurement" codeScheme="MedstMeasurementUsers" code-
Value="MSTMEAS_ADMIN" codeMeaning="Misurazioni MedStation- Admin" codeSchemeVersion="1.0">
<calculationsSet codeScheme="MedstMeasurementUsers" codeValue="2D" codeMeaning="Immagini 2D">
<calculationsSet codeScheme="MedstMeasurementUsers" codeValue="DIMENSIONI" codeMean-
ing="Dimensioni">
<calculation codeScheme="MedstMeasurementUsers" RegionSpatialFormat="" RegionDataType="" code-
Value="RADIUS" codeMeaning="Raggio" description="Raggio della sfera" example="" unitOfRe-
sult="mm">Line.LENGTH
</calculation>
<calculationsSet codeScheme="MedstMeasurementUsers" codeValue="AREE" codeMeaning="Aree">
<calculation codeScheme="MedstMeasurementUsers" codeValue="EQUATOR_AREA" codeMeaning="Area
Equatore" description="Area Equatore" example="" unitOfResult="mm2">
pi * (MedstMeasurementUsers::RADIUS[mm])^2
</calculation>
</calculationsSet>
<calculationsSet codeScheme="MedstMeasurementUsers" codeValue="VOLUMI" codeMeaning="Volumi">

<calculation codeScheme="MedstMeasurementUsers" codeValue="SPHERE_VOLUME" codeMeaning="Volume
Sfera code" description="" example="" unitOfResult="mm3">
(4 / 3) * pi * (MedstMeasurementUsers::RADIUS[mm]/10)^3
</calculation>
</calculationsSet>
</calculationsSet>
</calculationsSet>
</calculationsDictionary>
```

Preset measurements (still to be validated)

- 2D/Colour
  - *Size*
    - **LVOT diam** codeValue=DIAMLVOT, Line.LENGTH
    - **Ao rad. Diam. (2D)** codeValue=DIAMRADAO2D, Line.LENGTH
    - **LA size (2D)** codeValue=DIMENSLA2D, Line.LENGTH
  - *Vessels*
    - **Ascend. Ao diam.** codeValue=DIAMAOASC, Line.LENGTH
    - **Descend. Ao diam.** codeValue=DIAMAODISC, Line.LENGTH
    - **MPA diam.** codeValue=DIAMMPA, Line.LENGTH
    - **RVOT diam.** codeValue=DIAMRVOT, Line.LENGTH

- *EF and Volume*
  - *Simpson*
    - **LAd vol** codeValue=LADVOL, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
    - **LAs vol** codeValue=LASVOL, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
    - **EDV (A2C)** codeValue=EDVA2C, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
    - **ESV (A2C)**codeValue=ESVA2C, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
    - **EDV (A4C)** codeValue=EDVA4C, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
    - **ESV (A4C)**codeValue=ESVA4C, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
    - **EDV (BP)** codeValue=EDVBP, Cardiac EchoBiplaneVolume.VOLUME
    - **ESV (BP)** codeValue=ESVBP, Cardiac EchoBiplaneVolume.VOLUME
  - *A/L*
    - **EDV (A/L)** codeValue=EDVAL, EcoCardioAreaVolume.VOLUME(ELLIPSOIDSINGLEPLANE)
    - **ESV (A/L)** codeValue=ESVAL, EcoCardioAreaVolume.VOLUME(ELLIPSOIDSINGLEPLANE)
- *Mass*
  - **LVAd Sax Endo** codeValue=LVADSAXENDO, Polygon.AREA
  - **LVAd Sax Epi** codeValue= LVADSAXEPI, Polygon.AREA
  - **LVLd apical** codeValue= LVLDAPICAL, Polygon.AREA
- *Valves*
  - **AV area** codeValue= AREAAV, Polygon.AREA
  - **RVOT diam.** codeValue= DIAMRVOT, Line.LENGHT
  - **TV diam.** codeValue= DIAMTV, Line.LENGHT
  - **MV area (planim.)** codeValue= AREAMV, Polygon.AREA
  - **PISA (AI)**
    - **LVOT diam.** codeValue= DIAMLVOT, Line.LENGHT
    - **AI radius** codeValue= RADIUSAI, Line.LENGHT
    - **AI alias. vel.** codeValue= VELALIASAI, EcoCardioVelocityMeasure.VELOCITY
  - **PISA (MR)**
    - **MV diam.** codeValue= DIAMMV, Line.LENGHT
    - **MR radius** codeValue= RADIUSMR, Line.LENGHT
    - **MR alias. vel.** codeValue= VELALIASMR, EcoCardioVelocityMeasure.VELOCITY
  - **MVA (PISA)**
    - **MV radius** codeValue= RADIUSMV, Line.LENGHT
    - **MV alias. vel.** codeValue= VELALIASMV, EcoCardioVelocityMeasure.VELOCITY
- *Atrium*
  - *Left atrium*

- **LAd vol** codeValue= LADVOL, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
- **LAs vol** codeValue= LASVOL, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
- **LA size (2D)** codeValue= DIMENSLA2D, Line.LENGHT
- **LA area** codeValue= LAAREA, Polygon.AREA
- **LA volume** codeValue= VOLUMELA, EcoCardioAreaVolume.VOLUME(ELLIPSOIDSINGLEPLANE)

▪ *Right atrium*

- **RAd vol** codeValue= RASVOL, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
- **RAs vol** codeValue= RADVOL, EcoCardioAreaVolume.VOLUME(SIMPSONMONOPLANO)
- **Rad size (2D)** codeValue= DIMENSRAD2D, Line.LENGHT
- **RAs size (2D)** codeValue= DIMENSRAS2D, Line.LENGHT
- **RAd Area** codeValue= RADAREA, Polygon.AREA
- **RAd volumed** codeValue= VOLUMERAD, EcoCardioAreaVolume.VOLUME(ELLIPSOIDSINGLEPLANE)
- **RAs volume** codeValue= VOLUMERAS, EcoCardioAreaVolume.VOLUME(ELLIPSOIDSINGLEPLANE)

o *Kidney*

▪ **Kidney height** codeValue=ALTRENE, Line.LENGTH
▪ **Kidney width** codeValue= LARGRENE, Line.LENGTH
▪ **Kidney length** codeValue= LUNGRENE, Line.LENGTH

o *Spleen*

▪ **Spleen height** codeValue=ALTMILZA, Line.LENGTH
▪ **Spleen width** codeValue= LARGMILZA, Line.LENGTH
▪ **Spleen length** codeValue= LUNGMILZA, Line.LENGTH

o *Bladder*

▪ **Bladder height** codeValue=ALTVESCICA, Line.LENGTH
▪ **Bladder width** codeValue= LARGVESCICA, Line.LENGTH
▪ **Bladder length** codeValue= LUNGVESCICA, Line.LENGTH
▪ **Post-mict. bladder height** codeValue= ALTVESCICAPOSTMINZ, Line.LENGTH
▪ **Post-mict. bladder width** codeValue= LARGVESCICAPOSTMINZ, Line.LENGTH
▪ **Post-mict. bladder length** codeValue= LUNGVESCICAPOSTMINZ, Line.LENGTH
▪ **Lat. bladder** codeValue= VESCICALAT, Line.LENGTH

o *Liver*

▪ **Liver length** codeValue= LUNGFEGATO, Line.LENGTH

o *2D measurements*

▪ **Ao. arch diam..** codeValue= DIAMARCAO, Line.LENGTH
▪ **Ao isthmus diam.** codeValue= DIAMISTMOAO, Line.LENGTH
▪ **LPA diam.** codeValue= DIAMLPA, Line.LENGTH
▪ **RPA diam.** codeValue= DIAMRPA, Line.LENGTH
▪ **IVSd (2D)** codeValue= IVSD2D, Line.LENGTH
▪ **IVSs (2D)** codeValue= IVSS2D, Line.LENGTH
▪ **LVIDd (2D)** codeValue= LVIDD2D, Line.LENGTH

- **LVIDs (2D)** codeValue= LVIDS2D, Line.LENGTH
- **LVLd apicale** codeValue= LVLDAPICAL, Line.LENGTH
- **LVPWd (2D)** codeValue= LVPWD2D, Line.LENGTH
- **LVPWs (2D)** codeValue= LVPWS2D, Line.LENGTH
- **TR radius** codeValue= RADIUSTR, Line.LENGTH
- **TV radius** codeValue= RADIUSTV, Line.LENGTH
- **RAs area** codeValue= RASAREA, Polygon.AREA
- **RVAWd (2D)** codeValue= RVAWD2D, Line.LENGTH
- **RVIDd (2D)** codeValue= RVIDD2D, Line.LENGTH
- **CBD diam.** codeValue= DIAMCBD, Line.LENGTH
- **Ao dist. diam.** codeValue= DIAMDISTAO, Line.LENGTH
- **Ao med. diam.** codeValue= DIAMMEDAO, Line.LENGTH
- **Cholecyst wall diam.** codeValue= DIAMPARTECISTIF, Line.LENGTH
- **Ao prox. diam.** codeValue= DIAMPROSSAO, Line.LENGTH

o *Other 2D*

- **A2Cd** codeValue=A2CD, EcoCardioAreaVolume(SIMPSONMONOPLANO)
- **A2Cd – LV length** codeValue=A2CD_LUNGHEZZALV, MedstMeasurement::A2CD->DIAMETER
- **A2Cd - LV area** codeValue=A2CD_AREALV**,** MedstMeasurement::A2CD->AREA
- **A2Cd - LV volume** codeValue=A2CD_VOLLV, MedstMeasurement::A2CD->VOLUME
- **A2Cs** codeValue=A2CS, EcoCardioAreaVolume(SIMPSONMONOPLANO)
- **A2Cs - LV length** codeValue=A2CS_LUNGHEZZALV, MedstMeasurement::A2CS->DIAMETER
- **A2Cs – LV area** codeValue=A2CS_AREALV, MedstMeasurement::A2CS->AREA
- **A2Cs - LV volume** codeValue=A2CS_VOLLV, MedstMeasurement::A2CS->VOLUME
- **A4Cd** codeValue=A4CD, EcoCardioAreaVolume(SIMPSONMONOPLANO)
- **A4Cd - LV length** codeValue=A4CD_LUNGHEZZALV, MedstMeasurement::A4CD->DIAMETER
- **A4Cd - LV area** codeValue=A4CD_AREALV, MedstMeasurement::A4CD->AREA
- **A4Cd - LV volume** codeValue=A4CD_VOLLV, MedstMeasurement::A4CD->VOLUME
- **A4Cs** codeValue=A4CS, EcoCardioAreaVolume(SIMPSONMONOPLANO)
- **A4Cs - LV length** codeValue=A4CS_LUNGHEZZALV, MedstMeasurement::A4CS->DIAMETER
- **A4Cs – LV area** codeValue=A4CS_AREALV, MedstMeasurement::A4CS->AREA
- **A4Cs - LV volume** codeValue=A4CS_VOLLV, MedstMeasurement::A4CS->VOLUME

- **LVAd (A/L)** codeValue=LVADAL. EcoCardioAreaVolume(ELLIPSOIDSINGLEPLANE).AREA
- **LVAd (A2C)** codeValue=LVADA2C, MedstMeasurement::A2CD->AREA
- **LVAd (A4C)** codeValue=LVADA4C, MedstMeasurement::A4CD->AREA
- **LVAs (A/L)** codeValue=LVASAL, EcoCardioAreaVolume(ELLIPSOIDSINGLEPLANE).AREA
- **LVAs (A2C)** codeValue=LVASA2C, MedstMeasurement::A2CS->AREA
- **LVAs (A4C)** codeValue=LVASA4C, MedstMeasurement::A4CS->AREA
- **LVLd (A/L)** codeValue=LVLDAL, EcoCardioAreaVolume(ELLIPSOIDSINGLEPLANE).DIAMETER
- **LVLd (A2C)** codeValue=LVLDA2C, MedstMeasurement::A2CD->DIAMETER
- **LVLd (A4C)** codeValue=LVLDA4C, MedstMeasurement::A4CD->DIAMETER
- **LVLd (A/L)** codeValue=LVLSAL, EcoCardioAreaVolume(ELLIPSOIDSINGLEPLANE).DIAMETER
- **LVLd (A2C)** codeValue=LVLSA2C, MedstMeasurement::A2CS->DIAMETER
- **LVLd (A4C)** codeValue=LVLSA4C, MedstMeasurement::A4CS->DIAMETER

- MMode measurements
  - *Size*
    - *All points*
      - **RVAWd (MM)** codeValue= RVAWDMM, MModeLine.LENGTH
      - **RVIDd (MM)** codeValue= RVIDDMM, MModeLine.LENGTH
      - **IVSd (MM)** codeValue= IVSDMM, MModeDias-tole.IVS
      - **LVIDd (MM)** codeValue= LVIDDMM, MModeDiastole.LVID
      - **LVPWd (MM)** codeValue= LVPWDMM , MModeDiastole.LVPW
      - **IVSs (MM)** codeValue= IVSSMM, MModeSistole.IVS
      - **LVIDs (MM)** codeValue= LVIDSMM, MModeSis-tole.LVID
      - **LVPWs (MM)** codeValue= LVPWSMM, MModeSistole.LVPW
    - **Ao rad. diam. (MM)** codeValue= DIAMRADAOMM, MModeLine.LENGTH
    - **LA size (MM)** codeValue= DIMENLAMM, MModeLine.LENGTH
    - **AV cusp. sep.** codeValue= SEPCUSPAV, MModeLine.LENGTH
  - *Aortic valve*
    - **AV cusp. sep.** codeValue= SEPCUSPAV, MModeLine.LENGTH
    - **LV ET** codeValue= LVET, MModeLine.LENGTH
    - **LV PEP** codeValue= LVPEP, MModeLine.LENGTH
  - *Mitral valve*
    - **MV D-E esc.** codeValue=ESCDEMV, MModeLine.LENGTH

- **MV D-E slope** codeValue=PENDDEMV, MModeLine.DERIVATIVE
- **MV E-F slope** codeValue=PENDEFMV, MModeLine.DERIVATIVE
- **MV EPSS** codeValue=MVEPSS, MModeLine.LENGTH
- **MV E-E sep.** codeValue=SEPEEMV, MModeLine.LENGTH
- **MV A-C interval** codeValue=INTERVACMV, MModeLine.MMODETIME

o *Tricuspid valve*

- **TV D-E esc.** codeValue="ESCDETV, MModeLine.LENGTH
- **TV D-E slope** codeValue=PENDDETV, MModeLine.DERIVATIVE
- **TV E-F slope** codeValue=PENDEFTV, MModeLine.DERIVATIVE
- **TV A-C interval** codeValue=INTERVACTV, MModeLine.MMODETIME

o *Pulmonary valve*

- **Late diast. slope** codeValue=PENDDIASTTARDIVA, MModeLine.DERIVATIVE
- **A wave amp.** codeValue=AMPWAVEA,MModeLine.LENGTH
- **B-C slope** codeValue=PENDBC, MModeLine.DERIVATIVE
- **RV ET** codeValue=RVET, MModeLine.MMODETIME
- **RV PEP** codeValue=RVPEP, MModeLine.MMODETIME

o *Other*

- **EDV (MM-Teich)** codeValue= EDV (MM-Teich), MModeDias-tole.TEICHOLZ
- **ESV (MM-Teich)** codeValue= ESV (MM-Teich), MModeDiastole.TEICHOLZ

- Doppler measurements

o *Aortic valve*

- **AI dec. slope** codeValue=PENDDECAI, EcoCardioTimeMeasure.DERIVATIVE
- **AI accel. time** codeValue=TIMEACCELAI, EcoCardioTimeMeasure.TIME
- **AV accel. time** codeValue=TIMEACCELAV, EcoCardioTimeMeasure.TIME
- **AV decel. time** codeValue=TIMEDECELAV, EcoCardioTimeMeasure.TIME
- **LVOT accel. time** codeValue=TIMEACCELLVOT, EcoCardioTimeMeasure.TIME
- **Telediast. v. AI measure** codeValue=VTELEDIASTAI_MEAS, EcoCardioVelocityMeasure
- **AI telediast. v.** codeValue=VTELEDIASTAI, MedstMeasurement::VTELEDIASTAI_MEAS->VELOCITY
- **AI telediast. v. – max. PG** codeValue=VTELEDIASTAI_PGMAX MedstMeasurement::VTELEDIASTAI_MEAS->PRESSUREGRAD
- **AI PHT** codeValue=AIPHT, EcoCardioPressureHalfTime.PHT
- **AVA (V. max.)**
  - **Max. V. AV measure** codeValue=VMAXAV_MEAS, EcoCardioVeloc-ityMeasure
  - **Max. V. AV** codeValue=VMAXAV, MedstMeasurement::VMAXAV_MEAS->VELOCITY
  - **Max. V. AV – max. PG** codeValue=VMAXAV_PGMAX, MedstMeasurement::VMAXAV_MEAS->PRESSUREGRAD
  - **LVOT diam.** codeValue=DIAMLVOT, Line.LENGTH

- **Max. V. LVOT measure** codeValue=VMAXLVOT_MEAS, EcoCardioVelocityMeasure
- **Max. V. LVOT** codeValue=VMAXLVOT, MedstMeasurement::VMAXLVOT_MEAS->VELOCITY
- **Max. V. LVOT – max. PG** codeValue=VMAXLVOT_PGMAX, MedstMeasurement::VMAXLVOT_MEAS->PRESSUREGRAD

▪ **AVA (VTI)**
- **LVOT diam.** codeValue=DIAMLVOT, Line.LENGTH
- **LVOT VTI** codeValue=LVOTVTI, MedstMeasurement::LVOT->VTI
- **AV** codeValue=AV, EcoCardioPressureGradient
- **AV VTI – mean PG** codeValue=AV_PGMEAN, MedstMeasurement::AV->MEAN_GRAD
- **AV VTI – mean V**codeValue=AV_VMEAN, MedstMeasurement::AV->MEAN_VEL
- **AV VTI** codeValue=AVVTI, MedstMeasurement::AV->VTI

▪ **PISA (AI)**
- **AI alias. vel.** codeValue=VELALIASAI, EcoCardioVelocityMeasure.VELOCITY
- **AI VTI** codeValue=AIVTI, MedstMeasurement::AI->VTI
- **AI radius** codeValue=RADIUSAI, Line.LENGTH
- **Max. V. AI measure** codeValue=VMAXAI_MEAS, EcoCardioVelocityMeasure
- **Max. V. AI** codeValue="VMAXAI, MedstMeasurement::VMAXAI_MEAS->VELOCITY
- **Max. V. AI – max. PG** codeValue=VMAXAI_PGMAX, MedstMeasurement::VMAXAI_MEAS->PRESSUREGRAD
- **LVOT diam.** codeValue=DIAMLVOT, Line.LENGTH
- **LVOT VTI** codeValue=LVOTVTI, MedstMeasurement::LVOT->VTI

▪ **CO (LVOT)**
- **LVOT diam.** codeValue=DIAMLVOT, Line.LENGTH
- **LVOT VTI** codeValue=LVOTVT, MedstMeasurement::LVOT->VTI

o *Mitral valve*

▪ **MV PHT measure** codeValue=MVPHT, EcoCardioPressureHalfTime
▪ **MV PHT – max. V** codeValue=MVPHT_VMAX, MedstMeasurement::MVPHT->PEAK_VEL
▪ **MV PHT** codeValue=MVPHT_PHT, MedstMeasurement::MVPHT->PHT
▪ **MV A dur.** codeValue=DURAMV, EcoCardioTimeMeasure.TIME
▪ **MV accel. time** codeValue=TIMEACCELMV, EcoCardioTimeMeasure.TIME
▪ **MV dec. slope** codeValue=PENDDECMV, EcoCardioTimeMeasure.DERIVATIVE
▪ **MVA (VTI)**
- **LVOT diam.** codeValue=DIAMLVOT, Line.LENGTH

- **LVOT VTI** codeValue=LVOTVTI, MedstMeasurement::LVOT->VTI
- **MV VTI** codeValue="MVVTI_VTI, MedstMeasurement::MVVTI->VTI

▪ **MVA (PISA)**
- **MV radius** codeValue=RADIUSMV, Line.LENGTH
- **MV alias. vel.** codeValue=VELALIASMV, EcoCardioVelocityMeasure.VELOCITY
- **MV E peak vel.** codeValue=VELPICCOEMV, MedstMeasurement::VELPICCOEMV_MEAS->VELOCITY

▪ **PISA (MR)**
- **MR alias. vel.** codeValue=VELALIASMR, EcoCardioVelocityMeasure.VELOCITY
- **MR VTI** codeValue=MRVTI, MedstMeasurement::MR->VTI
- **MR radius** codeValue=RADIUSMR, Line.LENGTH
- **Max. V. MR measure** codeValue=VMAXMR_MEAS, EcoCardioVelocityMeasure
- **Max. V. MR** codeValue=VMAXMR, MedstMeasurement::VMAXMR_MEAS->VELOCITY
- **Max. V. MR – max. PG** codeValue=VMAXMR_PGMAX, MedstMeasurement::VMAXMR_MEAS->PRESSUREGRAD
- **MV VTI** codeValue=MVVTI_VTI, MedstMeasurement::MVVTI->VTI
- **MV diam.** codeValue=DIAMMV, Line.LENGTH

▪ **E/A (MV)**
- **MV A peak vel. measure** codeValue=VELPICCOAMV_MEAS, EcoCardioVelocityMeasure
- **MV A peak vel. – PG** codeValue=VELPICCOAMV_PG, MedstMeasurement::VELPICCOAMV_MEAS->PRESSUREGRAD
- **MV peak vel. measure** codeValue=VELPICCOEMV_MEAS, EcoCardioVelocityMeasure
- **MV E peak vel. – PG** codeValue=VELPICCOEMV_PG MedstMeasurement::VELPICCOEMV_MEAS->PRESSUREGRAD
- **MV decal. time** codeValue=TIMEDECELMV, EcoCardioTimeMeasure.TIME
- **MV EA measure** codeValue=MVEAMEAS, EcoCardioDecelerationTime
- **MV A peak vel.** codeValue=VELPICCOAMV, MedstMeasurement::MVEAMEAS->PEAK_VEL_A
- **MV E/A** codeValue=MVEA, MedstMeasurement::MVEAMEAS->RATIO_EA

o *Tricuspid valve*

▪ **RVSP**
- **Max. V. TR measure** codeValue=VMAXTR_MEAS, EcoCardioVelocityMeasure
- **Max. V. TR** codeValue=VMAXTR, MedstMeasurement::VMAXTR_MEAS->VELOCITY
- **Max. V. - PG max** codeValue=VMAXTR_PGMAX, MedstMeasurement::VMAXTR_MEAS->PRESSUREGRAD

- **E/A (TV)**
  - **TV A peak vel. measure** codeValue=VELPICCOATV_MEAS, EcoCardioVelocityMeasure
  - **TV A peak vel.** codeValue=VELPICCOATV, MedstMeasurement::VELPICCOATV_MEAS->VELOCITY
  - **TV A peak vel. – PG** codeValue=VELPICCOATV_PG, MedstMeasurement::VELPICCOATV_MEAS->PRESSUREGRAD
  - **TV E peak vel. measure** codeValue=VELPICCOETV_MEAS, EcoCardioVelocityMeasure
  - **TV E peak vel.** codeValue=VELPICCOETV, MedstMeasurement::VELPICCOETV_MEAS->VELOCITY
  - **TV E peak vel. – PG** codeValue=VELPICCOETV_PG, MedstMeasurement::VELPICCOETV_MEAS->PRESSUREGRAD
  - **TV accel. time** codeValue=TIMEACCELTV, EcoCardioTimeMeasure.TIME

- *Pulmonary valve*
  - **PV accel. time** codeValue=TIMEACCELPV, EcoCardioTimeMeas-ure.TIME
  - **PVA (V. max.)**
    - **RVOT diam.** codeValue=DIAMRVOT, Line.LENGTH
    - **Max. V. RVOT measure** codeValue=VMAXRVOT_MEAS, EcoCardioVelocityMeasure
    - **Max. V. RVOT** codeValue=VMAXRVOT, MedstMeasurement::VMAXRVOT_MEAS->VELOCITY
    - **Max. V. RVOT - PG max** codeValue=VMAXRVOT_PGMAX, MedstMeasurement::VMAXRVOT_MEAS->PRESSUREGRAD
    - **Max. V. PV measure** code-Value="VMAXPV_MEAS,EcoCardioVelocityMeasure
    - **Max. V. PV** codeValue=VMAXPV, MedstMeasurement::VMAXPV_MEAS->VELOCITY
    - **Max. V. PV - PG max** codeValue=VMAXPV_PGMAX, MedstMeasurement::VMAXPV_MEAS->PRESSUREGRAD
  - **PVA (VTI)**
    - **RVOT diam.** codeValue=DIAMRVOT, Line.LENGTH
    - **RVOT VTI** codeValue=RVOTVTI_VTI, MedstMeasurement::RVOTVTI->VTI
    - **PV VTI** codeValue=PVVTI_VTI, MedstMeasurement::PVVTI->VTI
  - **CO (RVOT)**
    - **RVOT diam.** codeValue=DIAMRVOT, Line.LENGTH
    - **RVOT VTI** codeValue="RVOTVTI_VTI, MedstMeasurement::RVOTVTI->VTI

- *Hepatic and pulmonary veins*
  - **Hepat. A inv. dur.** codeValue=DURINVAEPAT, EcoCardioTimeMeasure.TIME

- **Pulm. A. inv. dur.** codeValue=DURINVAPOLM, EcoCardioTimeMeasure.TIME
- **Hepat. diast. V. Measure** codeValue=VELDIASTEPAT_MEAS, EcoCardioVelocityMeasure
- **Hepat. diast. vel.** codeValue=VELDIASTEPAT, MedstMeasurement::VELDIASTEPAT_MEAS->VELOCITY
- **Hepat. diast. vel. - PG** codeValue=VELDIASTEPAT_PG, MedstMeasurement::VELDIASTEPAT_MEAS->PRESSUREGRAD
- **Hepat. Syst. V. Measure** codeValue=VELSISTEPAT_MEAS, EcoCardioVelocityMeasure
- **Hepat. Syst. vel.** codeValue=VELSISTEPAT, MedstMeasurement::VELSISTEPAT_MEAS->VELOCITY
- **Hepat. syst. A. - PG** codeValue=VELSISTEPAT_PG, MedstMeasurement::VELSISTEPAT_MEAS->PRESSUREGRAD
- **Hepat. A. inv. vel. Measure** codeValue=VELINVAEPAT_MEAS, EcoCardioVelocityMeasure
- **Hepat A. inv. vel.** codeValue=VELINVAEPAT, MedstMeasurement::VELINVAEPAT_MEAS->VELOCITY
- **Hepat A. inv. vel. - PG** codeValue=VELINVAEPAT_PG, MedstMeasurement::VELINVAEPAT_MEAS->PRESSUREGRAD
- **Pulm. diast. V. Measure** codeValue=VELDIASTPOLM_MEAS, EcoCardioVelocityMeasure
- **Pulm. diast. vel.** codeValue=VELDIASTPOLM, MedstMeasurement::VELDIASTPOLM_MEAS->VELOCITY
- **Pulm. diast. V. – PG** codeValue=VELDIASTPOLM_PG, MedstMeasurement::VELDIASTPOLM_MEAS->PRESSUREGRAD
- **Pulm. sist. V. easure** codeValue=VELSISTPOLM_MEAS, EcoCardioVelocityMeasure
- **Pulm. Syst. vel.** codeValue=VELSISTPOLM, MedstMeasurement::VELSISTPOLM_MEAS->VELOCITY
- **Pulm. Syst. V. – PG** codeValue=VELSISTPOLM_PG MedstMeasurement::VELSISTPOLM_MEAS->PRESSUREGRAD
- **Pulm. A. inv. vel. Measure** codeValue=VELINVAPOLM_MEAS, EcoCardioVelocityMeasure
- **Pulm. A. inv. vel.** codeValue=VELINVAPOLM, MedstMeasurement::VELINVAPOLM_MEAS->VELOCITY
- **Pulm. A inv. vel. - PG** codeValue=VELINVAPOLM_PG, MedstMeasurement::VELINVAPOLM_MEAS->PRESSUREGRAD
- **TDI**
  - **E/E'**
    - **Med. E' vel.** codeValue=VELEMED, EcoCardioVelocityMeasure.VELOCITY
    - **Lat. E' vel.** codeValue=VELELAT, EcoCardioVelocityMeasure.VELOCITY
  - **Vel. and TDI ratio**
    - **Med. S vel.** codeValue=VELSMED, EcoCardioVelocityMeasure.VELOCITY

- **Med. E' vel.** codeValue=VELEMED, EcoCardioVelocityMeasure.VELOCITY
- **Med. A' vel.** codeValue=VELAMED, EcoCardioVelocityMeasure.VELOCITY
- **Lat. S vel.** codeValue=VELSLAT, EcoCardioVelocityMeasure.VELOCITY
- **Lat. E' vel.** codeValue=VELELAT, EcoCardioVelocityMeasure.VELOCITY
- **Lat. A' vel.** codeValue=VELALAT EcoCardioVelocityMeasure.VELOCITY

▪ **TDI area**

- **Lat. A' area** codeValue=AREAALAT, EcoCardioPressureGradient
- **Lat. A' area – max. V max** codeValue=AREAALAT_VMAX, MedstMeasurement::AREAALAT->PEAK_VEL
- **Lat. A' area - mean V** codeValue=AREAALAT_VMEAN, MedstMeasurement::AREAALAT->MEAN_VEL
- **Lat. A' area – VTI** codeValue=AREAALAT_VTI, MedstMeasurement::AREAALAT->VTI
- **Med. A' area** codeValue=AREAAMED, EcoCardioPressureGradient
- **Med. A' area – max. V** codeValue=AREAAMED_VMAX, MedstMeasurement::AREAAMED->PEAK_VEL
- **Med. A' area. – mean V** codeValue=AREAAMED_VMEAN, MedstMeasurement::AREAAMED->MEAN_VEL
- **Med. A' area – VTI** codeValue=AREAAMED_VTI, MedstMeasurement::AREAAMED->VTI
- **Lat. E' area** codeValue=AREAELAT, EcoCardioPressureGradient
- **Lat. E' area – max. V** codeValue=AREAELAT_VMAX, MedstMeasurement::AREAELAT->PEAK_VEL
- **Lat. E' area – mean V** codeValue=AREAELAT_VMEAN, MedstMeasurement::AREAELAT->MEAN_VEL
- **Lat. E' area - VTI** codeValue=AREAELAT_VTI, MedstMeasurement::AREAELAT->VTI
- **Med. E' area** codeValue=AREAEMED, EcoCardioPressureGradient
- **Med. E' area - V max** codeValue="AREAEMED_VMAX, MedstMeasurement::AREAEMED->PEAK_VEL
- **Med. E' area - V media** codeValue="AREAEMED_VMEAN, MedstMeasurement::AREAEMED->MEAN_VEL
- **Med. E' area – VTI** codeValue="AREAEMED_VTI, MedstMeasurement::AREAEMED->VTI

o *TDI*

▪ **TDI time**

- **Lat. E' time** codeValue=TIMEELAT, EcoCardioTimeMeasure.TIME
- **Med. E' time** codeValue=TIMEEMED, EcoCardioTimeMeasure.TIME
- **Lat. S time** codeValue=TIMESLAT, EcoCardioTimeMeasure.TIME
- **Med. S time** codeValue=TIMESMED, EcoCardioTimeMeasure.TIME

- **Lat. accel. time** codeValue=TIMEACCELLAT,EcoCardioTimeMeasure.TIME
- **Lat. decel. time** codeValue=TIMEDECELLAT,EcoCardioTimeMeasure.TIME
- **Med. accel. time** codeValue=TIMEACCELMED,EcoCardioTimeMeasure.TIME
- **Med. decel. time** codeValue=TIMEDECELMED,EcoCardioTimeMeasure.TIME

▪ **IVRT and IVCT**
- **IVCT** codeValue=IVCT, EcoCardioTimeMeasure.TIME
- **Lat. IVCT** codeValue=IVCTLAT, EcoCardioTimeMeasure.TIME
- **Med. IVCT** codeValue=IVCTMED, EcoCardioTimeMeasure.TIME
- **IVRT** codeValue=IVRT, EcoCardioTimeMeasure.TIME
- **Lat. IVRT** codeValue=IVRTLAT, EcoCardioTimeMeasure.TIME
- **Med. IVRT** codeValue=IVRTMED, EcoCardioTimeMeasure.TIME

▪ **MV E/A flow**
- **MV EA measure** codeValue=MVEAMEAS, EcoCardioDecelerationTime
- **MV A peak vel.** codeValue=VELPICCOAMV, MedstMeasurement::MVEAMEAS->PEAK_VEL_A
- **MV E/A** codeValue=MVEA, MedstMeasurement::MVEAMEAS->RATIO_EA

o *Other*

▪ **AI** codeValue=AI, EcoCardioPressureGradient
▪ **AI VTI** codeValue=AIVTI, MedstMeasurement::AI->VTI
▪ **AI – mean PG** codeValue=AIPGMEAN, MedstMeasurement::AI->MEAN_GRAD
▪ **AI – mean V** codeValue=AIVMEAN, MedstMeasurement::AI->MEAN_VEL
▪ **LVOT** codeValue=LVOT, EcoCardioPressureGradient
▪ **LVOT – mean PG** codeValue=LVOTPGMEAN, MedstMeasurement::LVOT->MEAN_GRAD
▪ **LVOT – mean V** codeValue=LVOTVMEAN, MedstMeasurement::LVOT->MEAN_VEL
▪ **LVOT VTI** codeValue=LVOTVTI, MedstMeasurement::LVOT->VTI
▪ **MR** codeValue=MR, EcoCardioPressureGradient
▪ **MR – mean PG** codeValue=MRPGMEAN, MedstMeasurement::MR->MEAN_GRAD
▪ **MR – mean V** codeValue=MRVMEAN, MedstMeasurement::MR->MEAN_VEL
▪ **MR VTI** codeValue=MRVTI, MedstMeasurement::MR->VTI
▪ **MV VTI measure** codeValue=MVVTI, EcoCardioPressureGradient
▪ **MV VTI – mean PG** codeValue=MVVTIPGMEAN, MedstMeasurement::MVVTI->MEAN_GRAD
▪ **MV VTI – mean V** codeValue=MVVTIVMEAN, MedstMeasurement::MVVTI->MEAN_VEL
▪ **MV VTI** codeValue=MVVTI_VTI, MedstMeasurement::MVVTI->VTI
▪ **PV VTI measure** codeValue=PVVTI, EcoCardioPressureGradient
▪ **PV VTI – mean PG** codeValue=PVVTIPGMEAN, MedstMeasurement::PVVTI->MEAN_GRAD
▪ **PV VTI – mean V** codeValue=PVVTIVMEAN,

MedstMeasurement::PVVTI->MEAN_VEL

- **PV VTI** codeValue=PVVTI_VTI, MedstMeasurement::PVVTI->VTI
- **RVOT VTI measure** codeValue=RVOTVTI, EcoCardioPressureGradient
- **RVOT VTI – mean PG** codeValue=RVOTVTIPGMEAN, MedstMeasurement::RVOTVTI->MEAN_GRAD
- **RVOT VTI – mean V** codeValue=RVOTVTIVMEAN, MedstMeasurement::RVOTVTI->MEAN_VEL
- **RVOT VTI** codeValue=RVOTVTI_VTI, MedstMeasurement::RVOTVTI->VTI
- **TR VTI measure** codeValue=TRVTI, EcoCardioPressureGradient
- **TR VTI – mean PG** codeValue=TRVTIPGMEAN, MedstMeasurement::TRVTI->MEAN_GRAD
- **TR VTI – mean V** codeValue=TRVTIVMEAN, MedstMeasurement::TRVTI->MEAN_VEL
- **TR VTI** codeValue=TRVTI_VTI, MedstMeasurement::TRVTI->VTI
- **TV VTI measure** codeValue=TVVTI, EcoCardioPressureGradient
- **TV VTI – mean PG** codeValue=TVVTIPGMEAN, MedstMeasurement::TVVTI->MEAN_GRAD
- **TV VTI – mean V** codeValue=TVVTIVMEAN, MedstMeasurement::TVVTI->MEAN_VEL
- **TV VTI** codeValue=TVVTI_VTI, MedstMeasurement::TVVTI->VTI
- **Max. V. MV measure** codeValue=VMAXMV_MEAS, EcoCardioVelocityMeasure
- **Max. V. MV** codeValue=VMAXMV, MedstMeasurement::VMAXMV_MEAS->VELOCITY
- **Max. V. MV – max. PG** codeValue=VMAXMV_PGMAX, MedstMeasurement::VMAXMV_MEAS->PRESSUREGRAD
- **Max. V. TV measure** codeValue=VMAXTV_MEAS, EcoCardioVelocityMeasure
- **Max. V. TV** codeValue=VMAXTV, MedstMeasurement::VMAXTV_MEAS->VELOCITY
- **Max. V. TV – max. PG** codeValue=VMAXTV_PGMAX, MedstMeasurement::VMAXTV_MEAS->PRESSUREGRAD
- **Telediast. V. PI measure** codeValue=VTELEDIASTPI_MEAS, EcoCardioVelocityMeasure
- **Telediast. V. PI** codeValue=VTELEDIASTPI, MedstMeasurement::VTELEDIASTPI_MEAS->VELOCITY
- **Telediast. V. PI – max. PG** codeValue=VTELEDIASTPI_PGMAX, MedstMeasurement::VTELEDIASTPI_MEAS->PRESSUREGRAD
- **AI alias. vel.** codeValue=VELALIASAI, EcoCardioVelocityMeasure.VELOCITY
- **MR alias. vel.** codeValue=VELALIASMR, EcoCardioVelocityMeasure.VELOCITY
- **MV alias. vel.** codeValue=VELALIASMV, EcoCardioVelocityMeasure.VELOCITY
- **TR alias. vel.** codeValue=VELALIASTR,

EcoCardioVelocityMeasure.VELOCITY
- **TV alias. vel.** codeValue=VELALIASTV, EcoCardioVelocityMeasure.VELOCITY

Preset calculations (still to be validated)

- 2D calculations/Colour
  - *Size*
    - **LVOT area**[cm2]**=** *(pi/4)*((DIAMLVOT[cm])^2)* codeValue=AREALVOT
    - **LA/Ao (2D)**[]= *DIMENSLA2D[cm]/ DIAMRADAO2D[cm]* codeValue=LAAO2D
  - *EF and Volume*
    - *Simpson*
      - **EDV (2D-Cubic)**[ml]= *(LVIDD2D[cm])^3* codeValue=EDV2DCUBIC
      - **ESV (2D-Cubic)**[ml]= *(LVIDS2D[cm])^3* codeValue=ESV2DCUBIC
      - **EF (A2C)**[%]= ((EDVA2C[ml]- ESVA2C[ml])*100)/(EDVA2C[ml]) codeValue=EFA2C
      - **EF (A4C)**[%]= ((EDVA4C[ml]- ESVA4C[ml])*100)/(EDVA4C[ml]) codeValue=EFA4C
      - **EF (BP)**[%]= ((EDVBP[ml]-ESVBP[ml])*100)/(EDVBP[ml]) codeValue=EFBP
      - **EF (2D-Cubic)**[%]= ((EDV2DCUBICO[ml]- ESV2DCUBICO[ml])*100)/(EDV2DCUBICO[ml] codeValue= EF2DCUBICO
      - **SV (A2C)**[ml]= (EDVA2C[ml])-(ESVA2C[ml]) codeValue=SVA2C
      - **SV (A4C)**[ml]= (EDVA4C[ml])-(ESVA4C[ml]) codeValue=SVA2C
    - *A/L*
      - **EF (A/L)**[%]= ((EDVAL[ml]-ESVAL[ml])*100)/(EDVAL[ml]) codeValue= EFAL
      - **SV (A/L)**[ml]= (EDVAL[ml])-(ESVAL[ml]) codeValue=SVAL
    - **EDV (2D-Teich)**[ml]= ((LVIDD2D[cm])^3)*7/(2.4+LVIDD2D[cm]) codeValue= EDV2DTEICH
    - **ESV (2D-Teich)**[ml]= ((LVIDS2D[cm])^3)*7/(2.4+LVIDS2D[cm]) codeValue= ESV2DTEICH
    - **EF (2D-Teich)**[%]= ((EDV2DTEICH[ml]- ESV2DTEICH[ml])*100)/EDV2DTEICH[ml] codeValue= EF2DTEICH
  - *Valves*
    - **LVOT area**[cm2]= (pi/4)*((DIAMLVOT[cm])^2) codeValue=AREALVOT
    - **MV area**[cm2]= (pi/4)*((DIAMMV[cm])^2) codeValue=AREAMV
    - **RVOT area**[cm2]= (pi/4)*((DIAMRVOT[cm])^2)

codeValue=AREARVOT
- **TV area**[cm2]= (pi/4)*((DIAMTV[cm])^2)
codeValue=AREATV

- *Atrium*
  - **LA (BP)**[%]= (LADVOL[ml]- LASVOL[ml])*100/ LADVOL[ml]
codeValue= LABP
  - **RA (BP)**[%]= (RADVOL[ml]- RASVOL[ml])*100/ RADVOL[ml]
codeValue= RABP
- *2D calculations*
  - **Spleen vol.**[ml]=
(4/3)*pi*((LUNGMILZA[cm]/2)*(LARGMILZA[cm]/2)*(ALTMILZA[cm]/2))
codeValue= VOLMILZA
  - **Kidney vol.**[ml]=
(4/3)*pi*((LUNGRENE[cm]/2)*(LARGRENE[cm]/2)*(ALTRENE[cm]/2))
codeValue= VOLRENE
  - **Bladder vol.**[ml]= (4/3)*pi*((LUNGVESCICA[cm]/2)*(LARGVESCICA
[cm]/2)*(ALTVESCICA[cm]/2))
codeValue= VOLVESCICA
  - **Post-mict bladder vol.**[ml]= (4/3)*pi*((LUNGVESCICAPOSTMINZ[cm]/2)*(
LARGVESCICAPOSTMINZ[cm]/2)*(ALTVESCICAPOSTMINZ[cm]/2))
codeValue= VOLVESCICAPOSTMINZ
  - **SV (2D-Cubic)** [ml]= EDV2DCUBICO[ml]-ESV2DCUBICO[ml]
codeValue= SV2DCUBICO
  - **SV (2D-Teich)**[ml]= EDV2DTEICH [ml]- ESV2DTEICH [ml]
codeValue= SV2DTEICH
  - **FS (2D-Cubic)**[%]= (LVIDD2D[cm]-LVIDS2D[cm]) *100/ LVIDD2D[cm]
codeValue= FS2DCUBICO
  - **FS (2D-Teich)**[%]= (LVIDD2D[cm]-LVIDS2D[cm]) *100/ LVIDD2D[cm]
codeValue= FS2DTEICH
  - **IVS % (2D)**[%]= (IVSS2D[cm] - IVSD2D[cm]) *100/ IVSD2D[cm]
codeValue= IVSPERCENT2D
  - **IVS/LVPW (2D)**[]= IVSD2D[cm]/ LVPWD2D[cm]
codeValue= IVSLVPW2D
  - **LVPW % (2D)**[%]= (LVPWS2D[cm] - LVPWD2D[cm]) *100/ LVPWD2D[cm]
codeValue= LVPWPERCENT2D

- MMODE calculations
  - *Size*
    - *All points*
      - **EDV (MM-Teich)** [ml]= ((LVIDDMM[cm])^3)*7/(2.4+ LVIDDMM[cm])
codeValue= EDVMMTEICH
      - **ESV (MM-Teich)** [ml]= ((LVIDSMM[cm])^3)*7/(2.4+ LVIDSMM[cm])
codeValue= EDVMMTEICH
      - **ESV (MM-Teich)** [ml]= ((LVIDSMM[cm])^3)*7/(2.4+ LVIDSMM[cm])
codeValue= EDVMMTEICH
      - **EF (MM-Teich)** [%]=(EDVMMTEICH[ml]-
ESVMMTEICH[ml])*100/EDVMMTEICH[ml]

codeValue= EFMMTEICH
- **FS (MM-Teich)**[%]**=**(LVIDDMM[cm]- LVIDSMM[cm])*100/ LVIDDMM[cm]
codeValue= FSMMTEICH
- **IVS % (MM)**[%]= (IVSSMM[cm]-IVSDMM[cm]) *100/ IVSDMM[cm]
codeValue= IVSPERCENTMM
- **IVS/LVPW (MM)** []=IVSDMM[cm]/ LVPWDMM[cm]
codeValue= IVSLVPWMM
- **LVPW % (MM)**[%]=(LVPWSMM[cm]-LVPWDMM[cm])*100/LVPWDMM[cm]
codeValue= LVPWPERCENTMM
- **SV (MM-Teich)**[ml]= EDVMMTEICH[ml]- ESVMMTEICH[ml]
codeValue= SVMMTEICH

▪ **LA/Ao (MM)**[]= DIMENLAMM[cm]/ DIAMRADAOMM[cm]
codeValue=LAAOMM

o *Aortic valve*

▪ **LV PEP/ET** []=LVPEP[s]/ LVET[s]
codeValue= LVPEPET

o *Pulmonary valve*

▪ **RV PEP/ET** []=RVPEP[s]/ RVET[s]
codeValue= RVPEPET

o *Other*

▪ **EDV (MM-Cubic)**[ml]= LVIDDMM[cm]^3
codeValue= EDVMMCUBICO

▪ **ESV (MM-Cubic)**[ml]= LVIDSMM[cm]^3
codeValue= ESVMMCUBICO

▪ **EF (MM-Cubic)**[ml]= (EDVMMCUBICO[ml]-ESVMMCUBICO[ml])*100/EDVMMCUBICO[ml]
codeValue= EFMMCUBICO

▪ **FS (MM-Cubic)**[ml]= (LVIDDMM[cm]- LVIDSMM[cm])*100/LVIDDMM[cm]
codeValue= FSMMCUBICO

▪ **LV weight (Cubic)**[g]= 0.8*1.04*(((IVSDMM[cm]+LVIDDMM[cm]+LVPWDMM[cm])^3)-LVIDDMM[cm]^3)+0.6
codeValue= MASSALVCUBICO

▪ **SV (MM-Cubico)**[ml]= EDVMMCUBICO[ml]-ESVMMCUBICO[ml]
codeValue= SVMMCUBICO

- DOPPLER calculations

o *Aortic valve*

▪ *PISA (AI)*

- **PISA (AI)**[cm2]= 2*pi*(RADIUSAI[cm] ^2)
codeValue= PISAAI
- **AI flow rate** [ml/s]= PISAAI[cm2]* VELALIASAI[cm/s]
codeValue= VELFLUSSOAI
- **AI ERO** [cm2]= VELFLUSSOAI[ml/s] /VMAXAI[cm/s]
codeValue= AIERO
- **AI volume**[ml]= AIERO[cm2]* AIVTI[cm]
codeValue= VOLUMEAI

- **AI fraction**[%]=VOLUMEAI[ml]*100/ SVLVOT[ml]
  codeValue= FRAZIONEAI

▪ *CO (LVOT)*
- **SV (LVOT)**[ml]= LVOTVTI[cm]*AREALVOT[cm2]
  codeValue=SVLVOT
- **Qp/Qs**[ml]= SVRVOT[ml])/ SVLVOT[ml]
  codeValue=QPQS

▪ **AVA (max. V.)**[cm2]=AREALVOT[cm2] *VMAXLVOT[cm/s] /VMAXAV[cm/s]
codeValue= AVAVMAX

▪ **AVA (VTI)**[cm2]= AREALVOT[cm2]* LVOTVTI[cm]/AVVTI[cm]
codeValue= AVAVTI

o *Mitral valve*

▪ *PISA (MR)*
- **PISA (MR)**[cm2]= 2*pi*RADIUSMR[cm]^2
  codeValue= PISAMR
- **MR flow rate** [ml/s]= PISAMR[cm2]*VELALIASMR[cm/s]
  codeValue= VELFLUSSOMR
- **MR ERO**[cm2]=VELFLUSSOMR[ml/s]/ VMAXMR[cm/s]
  codeValue= MRERO
- **MR volume**[ml]= MRERO[cm2]*MRVTI[cm]
  codeValue= VOLUMEMR
- **MR fraction**[%]=VOLUMEMR [ml] *100/ SVMV[ml]
  codeValue= FRAZIONEMR
- **TEI index** []=(IVRT[s] +IVCT[s])/ LVET[s]
  codeValue= INDEXTEI

▪ **MVA (PHT)**[cm2]= 220/(MVPHT_PHT[s]*1000)
codeValue= MVAPHT

▪ **MVA (PISA)**[cm2]=
2*pi*(RADIUSMV[cm]^2)*VELALIASMV[cm/s]/VELPICCOEMV[cm/s]
codeValue= MVAPISA

▪ **MVA (VTI)**[cm2]= AREALVOT[cm2]*LVOTVTI[cm]/ MVVTI_VTI[cm]
codeValue= MVVTI

o *Tricuspid valve*

▪ *PISA (TR)*
- **PISA (TR)**[cm2]= 2*pi*RADIUSTR[cm]^2
  codeValue= PISATR
- **TR flow rate** [ml/s]= PISATR[cm2]*VELALIASTR[cm/s]
  codeValue= VELFLUSSOTR
- **TR ERO**[cm2]=VELFLUSSOTR[ml/s]/ VMAXTR[cm/s]
  codeValue= MRERO
- **TR volume** [ml]= TRERO[cm2]* TRVTI_VTI [cm]
  codeValue= VOLUMETR
- **TR fraction**[%]= VOLUMETR[ml]* SVTV[ml]
  codeValue= FRAZIONETR
- **TVA (PISA)**[cm2]=
  2*pi*RADIUSTV[cm]^2*VELALIASTV[cm/s]/VELPICCOETV[cm/s]
  codeValue=TVAPISA

- **TV E/A**[]=VELPICCOETV[cm/s] /VELPICCOATV[cm/s]
  codeValue=TVEA
- *Pulmonary valve*
  - **PVA (VTI)**[cm2]=AREARVOT[cm2]*RVOTVTI_VTI[cm]/PVVTI_VTI[cm]
    codeValue=PVAVTI
  - *CO (RVOT)*
    - **Qp/Qs**[]=SVRVOT[ml]/ SVLVOT[ml]
      codeValue= QPQS
- *Hepatic and pulmonary veins*
  - **Hepat. S/D**[]= VELSISTEPAT[cm/s]/ VELDIASTEPAT[cm/s]
    codeValue= SDEPAT
  - **Pulm. S/D**[]= VELSISTPOLM[cm/s]/ VELDIASTPOLM[cm/s]
    codeValue= SDPOLM
- *TDI*
  - *E/E'*
    - **E/Lat E'**[{ratio}]= VELPICCOEMV[cm/s]/VELELAT[cm/s]
      codeValue= ELATE
    - **E/Med E'**[{ratio}]= VELPICCOEMV[cm/s]/VELEMED[cm/s]
      codeValue= EMEDE
  - *Vel. and TDI ratio*
    - **Lateral E'/A'** [{ratio}]= VELELAT[cm/s]/ VELALAT[cm/s]
      codeValue= EALATERALE
    - **Medial E'/A'** [{ratio}]= VELEMED[cm/s]/ VELAMED[cm/s]
      codeValue= EAMEDIALE
- *Other*
  - **PVA (V. max.)**[cm2]=AREARVOT[cm2]*VMAXRVOT[cm/s]/VMAXPV[cm/s]
    codeValue= PVAMAX
  - **SV (LVOT)**[ml]= LVOTVTI[cm]* AREALVOT[cm2]
    codeValue=SVLVOT
  - **SV (MV)**[ml]= MVVTI_VTI[cm]* AREAMV[cm2]
    codeValue=SVMV
  - **SV (RVOT)**[ml]= RVOTVTI_VTI[cm]* AREARVOT[cm2]
    codeValue=SVRVOT
  - **SV (TV**)[ml]= TVVTI_VTI[cm]* AREATV[cm2]
    codeValue=SVTV

ROI[28]

The **ROI** side panel is used to manage regions of interest (ROI) or volumes of interest (VOI). It is accessed by selecting the **Window | ROI** menu item or clicking on the **ROI** button on one side of the work area. At the top of the panel there are buttons for activating the functions, at its center there are the parameters for drawing the ROIs on the current image and at the bottom there are any statistics calculated on the basis of ROIs drawn on a set of images of the study (statistical information on the pixels of the current ROI: number of pixels, minimum, maximum and mean value, standard deviation, area and volume).

[28] Function available only in MedStation but not in MedStation Express.

A 2D region of interest is made up of one or more areas and is identified by a name and a colour.

To select a 2D ROI on an image:

- Choose one of the 24 name-colour combinations from the **Name** menu
- Select a drawing mode:
    - **Automatic** If you select this, set a **Tolerance** value to indicate what pixel values are to be added to the ROI according to the pixel value selected on the image by the user
    - **Free hand** or **Polyline** If you select this, choose the **Pen size**.
- Press the **Draw** button
- Draw the region of interest on the current image
- Having completed the drawing, press the **Stop** button

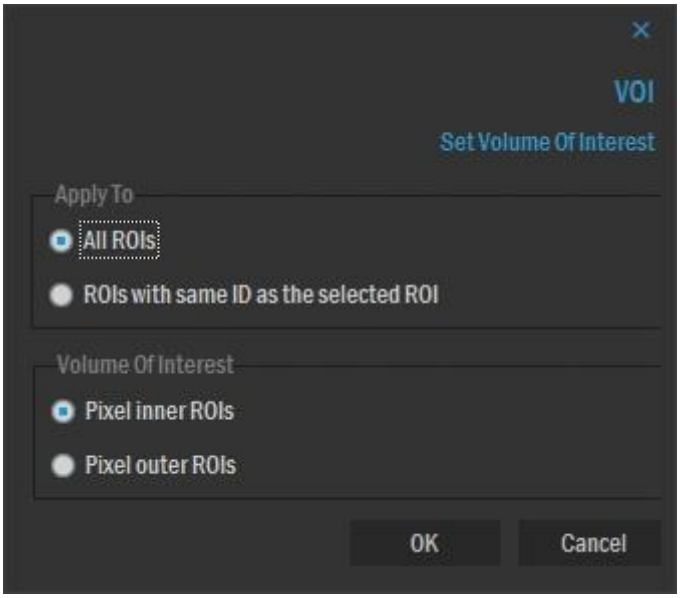
Having drawn a ROI, if you move onto another image and press the **Import** button, a new ROI identical to the one on the previous image will be added. This ROI can be modified using the tools described above.

The **Clear** button removes the current ROI from the current image (it does not clear all the ROIs from the current image or the range of images indicated by "Apply to…".

The **Polygonal**, **Propagate** and **3D ROI** buttons are used to create three-dimensional reconstructions (with which to interact using the 3D environment described in Chapter 7 of this manual) starting from portions of images. Proceed as follows:

- Select the outline of a region on an image using the **Polygonal** tool (this measures the area and the perimeter -if the image is calibrated and has the same unit of measurement in both dimensions -, the mean, the standard deviation and the maximum number of pixels - if the image is grayscale - contained in the polygonal area defined. Each click 'anchors' a point of the polygon, and it is thus possible to trace any area of the image accurately. Right click while drawing the ROI to cancel the operation. The ROI polygon is identical to the *Area* tool of *Measurements.*
- **Propagate** propagates the ROI selected to all images of the current display in accordance with the rules of application defined in "*Apply to…".* The images may then be scrolled and the polygon areas modified on each one.
- Finally, press the **3D ROI** button to view the 3D volume (VOI *Volume Of Interest*) generated from the ROIs in the current series. The volume of interest is selected from the dialog box shown in the figure.

Figure 13. Defining the volume of interest (VOI)



The *Apply to* group is used to select the desired range of ROIs. The range of the images must be selected in advance by selecting the series or images of interest. The *Volume of interest* group is used to select the portion of each source image to be considered in the volume to be displayed.

Geometrical functions

The **Tools | Geometry** submenu and the **Geometry** sheet of the side panel provide image rotate and flip functions.

Rotate+ Rotates the image 90° clockwise.
Rotate- Rotates the image 90° anticlockwise.
Rotate180° Rotates the image 180°.
Mirror Mirrors the image.
Flip Flips the image.
Original It returns the image to the initial condition, without changes.

Advanced[29]

The **Tools | Advanced** submenu and the **Advanced** sheet of the **Tools** side panel provide functions for removing and adding images.

[29] Function available only in MedStation but not in MedStation Express.

Cut is used to extract part of the image. Depending on the parameter chosen in configuration, the sub-image extracted will replace the image itself or create a new image at the end of the exam. The user clicks on the current image to open a rectangle, which can be sized and which indicates the selected area.

Right click to cancel the operation.

This option is disabled for some types of image.



RC-07

Delete image deletes the selected image from the study, having received confirmation from the user.



RC-07

Delete series deletes from the study all of the images belonging to the series of images selected, having received confirmation from the user.



RC-07

Delete study deletes all images displayed from the current exam, having received confirmation from the user.

Note: *Diagnostic images can be acquired in two ways:*

1. *by transferring a complete study (descriptive date and images) from a connected digital diagnostic source. A typical example would be diagnostic equipment connected through a DICOM SCP;*
2. *by directly acquiring the individual images that make up the exam.*

In the first case no action is required on the MedStation client as exams are transferred and made available using an external module: the DICOM Server (or DICOM SCP).

The direct image acquisition functions modes are described below.



RC-03

The addition of images to studies must be performed with extreme caution to avoid associating images with the wrong patients. If you attempt to add DICOM files or images to a study with patient data such as Patient Name and/or Date of Birth different from those contained in the study itself, the operation will be blocked and an error message displayed.

Add from file the window for naming the files(s) containing the image(s) to be acquired appears. Having confirmed by pressing the Open button, the selected file(s) will be added as a new series of the current study.

Add from clipboard The acquisition of images from the clipboard uses the Windows "copy to clipboard" or "paste from clipboard" functions. The **Add from Clipboard** option inserts the image present in the Windows clipboard as the first image of a new series of the current study.

Add from module This option activates an external application for acquisition of images

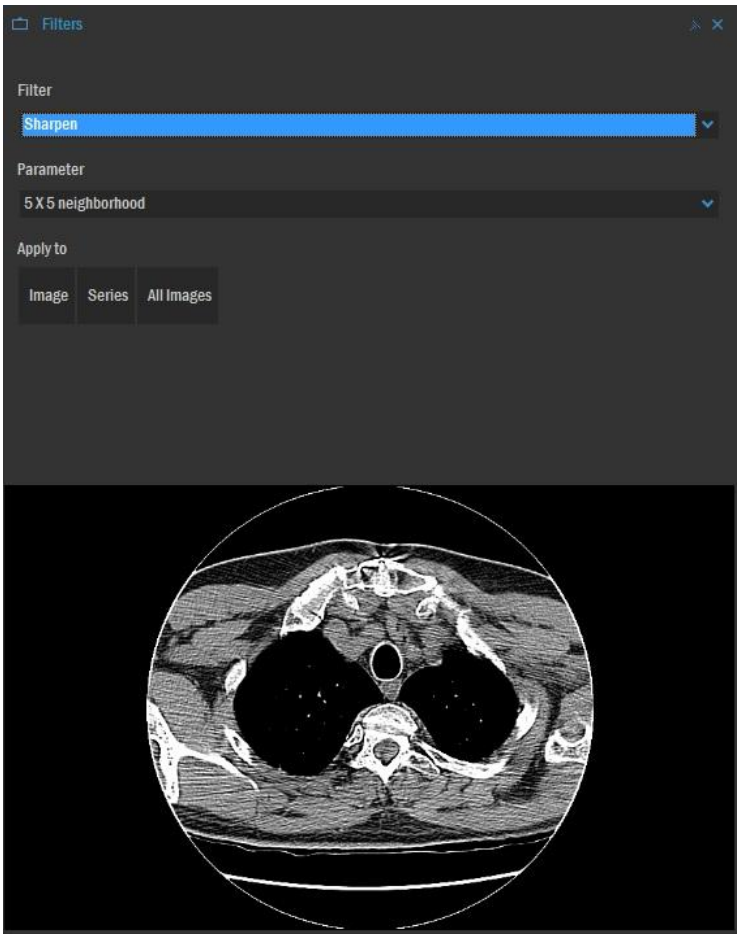
(for example a radiology scanner or video capture card). The images are added as a new series of the current study. The application and implementation modes used depend on the MedStation configuration settings.

Filters[30]

The **Filters** side panel give access to an environment for processing images like the one shown in the figure.

Using the functions provided here, a new series, obtained by processing the images according to the range of application chosen for the transformations, is added to the end of the study.

Figure 14. Image processing environment



The lower image view shows the preview of the image obtained having applied the filter chosen.

The *Filter* menu lists all of the processing operators available. Reduction or enhancement of details; Prewitt filter, Sobel filter for image edge detection; display in relief; edge improvement using the gradient or Laplacian method; average or median filter to reduce image noise;

[30] Function available only in MedStation but not in MedStation Express.

changes in grey levels (histogram equalization, gamma correction, false colours). When a filter has been selected, the "*Parameters*" menu can be used to select a suitable processing parameter.

The buttons in the "*Apply to"* group are used to select the range of application of the filter selected.

General information

The **General information** side panel includes a window with general information about the current image, series and study.

The **Image info** sheet shows the type and characteristics of the current study, series and image, the dimensions, acquisition mode, the local storage folder, if applicable, and the space it occupies on the disk.

The **DICOM** sheet contains a list of the principal DICOM attributes of the current image in "DICOM tag name" | "Tag value" format.

Key images

The **Edit | Key image** option enables you to declare that the current image is or is not a key image

Note: Key images are the images of a given study considered to be of the utmost importance.

Using the *Export* function, you can export only the images of a study set as key images.

The **Edit | Clear key images** option removes the key attribute from all images.

When opening a study you can load only key images as though they belonged to a single series.

After setting the "key image" flag, saving the study you will create a DICOM file with KO modality and save on the server where the images are. To add a note to the KO files with images of interest, you can use the menu item *File | Save Key Image Notes*, which also offers the user a DICOM dictionary of terms for the classification of the new file according to IHE directions.

If there are multiple key object in a studio, MedStation automatically apply the latest one. In the *View* menu, the voice *Key Image Note* appears, if the study has at least one key object. In correspondence of this entry, you can open a submenu containing the complete list of key object in the study.

Presentation States

In accordance with the DICOM standard, *Presentation State* objects define how the images to which they refer should be represented/displayed in a grayscale or colour space regardless of device; parameters defined include graphic annotations and the spatial changes to be made to the pixels in the images themselves.

MedStation can read, apply, and save presentation states, if the node from which the exam is opened supports PR modality DICOM objects.

If a number of presentation states are present for the same image, MedStation will automatically apply the most recent presentation state. The **View** menu and the shortcut menu include a **Presentation State** item if the image has one or more presentation states. The item opens a submenu containing a list of all exam presentation states. *The presentation states applicable to the image are marked with an asterisk, while the presentation state currently applied is marked with a check.* Click on any of the available presentation states in this list to apply the presentation state to the range defined using the "Apply to…" function.

If the presentation state currently applied to the image contains a list of window/level values and/or a list of VOI LUT, they will be displayed on a submenu of the *Current Presentation State* item on the popup menu of the image, among the items containing DICOM window/level values.

Chapter

4
Hanging Protocols

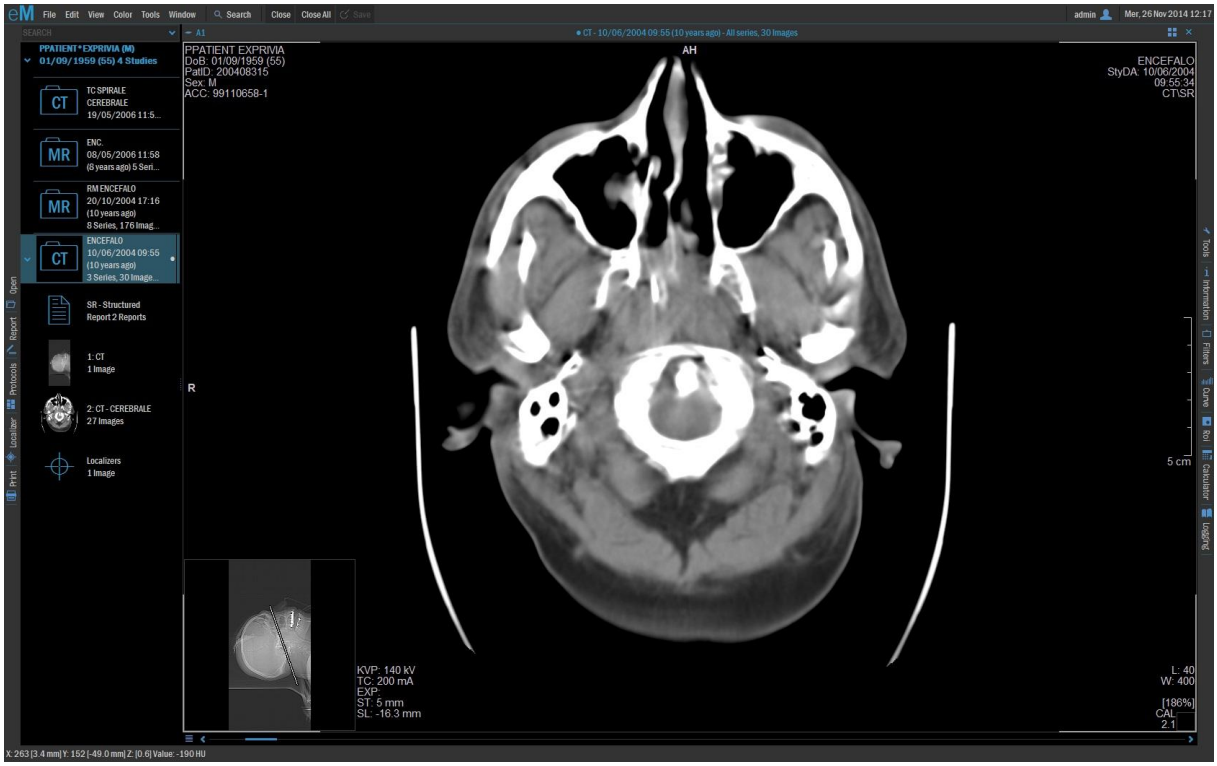
What a Hanging Protocol is

Hanging Protocols are used to save and reproduce layouts and to associate them with a specific type of study. Every user that has access to MedStation, can save customized Hanging Protocols (abbreviated to *Hp*) and therefore find his favourite layouts whenever he/she opens a study.

The environment for managing Hps in MedStation is situated on the **Protocols** side panel.

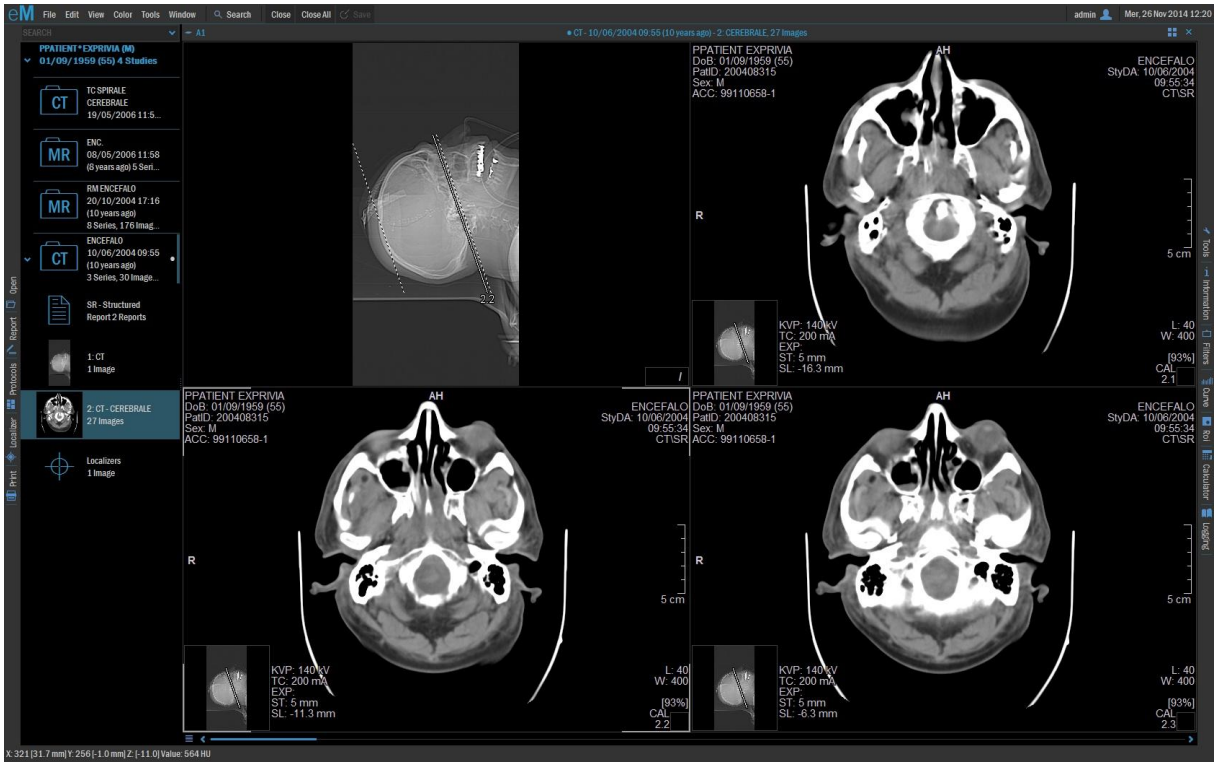
We shall take an example to better illustrate the concept. Imagine that you are opening a ENCEFALO CT image without a Hanging Protocol. An image similar to the one shown in the figure below will appear on the screen

Figure 15. Study opened without a Hp



If we are used to displaying a *ENCEFALO CT* studies in four boxes, the first containing the localizer image and the other three the remaining series, we can save a Hanging Protocol with this layout so that every time we open a *ENCEFALO CT* study, it will be displayed with this layout (example in Figure 16).

Figure 16. Study opened with a Hp



How an Hp works

Usually, each study is characterized by three fundamental items of information: *Modality, Body part or Protocol name, and Description.*

Modality: indicates the type of diagnosis with which the image was acquired. This information is always present in the study.

Body part: indicates the body part of the body to which images relate. Body parts are defined by DICOM standard. In some studies, they may not be specified. In other studies, there may be images of a series acquired for different body parts.

Protocol name: indicates the name of the protocol used by the diagnostic programs to conduct the study. In some studies it may not be specified.

Description: as the name itself suggests, it provides a description of the type of study. This data may not be present.

These three items (which we also define as *search parameters*) can be used to determine which Hp should be applied. In the example, the values read are:

Modality: CT

Body part: HEAD

Description: ENCEFALO

First MedStation checks if there are protocols for the study *CT, HEAD, ENCEFALO.*

- **Some HPs are present**

  There may be more than one Hp applicable to the study *CT, ENCEFALO, TC CEREBRAL.* Among those available, the system chooses the type designed as "predefined" (default). On the following pages, we will see how to define predefined HPs (default).

- **No HPs are present**

  If the system doesn't find any Hps, it searches for Hps that can be applied to the CT study, *<Protocol name>, CEREBRAL CT*

  If the system find no Hps for these values either, it broadens the search specifications and checks for protocols for *CT, ENCEFALO* or for *CT, <Protocol name>*.

  If no Hps are found even in this case, the system broadens the search further: it checks for the presence of protocols for *CT*

If even in the latter case, no Hps are found and the search parameters cannot be broadened any further, no HP will be applied to the study.

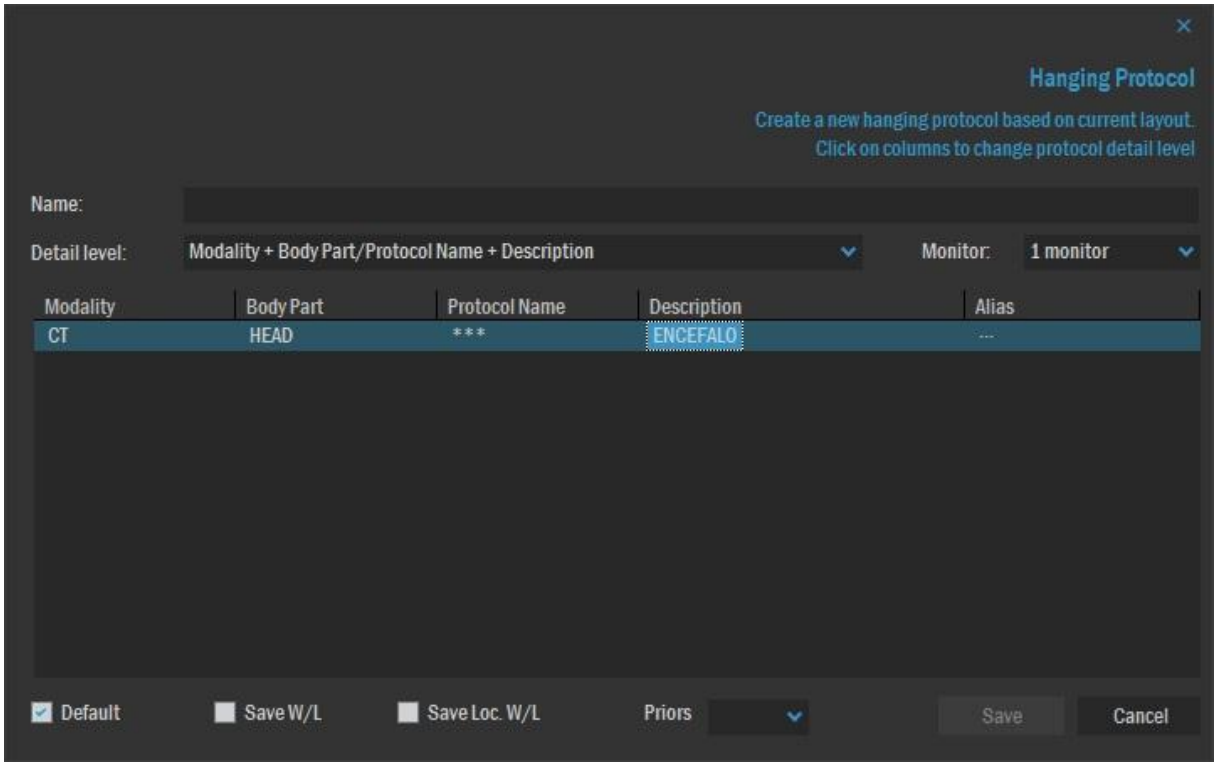
Saving an Hp

Saving an Hp is an easy operation. We will describe how to proceed step by step. Once you open the study for which you want to save an Hp, we arrange images and series in the way we usually want to. Referring to the example of study *ENCEFALO CT*, you can divide the monitor in four boxes, put the reference image on the first and the study series on the three remaining boxes. As soon as you have set your favourite layout, simply open the **Protocols** side panel and press the **New** button and the window for saving it will appear (Figure 17).

Description of the Hp save options

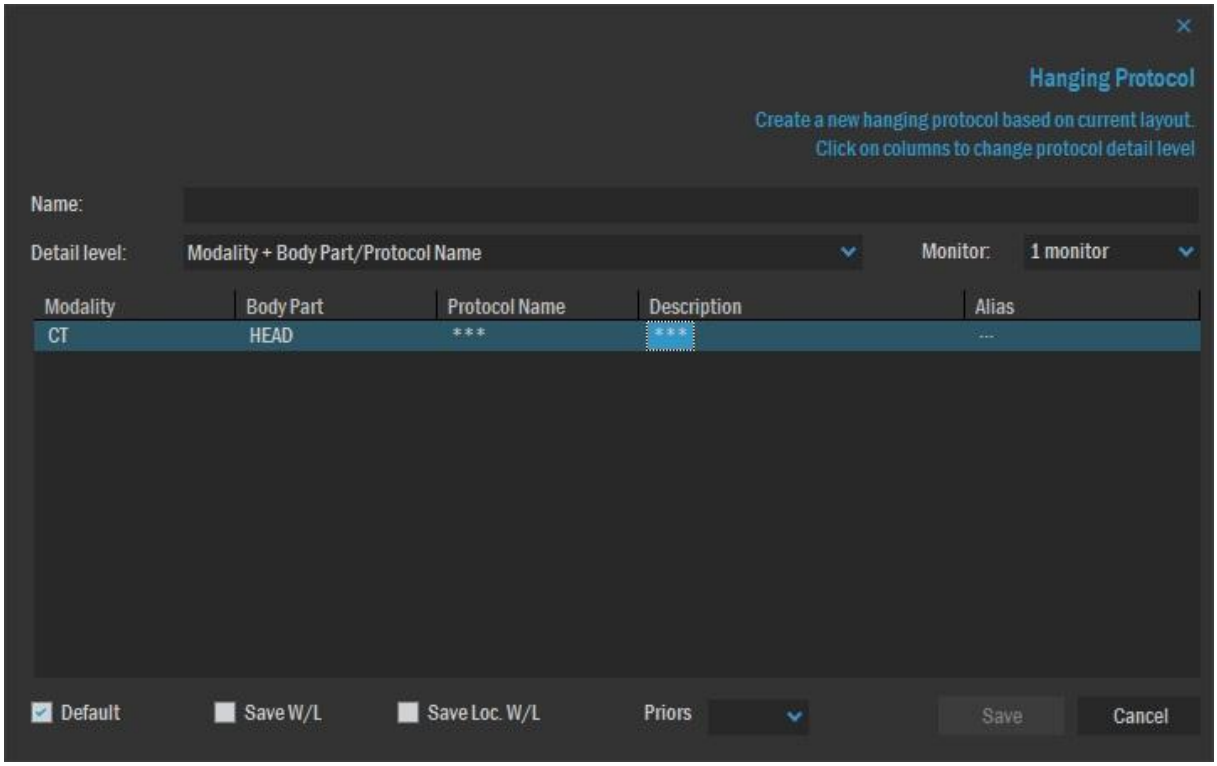
In Figure 17 we can see that the *level of detail* box contains the words *"Diagnostics + Body part /Protocol name + Description"*. This means that if we save the HP with this level of detail, the layout will only be applied to studies with following parameters: **Modality:** *CT***, Body part:** *HEAD* and **Description:** *ENCEFALO*.

Figure 17. Window for saving an Hp



If you want to make the Hp more generic, reduce the level of detail in *Diagnostics + Body part* (see Figure 18).

Figure 18. Window for saving an Hp with the generic description field

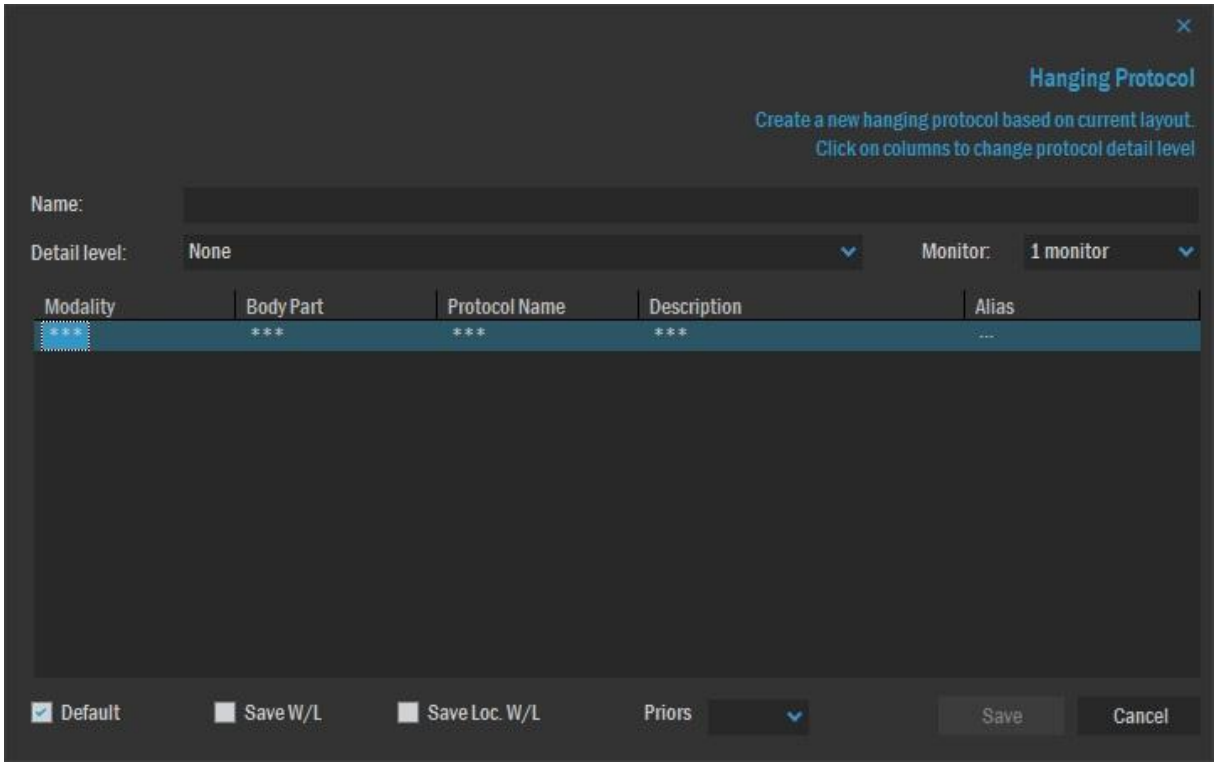


The "Description" column will contain asterisks to indicate that no field description has been specified. In this case, the Hanging Protocol will be applied whenever you open a study with **Modality** *CT* and **Body part** *HEAD*, regardless of the type of description that it contains.

You may want the layout to be valid for all CTs, regardless of the values of the fields **Body part** and **Description**. All you have to do is set the Body part, Protocol name and Description fields as generic so whenever a CT is opened, it will appear with the layout chosen.

The more general level of detail is obtained by setting also the modality to generic (Figure 19).

Figure 19. Saving a completely generic Hp



In this last case, the layout we have created will be applicable to every type of study opened.

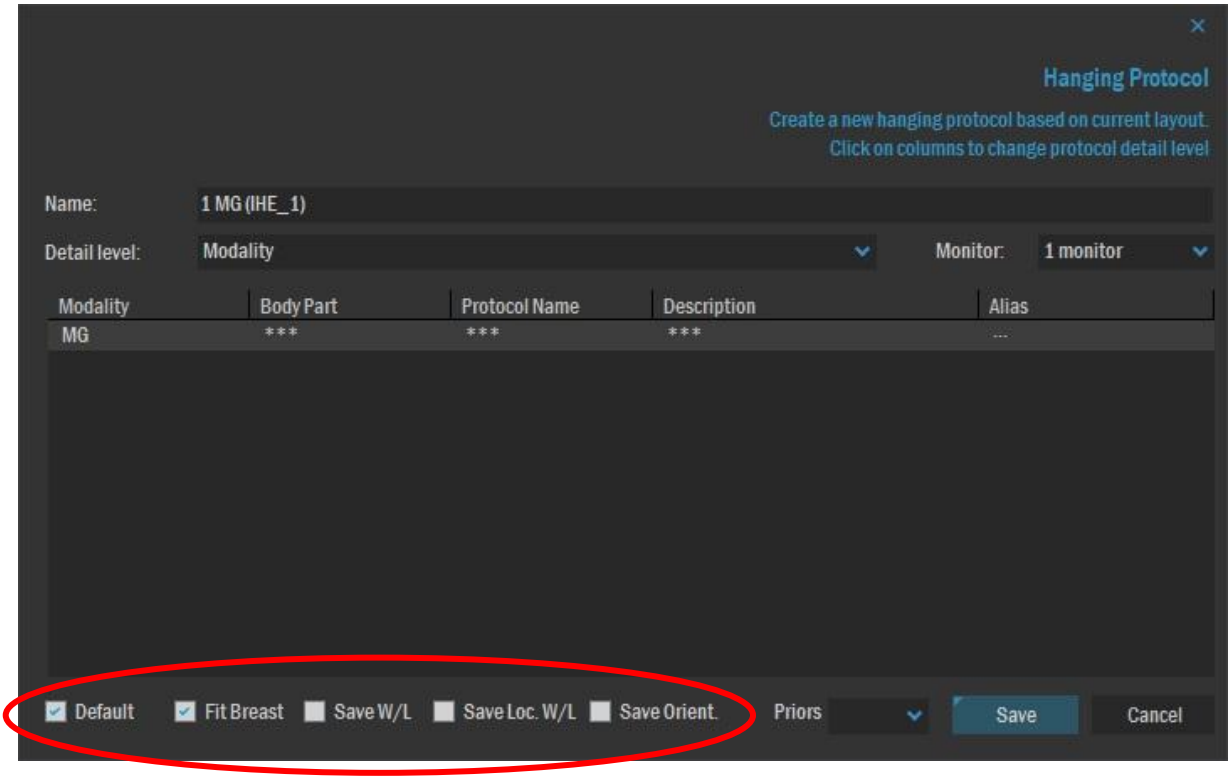
***Alias**. It is possible to associate one or more alias to a description. If our description is "CT ENCEFALO" and we want the protocol will be applied to each study that contains the word "ENCEFALO" , we have to write "*ENCEFALO*" on the list of aliases.*

***Note:** When we save an Hp, we can decide whether this will be the default layout for this level detail, or not. Moreover, when we save an Hp we can decide whether to save the window/level values of the series involved or not. The type of applied zoom, the image position within the boxes and possible alignments are automatically saved. Values saved and then re-applied are those of current image or of the first image in each series.*

For Hps involving mammographic studies (modality MG), you can save the flag "Fit breast", which will ensure that the Hp will apply the "Fit Breast" visualization at the end of the loading and displaying of the studies. ("Fit Breast" feature allows the arrangement of mammography images displayed in different boxes with FIT breast profile (excluding side air zones) and subsequent display in "Same size" taking as reference the spacing of the largest profile. The image of the breast that occupies more space within the view will be scaled so that the part of the air above, below and to the contour of the breast side is minimized (fit excluding the surrounding air), and all other views will be rescaled so as to have the same physical-dimension of this image.)

With the flag "Save Orient." you can save the preferential orientations of the visualized images - for each box will be saved in the HP the current image orientation. The orientation of the images is related to the reference system of the patient, deduced from the directions of the direction cosines of the rows and columns of the images themselves. To view the images with the orientation shown in the HP, the system will apply some geometric transformations; if it were not possible (multi-frame images, orientations not deductible from DICOM data, incom-

patible directions, ...) the images will be left unprocessed.



The Hps, besides these data and the subdivision of monitors into boxes, save also possible links between boxes, the parameter for transformation propagation, the range of transformation application, the display mode (2D, MPR, CINE, 3D) in each box.

Some considerations

When you open a study, the system searches the most detailed protocol for that kind of study so, if you have saved two protocols, a generic one without indicating the body part or giving a description and a more specific one as in Figure 17, when you open a *ENCEFALO CT* the system will choose a protocol as in Figure 17. While, if you open a *CT* with body part different from *ENCEFALO*, the system will choose the protocol for CTs.

Once you have decided the level of detail, you can enter the protocol name in the field "*Protocol Name*" and then you can save it using the button Save. In previously described case, the protocol will be available for reporting workstation with one monitor, as indicated in the *Monitor* field.

In case of multi-monitor[31] workstations, the **Monitor**[32] field will indicate the number of monitors used by the application. The saved Hp will be considered every time when the application

[31] If the application uses more than one monitor, when you save an Hp you can choose a lower value in the **Apply to** field than the one presented. For example, if the reporting workstation uses four monitors and in the **Apply to** field you set the value "2 monitors", the saved HP will only save the configuration of the first two monitors. This Hp can also be used on reporting workstations with two monitors.
[32] Function available only in MedStation but not in MedStation Express.

uses the same number of monitors.

It is also possible to save values of images window/level (the value of the first image in each box) and of images localizers.

In case of *studies with many body parts*, when you save an Hp you can choose whether to save in detail every body part of the study or only few, by setting the corresponding field. The "Body part" field contains all body parts present in the study. It is possible to modify the text with a double-click or by selecting the field and holding F2 (a single click activates level selection). Values in the field "Body part" should be separated by a DICOM separator '\', the insertion order is not significant and the recognition is "case insensitive". When you apply an HP to specified body parts, the correspondence must be complete, i.e. the study should contain series with every body part specified in the HP.

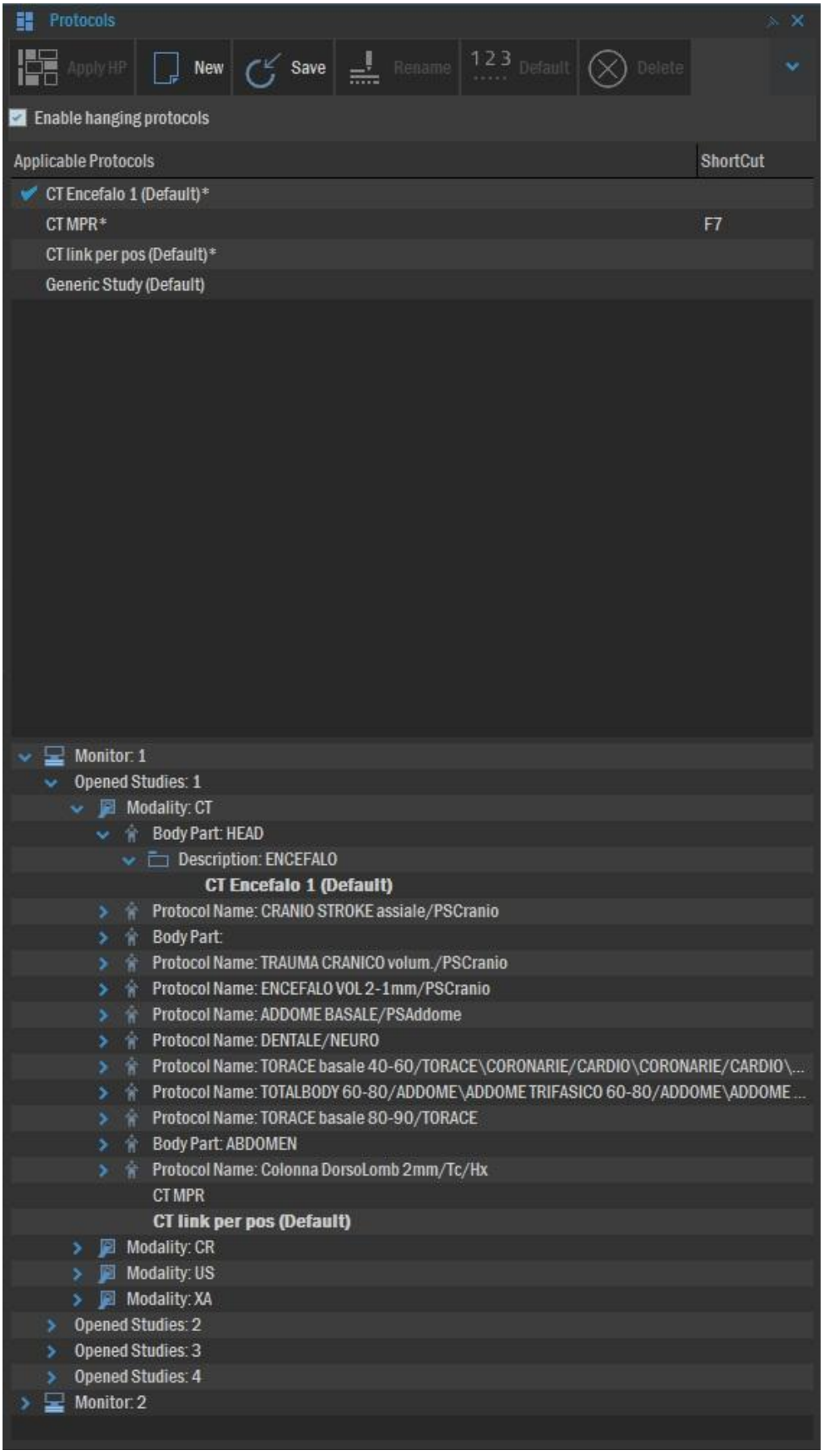
Creating a list of Hps

We will name the previously saved protocol for the study *ENCEFALO* - **2x2 Encefalo CT**. Suppose you normally need, besides this protocol, also another display layout with two boxes, one containing the localizer and the other used to scroll through the images. We name this protocol **1x2 Encefalo CT**. When you open a CT ENCEFALO study, you can decide which protocol to use from the menu for HP managing by clicking the option ***default*** or ***predefined***.

To switch from one protocol to the other, simply open the **Protocol** panel and choose a protocol from the list of those compatible with the study (Figure 20). The list is ordered so that the first protocol is the most specific one and the last is the most generic one.

You can apply in sequence the Hp of the applicable Hps list by pressing the F6 and F7 keys, respectively, to select the item that precedes the one applied in the list or to choose the next one.

Figure 20. Selecting a protocol from the list.

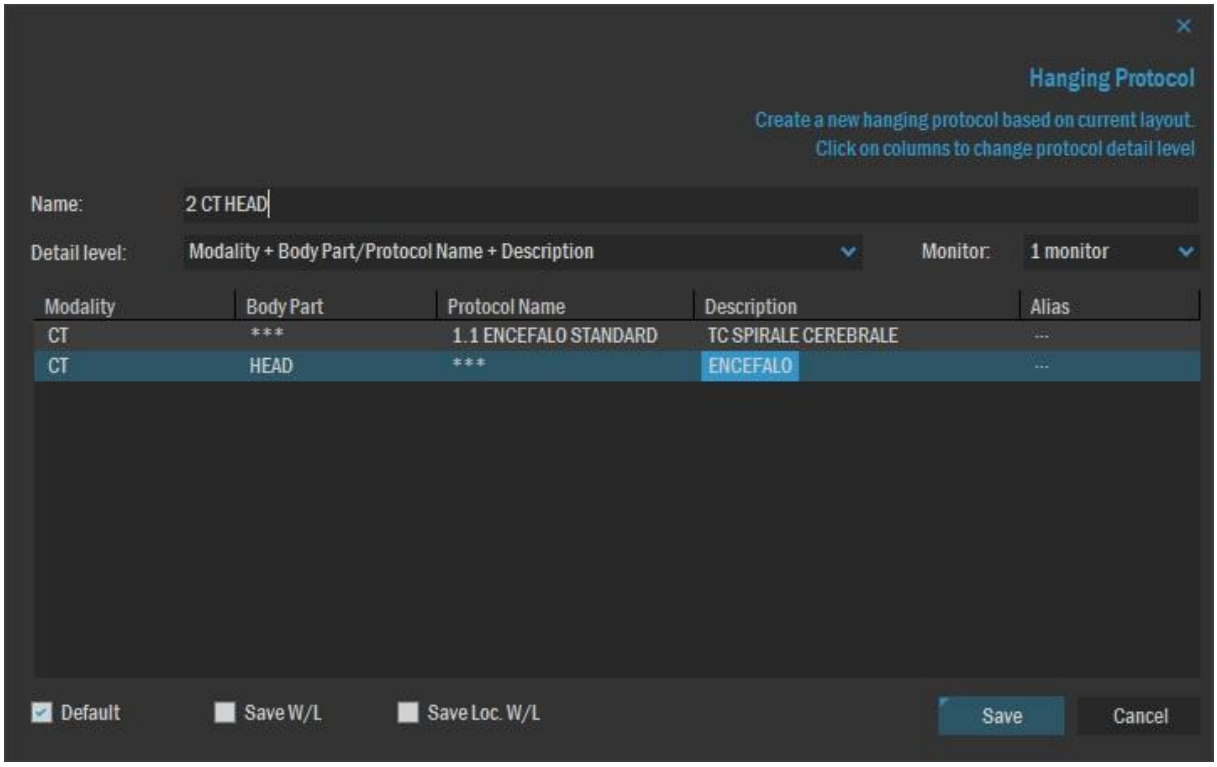


Protocols for viewing several studies

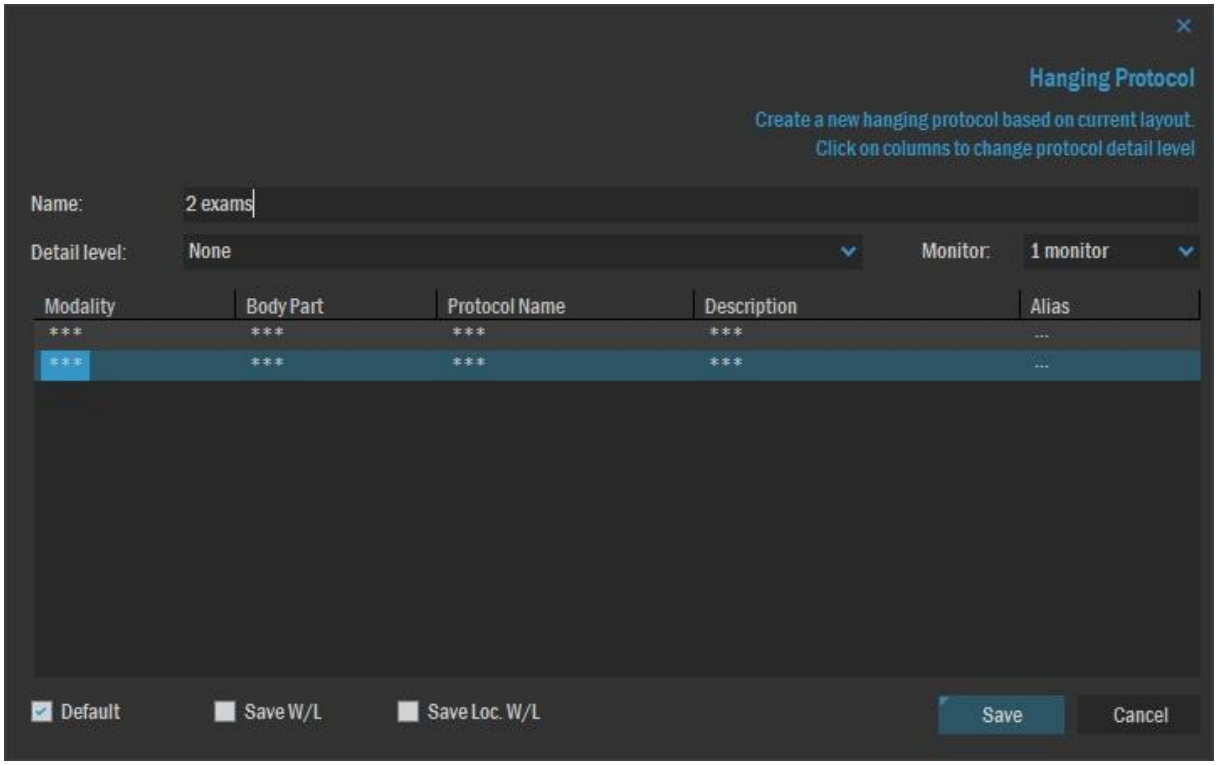
It is sometimes necessary to view several studies at the same time. This is the case, for example, when we want to compare a study with a previous one.

Having arranged the two studies in the desired layout, click on the **New** button on the **Protocols** panel.

Saving an Hp for two studies



Alternatively, you may want the HP to be applied whenever you compare two studies of any type. In this case, you have to define the HP irrespective of the study modality by clicking on the “Modality” box and making asterisks appear in the column.



When you compare two studies, the system will choose this HP.

Automatically opening previous studies

MedStation can automatically open one or more studies previous to the study displayed. To do this, the Hps must be appropriately configured.
When you save an Hp to display a single study, indicate the number of previous studies that you want to be opened automatically (using the drop-down menu in the bottom area of the window for saving a new Hp).

When you open studies to which the Hp saved is applicable, the system will search for previous studies and if it finds any, it will open them automatically, applying, where present, Hps suitable for the number of studies open after this operation or will create new image views to show all the studies opened (keeping the most recent study in the first view).

Previous studies will only be found and opened if the storage node from which the current study was opened contains other studies with the following characteristics:

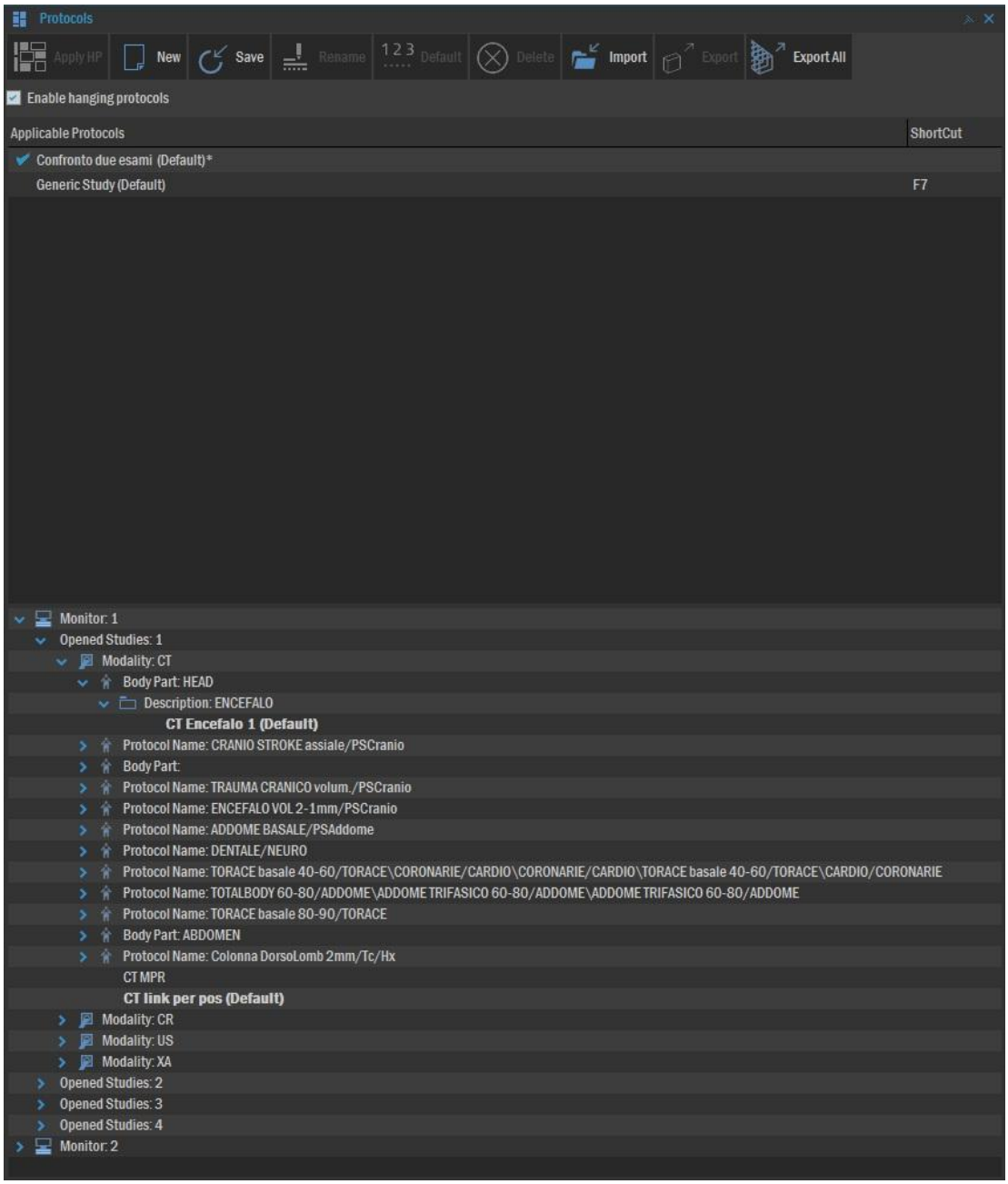
- Same patient
- Same study acquisition mode (excluding SR, PR, KO, DOC, and OT if it is not the only one). The modes in the following sets are considered equivalent:
  - MG, CR, DX
  - CR, DX
  - CT/PET, PET/CT

- Same study description (apart from multiple spaces, accented letters, apostrophes and non-alphanumeric characters)
- The study displayed by the user is the most recent with these characteristics

Managing Hanging Protocols

From the **Protocols** side panel (see Figure 21) you can access the window for managing and modifying Hps.

Figure 21. Modifying Hanging Protocols



Functions:

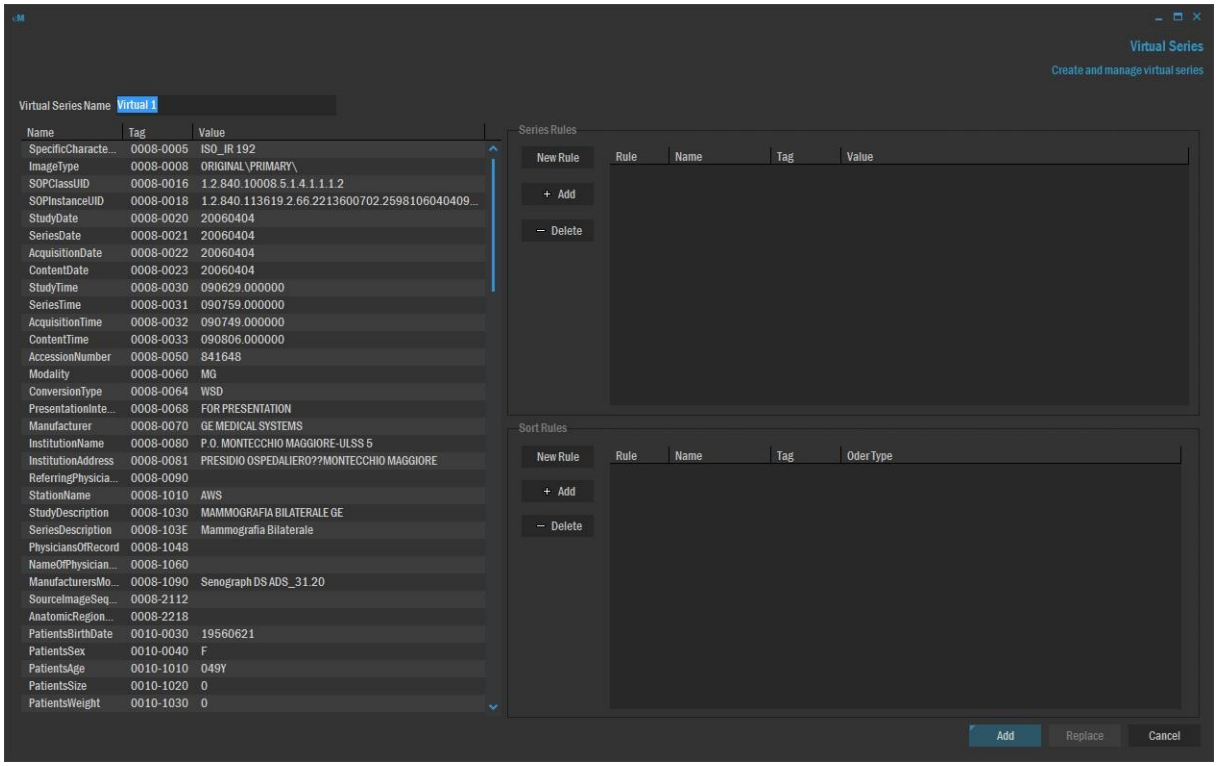
- **Enable Hanging Protocol:** if selected, saved HPs are analysed and applied whenever you open a study or a series.
- **Apply Hp:** applies the hanging protocol displayed to the current study.
- **Rename:** Changes the name of the selected HP on the tree structure that appears at the bottom of the panel.
- **Delete:** Deletes the HP selected on the tree structure that appears at the bottom of the panel.
- **Default:** Sets the HP selected on the tree structure that appears at the bottom of the panel as default. Setting a hanging protocol as *default* means that if there is more than one Hp available with the same level of detail for the study opened, the system will choose the predefined, or default, one.
- **Import** Allows you to search for and choose a previously exported file with the extension *fhp* containing a set of already saved HPs and to import them.
- **Export all** Exports a file containing all hanging protocols of the user connected to MedStation instance to a selectable path.

Virtual series

For some modalities of studies, the subdivision of images in series does not allow to create effective hanging protocols. In order to obtain HPs for these kind of studies, MedStation disposes of a tool that creates new *virtual* series, that combine images with particular values of DICOM tags and that can belong to one or several effective series.

To see in detail how to create and use virtual series, we consider a mammographic study (MG modality) which has two series, the first with non-processed images and the second with processed images ready to be reported. Suppose we are interested in a protocol in which there are only processed images, in a monitor subdivided in two displays, where in the left one you want to see the views of the right breast and in the right one the left breast. We subdivide the monitor into two boxes disposed in two columns. In the first box, we open the series with processed images and we place on the first view of the right breast. Right click on it. If you select the **Modify | Set virtual series** item, a window will appear, enabling you to create a virtual series from the data of the current image (Figure 22).

Figure 22. Window for creating virtual series

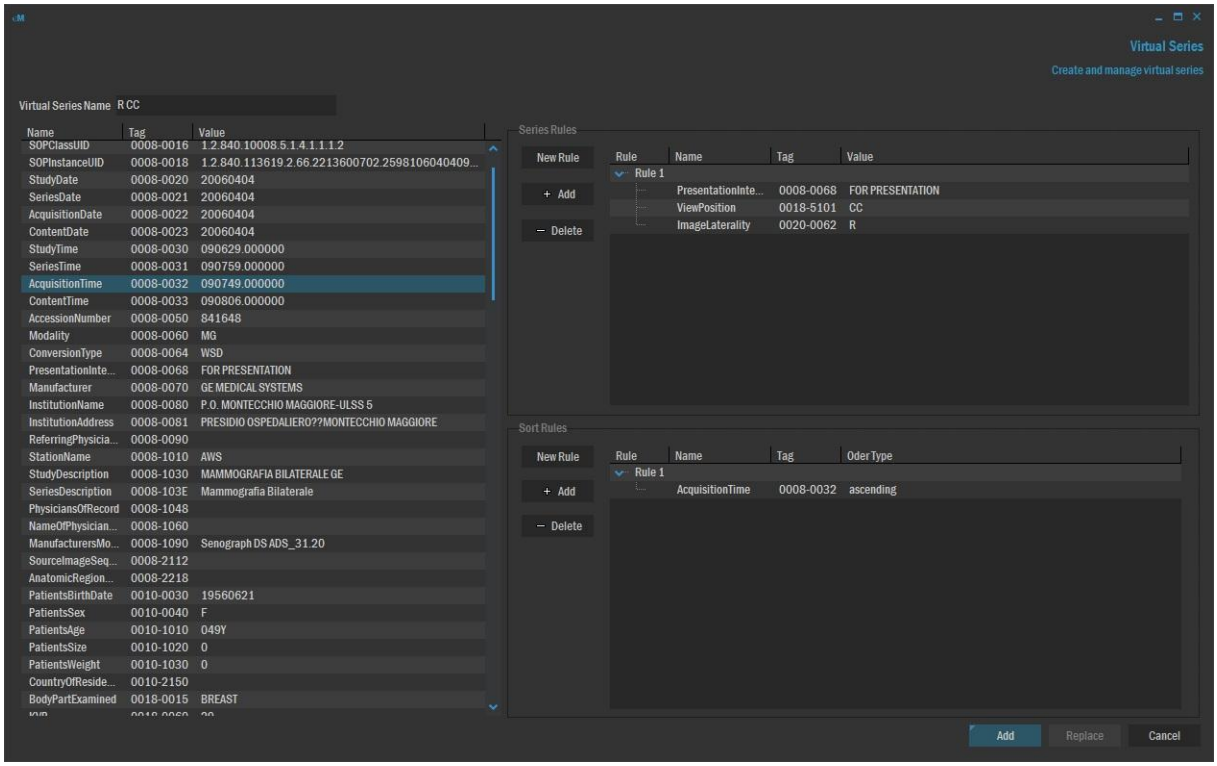


In the left part of this screen, you find the list of all even tags of the image, with their names and values in that image. In the right part of the screen, you find a space where you can generate the rules with which to create a virtual series and a space where you can generate the rules with which you can order the images of the virtual series you have just created.

To create a virtual series that contains all processed images of the right breast, you have to select in the left part all tags corresponding to this information and add them to the rule by clicking the button *Add*, available beside the window for rules creation, or by means of drag&drop in this window. So you create a rule. An image matches a rule if it has all tags that characterize such rule and if the rules have the indicated values. You can add several rules. Each rule will contribute to create the virtual series by including images, whose tags match at least one of present rules. In a similar way, you create rules with which you can order images within the virtual series when you display them.

Note: *Values assigned to tags that constitute a rule for virtual series creation can be assigned by wildcards. In this way, you can include also modalities that contain slightly different values for the same tag. If you want the value of a tag to contain the strings and you do not know the order in which they appear, you can include a character '&' between a string and the other.*

Figure 23. Example of how to create a virtual series



If you assign a name to the new series and press the button *Add*, the series will be created and displayed in current box. An icon will be added to the list of miniatures of the series on the series navigation panel.

In our example, you can create a virtual series containing all and only the processed images of the left breast. In this way, from a single series containing all the views of the right and left breast, we have created two separate series that can be displayed separately in different boxes.

Virtual series can be considered similar to real and effective series and you can create HP with them.

Note *You can create "on the fly" virtual series that contain images of two series already present in the study. After having created a single series you add other series of the study in the same box by selecting them from the series navigation panel and holding the button* CTRL + left button of the mouse *(displayed series will be indicated by names of virtual series contained in it).*

Note *MedStation, independently from the applied HP, automatically creates virtual series based on a single DICOM tag specified in the configuration. With the voice* SplitMixedSeriesTag *in settings_<user file>.cfg you can change the default tag (0020,0012) Acquisition Number, writing for example SplitMixedSeriesTag = 0020-0013. This functionality is active if the menu item* View | Separate series *is selected. In this case, the split is done automatically when the exam is loaded, and will be created, "breaking" each effective series, a virtual series for each different value of the tag specified in parameter SplitMixedSeriesTag found in images for loaded series.*

The Hp administrator[33]

You can define Hps that are common to all users. If you enter MedStation with the login of Hp administrator, you can define and modify generic HPs valid for each user.

When MedStation searches for a HP, it starts by searching for the logged user's Hps, and then, before broadening the search specifications, it checks for a generic HP on the same level of detail.

[33] Function available only in MedStation but not in MedStation Express.

Chapter

5
Printing studies

This chapter describes the methods for printing the images displayed.

To print a study

1. Use **File | Add to print** option or the **Add** button on the **Print** side panel or **P** to add the image, the series or the displayed part of the study or the set of selected images (according to the MedStation **Apply to** settings or print setup) to the print job.
2. Repeat to select all images you want to print.
3. Print the job by selecting **File | Print**, clicking on the **Print** button on the **Print** side bar or pressing CTRL+P.

Note: *The* ***Print key*** *starts adding all the key images to the print job and displays the dialog box for actually printing them.*

Note: *The* ***Cursor | Selection*** *tool shows a rectangular region of interest of the image. Move on the image to a point that is to be the top left-hand corner of the rectangular area and drag the mouse to the point that is to be the bottom right-hand corner of it and then release the mouse button. At this point, the following buttons will appear in the rectangular area:*

- ***print*** *the part of the image enclosed in the rectangle*
- ***copy*** *to the Windows clipboard a bitmap image containing the part of the image enclosed in the rectangle*
- ***apply*** *to the image the optimized window/level calculated on the area selected*
- ***cancel*** *to remove the rectangle*

You can change the size of the rectangle by moving the mouse cursor onto one of the squares on the border of the rectangle, clicking on it and dragging the mouse, with the left button pressed.

By clicking on the area enclosed in the rectangle you can drag it to the print preview, thus adding the part of the image inside the rectangle to the print job.

Note: *If images are added to the print job using the buttons or the items in the* **File | Print** *section (except for the* Print key *item), the function respects the range of application chosen in*

the print setup and may not correspond to that of the other functions of MedStation.

In particular, if the range of application is Set*, the printing of images using the "Add" commands or shortcut* P *is applied only to selected images (in all the boxes used by MedStation, even if they belong to different studies), omitting to print the current image if it is not marked as set.*

If images "caught" by the selection box in the bottom right-hand corner are dragged with the mouse onto the Print panel, the function follows a slightly different logic. Irrespective of the range of application, if you drag an image (having clicked on the selection box in the bottom right-hand corner) onto the print preview panel and you hold down CTRL *+ left button of the mouse, all and only images marked as set will be added to the print job. Irrespective of the range of application, if you drag an image (having clicked on the selection box in the bottom right-hand corner) onto the print preview panel and hold down only the left mouse button, only the dragged image will be added to the print job.*



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Note *The system allows you to add images of different patients and images from different studies to a single print job. The information shown on each image is consistent with the patient/study data but, to avoid printing images of different patients or studies on the same page, a dialog box will appear to warn you that images have been added to the print job. Whenever you add images to the print job (by pressing the* Add *button on the* Print *panel, selecting the* File | Add *item or the key* P*, by selecting a rectangular area using* Rect *or* Selection*, by sending the key images to the print job using* Print key*, or by dragging an image or the selected images from the image views to the print preview) a comparison is made with the data of the images already present on the pages to be printed. If discrepancies are found in the patient data (different* Name, Patient ID, Sex or date of birth*) or the study data (different* DICOM UID Study Instance*), a warning box appears indicating the first image of the patient/study different from those that are about to be added. From the warning box you can choose to* Cancel the print job *present before adding the images chosen,* Print the pages of the print job *present before adding the other images chosen,* Add the images chosen to the print job *or* leave the previous job unchanged without adding the images. *The latter option will be saved by the system so that it can be reapplied by pressing* Enter *when other images from different studies or patients are added subsequently.*
Another warning message will appear when the printer is about to actually start printing the job if it includes images of different patients or from different studies.

When you choose the **Window | Print** option or click on the **Print** tab beside the work area, the panel with the print previews will appear on the left side of the work area of each monitor.

Note: *The following three different types of printer are supported:*

1. *Windows printers*
2. Printers connected using the 3M-952 protocol
3. *DICOM printers*

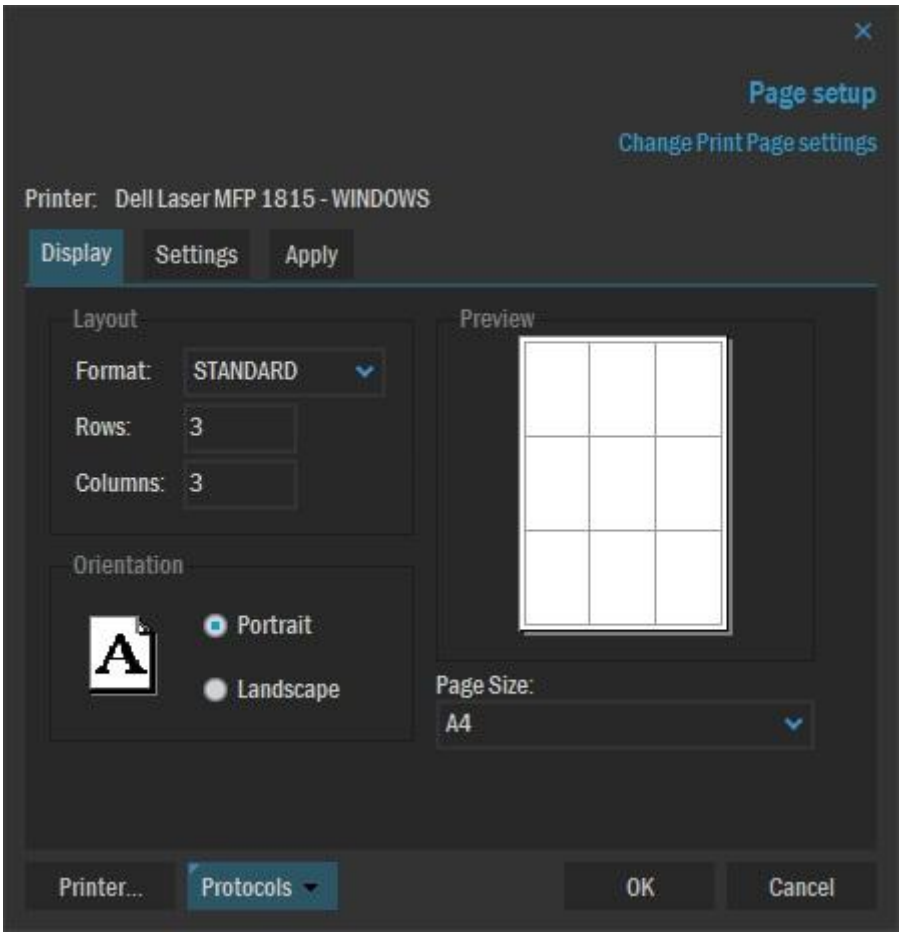
Page setup

The **File | Page setup** option or the **Setup** button on the **Print** side panel opens the print setup window, which has three sheets: *Display*, *Options* and *Apply* (see Figure 24).

The **Printer** button opens a window for setting up the current printer (see the "Print" section).

The **Protocols** button allows you to choose print protocols defined during the setup phase (see Appendix C).

Figure 24. Page setup

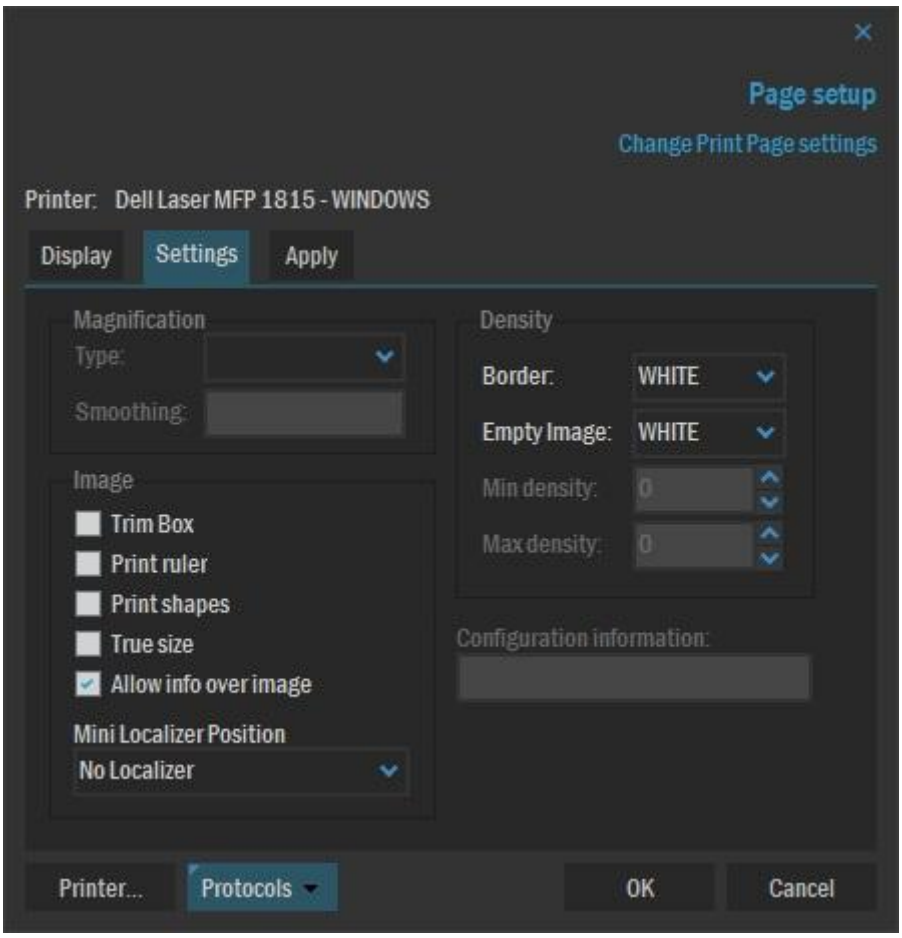


You can set the layout and orientation of the page, and the page format using the "Display" sheet.

Field	Description
Layout	Definition of the image grid in the page setup. It can have the values: STANDARD (*image matrix*: the number of rows and columns are respectively specified in the "Rows" and "Columns" fields);

	ROW (*sequence of rows*: the number of images in each row are specified in the "Rows" field separated by a comma); COL (*sequence of columns*: the numbers of images in each column are specified in the "Columns" field separated by a comma).
Orientation	Page orientation: Vertical or Horizontal
Preview	Displays an image preview of the layout chosen in the *Layout* section.
Page size	Size of the page or film for printing. ***Note.*** *You can change the page size from MedStation Configuration (see Appendix C).*

Figure 25. Image print settings

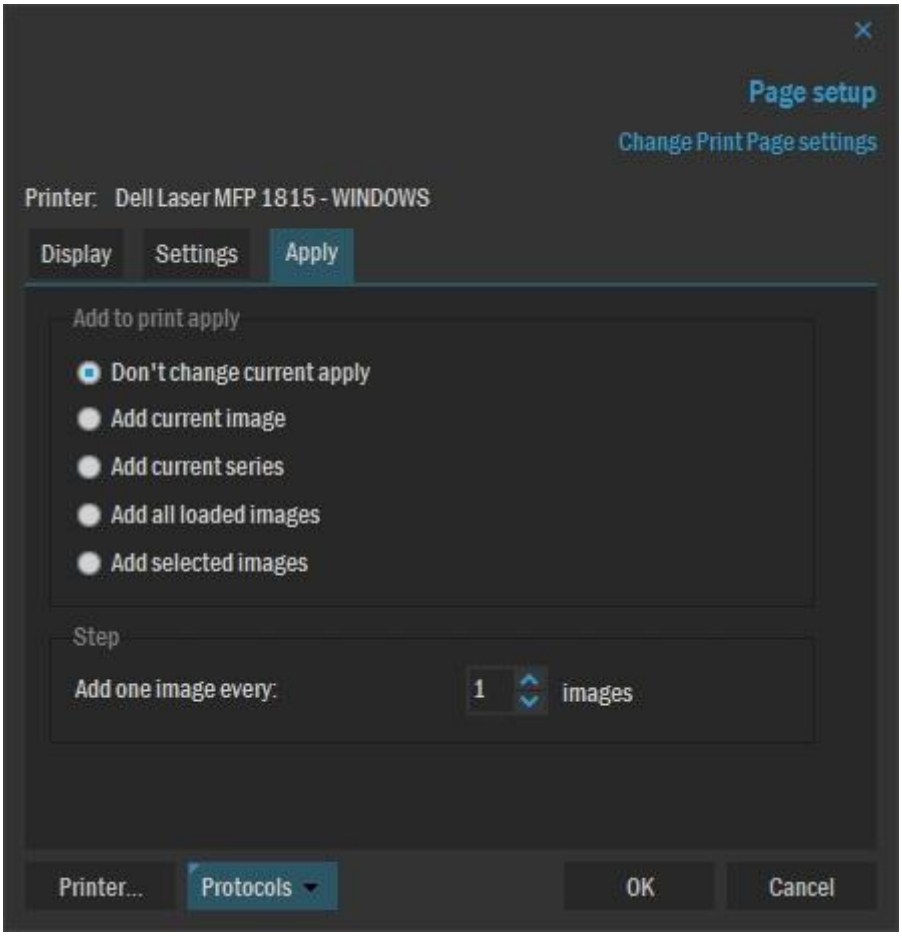


The "Settings" page is used to configure the appearance of the images, borders, empty image and enlargement filters for the image.

Field	**Description**
Magnification	Type of interpolation used by the printer to adapt the image to the image

Type	frame in the page setup. In the case of DICOM, it takes on the following values: REPLICATE, BILINEAR, CUBIC, NONE. In the case of Windows it uses the Windows basic primitives
Magnification | Smoothing	Specifies the type of interpolation function defined in the printer Conformance Statement. This is used only for DICOM printers.
Density | Border Color	Border color around the page images. Can have the values: BLACK, WHITE or n, where in DICOM n represents the optical density and in Windows it represents the grayscale level.
Density | Empty image	Density of the area in the frame not covered with images. Can have the values: BLACK, WHITE or n, where in DICOM n represents the density in OD*100 (e.g. 150 correspond to 1.5 OD) and the grayscale level in Windows.
Density | Min density	Minimum image density, expressed in OD*100. Lower density values will be forced to the *Min density*. This is only used for DICOM printers.
Density | Max density	Maximum image density, expressed in OD*100. Greater intensity values will be forced to the *Max density*. This is only used for DICOM printers.
Image | Trim Box	Specifies whether an internal border has to be created for each image on the page.
Image | Print Ruler	Prints a ruler on the image.
Image | Print Shapes	Prints measurements and symbols on the image.
Image | True Size	Print the images with their actual dimension.
Image | Allow info over image	The annotations are printed over the images.
Image | Mini Localizer position	Enables the possibility to print possible current localizer over the image area indicating the intersection slice. It is possible to choose one of the four image corners and to omit to print the mini localizer superimposed on the image.
Configuration information	String of specific configuration characters for the DICOM printer as detailed in the Conformance Statement.

Figure 26. Apply section



In the "Apply" section, you can set further parameters directly from MedStation before printing.

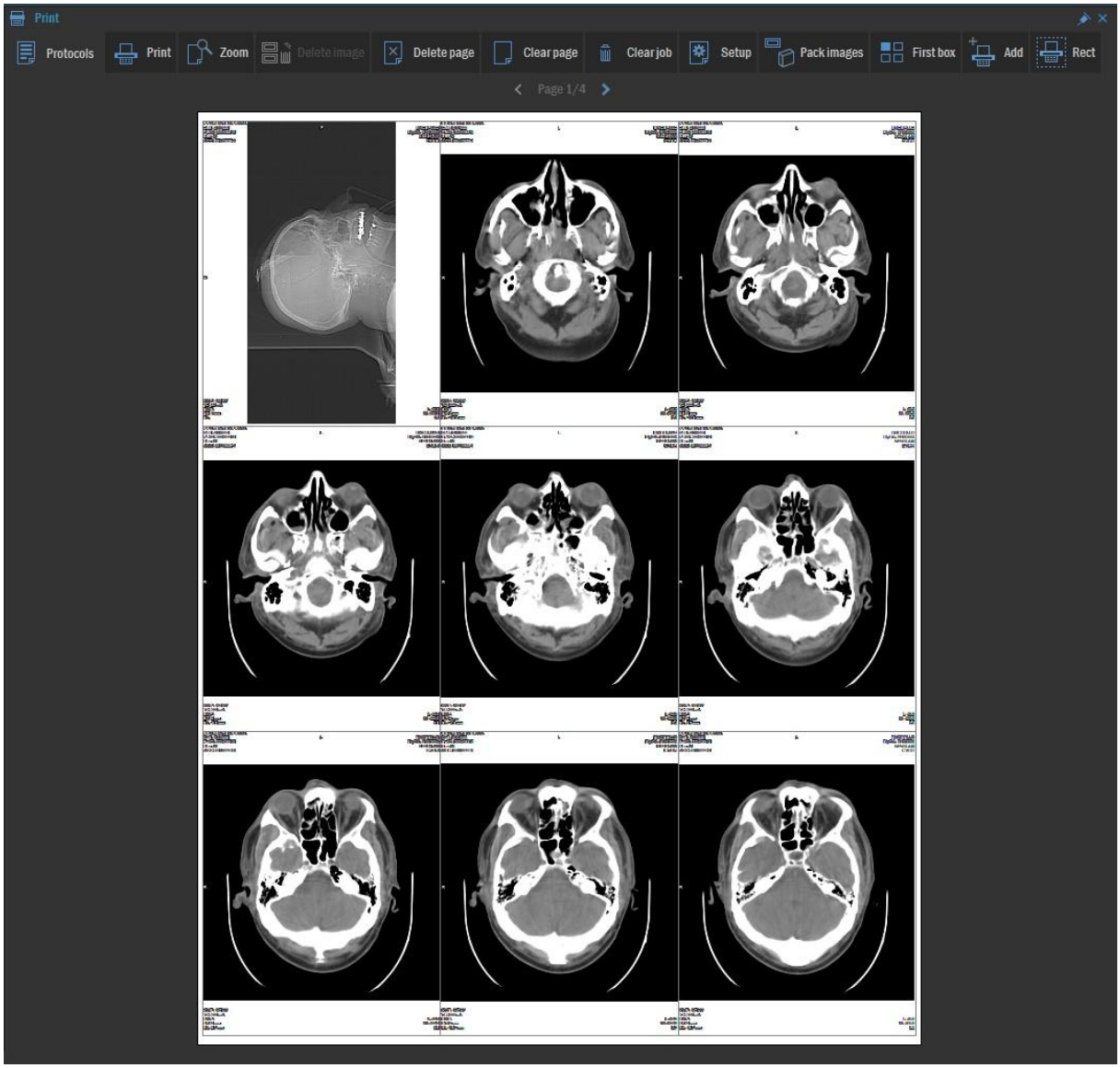
Don't change current apply	Doesn't change default setup
Add current image	Adds current image to print
Add current series	Adds all images of current series to print
Add all loaded images	Adds all images of current study to print
Add selected images	Adds the set of selected images to print
Add one image every	Adds to print images whose number is included in an interval. e.g. if the series is constituted by 10 images and we set to 2 the parameter *Add one image every*, the first operation of "add image" will send to print the first image, the second operation will send the third image (1+2), the third operation will

	send the fifth one (3+2) and so on.

Print preview

If you click on the **File | Print preview** option or open the **Print** side panel (from the label to the left of the work area or from the **Window | Print** menu), the panel will appear on the display (Figure 27).

Figure 27. Print side panel



The following buttons are available on the toolbar in the print preview and print management window:

Add Adds the selected image (or series to which it belongs, the entire study or the set of images selected, according to the range of application chosen and confirmed by the user) to the print job
Rect used to select a rectangular area of the image and send it to the print job
Protocols used to choose a layout for the images on the pages to be printed and other options concerning the page setup and the addition of images to the print job
Print job starts printing.
Zoom enables you to view the print preview with a greater zoom factor
Delete image deletes the selected image from the page to be printed.
Delete page deletes the images and current page and moves onto the next one, if present.
Clear page clears all images from the current page.
Clear job clears all the pages of the current print job.
Setup used to set the layout of the page to be printed.
Pack images compresses images, removing frames and empty images.
First box this control field, if enabled, places the new images to be printed in the first empty frame. If disabled, they will be added to the end of the job.

To select an image from the print preview, simply click on it. To select more than one image, hold the CTRL key down while you click on the images of interest.

Setting a Header/Footer

Having appropriately configured the page to be printed from MedStation Configuration (see Appendix C), you can have the following indicated on each page printed:

- A text box at the top of the page containing patient data (Header)
- A text box at the bottom of the page containing department data (Footer)

Printing

The job can be printed by selecting the **File | Print** command or by pressing the **Print** button on the **Print** side panel.

A window is displayed enabling you to select and set up the printer, the number of pages, the number of copies, the medium used and the destination of the images to be printed.

Field	Description

Name	Name of the printer.
Type	Type of printer. Can have the values: Windows, DICOM, 3M.
Where	Printing output route: In the case of 3M or DICOM, printing indicates the spool folder.
Film destination	Film destination, used only for DICOM printers. Can have the values: MAGAZINE (archived film), PROCESSOR (developed film).
Medium type	Type of print media used for DICOM printers only. Can have the values: PAPER, CLEAR FILM, BLUE FILM.
Priority	Specifies the print priority, used only for DICOM printers. Can have the values: High, Medium or Low
Number of copies	Number of copies to be printed for each page.
All	Prints all the pages
Pages	Prints all pages from/to.
Font	Sets the style and size of characters to be used for printing.

If you press the **Print Spool** button, the print queue will be displayed, enabling you to cancel jobs being printed or spooled.

Chapter

6
MPR Display Mode

This chapter describes the functions of the add-on **MPR** (*Multi-Planar Reformatting*) modules for creating oblique slices of tomographic studies and **2D Curved MPR** for creating series of landscape images or images perpendicular to polygonal curves drawn a 2D image.

Accessing MPR Display Mode

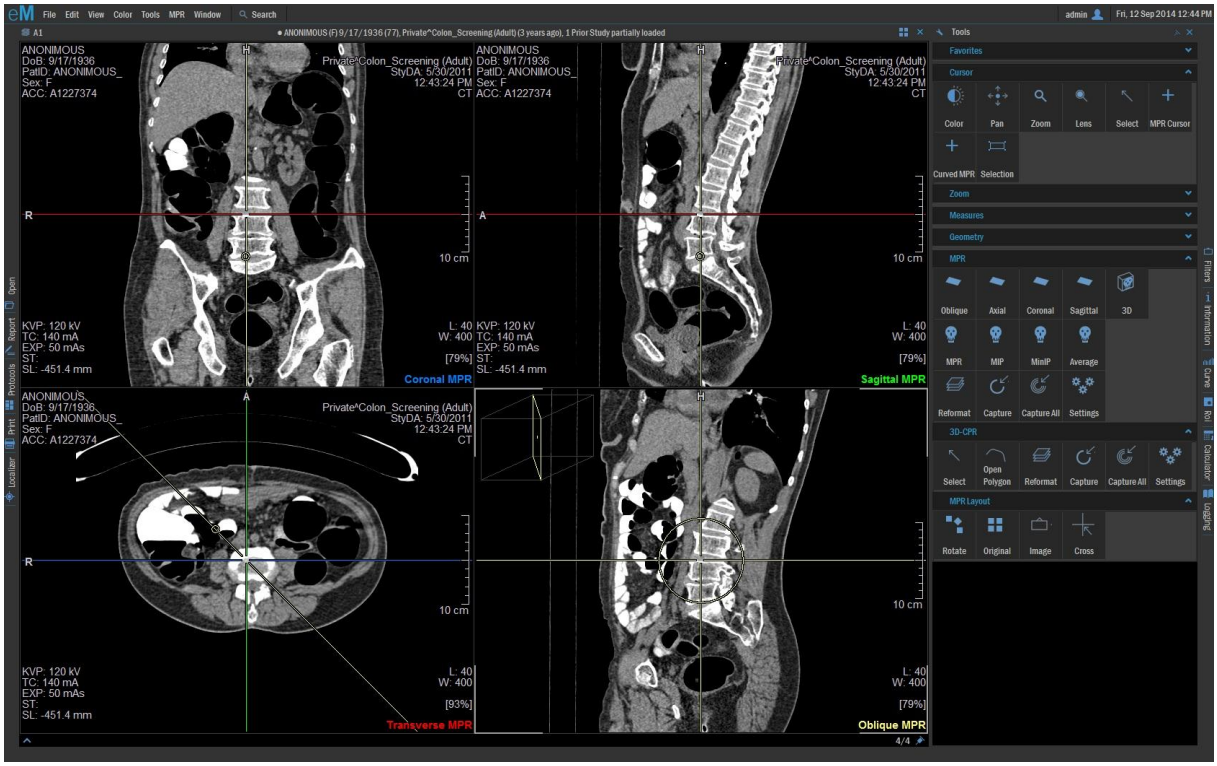
The same window used for image display and standard management is used for the **MPR** display mode.

To activate the MPR display mode:

1. Click on an image in the series to be displayed in MPR.
2. Select the **View | Mode | MPR** item or the **MPR** button on the menu that appears when you click on the name of the view in which the series is displayed.

Note: *All the images in the current series parallel to the selected image are used for MPR display. The MPR display mode will be activated for CT or MR images, if the series has at least two images and if the images are slices of a three-dimensional volume.*

Figure 28. MPR display of a series



MPR display window

The graphic area is automatically subdivided into four views in the MPR environment: axial, coronal, sagittal, and oblique planes of the volume reconstructed from images of the selected series (as in Figure 28).

On each view there are:

- Image, patient, study data as in 2D images
- a small square which identifies the view
- the navigation lines

Each line is the intersection of current view with another one, the line is drawn in the same color and with the same number as the view which it represents.

Note: *To hide/show lines of intersection among views, use the item* Show | Display reference line.

The intersection of lines is called “pivot”, which is the point through which all the sections pass.

Navigation takes place in the currently selected view and acts differently for the three axial, coronal, sagittal views with respect to oblique image.

- *Sagittal, axial, coronal planes.* With the "MPR cursor" (default setting, which can also be found under **Tools | Cursor**), by moving the mouse with the left key hold, you enter the "navigation" status. Depending on the line or point on which you point your mouse, you will shift the pivot or turn the oblique view. Other views will change to reflect the new intersections with the current view. It is also possible to change a single horizontal or vertical line. The intersection line with the oblique view has a small circle, which can be used to rotate the line around the pivot with the mouse. To exit the "navigation" status and fix current position, simply stop moving the mouse and release the key.
- *Oblique plane.* Not only can you move the pivot, you can also rotate the image around its center by clicking on the circumference shown on the image.

On top left corner of the image cross section, is drawn a parallelepiped that represents a volume generated by the images of the chosen series and it's constituted by: horizontal plane xy which is always the plane of images of the chosen series; the height represented on axis z depends on how many images are contained in the series and the space between them. Therefore *the orientation of the drawn cube is not closely related to the orientation of the patient (according to the reference system of patient described by the DICOM standards) but changes from time to time depending on the choice of the series on which you perform the MPR reconstruction.* Within this cube is drawn the plane containing the oblique view that reflects each movement that occurs while navigating through the views.

For all views, if no line is selected, you can enter the navigation mode **stack view**. In navigation mode (cursor MPR), simply by rotating the mouse wheel; in pan mode, by holding the central wheel of the mouse pressed and by moving the cursor within the display area of an image. In stack view mode, you will see a sequance of parallel images scroll one after the other in the same view.

MPR tools

The **Tools | MPR layout** menu and the **MPR layout** sheet on the **Tools** side panel include the following functions:

Rotate rotates axial, sagittal and coronal views in the window counter clockwise.
Original cancels all volume navigation operations and returns the views (axial, sagittal, and coronal) to the original positions that are at the center of the volume. If visible, the oblique view is also returned to the original position.
Image centres all the images within the current views on the screen
Cross moves the image so that the pivot is located at the center of the current views

The **Tools | MPR** menu and the **MPR layout** sheet on the **Tools** side panel include all the

functions available in MPR mode.

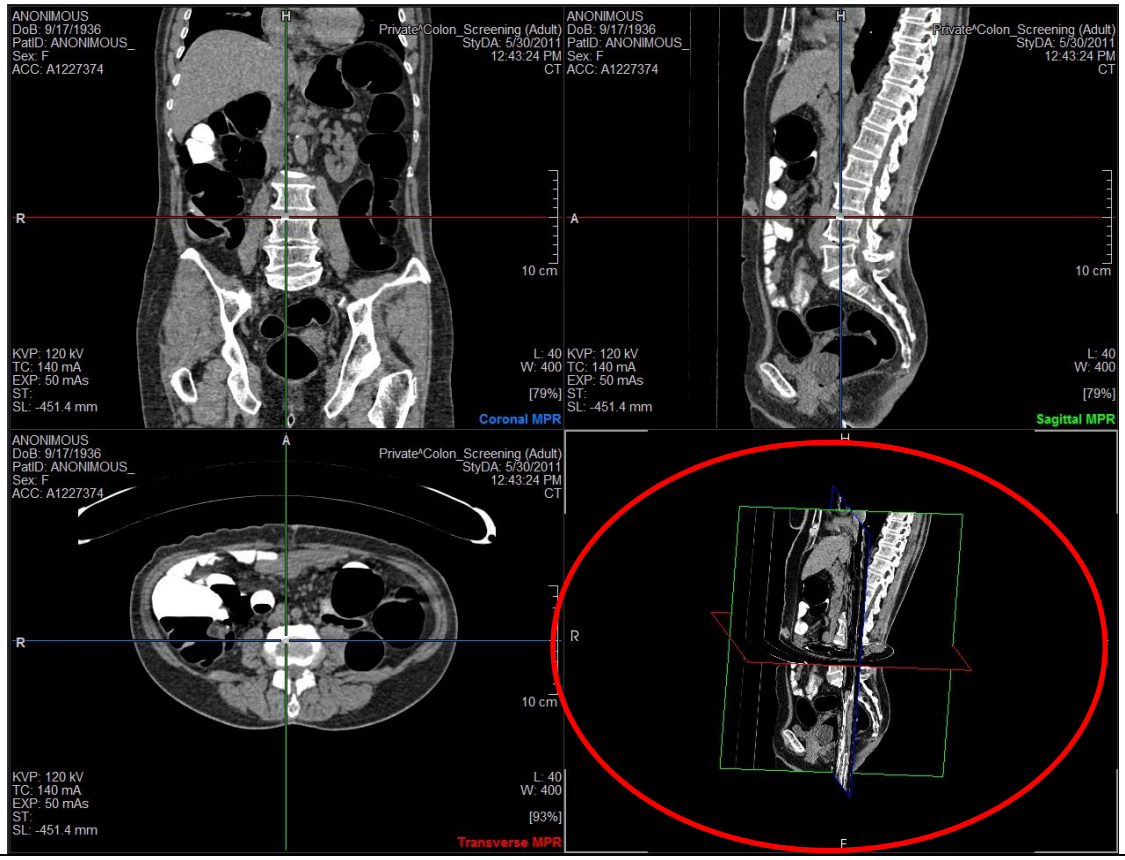
Oblique displays as oblique view a section perpendicular to the transverse and rotated of 45° with respect to coronal and sagittal sections

Axial displays axial section as oblique

Coronal displays coronal section as oblique

Sagittal displays sagittal section as oblique

3D displays the three fundamental sections in a three-dimensional space and predisposes environment for interaction (see following figure)

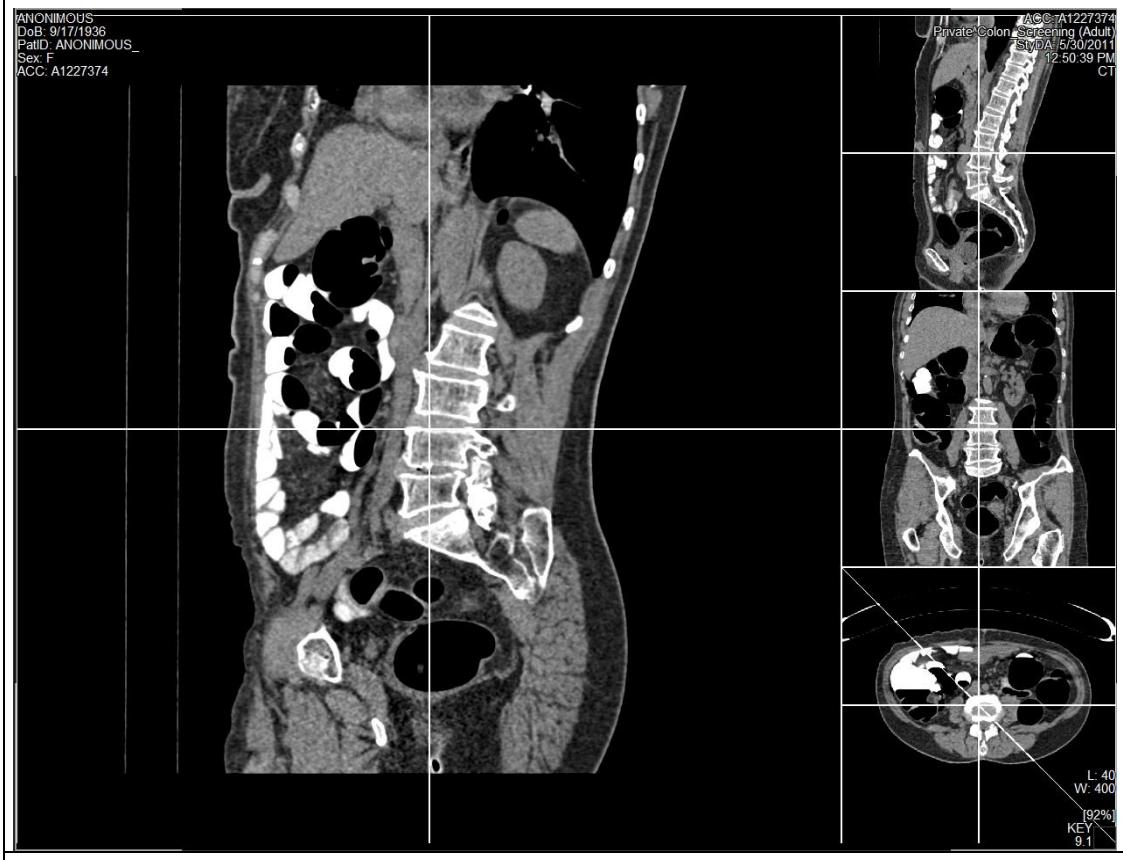


Reformat enables the generation of a new series of slices parallel to the current oblique plane and evenly distributed along space at a specified distance. A dialog box is displayed in which the user can specify the number of images to be generated and the distance between them, expressed in mm.

The new series of images will be added to the current study

Capture adds to the study an image with selected view

Capture all adds to the study an image with the oblique view besides the axial, sagittal and coronal views. As in the following example



MPR *(Multi-Planar Reformatting)* brings the display back to MPR standard views having used the MIP, MinIP or Media functions.

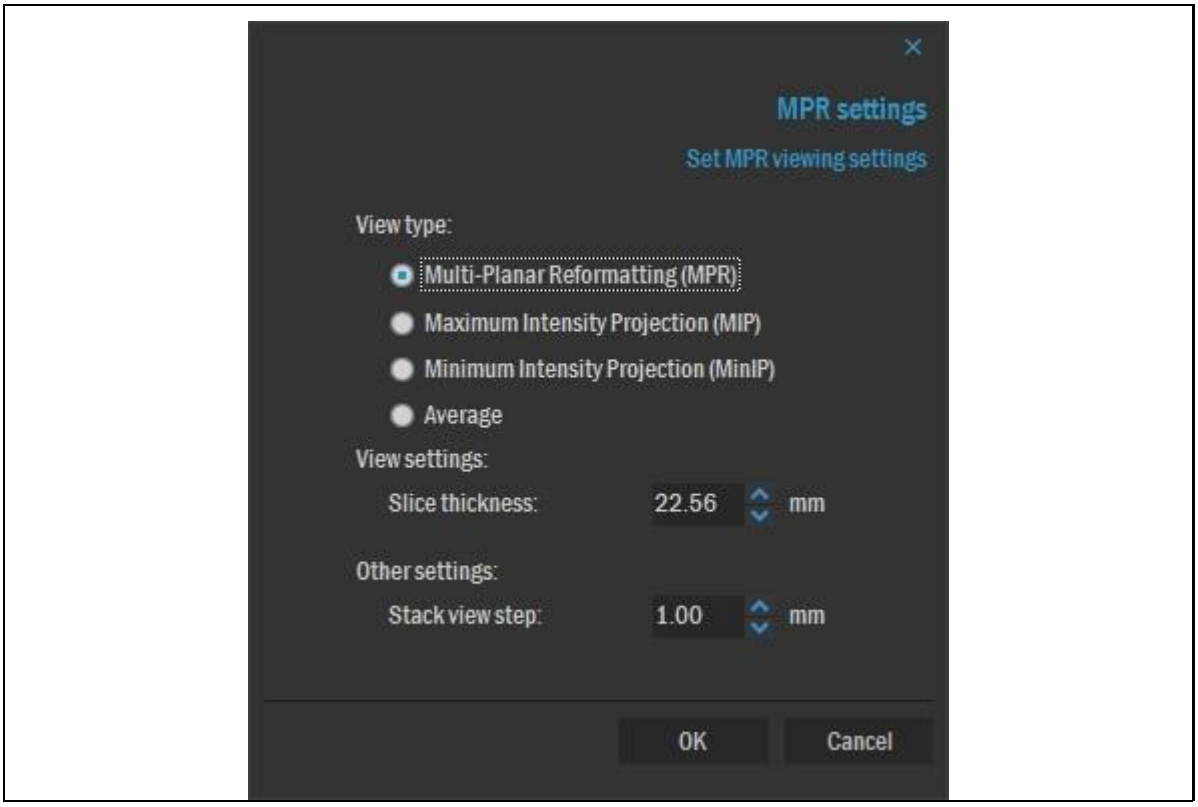
MIP (*Maximum Intensity Projection*) activates a grayscale method to emphasize the tissues (as bones and vascular tissues) represented with the highest pixel value in the spatial range set using the "Option" mask or chosen interactively on current image by acting on lines parallel to the section of which you want to calculate the MIP.

MinIP (*Minimum Intensity Projection*) activates a grayscale method to emphasize the tissues (like structures filled with air) represented with the lowest pixel value in the spatial range set using the "Option" mask or chosen interactively on current image by acting on lines parallel to the section of which you want to calculate the MinIP.

Average activates a grayscale method to display the medium pixel value in the range set using the "Option" mask or chosen interactively on current image by acting on lines parallel to the section of which you want to calculate the Average.

Options allow setting the display of views applying algorithms of MPR, MIP, MinIP, Average and, for these last three, choosing the thickness of the volume on which to act (which will be the same for every section). You can also set the distance between an image and the following during stack-view navigation.

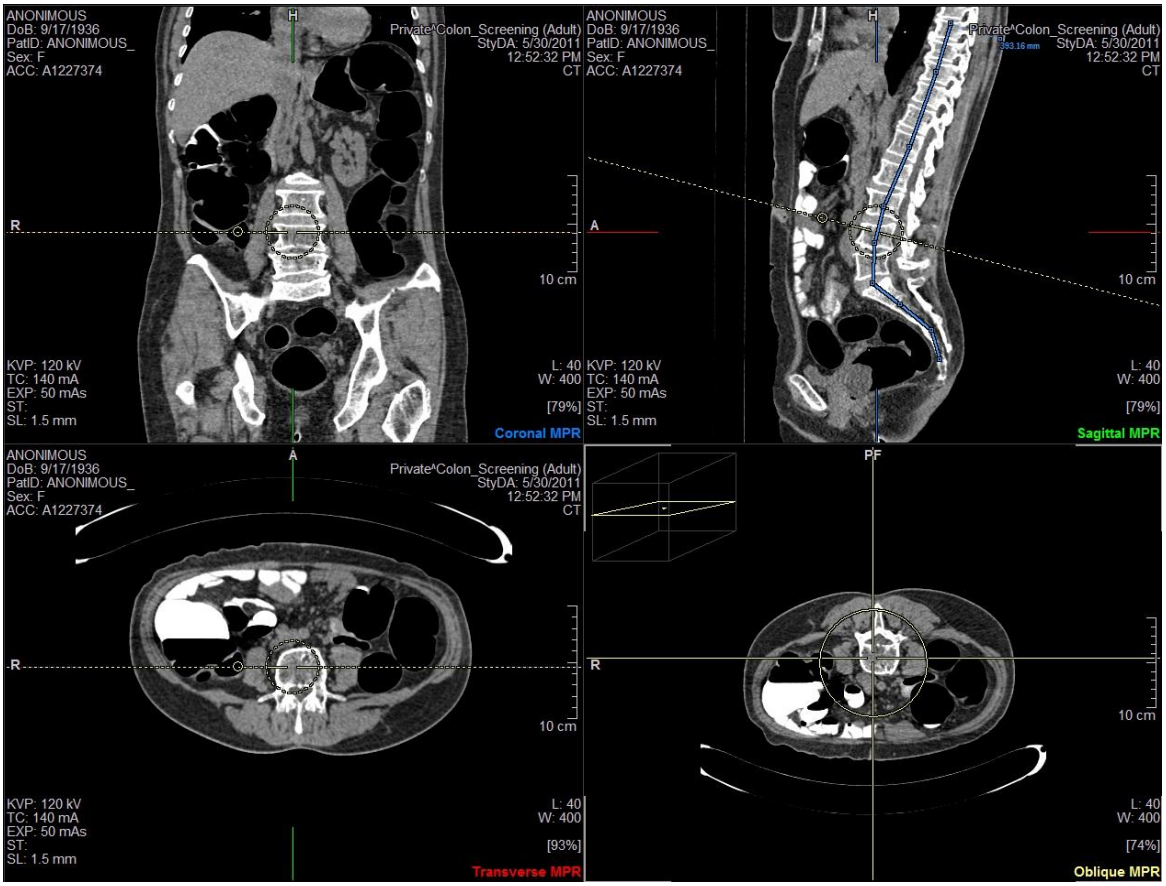
Figure 29. MPR Options



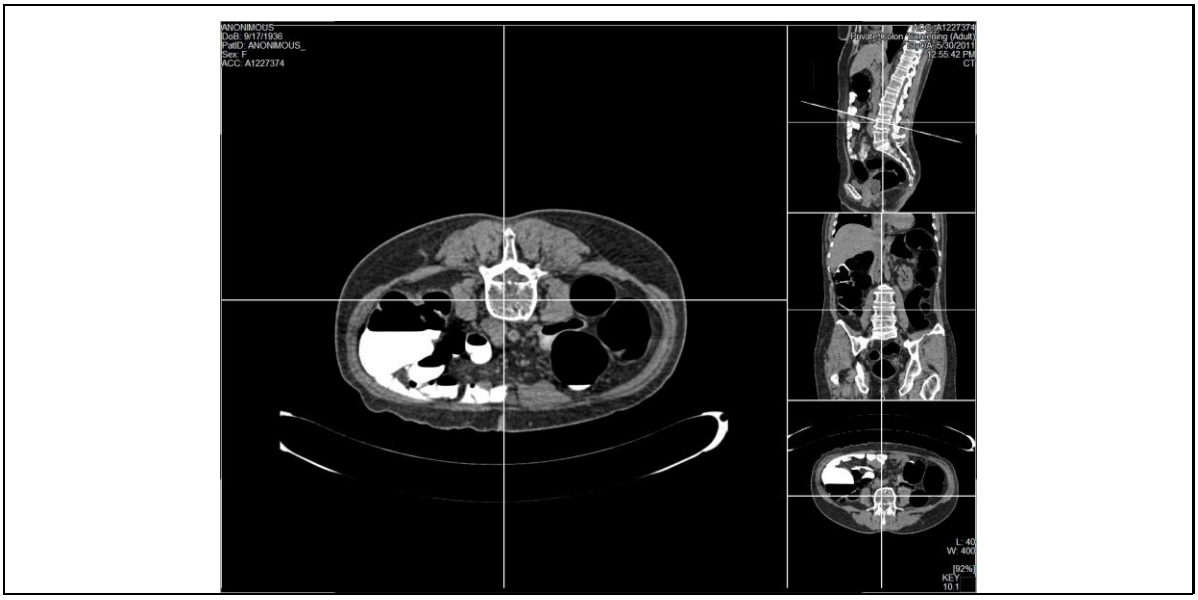
Warning! *Any new series of images, generated by re-formatting, are definitively stored in the archive only when you save the whole study (**File | Save** option).*

The **Tools | 3D Curved MPR** menu and the **3D Curved MPR** sheet on the **Tools** side panel contain the tools for moving the oblique plane along a polygonal curve drawn on one of the main three views (Figure 30).

Figure 30. Navigation along a curved slice (3D curved MPR)



Select enables you to select curves drawn on the current view
Open polygon enables you to draw an open polygonal curve
Options opens a window that allows you to set the interval (in mm) between the oblique views along the curve and perpendicular to it
Reformat enables the generation of a new series of images made up of slices perpendicular to the point of selected curves on one of the three main sections and equidistant from each other of a distance defined by user in MPR Curved 3D options.
Capture adds an image with the selected view to the study.
Capture all adds an image showing the oblique view with the axial, sagittal and coronal views beside it, as shown in the following example, to the study.



Note: *The* ***Tools | Geometry*** *menu contains some geometrical transformations that you can use on images in MPR mode. Unlike similar functions in 2D that operate according to settings of Apply to, in MPR mode they are applied to every view.*

Mirror performs a reflection with respect to the vertical axis
Flip performs a reflection with respect to the horizontal axis

2D curved MPR mode

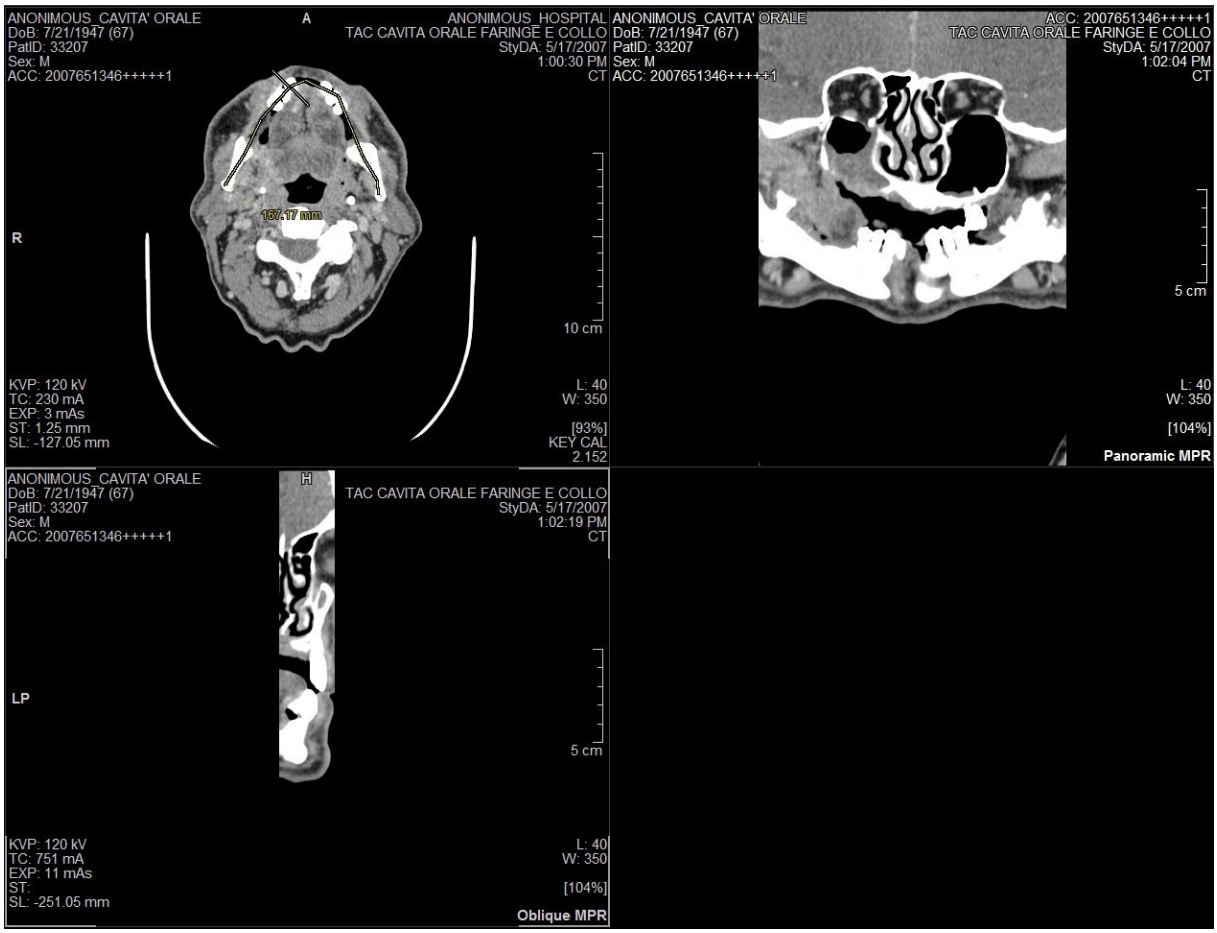
To display a study in **MPR curved 2D** mode is used the standard display and management box

To enable 2D curved MPR display mode

1. Click on one image of the series to display in MPR curved 2D mode.
2. Select the **Display | Mode | 2D curved MPR** option or click on the **2D curved MPR** button on the bar in the box in which the series is displayed.

Note: *In MPR curved 2D display mode, the system employs only images of current series parallel to the selected image. MPR mode will be actived if the series has at least two images and if images are parallel sections of a three-dimensional volume.*

Figure 31. Series displayed in 2D curved MPR mode



2D curved MPR display windows

In MPR curved 2D environment, the graphic area will be automatically subdivided into four views. The first box will always contain the images of the series of the selected image. Select in one of these images a polygonal measurement on the image in the view in the top-left-hand area or draw one, thus another box will contain the image constructed with the points of the curve projected on all images in the series (panoramic view). The third box will display the sections perpendicular to the points of the curves (calculated images are equidistant from each other of a distance defined by user in the options).

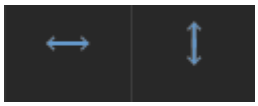
Navigation is different in the three views.

- *Source image* The stack-view in this box scrolls the images of the series to which current image belongs in the passage to MPR curved 2D mode. When in this box the current image changes, the other boxes update automatically showing a perpendicular slice and a panoramic view of one of the curves of the source image or empty boxes if the source image has no curve.
- *Section perpendicular to the curve* If you scroll images in this box, you will see a sequence of volume sections built perpendicular to the curve selected on source image, on which you will see the intersection line between the two image planes.
- *Panoramic view* In this box, you will see the panoramic views, i.e. images obtained by cutting the volume of source image along the selected curve and by displaying the flattened slice. Scrolling the images in this view, you will obtain slices of curves – always belonging to the source image in the first box – obtained by means of horizontal or vertical translation of the original curve, or of curves obtained from original curve by moving all its points so that the identified segments are parallel to the originals.

2D curved MPR tools

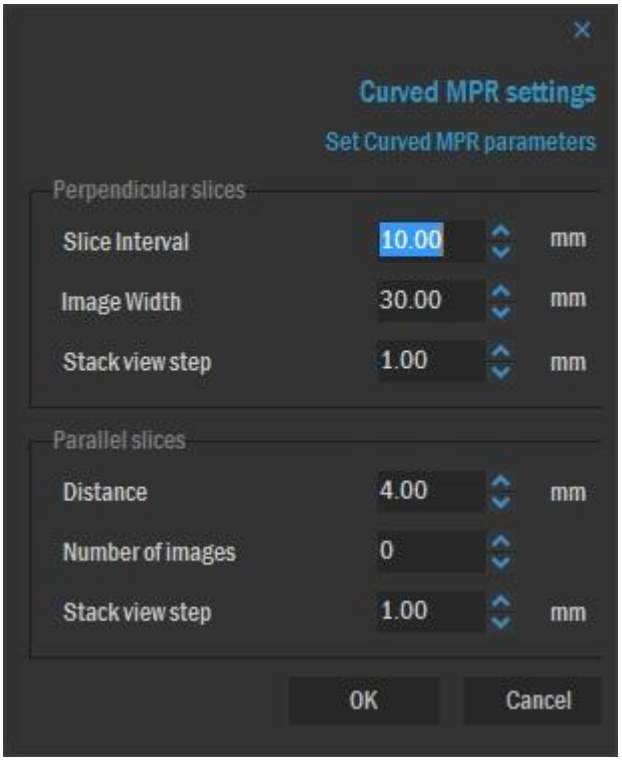
The **Tools | 2D curved MPR** menu and the **2D curved MPR** sheet of the **Tools** side panel contain the following functions:

Select Enables you to select the curves drawn on the current view
Open polygon Allows you to draw an open polygonal curve
Calculate parallel Stack operations on panoramic view increase and decrease the extension of the navigation curve maintaining its proportions
Translate Curve Stack operations on panoramic view translate the navigation curve in a vertical or horizontal way depending on the selection



Options A dialog box appears, enabling you to set the interval (in mm) between oblique slices perpendicular to the curve and the width (in mm) of new images. A width of 0 mm indicates to the system to create images of the same size as originals.

Figure 32. 2D curved MPR settings



You can generate an additional series of slices parallel to the navigation curve by using parameter in *"Parallel Slices"* section.

Reformat enables you to create two new series of images. A series will be constituted by sections perpendicular to the points of selected curves on a source image, equidistant from each other of a distance defined by user. The other series will be constituted by panoramic sections of the same curves in set of images obtained by means of parallel slices of as many curves and at what distance as set in options.

Chapter

7

3D Display Mode[34]

Accessing 3D Display Mode

To view a study in **3D** display mode, you can:

- Use the corresponding environment of the application or.
- Run an external application (see Appendix C of this manual to configure integration between MedStation and this application) for advanced 3D processing. The external application configured is started after opening the study displayed in MedStation, by selecting the **Display | Mode | External 3D** menu item or the **External 3D** item on the menu that appears when you click on the name of the image view of the study. In this way, the 3D processing application will be opened; in general, this application will process the data of the current series. After processing, work can be continued in MedStation.

Below is a description of the internal environment for viewing studies in 3D mode.

A study in 3D mode is displayed in the standard display and management box.

To activate 3D display mode:

1. Click on an image in the series to be displayed in 3D mode.
2. Select the **View | Mode | 3D** option or the **3D** button from the toolbar of the box in which the series is displayed.

Note: *In 3D display mode, only the images in the current series parallel to the selected image are used. The 3D display mode will be activated if the series has at least two images and if the images are parallel slices of a three-dimensional volume.*

[34] Function available only in MedStation but not in MedStation Express.

Figure 33. 3D Reconstruction



3D display window

In a 3D environment, initial reconstruction presents a front coronal view of the volume, reconstructed from images of the selected series.

On the images, you can see:

- Letters regarding the positioning of the volume in space according to DICOM standard DICOM (R, L, A, P, …)
- A system of axes orthogonal to the position of the volume in space
- Window/level information used for drawing

Navigation of the volume occurs by clicking the left mouse button and moving it in the desired direction of rotation. The **3D** menu and the **3D** sheet of the **Tools** contain the items for viewing the standard orthogonal positions: coronal (front and rear), sagittal (left and right) and axial (upper and lower).

To change level and quantity of displayed tissues click the right mouse button and drag from left to right or from top to bottom (standard *windowing* as in 2D mode). The *LUT* section of the **Color** menu contains the items for selecting preset window/level values, color and opacity tables that allow you to select the quantity, color and transparency of reconstructed tissues, respectively.

Note *When you work with a multi-monitor workstation, you can move the window to a moni-*

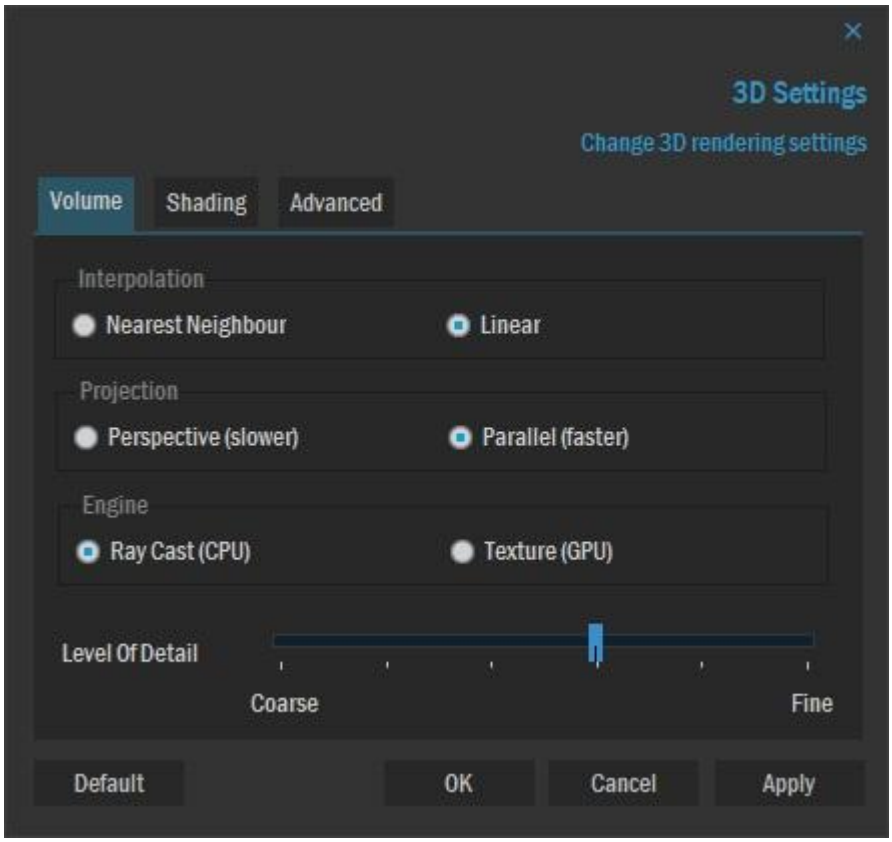
tor that allows a better rendering of colors, simply by clicking on the items of the ***Window | Monitor*** *submenu.*

3D tools

The **3D** menu and the **3D** sheet of the **Tools** side panel contain the functions available in 3D mode.

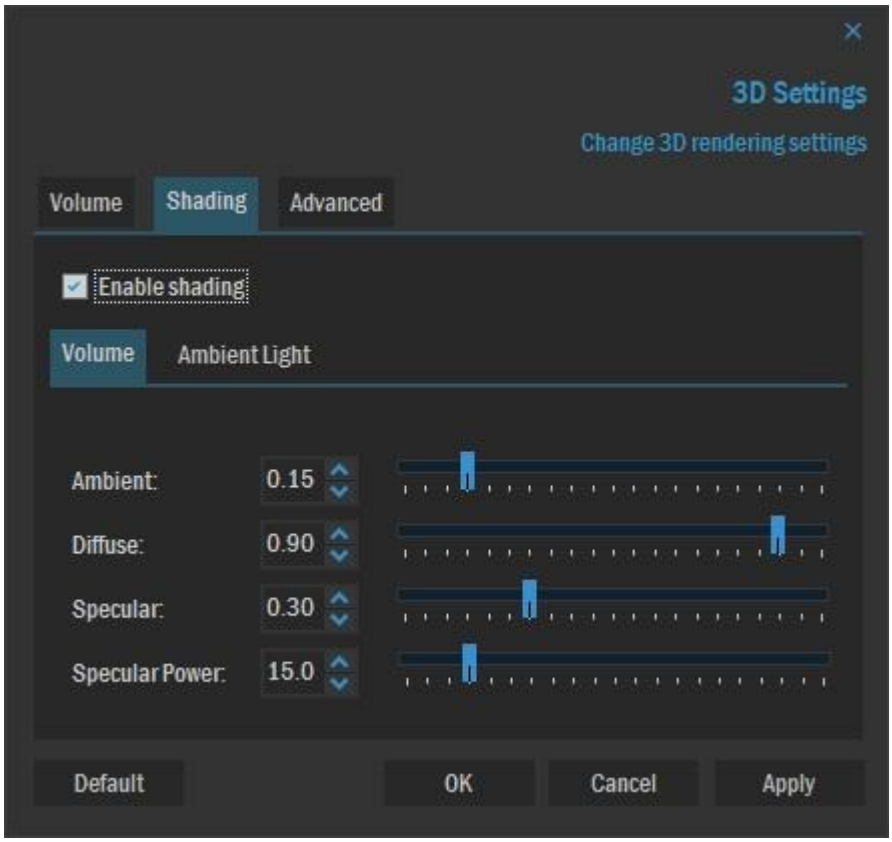
Original cancels all the operations of navigation in the volume and goes back to original position
Coronal shows the front coronal view of the volume; if you simultaneously click the button ALT, it shows also the back coronal view
Sagittal shows the left sagittal view of the volume; if you simultaneously click the ALT button, it displays also the right sagittal view
Axial shows the upper axial view of the volume; if you simultaneously click the ALT button, it displays also the back coronal view
3D displays the volume in standard modality, without scalar projection algorithms
MIP displays the volume using the Maximum Intensity Projection algorithm
3D Surface displays an isosurface of volume calculated by current window/level values
Best takes a snapshot of the volume at the maximum quality of drawing set in the options. If you simultaneously click the button ALT, it uses a unitary level of detail (a radius for each vertex). The action is available only with Ray Cast engine for drawing (see *3D Settings*).
Colour opens a window for changing the colour and opacity options of the 3D drawing (a more detailed description is given in the following section)
Cropping Box enables/disables the cropping box with planes parallel to system of reference. To move the planes you can drag the anchor points highlighted by colored globes
Cutting plane enables/disables and oblique cutting plane of the volume. To translate the plane you can drag a point of the plane, while to rotate it you have to drag the vector normal to the plane
Bone Removal enables the tool for removing bone parts. To remove a part you can modify the widow/level of the volume to show the desired bone structures and then click the left mouse button on the structure to be removed. You cannot cancel this operation. You can set the level of selection in 3D settings
Capture adds an image with current 3D view to the study
Settings allows you to set specific 3D display parameters.

Figure 34. 3D volume settings



- **Interpolation** changes the used interpolation algorithm: adjacent or linear (default)
- **Projection** changes the view projection type: perspective and parallel (default)
- **Engine** changes the type of engine for drawing: ***Ray Cast*** uses only the algorithmic calculation, ***Texture*** uses the graphics processing capabilities of the video card
- **Level of detail (LOD)** changes the level of detail with which the volume is drawn by using the Ray Cast algorithm. The finer the LOD the greater the number of rays used for the calculation of every single volume cell and the greater the definition of the resulting image.

Figure 35. 3D shading settings



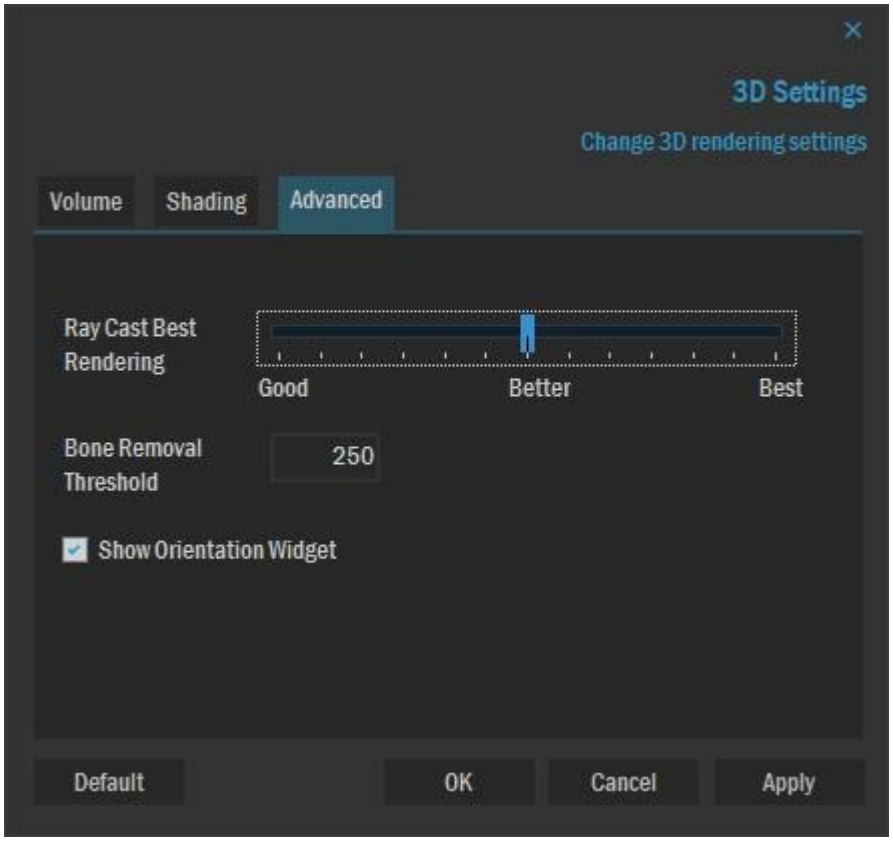
To enable the color gradient of the volume or change the shading, select the box in top left-hand corner of this section.

- **Volume** controls the gradient parameters of the volume:
    - **Ambient**: represents the total fraction of incident light reflected by the volume.
    - **Diffuse**: represents the fraction of light reflected by the volume for opaque objects. Diffuse lighting is a function of the angle between incident light and light normal to the volume surface.
    - **Specular**: represents the intensity (relative) of incident light reflected by shiny objects. Specular light is a function of the angle between the incident light, the light normal to volume surface and the angle of sight.
    - **Specular power**: indicates how shiny an object is, or, more specifically, how quickly the intensity of specular light decreases at the diverging of incident angle from total reflection angle.
- **Ambient light** controls the light parameters:
    - **Warmth** represents a special color spectrum from which one can deduce the incident light (from 0 for a cool blue, 0.5 for a natural white, up to 1 for a red sunset)
    - **Intensity** represents the intensity of light incident to the volume
    - **Height** is the latitude in degrees of the light incident to the volume. Positive

values of this parameter move the light above the volume.

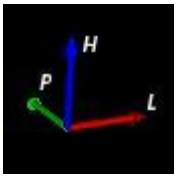
- **Azimuth** is the longitude in degrees of the incident light. Negative values of longitude move the light clockwise around the light.

Figure 36. Advanced 3D settings



- **Ray Cast Best Rendering** changes the level of detail used during the snapshots with highest precision quality
- **Bone Removal Threshold** changes the level used during the algorithm of bone structure removal
- **Show Orientation Widget** displays a box with orientation labels as regards to the patient

Figure 37. 3D Orientation Widget

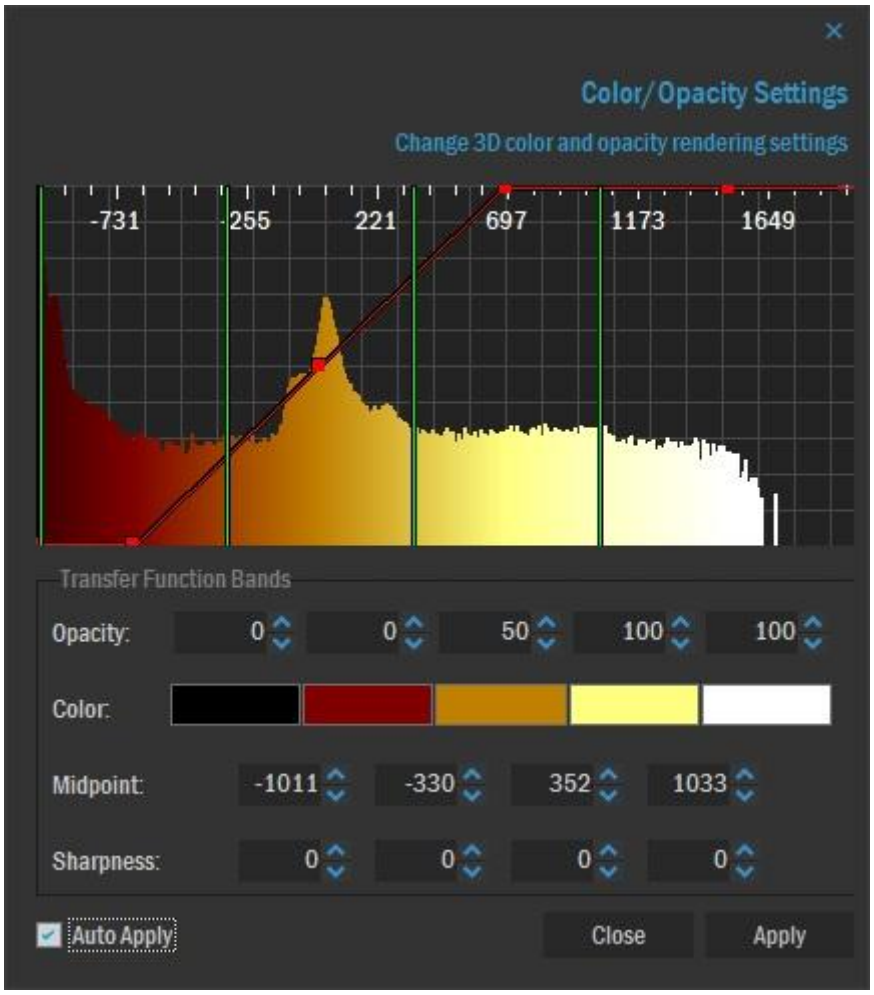


Default restores the default values of all parameters, to activate them, simply click on the OK or Apply button.

Color/Opacity settings

This tool (activated from the **3D | Color** menu or the **Color** button on the **3D** sheet of the **Tools** side panel) is used to modify the curves of color and opacity of displayed volume.

Figure 38. 3D Color/Opacity settings



The Color/Opacity dialog window displays a histogram with five bands (separated by four lines called *middle points*) related to the entire distribution of pixel values in the volume. The opacity of each band is shown by the red square in the center of the band. To change the opacity, you have to change the value of the corresponding box. The value can be between 0 and 100, where 0 is completely transparent and 100 is completely opaque.

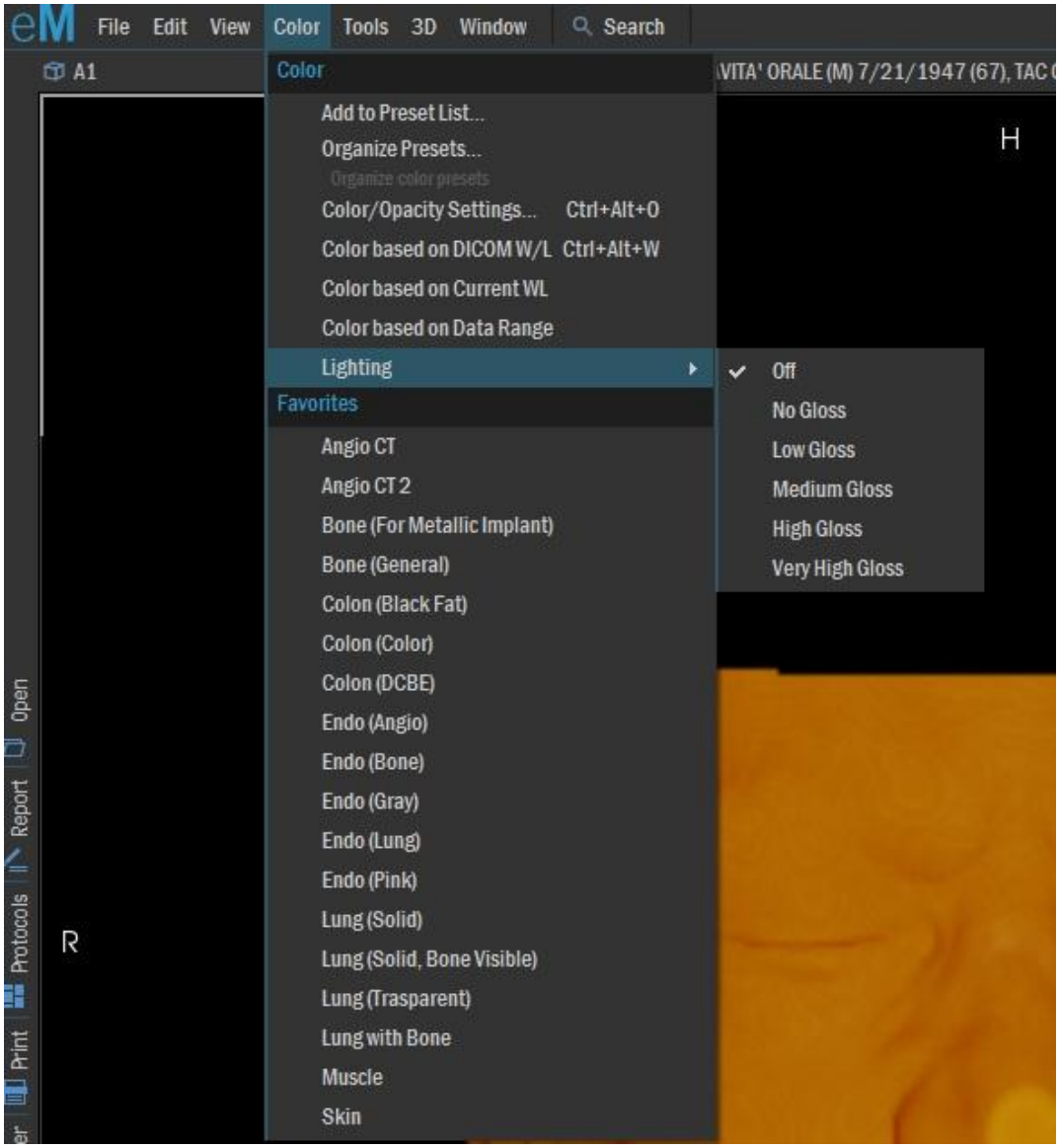
To change the color of a band click on the color bar corresponding to the desired band. To change the width of a band you must change the value of the corresponding middle point.

To change the way in which the values of opacity and color blend between two adjacent bands, you have to change the steepness value in the corresponding box. The value can be between 0 and 100 at intervals of 5, where 0 denotes a linear trend and 100 a step trend.

Preset Color/Opacity values

The application enables you to change the color/opacity values of the volume by using predefined settings. The corresponding menu is located in the **Color** menu

Figure 39. Default 3D Color/Opacity settings



Select the desired predefined element from the menu:

- **Color based on DICOM W/L**: changes color, opacity and in order to be appropriate with DICOM window/levels saved in original images.
- **Color based on current W/L**: changes color, opacity and lighting in order to be appropriate with current DICOM window/levels.
- **Color based on data range**: changes color, opacity and lighting in order to be appro-

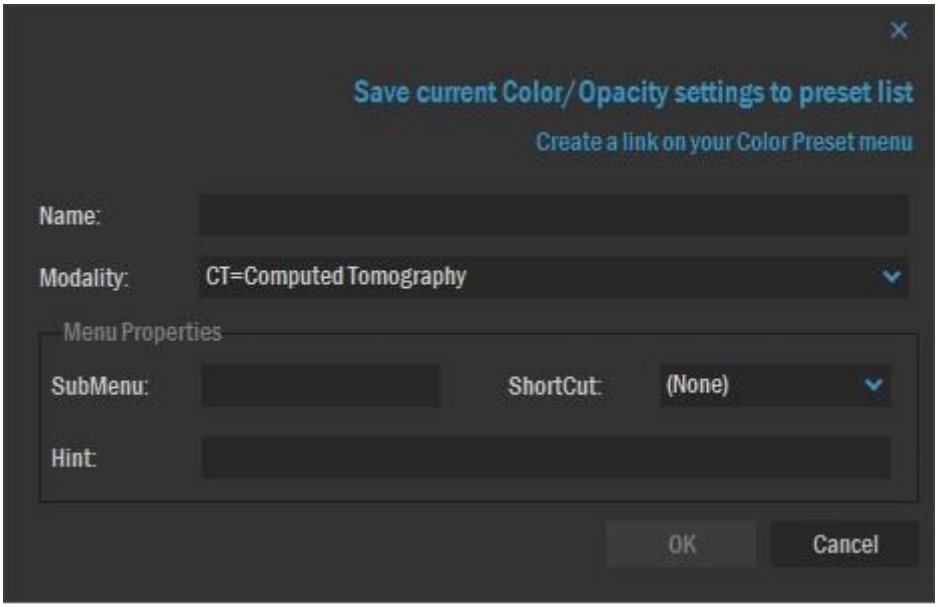
priate with the entire interval of pixel values of the volume.

- Remaining elements are values defined by the user.

Saving preset values

To save the current color, opacity and lighting settings click on the "**Add to preset list**" item on the **Color/Opacity** submenu.

Figure 40. Saving predefined Color/Opacity settings

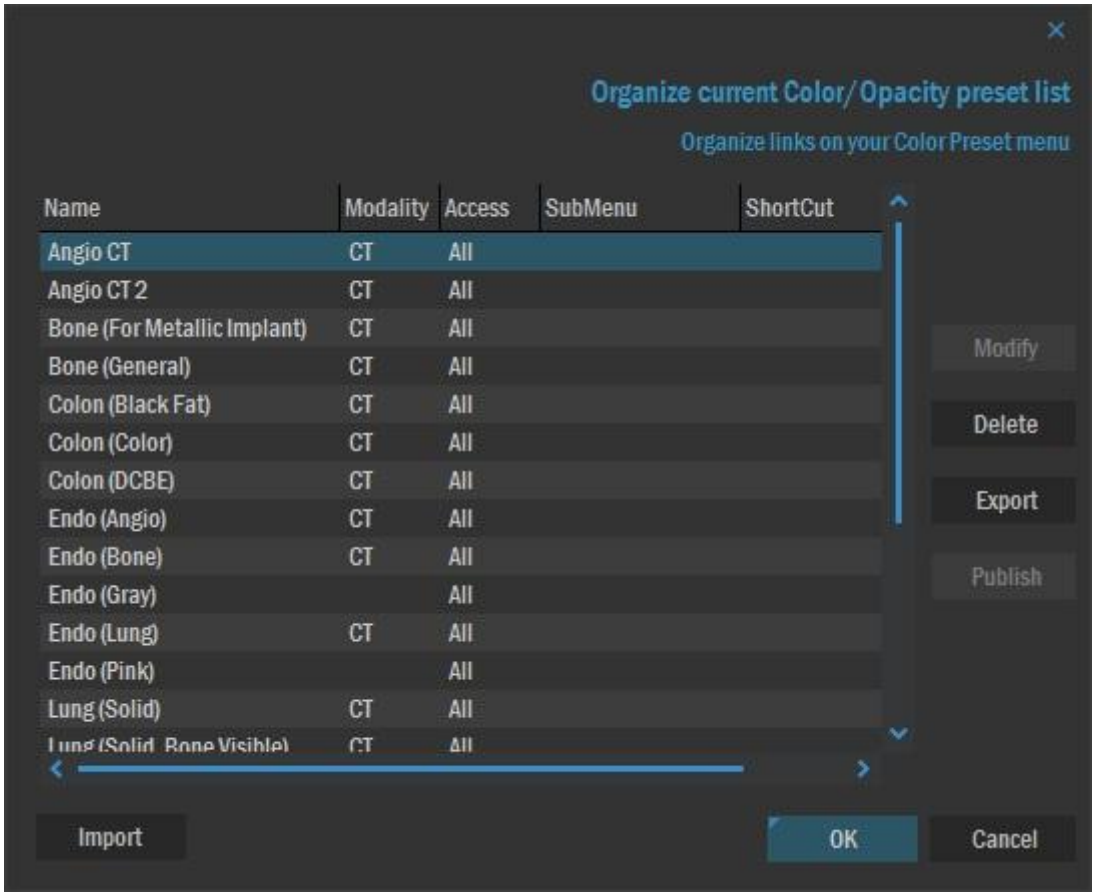


The creation window allows you to assign a unique name to the link and add it to a specific sub-menu. You can also assign a keyboard shortcut to the element and a hint for the description of the element when the mouse in positioned on it.

Modifying preset values

To change or delete predefined color, opacity and lighting elements created previously, click on "**Organize Presets...**" item on the **Color** menu.

Figure 41. Organizing 3D Color/Opacity presets



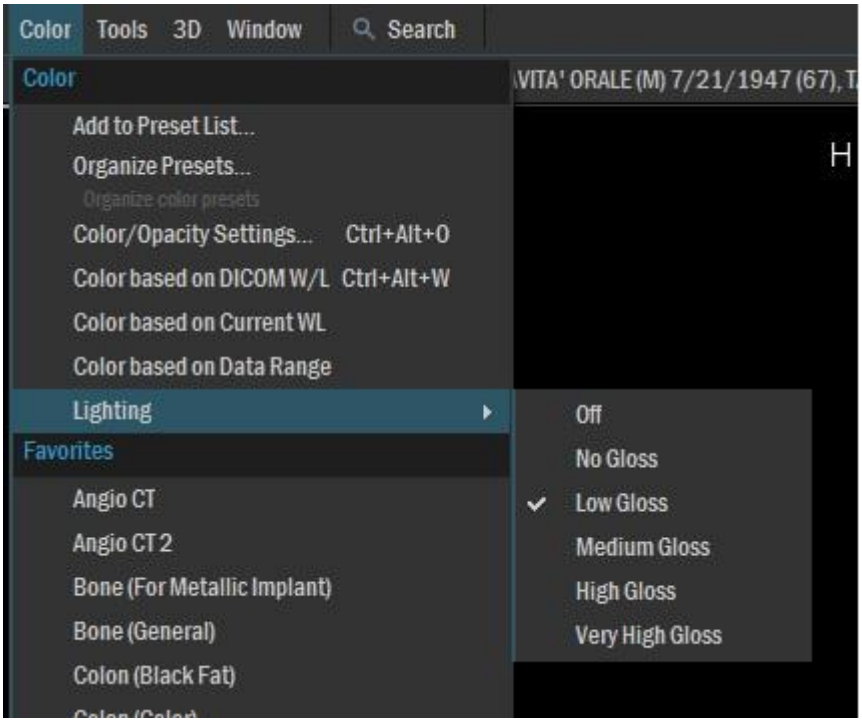
The preset organizing window allows you to change, delete and export items from the **Color**/**Opacity** menu. Newly created items can only be viewed by the user that created them but, by clicking on the **Publish** button, you can allow all users to view them.

By clicking on the **Import** button, you can import the Color/Opacity settings saved in an external file.

Preset lighting values

The application allows you to change the lighting and brightness of the volume using presets. To display the corresponding menu click on the **Color | Lighting** menu item.

Figure 42. Preset 3D lighting settings



The "*Off"* item displays the volume without any directional ambient lighting and without any shading.

The "*No gloss"* item displays the volume with directional ambient lighting and without any shading.

The other items display the volume with directional ambient lighting and with various degrees of shading and brightness.

Chapter

8
Cine/Loop Mode

This chapter describes the functions of the *Cine/Loop* environment for displaying series of tomographic images or *clips* in DICOM Multiframe or MPEG or AVI format.

Cine environment

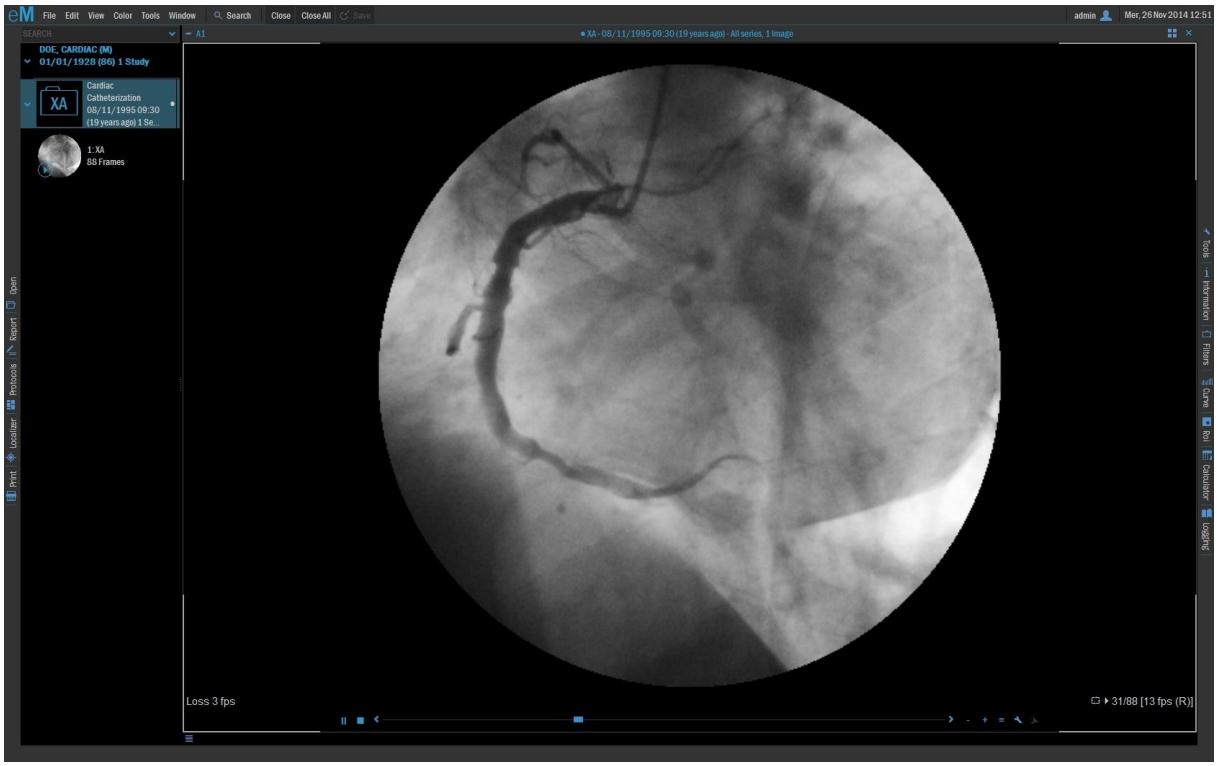
To activate CINE display:

1. Click on the image of the series to be displayed.
2. Press the space bar to start the video if the image contains one (multiframe image or MPEG file), or to start the loop of static images in the series to which the image belongs. The video is displayed in the same image view as the initial image; this view will take on video management characteristics.
3. (Alternative to 2.) Another way of starting a series of images or a video is to select it and run it from the study/series navigation panel. The study/series navigation panel shows the structure of the current study. In particular, there are icons representing the series of images that make up the study. The data beside the icon include the number of the series, the modality of the images, a description (if any) and the number of images present in the series. If any of the images in the series are ***videos*** (multi frame images or MPEG videos), beside the icon of the entire series will appear a list with an icon for each video image and, finally, an icon representing all and only the static images present. When you double click on the icon of a video, it will be played in a box and this box will show all the commands for managing Cine display options. If you double click on the same icon again, the video will be stopped and the image display grid will be restored in the work area. If you press the icon of the set of static images, only the *non*-video images of the series will be displayed in the image view.
4. (Alternative to 2. and 3.) Another way of starting an image containing a video is to press the *play* button, which can be found among the tools on the shortcut bar of the image. In fact, if the image contains a film (multiframe image or video), at the bottom of the image display area there will be a bar giving access to a set of tools for controlling the display of the images that make up the film. Clicking on the button will start the film.

CINE display mode works as follows:

- If the selected image contains a video in DICOM Multiframe or MPEG format (recognizable from the indication that appears in the bottom right-hand area “Fr: <No. current frame / Tot. no. of frames>”), the video is played.
- If the selected image contains a video in AVI format (also recognizable from the “Fr” indication in the bottom right-hand area of the image) the video is played.
- If the image selected belongs to a series of static images, the video played with consist of the images in the series displayed in sequence (in the order set for viewing).

Figure 43. CINE display window



In the bottom right-hand corner there will be a symbol indicating that all the frames have been loaded or are in the process of being loaded, the number of the current frame with respect to the total number of frames that make up the video and the display speed expressed in frames per second. The letter “R” indicates that the speed set corresponds to acquisition speed.

Management functions

At the bottom of the viewing area of a video being played there is a bar that shows the frame scrolling and provides access to some tools for controlling the display of the images making up the video. The ▶ button starts the video, while ■ stops it and the ◀ and ▶ buttons may be used to scroll back or forwards through the frames of the sequence.

The ◀◀ and ▶▶ buttons are used to regulate the play speed. In addition, while the video is being

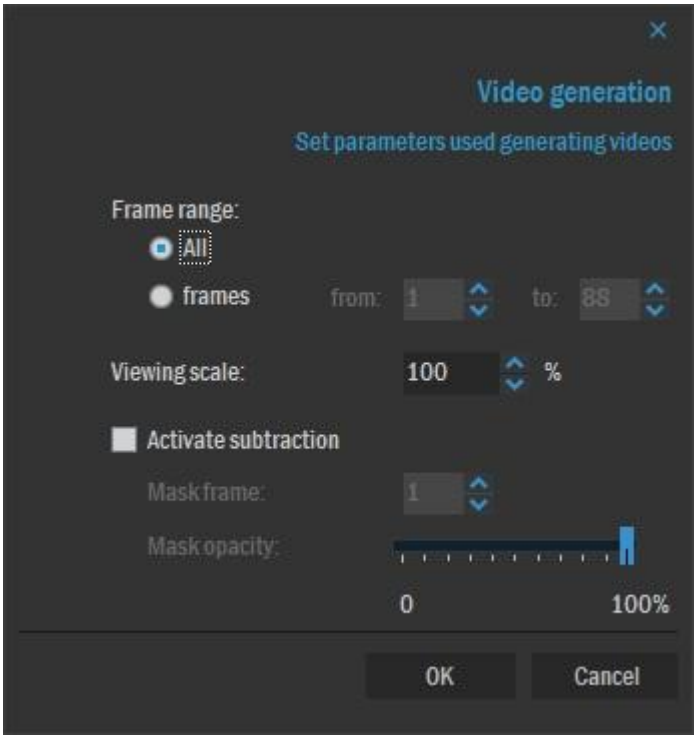
played, to *increase its speed*, that is, to reduce the amount of time between the display of one frame and the next, press the right arrow; while, to *reduce its speed*, that is, to increase the time between the display of one frame and the next, press the left arrow.

Press the  button to *Pause* the video. The same effect is obtained by pressing the space bar.

If the mouse has a scroll wheel, it can be used to interact with viewing in *cine* modality. If the video is running, moving the wheel will increase or decrease its speed. If the video is in pause, you can move the wheel to scroll through the frames.

The button after those for regulating the speed of the video opens a menu with the following items.

Synchronize scroll with	If there are several boxes for viewing studies and there are videos in two of them, you can create a link between them so that, when they are started, they are played together within a range of frames. ***Note:*** *If two boxes linked in this way contain the same video, they will be synchronized frame by frame.*
Disconnect all	Breaks any links between boxes in CINE mode
Go to	Opens a submenu with the following items: **First frame** shows the first frame in the sequence. The same effect is obtained by pressing the HOME key. **Last frame** shows the last frame in the sequence. The same effect is obtained by pressing the END key. **Next frame** shows the frame after the current image. The same effect is obtained by pressing the down arrow key. **Previous frame** shows the frame before the current image. The same effect is obtained by pressing the up arrow key. **Reference frame** shows the frame indicated in the DICOM tags of the current image as the frame representing the video.
Loop	Opens a submenu with the following items: **Set first frame** Sets the current image as the first in the cine sequence **Set last frame** Sets the current image as the last in the cine sequence **Reset start/end frame** Cancels the current first and last frame settings.
Repeat continuously	Activates automatic repetition of the cine sequence; the video is played non-stop, when it reaches the end it starts from the beginning again
Yo-Yo display	Activates automatic repetition of the video, playing the video from the start to the end and then from the end to the start.
Real time speed	Runs the video in real time, that is, it is played with the same time interval between images as when it was acquired. This function is obligatory for images in AVI format while it is optional for images in DICOM Multiframe format.

Subtraction	Enables mask subtraction mode for all images.
Use frame as mask	Uses the current image as a mask to be subtracted from all the others.
Selected figures	Opens a submenu with items for choosing the frames on which the measurements and notes selected on the current frame are to be displayed **First frame** makes the current frame the first in a range for displaying figures **Last frame** makes the current frame the last in a range for displaying figures **Show on this frame only** shows figures on the current frame and none of the others making up the video **Restore frame range** cancels the settings made using the items listed above
Capture	Creates an image (to be added to the study) with the image of the current frame.
Save video	For images containing a video, it opens a window for creating and saving a video from the frames that make up the study displayed. **Figure 44.** Creating a video  To create a new video, you can choose all the frames or those included within a range (**Frame range**), as well as the display scale (**Scale**). If you select the **Activate subtraction** box**,** the mask image will be subtracted

	from all other images and you can set the opacity of the subtraction mask on a scale from 0 to 100. When you press the **OK** button, the window for saving the video created will appear. Finally, you can choose the type of compression to be applied to the video created.

Chapter

9
The Options menu

The **eM | Options** menu allows you to configure information displayed on images and some operating parameters of the application.

Information on images

Using the **eM | Option | Info on images** command you enter a window from which you can configure information superimposed on displayed images.

The user can decide type and location of each single inscription by clicking on present boxes. You can specify nine lines of information to be displayed in the upper left corner, as many as in the upper right and in the bottom left corner. The list of information you can choose is preset (but can be expanded) and comprises some DICOM tag values that can be in the images.

Pressing the **Color** button opens a dialog box in which you can set the color of the information.

A preview window shows you the final result of the choices.

The mask is divided into tabs, each of which specifies a study modality, or a modality combined with a specific SOP Class. If there are no specific tabs for some modality, images will be displayed with the information indicated in the "Default" tab.

The **Add** button opens a window for choosing diagnostics for which configure the information to be superimposed on images of such modalities. In MedStation, adding a tab when there is a displayed study, the system will propose the modality combined with the SOP Class of the current image, if you want to create a generic tab only for the modality choose it from the drop down menu. While, on MedConf you can only create tabs associated with a modality without being able to combine with a SOP Class. Once you have created the new card, you can configure / change the lines of information for each corner choosing value from those that appear in the menu dropdown that opens for each row.

The **Delete** button eliminates the specific sheet of a diagnostic modality.



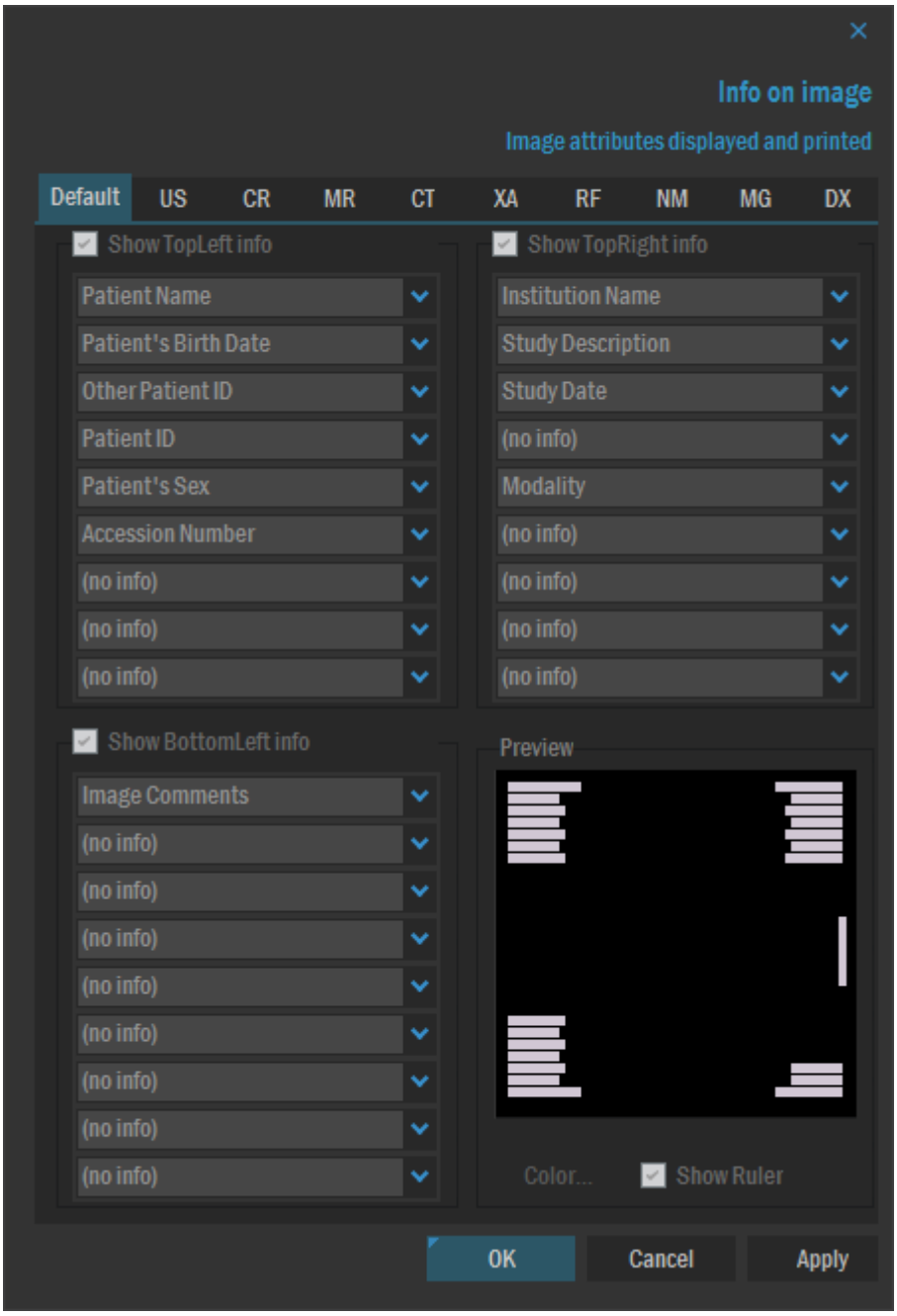
RC-05

***Note** The display of patient data on images minimizes the risk to visualize another patient's images during the reporting.*

RC-14

Note *The display of study data on images minimizes the risk of confusion between current and previous studies during the reporting phase.*

Figure 45. Configuring information superimposed on images



Application preferences

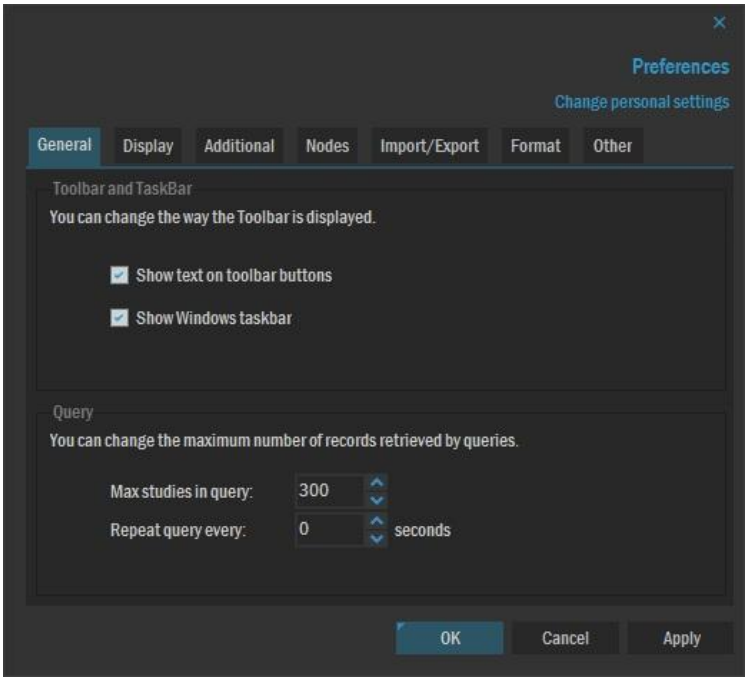
When you select the **eM | Option | Preferences…** command, a set of sheets for configuring

the application are activated.

Using the **General**[35] sheet (Figure 46), you can:

- Choose whether to display the Windows status bar or not.
- Choose whether to show text beside the buttons on the user-defined toolbar (for buttons that have an icon, otherwise the text is always shown)
- decide the maximum number of studies to be returned by a query and choose a time interval for automatically repeating the search functions (queries to a study server).

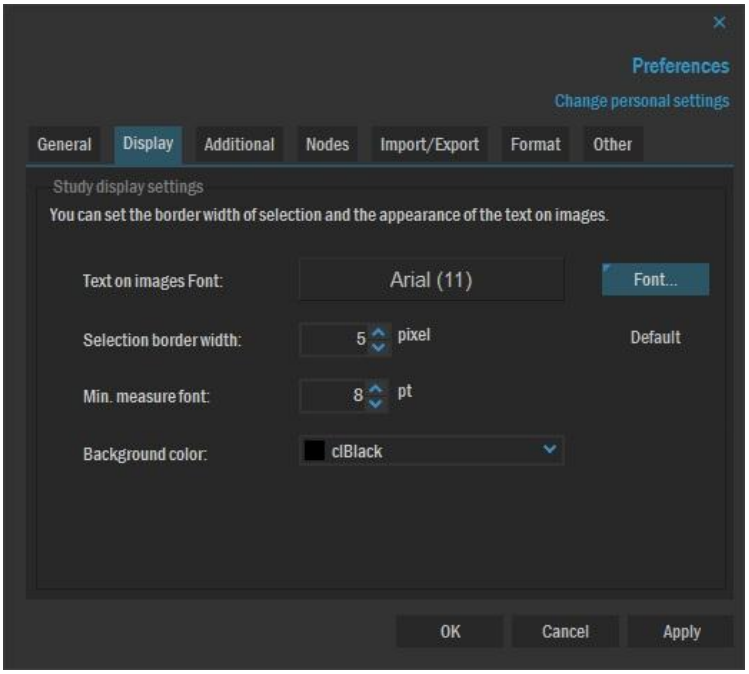
Figure 46. *General* configuration sheet



On the **Display** sheet (Figure 47) you can specify the border thickness of the image selected, the font type and size of the text to be superimposed on images, the minimum (in pixel) of texts displayed with measurements.

[35] Function available only in MedStation but not in MedStation Express.

Figure 47. *Display* configuration sheet

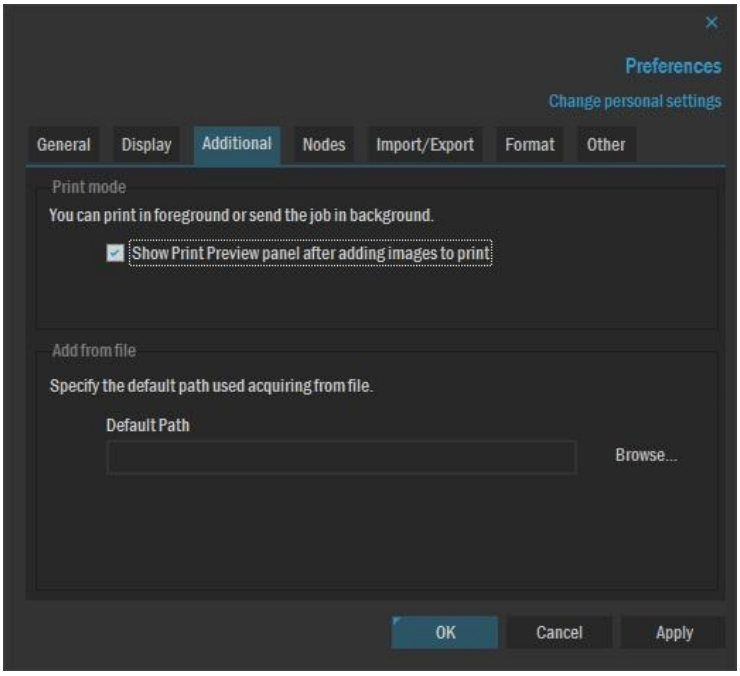


On the **Additional**[36] sheet (Figure 48) you can specify whether to show the print preview (if the **Print** side panel is closed) having added images to the print job. If this option is not selected, to see the print preview, use the relevant buttons or menu items.

You can also specify the default directory from which to add images to the current study, when you use the **Add from file** function.

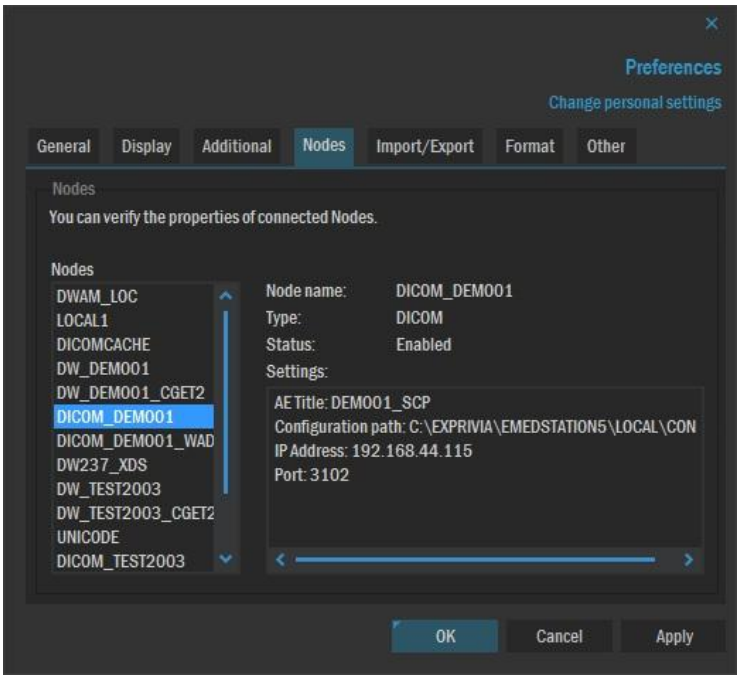
[36] Function available only in MedStation but not in MedStation Express.

Figure 48. *Additional* configuration sheet



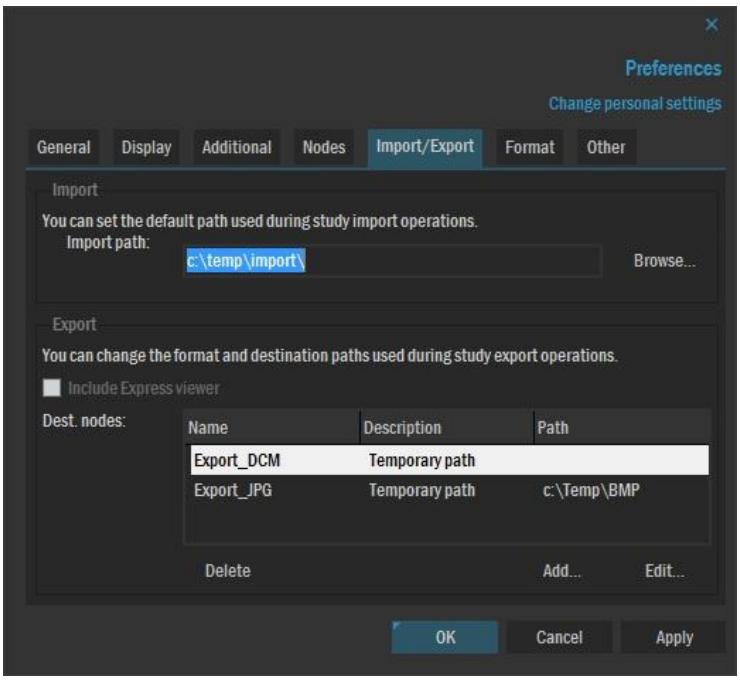
On the **Nodes**[36] sheet (Figure 49) you can check the properties of connected nodes. In a box to the left of this sheet appears a list with a description of the nodes. If you select one of these, you will see the related information to the right.

Figure 49. *Nodes* configuration sheet



On the **Import/Export**[37] sheet (Figure 50) you can change the default path used to import studies, destination nodes for studies export and image format used for each node.

Figure 50. *Import/Export* configuration sheet

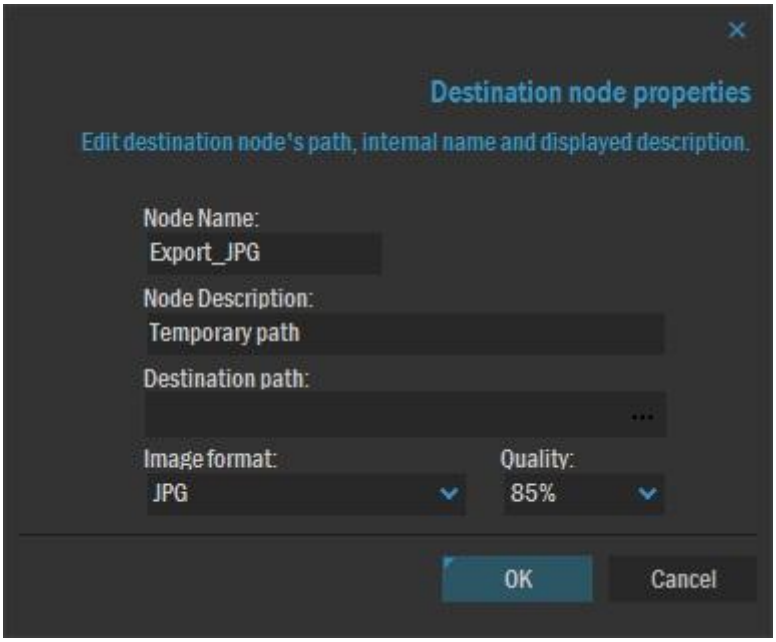


Using the **Add…** button you can add a new destination node by specifying: node name, description, destination directory, format and possible compression factor of the image (as in Figure 51).

Note: *If you do not specify any destination path, when you export a study, the system will ask you to choose a path.*

[37] Function available only in MedStation but not in MedStation Express.

Figure 51. Window for configuring a new study export node

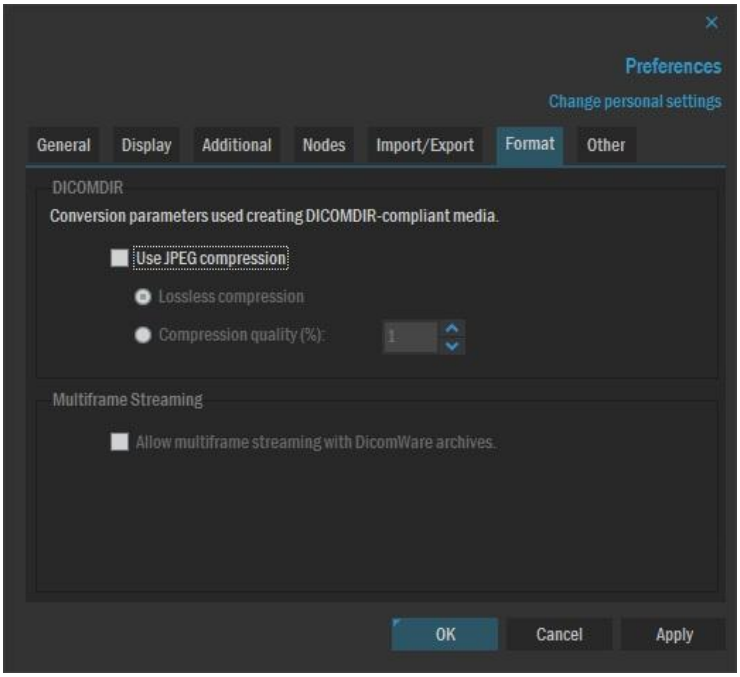


The **Delete** button eliminates the selected node form the list of destination nodes. Pressing the **Modify** button will show a dialog box similar to the one shown in Figure 51, in which you can change properties of a destination node.

In the **Format**[38] sheet it is possible to specify conversion parameters used for the creation of DICOMDIR media and enable/disable the STREAMING for the file MULTIFRAME from DWAM nodes.

[38] Function available only in MedStation but not in MedStation Express.

Figure 52. *Format* configuration sheet

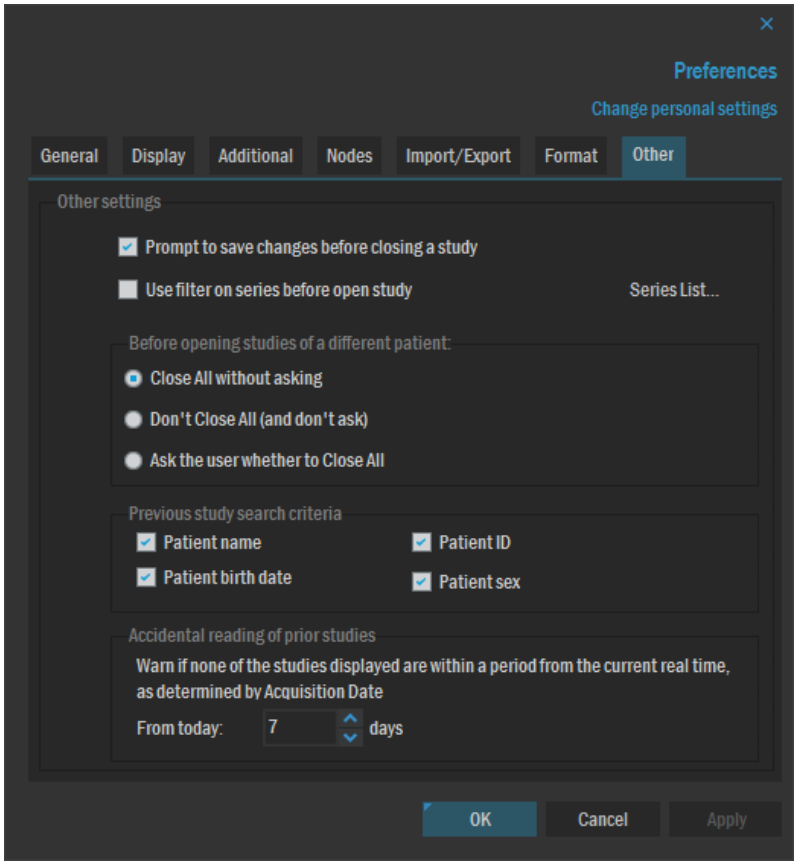


The **Other** sheet (Figure 53) groups various settings to customize the application according to user's needs.

You can set the application so that it asks the user to save the changes made on images of a study before closing it. If you exclude this option, by closing studies you will lose all changes made on them that have not been saved.

If you enable the option that applies a filter to the series before opening the study, MedStation controls the "Excluded Series List" of the series that should not be considered at the opening of studies with defined modalities. Some modern diagnostic modalities, effect studies with a huge quantity of images. Some series of images are not interesting for the reporting of the study. MedStation allows to filter these series thus avoiding to load and show them along with the rest of the study (unless you select them explicitly); in this way you simplify and speed up the work for loading and viewing of the study. In order to choose the series to avoid, press the *Excluded series list…* button and in the following window insert modalities and descriptions (separated by ';') of the series that you don't want to view when you open the whole study.

Figure 53. *Other* options sheet



RC-05 *Opening more than one study in MedStation could lead you to associate images of studies with the wrong patients.*

For this reason, the system displays warning messages if potentially risky situations arise.

The *Before opening a study of a different patient* section allows you to choose the type of behaviour to be assumed by the application when you display a study and you want to open a study of another patient:

RC-05 *Close all without asking.* When you open a study of a patient different from that of currently open studies, they will be closed without asking confirmation to the user.

RC-05 *Don't Close All (and don't ask).* When you open a study of a patient different from that of currently open studies, they will not be closed and the user will not be advised that the system is opening a study of a new patient and that open studies won't be closed.

RC-05 *Ask the user whether to close all.* When you open a study of a patient different from that of currently open studies, a message appears to advise the user that the system is opening a study of a new patient and to ask the user whether to close or not already open studies.

RC-05

The section "*Previous study search criteria"* allows to choose which filters (among date of birth, sex or patient ID, besides patient name) to be used for searching previous studies of a patient with a certain name.

RC-14

The section "*Accidental reading of prior studies*" allows to specify a number of days to warn the user if none of the studies being displayed are within a user configurable period from the current real time, calculated using the acquisition dates of the exams. For each open study the system searches for the date of acquisition, controlling the DICOM data of the first image of each series of studies and finding the oldest date (so that it is considered to be the date of acquisition on diagnostics and not of any subsequently reconstructed series).
Specify 0 to disable the control.

Appendix

A

Using the keyboard

This chapter describes how to use the keyboard in MedStation.

Image management

The following table lists all the shortcut keys for image management.

Table 1 Image management

Key	Description
F2	It changes the range of application of subsequent modifications. Cyclically it will change from application to the selected image only to the series of the selected image.
CTRL+L	It assigns/removes the localizer attribute to/from images
CTRL+A	It selects all images displayed in the current view
CTRL+SHIFT+A	It deselects all selected images in the current view
P	It adds images to the printing page
K	It assigns/removes the key image attribute to/from images
CTRL+F6	It adds the current window/level values to favourites
CTRL+I	It applies or removes interpolation to/from images
I	It shows/hides the text on images
+	Zoom In
-	Zoom Out
F	Zoom Fit (fit to window)

1	Zoom 1:1
. (Point – Numeric keypad)	Select cursor
Esc	Pan cursor
2 and 8 (Numeric keypad)	Flip (vertical reflection)
4 and 6 (Numeric keypad)	Mirror (horizontal reflection)
3 (Numeric keypad)	Rotate 90° clockwise
9 (Numeric keypad)	Rotate 90° anticlockwise
L or CTRL++(Plus – Numeric keypad)	It enables magnifying glass cursor
CTRL + Arrows	It changes the Win/Level values in 10 unit steps.
CTRL+Shift+Arrows	It changes the Win/Level values in 1 unit steps.
ALT+right-click	It set Win/Level optimized on the rectangular area defined by dragging the mouse (with the right mouse button pressed)
Up arrow	**Normal cursor**: Shows a row of previous images and the active image becomes the first one displayed.
	Magnifying glass: increases the zoom factor
Down arrow	**Normal cursor**: Shows a row of subsequent images and the active image becomes the first one displayed
	Magnifying glass: decreases the zoom factor
Left arrow	**Normal cursor**: moves to previous image and makes it the active image
	Magnifying glass: decreases the area occupied by the magnifying glass
Right arrow	**Normal cursor**: moves to the next image and makes it the active image
	Magnifying glass: increases the area occupied by the magnifying glass
HOME	It goes to the first image
END	It goes to the last image
S	It activates navigating between images in stack view mode
ENTER	It toggles between current layout and 1x1 layout

N	It inverts the colours of the image
BACKSPACE	It resets the original window/level values of the images, or the last applicable presentation state, according to transformation application range
Space bar	It activates CINE mode When this mode is active, it starts/pauses the sequence of images
Del	It deletes the measurements selected
D	It selects the Distance measurement
A	It selects the Angle measurement
Q	It selects the Area measurement
C	It selects the Circle measurement
CTRL+Z	Original: it cancels unsaved changes to the current image

Study management

The following table lists all the shortcut keys for managing studies.

Table 1. Study management

Key	Description
CTRL+O	It opens study search and select window
CTRL+S	It saves changes to the current study
CTRL+F4	It closes the current study
R	It opens the Reporting environment
CTRL+P	It starts printing if there are pages with images to be printed
SHIFT+CTRL+P	It opens the print preview panel
CTRL+E	It exports study
CTRL+C	It copies images to the clipboard
CTRL+V	It pastes images from the clipboard
F5	It redraws the entire window
F6	It applies the previous display protocol on the list
F7	It applies the next display protocol on the list
F9	It closes all studies
F12	It starts the external acquisition module
CTRL+H	It enables/disables the application of hanging protocols when studies are opened
O	It shows/hides the drawing of the intersection line of the selected image and the series to which it belongs on the images of the same study displayed in different boxes

Screen management

The following tables list all the shortcut keys for managing the screen.

Table 2. Display management

Key	Description
CTRL+T	It shows/hides the Tools panel

CTRL+O	It shows/hides the study search and opening panel
R	It shows/hides the Report panel
CTRL+SHIFT+P	It shows/hides the print preview panel
CTRL+H	It shows/hides the Protocols panel
CTRL+B	It shows/hides the status bar
F11	It toggles between full-screen mode and the display mode with control bars

Using menus and closing windows

The following table lists all the shortcut keys for using the menus and closing windows.

Table 3. Using menus and closing windows

Key	Description
ALT or F10	It activates the menu bar.
Arrow key and ENTER	(with menu active) It selects a command from the menu.
ALT +F4	It exits from the application
F1	It opens the manual in pdf format

Using dialog boxes

The following table lists all the keys for using the dialog boxes.

Table 4. Using dialog boxes

Key	Description
ENTER	It executes a command.
ESC or ALT +F4	It closes the dialog box.
ALT +*Down arrow*	It opens or closes a selected list.
Arrow keys	It moves between menu commands, between text characters or between the items in a list.
TAB	It moves to the next item in a window.
SHIFT +TAB	It moves to the previous item in a window.
ALT + *underlined character in the item name*	It moves directly to the element in a window.

HOME	It moves to the beginning of a row, a list or screen.
END	It moves to the end of a row, a list or screen.
Page Up	Display of previous study or series listed in the navigation panel of exams/series.
Page Down	Display of next study or series listed in the navigation panel of exams/series.
SHIFT +Home	It moves back to the beginning of the first line.
SHIFT +End	It moves back to the end of the last line.
SHIFT +CTRL+ *right arrow*	It moves to the next word.
SHIFT +CTRL+*left arrow*	It moves to the previous word.
SHIFT +*left arrow*	It selects one character at a time from left to right.
SHIFT +*Right arrow*	It selects one character at a time from right to left.
Space Bar	It selects/deselects one item on a list or activates a check box.

Editing text

The following tables list the functions available for changing information entered in text boxes or in window fields.

Table 5. Editing text

Key	Description
BACKSPACE	It deletes the character to the left or all the highlighted text.
DEL	It deletes the character to the right or all the selected text
CTRL+C *or* CTRL+INS	It copies the selected text to the clipboard
CTRL+X o*r* SHIFT+DEL	It cuts selected text and places it on clipboard
CTRL+V *or* SHIFT+INS	It pastes text from clipboard
CTRL+Z *or* ALT+BACKSPACE	It undoes the last change made

List of preset Window/Level values

Tabella 1. Preset window/level values for CT studies

Key	Description	Level	Window
	Brain	40	80
	Posterior cranial fossa	30	110
	Orbits	30	450
	Temporal bone	650	3200
	Maxillae	220	1400
	Paranasal sinuses	220	1600
	Turkish saddle	50	400
	Head and neck	80	300
	Cervical column	50	300
	Lumbar column	40	350
	Thorax for mediastinum	40	400
	Thorax for parenchyma	-600	1600
	Thorax for embolism	150	800
	Aorta	150	600
	Liver	50	300
	Arterial phase liver	40	450
	Portal phase liver	50	400
	Inferior abdomen	50	500
	Knee	50	200
	Bones	600	1900
	Skull	40	400
	Bones and cones	600	3000
	Vertebrae	300	2000
← (BackSpace)	All original presentation window/level values		
Alt+ ← (BackSpace)	All original window/level values of the images		

Apendix

B

User Manager[39]

This appendix describes the application for managing users in MedStation.

RC-07 *This program can only be executed by the system supervisor. Unauthorized changes to configuration files of MedStation may cause the application to malfunction. Contact Exprivia S.p.A. support before making any changes.*

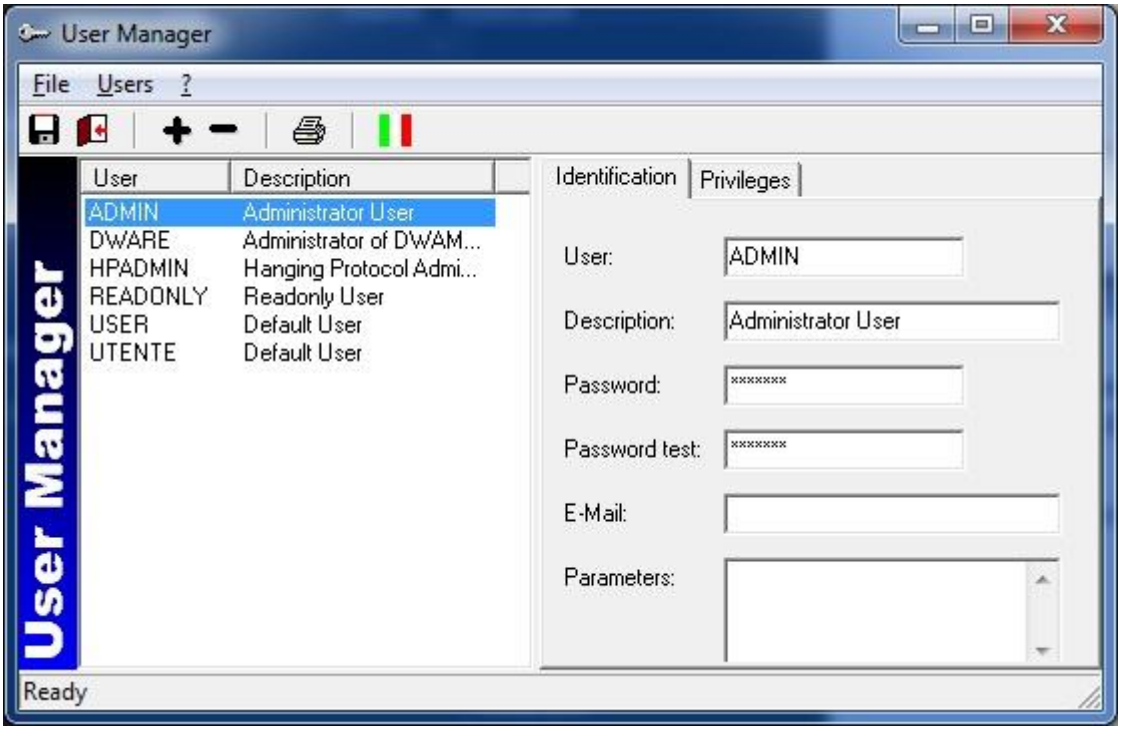
Running the User Manager application

To start the program click on the *User Manager* application or select the *Users and Privileges* box on the Properties Configuration sheet of a node displayed using **MedStation Configuration.**

After prompting the user for his credentials, the window described Figure 54 is displayed

[39] Function available only in MedStation but not it in MedStation Express.

Figure 54. User manager window



The window is divided into four areas:

1. The toolbar.
2. The display area for the list of users present.
3. The identification page for the current user.
4. The configuration page for the current user's privileges.

The toolbar

	Save user settings
	Exit the application
	Add a user
	Delete the selected user
	Print the list of users
	Change the application language (English/Italian).

To insert a new user

Press the + button or the **Users | Add** command and enter the identification data of the new user in fields to the right of the window.

Note: *When you add a new user, he can enter only the node from which he was created. To create a user able to enter all the nodes, it is necessary to define him in each node.*

To delete a user

Select the user that is to be deleted from the list and press the – button or use the command **Users | Delete**.

The users display area

The complete list of users and associated description is displayed to the left of the window.

In order to display the properties for each individual user, it is sufficient to select it from the list.

The user identification page

The current user is identified by a name *(User)*, a description (*Description*), a password *(Password)*, an e-mail address (*E-Mail*) and certain other personalized parameters (*Parameters*).

The parameters that are always mandatory are *User* and *Password* (with the relative *Test Password*), the other fields can be specified or not.

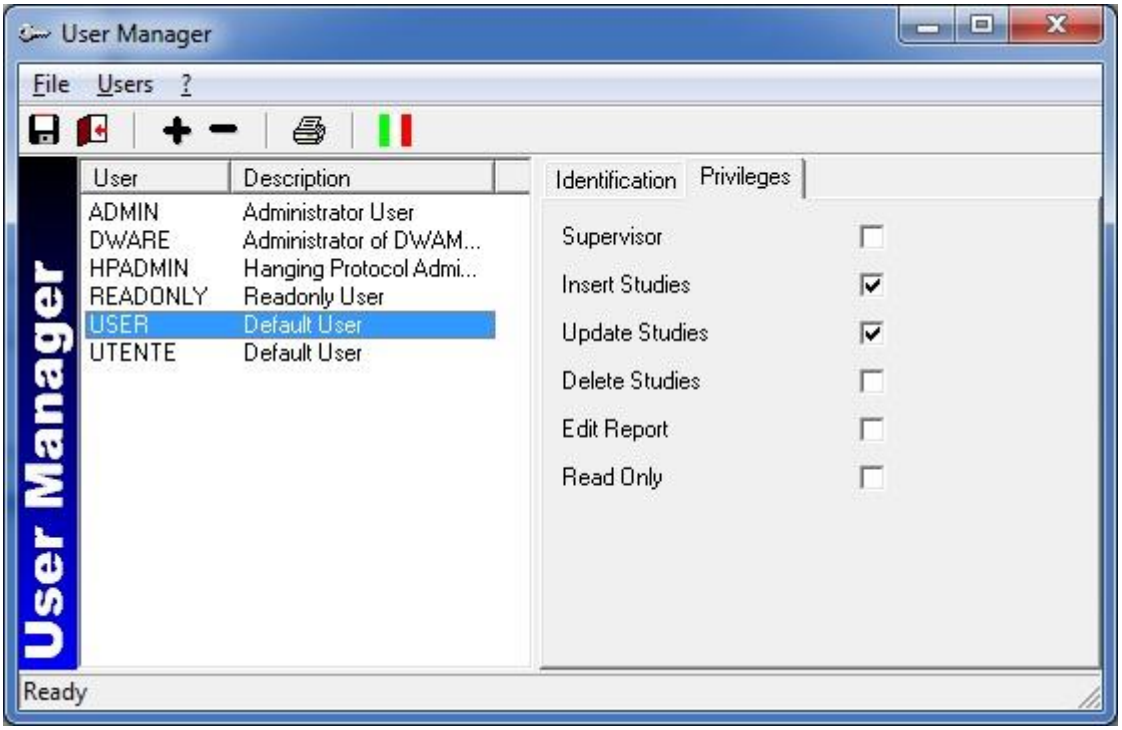
Note: The password attributed to the user must be entered both in the "Password" and in the "Test password" fields. The data entered are concealed with asterisks.

The user privileges configuration page

In this area it is possible to assign to the user the privileges he needs. ⚠ *To limit some operations to the authorized users, each user can be assigned the following privileges*:

- **Supervisor**: System supervisor. Can execute all functions and configuration activities, including the user and profile manager programs described here.
- **Insert Studies**: Administrator user. Can execute all functions, insert and update studies.
- **Update Studies:** Administration user. Can execute all functions and edit already existing studies.
- **Write and configure Report:** The user can write reports and create templates for writing structured documents
- **Edit Report:** The user can use the data of a read-only report to create a new DICOM SR report.
- **Delete Studies**: User manager. Can execute functions and delete already existing studies.
- **Read Only**: Consultation user. Can access all functions for consultation only. Cannot edit any files.

Figure 55. User privileges manager window



C

Configuration[40]



RC-07

Unauthorized changes to configuration files of MedStation may cause the application to malfunction. Contact Exprivia S.p.A. support before making any changes.

The **MedStation Configuration** program is used to configure the parameters of the **MedStation** application.

To start the application select **Start | Programs | Exprivia | MedStation® 5 | MedStation Configuration**. A dialog box will appear prompting you to enter the password.



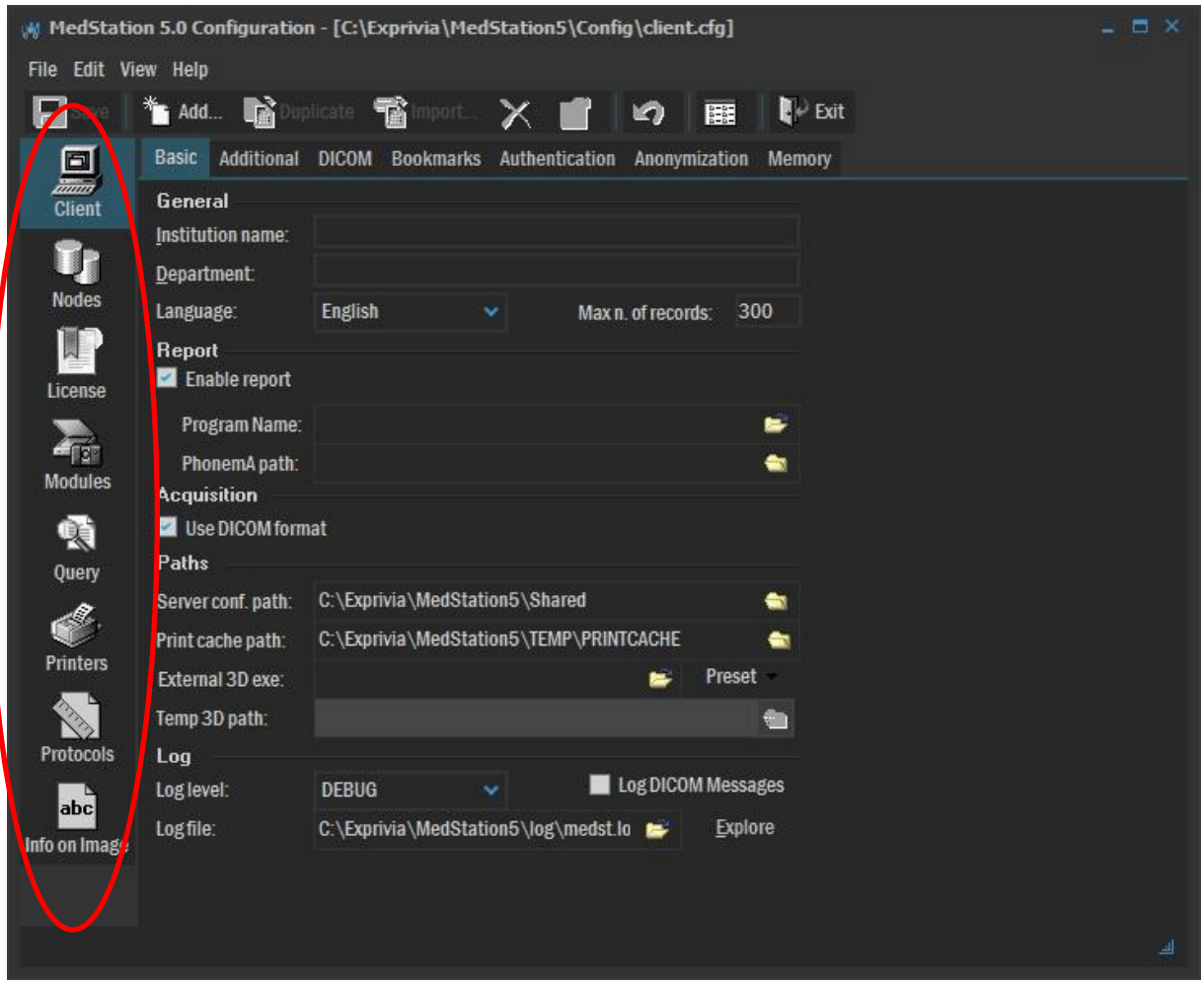
RC-07

***Note:** For security reasons, only specialized technicians know the password.*

At the end of the authentication process, the configuration program is opened. It is divided into **sections,** which can be accessed using the buttons in the left part of the main window (see Figure 56).

[40] Function available only in MedStation but not it in MedStation Express.

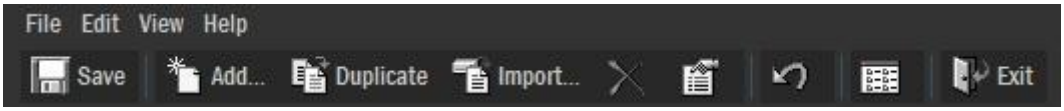
Figure 56. MedStation Configuration: main window



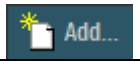
The toolbar

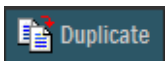
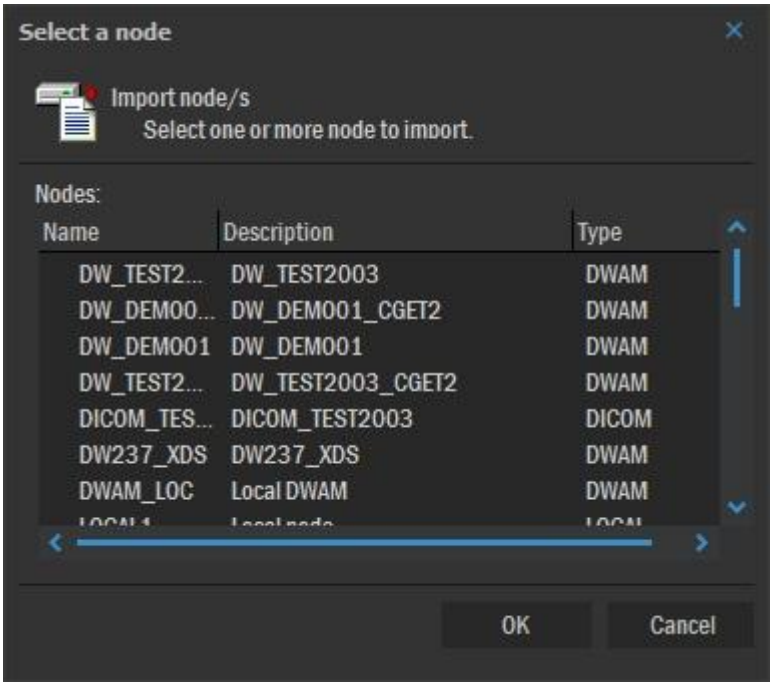
The MedStation Configuration toolbar is used to perform common item management operations (storage nodes, printers etc.).

Figure 57. MedStation Configuration: toolbar



It provides the following functions:

	Adds a new element (the type of element depends on the context)
	Saves changes

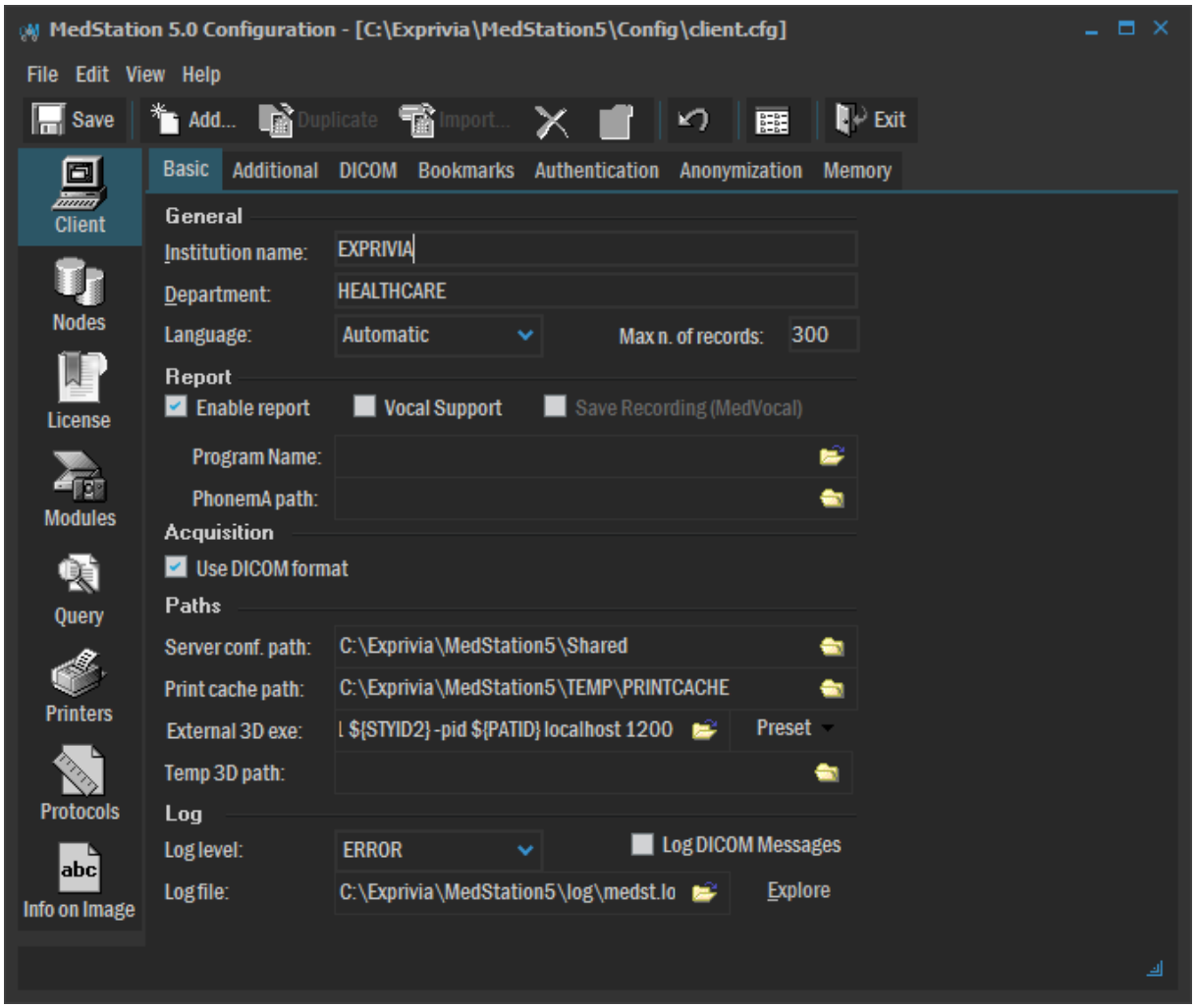
	Creates a new item by duplicating the settings of the selected item (the type of element depends on the context)
	It is active only in the section for nodes configuration. It allows importing one or more nodes from an external file belonging to a previous version of MedStation (in versions prior to 3.5, the file that contained the nodes configuration, was named `client.cfg`, in 3.5 and subsequent versions its name is `nodes.cfg`). Once you select the file, it appears the following window where you can select the nodes to be imported. 
	*(Delete)* Deletes the selected object
	*(Properties)* Displays the properties of selected item
	*(Undo changes)* Undoes changes made since the last saving
	*(List type)* Selects the list type
	Exits from the application

Basic configuration

In the "*Client*" section there are seven sheets: *Basic*, *Additional*, *DICOM*, *Bookmarks*, *Authentication*, *Anonymization* and *Memory*.

Basic sheet

Figure 58. Client section (Basic sheet)



Institution name	Name of Institute/Hospital where MedStation is installed. This data is placed on new acquired images together with *Department.*
Department	Department name
Language	MedStation language. The languages supported are *Automatic, English, German, Italian, Spanish, Portuguese.* If you specify *Automatic,* MedStation will use the same language as the operating system; if the language of the operating system; if the language of the operating system is not included into those listed above, MedStation will use English.
Max. no. of records	Maximum number of records displayed in the study search

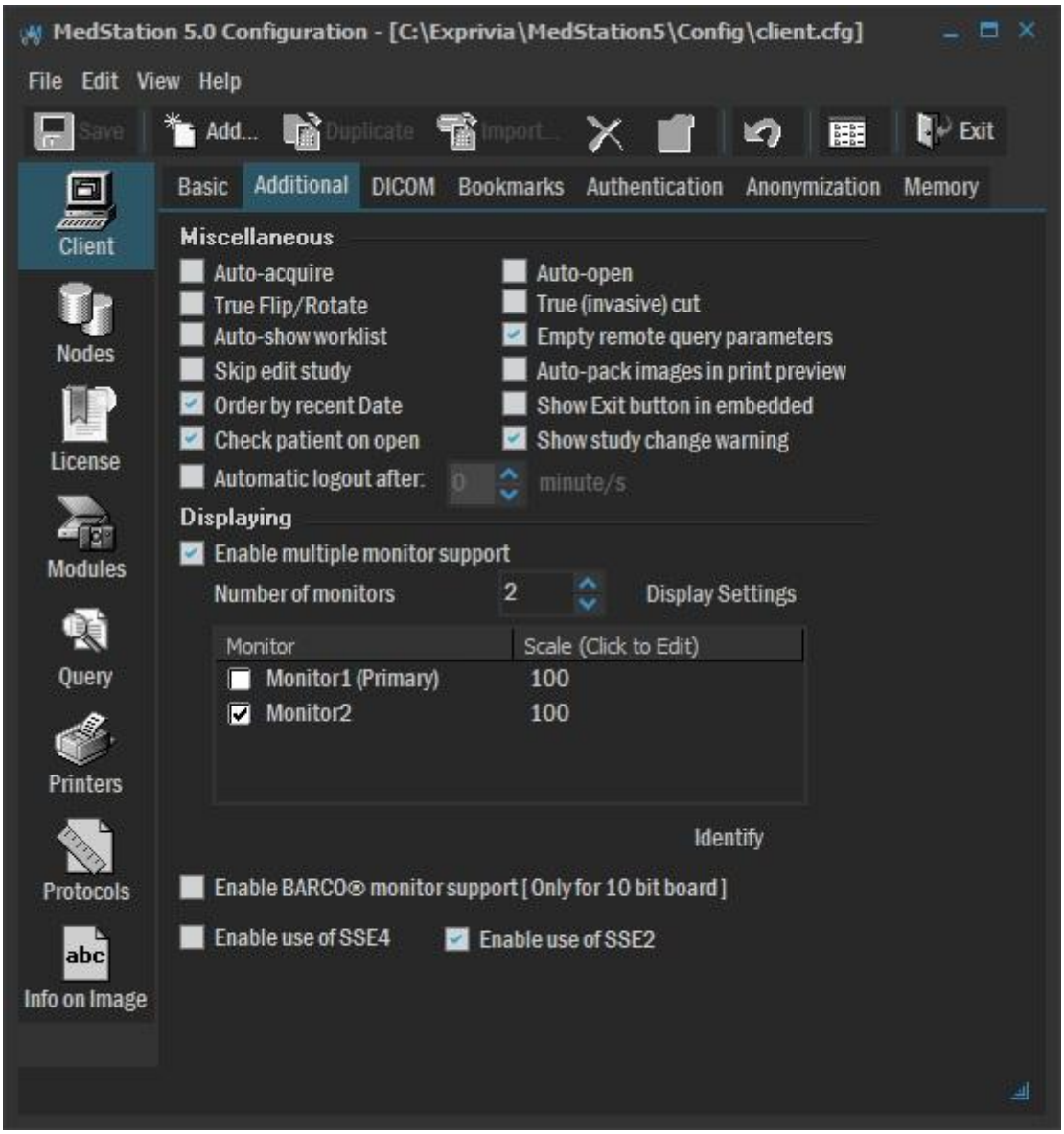
Enable report	Enable the reporting environment within MedStation
Vocal Support	Enables Phonema OCX voice reporting setting automatically edit box *Program name* to value "***PHONEMAOCX***".
Save Recording (MedVocal)	Specific option for MedVocal speech engine that enables the updating of the user dictionary on the server, in case of writing and saving completed and verified report.
Program Name	Name of the external application for editing reports, if present. Following parameters are added to the application name: 'USR=*UserName* PWD=*Password* DIR=*StudyDirectory* ACCESS=*AccessMode*' where *UserName* and *Password* are respectively the logged user and password, *StudyDirectory* is the directory in which study data are stored and *AccessMode* is 'R' if the user enters the study in read-only mode or 'W' in read/write mode. If you omit *Program name*, MedStation will use its internal editor for study reporting. If you assign the value "***EXTERNAL***" to *Program name*, MedStation will assign to the studies the status of *reported* only when you select the **File | Reported…** menu item If you assign the value "***PHONEMAOCX***" to *Program name*, and Phonema OCX is installed, at opening of MedStation reporting window, the environment of Phonema reporting will be activated (See *Vocal Support*) ***Note:*** In this case (*Program name* = ***PHONEMAOCX***) it is not necessary to choose any in *PhonemA path*. In MedStation reporting interface, the icon Phonema does not appear and Ocx will start automatically.
PhonemA path	Directory (optional) for the installation of PhonemA for voice reporting
Use DICOM format	When this opting is active, all acquired images, (from clipboard, from external module, from file) are converted from their native format in DICOM format. This option has precedence over image format as specified in *Configuration* form of single storage nodes. In other words, when this option is active, acquired images will be saved in DICOM format regardless of the format specified for the nodes.
Server conf. path	It is a parameter used to share (centralize) the same configuration files among different workstations. It indicates the path of the shared directory where you can find the directory `config` which contains the configuration files (for example: *\\computername\drive\exprivia\medst5*, or *m:\Exprivia\Medst5\Shared* where *m*: is a shared drive). Only some configuration files can be centralized, including: `IMGINFO.CFG`, `WINLEVEL.CFG`, `ACQMODE.CFG`, `PRINTERS.CFG`, `PROTOCOLS.CFG`, `HP_`*`nomeutente`*`.XML`, `MODALITIES.DAT`

External 3D exe	Name of any external module 3D processing of the current series, preset values are: • **Terarecon 3D**; *"C:\AQi\bin\AQi.exe" -l ${USER} -p ${PASSWD} -s1 ${STYID2} -pid ${PATID} localhost 1200"* The internet address *localhost* and default port *1200* shall be replaced by the correposnding available on the network. In the case of domain authentication parameters *-l ${USER} -p ${PASSWD}* can be omitted and the system will use the credentials of the user authenticated in the operating system. The external module is launched allowing the user to choose the range of interest (when study have multiple series). If you want to turn directly to the navigation of the current series Series Instance UID shall be specified as: *-s2 ${SERID2}* • **Voxar 3D:** *"C:\Program Files (x86)\Barco\Voxar3D\Voxar3D.exe"* • **Vitrea 3D:** *"C:\Program Files (x86)\Internet Explorer\iexplore.exe" "http://127.0.0.1/VCAccess.aspx?id=<URLRequest User="${USER}" Pass="${PASSWD}" Domain="${DOMAIN}" Method="OpenSeriesByStudyUID" StudyUID="${STYID2}" SeriesUID="" StudyMode="0" />"* The internet address http://127.0.0.1/VCAccess.aspx must be replaced by the corresponding available in the network. In the case of domain authentication parameters *User="${USER}" Pass="${PASSWD}" Domain="${DOMAIN}"* can be omitted and the system will use the credentials of the user authenticated in the operating system. The external module is launched allowing the user to choose the range of interest (when study have multiple series). If you want to turn directly to the navigation of the current series Series Instance UID shall be specified as: *SeriesUID="${SERID2}"* The external module is started in 2D mode, if you want to enable advanced 3D mode directly set the parameter as follows*: StudyMode="1"* • **3D Biotronics:** *"C:\Program Files (x86)\Biotronics3D\3DNet\b3d_examiner.exe"* • **Alma 3D:** *"C:\Program Files (x86)\Internet Explorer\iexplore.exe" "a3dcon:?requestType=CONNECT&messageName=OpenStudies&StudyUID=${STYID2}"* To enable searching and loading from a DICOM server use the following specific path of integration:

	"C:\Program Files (x86)\Internet Explorer\iexplore.exe" "a3dcon:?requestType=CONNECT&messageName=OpenStudies&StudyUID=${STYID2}&QueryString=dicom#AETitle1/IP1:Port1&RetrieveString=dicom#AETitle2/IP2:Port2" where *Tittle, IP* and *Port* are the connection parameters of the DICOM SCP servers of QUERY and MOVE. The parameters ${...} are replaced before launch of external module with the corresponding runtime values. The name of the folder *"C:\Program Files (x86)\"* shall be replaced by the value of *Program-Files* environment variable for x86 or operating systems.
Temp 3D path	Temporary file directory for generation of 3D models.
Log level	Application log level (predefined value ERROR). For log levels such as DEBUG and TRACE application performance could significantly reduce.
Log File	Path of application log file
Log DICOM messages	If you select it, it outlines the DICOM communication between the application and remote clients.
Audit Node	DWAM server that will act as proxy for log messages to a ATNA server.

Additional sheet

Figure 59. Client section (Additional sheet)



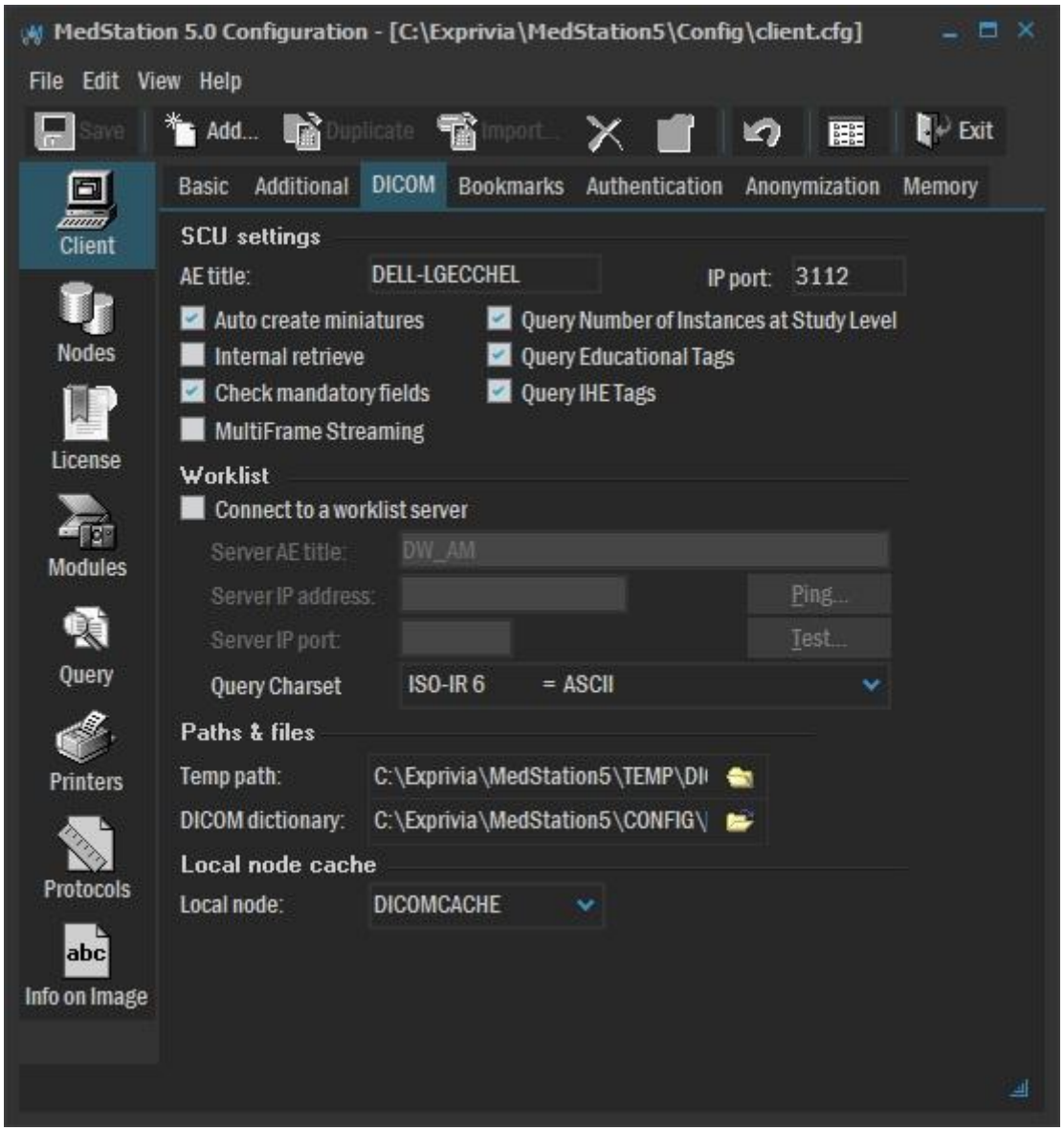
Auto-acquire	Automatically activate the acquisition module when creating a study.
True Flip/Rotate	If not activated, the operation of flip / rotate are handled internally as a status and the image file is not physically changed. If enabled, the operation of flip / rotate are physically applied to the file.
Automatic logout after	If enabled, the user will be logged out from MedStation after the period of time set in minutes.
Auto-show worklist	When you create a new study, a worklist appears from which you can select the data of a patient/study. The data of connection to the worklist are those stated on the DICOM sheet

Empty remote query parameters	Used only when study search queries are performed by external applications through integration (from the command line or COM). If active, indicates to reset the search parameters set by the query coming from the external application.
Auto-open	On starting the application, the study selection window is opened automatically.
Skip edit study	Allows confirmation of study data to be skipped, on creation of a study.
True (invasive) cut	If not enabled, when you perform a CUT (cut), the starting image remains unchanged and a new image containing the selected area is added to the series. On the contrary, if enabled, CUT operations overwrite the original image with the selected sub-region. In this case, when you save the study, the original image is lost permanently.
Auto-pack images in print preview	In the composition of pages to print, it automatically fills the holes left empty by images eventually deleted from the print job, and repositions the images left.
Order by recent Date	On the search and selection sheet, studies are sorted by most recent ones
Check patient on open	At a study opening and when a study is already open, it allows MedStation to check that the studies belong to the same patient. Otherwise, it will show the user a warning message. This helps to avoid that, by mistake, you can compare studies of different patients.
Show Exit button in embedded	It shows/hides the button to exit from MedStation when it is integrated as a COM object.
Show Study change warning	It shows an alert message when you open two or more studies of different patients.
Enable multiple monitor support	It enables the use of one or more monitors. *Number of monitors* indicates the number of monitors in use. To indicate which of the monitors connected are not to be used by MedStation to display data, deselect the flag beside the name of the monitor. This parameter is typically used when one of the monitors is dedicated for use with other applications, typically with a RIS integrated with MedStation. Beside the name of the monitor, you can indicate the enlargement scale of the windows and text on the MedStation interface on that monitor. This parameter is normally used when the workstation has a monitor with an extremely high resolution, which makes it difficult to read very small characters. The default value is 100%, which corresponds to no enlargement. Scale values of over 100% enlarge the windows and text.
Enable Barco® monitor support	It enables the support to the extended palette of Barco® monitors. This parameter will be considered only if the system is provided with a Barco® card that supports a 10-bit palette.

Enable use of SSE4	It enables the calculation of image interpolation with algorithms written with SSE4 technology
Enable use of SSE2	It enables the calculation of image interpolation with algorithms written with SSE2 technology

DICOM sheet

Figure 60. Client section (DICOM sheet)



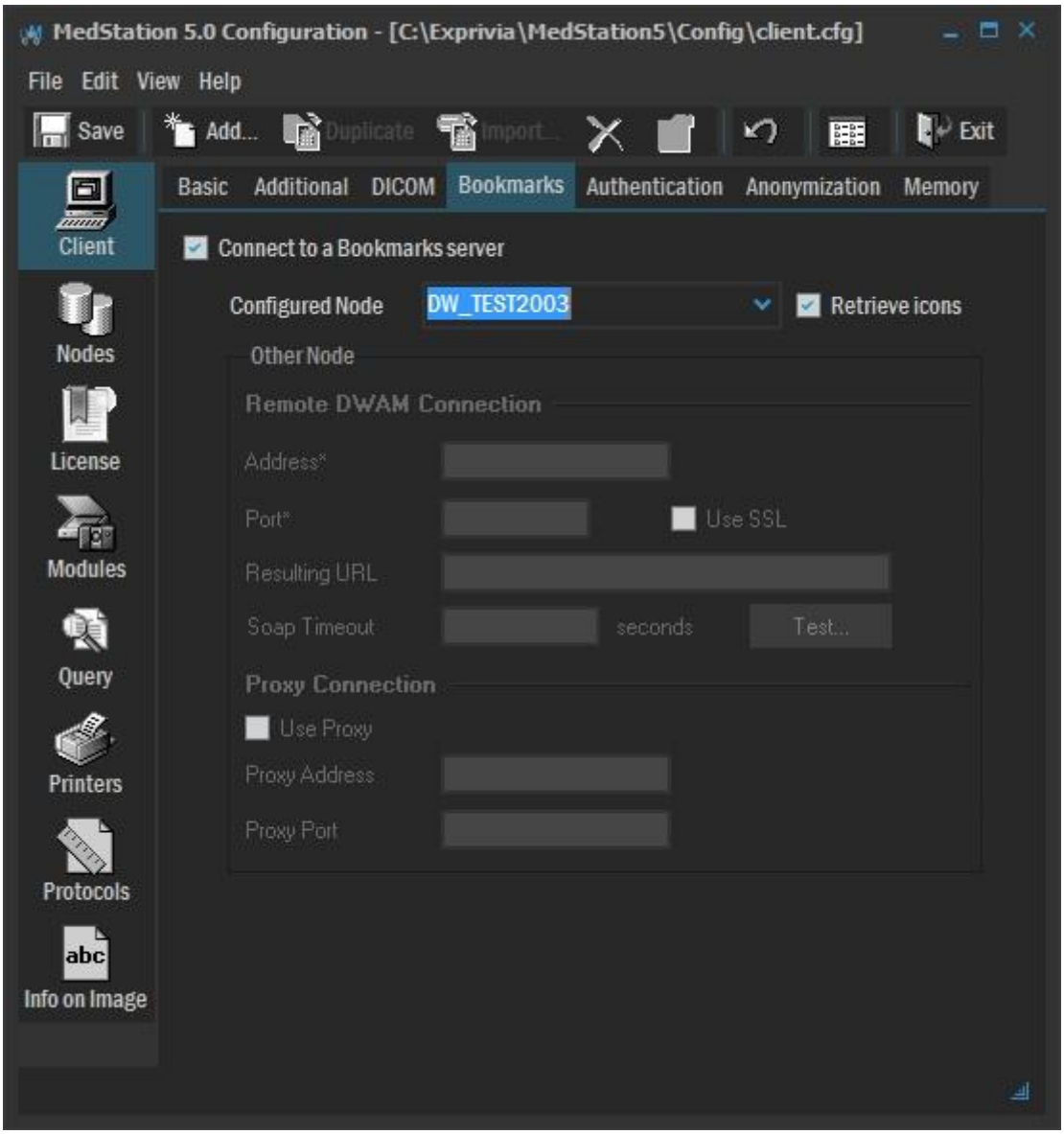
On this sheet you can configure DICOM connection parameters.

AE Title	Application Entity (AE) Title is used by MedStation to identify DICOM connections. Predefined value is <MachineName_MS>

IP port	Identification number of IP port used in DICOM connections. Default value is 3112.
Auto create miniatures	It indicates the "old" *Dicom Store* service able to automatically create miniatures of every image received.
Internal Retrieve	
Check mandatory fields	It checks the presence of compulsory DICOM TAG. If active, images without compulsory tags are rejected. If not active, the system also allows the acquisition of studies in which one or more of the mandatory fields are empty.
Query number of instances at study level	It indicates whether or not to ask for the number of DICOM instances (images and other study files) to DICOM servers on which you make a query. This can speed up response times to queries of some DICOM "slow" server. It has effect only for queries at study-level.
Query Educational Tags	It adds queries to educational fields.
Query IHE Tags	It makes an IHE compatible query adding special tags provided by the standard.
Multiframe Streaming	It indicates whether or not to enable multiframe streaming with DicomWare 4 or later DICOM archives.
Connect to a worklist server	It enables connection to a DICOM Worklist server to be accessed to select the data when you create a new study. With the Ping and Test buttons you can run, respectively: the test of network connection and the test of connection with the DICOM Worklist Server.
Server AE title	Application Entity Title DICOM of Worklist server.
Server IP address	IP address of Worklist server.
Server IP port	Worklist Server listening port.
Query Charset	The charset to be used to encode the strings that make up the query made to the worklist server.
Temp path	Temporary directory for study writing
DICOM dictionary	DICOM dictionary path and name
Local node	Parameter used by the "old" service Dicom Store, which indicates the local node to use as a database in which to write the studies received.

Bookmarks sheet

Figure 61. Client section (Bookmarks sheet)



MedStation can be connected to a DicomWare server on which you can save and read lists of studies indicated as favourites (these studies are not necessarily stored on the same server that manages bookmarks to favourite studies).

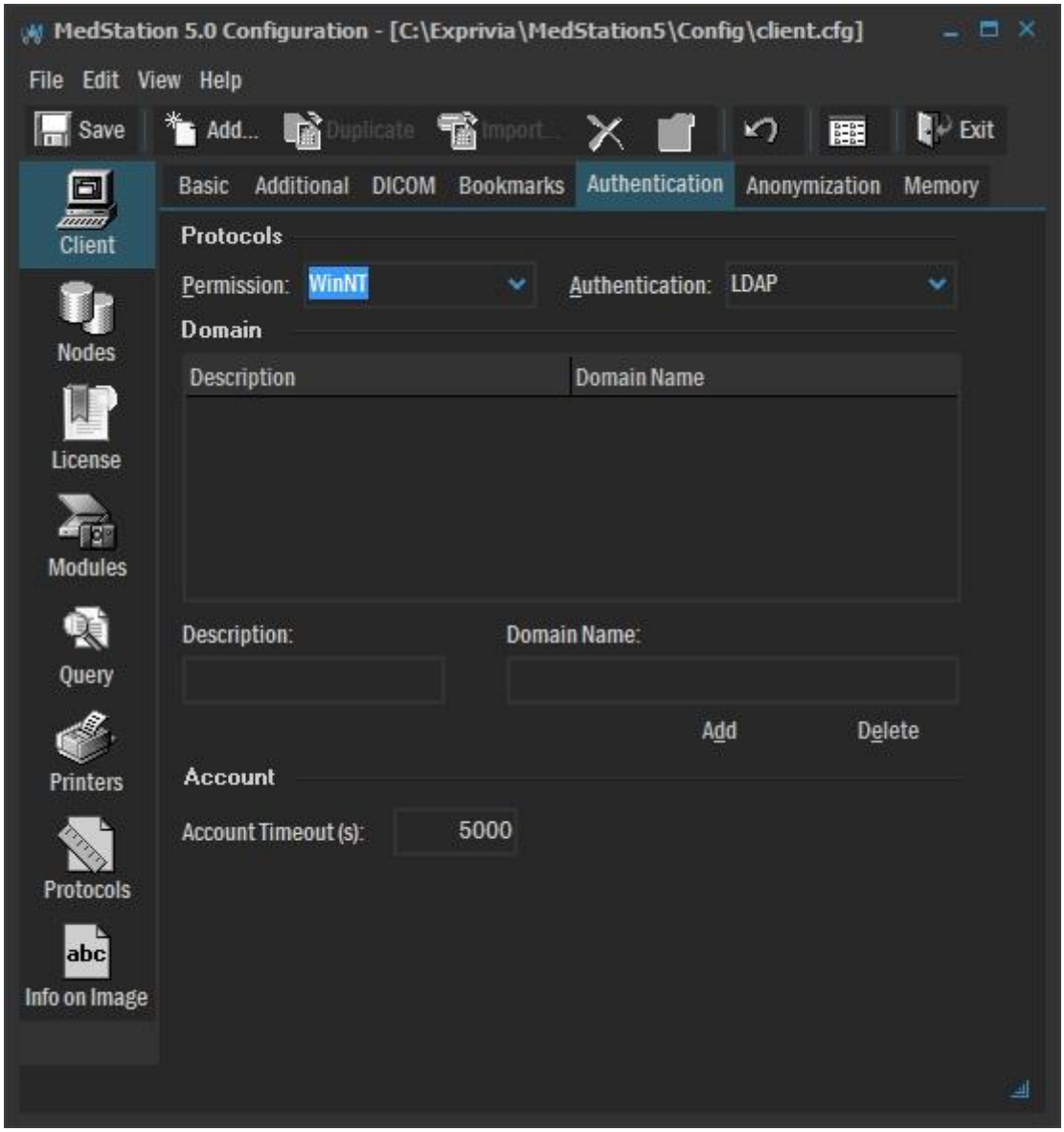
On this sheet you can enable and disable the management of favourite studies.

The connection with a bookmarks server is activated by selecting the *Connect to Bookmarks Server* check box. This function is only available if you have a DWAM server version 4.8 or later. The server can be chosen from one of the nodes configured in the *Nodes* section. If you leave the *Configured Node* box blank, the lower section (***Other Node***) will be enabled and you will be able to configure the SOAP connection with another server, by entering in the dialog box all the data required to communicate with this DWAM archive.

The *retrieve icons* option can be used to download the icons representing the studies (these icons will be shown on the list of favourites in the MedStation study search and opening screen), but you must make sure that they are enabled on the DWAM server. The WADO connection must also be enabled on it and be configured on the client nodes that allow access to the favourite study.

Authentication sheet

Figure 62. Client section (Authentication sheet)



MedStation offers the possibility of using a network domain and login with users defined therein. To do this it uses the standard protocol for managing de-LDAP users and the protocol for managing WINNT MedStation permissions.

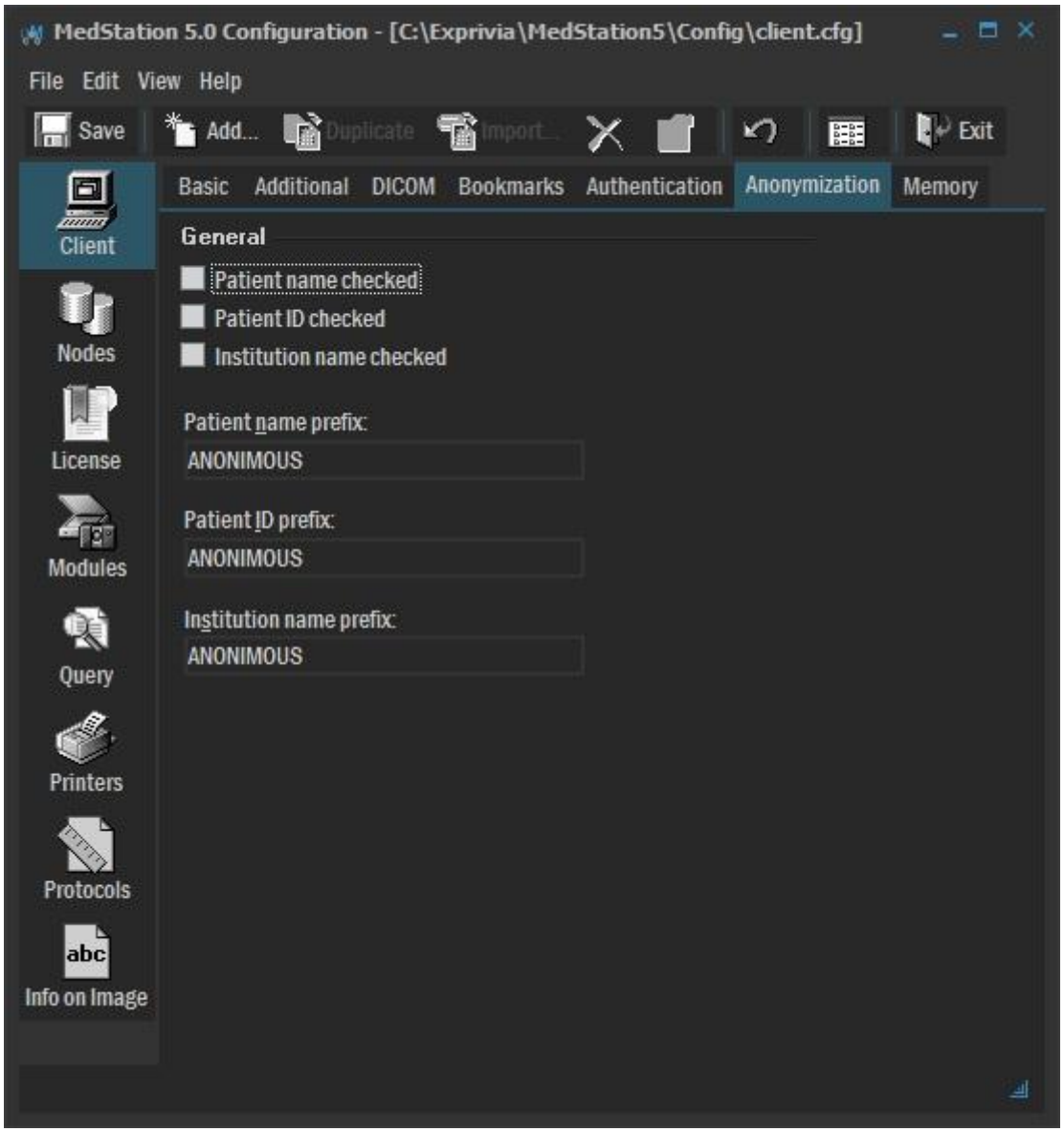
From the drop-down menu of the **Protocols** section, you can choose which protocols to use

for the management of permissions and authentication.

In the **Domain** section, you insert the domains that you want to access. You can simply enter a description and the domain name and press "Add". Startup MedStation from the login window, you can choose the domain to be used for authentication.

Anonymization sheet

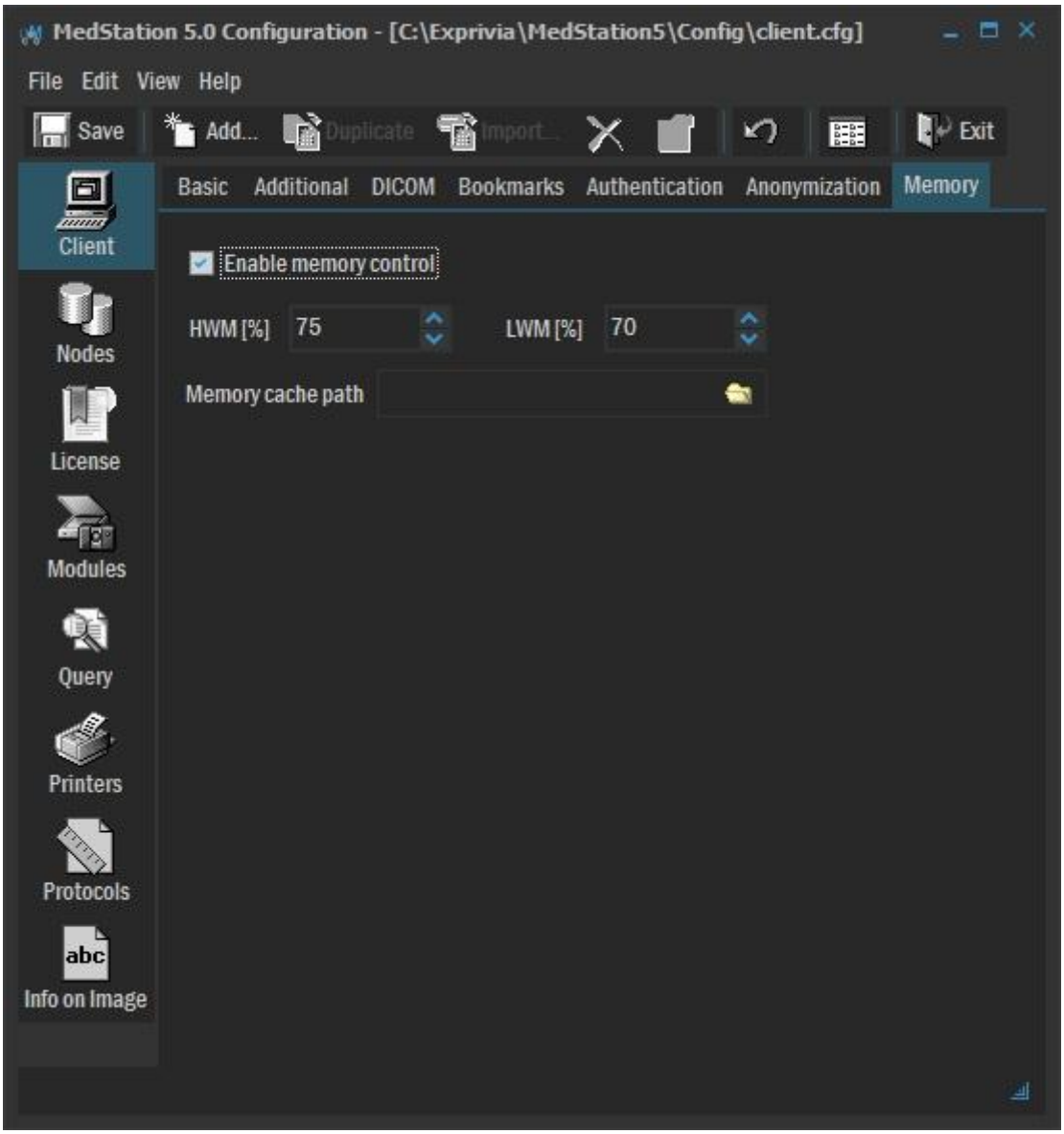
Figure 63. Client section (Anonymization sheet)



On this sheet you can determine the prefix to be applied to data to be anonymized during the study export phase.

Memory sheet

Figure 64. Client section (Memory sheet)



On this sheet, you enable / disable management of memory allocation used by MedStation. If this function is active and if you exceed the HWM level of the memory used, a part of data of the displayed studies will be mapped to the directory indicated in the *Memory cache path* (or, if not indicated, in the temporary folder of the user) so that the RAM will be emptied until it reaches the LWM level.

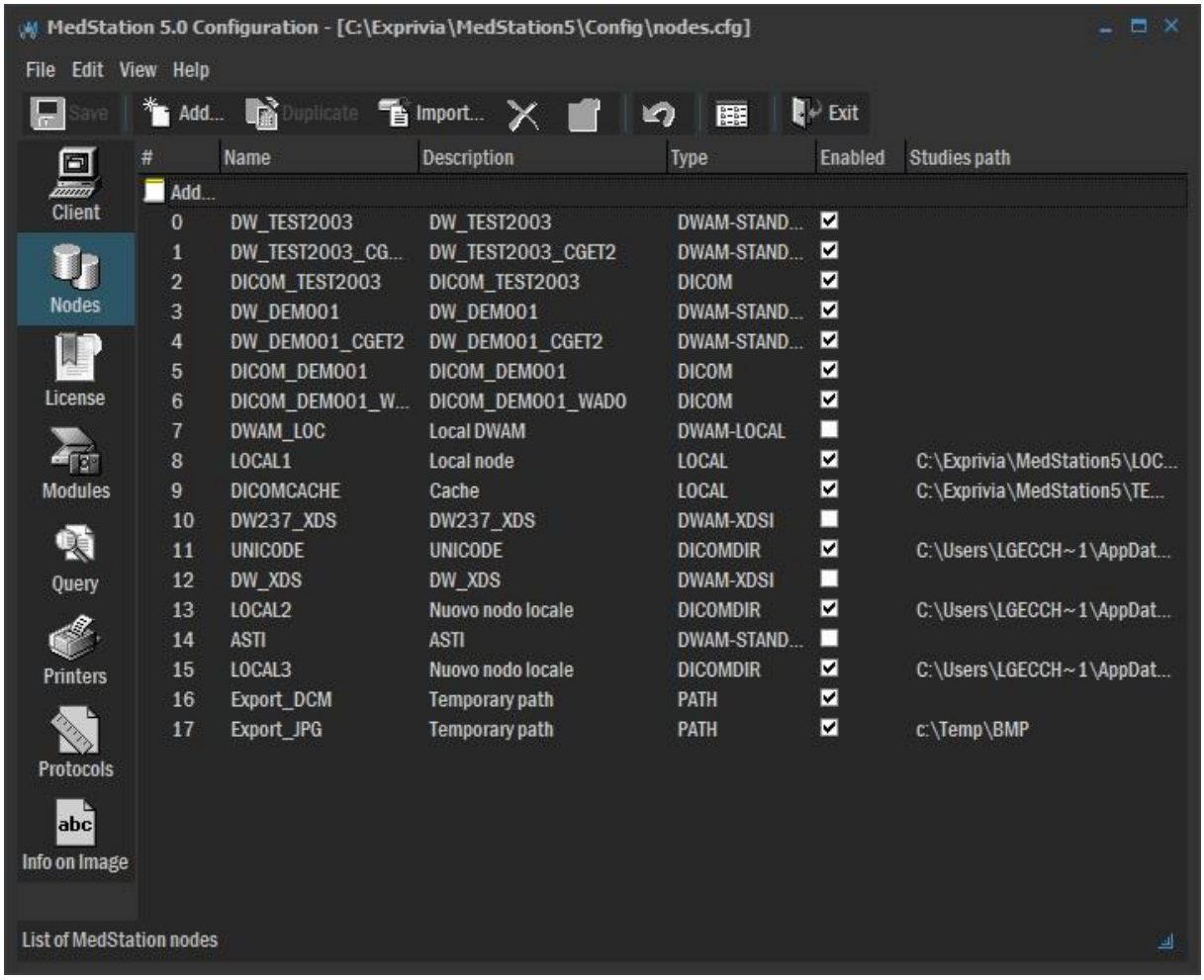
Storage node configuration

The *Nodes* section enables the creation and configuration of the different types of storage

nodes provided for by MedStation: LOCAL, DWAM, DICOM, DICOMDIR, METANODE and PATH nodes. The PATH node IS only used when exporting diagnostic studies.

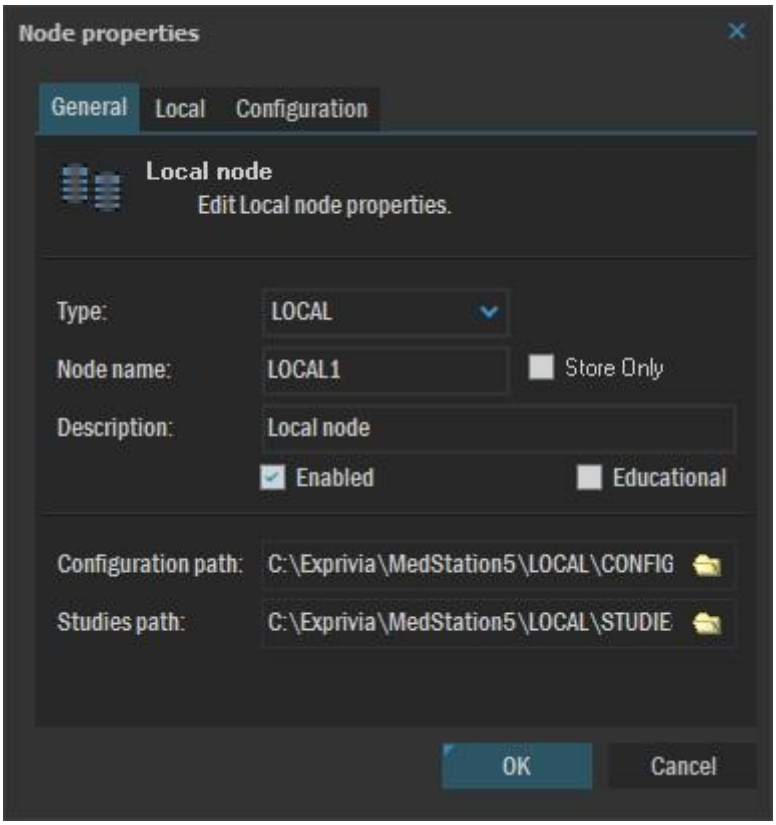
To create a new node, simply click on the *Add* button on the toolbar; to modify the properties of a node use the **Properties** button**.** Figure 65 shows the configuration window of the *Nodes* section whilst the later diagrams show and describe each individual type of storage node.

Figure 65. Nodes section



Local node properties

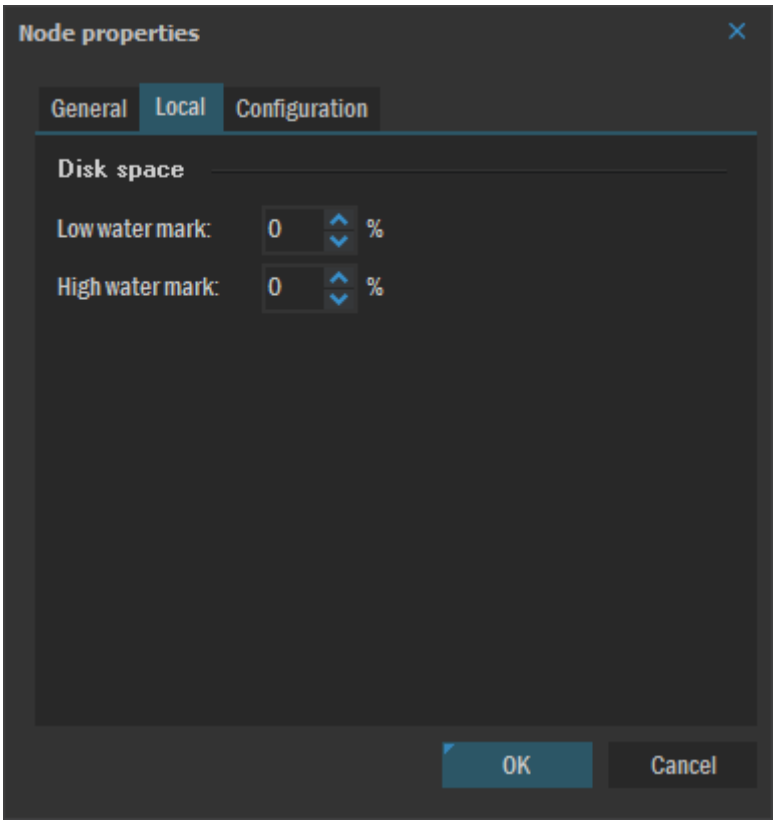
Figure 66. Local node properties



General page

Type	Type of node: LOCAL
Node name	Internal node name. This name must uniquely identify the node within the list of nodes MedStation
Description	Node description
Store Only	Sola archiviazione. Se attivo, nasconde il nodo dall'ambiente di selezione esami e lo rende disponibile solo come nodo di destinazione di una copia.
Enabled	Enabling/disabling node. If active, the user can access the node and perform all the operations allowed. If not active, the node is ignored.
Educational	Enabling educational data management
Configuration path	Configuration file path
Studies path	Stored studies path

Figure 67. Local sheet of local node.

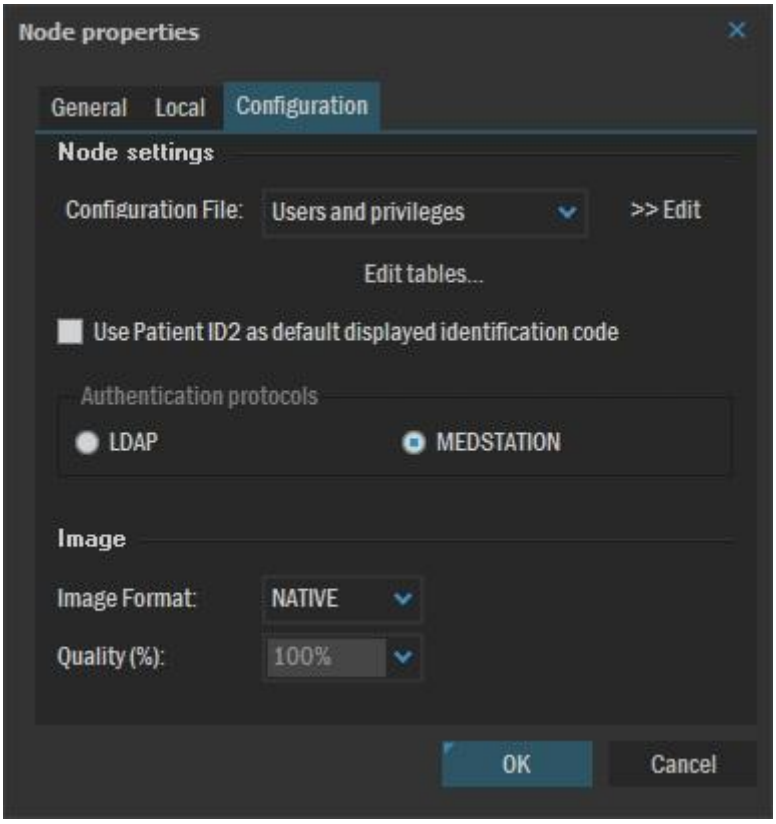


Local sheet

The *Disk Space* section is used to activate automatic management of space on the installation disk of the local node.

When this management is not active, there is no control over the space occupied by the studies. It is activated when the high watermark and low watermark values are different from zero.

High water mark	Indicates the maximum percentage of space occupied on disk. When adding studies, you reach or exceed this level, is activated the cancellation proceedings under the FIFO rules (First In First Out). That is, some less recent studies will be erased to make room on the disk.
Low water mark	Indicates the percentage of disk space you are trying to achieve during the cancellation tests according to the FIFO rules.



Configuration sheet

Image Format	Image format: BMP, JPG, etc. Only 1, 8 and 24-bit formats are allowed. This format is used when the user captures images from files, the clipboard or an external module. ***Note:*** *This parameter is ignored if 'Use DICOM format' (in the Client section, Basic sheet) is active*
Quality (%)	Image compression factor. It is only considered for CMP and JPG formats.

Users and privileges

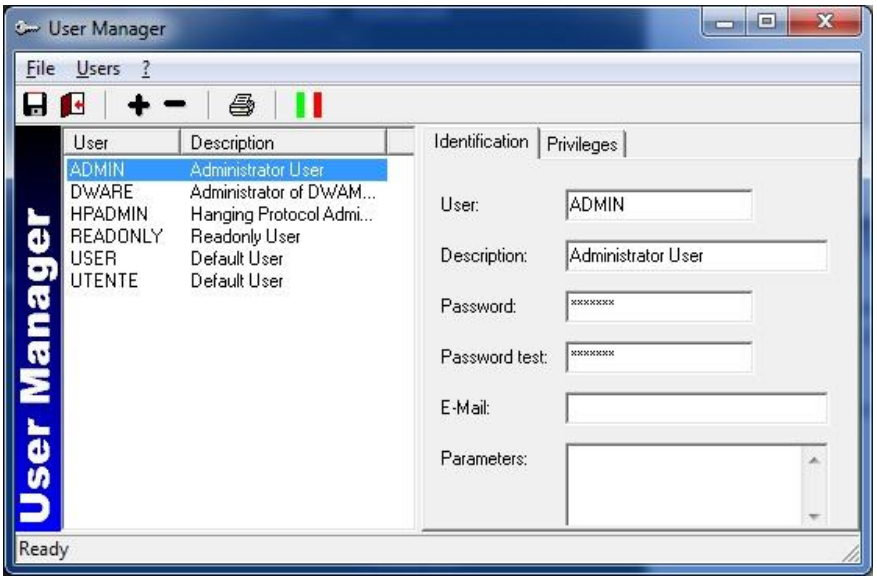
To enter the application for User per node management, select *Users and privileges* in the *Configuration file* box and press *Edit*. The window shown in Figure 68 will appear.

Figure 68. Node user management



Having entered the user name and password of the administrator, the window for creating and modifying users will be displayed.

Figure 69. Node user management: creating a user



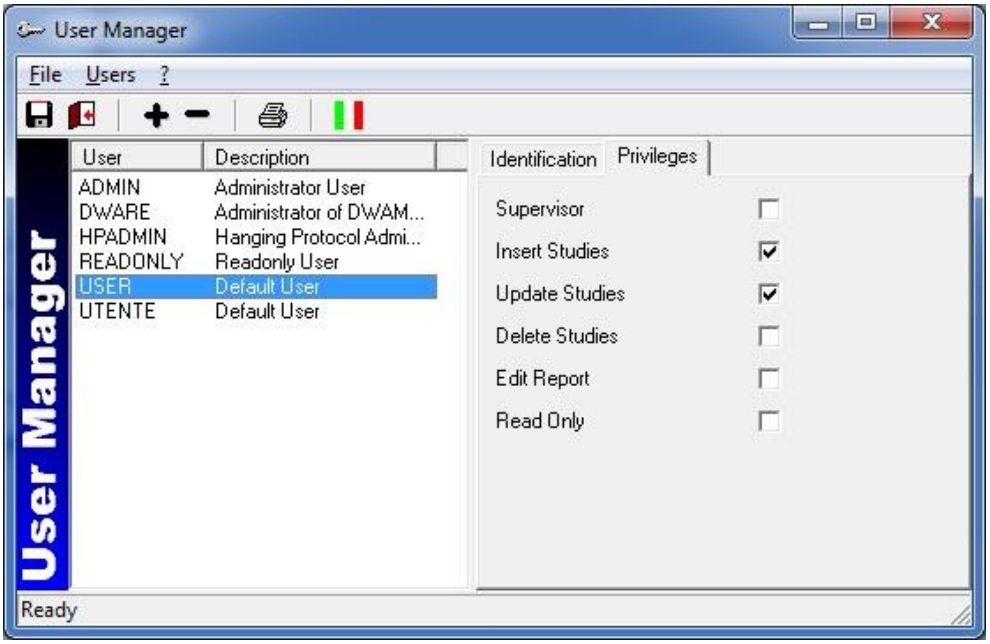
To create a new user click the + button or select *User* | *Add* from the menu.

Each user is characterized by following data:

- Description
- Password
- Password test (re-enter the password you entered in the previous box)
- E-mail
- Parameters, if any

From the *Privileges sheet* (Figure 70) you can assign privileges to the new user.

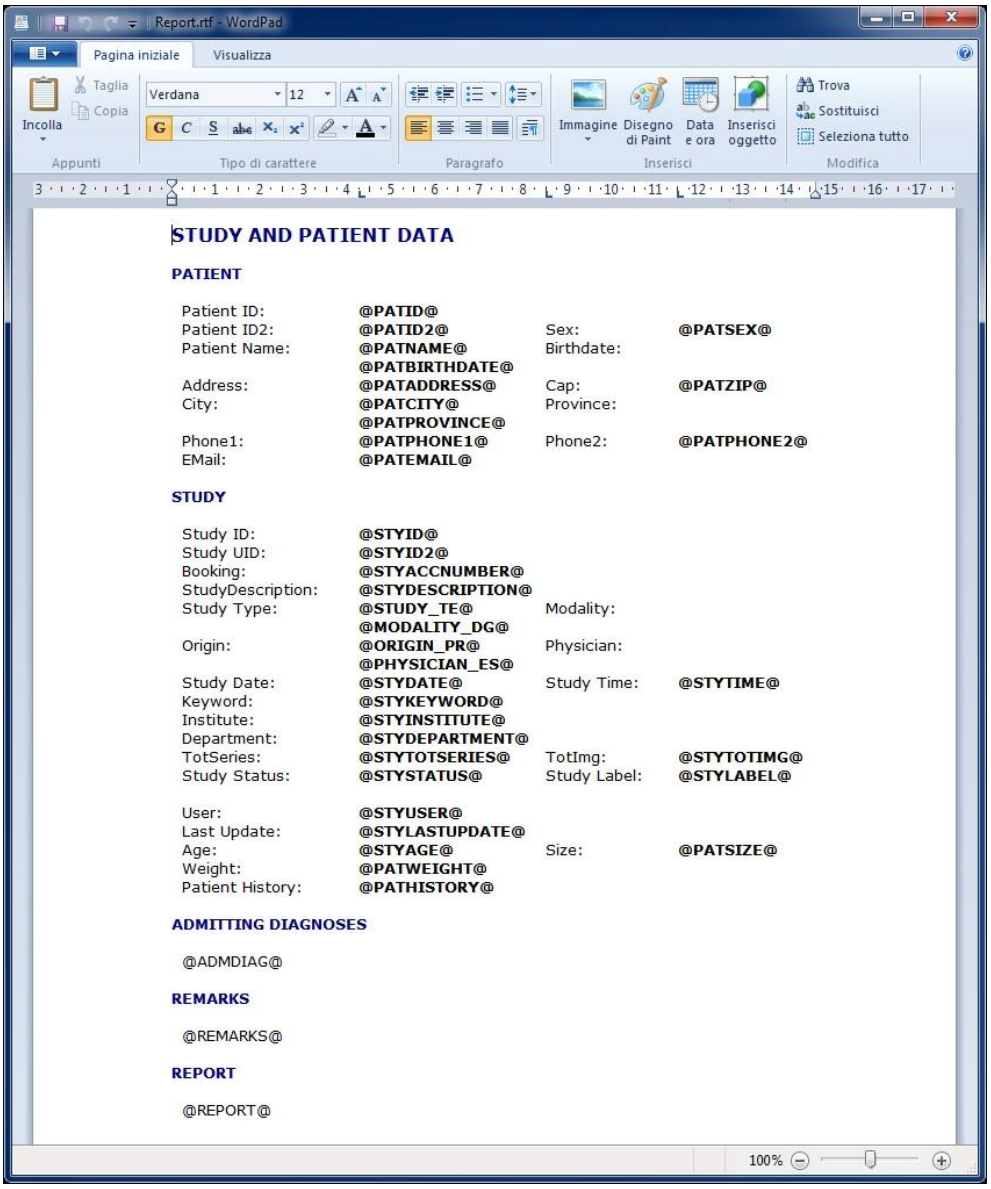
Figure 70. Node user management: user privileges

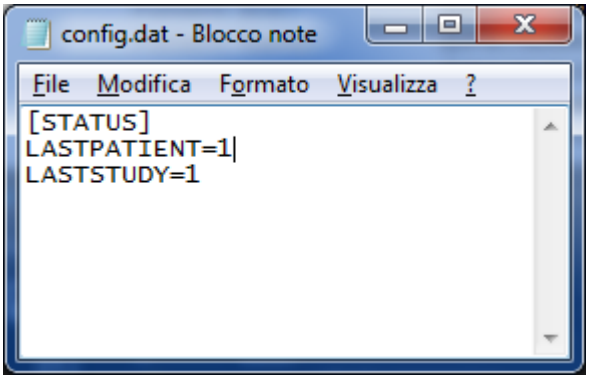


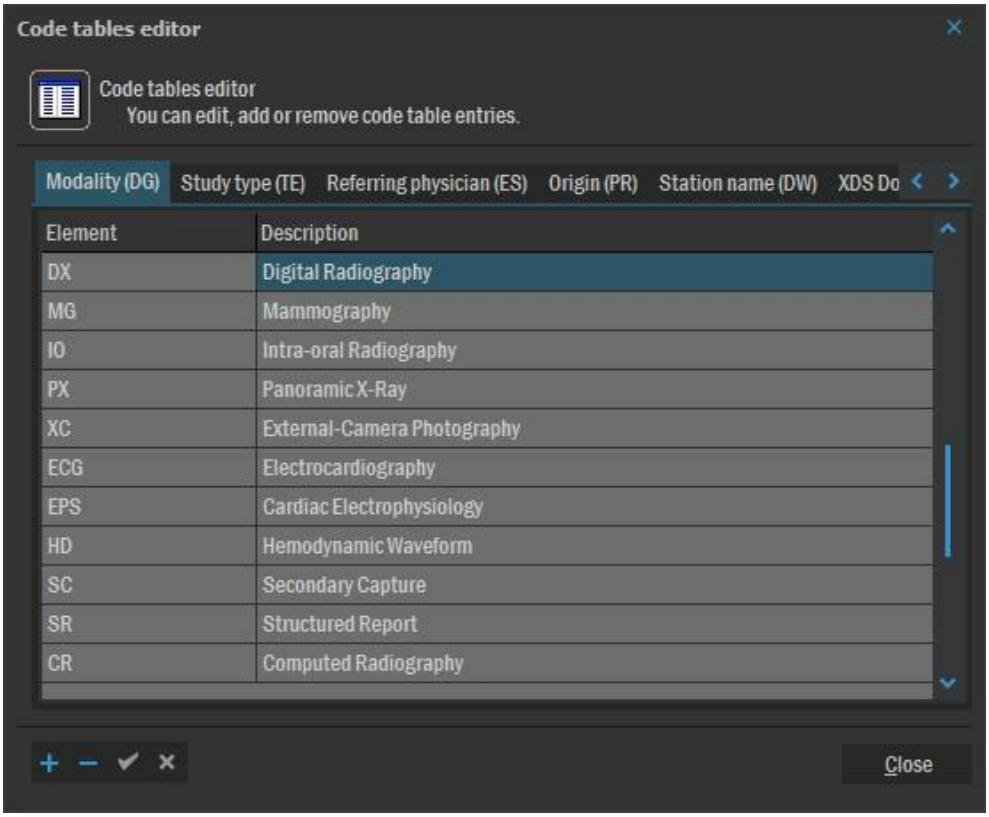
The user may have the following privileges:

RC-07

- Administrator (Supervisor)
- Insert new studies (Insert Studies)
- Modify studies (Update Studies)
- Delete studies (Delete Studies)
- Read only (Read Only)
- Configure report workspace (Write and configure Report)
- Use of a reading report data to compile a new report (Edit Report)

Info Print Format	By selecting *Info Print Format* from *Configuration file* box and by clicking on *Edit*, you enter the environment printing information changes in the study data summary. (You obtain this summary from MedStation if you click *Print* in the window for study data). **Figure 71.** Printing information configuration 

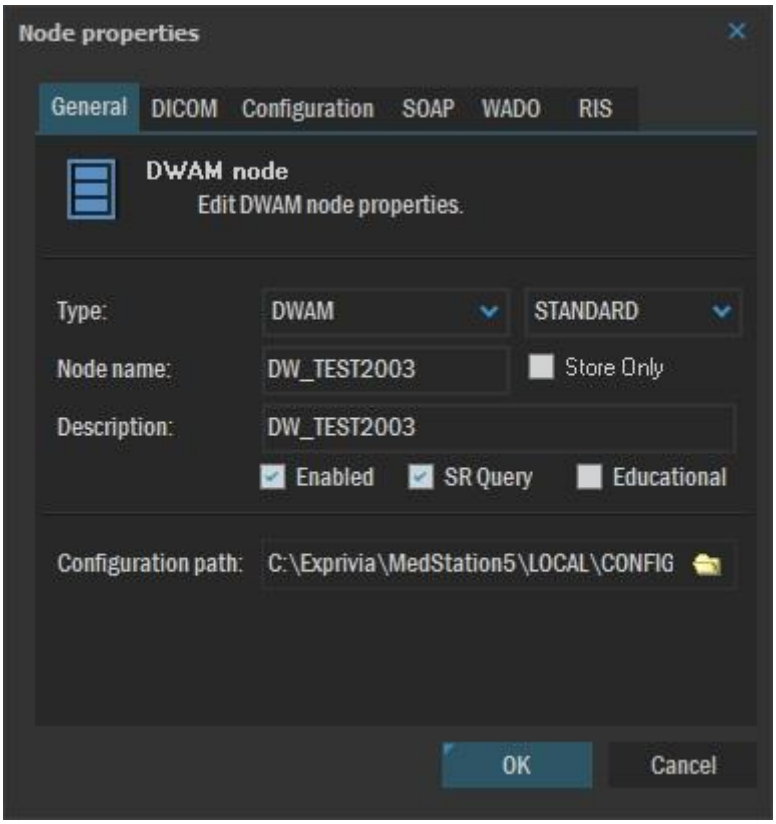
Counter Status	Counter status of studies and patients. To change them select *Counter Status* in the *Configuration file* box and press *Edit*. **Figure 72.** Config.dat file: last patient/study  This file contains the counters of the number of studies and the number of patients used to generate of patient and study ID when you create a new one. Normally there is no reason to change these values, modify them is allowed only for special cases.

Edit Tables	Code tables editor. A code table contains the description to be associated to following fields: Modality, Study Type, Referring physician, Origin and Station name. **Figure 73.** Code table 
Use Patient ID2 as default displayed identification code	If active, the Patient ID2 filed is displayed (patient DICOM code) as patient ID, whereas normally (i.e. when this option is not active) the Patient ID field is displayed (MedStation patient code).

DWAM node properties

Note: *From DWAM 4.4 version, management of user privileges is operated within DWAM server and not within MedStation client. User privileges will be received during the initialization of the communication with the server DWAM so you will not need to configure the section "User and privileges in the DWAM nodes configuration through MedConf. Configuration should be effected in the DWAM server in the* `DWMGR|Users` *section.*

Figure 74. DWAM node properties: General sheet



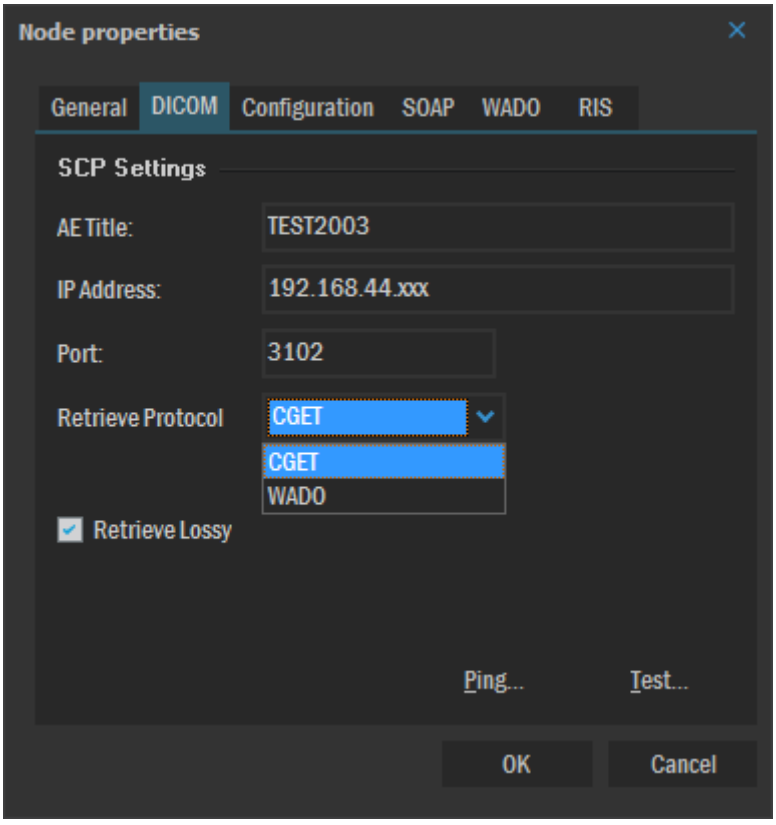
General sheet

Type	Type of node: DWAM. Beside, you can specify the type of DWAM node: LOCAL, STANDARD, http, XDS-I. LOCAL nodes are those related to the archive installed in the same machine (DicomWare server and study archive are on the same machine of MedStation. In this way, MedStation uses the COM interface and activates the retrieval of images via file system). STANDARD nodes represent a remote DWAM archive (if server and archive do not reside in the local machine. In this case, the communication with DicomWare will be effected through soap interface and you have to configure *DWAM connection* appropriately*)*. You choose HTTP if the DWAM archive resides on the wide area network. XDS-I nodes represents DWAM nodes. They are a gateway for research and display of XDS documents on remote nodes.
Node name	Internal node name. This name must uniquely identify the node within the list of MedStation nodes.
Store Only	Sola archiviazione. Se attivo, nasconde il nodo dall'ambiente di selezione esami e lo rende disponibile solo come nodo di destinazione di una copia.
Description	Description of the node shown to the user

Configuration

Educational	Management of educational data (not present for HTTP nodes)
SR Query	If active, while searching for studies in this node, you could set search parameters for structured DICOM reports (they will be displayed in a box in the *Advanced search criteria* window from the window for studies search and selection in MedStation.) **Warning!** The query on these parameters will only be performed properly if the *Query IHE Tags* flag is enabled on the *Client* | *DICOM* configuration sheet.
Configuration path	File configuration path

Figure 75. DWAM node properties: DICOM sheet



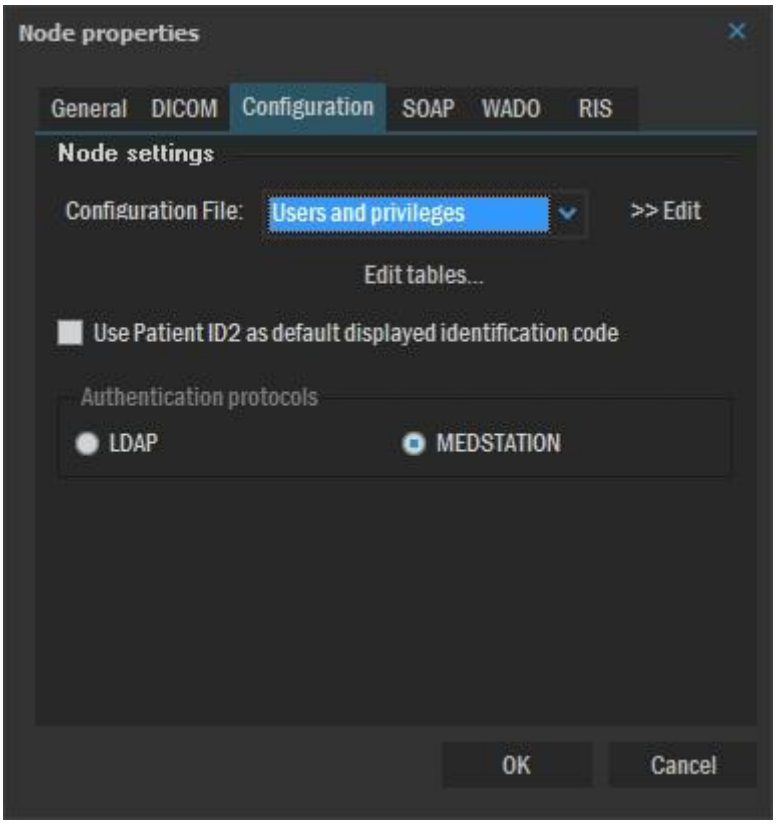
DICOM sheet

For HTTP nodes, on this sheet all you have to do is set the AE Title field.

AE Title	Title of Application Entity (AE) of the DicomWare server to which you want to connect by using this node.
Port	Port number of DicomWare server
IP Address	IP address of DicomWare server
Retrieve Proto-	Choose the communication protocol to DicomWare server

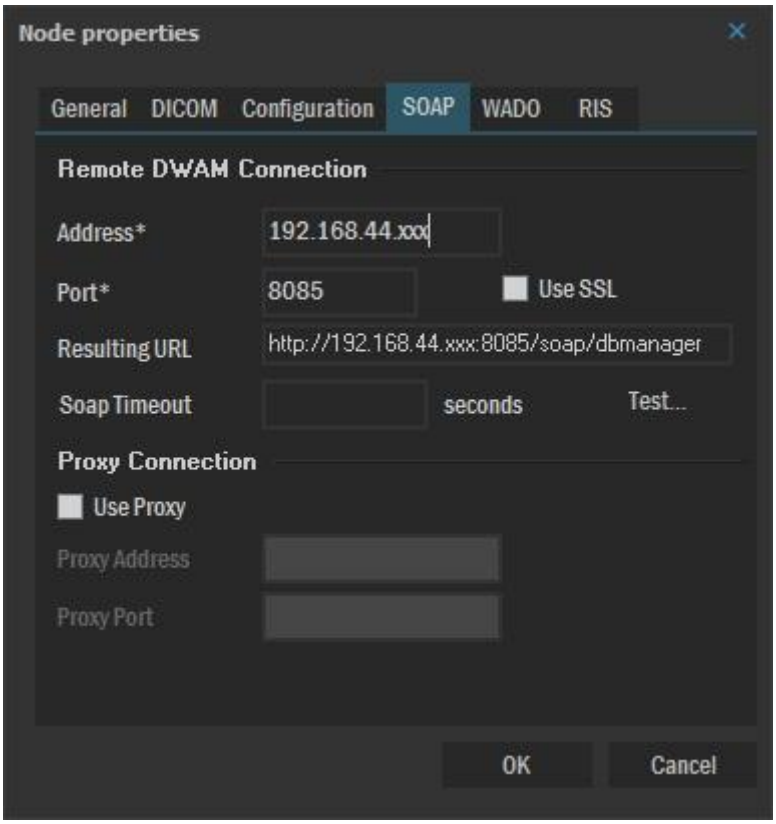
col	
Retrieve lossy	If active, images retrieval will be effected by searching in an archive where images are compressed with a lossy format. Otherwise, despite of a compressed archive, images retrieval will be effected in the not compressed archive.
Ping	Tests the TCP/IP connection with the destination machine: runs the command `ping` of MS-DOS.
Test	Tests the connection with the DicomWare server

Figure 76. DWAM node properties: Configuration sheet



The *Configuration* sheet is managed in the same way as described for *Local* nodes, except for Counter Status section.

Figure 77. DWAM node properties: SOAP sheet

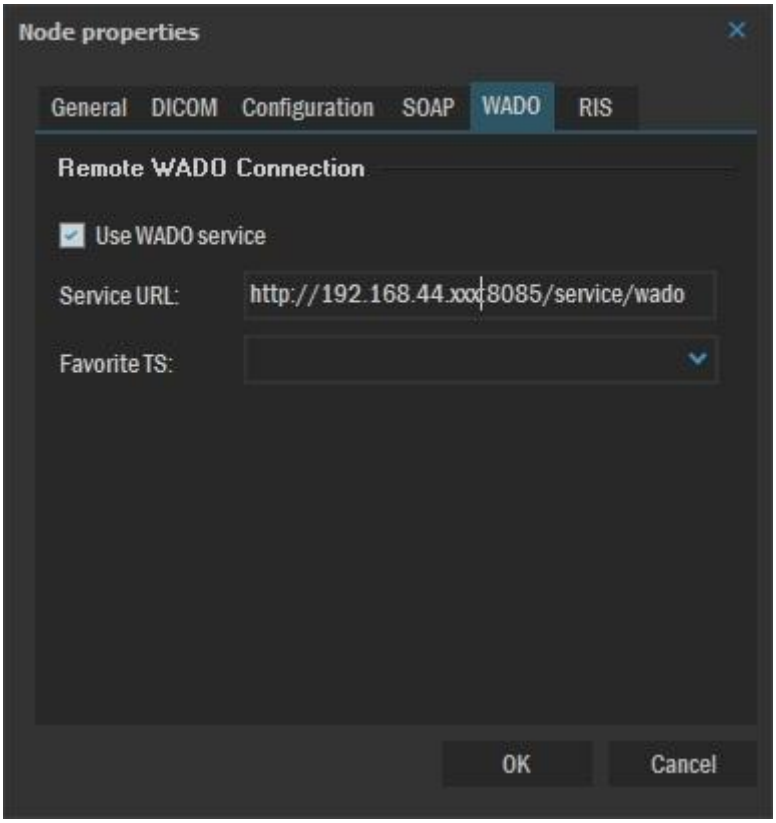


This sheet is available only when the DWAM node is not LOCAL and is used to indicate parameter for the SOAP connection.

DWAM connection sheet

Address	IP address of remote DicomWare server (automatic filling)
Port	Port number for SOAP communication in remote DicomWare server (value of field Port number in the HTTP Server section of remote DicomWare if the nodes is *DWAM STANDARD*; on the contrary, it is the value of field Port Number in the SSL Server section of remote DicomWare if the node is *DWAM HTTP with SSL active*)
Use SSL	Activates the secure connection HTTPS (only http nodes)
Resulting Url	Url automatic filling if previous values *Address* and *Port* are correctly inserted
Soap Timeout	Time expressed in second before soap connection timeout (only for Standard and Http nodes)
Test	Testing the connection to DicomWare server
Use Proxy	Allows to select a proxy to access the network
Proxy Ip	Proxy IP address
Proxy port	Proxy port

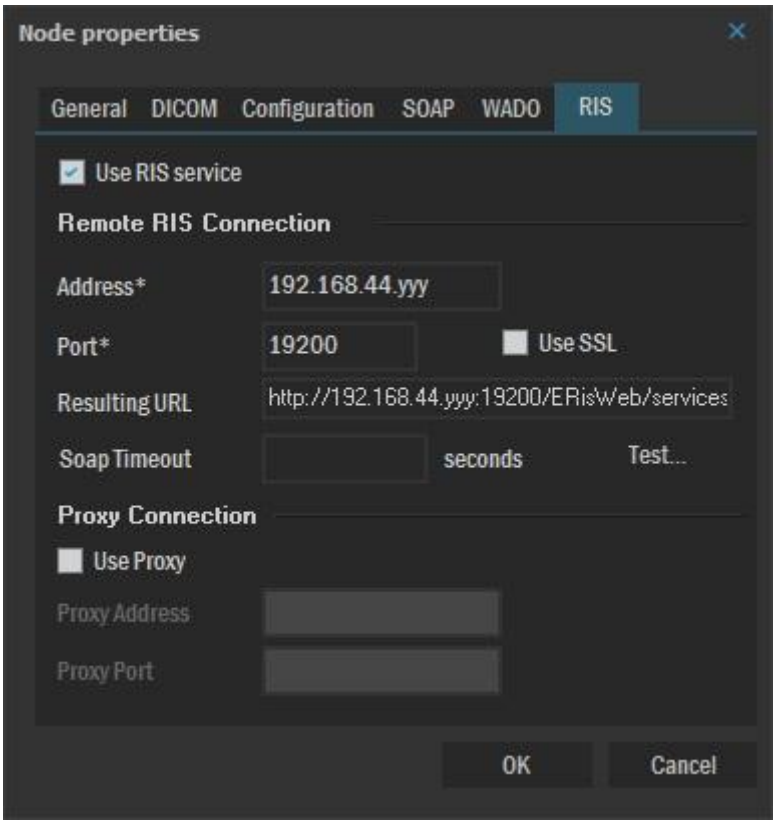
Figure 78. DWAM node properties: WADO sheet



WADO sheet

Use WADO Service	It activates the retrieval of images using the DICOM WADO protocol from a remote web service for the preview of images within structured reports and in the search form for the tree of bookmarks, for the recovery of movies, MPEG, ...
Service Url	Url address of WADO service
Favorite TS	(Optional field) Transfer syntax preferable to receive images via WADO protocol. It will be used by the server only if it supports this TS.

Figure 79. DWAM node properties: RIS sheet



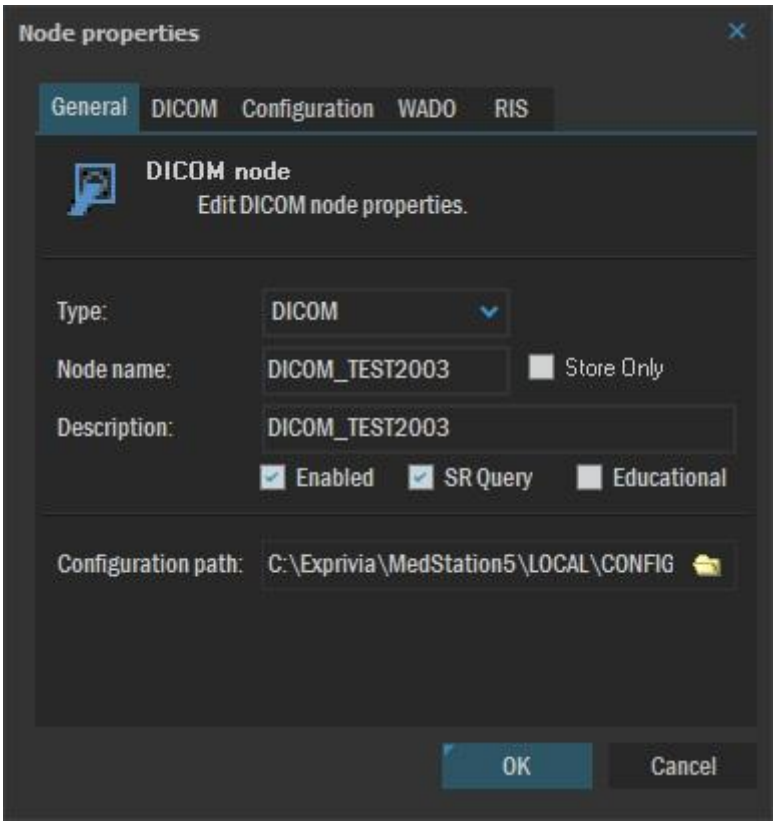
RIS sheet

This sheet only appears if the node is of the DICOM or DWAM type and is used to indicate the parameters for the SOAP connection with the eRis server, version 1.8 or later.

Use RIS service	It activates a connection with a *RIS* server
Server host	IP address of the remote e*Ris* server
Port	Number of the port for SOAP communication of the remote e*RIS* server
Resulting Url	Url that is set automatically if the two previous values are entered correctly, but can be edited manually.
Soap Timeout	Time expressed in seconds before a SOAP connection is considered failed if it does not respond.
Test	It tests the connection with the *RIS* server
Use Proxy	Used to select a proxy for access to the network
Proxy Ip	IP address of the proxy
Proxy port	Port of the proxy

DICOM node properties

Figure 80. DICOM node properties: General sheet

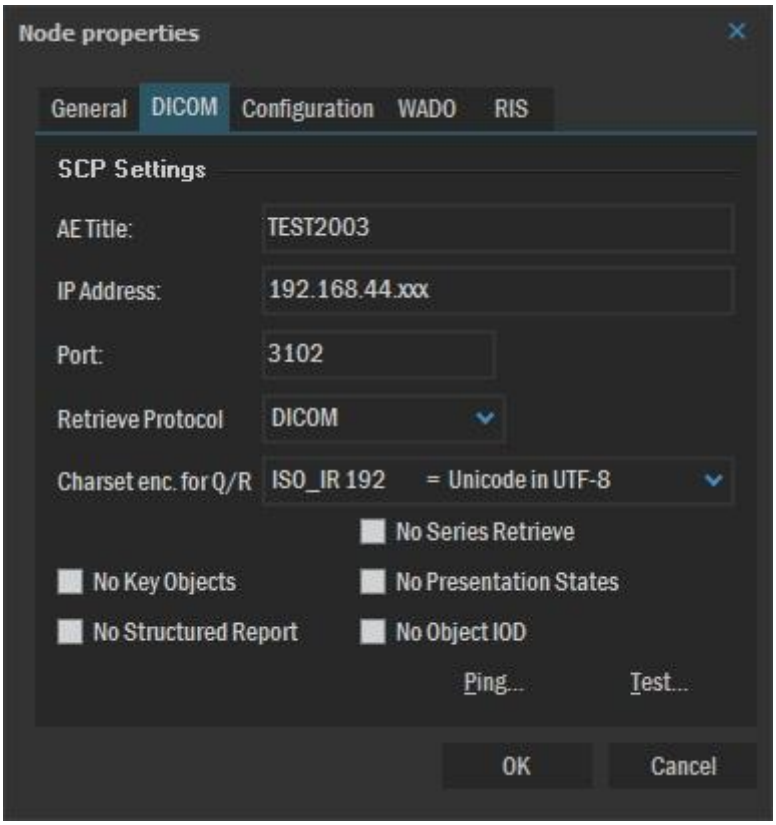


General sheet

Type	Type of node: DICOM
Node name	Internal node name. This name must uniquely identify the node within the list of MedStation nodes
Store Only	Storing only. If active, it hides the node from the environment of study selection available only as destination node of a copy.
Description	Node description
Enabled	Enabling/disabling node. If active, the user can access the node and perform all the operations allowed. If not active, the node is ignored.
Educational	Educational data management
SR Query	If active, while searching studies in this node, you could set search parameters for structured DICOM reports (they will be displayed in a box in the *Advanced search criteria* window from the window for studies search and selection in MedStation.) **Warning!** The query on these parameters will be done properly only if the flag *Query IHE Tags* is enabled in the *Client* | *DICOM* configuration.

Configuration path	File configuration path

Figure 81. DICOM node properties: DICOM sheet



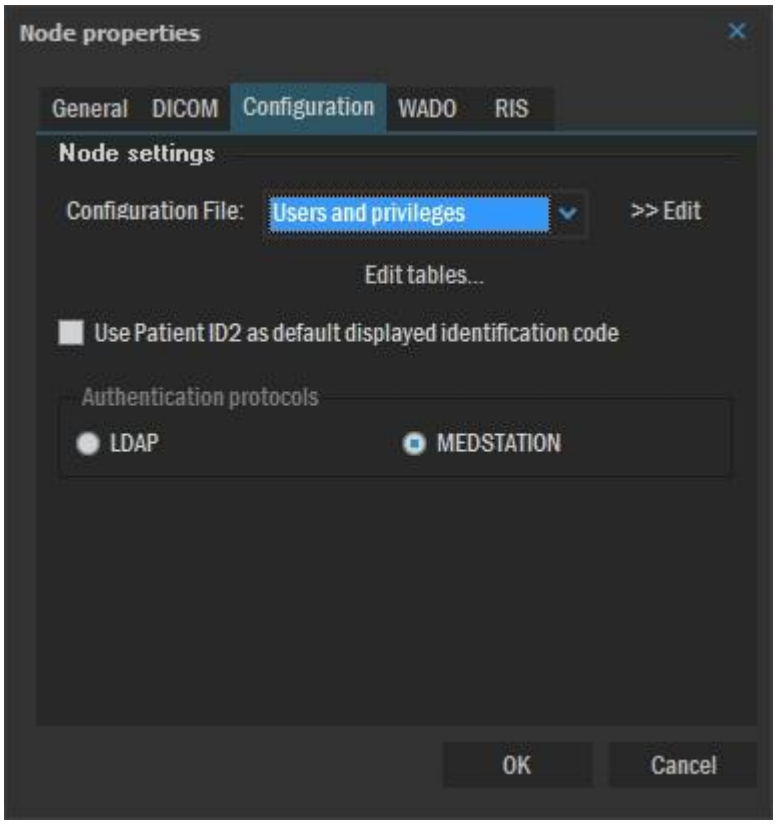
DICOM sheet

AE Title	Title of Application Entity (AE) of the DICOM server to which you want to connect by using this node.
Port	Port number of DICOM server
IP Address	IP address of DICOM server
Retrieve Protocol	Choice of communication protocol with the server. Possible values DICOM and WADO.
Charset enc. for Q/R	Charset used to encode strings that make up the query and retrieve messages between the client and the server.
No Key Objects	It excludes the downloading and saving of DICOM objects in KO modality
No Structured Report	It excludes the downloading and saving of DICOM objects in SR modality
No Series Retrieve	If active, the DICOM retrieve occurs only at STUDY level and can be useful with SCP that does not support QUERY/RETRIEVE actions at SERIES level.
No Presentation	It excludes the downloading and saving of DICOM objects in PR modality

Configuration

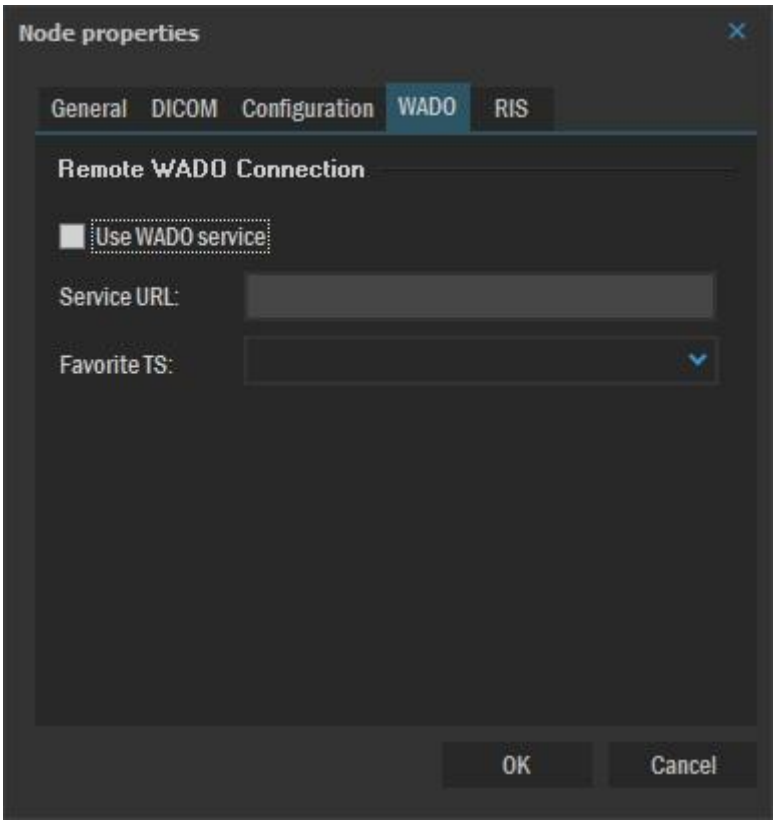
States	
No Object IOD	Predisposed Flag for downloading and saving of DICOM objects that are not images. Currently it acts only on DICOM objects with ECG modality.
Ping	Tests the TCP/IP connection with the destination machine: runs the command `ping` of MS-DOS.
Test	Tests the connection to DICOM server

Figure 82. DICOM node properties: Configuration sheet



The *Configuration* sheet is managed in the same way as described for *Local* nodes, except for the Counter Status section.

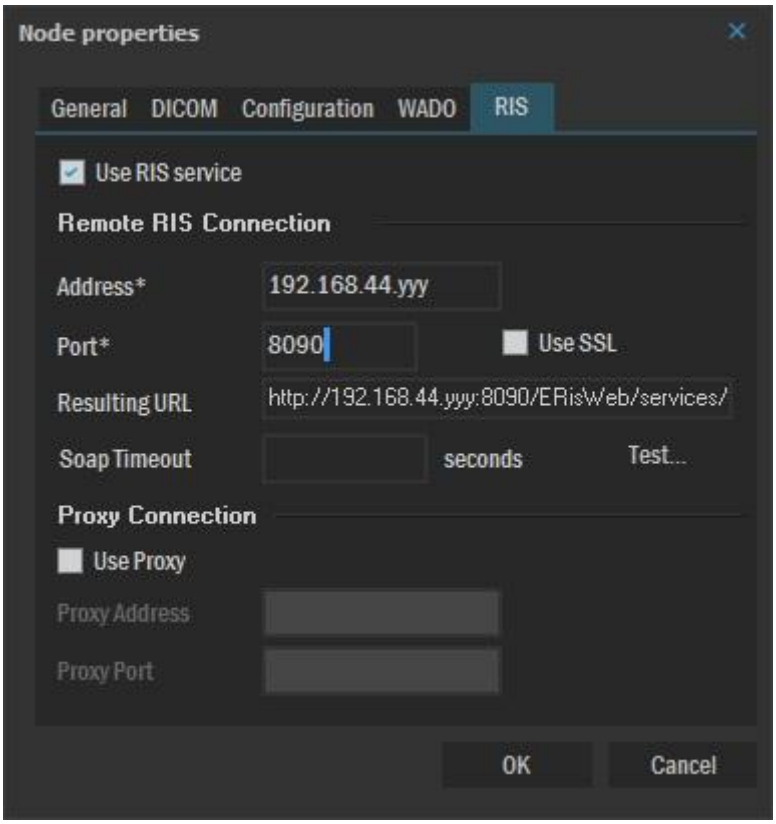
Figure 83. DICOM node properties: WADO sheet



WADO sheet

Use WADO service	It activates the retrieval of images using the DICOM WADO protocol from a remote web service for the preview of images within structured reports and in the search form for the tree of bookmarks, for the recovery of movies, MPEG, ...
Service URL	URL base of WADO service.
Favorite TS	(Optional field) Transfer syntax preferable to receive images via WADO protocol. It will be used by the server only if it supports this TS.

Figure 84. DICOM node properties: RIS sheet



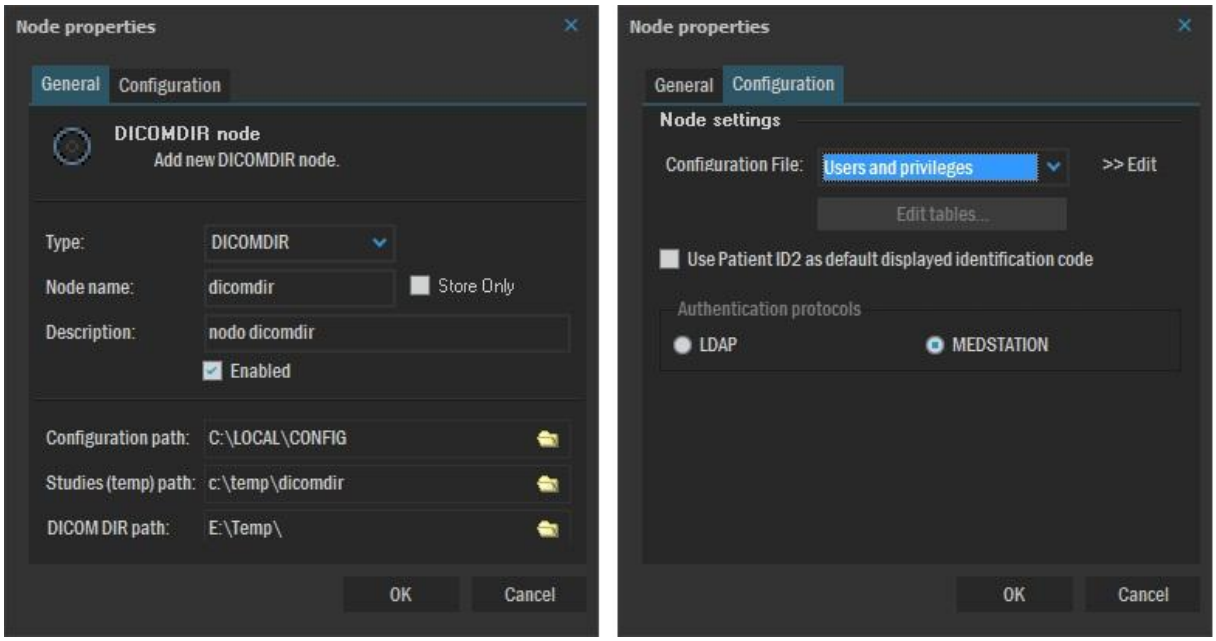
RIS sheet

This sheet only appears if the node is of the DICOM or DWAM type and is used to indicate the parameters for the SOAP connection with the eRis server, version 1.8 or later.

Use RIS service	It activates a connection with a *RIS* server
Server host	IP address of the remote e*Ris* server
Port	Number of the port for SOAP communication on the remote e*Ris* server
Resulting Url	Url that is set automatically if the two previous values are entered correctly, but can be edited manually.
Soap Timeout	Time expressed in seconds before a SOAP connection is considered failed if it does not respond.
Test	It tests the connection with the e*Ris* server
Use Proxy	Used to select a proxy for access to the network
Proxy Ip	IP address of the proxy
Proxy port	Port of the proxy

DICOMDIR node properties

Figure 85. DICOMDIR node properties



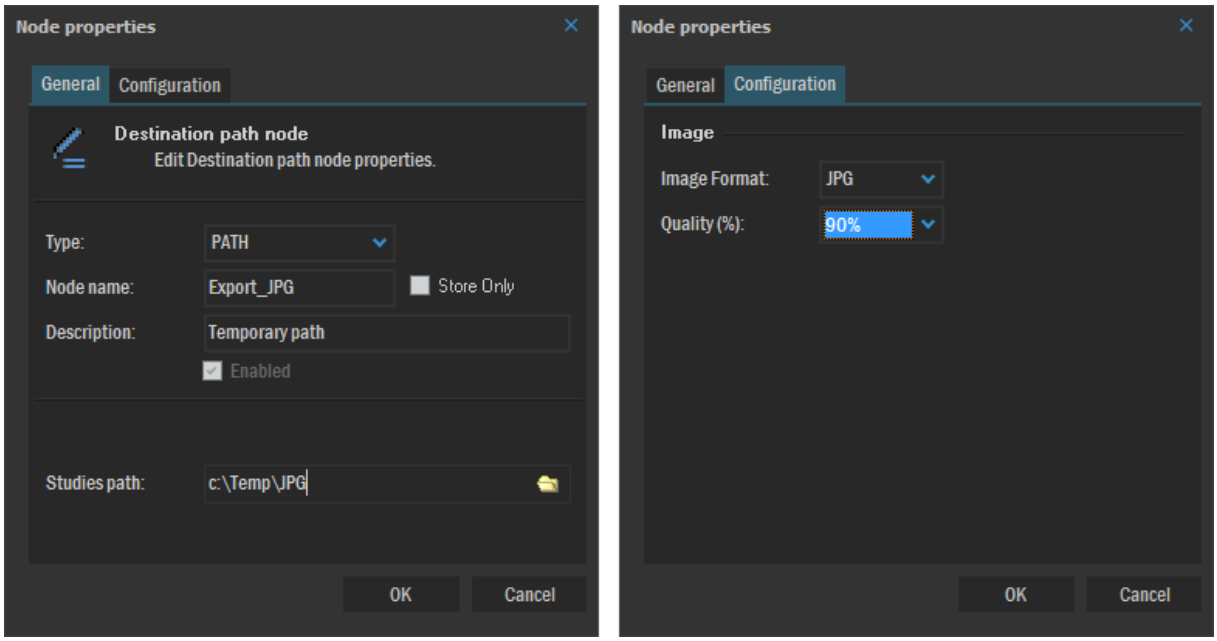
General sheet

Type	Type of node: DICOMDIR
Node name	Internal node name. This name must uniquely identify the node within the list of MedStation nodes.
Description	Node description
Enabled	Enabling/disabling node. If enabled, the user can access the node and perform all the operations allowed. If disabled, the node is ignored.
Configuration path	File configuration path
Studies path	Temporary directory for downloading studies
DICOMDIR path	Root directory of the drive containing studies in DICOMDIR format

The *Configuration* sheet is managed in the same way as described for *Local* nodes, except for Counter Status section.

PATH node properties

Figure 86. PATH node properties



General sheet

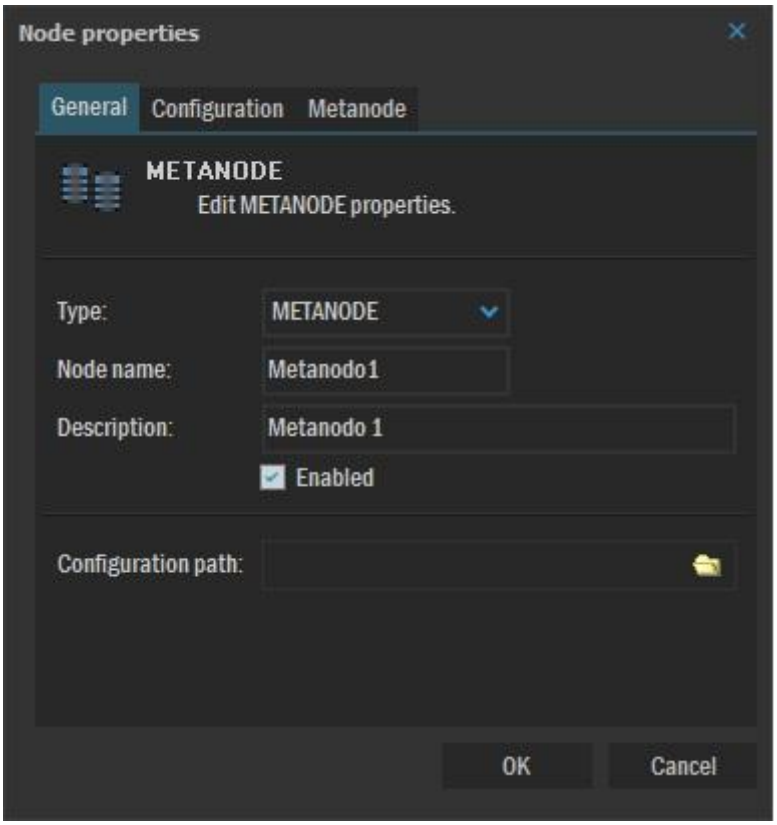
Type	Type of node: PATH
Node name	Internal node name. This name must uniquely identify the node within the list of MedStation nodes.
Description	Node description
Studies path	Temporary directory for study downloading.

Configuration sheet

Image Format	Image format: BMP, JPG, etc. Only 1, 8 and 24-bit formats are allowed. This format is used when the user captures images from files, from clip-board or from external module. ***Note:*** *This parameter is ignored if 'Use DICOM format' (in the section Client, Basic sheet) is active*
Quality (%)	Image compression factor. To be considered only with JPG format.

Metanode properties

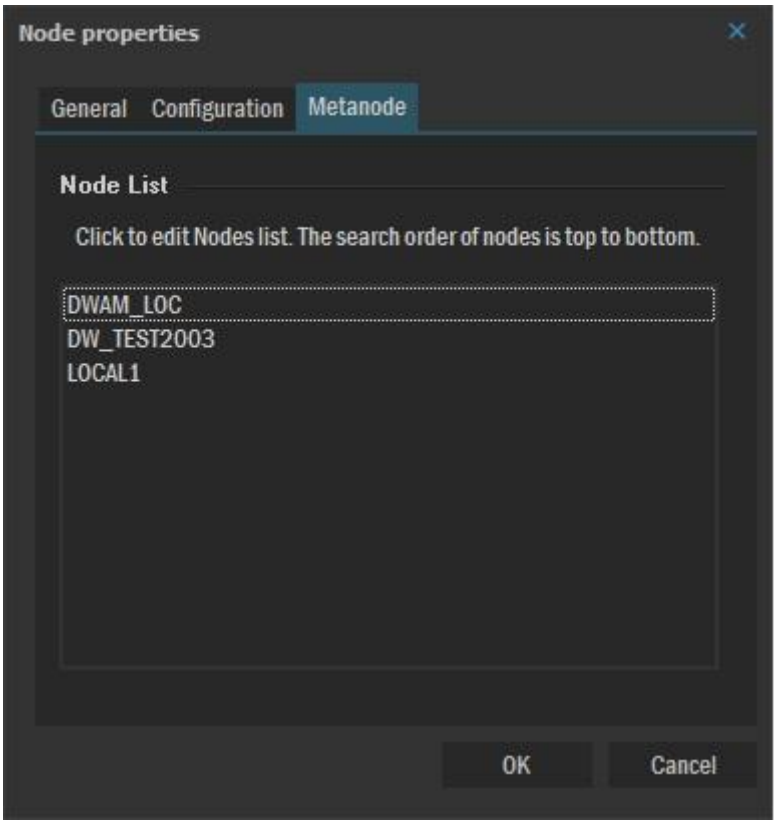
Figure 87. Metanode properties: General sheet



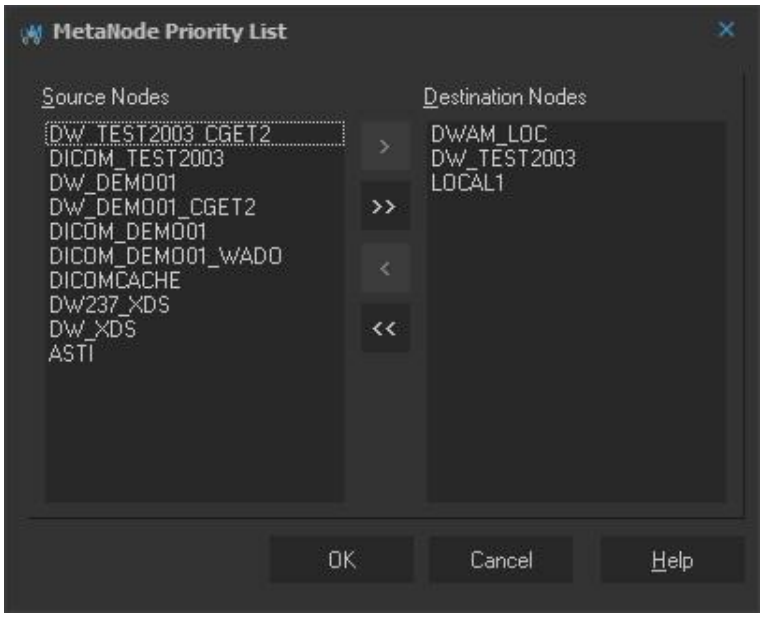
General sheet

Type	Type of node: METANODE
Node name	Internal node name. This name must uniquely identify the node within the list of MedStation nodes.
Description	Node description
Enable	Enabling/disabling node. If active, the user can access the node and perform all the operations allowed. If not active, the node is ignored.
Configuration path	File configuration path

Figure 88. Metanode properties: Metanode sheet



Metanode sheet

Nodes List	Manage of the list of nodes that should be part of a metanode. Click on the list to modify it; through a secondary window, you can select the nodes. 

	On the left, you have the list of all existing nodes on the right of the nodes to be considered by the metanode. Select a node and push the '>' or '<' to move it from on list to the other. Buttons '<<' and '>>' move all the nodes from one section to the other. The order in which nodes are listed corresponds to the order in which Med-Station will affect the search. In the following example, the search will start from the DWAM_LOC node to go to LOCAL1. ***Note:*** *if you're opening a study from Metanode and the same study is present in more than one node, only the first study will be added to the list, the other will be ignored; this because we suppose that all nodes of the Metanode have been ordered (so that the first node is the quickest to open and the following the slower to open). To disable this operation, and show all the duplicates, hold down the Ctrl key.*

Setup of the license server

Starting with version 5.0 of MedStation, the management of licenses has changed. A DicomWare server will manage them. The management of licenses is therefore centralized and is no longer dependent on the individual client where MedStation is installed.

In this section of the configurator you have to specify the data of the license server.

Address	IP address of the DicomWare server designed for license management
Port	Number of the SOAP port of the server
Resulting URL	String automatically composed after insertion of the two previous items
Timeout	Time in seconds before a soap connection is considered as failed if is not responding.
Test	Tests the connection to the server
Proxy Address	Ip address of the proxy
Proxy port	Proxy port

Figure 89. Data of the license server

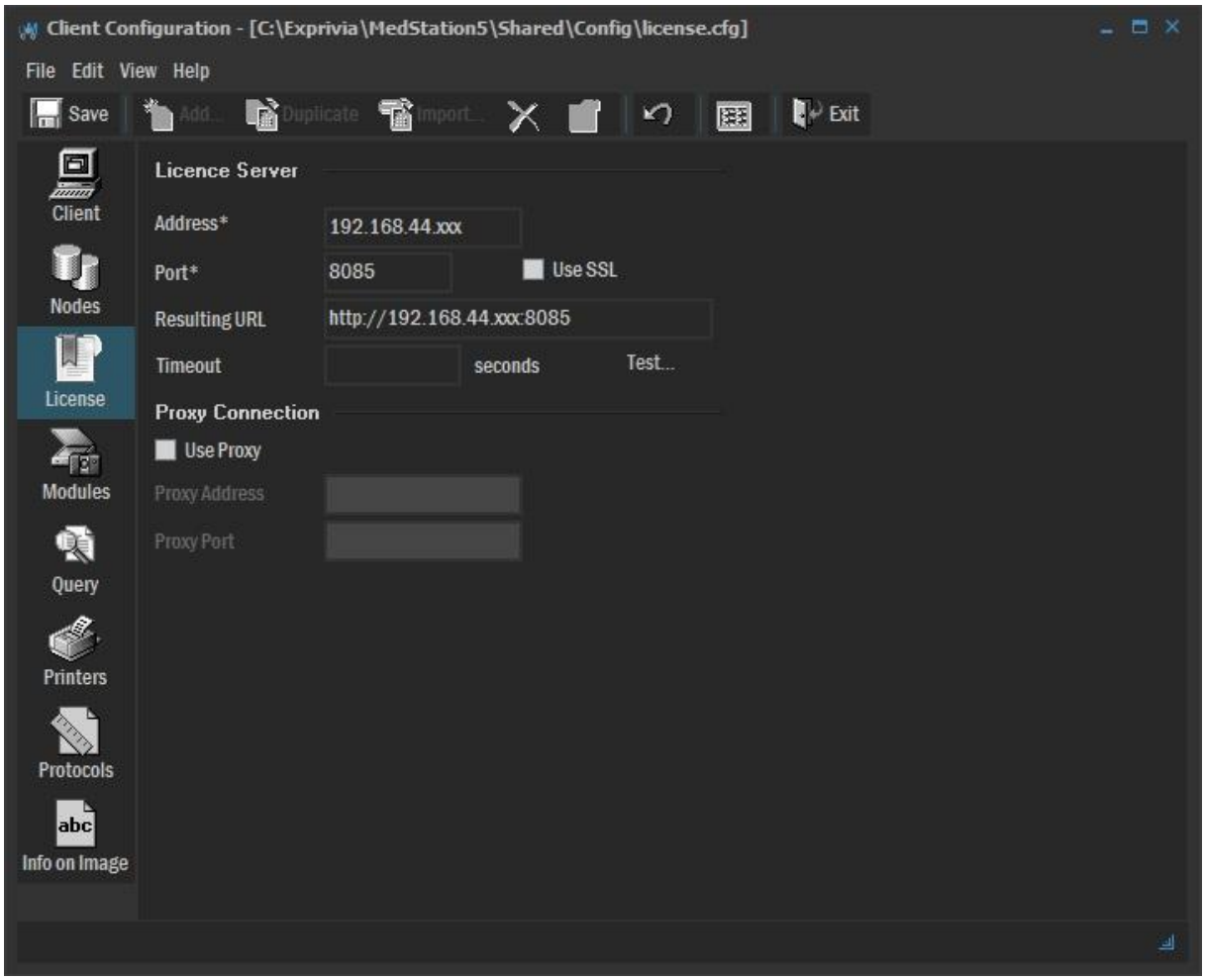
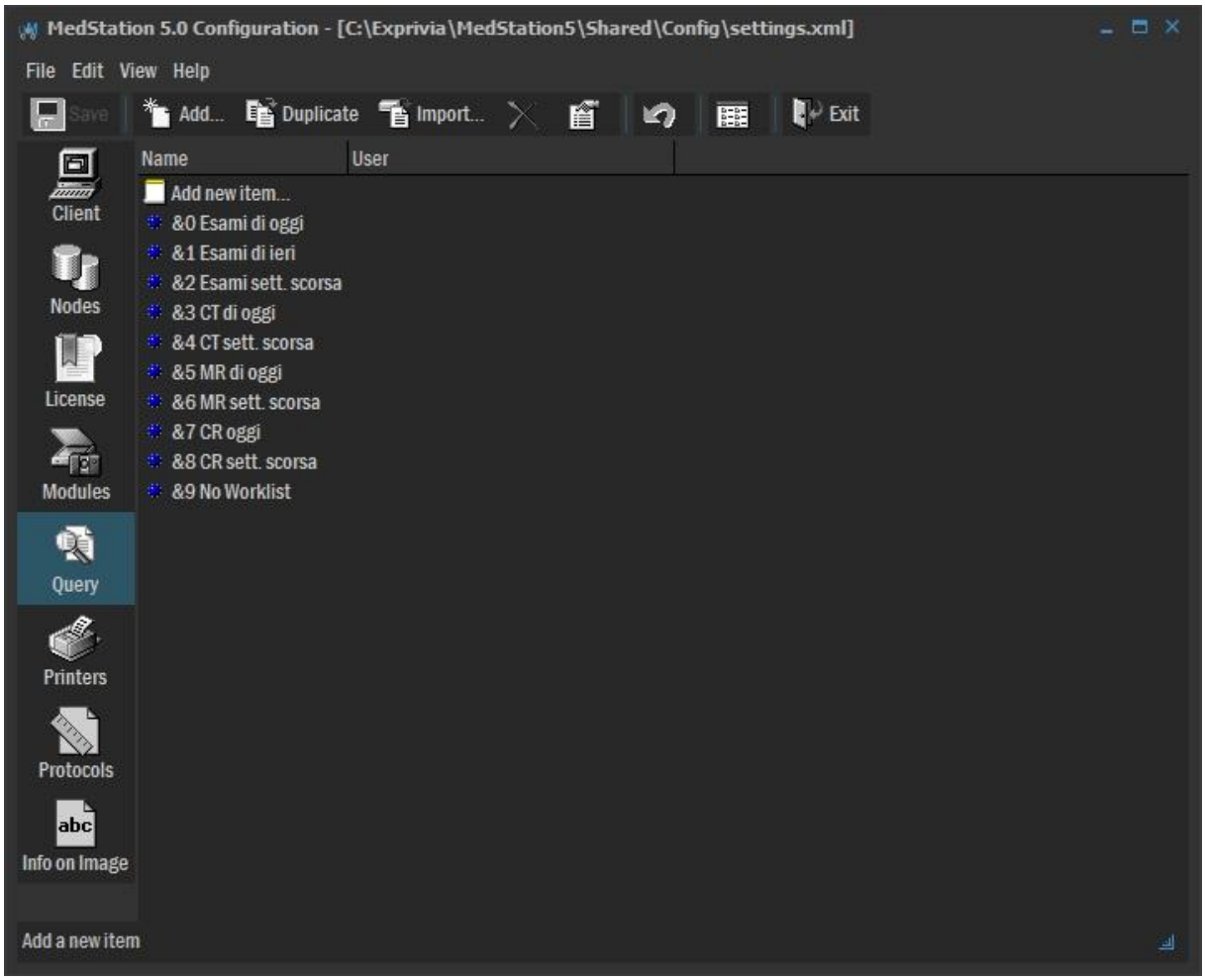


Figure 90. XML Query section



This sheet allows configuring predefined queries that are displayed in the window for study searching and selection in MedStation.

To create a new query press button *Add*, to modify an existing query select it and press button *Properties*. In both cases, a window will appear where to choose the parameters of the query. Available parameters are the same as in the study selection window in MedStation, included advanced criteria. Every user can have a different list of predefined queries.

Configuring acquisition modules

In this section, you can configure external modules through which MedStation acquires diagnostic images from non-DICOM source.

Figure 91. Acquisition module configuration section

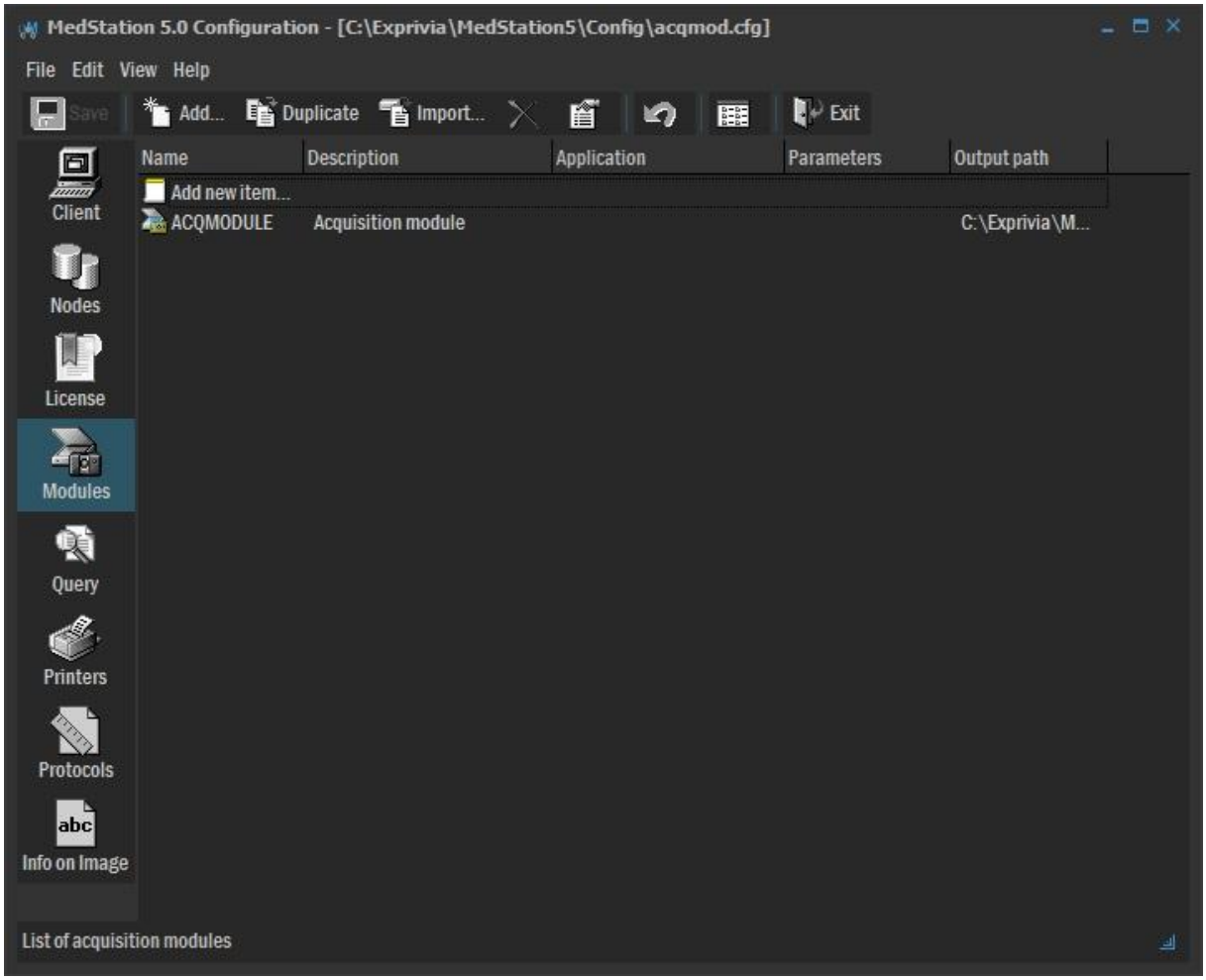
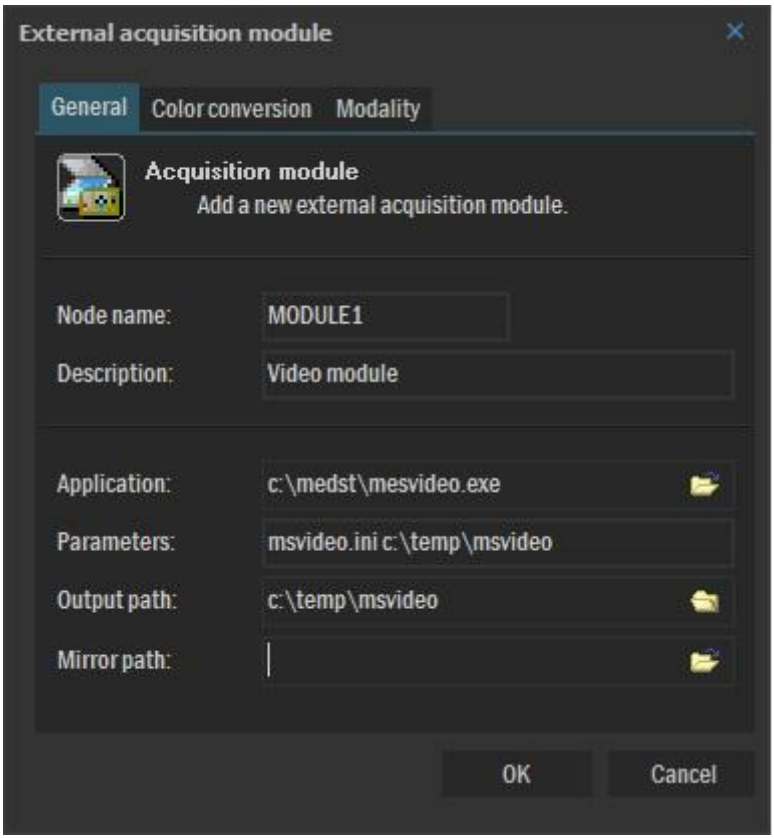


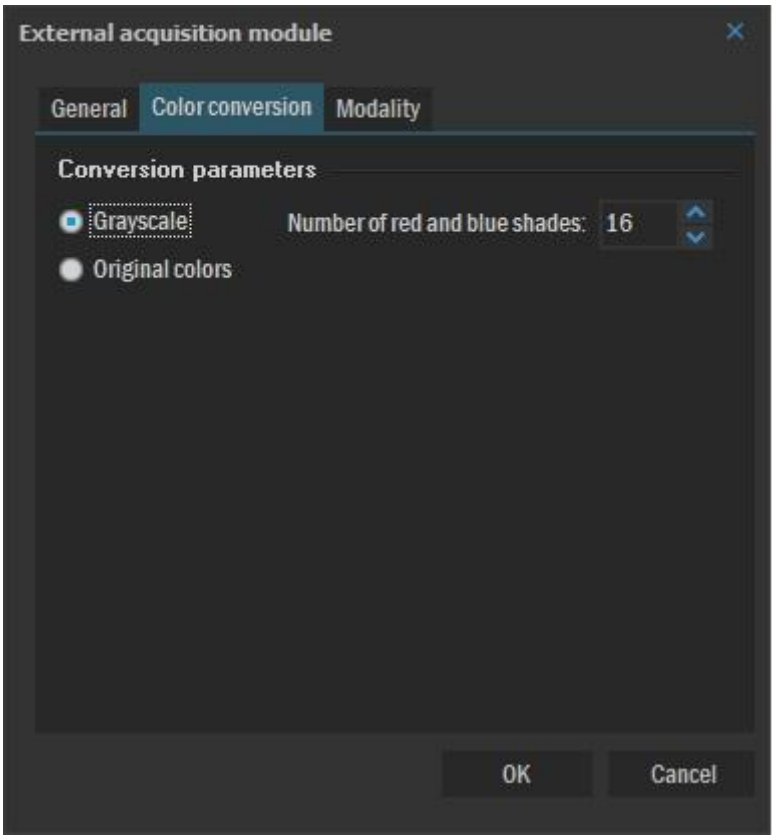
Figure 92. External acquisition module: General sheet



General sheet

Node name	Internal node name. This name must uniquely identify the node within the list of MedStation nodes.
Description	Module description
Application	Path of the application used as images acquisition module
Parameters	Possible module configuration parameters. In general, for modules supplied by Exprivia you have to specify the configuration file name and the destination directory where the acquired files are saved. If you start the application without parameters, a window with the correct syntax is displayed.
Output path	Directory where the acquisition application will save acquired images. When you quit the acquisition application, MedStation reads acquired files from this directory, adds them to current study and eliminates them from the directory.
Mirror path	All acquired images are replicated in the directory specified by *Mirror Path*. This function allows connecting one after the other applications that consider images contained in this directory.

Figure 93. External module acquisition: Color Conversion sheet

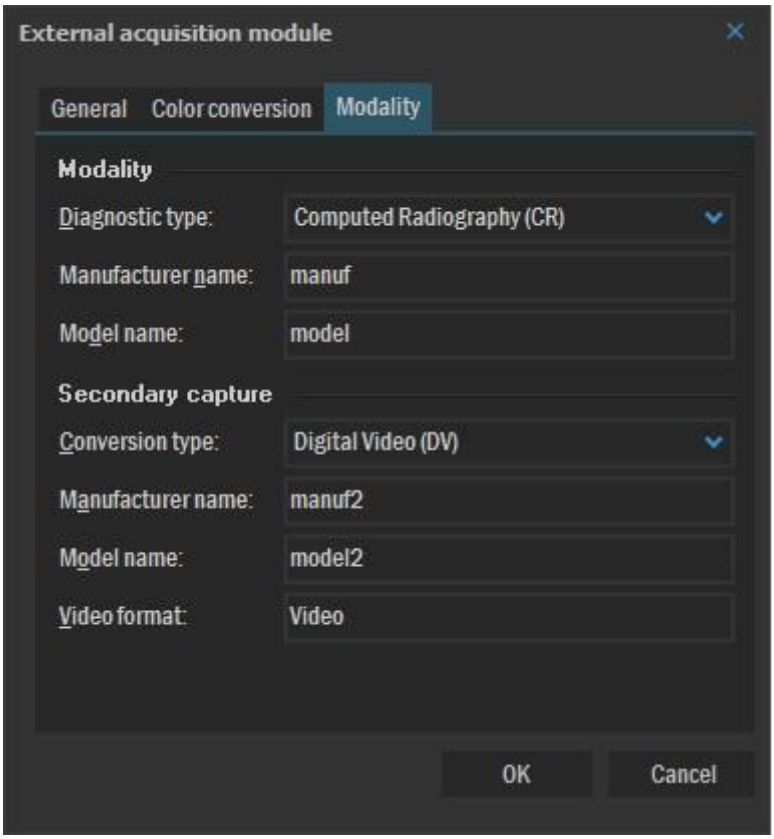


Color conversion sheet

The "Color conversion" sheet defines the color conversion modality for images acquired at 8 (256 grayscale) or 24 bit (*true-color*).

Grayscale	You can force the grayscale acquisition with possible recognition of a pre-determined number of shades of red and blue. Forcing to a grayscale is used in the case of a frame grabber connected to a monitor in black and white, while the recognition of shades of red and blue is generally used in echo-Doppler systems.
Original colors	Used to maintain images original colors.

Figure 94. External module acquisition: Modality sheet



Modality sheet

Diagnostic type	It specifies the type of diagnostic modality
Manufacturer name	Diagnostic manufacturer name
Model name	Diagnostic model name
Conversion type	Type of conversion from Secondary capture
Model name	Secondary capture model name
Video Format	It specifies video format

Configuring installed printers

The *Printers* section enables installed printers to be configured. The types of printers managed are Windows, DICOM and 3M.

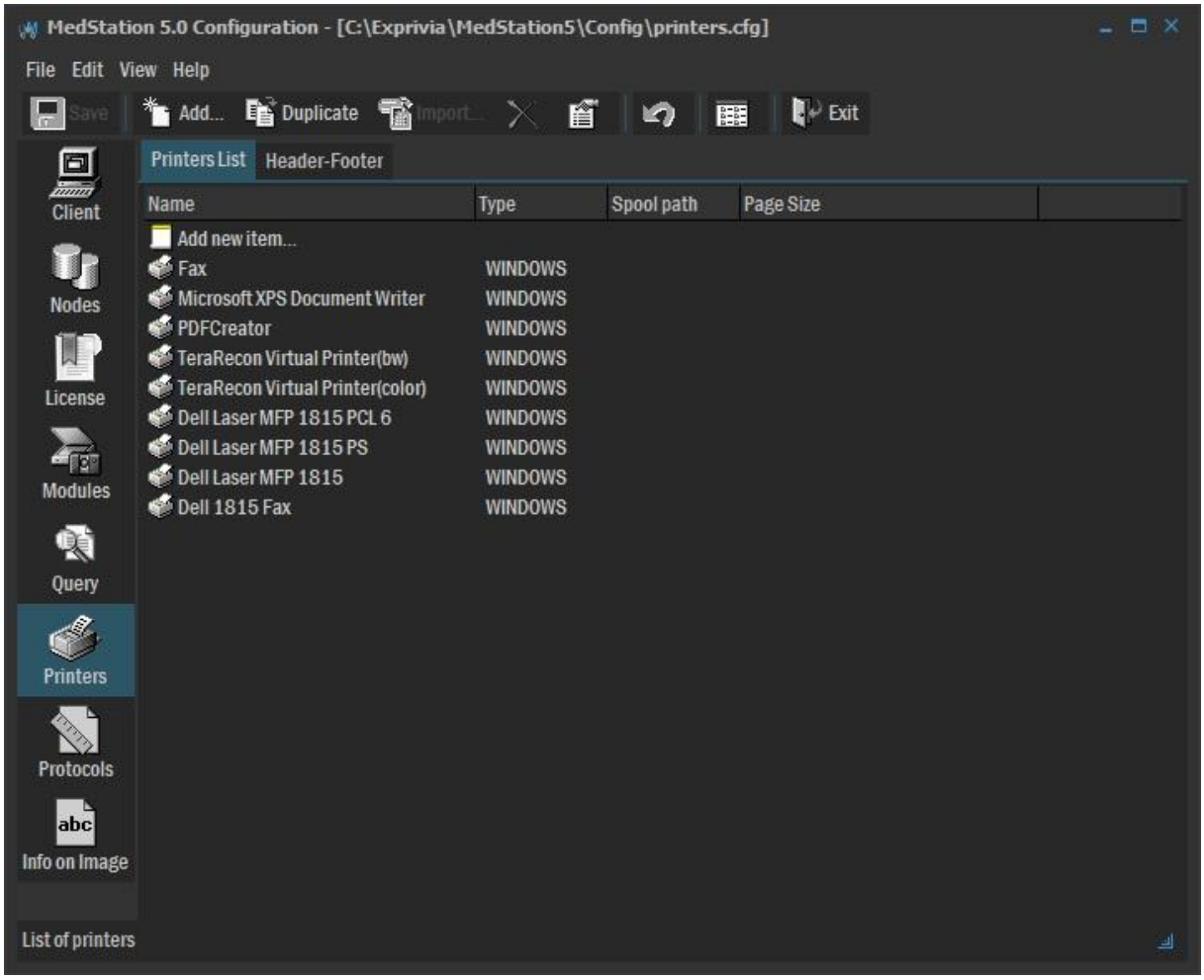
Pages sent to printers are then processed by the print system with size and color changes. Exprivia does not assume any liability for the compliance of the printed files with the originals generated by the diagnostic device.

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Validation is the responsibility of the user in each plant and each printer used.

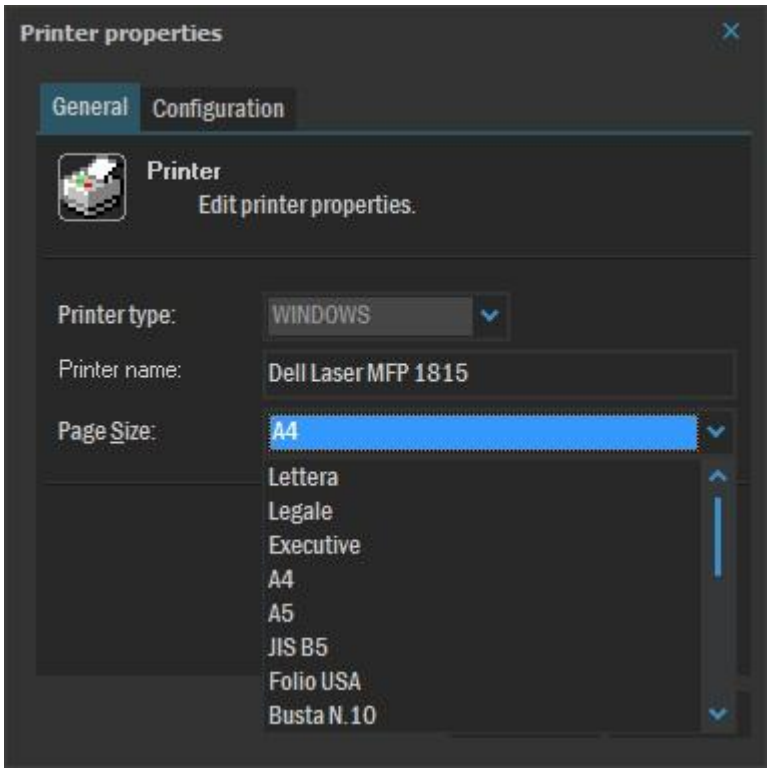
To configure a new printer, press **Add** in the toolbar in the *Printers* section shown in Figure 95. Access is given to the properties window of the printers (Windows, DICOM and 3M) shown in following figures, in which you can configure the type of printer, the name, the spool directory and the resolution.

Figure 95. Configuration application: Printers section



Windows Printers

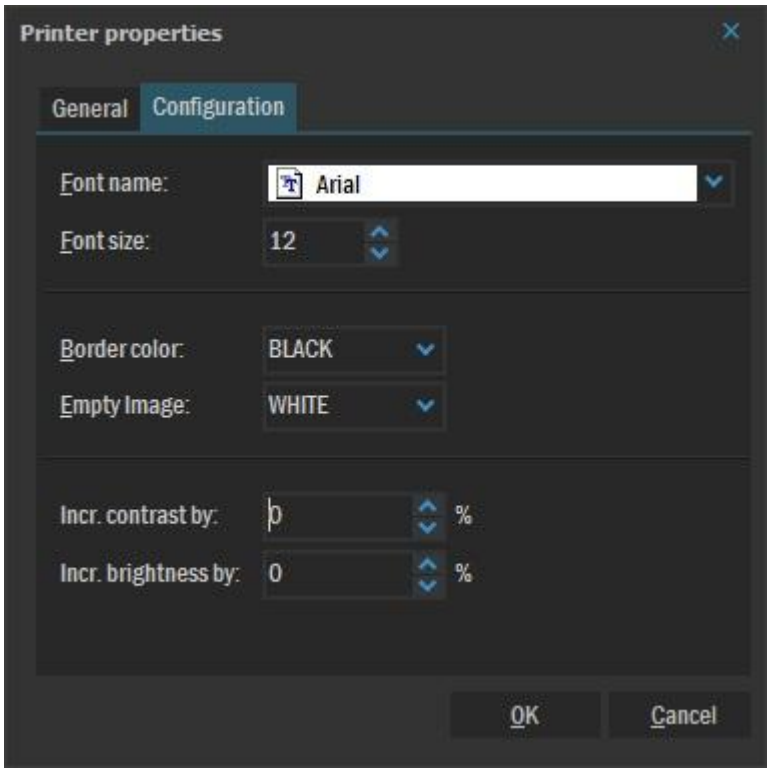
Figure 96. Configuring a Windows printer – General sheet



General sheet

Printer Type	Type of printer to configure
Printer Name	Printer name assigned by user
Page Size	Dimension of page to print

Figure 97. Configuring a Windows printer – Configuration sheet



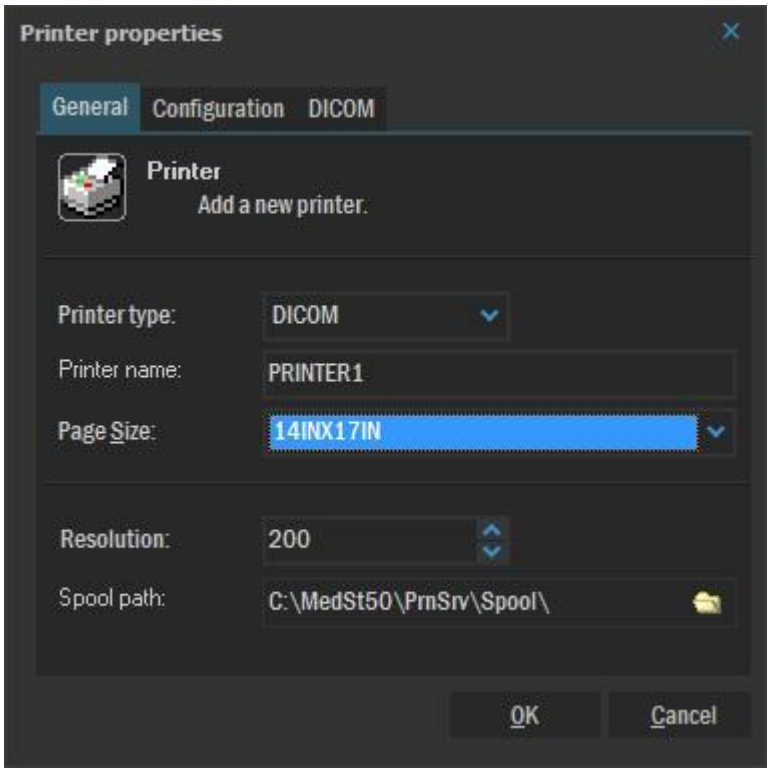
Configuration sheet

Font name	Name of the font to use
Font size	Font size of the text to print
Border color	Border color of the page to print
Empty Image	Color of empty images
Incr. Contrast by	Increasing contrast of the page to print
Incr. Brightness by	Increasing brightness of the page to print

DICOM printers

DICOM printers need the installation of Printer Server service to function. The application generates printer files saving them in the spool directory controlled by the Printer Server service.

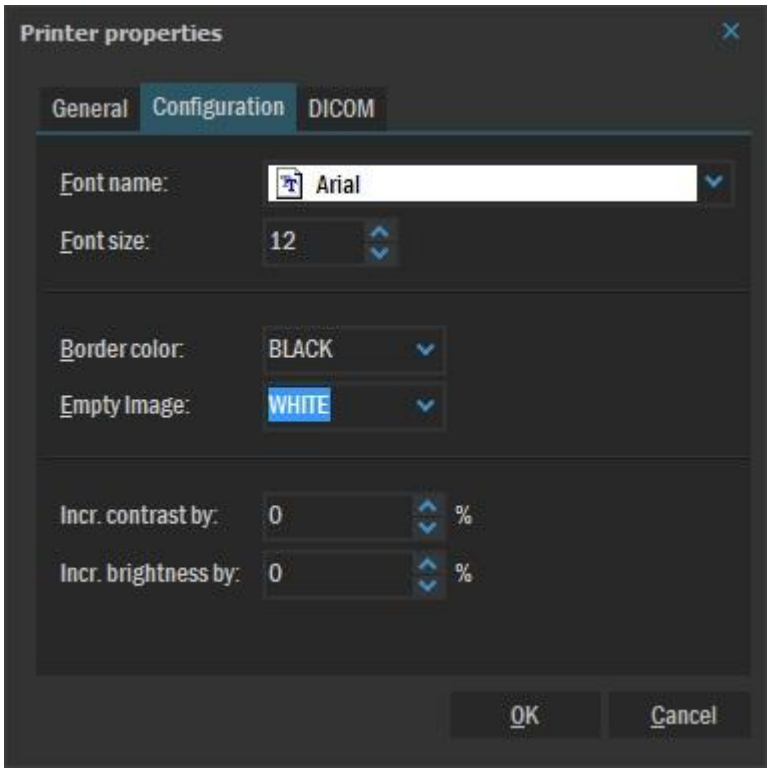
Figure 98. Configuring a DICOM printer – General sheet



General sheet

Printer Type	Type of printer to configure
Printer Name	Printer name assigned by user
Page Size	Page size to print: it is possible to select a standard format or to define new page dimensions by modifying the printer configuration file `printers.cfg` as follows: PAGESIZE*nn*=*x*INX*y*IN^*x_in_mm*^*y_in_mm* Where *nn* is progressive and starts from 00, the dimension of *x* in mm can be calculated by *x*IN*254. For example: PAGESIZE00=14INX17IN^3560^4320 where 14*254=3560 After this operation, also new formats are displayed
Spool path	Temporary directory
Resolution	Print resolution. Inserted value is expressed in dpi (Dots Per Inch). Its value is calculated according to the page format and to the matrix representing the useful area of image to print. Page layout and dimension are provided by the printer. For example, if *Page Size* is 14INX17IN and the print matrix is 1000x1500 point, the resolution R is 14 * R = 1000 o 17 * R = 1500.

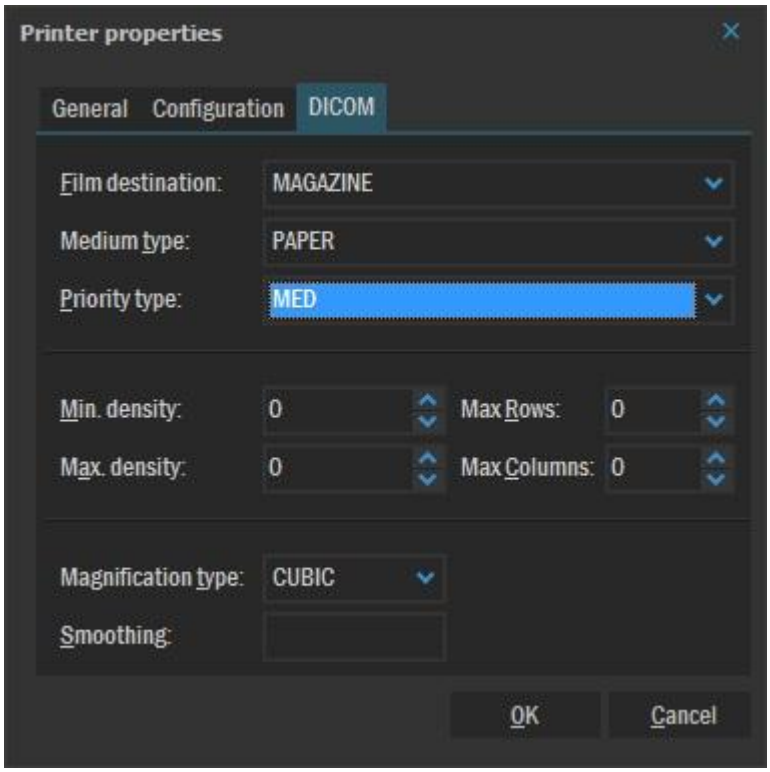
Figure 99. Configuring a DICOM printer – Configuration sheet



Configuration sheet

Font name	Name of the font to use
Font size	Font size of the text to print
Border color	Border color of the page to print
Empty Image	Color of empty images
Incr. Contrast by	Increasing contrast of the page to print
Incr. Brightness by	Increasing brightness of the page to print

Figure 100. Configuring a DICOM printer – DICOM sheet



DICOM sheet

The meaning of following parameters is described in detail in part 3 of DICOM Standard and in Conformance Statement of the printer.

Film destination	Destination for the film. Legal values of MAGAZINE and PROCESSOR.
Medium type	Print media used. Legal values: PAPER, CLEAR FILM, BLUE FILM.
Priority Type	Specifies the print priority. Legal values: High, Medium, Low.
Min density	Minimum pixel intensity for the image printed, expressed in OD*100. Inferior density values are forced to *Min density*.
Max density	Maximum pixel intensity for the image printed, expressed in OD*100. Superior density values are forced to *Max density*.
Max Rows	Maximum rows number of matrix to print (value expressed in points).
Max Cols	Maximum rows number of columns to print (value expressed in points).
Magnification type	Interpolation algorithm used when resizing the image to fit it in its print box. Legal values: REPLICATE, BILINEAR, CUBIC, NONE. (Windows uses Windows primitive base)

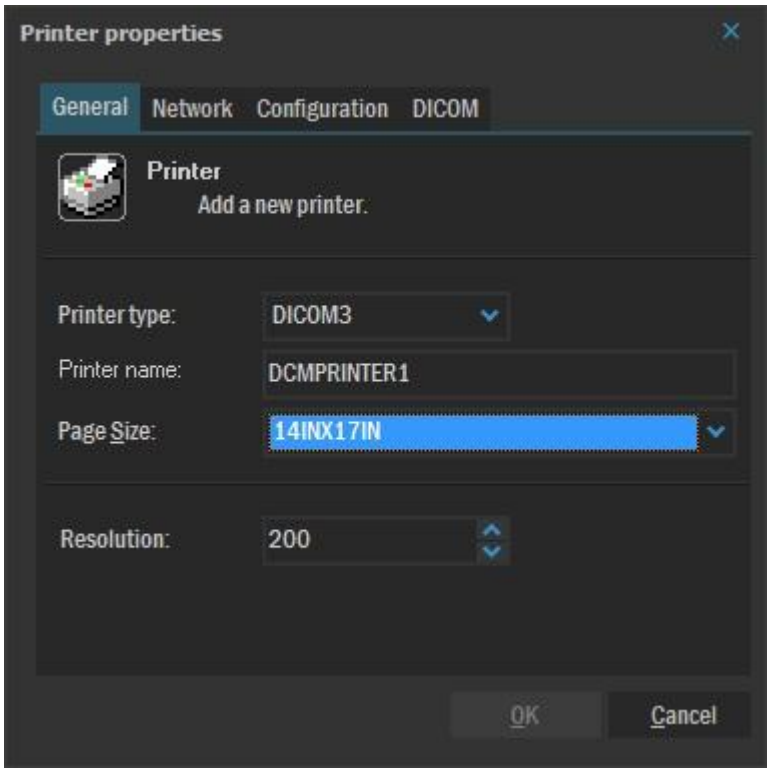
Smoothing	Specifies the type of interpolation function to be used as indicated in the printer's Conformance Statement.

Configuring a 3M printer is similar to configuring a DICOM printer as described in General and Configuration sheets. The DICOM page is not present.

DICOM3 Printers

These printers do not need the installation of Printer Server module, images to print are sent directly to the remote DICOM printer.

Figure 101. Configuring a DICOM3 Printer – General sheet

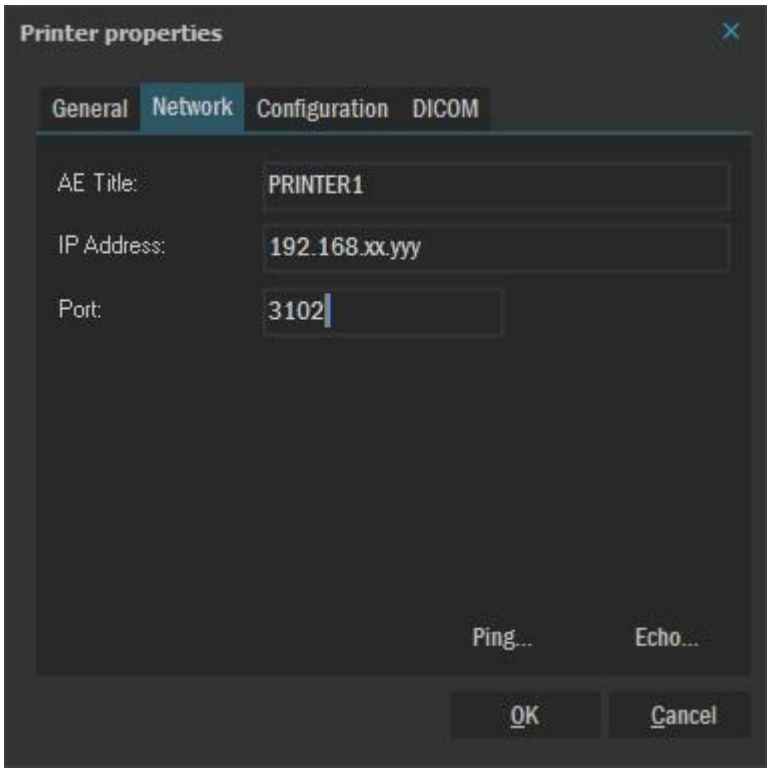


General sheet

Printer Type	Type of printer to configure (DICOM3)
Printer Name	Printer name assigned by user (Compulsory)

Page Size	Page size to print: it is possible to select a standard format or to define new page dimensions by modifying the printer configuration file `printers.cfg` as follows: PAGESIZE*nn*=*x*INX*y*IN^*x_in_mm*^*y_in_mm* Where *nn* is progressive and starts from 00, the dimension of *x* in mm can be calculated by *x*IN*254. For example: PAGESIZE00=14INX17IN^3560^4320 where 14*254=3560 After this operation, also new formats are displayed
Resolution	Print resolution. Inserted value is expressed in dpi (Dots Per Inch). Its value is calculated according to the page format and to the matrix representing the useful area of image to print. Page layout and dimension are provided by the printer. For example, if *Page Size* is 14INX17IN and the print matrix is 1000x1500 point, the resolution R is 14 * R = 1000 o 17 * R = 1500.

Figure 102. Configuring a DICOM3 Printer – Network sheet



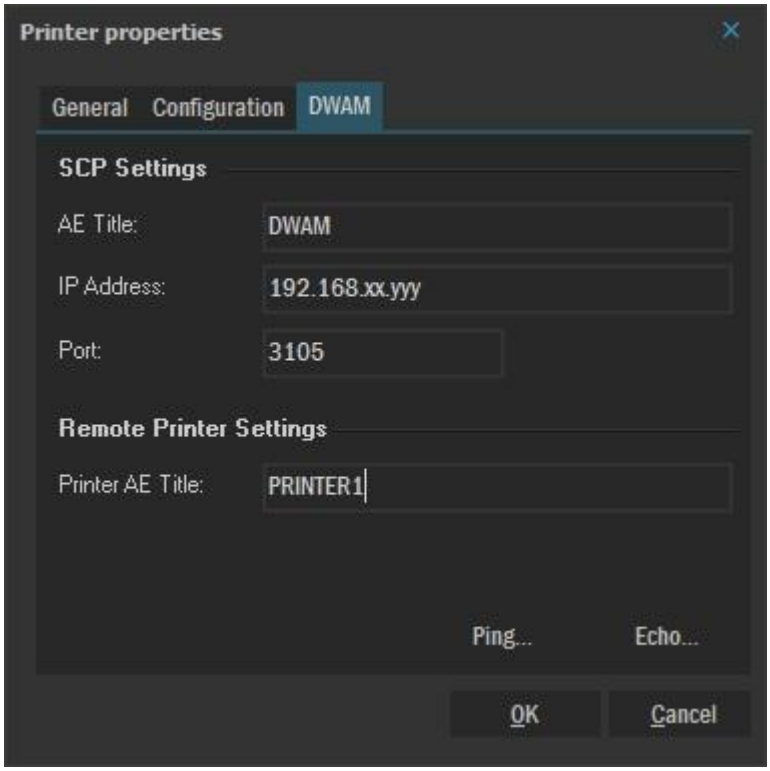
Network sheet

AE-Title	DICOM Application Entity Title of the printer (Compulsory)
IP Address	IP Address of the printer (Compulsory)
Port	Internet Port of the printer (Compulsory)

DWAM Printers

They use a DicomWare server as printer gateway. Images to print are sent through a proprietary protocol to the DWAM gateway, which redirects them to the destination DICOM printer.

Figure 103. Configuring a DWAM Printer –DWAM sheet



DWAM sheet

AE-Title	DICOM Application Entity Title of server DicomWare that act as gateway for prints (Compulsory)
IP Address	Internet IP of gateway (Compulsory)
Port	Internet Port of gateway (Compulsory)
Printer AE Title	DICOM Application Entity Title of the remote printer configured in the DWAM gateway.

Print protocols

The Protocols (print protocols) section allows to configure print protocols used by MedStation. In particular, it is possible to define the print format, page orientation and additional parameters (print ruler, print image in real size, etc.).

To define a new protocol, press Add in the toolbar in section Protocols as in Figure 104. A dialog box that gives access to the protocol properties is opened as in Figure 105. The same

window appears if you select and double-click one of the existing protocols, and can be used to modify its properties.

Figure 104. Protocols section

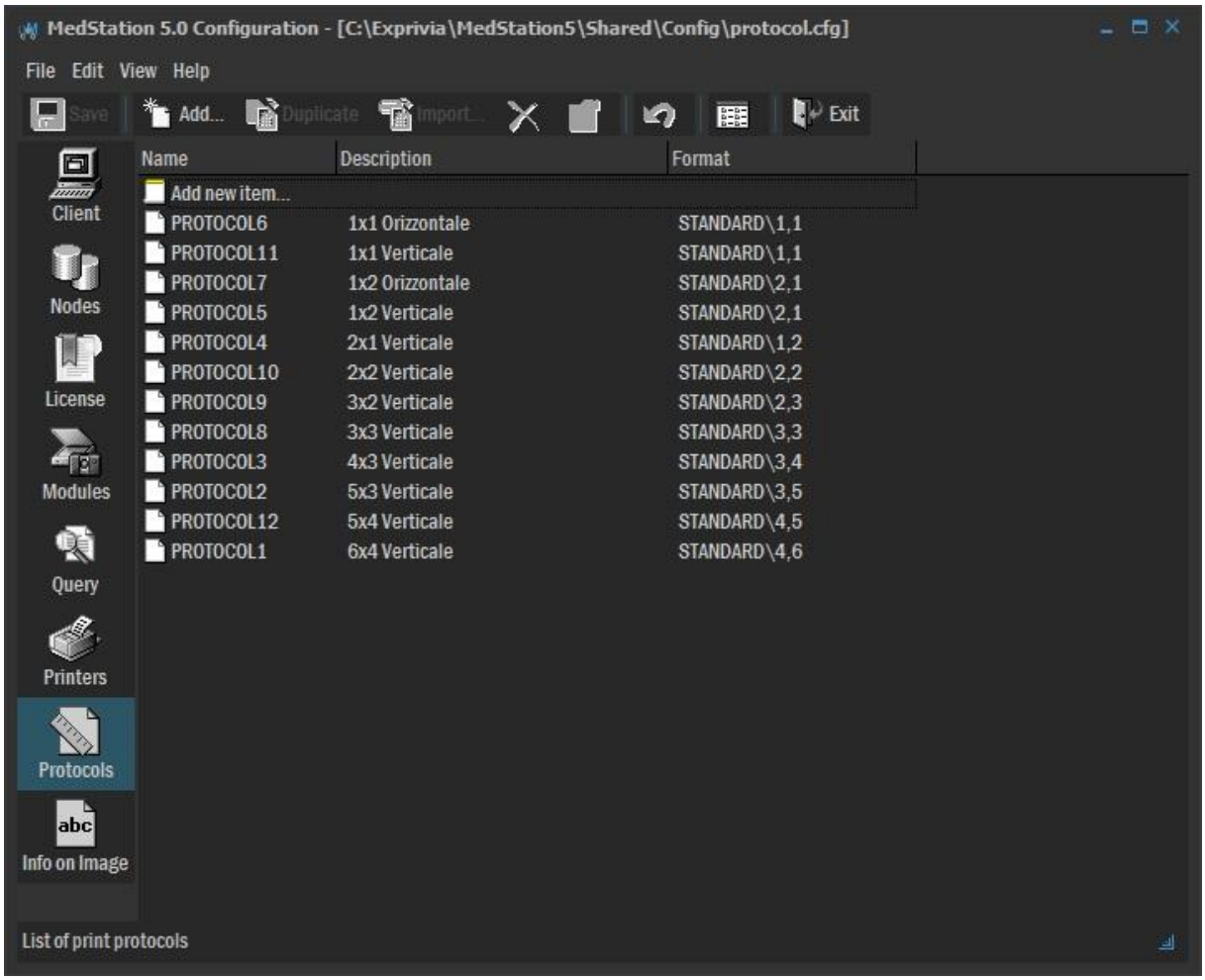
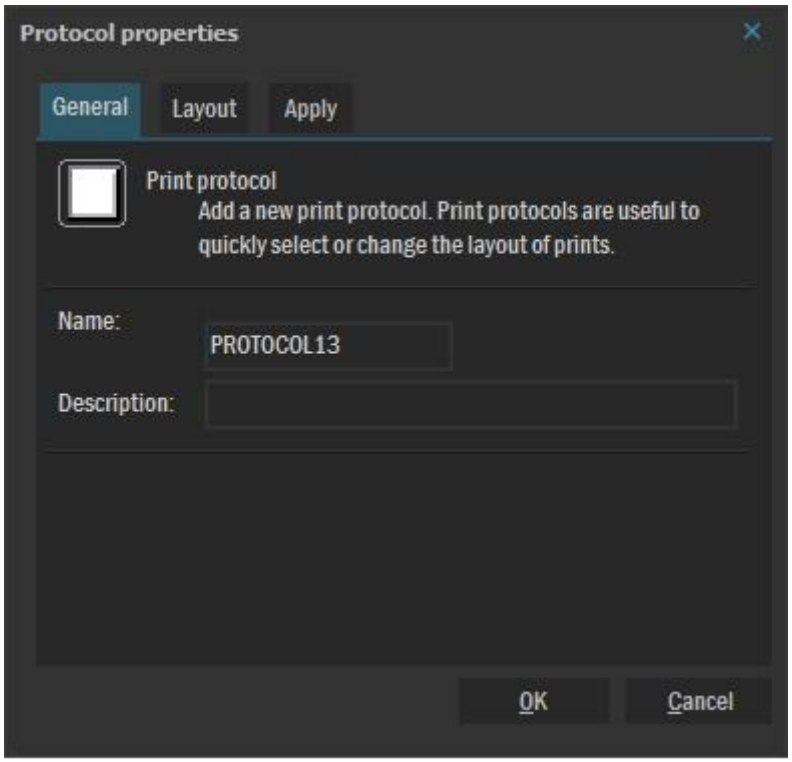


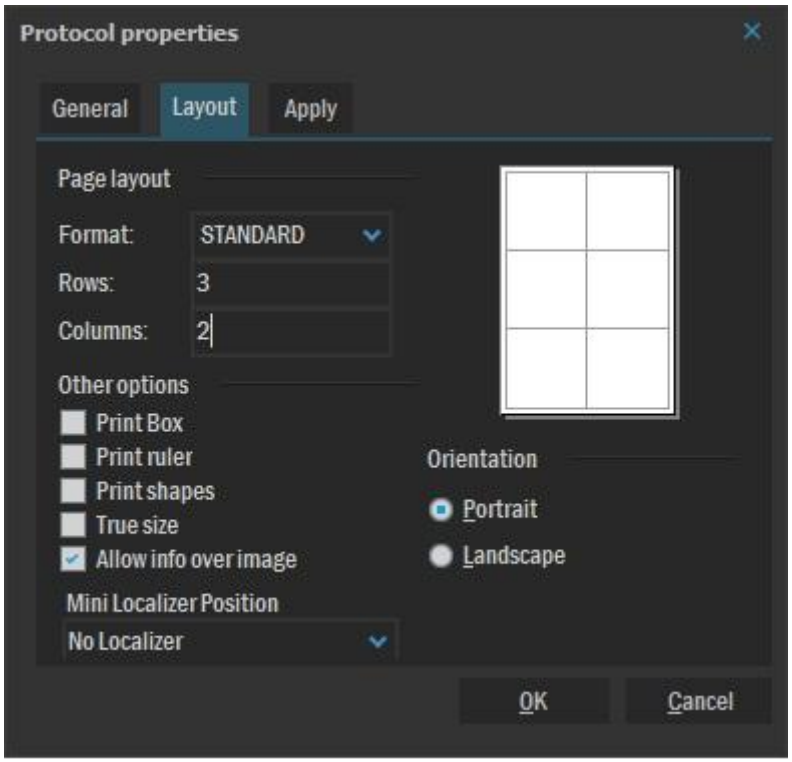
Figure 105. Configuring a Printer Protocol: General sheet



General sheet

Name	Internal name of Printer Protocol
Description	Protocol description

Figure 106. Configuring a Printer Protocol: Layout sheet



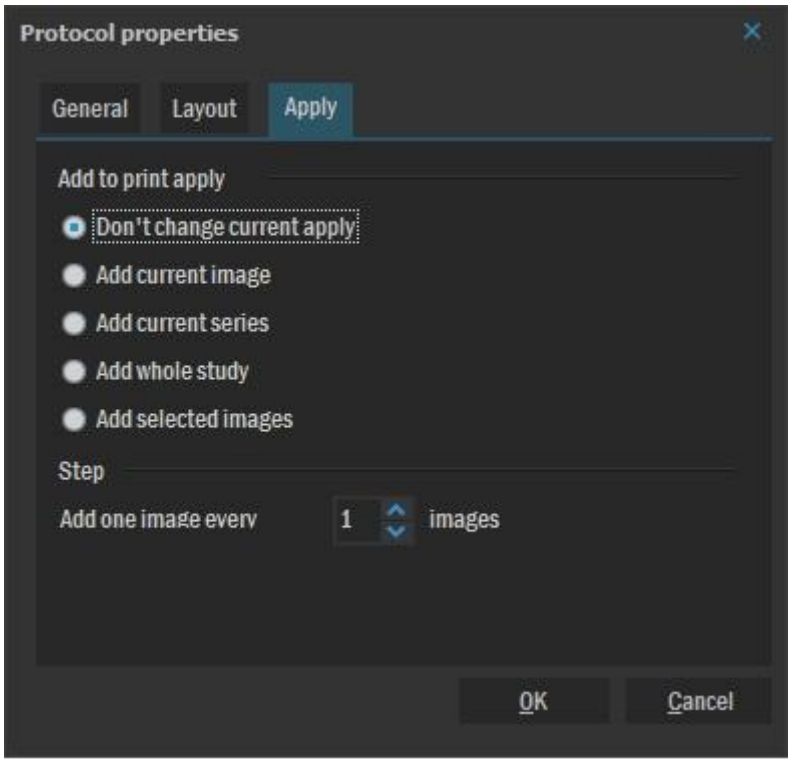
Layout sheet

Format	Format. Possible values are • STANDARD the composition happens by subdividing the printed page into rows and columns (according to values assigned to parameters *Rows* and *Columns*): • ROW the composition happens by choosing the number of columns in each line of the page to print. In the *Rows* field you indicate (separated by a comma) the number of columns you want in the corresponding row. For example, if you want that the page to print has two rows: the first with two images and the second with three, you'll write 2,3 in the field *Rows* • COL the composition happens by choosing the number of rows in each columns of the page to print. In the *Columns* field you indicate (separated by a comma) the number of rows you want in the corresponding columns. For example, if you want that the page to print has two columns: the first with two images and the second with three, you'll write 2,3 in the field *Columns*
Rows	Number of rows
Columns	Number of columns
Print Box	Image: Print Border around the boxes that contain images
Print ruler	Image: Print Ruler on the calibrated images

Configuration

Print shapes	Image: Print Measure on images sent to print
True size	Image: print images with their original size
Allow info over image	Allows the presence of info over the image. As in images displayed by MedStation, the info is placed over images. If this option is not active and images sent to print have superimposed info, this info is printed around the image.
Mini Localizer position	Positioning mini localizer on images sent to print
Portrait	Page orientation: Vertical
Landscape	Page orientation: Horizontal

Figure 107. Configuring a Printer Protocol: Apply sheet



Apply sheet

Don't change current apply	Don't change current settings
Add current image	Adds current image to print
Add current series	Adds current series to print
Add whole study	Adds to print all images of the study

Add selected images	adds to print all selected images
Add one image every	You can decide to send to print an image every n, where n is the set value, within a series or a whole study

Information on images

The *Info on Image* section let the user define the information display on the images according to their modality (CR, CT, MR, etc.). In order to introduce the annotations for a new modality the user must press the *Add* button in the toolbar as shown in Figure 108. Subsequently you enter the sheets in Figure 109 and Figure 110 to specify configuration info.

Figure 108. Configuration Apply: Info on Image section

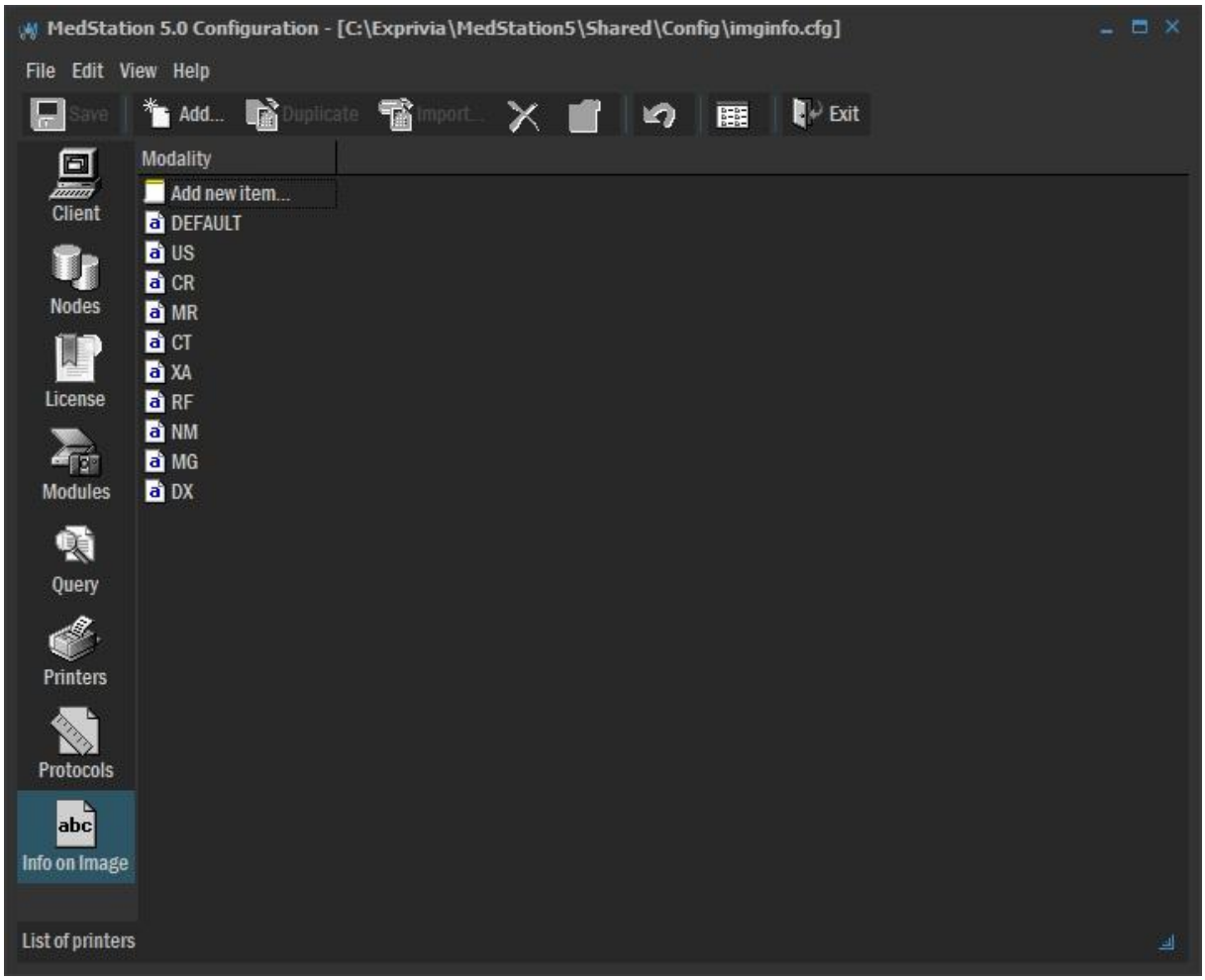
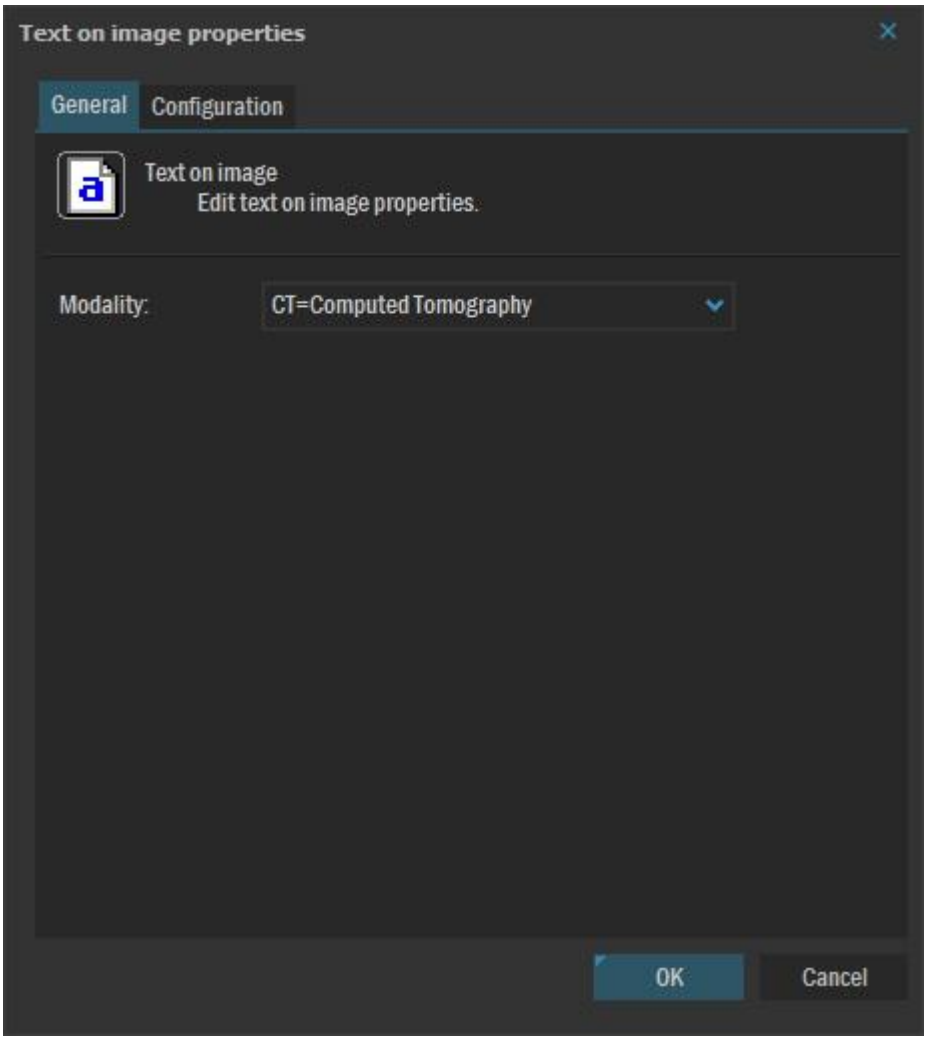


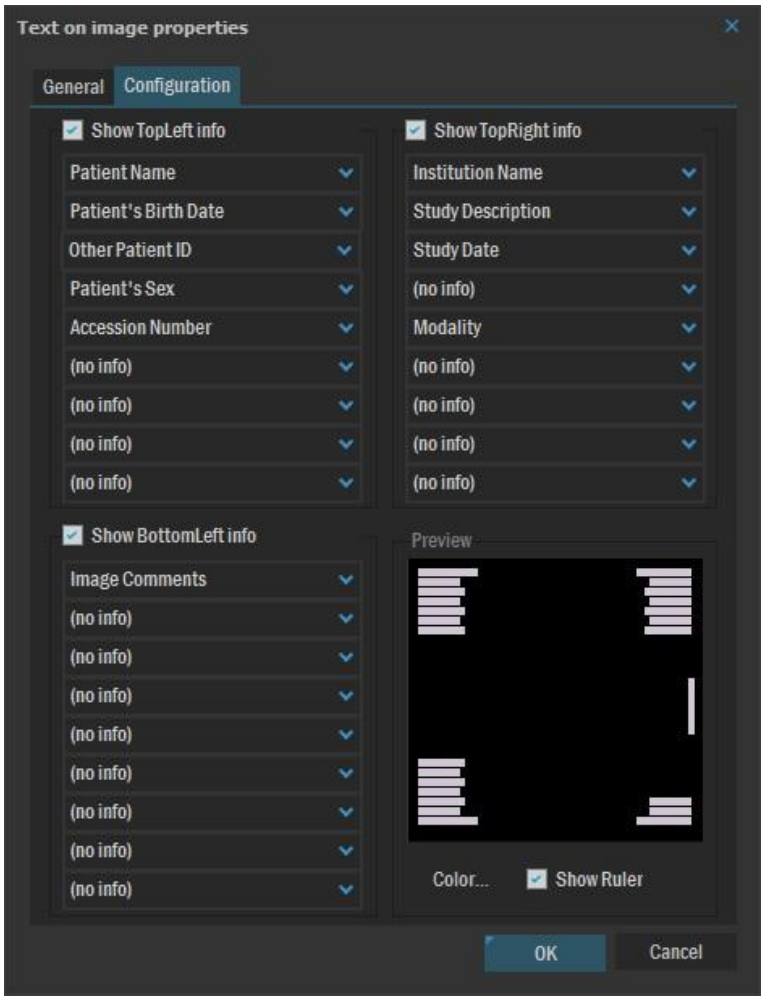
Figure 109. Info on images: General sheet



General sheet

Modality	Specifies diagnostic modality: CR, CT, MR, etc. According to selected modality, settings of following sheet will regard all images coming from a diagnostic of this modality.

Figure 110. Info on images: Configuration sheet



Configuration sheet

Show TopLeft info	Show info on top left images
Show TopRight info	Show info on top right images
Show BottomLeft info	Show info on bottom left images
Preview	Preview
Color	Allows to specify text color
Show Ruler	If active, allows the display a ruler

To choose which info is to be shown on images, you have to choose the interested info from the menu you can open by clicking on the arrow next to each possible choice.

For detailed info, please see the paragraph *Info on images* in Chapter 8 of this manual.

Appendix

D

Execution parameters[41]

Introduction

MedStation, among its main features, has the ability to open multiple studies simultaneously on one or more monitors in the same instance. Each monitor has one or more boxes depending on the layout chosen. Inside each box you can manage a study independently from others. Each part of a study is uniquely identified by the pair monitor / box. We have chosen to identify the monitors with letters from 'A' and to number the boxes from 1 within each monitor.

MedStation exposes a command line interface that lets you launch and close instances of the application, to log-in, to open and close studies by choosing the monitor and the box, to choose the layout of monitor and box, to open a study as a continuation of another, to link different displayed studies.

There is also the opportunity to query **MedStation**; in response to a query of this type, MedStation will create a file that describes the state of the program at that time.

Note: *Request is not processed if the active window is not the main one.*

Interface

At the time of executing MedStation it is possible to specify certain parameters that enable the automation of some operations. These parameters can be specified directly from the command line (prompt) or by means of a text file.

The execution parameters enable the following operations to be carried out automatically**:**

- User authentication (Login).
- Direct access to images making up a diagnostic study.
- Search or QUERY of diagnostic studies on the basis of search criteria on DICOM and

[41] Function available only in MedStation but not in MedStation Express.

DWAM nodes

- Choose the layout for each monitor
- Choose the layout for each study box
- View study reports
- Open studies continuously (Link per page)
- Scroll link of studies
- Close study

The beginning of the parameter string is identified by '?'. The string itself is constituted by pairs ATTRIBUTE=VALUE separated by '&'. Pairs ATTRIBUTE=VALUE can be specified in each order. Parameter string will have following appearance:

```
<path>\Medst.exe ?<nome1=valore1>&...&<nomeN=valoreN>
```

Warning! In Windows 2000, parameter list `?<nome1=valore1>` should be enclosed in " " (quotation marks).

Example: "`?USER=UTENTE&PASSWD=PASSWD`"

Parameters can be specified as list of pairs ATTRIBUTE=VALUE within a file, typically with the extension '.MST'; in this case the file itself will be passed to the program as a parameter:

```
<path>\Medst.exe <nomefile>
```

Parameter list

Table 2 List of allowed execution parameters

	TYPE	Indicates how to interpret the other specified fields
	USER	User access (the value of this parameter can be a domain user. In this case it will be of the type <DOMAIN>\<USER>)
	PASSWD	Access password
	ACCOUNT	Logon Ticket ID for secure access to system
	STYNODE	Node index (in base 0)
	PATID	Patient ID
*	PATID2	Alternative patient identification code
	PATNAME	Name of patient
	PATSEX	Sex of patient
	PATDATEFROM	Start date of birth
	PATDATETO	End date of birth
	SERID	Internal ID of a series of the study

	SERID2	Series Instance UID DICOM of the series
	STYID	Study ID
	STYID2	Alternative study identification code
	STYACCNUMBER	Study appointment number
	STYDESCR	Study description
*	STYSTATUS	Study status (can be: A,V,S,B,R)
	STYDATEFROM	Start study date
	STYDATETO	End study date
*	STYMODALITY	Modality code (CT, MR, …)
*	STYPHYS	Examining physician
*	STYTYPE	Study type code

From the command line you can specify LOGON parameter:

LOGON	Direct access to the application without going through the user identification. Equivalent to run MedStation specifying as user the same name used to log on to Windows and leave the password blank. Obviously, you should have previously defined a user with that name and blank password in MedStation.

Options to use together with other commands:

	NEWWIN	Set to 1 and used together with QUERY or OPEN tries to open the study creating a new box in the specified monitor.
	DESTWIN	It specifies which monitor and box where you want to work; In <LetterNumber> (‘A1’, ‘B2’) format, the letter represents the monitor and the number represents the box; In Number format, the number indicates the box; the monitor and the box are calculated considering the number (in base 0) passed from the first box of the first monitor to the last box of the last monitor Optional, with TYPE=EXECUTE and option CINE you can specify the view number where you want to work in the form ‘A1|N’ where N is the view number with base 0 ordered from left to right and from top to bottom. If not specified, the command is applied to the first view of destination BOX.

	GRID	If used with TYPE=EXECUTE in the form NumberRows|NumberColumns, it changes the layout of box identified by DESTWIN
	LAYOUT	If used with TYPE=EXECUTE in the form NumberRows|NumberColumns, it changes the layout monitor identified by DESTWIN
	LINK	If used with TYPE=EXECUTE in the form IndexBox|Mode, it runs the link per page (Mode = 2) or per scroll (Mode=1) or destroys an existing link (Mode=0) of the box identified by DESTWIN to the box identified by IndexBox.
	FILE	Used together with GETPROCESSLIST to identify the file which will contain the description of MedStation status
	BEEP	The command makes a sound in the occurrence of a particular event, useful for debugging.
	SHOWREPORT	Used together with TYPE=QUERY o TYPE=OPEN it displays a study report
	LANGUAGE	It defines the language (Italian, English or German) of MedStation. LANGUAGE=ITA, ENG, DEU. Default language is Italian
	CINE	If used with TYPE=EXECUTE, it runs a cine command on the view identified by DESTWIN (this can also be specified in the format similar to 'A1|N' where N is the number of the view in base 0 and sorted from left to right and from top to bottom. If not specified, the command is applied to the first view of the destination monitor or the first, if not indicated). CINE can have following values: STOP, PLAY, PAUSE, FIRST, PREV, NEXT, LAST.
	USE_XDSI_GATEWAY	If used with TYPE=OPEN, it enables you to browse through documents on XDS registry.
	REPOSITORY_UID	Univocal ID XDS repository
	DOCUMENT_UID	Univocal ID XDS document
	HOME_COMMUNITY_ID	ID of remote XDS node

Note: *The parameters marked with an asterisk (*) are not managed by DICOM nodes.*

TYPE parameter

- the TYPE parameter is particularly important because its value determines how other fields are interpreted by the program. The values that TYPE can assume are:

	NEW	Allows creating a new study in MedStation.
	QUERY	Allows a Query when you open an instance or when an instance is already opened.
	OPEN	Allows opening a study when you open an instance or when an instance is already opened.
	CLOSE	Allows closing a study or all studies of a monitor, while leaving the instance opened.
	EXIT	Allows to close an instance
	GETPROCESSLIST	Allows creating a file that describes the instance status. Each line in the file will be related to a box of the instance and will be constituted by 3 pairs ATTRIBUTE=VALUE separated by '|' describing: PROCID=Process ID WINDOW=Pair LetterNumber that identifies the box. E.g. 'A1,'B2'…. TITLE=Descriptive of box: if a study is open, the string carries the name, the date of birth and the study description. As in the examples: PROCID=1560|WINDOW=A1|TITLE=MedStation 4.0 PROCID=1560|WINDOW=B1|TITLE=ROSSI*MARIO M 30/12/1949 RM ASSIALE E SAGITTALE - MedStation 4.0
	EXECUTE	To be used with other parameters that specify the action to do.

- TYPE not specified, parameters USER and PASSWD are considered to logon: E.g.

```
<Path>\MedSt.exe?USER=USER&PASSWD=PASSWD&LANGUAGE=ENG
Runs the logon to MedStation, launches the program in English.
```

- TYPE=NEW Parameters STYNODE and DESTWIN are considered to identify the node and the study box

```
<Path>\MedSt.exe  ?TYPE=NEW&DESTWIN=A2&STYNODE=0.
It creates a new study in the node 0 and opens it in the box A2
```

- TYPE=QUERY Parameters USER, PASSWD are considered for the logon, all search

parameters DESTWIN, NEWWIN for identifying the study box. MedStation runs a query between the parameters in the specified database to search for all studies where data correspond to the criteria. In case the search result corresponds to two or more of these studies, they are displayed in the search/selection window. Instead, if the search results in a single test, this study is opened directly, without displaying the selection window. In the search for alphanumeric fields, the use of wildcards is allowed '%' (any character sequence) and '_' (exactly any type of character). In case of patient name, it will be automatically added to the end of wildcard'%'. Il TYPE=QUERY functions only on DICOM and DWAM nodes while the other values in the field TYPE function with every type of node

```
<Path>\MedSt.exe ?TYPE=QUERY&STYNODE=2&STYID2=1.1&DESTWIN=A3
```

It runs a study search and tries to open box 3 of monitor A; If a box doesn't exist, it automatically changes the monitor layout until the creation of a box.

```
<Path>\MedSt.exe ?TYPE=QUERY&STYNODE=2&STYID2=1.1&DESTWIN=A&NEWWIN=1
```

It runs a study search and tries to open a new box in monitor A.

```
<Path>\MedSt.exe
&TYPE=QUERY&STYNODE=2&STYID2=1.1&DESTWIN=B2&BEEP=1&SHOWREPORT=1
```

It runs a study search and tries to open box 2 of monitor B. If a box does not exist, it automatically changes the monitor layout until the creation of a box. As soon as the study is opened, it displays the report.

- TYPE=OPEN Only fields USER, PASSWD are considered for the logon, STYNODE , STYID for the search, DESTWIN, NEWWIN for the study box identification. To browse through XDS documents, fields `REPOSITORY_UID`, `DOCUMENT_UID` e `HOME_COMMUNITY_ID` are considered.

```
<Path>\MedSt.exe ?&TYPE=OPEN&STYNODE=2&STYID=00000001&DESTWIN=A1
```

Tries to open the study in box 1 of monitor A. If a box does not exist, it automatically changes the monitor layout until the creation of a box.

```
<Path>\MedSt.exe
?TYPE=OPEN&STYNODE=2&STYID=00000001&DESTWIN=B&NEWWIN=1
```

It automatically changes the monitor B layout to create a new box and tries to open the study.

```
<Path>\MedSt.exe     ?TYPE=OPEN&STYNODE=2&DESTWIN=B&NEWWIN=1&
USE_XDSI_GATEWAY=True&REPOSITORY_UID=1.19.6.24.109.42.1.1&DOCUMENT_UID=1
.3.76.13.500.192.168.24.69.2796.1229945352.2
```

Tries to open an XDS document through a XDS-I gateway, identified by a STYNODE node. Parameters REPOSITORY_UID and DOCUMENT_UID are compulsory.

- TYPE=CLOSE Considers the parameter DESTWIN. If the destination is not an existing box, all the open studies in MedStation are closed.

```
<Path>\MedSt.exe ?TYPE=CLOSE&DESTWIN=0
```

Closes the study in box A1 (Calculated by index 0)

```
<Path>\MedSt.exe ?TYPE=CLOSE&DESTWIN=3
```

If the layout of monitor A and 2*2, closes the study in box A4 (Calcu-

lated by index 0). If the layout of monitor A and 1*2 and that of B is 2*2, closes the study in box B2 (Calculated by index 0)

<Path>\MedSt.exe ?TYPE=CLOSE&DESTWIN=A2

Closes the study in box A2

- TYPE=EXIT Doesn't consider the parameters

<Path>\MedSt.exe ?TYPE=EXIT

Exit the instance.

- TYPE= GETPROCESSLIST

<Path>\MedSt.exe ?TYPE=GETPROCESSLIST&FILE=C:\PIPPO.TXT&BEEP=1

Downloads the instance status description in the file C:\pippo and emits a Beep.

- TYPE= EXECUTE With GRID and DESTWIN changes the layout of box identified by DESTWIN; With LAYOUT and DESTWIN changes the layout of box identified by DESTWIN; With LINK and DESTWIN runs the link per page or per scroll of box identified by DESTWIN to the study open in the box identified by LINK; with CINE and DESTWIN runs the cine command on a view identified by DESTWIN:

<Path>\MedSt.exe ?TYPE=EXECUTE&LAYOUT=2|2&DESTWIN=A&BEEP=1

Changes the layout of monitor A to 2*2

<Path>\MedSt.exe ?TYPE=EXECUTE&GRID=2|2&DESTWIN=B1&BEEP=1

Changes the layout of box B1 to 2*2 if existing and if there is an open study and emits a beep;

<Path>\MedSt.exe ?TYPE=EXECUTE&LINK=A1|2&DESTWIN=B5

Runs the link per page (Continues) of box B5 to the study open in box A1

<Path>\MedSt.exe ?TYPE=EXECUTE&LINK=A1|1&DESTWIN=B5

Runs the link per scroll of the study open in box B5 to the study open in box A1;

<Path>\MedSt.exe ?TYPE=EXECUTE&LINK=|0&DESTWIN=B5

Runs the Unlink per page of study open in box B5;

<Path>\MedSt.exe ?TYPE=EXECUTE&CINE=PLAY

Starts cine on the first view of the study open in box A1;

<Path>\MedSt.exe ?TYPE=EXECUTE&CINE=STOP&DESTWIN=A2

Stops cine on the first view of the study open in box A2;

<Path>\MedSt.exe ?TYPE=EXECUTE&CINE=LAST&DESTWIN=A2|1

Displays last frame of the second view of the study open box A2;

Other examples

- <Path>\Medst.exe ?USER=UTENTE&PASSWD=PASSWD&TYPE=QUERY&STYNODE=1&PATNAME=MARIO*ROSSI

Searches all studies of patient MARIO*ROSSI in the second node (of index 1). If it finds only one, it opens it.

- <Path>\Medst.exe 99006338.MST

Launches MedStation taking parameters from file 9906338.MST containing, for example, the list:

TYPE=OPEN

USER=UTENTE

PASSWD=PASSWD

STYNODE=2

STYID=99006338

Opens directly the study 99006338 from the third node (because STYNODE=2).

- <Path>\Medst.exe ?LOGON

Opens MedStation directly using current Windows 9x/NT user name. The user must have been previously defined in MedStation and have a blank Password.

- <Path>\Medst.exe 99006338.MST

Launches MedStation taking parameters from file 9906338.MST containing the list:

TYPE=QUERY

USER=UTENTE

PASSWD=PASSWD

STYID=99006338

STYNODE=2;3

STYDATEFROM=01/01/1999

STYDATETO=31/12/1999

STYMODALITY=CT

STYSTATUS=Blocked

PATID=9

Selects all studies of patient 99006338 conducted between 01/01/1999 and 31/12/1999 with status of 'CT' modality 'blocked' by nodes 2 and 3.

Appendix

E

COM interface[42]

Introduction

MedStation, among its main features, has the ability to open multiple studies simultaneously on one or more monitors in the same instance. Each monitor has one or more boxes depending on the layout chosen. Inside each box you can manage a study independently from others. Each study is uniquely identified by the pair monitor / box. We have chosen to identify the monitors with letters from 'A' and to number the boxes from 1 within each monitor. Open studies remain in memory also without box display, until the call of command Close All, by means of key, menu item.

MedStation exposes an interface that allows you to launch and close instances of the application as COM objects, to log-in, to open and close studies by choosing the monitor and the box, or to leave MedStation decide, by means of Hanging Protocols application, which display to apply to the study, to choose monitor layout.

There is also a notification mechanism by which open instance of MedStation, which acts as a server, notifies the client (the application that launches MedStation) certain events including:

- Instance opening and closing
- Monitor opening and closing
- Changing monitor layout
- Beginning and end of study search by means of query
- Adding and releasing of a study box
- Opening and closing of a study (i.e. loading and releasing of a study to memory)
- Logic opening and closing of a study box
- Changing a study display mode (2D, MPR…)
- Some type of errors and info
- Studies link per page and per scroll

[42] Function available only in MedStation but not in MedStation Express.

To intercept the notification events, the client must be connected to MedStation with the mechanism of connection points through the implementation of an output interface. With output interface, we mean an interface defined in the object itself, but implemented by the client. An object defined *sink* that resides within the client is an object that implements the output interface of the client. You can use the interface in one-way mode without implementation of the sink.

Flow example for the opening of study by a client

- Creation of IMedstEngine (Starts the creation of an instance of MedStation); MedStation puts itself in a state of waiting for the login for a few seconds; if it doesn't receive the login request within this period, it goes in a timeout state;
- Creation of a sink object
- Connection of the sink object to MedStation COM object
- Login
- Reception of events: INS_OPEN, MON_OPEN, STY_CONTROLLER_ADDED;
- Query;
- Reception of eventsMON_INITSEARCH, STY_AFTERPHISOPEN, STY_AFTEROPEN, MON_ENDSEARCH.
- CloseInstance
- Reception of events: STY_BEFORECLOSE, STY_AFTERCLOSE , STY_AFTERPHISCLOSE, STY_CONTROLLER_DELETED, MON_CLOSED, INS_CLOSED
- Disconnecting form sink object
- Free memory associated to object ImedstEngine

.

COM interface: functions

The interface exposed by **MedStation** is IMedstEnginexx. To register the interface, install **MedStation** and run the executable file with the parameter *regserver*.
A new instance is opened through the creation of a COM object.

COM interface: basic functions

The basic functions that can be activated by the customer are:

- *function **Login**(const Username, Password, Params: WideString): Integer;*

  Authentication in MedStation.

  - *Username*
  - *Password*
  - *Params*: a string of the 'ATTRIBUTE=VALUE' type. The attributes can be chosen from the following (the values available for each one are also indicated)
    - *DOMAIN*: if the user does not belong to the *MEDSTATION* domain, the function is to be invoked with this parameter and its value must be the name of the access domain
    - *ENABLENEW*: if set to 0 disables the function for creating a new study
    - *ENABLEIMPORT*: if set to 0 disables the function for importing a study
    - *ENABLEEXPORT*: if set to 0 disables the function for exporting the studies
    - *ENABLEOPENCLOSE*: if set to 0 disables the functions for opening and closing the studies from the MedStation interface
    - *ENABLEREPORT*: if set to 0 disables the function for viewing/creating reports
    - *OPENSTUDYSEL*: if set to 0 disables the function for searching for studies on the system interface
    - *SHOWLOGINERROR*: if set to 0, MedStation will not show a warning when a login error occurs
    - *ACCOUNT*: to pass the encrypted string containing the user name and the password for login to the function
  - *result:*
    - *1* if no errors occurred
    - *0* if errors occurred during the login procedure

***Note:** There is a timeout of 10 seconds between the moment in which the server object is created and the moment in which the client can log on.*

- *function **Query**(const HController: WideString; const Node: WideString; QueryParams: Widestring): Integer;*

Study search and opening request.

- *HController:* ID of the destination box of the study that is to be opened (e.g. 'A1' or 'B3'). If Hcontroller=' the box in which to open the study is not specified. The box is automatically chosen by MedStation by means of Hanging Protocols
- *Node:* Id of the node or nodes in base 0, in which to effect the search. If you specify more than one node, indices should be separated by ';' (e.g.: 0;1;2)
- *QueryParams:* MedStation runs a query in the databases corresponding to the nodes specified in the *Node* parameter to search for all studies whose data satisfy the specified criteria. If the search finds two or more studies, they will be displayed in the selection window while if it only finds one study, this study will be opened directly in the box indicated.

  When searching alphanumeric fields you can use the wildcard characters '%' (any sequence of characters) and '_' (exactly any character). In patient names, the wildcard '%' is automatically added at the end. This function is only to be used on DICOM and DWA nodes. The search parameters should be passed as a string encoded as 'CONDITION1=VALUE1' 'CONDITION2=VALUE2' Each condition/value pair should be separated by a Line Feed character. Several conditions can be specified simultaneously. The parameters that can be specified are

	PATID	Patient ID
*	PATID2	Alternative patient identification code
	PATNAME	Patient name
	PATSEX	Sex of patient
	PATDATEFROM	Start date of birth
	PATDATETO	End date of birth
	STYID	Study ID
	STYID2	Alternative study identification code
	STYACCNUMBER	Study appointment number
	STYDESCR	Study description
*	STYSTATUS	Study status (may be set to: A,V,S,B,R)
	STYDATEFROM	Start study date
	STYDATETO	End study date
*	STYMODALITY	Modality code (CT, MR, …)
*	STYPHYS	Examining physician
*	STYTYPE	Study type code

Note: *Parameters marked with an asterisk (*) are not managed on DICOM nodes.*

  - *result:*
    - *n* number of studies found by the query
    - *-1* if the call was made with all the parameters of the function blank or if errors occurred

- *function* ***OpenStudiesGroup****(const iNode: WideString; const IParams: IUnknown): Integer;*

Requests to search for and open all the studies returned by the query made with the parameters contained in *IParams*

  - *iNode:* like the *Node* parameter of the *Query* function
  - *iParams:* like the *QueryParams* parameter of the *Query* function
  - *result:*
    - *n* number of studies found by the query
    - *-1* if the call was made with all the parameters of the function blank or if errors occurred

- *function* ***SetLayout****(const HMonitor: WideString; Rows, Cols: Integer): Integer;*

  Changes the layout of a monitor, subdividing it in a grid of boxes (image views)

  - *HMonitor*: Monitor ID (e.g. 'A', 'B'…)
  - *Rows*: number of rows in the grid
  - *Cols*: number of columns
  - *result:*
    - *1* if completed successfully
    - *0* if errors occurred

- *function* ***SetImageLayout****(const HController: WideString; Rows, Cols: Integer): Integer;*

  Changes the layout of a box, subdividing it in a grid of images.

  - *HController*: ID of the box (e.g. 'A1', 'B3'…)
  - *Rows*: number of rows in the grid
  - *Cols*: number of columns
  - *result:*
    - *1* if completed successfully
    - *0* if errors occurred

- *function* ***LinkTo****(const HController: WideString; const HPrevController: WideString; Mode: Integer): Integer;*

  Creates a link between two image views.

  - *HController*: ID of the box to be linked (e.g. 'A1', 'B3'…)

- *HPrevController*: ID of the box to which the other box is to be linked (e.g. ‘A2’, ‘B1’…)
- *Mode*: Type of link:
  - *1* Scroll link
  - *2* Page link
  - *3* Localizer link
  - *4* Position link
- *result:*
  - *1* if completed successfully
  - *0* if errors occurred

- *function **CloseStudy**(const HController: WideString): Integer;*

  Logically closes a study (the study remains on line but not displayed).

  - *HController*: ID of the box (e.g. ‘A1’, ‘B3’)
  - *result:*
    - *1* if closed successfully
    - *0* if an error occurred during closure or the study could not be removed from the display for some reason

- *function **CloseAll**; Integer;*

  Instructs MedStation to physically close all open studies (the studies will be taken off line).

  - *params:* ---
  - *result*:
    - *1* if closed successfully
    - *0* if an error occurred during closure
    - *-2* if the studies could not be closed due to modal windows being open in MedStation as they must be closed before activating the CloseAll function

- *function **ChangeLogon**(const iUser: WideString; const iPasswd: WideString): Integer;*

  Enables you to change user in MedStation without closing the instance to reopen it subsequently.

  - *iUser*: user name
  - *iPasswd*: password
  - *result:*
    - *1* if the change user command was executed successfully
    - *0* if an error occurred
    - *-2* if the change user command could not be executed due to modal windows being open in MedStation as they must be closed before invoking this function

- *function **CloseInstance**: Integer;*

  Closes the MedStation instance.
  Note: the Client will have to free the memory associated with the COM object created.

  - *params: ---*
  - *result:*
    - *1*if closed successfully
    - *0* if an error occurred during closure
    - *-2* if the instance could not be closed due to modal windows being open in MedStation as they must be closed before invoking this function

- *procedure **StudySync**(const AccNumNew: WideString; out UID: WideString; out AccNumOld: WideString);*

  Changes the Accession Number of the current study displayed in MedStation
  - *AccNumNew:* new Accession Number to be assigned to the study
  - *UID:* study UID
  - *AccNumOld:* Accession Number of the study before the change

- *procedure **GetSelectedStudy**(out StudyData: WideString);*

  - *StudyData:* data (see **Encoding of patient and study data**) of the active study in MedStation

- *function **Active**: Integer;*

  Checks whether a MedStation instance is active

  - *result:*
    - *0* if there is no MedStation instance active
    - *otherwise a positive value*

- *function **GetOpenedStudies**(out sList: WideString): Integer;*

  Returns the data of all studies loaded

  - *sList:* list of the data (see **Encoding of patient and study data**) of all the studies loaded in MedStation (the data of one study are separated from those of another by the "|" character)
  - *result: 0*

- *function **SendCalcMemory**: Integer;*

  Sends the entire contents of the calculator's memory (for realignment, where necessary)

- *result:*
  - *0* if an error occurs
  - Otherwise a positive value

- *function **ShowInstance**(nCmdShow: Integer): Integer;*

  Minimizes or maximizes the MedStation main window

  - *nCmdShow:* may be set to one of the following values
    - SW_HIDE to minimize the window
    - SW_SHOW
    - SW_SHOWNA
    - SW_SHOWNORMAL
  - *result:*
    - *0* if an error occurs
    - The return value of the *ShowWindow(Application.Handle, nCmdShow)* function

COM interface: using measures, measurements and calculations

On the COM interface displayed by MedStation, the functions concerning the use of measures, measurements and calculations that can be activated from the client are:

- *function **DoMeasure**(const RequestID, Params: WideString; out Error: WideString): Integer;*

  Sends MedStation a request for measures or measurements and calculations to be processed by MedStation by setting the quick measuring tools and allowing the user to draw the corresponding figures on the images of a study shown on the display.

  - *RequestID*: unique ID of the request
  - *Params*: xml message with the contents of the request
  - *Error*: code indicating whether the request was sent successfully or not
  - *result*: 0 if the request was sent correctly, != 0 otherwise

- *function **GetMedstToolList**(const toolKind: WideString; out listResult: WideString): Integer;*

  Sends MedStation a request for the quick or derived measuring tools at its disposal.

  - *toolKind*: must be one of the following strings
    - '<*measureDictionary/*>' to obtain a list of the quick measuring tools, with the name of the tool and a list of all the possible return values

        - '<*measurementsDictionary/*>' to obtain a list of the measurements configured on the system
        - '<*calculationsDictionary/*>' to obtain a list of the calculations configured on the system
    - *listResult:* result of the request, list of all the tools available
    - *result*: 0 if the request was successful and the list was returned, otherwise !=0

COM interface: creating breast screening reports

Functions used in eRis/MedStation integration. The report forms in eRis may have "statuses". When one of them is selected, a sequence of operations is triggered, for example, part of the form is filled in or the report is closed and the program moves on to the next one. In order to be able to set one of these statuses, you must press a button that appears on the eRis interface at the same time as on the form or enter the corresponding shortcut command. If eRis is integrated with MedStation, you must press buttons or enter the same shortcuts associated with the statuses of the form and trigger the sequence of operations associated with the status chosen in eRis. For this to be possible, MedStation and IntEng implement functions for managing in MedStation some tabs that contain buttons associated with the statuses of the report form being filled in eRis. When activated, the buttons on these tabs or the corresponding shortcut commands send messages that set one of the statuses of the form via COM to eRis.

- *function **AddToolTABsAction**(const TabStr: WideString; const ActionStr: WideString): Integer;*

  Adds a tab with buttons to the toolbar of the MedStation tools:

    - *TabStr*: is a string of the 'TAB_ID$TAB_Caption' type, where
        - TAB_ID is an ID of the tab to be created
        - TAB_Caption is the name of the tab that will appear on the MedStation user interface
    - *ActionStr*: is a string of the 'BtnActionID_1$BtnCaption_1$BtnShortcut_1|BtnActionID_2$BtnCaption_2$BtnShortcut_2|...' type where
        - BtnActionID is the ID of the status associated with the button
        - BtnCaption is the name of the button that will appear on the MedStation interface
        - BtnShortcut is the shortcut associated with the same function as the button
    - *result*:
        - *0* if completed successfully
        - otherwise *a negative value*

***Note:** Separator between the parameters for creating the button is "$" Separator between the buttons is "|"*

The tab can contain as many buttons as desired. For the moment, all the button icons are the same. Every button must have an ID and Caption, while shortcuts are optional.

Pressing one of these buttons /shortcuts sends a message via COM with message code 329 (STY_SEND_COM_BTN) and a string of the 'TAB_ID|BtnActionID' type.

- *function **DeleteToolTAB**(const ToolTabStr: WideString): Integer;*

Removes from the MedStation toolbar one of the custom tabs added using the *AddToolTABsAction* function

  - *ToolTabStr*: is a string of the 'TAB_ID$TAB_Caption' type
    - TAB_ID the ID of the tab to be destroyed
    - TAB_Caption the name of the tab (which appears on the MedStation user interface)
  - *result:*
    - *0* if completed successfully
    - otherwise a *negative value*

- *function **DisableToolTAB**(const ToolTabStr: WideString; Disabled: Smallint): Integer;*

Disables/enables all the buttons/shortcuts on one of the custom tabs added to MedStation using the *AddToolTABsAction* function

  - *ToolTabStr*: is a string of the 'TAB_ID$TAB_Caption' type
    - TAB_ID the ID of the tab to be disabled/enabled
    - TAB_Caption the name of the tab (which appears on the MedStation user interface)
  - *Disabled:* is short for a Boolean. It must be true to disable, false to enable
  - *result:*
    - *0* if completed successfully
    - otherwise a *negative value*

- *function **DisableToolBTN**(const ToolBTNstr: WideString; Disabled: Smallint): Integer;*

Disables a button /shortcut of one of the custom tabs added to MedStation using the *AddToolTABsAction* function

  - *ToolBTNStr*: is a string of the 'TAB_ID$BTN_ID' type
    - TAB_ID the ID of the tab to which the button to be disabled/enabled belongs
    - BTN_ID the ID of the button to be disabled/enabled
  - *Disabled:* it is shortcut for a Boolean. It must be true to disable or false to enable
  - *result:*
    - *0* if completed successfully

- otherwise a *negative value*

Notification functions

The outgoing interface displayed by **MedStation** is ImedstEngineEvents. This interface should be implemented by the client.
The callback functions of **MedStation** instances are

NotifyEvent	Generic notification. The meaning of the notification can be seen from the interpretation of the parameters.

- *procedure* NotifyEvent(Status: Integer; StrParam1: WideString, StrParam2: WideString; Param1: Integer, Param2: Integer);

Status	Specifies notification type
StrParam1	Can take on significant values or not depending on the value of parameter Status
StrParam2	Can take on significant values or not depending on the value of parameter Status
Param1	Can take on significant values or not depending on the value of parameter Status
Param2	Can take on significant values or not depending on the value of parameter Status

Notification parameters

For each possible value of the Status parameter, the values of the following parameters StrParam1, StrParam2, Param1 and Param2 are specified when they assume significant values;

- **INS_OPEN** (201):
  Sent when the instance is opened

StrParam1	Id of instance handle
StrParam2	‘’
Param1	-1
Param2	-1

- **INS_CLOSED** (202):
  Sent when the instance is closed

StrParam1	Id of instance handle
StrParam2	‘’
Param1	-1
Param2	-1

- **INS_INITSTYOPEN** (203):
  Sent at the beginning of a study opening operation performed by MedStation

StrParam1	Id of instance handle
StrParam2	‘’
Param1	Number of studies selected for opening
Param2	-1

- **INS_ENDSTYOPEN** (204):
  Sent at the end of a study opening operation performed by MedStation

StrParam1	Id of instance handle
StrParam2	‘’
Param1	-1
Param2	-1

- **MON_OPEN** (101):
  Sent when the object that manages a monitor is created

StrParam1	Monitor Id (e.g. ‘A’, ‘B’…)
StrParam2	‘’
Param1	-1
Param2	-1

- **MON_CLOSED** (102):
  Sent at the elimination of the object that manages a monitor

StrParam1	Monitor Id (e.g. ‘A’, ‘B’…)
StrParam2	‘’
Param1	-1
Param2	-1

- **MON_LAYOUT** (103):
  Sent when a monitor layout is changed

StrParam1	Monitor Id e.g. ‘A’, ‘B’…
StrParam2	‘’
Param1	Number of Rows

Param2	Number of Columns

- **MON_INITSEARCH** (104):
  Sent at the beginning of a search started after the function Query

StrParam1	Monitor Id (e.g. ‘A’, ‘B’…)
StrParam2	‘’
Param1	-1
Param2	-1

- **MON_ENDSEARCH** (105):
  Sent at the end of a search started after the function Query

StrParam1	Monitor Id (e.g. ‘A’, ‘B’…)
StrParam2	‘’
Param1	-1
Param2	-1

- **STY_CONTROLLER_ADDED** (301):
  Sent at the creation of a new study box

StrParam1	Box Id (e.g. ‘A’, ‘B’…)
StrParam2	‘’
Param1	-1
Param2	-1

- **STY_CONTROLLER_DELETED** (302):
  Sent at the elimination of a new study box

StrParam1	Box Id (e.g. ‘A’, ‘B’…)
StrParam2	‘’
Param1	-1
Param2	-1

- **STY_AFTERPHISOPEN** (304):
  Sent at the opening (Memory loading) of a study


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***Note** Managing the data returned through this notification message is useful to minimize the risk of displaying other patient images during reporting.*

StrParam1	Patient and Study data (See: **Encoding Patient and Study data**)
StrParam2	‘’
Param1	Index of study on the list of studies opened in MedStation

Param2	-1

- **STY_AFTERPHISCLOSE** (306):
  Sent when a study is actually closed (removed from the memory);

StrParam1	Patient and Study data (See **Encoding Patient and Study data**)
StrParam2	‘’
Param1	Index of study on the list of studies opened in MedStation
Param2	-1

- **STY_AFTEROPEN** (307):
  Sent after a study has been opened in a box


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Nota *Managing the data returned through this notification message is useful to minimize the risk of displaying other patient images during reporting.*

StrParam1	Box Id (e.g. ‘A’, ‘B’…)
StrParam2	Patient and Study data in case the opening occurs successfully (See: **Encoding Patient and Study data**)
Param1	-1
Param2	-1

- **STY_AFTERCLOSE** (308):
  Sent after a study has been logically closed;

StrParam1	Box Id (e.g. ‘A’, ‘B’…)
StrParam2	Patient and Study data in case the closing occurs successfully (See: **Encoding Patient and Study data**)
Param1	-1
Param2	-1

- **STY_MODE** (309):
  Sent when the display mode of a study is changed

StrParam1	Id of the box (e.g. ‘A’, ‘B’…)
StrParam2	‘’

Param1	Display modes available • 0=VNone; • 1=VView; • 2=V2D; • 5=V3D; • 8=VVoxar; • 10=VMPR2; • 11=VCURVEDMPR; • 12=VExternalController; • 13=VCine2;
Param2	-1

- **LINK_STY** (401):
  Sent when a scroll or page link is made between studies

StrParam1	Id of the box (e.g. ‘A’, ‘B’…)
StrParam2	Id of the box to which StrParam1 is linked
Param1	Type of link: • 1=scroll link • 2=page link • 3=localizer link • 4=position link
Param2	Number of links enabled for the StrParam1 box

- **UNLINK_STY** (402):
  Sent at the elimination of a link

StrParam1	Id of the box, e.g. ‘A1’, B2’….
StrParam2	‘’
Param1	Type of link: • 1=scroll link • 2=page link • 3=localizer link • 4=position link
Param2	0

- **GEN_ERROR** (501):
  Sent when you cannot perform an operation requested by the client, because the main window is not active or because the display mode is different from the standard mode;

StrParam1	Error message
StrParam2	‘’
Param1	-1

Param2	-1

- **PWD_ERROR** (502):
  Sent when the login fails because the user name or password is wrong

StrParam1	Please check username and password.
StrParam2	‘’
Param1	-1
Param2	-1

- **NSF_INFO** (503):
  Sent at the end of a query;

StrParam1	n studies found. (n= number of studies found)
StrParam2	‘’
Param1	Number of studies found
Param2	-1

- **STY_STUDY_PATIENT_DATA_MODIFY** (326)
  Sent if MedStation failed to make the changes to the patient’s data or information about a study*

StrParam1	Patient and study data if the opening operation was successful (see **Encoding Patient and Study data**)
StrParam2	‘’
Param1	-1
Param2	-1

- **STY_MEASURE_RESULT** (315)

Sent after all the measurements included in a request for quick measuring instruments have been drawn (for example, a request coming from a *MeasureGroup* component of a FormManager form in eRis/eVisit)

StrParam1	The xml message with the reply: values of the measurements, units of measurement, coordinates of the points on the figures, reference to the image on which they were drawn
StrParam2	ID of the request that is being replied.
Param1	-1
Param2	-1

- **STY_MEASUREMENTS_RESULT** (324)

Sent after all the measurements included in a request for derived measurements and/or calculations (for example the request came from a *text* component of FormManager configured in such a way as to have an expression that requests the return values processed by the MedStation calculator) have been drawn:

StrParam1	The xml message with the reply: values of measurements and/or calculations performed and corresponding units of measurement
StrParam2	The ID of the request that is being replied.
Param1	-1
Param2	-1

- **STY_MEASURE_UPDATE** (317)

  Sent when a figure drawn on a MedStation image is modified by the user and, as a result, one of its return values may change (so, for example, in FormManager in Eris/eVisit, the components of the form set using these values have to be updated, irrespective of whether they are components of a MeasureGroup o text fields with expression).

StrParam1	If the modified figure was drawn after a request for measurements/calculations, this parameter will contain the xml message with the data of the reassessed measurement/calculation data. If the modified figure was drawn after a request for a quick measurement, this parameter will contain the xml message with values only of the measurement modified, the unit of measurement, coordinates of the points, reference to the image on which it was drawn.
StrParam2	If the figure modified was drawn after a request for measurements/calculations, this parameter will contain the ID of the initial request. If the figure modified was drawn after a request for a quick measurement, StrParam2 will contain the unique ID of the figure modified.
Param1	-1
Param2	-1

- **STY_MEASURE_DELETE** (318)

Sent when a figure drawn on a MedStation image is deleted.

StrParam1	‘’

StrParam2	Unique ID of the deleted figure.
Param1	-1
Param2	-1

- **STY_CURRIMG_INFO** (320)

Sent when you click on a point of an image displayed in MedStation in order to give the client some information about the modality of the image and the properties of the region containing the selected point. (For example, in FormManager, this information can be used in the scripts associated with the events concerning the components of the forms; they can also be used to filter the display of the lists of tools available in MedStation that can be used in expressions (if the lists are configured correctly)).

StrParam1

Xml with some information about the image at the point selected by the user, in particular the values of the following DICOM tags:

- SOP Instance UID
- Modality
- Region Spatial Format
- Region Data Type

To be more precise, the information notified is grouped in an xml message of the following type

```
<?xml version="1.0" encoding="ISO-8859-1"
standalone="yes" ?>
<Body Version="1.0">
    <Image>
        <SOPInstanceUID
Value="1.2.840.113663.1500.1.246279593.3.5.201
00506.124322.359" />
        <Modality Value="US" />
        <RegionSpatialFormat Value="3" />
        <RegionDataType Value="3" />
    </Image>
</Body>
```

The unique DICOM ID (SOP Instance UID) and the modality (Modality) of the image selected are indicated. If the image has calibration regions, the format and type of the region in which the point selected on the currently displayed image are also indicated. The value of the format is that indicated by the DICOM *Region Spatial Format* (0018,6012) tag, which indicates the spatial organization of the data in the region, and can be set to the following values:

- 0000H None or not applicable
- 0001H 2D(tissue or flow)
- 0002H M-Mode(tissue or flow)
- 0003H Spectral(CW or PW Doppler)
- 0004H Wave form(physiological traces, doppler traces,....)
- 0005H Graphics

DICOM *Data* nella 0001H

- 0002H Color Flow
- 0003H PW Spectral Doppler0004H CW Spectral Doppler

	The value of the type is that indicated by the DICOM *Region Data Type* tag (0018,6013), which indicates the type of data in the region, and can be set to the following values ‘’
StrParam2	
Param1	-1
Param2	-1

- **STY_COPY_IMG_URL (328)**

Sent when an image displayed in MedStation has been copied to the clipboard of the system (*Modify | Copy (CTRL+C)*)

StrParam1	Xml message containing the dataset of the image and some information for identifying the images on the server
StrParam2	‘’
Param1	-1
Param2	-1

Note: *Some events are only notified if these events have been recorded*. The function for recording events is

- *function* ***RegisterEvent****(EventID: Integer; Value: Integer): Integer;*
    - *EventID*: the ID of the event to be recorded. The available values are
        - *STY_CURRIMG_INFO* = 320, for the notification of data about the image or a region of it on which the user has clicked with the mouse
        - *STY_CALC_UPDAT* = 327, for notification of the addition or modification of a quick measurement or a measurement or calculation requested via the calculator
        - *STY_COPY_IMG_URL* = 328, for notification of the copy of a displayed image to the clipboard
    - *Value*:
        - *0* to disable notification
        - *1* to enable notification
    - *result*:
        - *1* if the event was recorded
        - *0* if the event was not recorded

Encoding of patient and study data

Parameter StrParam2 in the notification function for the events: STY_AFTERPHISOPEN, STY_AFTERPHISCLOSE, STY_BEFOREOPEN, STY_AFTEROPEN and STY_BEFORECLOSE consists of a string in the form: ‘ATTRIBUTE0=VALUE0$....$ATTRIBUTEn=VALUEn‘

ATTRIBUTE=VALUE pairs refer to following patient and study data;

PATIENT:

PATID, PATID2, PATNAME, PATBIRTHDATE, PATSEX, PATADDRESS, PATCITY, PATZIP, PATPROVINCE, PATPHONE1, PATPHONE2, PATEMAIL;

STUDY:

STYID, STYID2, STYACCNUMBER, PATID, STYDESCRIPTION, STUDY_TE, MODALITY_DG, ORIGIN_PR, PHYSICIAN_ES, STYDATE, STYDATE, STYTIME, STYKEYWORD, STYINSTITUTE, STYDEPARTMENT, STYTOTSERIES, STYTOTIMG, STYSTATUS, STYLABEL, STYUSER, STYLASTUPDATE, STYAGE, PATSIZE, PATWEIGHT

‘’ is passed for values that are not available. Dates are in ‘yyyymmdd’ DICOM format.

Implementing the client sink object

To receive event notification from the server, the client has to implement the ImedstEngineEvents interface. A connection with server is established by the point-to-point method; The steps to be taken by the client are:

- The Client calls the *IUnknown::QueryInterface* method of the connectable object to request a pointer to the *IConnectionPointContainer* interface**.**
- The Client calls the *IConnectionPointContainer::FindConnectionPoint* method to request a pointer to the *IMedstEngineEvents* interface connection.
- The Client calls the *IConnectionPoint::Advise* method to provide the object with a pointer connectable to the *IUnknown* interface of the relative sink object.
- The Connectable object calls the IUnknown::QueryInterface method of the sink object of the client to request a pointer to the *IMedstEngineEvents* interface.
- The Connectable object can call the *IMedstEngineEvents* interface methods implemented by the client’s sink object;

F

Use of measures, measurements and calculations on eRis/eVisit forms[43]

RC-07 *Users must have followed a training course held by qualified staff and read this manual to be able to use the tools described in this chapter properly.*

MeasureGroup

MeasureGroup is a component provided by FormManager (a component of Exprivia eRis/eVisit) to manage the integration between the report form and the measurements on the images displayed in MedStation. The node corresponding to the MeasureGroup component on the data form must have *Data type* = Group and the *Measure group* flag enabled. In this way, you can load the list of tools provided by MedStation onto the *Dictionary* sheet of the *Form element* configuration screen (press the "MedStation" button when a MedStation instance is open via COM from FormManager). By selecting the desired tools from the list on the left-hand side of the screen, you can add them to the list of tools used by the component when the form is being filled in.
To be able to use this component, it must have a *button* and a few text components in which one of the results of the measurements can be displayed (each one may have several return values) as child components. If you select the MeasureGroup component on the view, you will gain access to its properties, which include the *Measures* tab. Here you can assign a return value of one of the measurements associated with the group to each text component. The *"Take Measure" relation* must be associated with the button. During compilation, press the button so that the tools chosen during the configuration phase will appear in sequence in MedStation. Once the measuring operations have been completed, the components of the form will receive and display the results.
All the tools available for use with the MeasureGroup components and their values that can be recorded in the text components of the group are listed here below.

[43] Function available only in MedStation but not in MedStation Express.

- **Angle** codeValue="Angle"
    - Angle Value
    - Angle Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Angle between lines** codeValue="AngleLine"
    - Angle Line Value
    - Angle Line Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Circle** codeValue="Circle"
    - Radius
    - Radius Unit of Measure
    - Circumference
    - Circumference Unit of Measure
    - Area
    - Area Unit of Measure
    - Mean
    - Mean Unit of Measure
    - Standard Deviation
    - Standard Deviation Unit of Measure
    - Maximum
    - Maximum Unit of Measure
    - Minimum
    - Minimum Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Distance** codeValue="Line"
    - Distance
    - Distance Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Polygon** codeValue="Polygon"
    - Area
    - Area Unit of Measure
    - Perimeter
    - Perimeter Unit of Measure
    - Mean

    - Mean Unit of Measure
    - Standard Deviation
    - Standard Deviation Unit of Measure
    - Maximum
    - Maximum Unit of Measure
    - Minimum
    - Minimum Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Ellipse** codeValue="Ellipse"
    - Area
    - Area Unit of Measure
    - Perimeter
    - Perimeter Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Vertebral morphometry** codeValue="Morphometry"
    - Ha
    - Ha Unit of Measure
    - Hm
    - Hm Unit of Measure
    - Hp
    - Hp Unit of Measure
    - Hpp
    - Hpp Unit of Measure
    - HaonHp
    - HaonHp Unit of Measure
    - HmonHp
    - HmonHp Unit of Measure
    - HponHpp
    - HponHpp Unit of Measure
    - Vertebra Name
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Distance-Time-Slope in MMode** codeValue="MModeLine"
    - Length
    - Length Unit of Measure
    - Time
    - Time Unit of Measure
    - Derivative
    - Derivative Unit of Measure

    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **MMode in Diastole** codeValue="MModeDiastole"
    - Right Ventricular Internal Diastolic Dimension
    - Right Ventricular Internal Diastolic Dimension Unit of Measure
    - Interventricular Septum Diastolic Thickness
    - Interventricular Septum Diastolic Thickness Unit of Measure
    - Left Ventricle Internal End Diastolic Dimension
    - Left Ventricle Internal End Diastolic Dimension Unit of Measure
    - Left Ventricular End Diastolic Volume
    - Left Ventricular End Diastolic Volume Unit of Measure
    - Left Ventricular End Diastolic Volume Measurement Method
    - Left Ventricle Mass
    - Left Ventricle Mass Unit of Measure
    - Left Ventricle Mass Measurement Method
    - Left Ventricle Posterior Wall Diastolic Thickness
    - Left Ventricle Posterior Wall Diastolic Thickness Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **MMode in Systole** codeValue="MModeSistole"
    - Interventricular Septum Systolic Thickness
    - Interventricular Septum Systolic Thickness Unit of Measure
    - Left Ventricle Internal Systolic Dimension
    - Left Ventricle Internal Systolic Dimension Unit of Measure
    - Left Ventricular End Systolic Volume
    - Left Ventricular End Systolic Volume Unit of Measure
    - Left Ventricular End Systolic Volume Measurement Method
    - Left Ventricle Posterior Wall Systolic Thickness
    - Left Ventricle Posterior Wall Systolic Thickness Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Echocardiogram Area Volume** codeValue="EcoCardioAreaVolume"
    - Long Axis
    - Long Axis Unit of Measure
    - (Axis) Source of Measurement Sop Instance UID
    - (Axis) Source of Measurement Sop Class UID
    - (Axis) Source of Measurement Series UID
    - Area of defined region
    - Area of defined region Unit of Measure
    - (Area) Source of Measurement Sop Instance UID
    - (Area) Source of Measurement Sop Class UID

- (Area) Source of Measurement Series UID
- Volume estimated from single 2D region
- Volume estimated from single 2D region Unit of Measure
- Volume estimated from single 2D region Measurement Method
- (Volume) Source of Measurement Sop Instance UID
- (Volume) Source of Measurement Sop Class UID
- (Volume) Source of Measurement Series UID

- **Echocardiogram Volume with Biplane method** code-Value="EcoCardioBiplaneVolume"
  - Volume
  - Volume Unit of Measure

- **Echocardiogram Pressure gradients** codeValue="EcoCardioPressureGradient"
  - Peak Velocity
  - Peak Velocity Unit of Measure
  - Peak Gradient
  - Peak Gradient Unit of Measure
  - Peak Gradient Measurement Method
  - Mean Velocity
  - Mean Velocity Unit of Measure
  - Mean Gradient
  - Mean Gradient Unit of Measure
  - Mean Gradient Measurement Method
  - Velocity Time Integral
  - Velocity Time Integral Unit of Measure
  - Source of Measurement Sop Instance UID
  - Source of Measurement Sop Class UID
  - Source of Measurement Series UID

- **Echocardiogram Deceleration time** codeValue="EcoCardioDecelerationTime"
  - Mitral Valve E-Wave Peak Velocity
  - Mitral Valve E-Wave Peak Velocity Unit of Measure
  - Mitral Valve A-Wave Peak Velocity
  - Mitral Valve A-Wave Peak Velocity Unit of Measure
  - Mitral Valve E to A Ratio
  - Mitral Valve E to A Ratio Unit of Measure
  - Deceleration Time
  - Deceleration Time Unit of Measure
  - Peak Velocity
  - Peak Velocity Unit of Measure
  - Peak Gradient
  - Peak Gradient Unit of Measure
  - Peak Gradient Measurement Method
  - Mean Velocity
  - Mean Velocity Unit of Measure
  - Mean Gradient

    - Mean Gradient Unit of Measure
    - Mean Gradient Measurement Method
    - Velocity Time Integral
    - Velocity Time Integral Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Echocardiogram Acceleration time** codeValue="EcoCardioAccelerationTime"
    - Acceleration Time
    - Acceleration Time Unit of Measure
    - Aortic Valve Ejection Time
    - Aortic Valve Ejection Time Unit of Measure
    - Ratio of Aortic Valve Acceleration Time to Ejection Time
    - Ratio of Aortic Valve Acceleration Time to Ejection Time Unit of Measure
    - Peak Velocity
    - Peak Velocity Unit of Measure
    - Peak Gradient
    - Peak Gradient Unit of Measure
    - Peak Gradient Measurement Method
    - Mean Velocity
    - Mean Velocity Unit of Measure
    - Mean Gradient
    - Mean Gradient Unit of Measure
    - Mean Gradient Measurement Method
    - Velocity Time Integral
    - Velocity Time Integral Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Echocardiogram Pressure Half Time** codeValue="EcoCardioPressureHalfTime"
    - Velocity of Half Gradient
    - Velocity of Half Gradient Unit of Measure
    - Half Gradient
    - Half Gradient Unit of Measure
    - Half Gradient Measurement Method
    - Pressure Half-Time
    - Pressure Half-Time Unit of Measure
    - Area by Pressure Half-Time
    - Area by Pressure Half-Time Unit of Measure
    - Peak Velocity
    - Peak Velocity Unit of Measure
    - Peak Gradient
    - Peak Gradient Unit of Measure
    - Peak Gradient Measurement Method
    - Mean Velocity

    - Mean Velocity Unit of Measure
    - Mean Gradient
    - Mean Gradient Unit of Measure
    - Mean Gradient Measurement Method
    - Velocity Time Integral
    - Velocity Time Integral Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Echocardiogram Velocity** codeValue="EcoCardioVelocityMeasure"
    - Velocity
    - Velocity Unit of Measure
    - Pressure Gradient
    - Pressure Gradient Unit of Measure
    - Pressure Gradient Measurement Method
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

- **Echocardiogram Time** codeValue="EcoCardioTimeMeasure"
    - Time
    - Time Unit of Measure
    - Pressure Half-Time
    - Pressure Half-Time Unit of Measure
    - Derivative
    - Derivative Unit of Measure
    - Peak Velocity
    - Peak Velocity Unit of Measure
    - Area by Pressure Half-Time
    - Area by Pressure Half-Time Unit of Measure
    - Source of Measurement Sop Instance UID
    - Source of Measurement Sop Class UID
    - Source of Measurement Series UID

Expressions

The use of measurements and calculations on forms created with FormManager is based on the idea of linking an input field of a form to an expression. At the moment, expressions simply apply mathematical formulae. In other words, formulae can be implemented to set some components.
The *text* type components of FormManager present the *expression* property in which you can write a formula during the form configuration phase.
The expression creation environment can also be used during the execution of a form to modify the expression of a *text* component, if the *expressionEditorRuntime* property is set to *true*.

For the moment, use is limited to mathematical formulae whose variables indicate:

- Components of the form
- Constants and mathematical operators
- Measurements and calculations chosen from the lists provided by MedStation
    - *Preset measurements (to be validated)*
    - *Preset calculations (to be validated)*

The expressions that can be associated with the input fields of a form may therefore perform calculations of the following type:

[measurement1] * 0.5 + [measurement2] * [field1] + [calculation1].

When executing a form, the expression is activated by pressing a key that appears on the component only when the expression is present. Calling a measurement automatically prepares MedStation to make this measurement. Once the measurement has been drawn, the component that requested the measurement will obtain the result and can use its value to show it or process it in one of its formulas or scripts. Calling a calculation automatically prepares MedStation to make all the measurements necessary to set the variables in the formula in sequence. When all the measurements have been drawn, the MedStation calculator will perform the calculation and return the result. This data will be visible and available both on the Calculator panel and on any external component that requested the calculation.



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Note *The result of a calculation is only significant if the values of the measurements involved are significant and, in particular, if the units of measurement declared in the configuration of the formula coincide with those measured. For example, the spleen volume formula entails tracing three distances on the images of a study. These distances are declared in cm and the volume in ml in the formula. This means that only if the three distances were traced on images calibrated in cm can we be sure that the result of the formula returns a volume in ml. In MedStation, we make no conversion.*



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Note *In FormManager the final value returned by MedStation to the form can be converted, if the component waiting for the result is of the* text *type, the* inputIsNumber *property is* true*, and the corresponding node of the form also has its* Data type *set to* Number *and the expected unit of measurement has been declared.*

Note *In accordance with the DICOM standard, the units of measurement that may be used in calibrating non-US images are mm and undefined, while for US regions they are listed here below. The calibration function may therefore only use these units of measurement so, if you configure the expressions in the calculator in such a way that the elements of the formulae correspond to the possible calibration units of measurement and the derived units used in the return values of MedStation measurements, conversions do not have to be managed immediately in MedStation. If, for example, there were a formula that could be used for both US and CT, which, for 2D regions, are calibrated in cm and mm, respectively, you can duplicate the formula declaring the two different units of measurement in the two expressions.*

The units of measurement for regions of US calibrations are listed below:

Value Meaning
0000H = None or not applicable
0001H = Percent
0002H = dB
0003H = cm
0004H = second
0005H = hertz(second^{-1})
0006H = dB/second
0007H = cm/sec
0008H = cm2
0009H = cm2/sec
000AH = cm3
000BH = cm3/sec
000CH = degree

When a component has an expression that involves measurements/calculations chosen from the MedStation lists, communication is activated so that any changes or deletions of the measures drawn on the images (and thus the measurements or calculations that required these measures) update the measurement and calculation results and communicate them to the form.

Calculator error messages

The following errors may occur while making a measurement or performing a calculation.

- *Different unit of measurement*: if one of the units of measurement was not respected. For example, if the return value of a measurement involved has a unit of measurement different from that indicated in the definition of the formula being applied.
- *Unknown unit of measurement*: if one of the units of measurement is unknown. For example, if the return value of a measurement involved has a unit of measurement not present on the units of measurement list.
- *Null variable*: an attempt has been made to perform an operation with a variable having no value. For example, if you have requested the application of a formula but before starting it you request a different one or if you try to assess a formula whose variables have not yet been set.
- *Invalid operand*: if one of the operands has an invalid value.
- *Invalid left operand*: if the left operand is not valid.
- *Invalid right operand*: if the right operand is not valid.
- *Unknown operation*: Invalid operation