



MedDream
USER MANUAL
(version 7.8.1)

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Table of Contents

Table of Contents	3
General information	6
Personal data security breach	6
Serious incidents reporting	7
Availability of documentation	7
Questions	7
Explanation of symbols used	7
Summary of clinical evaluation report	15
List of applicable standards	17
Warnings regarding residual risks	21
Short product description	26
Product customization	27
Product labeling	27
License agreement and registration	28
Access to user documentation	29
Product installation	29
Minimal client side requirements	29
Installation verification	30
IT security measures	32
MedDream viewing functionalities	33
Logging on to MedDream	33
Search of studies	33
MedDream DICOM Viewer	39
Viewer window	39
Toolbar	39
System tools	41
Thumbnails bar	41
View zone	44
Viewport toolbar	45
Copy the viewport content to the clipboard	46
Quick access to additional data	46
Quick menu	47
Opening studies	49
Patient studies window	50
Patient history	51
Tools for image manipulation and analysis	54
Windowing	54
Pan	56
Zoom	56
Channels	57
Scroll	57
Magnifier	58
Layout and Multi image	59
Reset	60
MPR	61
Reference Line and Crosshair	66
Rotate	68
DICOM	69
Link scrolled series	71
Tools for measuring, and annotation saving	73
Measuring images	73
Line	74
Angle	74
Polyline	75
Area	75
Volume	76
Velocity Time Integral (VTI)	76
Ellipse	77
Cobb Angle	78

Tibial Plateau Angle	78
Norberg Angle	79
Verbal Heart Scale	80
Cardiothoracic ratio	82
Text annotations	83
Region Of Interest	84
Foot longitudinal arch	84
Calibration line	85
Show Angles	86
Intensity	86
Delete measurements	87
Save Annotation	87
Copy and paste measurement	87
Copy and paste ellipse	88
Annotations	89
Key Objects	92
Segmentation	95
Bounding Box	96
Free Draw	103
Viewing and measuring segments	107
Tools for study exchange	111
Share files via DICOM Library	111
Forward	113
Export	114
LiveShare	114
Fusion function for Positron Emission Tomography (PET CT)	117
Manipulating fusion series	119
Cine mode	122
Other Viewer tools	123
Series	123
Plugins	124
Full Screen	125
Theme	125
Thumbnails	125
Preload Series	125
Print	126
Hanging protocols	126
Report	128
Special views	128
ECG module	128
SR view	132
PDF view	133
Video view	134
Multi-frame view	134
MedDream DICOM Viewer Chrome browser extension for multi-monitors	135
Size and position of modal dialog window	139
Export and Forward	140
Forward window	140
Export / Burn to CD/DVD window	142
Report module	146
Managing report templates	151
System menu functions	154
About	154
License Agreement	155
Help	156
Shortcuts	156
Settings	157
Log Off	157
License registration	158
Settings	160
General settings	160
Search window settings	161

Viewer window settings.....	161
Info Label Properties	163
Toolbar Properties.....	165
Windowing settings	167
Report settings	169
Hanging protocol settings	169
MedDream Mobile mode	175
Search of studies in mobile mode	175
Viewer window in mobile mode	178
Opening studies in MedDream Mobile mode	181
Patient studies list in mobile mode	185
Manipulating images in MedDream Mobile mode	186
Setting window in mobile mode	188
Table of Figures	190
Index	197

General information

This user`s manual describes MedDream functionalities and operation with MedDream.

Seeking to ensure patient safety, software should be used by intended use. You should therefore ensure that you are thoroughly familiar with the user manual before setting up and using MedDream for the first time.

MedDream does not replace medical professionals and could be used only as an additional tool. No special facilities or special training of the medical software MedDream users are required.

Please note that medical images quality, sharpness, accuracy and other parameters, relevant to the users, directly depends on the technical capabilities of medical device, which is generating medical images, on the monitor and printer technical capabilities.

Indications for Use: MedDream is a software intended to aid in diagnosis by visualization various medical images, video and signals, measuring data in DICOM images and management DICOM images, when the patient is not in life-threatening state of health, time is not critical for medical decision and no major therapeutic interventions are required.



WARNING! Software usage not by intended use may cause patient death, potential injury or serious health impairment, requiring professional medical intervention.

Risk and Benefit: Using MedDream by its intended use does not cause risk, which could influence patient health status or health changes, but facilitate work of medical professionals, provide a better opportunity for accurate diagnosis.

Clinical data are collected, stored and managed as described below:

- By implementing post market clinical follow-up studies;
- By analyzing results of collected preclinical data;
- By implementing competitor analysis and literature analysis;
- By managing risk;
- By managing complaints and problems;
- By collection vigilance system data;
- By implementing biomedical research.

MedDream is continually tested. All critical issues are corrected immediately and users are informed about software functionality limitations and risks.

In case of MedDream bugs please immediately contact to Softneta support at this email: support@softneta.com.

Personal data security breach

In case of personal data breach (including but not limited to cybersecurity breach) please immediately (but not later than during 24 hours) inform medical software Manufacturer Softneta UAB by using below mentioned contacts:

SOFTNETA Data Protection Officer (contacts of Data Protection Officer are public available www.softneta.com).

Name, Surname: Raimundas Mikalauskas

Tel. +370 630 06808

Mail: dpo@softneta.com

Serious incidents reporting

Any serious incident that has occurred in relation to the device should be reported to the manufacturer (via email: support@softneta.com) and the competent authority of the Member State in which the user and/or patient is established.

Availability of documentation

Electronic version of MedDream User Manual in Lithuanian and English is free available on the Softneta UAB website (www.softneta.lt / www.softneta.com in the "Products" section) as well as access to the supporting software versions. Instructions are included in the "Product description" part in the section "Downloads". User Manual could be opened in a browser or saved in pdf format and downloaded to Your computer.

Software Install Manual is added as a separate document to the User Manual.

If You require paper version of User Manual, please ask us by email: support@softneta.com. Paper version of User Manual will be sent not later than in 72 hours after receiving Your request (to the address You specify).

Questions

Please visit our F.A.Q. in Softneta UAB webpage for answers to frequently asked questions or problems.



WARNING! In the event of malfunction of the device or changes in its performance that may affect safety, contact to manufacturer.



CAUTION! Incorrectly installed software could cause inconvenience to medical professionals using the software and disruption of the medical professional activities.

If you have any questions or comments regarding MedDream functionalities or this user's manual, please contact Softneta UAB Customer support: support@softneta.com.

Explanation of symbols used

During MedDream usage please pay attention to important information, related to patient safety, which is warning about software functions, whose implementation errors may pose a risk to patient health.

The symbols in this User Manual are intended to alert user about possible errors in the software or its use. Please read the information carefully as you see the symbols described below.



WARNING! This indicates a hazardous situation which may cause patient death, potential injury or serious health impairment, requiring professional medical intervention.



CAUTION! This indicates a hazardous situation which may cause minor potential injury, not requiring professional medical intervention, or simply cause inconvenience to medical professionals using software without affecting patient health status or health changes.



NOTE! Information, hints and advice for a better understanding of the instructions to be observed in the operation of the instrument.

Additional Symbols:



Tick box



Search



Export



Forward



View icon



Ascending/Descending



System menu



Language menu



Windowing function



Patient history



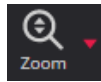
Windowing



Synchronize windowing



Invert



Zoom



Pan



Channels



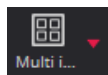
Scroll



Magnifier



Layout



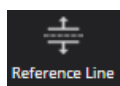
Multi image



Reset



MPR (multi-planar reconstruction)



Reference line



Crosshair



Rotate



DICOM



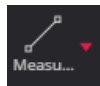
Link



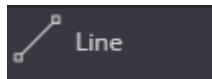
Automatic link



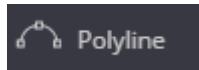
Manual link



Measure



Line



Polyline



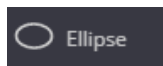
Angle



Area



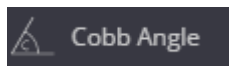
Volume



Ellipse



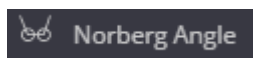
Velocity Time Integral (VTI)



Cobb Angle



Tibial Plateau Angle



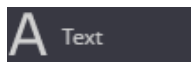
Norberg Angle



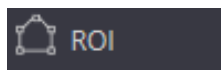
Verbal Heart Scale



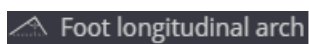
Cardiothoracic ratio



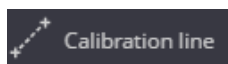
Text annotations



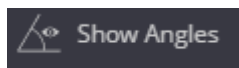
Region of interest



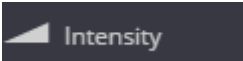


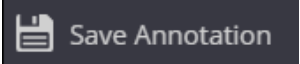










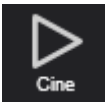



Foot longitudinal arch


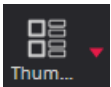

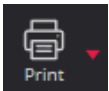


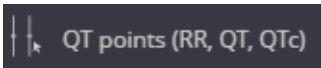



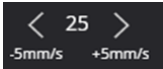
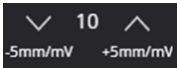
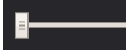




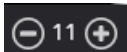






















Calibration line



Show Angles

	Intensity
	Delete all measurements
	Delete selected measurements
	Save annotation
	Key objects
	Segmentation
	Segmentation tool Bounding Box
	Segmentation tool Free Draw
	Share files via DICOM Library
	Live share
	Start live share
	Stop live share
	Copy live share link
	Fusion
	Cine mode
	Series
	Plugins
	Full Screen

	Theme
	Thumbnails
	Preload series
	Print
	Hanging protocols
	Measurement
	QT points
	HR
	QRS Axis
	Filter
	Change horizontal scale (mm per second)
	Change vertical scale (mm per mV)
	ECG view scrollbar
	Pause
	Play
	Previous Instance
	Next Instance
	Frame rate in multi-frame

	Stop playback
	Volume on
	Volume off
	Create report
	Open/Edit report
	Paste to report
	Edit report template, segment
	Delete report template, segment
 Download	Download
	Copy measurement
	Paste measurement
	Stop copy and paste measurement action
	Copy the image to the clipboard
	Create 2D Bounding Box segment
	Create 3D Bounding Box segment
	Create Free Draw segment
	Duplicate Bounding Box segment
	Locate segment
	Change color
	Erase segment contour



Segment measurement



Copy values to clipboard in CSV format



Save segments



Edit



To start recording



Take snapshot while recording



Delete images or complete video



Expand patient record



Close study



Open not saved (not converted to DICOM format) study in CURRENT STUDY window for more changes



Open already saved (converted to DICOM format) study in DICOM VIEWER window



Export the study to local or external drive



Forward study to hospital DICOM archive (requires to setup remote DICOM archive in 7.1.2 Network settings)



New study in the list, not reviewed



Study is not stored in hospital DICOM archive



Study is stored in hospital DICOM archive



Study and patient information are selected from scheduled modality worklist



Try run task again



Stop running task



Rollback the task. This button will appear on failed “CONVERT JPG/VIDEO to DICOM” task. Allow user to return all DICOM files to images of video for more study changes



Delete task



send DICOM C-ECHO and verify basic connectivity by DICOM protocol



Activate source profile - display video input source streaming window in application include on startup



Update or change source profile settings



Delete source profile



Reload all active sources



Add new source profile



Can copy full stream address



Download VLC media player format playlist file, that contains the same stream address



FDA cleared product, which means the manufacturer can demonstrate that the product is substantially equivalent to another (similar) legally marketed device that already has FDA clearance or approval



Product certified according to the Regulation (EU) 2017/745 by notified body TÜV Rheinland LGA Products GmbH



Manufacturer

Summary of clinical evaluation report

The device's risks were managed according to UAB “Softneta” internal risk management work instruction, which is based on the ISO 14971:2019 standard. During the risk management activities, the device was:

- Classified according to the Regulation (EU) 2017/745 on medical devices Annex VIII as a CLASS IIb medical device (the device's risk management file);
- Identified according to the EU 2007/47/EC directive and requirements defined in the ISO 14971:2019 standard's Appendix C (the device's risk management file);
- Ensured risk managed (implemented risk analysis, risk mitigation actions, residual risks verification) (the device's risk management file);
- Tested and verified for residual risks (retested) according to the risk management results and UAB “Softneta” Testing work instruction (software tests, user acceptance tests, clinical tests), (the device's risk management file).

- All the risk management activities were carried out by the risk management team.

Softneta gathers production and post-production information using the following Quality management system's areas: product realization; measurement analysis and improvement; change and problem management; auditing; post market data results. The above-mentioned activities ensure, that internal and external environments (in which the product exists) are constantly monitored and if changes occur all associated risks are re-managed.

Residual risks (hazard) with the "minor" severity (Results in injury or impairment requiring professional medical intervention) are mentioned in the section „Warning regarding residual risks“. We don't have any residual risk with "serious" (or higher) severity.

Calculated risk-benefit ratio (percentage) value is lower than 1 (one), therefore it is considered that the software benefit outweighs the risk that may be encountered while using the software.

List of applicable standards

Number	Requirements
EN ISO 13485:2016	Medical devices - Quality management systems - Requirements for regulatory purposes
EN ISO 14971:2019	Medical devices – Application of risk management to medical devices
IEC 82304-1:2016	Health software – Part 1: General requirements for product safety
EN 62304:2006 +A1:2015	Medical device software - Software life-cycle processes CONSOLIDATED EDITION
EN 62366-1:2015	Medical devices - Application of usability engineering to medical devices
EN ISO 15223-1:2021	Medical devices - Symbols to be used with information to be supplied by the manufacturer - Part 1: General requirements
EN ISO 12052:2017	Health informatics - Digital imaging and communication in medicine (DICOM) including workflow and data management (ISO 12052:2006)
EN ISO 14155:2020	Clinical investigation of medical devices for human subjects - Good clinical practice
EN 1041:2008 +A1:2013	Information supplied by the manufacturer with medical devices
IEC 82079-1:2019	Preparation of information for use (instructions for use) of products
2017/745	Directive concerning medical devices Regulation (EU) 2017/745 of the European Parliament and of the Council of 5 April 2017 on medical devices, Amending Directive 2001/83/EC, Regulation (EC) No 178/2002 and Regulation (EC) No 1223/2009 and repealing Council Directives 90/385/EEC and 93/42/EEC
GHTF/SG1/N055:2009	Definitions of the Terms Manufacturer, Authorised Representative, Distributor and Importer
GHTF/SG1/N063:2011	Summary Technical Documentation (STED) for Demonstrating conformity to the Essential Principles
MDCG 2020-8	Clinical Investigation and Evaluation: Post-market clinical follow-up (PMCF) Evaluation Report Template. A guide for manufacturers and notified bodies (EC)
MDCG 2020-7	Clinical Investigation and Evaluation: Post-market clinical follow-up (PMCF) Plan Template. A guide for manufacturers and notified bodies (EC)
MDCG 2020-10/1	Clinical Investigation and Evaluation: Safety reporting in clinical investigations of medical devices under the Regulation (EU) 2017/745 (EC)
MDCG 2020-10/2	Clinical Investigation and Evaluation: Clinical Investigation Summary Safety Report Form v1.0 (EC)
MDCG 2020-6	Clinical Investigation and Evaluation: Regulation (EU) 2017/745: Clinical evidence needed for medical devices previously CE marked under Directives 93/42/EEC or 90/385/EEC. A guide for manufacturers and notified bodies (EC)
MDCG 2020-1	Clinical Investigation and Evaluation: Guidance on Clinical Evaluation (MDR) / Performance Evaluation (IVDR) of Medical Device Software (EC)
MDCG 2020-5	Clinical Investigation and Evaluation: Clinical Evaluation – Equivalence. A guide for manufacturers and notified bodies (EC)

IMDRF MDCE WG/N56FINAL:2019 (IMDRF)	Clinical Investigation and Evaluation: Clinical Evaluation
IMDRF MDCE WG/N57FINAL:2019 (IMDRF)	Clinical Investigation and Evaluation: Clinical Investigation
IMDRF MDCE WG/N55 FINAL:2019 (IMDRF)	Clinical Investigation and Evaluation: Clinical Evidence
MDCG 2019-11	Software: Guidance on Qualification and Classification of Software in Regulation (EU) 2017/745 – MDR and Regulation (EU) 2017/746 – IVDR (EC)
SaMD WG/N41:2017	Software as a Medical Device (SaMD): Clinical Evaluation
IMDRF/GRRP WG/N52 FINAL:2019 (IMDRF)	Labelling: Principles of Labelling
MDCG 2018-5	UDI: UDI Assignment to Medical Device Software (EC)
MDCG 2018-6	UDI: Clarifications of UDI related responsibilities in relation to Article 16 of the Medical Device Regulation 2017/745 and the In-Vitro Diagnostic Medical Devices Regulation 2017/746 (EC)
IMDRF/UDI WG/N48 FINAL: 2019 (IMDRF)	UDI: UDI system
IMDRF/UDI WG/N7 FINAL:2013 (IMDRF)	UDI: UDI Guidance
MDCG 2019-7	PRRC. Guidance on Article 15 of the Medical Device Regulation (MDR) and in vitro Diagnostic Device Regulation (IVDR) regarding a 'person responsible for regulatory compliance' (PRRC) (EC)
MDCG 2019-16	Guidance on Cybersecurity for medical devices
MDCG 2020-3	Guidance on significant changes regarding the transitional provision under Article 120 of the MDR with regard to devices covered by certificates according to MDD or AIMDD
2014/30/EU	Directive 2014/30/EU, Electromagnetic Compatibility (EMC)
GFTF/SG3/N99-10:2004 (Edition 2)	Quality Management Systems – Process Validation Guidance
MEDDEV 2.12/1 Rev8	Report Form: Field Safety Corrective Action. Medical Devices Vigilance System
MEDDEV 2.12/1 Rev8	Report Form: Manufacturer's Incident Report. Medical Devices Vigilance System
MEDDEV 2.12/1 Rev8	Report Form: Manufacturer's Periodic Summary Report (PSR). Medical Devices Vigilance System
MEDDEV 2.12/1 Rev8	Report Form: Manufacturer's Trend Report. Medical Devices Vigilance System
MEDDEV 2.12/1 Rev8	MEDDEV 2.12-1 rev 8 on a medical devices vigilance system. Additional guidance on MEDDEV 2.12/1 rev 8
0.30.16-PROD	Manufacturer Incident Report (MIR) for Serious Incidents (MDR/IVDR) and Incidents (AIMDD/MDD/IVDD) reporting template version 7.2. Device specific vigilance guidance. New MIR form.
-	Template for a Field Safety Notice
207/2012 of 9 March 2012	Commission regulation on electronic instructions for use of medical devices
21 C.F.R. Part 801	U.S. FDA Medical Device Regulation: 21 C.F.R. Part 801 et seq. (Labeling)

21 C.F.R. Part 803	U.S. FDA Medical Device Regulation: 21 C.F.R. Part 803 (The Medical Device Reporting (MDR))
21 C.F.R. section 814.9.	U.S. FDA MAF Regulation: 21 C.F.R. section 814.9. (Medical Device Master File)
21 C.F.R. section 814.9.	U.S. FDA 510(k) Regulation: 21 C.F.R. section 814.9. (Premarket approval of medical devices)
21 C.F.R. Part 820	U.S. FDA Medical Device Regulation: 21 C.F.R. Part 820 (Quality System regulation)
78 Fed. Reg. 58785, 58785-58828	UDI-GUDID Regulations: 78 Fed. Reg. 58785, 58785-58828 (Unique Device Identification System)
FDA	Overview of Regulatory Requirements: Medical Devices
FDA	Software related documentation: Guidance for the Content of Premarket Submissions for Software Contained in Medical Devices
FDA	General Principles of Software Validation; Final Guidance for Industry and FDA Staff
FDA	FDA guidelines to User Manual
2016/679	General Data Protection Regulation (GDPR; Regulation (EU) 2016/679
IMDRF/CYBER WG/N60FINAL:2020 (IMDRF)	Cybersecurity: Principles and Practices for Medical Device Cybersecurity
45 C. F. R. Part 160, subparts A and E of part 164	45 C.F.R. Part 160 (Public Welfare: The HIPAA Privacy Rule)
45 C. F. R. Part 160, subparts A and C of part 164	45 C.F.R. Part 160 (Public Welfare: The Security Rule)
Guidance on the provisions in the HIPAA Security Rule.1 (45 C.F.R. §§ 164.302 – 318.)	Guidance on Risk Analysis Requirements under the HIPAA Security Rule
-	Guidance on Cybersecurity for Networked Medical Devices Containing Off-the Shelf (OTS) Software
-	Postmarket Management of Cybersecurity in Medical Devices (Contains Nonbinding Recommendations)
-	Content of Premarket Submissions for Management of Cybersecurity in Medical Devices; Guidance for Industry and Food and Drug Administration Staff
2015 m. rugsėjo 17 d. Nr. XII-1938	Biomedicininų tyrimų etikos įstatymas / Biomedical Research Ethics Law
2016 m. sausio 15 d. Nr. V-4	Įsakymas dėl prašymo išduoti leidimą atlikti biomedicininį tyrimą, paraiškos biomedicininiam tyrimui, biomedicininio tyrimo etinio vertinimo anketos pavyzdinių formų patvirtinimo / Order on the biomedical research forms approval: for of request for permission to implement biomedical research; biomedical research ethical evaluation form.
2017 m. gegužės 5 d. Nr. T1-683	Įsakymas dėl Valstybinės akreditavimo sveikatos priežiūros veiklai tarnybos prie Sveikatos apsaugos ministerijos generalinio direktoriaus 2004 m. rugpjūčio 5 d. įsakymo nr. T1-136 „Dėl pranešimų apie neatitinkančius reikalavimų medicinos prietaisais (budra) pateikimo tvarkos aprašo patvirtinimo“ pakeitimo / Order on the changes in vigilance system
Nr. T1-564, 2016-0412	Įsakymas „Dėl laisvos prekybos pažymėjimų išdavimo medicinos priemonėms (prietaisams) tvarkos aprašo patvirtinimo“ / Order “On Approval of the Description of the Procedure for Issuing Free Trade Certificates for Medical Devices”

Nr. T1-568, 2016-04-13	Dėl teikiamų rinkai medicinos prietaisų registravimo tvarkos aprašo patvirtinimo pakeitimo / Amendment of the approval of the description of the procedure for registration of medical devices placed on the market
2019-01-01 redakcija	LR asmens duomenų teisinės apsaugos įstatymas / Law on Legal Protection of Personal Data of the Republic of Lithuania
1T-63(1.12.E)	Duomenų subjekto teisių įgyvendinimo pavyzdinės taisyklės. 2018-07-09 Valstybinės duomenų apsaugos inspekcijos direktoriaus įsakymas Nr. 1T-63(1.12.E) / Model rules for the exercise of the rights of the data subject. Order of the Director of the State Data Protection Inspectorate on July 9, 2018.
1T-68(1.12.E)	Leidimų perduoti asmens duomenis į trečiąsias valstybes ar tarptautinėms organizacijoms išdavimo tvarkos aprašas. 2018-07-18 Valstybinės duomenų apsaugos inspekcijos direktoriaus įsakymas Nr. 1T-68(1.12.E) / Description of the procedure for the issuance of permits for the transfer of personal data to third countries or international organizations. Order of the Director of the State Data Protection Inspectorate, 2018-07-18.
1T-72(1.12.E)	Pranešimo apie asmens duomenų saugumo pažeidimą pateikimo Valstybinei duomenų apsaugos inspekcijai tvarkos aprašas. 2018-07-27 Valstybinės duomenų apsaugos inspekcijos direktoriaus įsakymas Nr. 1T-72(1.12.E). / Description of the Procedure for Submitting a Report on the Infringement of Personal Data Security to the State Data Protection Inspectorate. July 27, 2018 Order of the Director of the State Data Protection Inspectorate.
1T-73(1.12.E)	Duomenų subjekto teisių gauti informaciją, susipažinti su asmens duomenimis, reikalauti ištaisyti ar ištrinti asmens duomenis ir apriboti jų tvarkymą įgyvendinimo, kai duomenų subjektas šias teises įgyvendina per Valstybinę duomenų apsaugos inspekciją, tvarkos aprašas. 2018-07-30 Valstybinės duomenų apsaugos inspekcijos direktoriaus įsakymas Nr. 1T-73(1.12.E) / A description of the procedure for the data subject's right to receive information, access to personal data, request for the correction or deletion of personal data and the restriction of their processing when the data subject implements these rights through the State Data Protection Inspectorate. Order of the Director of the State Data Protection Inspectorate on July 30, 2018.

Warnings regarding residual risks

No	Hazard	Warning/ Caution/ Note
1	Illegal access	<p>WARNING! If integrated Viewer is used, the login window may be disabled in configuration.</p> <p>NOTE. Remote hospital DICOM archive and DICOM modality worklist server settings can be the same or not – depends on hospital infrastructure. Recommended to consult to your DICOM archive or worklist server administrator.</p>
2	Inadequate filtration process	<p>WARNING! It is not possible to search for Ideographic and Phonetic versions of patient names. The search is performed only against the basic version (Alphabetic), even if the image contains the other two versions and the PACS supports them.</p> <p>WARNING! One date interval value can be picked at a time. The ends of picked interval are displayed in the date fields on the left of the interval pick list. The fields are empty if no specific interval (Any) is picked.</p> <p>WARNING! The search according the picked modalities is performed automatically on any change in pick list.</p> <p>WARNING! The default selection on search window open is All and filtering by modality is not performed.</p> <p>WARNING! Be aware, that access to the storages may be restricted by the user rights. The storages list contains only the storages, that are granted for the user. Searching is performed only in the granted storages, if the All storages option is selected.</p> <p>WARNING! The system may be configured to search for patient studies either in all storages, or in the storage of the viewed studies.</p> <p>WARNING! Be aware, that access to the storages may be restricted by the user rights. If search for patient studies is configured in all storages, searching is performed in the storages, that are granted for the user</p> <p>WARNING! Patient history search is performed according to the Patient ID. Contact your system administrator, if multiple patients ID are displayed.</p> <p>WARNING! The mobile mode has the following search limitations comparing to desktop version: search according accession number and source AE title is not allowed; search according custom date interval is not allowed; the customization of modalities pick list and search according custom modality is not allowed.</p> <p>CAUTION! Please fill all fields correctly to identify patient and avoid editing patient with already existing studies.</p>
3	Incorrect configuration	<p>WARNING! If integrated Viewer is used, the search window may be disabled in configuration.</p> <p>WARNING! The first image opens, if AutoOpen First Image conditions are met (see description in Settings).</p> <p>WARNING! In case the first study image should be opened according to Settings, the image is opened in the first (top right) viewport and only if this viewport is empty.</p> <p>WARNING! The patient's history icon is visible only if the viewing patient's history is allowed by system configuration, and the user rights.</p> <p>WARNING! Key objects functionality may be disabled in configuration.</p> <p>WARNING! Any or all segmentation tools may be disabled in configuration, or by user rights.</p> <p>WARNING! Performing the Bounding Box segmentation, or viewing Bounding Box segments may be disabled by user rights.</p>

		<p>WARNING! Performing the Free Draw segmentation, or viewing Free Draw segments may be disabled by user rights.</p> <p>WARNING! Viewing any or all segments may be disabled in configuration, or by user rights.</p> <p>WARNING! Share files via DICOM Library function should be enabled and the required parameters should be set in configuration.</p> <p>WARNING! Forward function should be enabled and the required parameters (list of forward destination machines) should be set in configuration.</p> <p>WARNING! Export function should be enabled and the required parameters (path to DICOMDIR viewer and size of ISO archive) should be set in configuration.</p> <p>WARNING! LiveShare function should be enabled in configuration, and sockets connection to MedDream server from host's and guests' workplace should be allowed.</p> <p>WARNING! The media sizes may be supplemented or replaced with other values by system administrator.</p> <p>WARNING! The viewer may be included in ISO archive, if the appropriate viewer software is provided and system administrator configures to enclose it in export archive.</p> <p>CAUTION! To display correct DICOM modality worklist search result, please see Network settings and adjust correct worklist character set and wildcard options.</p> <p>NOTE. To record multiple signal inputs with pedals, do not forget to change source profile ENABLE RECORDING KEYS option in Recording settings. To setup pedals keys – see General settings.</p> <p>CAUTION! Try to set the same character set for the patient studies, try open one the same study and look for DICOM tag “<i>Specific Character Set</i>“(0008, 0005). Some PACS, during study import, will update patient name from DICOM file with different encoding – may lead to display incorrect patient name in the DICOM viewer (this will not change/damage any DICOM files – just database record).</p> <p>CAUTION! Do not activate multiple profiles for the same video input source. For e.g. added camera to profile A and the same camera to profile B and enabled both of them, to be active in VS application. In this situation, just profile A will start and profile B will fail, because input signal will be busy.</p> <p>It is possible to have A and B profiles active at the same time, if card allows this (for example, play input signal via windows direct show and other via capture card interface, if this exist). However, it does not make any sense to have 2 the same signals recording and it can cause unstable input stream recording process.</p> <p>NOTE. GUI validates and checks available recording device option combination by DICOM TRANSFER SYNTAX option.</p> <p>Requires to ensure, that PACS supports transfer syntax(ask PACS administrator or see PACS DICOM conformance statement document) and recorder DICOM files will be accepted by PACS</p> <p>Some options can be updated in C:\MedDreamStation\recorder\configurationSettings.json, but during re-installation – will be overridden.</p> <p>CAUTION! Registration requires internet access to https://lic.softneta.com.</p>
4	3rd party libraries / internal components work incorrectly / not available	<p>WARNING! The section described how to open the studies in Viewer window from the Search results list in Search window. For a description of opening studies in mobile mode, see the Opening studies in MedDream Mobile mode section. If Viewer is used in an integrated solution, the window is opened by an integrating information system, such as a hospital information system or a patient portal.</p> <p>WARNING! Annotation saving is implemented according to DICOM standard. The function is available only if the used study storage provides DICOM saving functionality.</p> <p>WARNING! Key object saving is implemented according to DICOM standard. The function is available only if the used study storage provides DICOM saving functionality.</p>

		<p>WARNING! 2D bounding box segmentation may be done only on images of CT, MR, PT, or MG modality.</p> <p>WARNING! 3D bounding box segmentation may be done only on images of CT, MR, or PT with more than two images in series.</p> <p>WARNING! Segments are saved in DICOM format. The function is available only if the used study storage provides DICOM saving functionality.</p> <p>WARNING! Free draw segmentation may be done only on images of CT, MR, PT, or MG modality.</p> <p>WARNING! Live sharing is dedicated for images. Multiframe, video, ECG, PDF, SR documents is not supposed to be live shared.</p> <p>WARNING! PDF file is opened with default PDF reader. Some Web browsers have built-in readers. In other cases, the additional software for pdf reading and displaying, like Adobe Acrobat Reader, should be deployed in user workplace.</p> <p>NOTE. See more details in section Selecting patient from DICOM modality worklist.</p> <p>NOTE. Some pedals producing different signal key combination on longer press. It is recommended to consult with active personal about pedal pressing habits (how long and how they press on snapshot or video recording buttons).</p> <p>NOTE. If profile has DIRECTSHOW enabled – all STREAM options will not be possible.</p> <p>CAUTION! On Windows OS it is recommended to have at least more than 2GB free space to function properly.</p>
5	Component / function is missing	<p>WARNING! The tool button in the Viewport toolbar is displayed only if it is applicable according to the Viewer configuration, the user actions, or the viewport content.</p> <p>WARNING! The tools in Measure button menu may vary depending on license type, active image type and system settings:</p> <ul style="list-style-type: none"> • Measure button is not displayed for structure reports (SR). • ECG studies has different set of Measure tools (see Special views). • Cobb Angle, TPA, Norberg Angle, and VHS measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types. • VTI measuring is applicable and displayed only for US modality. <p>WARNING! Access to Export, Forward, and Settings functionality may be not allowed either by Settings, or by user rights.</p> <p>WARNING! Systems menu options may be disabled in Settings. The Settings option may also be not allowed by user rights.</p> <p>WARNING! Annotations functionality may be disabled in configuration.</p> <p>WARNING! The Register button is visible only if user has administrator right granted by user rights and Settings menu is enabled in system settings.</p> <p>WARNING! License registration is required for legal software use. The license registration function is accessible only for users having administrator rights.</p> <p>CAUTION! Please ensure, that video recording is not active.</p> <p>WARNING! In order to ensure successful VS work, the settings must be modified only by the system administrator.</p> <p>CAUTION! When connecting pedal and keyboard, review SNAPSHOT or PLAY/STOP KEY settings and try to avoid pressing configured keys.</p>
6	Software problem usage	<p>WARNING! We recommend upgrade PC or reduce video quality, if it does not match minimal requirements for recording, playing and streaming at the same time.</p> <p>WARNING! Quick series images preview cannot be done for CT, PT, or MR series, if not displaying thumbnails is configured. Use scrollbar cursor dragging in viewport for quick series images preview.</p>

		<p>WARNING! It is not possible to sort and filter the patient's history list if working in mobile mode.</p> <p>WARNING! The internet connection and access to license server should be ensured for successful license registration.</p> <p>WARNING! You cannot change the size of particular image that is opened as one of multi images. If the viewport size is changed, the size of multi images is automatically adjusted.</p> <p>WARNING! The localization tools are mainly used for CT, MR and PT studies, that contains several series taken in several planes.</p> <p>WARNING! Note, that MedDream cannot guarantee that the manual series linking displays the images of the same patient and at the corresponding position.</p> <p>WARNING! VTI measuring tool is applicable only for the images of "US" modality with visible blood velocity profile.</p> <p>WARNING! TPA, Norberg Angle, and VHS measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.</p> <p>WARNING! Only one Copy and paste measurement actions sequence is allowed at a time.</p> <p>WARNING! Saved Annotations can only be viewed.</p> <p>WARNING! If Key object image is opened from thumbnail, Key object filter is not activated. To activate the filter, expand the key object menu by clicking the key object icon on the right of the image, and click the filter menu.</p> <p>WARNING! The 3D bounding box editing actions (move, rotate, resize) are not allowed in the images, that has other than tetragonal intersection contour.</p> <p>WARNING! Until not saved, the created, deleted or edited segments are held in program temporary storage and will be lost, if closing the Viewer or closing the study, that has segmentations with unsaved changes.</p> <p>WARNING! Windowing, Pan and Zoom functions are available during cine mode (see pages 19-20 on Manipulating and analyzing images).</p> <p>WARNING! Forward and Export functions are not available in Search window if working in mobile mode.</p> <p>WARNING! JPEG/MP4/pdf and TIFF/MP4/pdf formats are disabled in the following conditions:</p> <ul style="list-style-type: none"> - At least one study contains object of SR or ECG type, if study export (Save study) is selected. - The active series contains object of SR or ECG type, if series export (Save active series) is selected. - The active image is SR or ECG type, if image export (Save active image/video) is selected. <p>WARNING! Save active image/video and Save active series scopes are enabled only for active study export from Viewer window.</p> <p>WARNING! The size limits for one attachment file and one-time upload package, that are defined in system configuration, cannot be exceeded.</p> <p>WARNING! In Hanging protocol alpha version, the setting Do not fetch metadata for these modalities can only be modified in settings file. Note that for large-scale studies (for example CT, MRI) it is recommended not to use metadata due to long loading time.</p> <p>WARNING! Note, that browser's zoom function changes resolution and the software may automatically switch to mobile mode.</p> <p>WARNING! Forward and Export functions are not available in Search results window if working in mobile mode.</p> <p>WARNING! Software usage not by intended use may cause patient death, potential injury or serious health impairment, requiring professional medical intervention.</p>
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		<p>NOTE. During conversion to DICOM – user will not be able to open this study. User can stop the task and roll back to image and video. After roll back task is completed – can open study for editing in CURRENT STUDY window.</p> <p>After conversion complete – can open study in DICOM VIEWER window.</p> <p>NOTE. If cannot see any devices or some is missing – please check connection cables to the device. If problem persist - check Windows OS device list, if all drivers installed properly.</p> <p>NOTE. If parameter DELETE IF DISK SPACE IF LOWER THAN (GB) TO 5GB and MINIMUM MAKE FREE DISK SPACE (GB) value is 2.1GB – auto deletion expected result will be 7.1GB disk free space.</p>
7	Vulnerability of e-PHI (electronic personal health information)	<p>WARNING! Running MedDream software on shared user's account can lead to unauthorised access to patient's medical data.</p> <p>WARNING! For proper forward functioning the forward destination should be properly configured and the device should support DICOM saving functionality.</p> <p>CAUTION! Incorrectly installed software could cause inconvenience to medical professionals using the software and disruption of the medical professional activities.</p> <p>CAUTION! Please notice, that closing the program without Log Off (using browser window close 'x' button) is not safe and may lead to unauthorized access to medical data.</p> <p>CAUTION! The system does not anonymize the content of shared images and entered message. You take responsibility for sensitive data in shared information.</p> <p>WARNING! The system grants to the guests the access to all the studies, that are opened in host's Viewer window when starting live sharing, and these studies will be displayed in the thumbnail panel of the guests' Viewer window. Opening or closing the studies, while sharing is on, is not supported.</p>
8	Measurements inaccurate	<p>WARNING! MedDream cannot guarantee the accuracy of calibration data received from the modality. Note, that MedDream cannot guarantee that the manual calibration which is performed by users is done accurately.</p> <p>WARNING! Note, that measuring functions in MedDream is approximate.</p>

Short product description

MedDream is a HTML based package for PACS server which is designed to aid professionals in every day's decision-making process, connecting all the medical data into a unified and fast performing network. MedDream ensures a fast and reliable way to search, present and analyze the medical data (images and video files) on various devices: computers, smart phones, tablets and so forth. Intuitive user interface, simple, but very powerful software controllable by touchscreen Medical Panel PC. Storing locally more than 125 hours of HD videos and up to 100.000 of still images.

MedDream covers: radiology, cardiology, oncology, gastroenterology and many other fields of medical application. It seamlessly integrates with various medical imaging devices, such as: ultrasound (US), magnetic resonance (MRI), positron emission tomography (PET), computed tomography (CT), endoscopy (ES), mammography (MG), digital radiography (DR), computed radiography (CR), ophthalmology, and so forth.

Core MedDream uses are:

- Replacement of hard copies, e.g. film archives, paper documents, etc.
- Remote access. MedDream provides a possibility to be mobile and work from any place in the world where the Internet is accessible. More than one person can access and view medical records at one time. Such functionality speeds up the collaboration among the professionals. So, that a doctor in the hospital and a doctor that is in the different location may view the medical data and discuss about it simultaneously. The patient's medical history, various studies and images are found much faster comparing to the conventional paper-based methods.
- MedDream can be used as a standalone WEB Viewer or integrated into PacsOne PACS, dcm4chee Archive, Conquest PACS, ClearCanvas PACS systems. Moreover, MedDream can be adapted to client's PACS system and easily integrated into RIS/HIS workflow.
- MedDream has multiple functions such as search of studies, viewing, analyzing, saving, exporting, forwarding images and videos, etc.
- High-quality video recording into DICOM by using MPEG2 and MPEG-4 AVC/H.264 compression.
- Record/take multiple low and high (full HD) quality video/snapshots during the surgery or other procedures.
- Live stream video during the procedure.
- Record, stream, play video and take snapshots at the same time.
- Record video/take images from multiple connected devices (special video card needed).
- Flexible patient data assignment: selecting already existing patient, manually entering the patient details or selecting from hospital DICOM worklist server.
- Possibility to start a new study recording, while other video/snapshots is in progress for saving to DICOM or sending to DICOM archive.
- Review medical images/video during the surgery or other procedures.
- Trim the recorded video.
- Recorded studies can be stored locally, sent to the hospital DICOM archive (PACS) or exported to other storage devices.
- View saved images/videos with integrated DICOM Viewer.

Features of MedDream software:

- Multi language support (EN, LT);
- System administration via WEB interface;
- User identification by username and password, user rights;
- Ability to save image viewing settings;

- Secure data transfer (SSL support);
- Ability to open more than one study at a time;
- Image transformation (rotate, flip, align, pan, scale)
- Image inversion;
- Intensity (density of the point) measurement;
- Changing the Level/Window values;
- Measurements: Line, Reference line, Angle, Area, Volume, Cobb angle, Velocity time integral (VTI), Heart cardiothoracic ratio (CTR);
- Tools for localization of the images in intersecting planes;
- Multiplanar reconstruction (MPR);
- Additional data for image support (annotation and key object);
- ECG support (Tools: Beats per minute (bpm), time (s), millivolts (mV), QT points, heart rate (HR), QRS axis);
- Reports for study;
- Hanging protocols.

Product customization

Customizing the MedDream software allows providing the required set of functionalities to the system user:

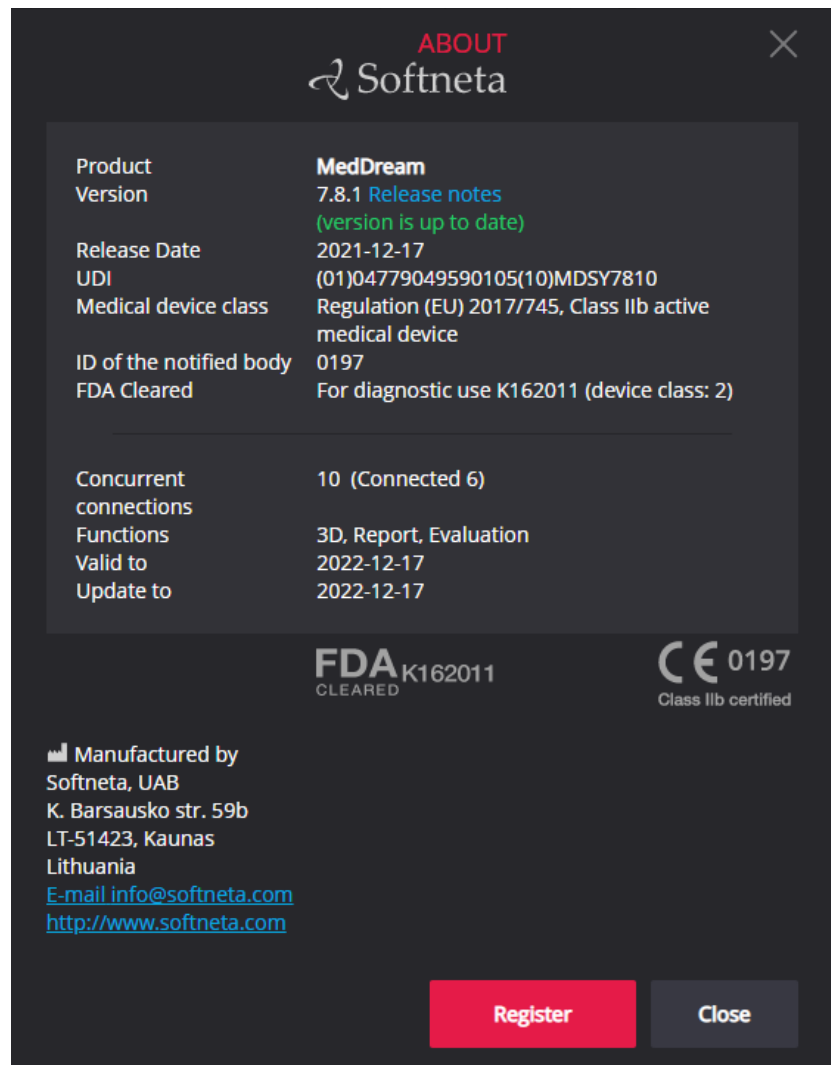
- MedDream Viewing functionalities,
- MedDream Video viewing and converting functionalities.

System appearance, and availability of tools may be also customized by changing the settings. See the detail functionalities description and description of Settings in annexes of this document.

Product labeling

The information about the product is provided to the system user in the About window:

- Product name.
- Product version.
- Release date.
- Unique Device Identification number (UID).
- Certification information: Medical device class, ID of the notified body, and FDA cleared mark.
- Contacts of product manufacturer.
- Licensing information: organization that owns the license of current product installation, and dates, until the current license is valid and will receive updates.



See the detail description of About window and how to access it in this document.

License agreement and registration



WARNING! License registration is required for legal software use.

The access to the Software License Agreement (EULA) and license registration is provided to the end user in the system. To register the license or license update, the user should do the following:

- apply for the license and receive the valid license number from system administrator or system provider,
- read the Software License Agreement and agree with it,
- enter the license information and register license.

See the detail description of license registration steps in annexes of this document.



WARNING! The internet connection and access to license server should be ensured for successful license registration.

Access to user documentation

The user manual user is available in MedDream under the Help menu. See the detail description how to access Help menu in annexes of this document.

Product installation

The requirements for MedDream server, detail instructions, how to install MedDream and verify the MedDream functioning after system installation or restart, are provided in Install Manual.

Current section provides the requirements for user workplace and instructions for verifying, that the user can access MedDream functionalities from his workplace.

Minimal client side requirements

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

Parameter	Requirements
Desktop Web HTML5	
Operating system	Windows 10 (32/64 bit), Mac OS X 10.9+
Web Browsers	Chrome 74+, Firefox 74+, Safari 10+, Microsoft Edge 85+
CPU	Modern x86/x64 Consumer CPU (5th generation Intel i3 2 core CPU or better)
RAM*	4+ GB of RAM, 256+ MB of VRAM
HDD	10 GB
Network Bandwidth**	>=2 Mbit/s for X-Ray, >=8 Mbit/s for CT, MRI
Mobile iOS Web	
Operating system	iOS 9+
Web Browsers	iOS 9+ Safari, Chrome
CPU	iPhone 6+, iPad Air+
RAM*	1 GB
HDD	2 GB
Network Bandwidth**	>=1 Mbit/s for X-Ray, >= 4 Mbit/s for CT, MRI
Mobile Android Web	
Operating system	Android 6+
Web Browsers	Android 6+ Chrome
CPU	ARMv7 processor with vector FPU, minimum 550MHz, OpenGL ES 2.0, H.264 and AAC HW decoders
RAM*	1 GB
HDD	2 GB
Network Bandwidth**	>=1 Mbit/s for X-Ray, >= 4 Mbit/s for CT, MRI

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

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

* for MG Mammography:

- 64-bit CPU and 64 bit operating system;
- Graphic board with ≥ 1 GB video memory;
- 12 GB of RAM.

* for MG Tomosynthesis:

- 64-bit CPU and 64 bit operating system;
- Graphic board with ≥ 1 GB video memory;
- 16 GB of RAM.

**Network bandwidth will directly affect image open speed.



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

NOTE! See Install Manual for MedDream viewing functionalities server system requirements.

The table describes the requirements for computer with locally installed MedDream video viewing and converting functionalities:

Parameter	Requirements
Processor	Intel® Core™ i5 or i7 When using FHD streaming, recording and playing at the same time: 4 threads, 4 GHz or 8 threads, 1.8 GHZ. Using intel media SDK (reduce CPU consumption), requires 3rd Generation (or later) Intel® Core™, selected Intel® Celeron™, Intel® Pentium™ and Intel® Atom® processors with integrated graphics supporting Intel® Quick Sync Video
Memory	4 GB RAM
Hard drive	SDD 500 GB (SATA) depends on usage workflow, can be ≥ 256 GB, ~7 days requires 56 GB
Onboard graphics	Intel® HD Graphics
Network Interface	1000 Mbit/s
Screen resolution	1920x1080 pixels (lower resolution not supported)
Supports following operating systems	Windows 7/8/10 (32 and 64 bit)

We recommend upgrade PC or reduce video quality, if it does not match minimal requirements for recording, playing and streaming at the same time.



If you faced with such a problem, please contact Softneta UAB Customer support – e-mail support@softneta.com and we will help you resolve it.

Installation verification

Section provides short check list for verifying, that the user can access MedDream functionalities from his workplace, view studies and use MedDream tools, required for daily operations.

To verify the MedDream viewing functionalities, perform the following steps:

- Open study in MedDream.
- Use your usual way to connect to MedDream service and open the MedDream Viewer: execute the known valid study open URL, or login with your credentials and select the study in MedDream search window.

- If you usually are working with studies from several network storages, try opening studies from all the used network places.
- Check, that study is correctly opened: thumbnails are displayed instead of exclamation marks, the chosen images opens as well.
- Check the Viewer toolbar for the opened image: make sure, that you usually used tools are displayed in common place and accessible.
- Verify the working of functions and tools, that are critical to you daily operations (like measuring, patient history, zoom, pan).

To verify the MedDream Video viewing and converting functionalities, perform the following steps:

- Use your usual way to connect to MedDream and open: execute the app, video source should be connected to PC;
- Check the video signal in view window. If no signal is displayed, try to refresh signal, otherwise check user manual chapter „Recording settings“;
- Try to create a new patient, or Try to select patient from worklist – (if worklist is available, check configuration chapter „Selecting patient from DICOM modality worklist“;
- After patient is created or selected from worklist try to record video. If having problem, check chapter „Recording settings“, otherwise contact system administrator or support@softenta.com

IT security measures

The “Security considerations” section in the Install Manual provides detail recommendations, how to install and configure the MedDream software in order to ensure the system security.

Current section describes actions, that should be taken by MedDream user, in order to secure his workplace and user's account against unauthorized access:

- It is highly recommended to run MedDream only from the devices and accounts, that are authorized for the user by company's security policy. Company's security policy should ensure, that work network and user's workplace is secure – servers and workplaces have on time security patches and updates, required antivirus software, firewalls and other protection means.
- Use MedDream shutdown function, after finishing your work.



WARNING! Running MedDream software on shared user's account can lead to unauthorised access to patient's medical data.

- It is recommended to use the browser, that is authorized according company's security policy, and is compatible with MedDream software. If company's security policy does not give recommendation for browser, we would recommend considering the Google Chrome or Mozilla Firefox as the most secure browser alternatives in the market at the moment.
- The authentication is required for MedDream software. However, the authentication ways may vary. If you are using login and password authentication, keep the password safe from unauthorized access:
 - do not expose the password to other persons;
 - do not allow the browser to save the password.
- Use MedDream log off function, after finishing your work and before closing browser window. Closing the program without Log Off (using browser window close 'x' button) is not safe and may lead to unauthorized access to medical data.



NOTE! Note for user, that share the computer and user's account. MedDream is designed with “zero footprint” concept, meaning that no patient data is left on a client machine: after the end user logs out from MedDream, its cache does not contain any server responses with patient data. However, there are known browser's security bug's, that allows to extract potentially sensitive data from browser's memory cache after the user logs out and doesn't close the entire browser application. Therefore, it is recommended to also close the entire browser (not just a particular tab or one of the windows) after logout.

MedDream viewing functionalities

Logging on to MedDream



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

To log on to MedDream, please do the following:

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

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

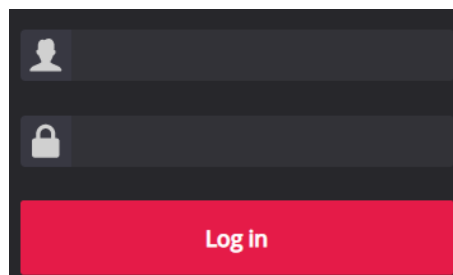


Figure 1. Log in window



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

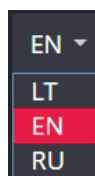


Figure 2. Language selection in a log in window



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

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

Search of studies

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

To

1d3d1w1m1yAnyAllCRCTDXMR

All storages

Q

DownloadIconEN

		ID	Anonymized	Accession	Modality	Description	Date Time	Received On	Source AE
<input type="checkbox"/>		0	ANONYMIZED		SR	L-SPINE^CLINICAL LIBRARIES	2015-04-27 16:24:29	2020-03-26T14:46:58	SENDPAC
<input type="checkbox"/>		0	ANONYMIZED		XC	TEST VIDEO HD	2014-05-05 13:55:31	2020-03-26T16:52:04	MEDDREAM
<input type="checkbox"/>		0	ANONYMIZED		OT	W/L TESTING	2013-05-21 10:44:52	2019-10-28T15:33:15	SENDTOPACS
<input type="checkbox"/>		0	ANONYMIZED		OT	MEASUREMENT: LINE	2012-12-04 14:47:25	2019-10-28T15:46:12	SENDTOPACS
<input type="checkbox"/>		0	ANONYMIZED		MG	SCREENING	2008-10-03 12:00:45	2019-10-28T15:33:18	SENDTOPACS
<input type="checkbox"/>		0	ANONYMIZED		CT	CT1 ABDOMEN	2006-10-12 09:02:58	2019-10-28T15:34:21	SENDTOPACS
<input type="checkbox"/>		0	ANONYMIZED					2019-10-28T15:33:13	SENDTOPACS
<input type="checkbox"/>		PACS-2023231696	ANONYMIZED		NM			2019-10-28T15:46:16	SENDTOPACS
<input type="checkbox"/>		0	Anonymized			C-stuburas	20150213 202950		
<input type="checkbox"/>		0	Anonymized				20180213 141352		

11 to 20 of 188

Previous12345...19Next

Figure 3. Search window



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

Description of search menu parameters:

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

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

ID	Q	↑	anonymous	Q	↑	Accession	Q	↑	Modality	Q	↑	Description	Q	↑	Date Time	↑	Received On	↑	Source AE	Q	↑
----	---	---	-----------	---	---	-----------	---	---	----------	---	---	-------------	---	---	-----------	---	-------------	---	-----------	---	---

Figure 4. Search criteria entry fields in search results list



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



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

NOTE! To perform the search click **Search** icon after the criteria is entered.

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

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

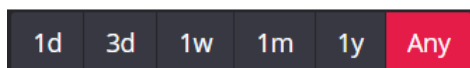


Figure 5. Quick pick list for choosing the study date interval



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



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

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

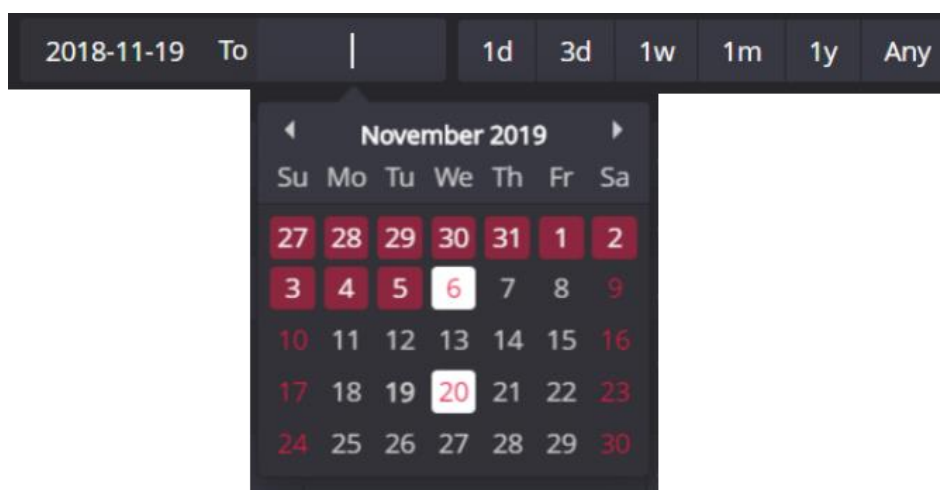


Figure 6. Study date interval entry fields



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

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



Figure 7. Pick list for choosing modality: CT is chosen



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

WARNING! The default selection on search window open is **All** and filtering by modality is not performed.

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

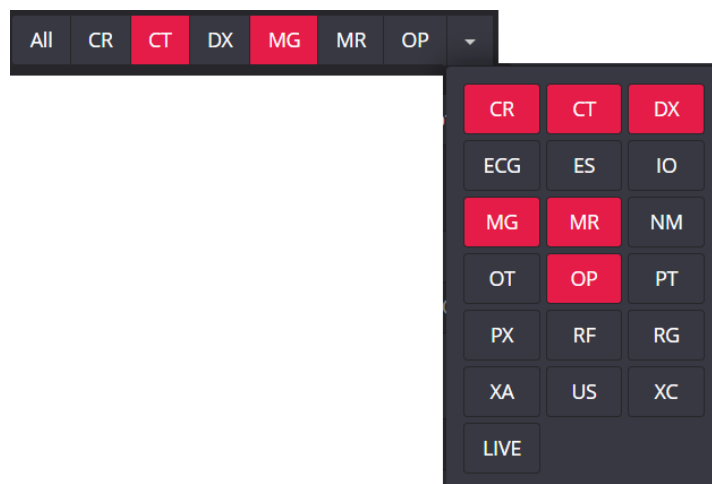


Figure 8. Customization of modalities pick list

The list of modalities:

CR – Computed Radiography

CT – Computed Tomography

DX – Digital Radiography

ECG – Electrocardiography

ES – Endoscopy

IO – Intra-Oral Radiography

MG – Mammography

MR – Magnetic Resonance

NM – Nuclear Medicine

OT – Other

OP – Ophthalmic Photography

PT – Positron emission tomography (PET)

PX – Panoramic X-Ray

RF – Radio Fluoroscopy

RG – Radiographic Imaging

XA – X-Ray Angiography

US – Ultra Sound

XC – External camera photography

LIVE – live stream



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

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

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

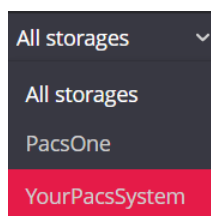


Figure 9. Picking the storage



NOTE! The storage selection control is visible only if multiple storages are configured. The default selection on search window open is **All storages** and searching is done in all configured storages. The search according the picked **storage** is performed automatically on selection change.



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




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

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



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

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

1. To sort the result list by any of data fields. Each field has **Ascending/Descending** button . You can arrange each of them in ascending  or descending  order. Click once and the order of the selected field will change from ascending to descending and vice versa.
2. To navigate through result list by picking the required page or using **Previous** and **Next** in page navigation controls:

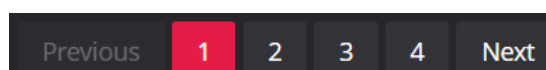


Figure 10. Page navigation in the search results list



NOTE! The number of studies per page is defined in Settings.

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

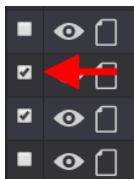




Figure 11. Marking the study

The forward and export functionality is activated by selecting the appropriate menu in the search window. See section [Export and Forward](#) for detail description.



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

4. To open the study in viewer by clicking the study in the search results list. See [Opening studies](#) section for detail description.

5. To open the Report window by clicking the Create report  icon, or Edit report  icon in the search results list. See [Report module](#) section for detail description.

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

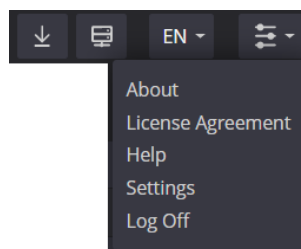


Figure 12. The other menu in Search window

1. Clicking the **Export** button opens the export window. Before doing so, mark the studies you want to export. See [Export and Forward](#) section for detail description.

2. Clicking the **Forward** button opens the forward window. Before doing so, mark the studies you want to forward. See [Export and Forward](#) section for detail description.

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

4. **System** menu in Search window contains the following options: About; License Agreement; Help; Setting; Log Off. See [System menu functions](#) section for detail description of each option.



WARNING! Access to Export, Forward, and Settings functionality may be not allowed either by Settings, or by user rights.

MedDream DICOM Viewer

Viewer window

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

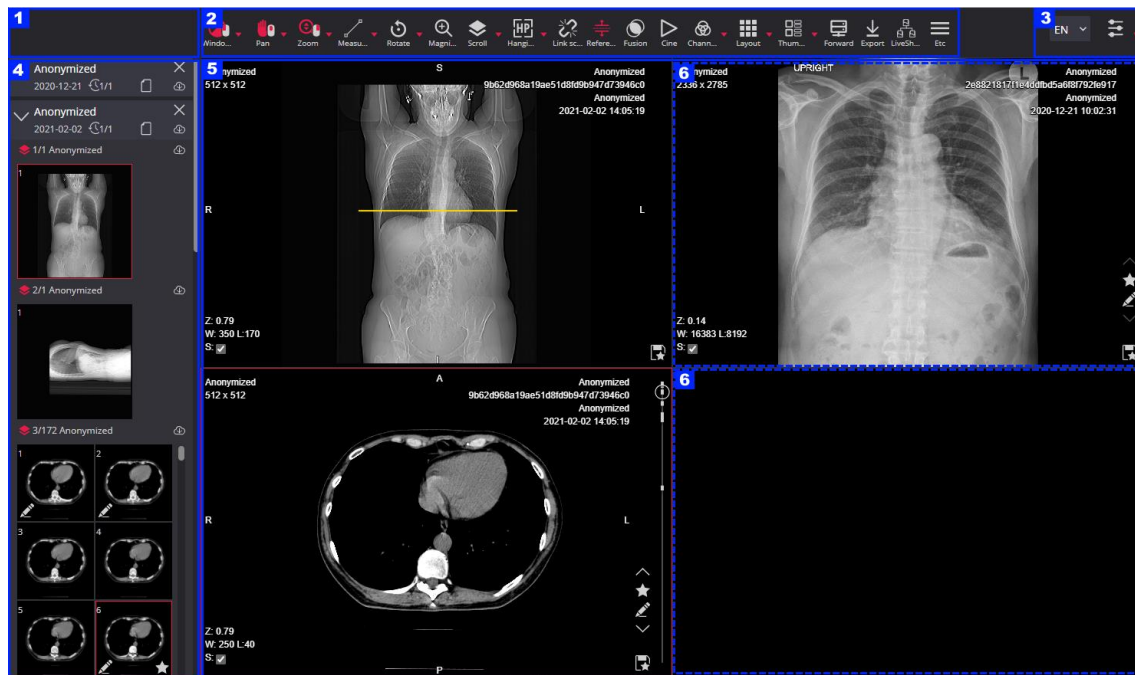


Figure 13. Viewer window zones

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

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



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

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

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

Toolbar

Image manipulation tools are displayed at the top of the Viewer window. In section [Toolbar Properties](#) you can configure what buttons and in what order are shown on toolbar. If there is not enough space for the buttons to be displayed, the **Etc** button is displayed at the end of the toolbar. Click the **Etc** button to see the missing tool buttons.

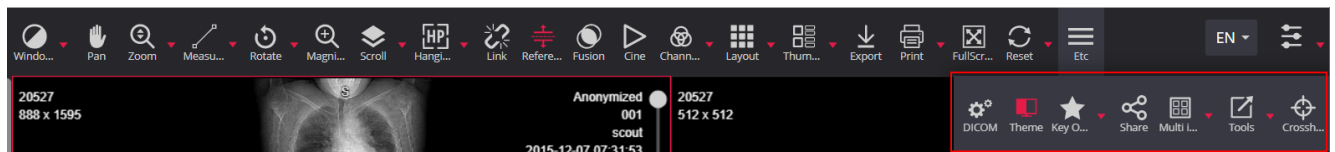


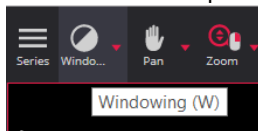
Figure 14. Expanded toolbar.




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

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

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



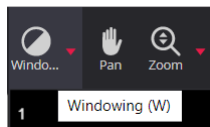
- Press the mouse key that you want to use for the mouse action
- Tool icon displays the activated mouse button: in example , the left mouse button is activated to change the brightness level.



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

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

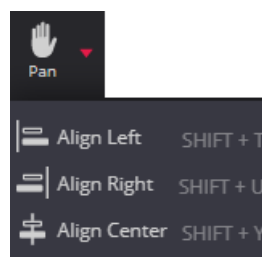
You can activate and deactivate the left mouse button usage for tools' mouse action with keyboard: press the letter



displayed in tooltip 1. Pressing 'W' activates the left mouse button usage for windowing function



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



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

System tools

The system tools zone contains two buttons:

- **Language** menu that enables language change by selecting the language in expandable list.
- Expandable **System** menu with the following options: About; License Agreement; Help; Shortcuts; Settings; Log Off. See [System menu functions](#) section for detail description.






WARNING! System menu options may be disabled in [Settings](#). The Settings option may also be not allowed by user rights.



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

Thumbnails bar

The Thumbnail holds the studies that are opened in Viewer window. If study description is expanded, the series description and series images thumbnails are displayed. For video and multi-frame images, the type indicator  is displayed at the top right thumbnail's corner. The Annotation icon  is displayed at the bottom left thumbnail's corner, if presentation state is saved for the image. The Key object icon  is displayed at the bottom right thumbnail's corner, if the image is marked as key object.



NOTE! By default, system is configured to not show the image thumbnails for CT, PT and MR series in order to decrease the study loading time. For CT, PT, and MR series without image thumbnails, only one series thumbnail is displayed. If the series has images with annotations or marked as key objects, the additional data thumbnail is displayed next to the series thumbnail.

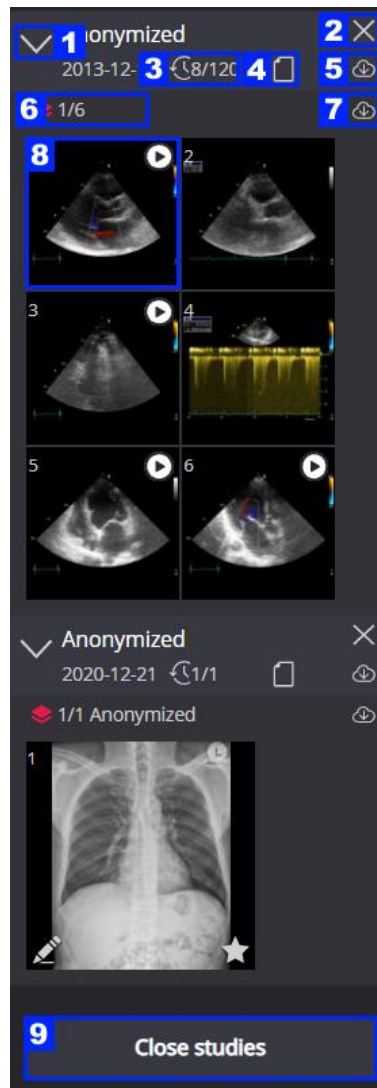






Figure 15. Action controls in Thumbnail

In thumbnail zone you can perform the following (see control numbers in Figure 15 and Figure 17):

- Expand or collapse the study description by clicking the chevron icon (number 1) at the top left corner of the study description.
- Remove the study from Viewer window if you are done with it. To remove the study from Viewer window, click on close study button (number 2) at the top right corner of the study description.
- Open patients' studies modal (see detail description in section [Patient history](#)) by clicking the patient's history icon  (number 3) in the study description.
- Open Report window by clicking the Create report  icon, or Edit report  icon (number 4) in study description. See detail description in section [Report module](#).
- Preload the data by clicking the preload icon . Clicking the preload icon on the right side of study description (number 5), preloads the whole study. Clicking the preload icon on the right side of series description (number 7), preloads the series. Study or series preload allows to scroll through the images much faster.



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

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

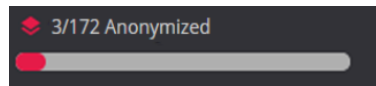


Figure 16. Preload progress bar



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

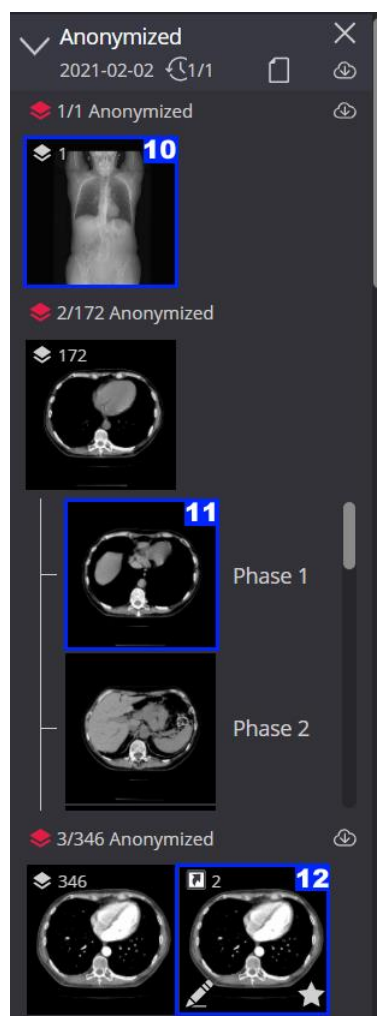


Figure 17. CT series default view without images thumbnails, and with phase filter

- Remove all the studies from Viewer window by clicking on **Close studies** button (number 9) at the bottom of the Thumbnail zone.
- Open images in the following ways:
 - To open any series in the viewport, drag the series description (number 6) to that viewport. System displays the first series image in the viewport, and automatically starts series images preload;

- To open any image from series with images thumbnails (number 8), find the image thumbnail and click it to open in active viewport, or drag it to selected viewport. If the image is currently viewed, the image picture is highlighted;
- To open CT, PT, or MR series without image thumbnails in the active viewport, click the series thumbnail (number 10), or drag it to selected viewport. System displays the first series image in the viewport. The series thumbnail image is highlighted, if at least one series image is displayed in viewer;



WARNING! Quick series images preview cannot be done for CT, PT, or MR series, if not displaying thumbnails is configured. Use scrollbar cursor dragging in viewport for quick series images preview.



NOTE! The automatic series preload for better scrolling performance may be done on CT, PT, MR series opening, if not displaying thumbnails is configured (see section [Scroll](#)).

- To open the first image with additional data for CT, PT, or MR series without image thumbnails in active viewport, click the additional data thumbnail (number 12), or drag it to selected viewport. The additional data thumbnail image is highlighted, if at least one series image with additional data is displayed in viewer;
- To open the phase images in the active viewport, click the selected phase thumbnail (number 11), or drag it to selected viewport. The middle of the phase images is displayed, and you can see images of the phase by scrolling forward and backward.



NOTE! Use the Study window (see description in section [Series](#)) as an alternative way to perform the actions: view study description and image thumbnails, preload series images, view the selected image, close the selected study.

View zone

The view zone takes the largest part of the Viewer window and is designated to view and analyze the images. The view zone may be divided to several sections, each section (dashed line in figure) working as separate viewport. The manipulation is allowed in one active viewport at a time. To activate the viewport, click on the viewport area – the active viewport is highlighted. The toolbar and quick menu are automatically adjusted according the content of the active viewport.

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

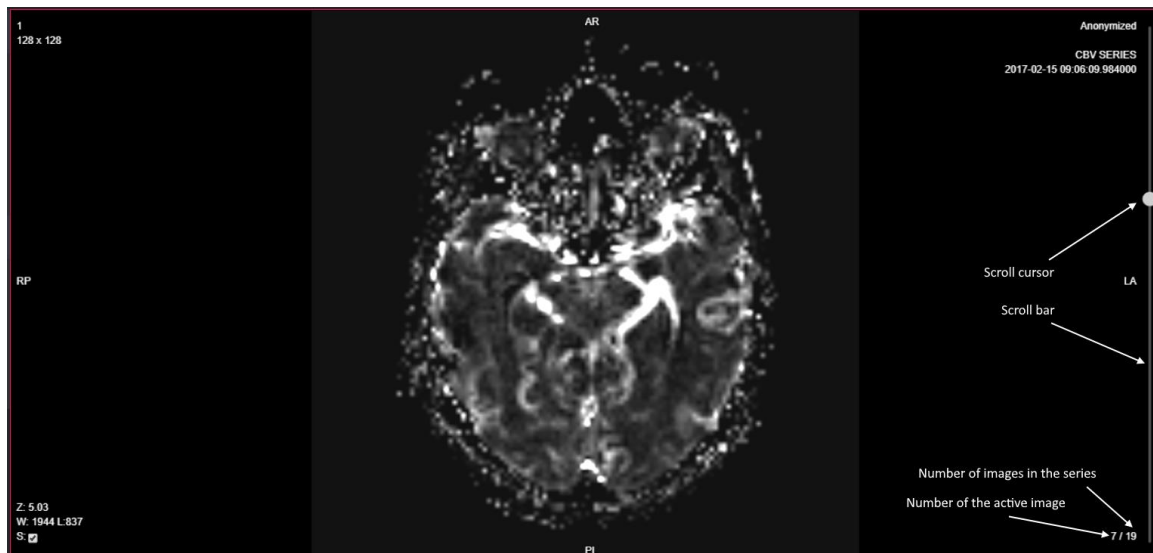


Figure 18. Image scroll bar



NOTE! The scrollbar is displayed for the series of PT, CT or MR modality, and having two or more images.

Viewport toolbar

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

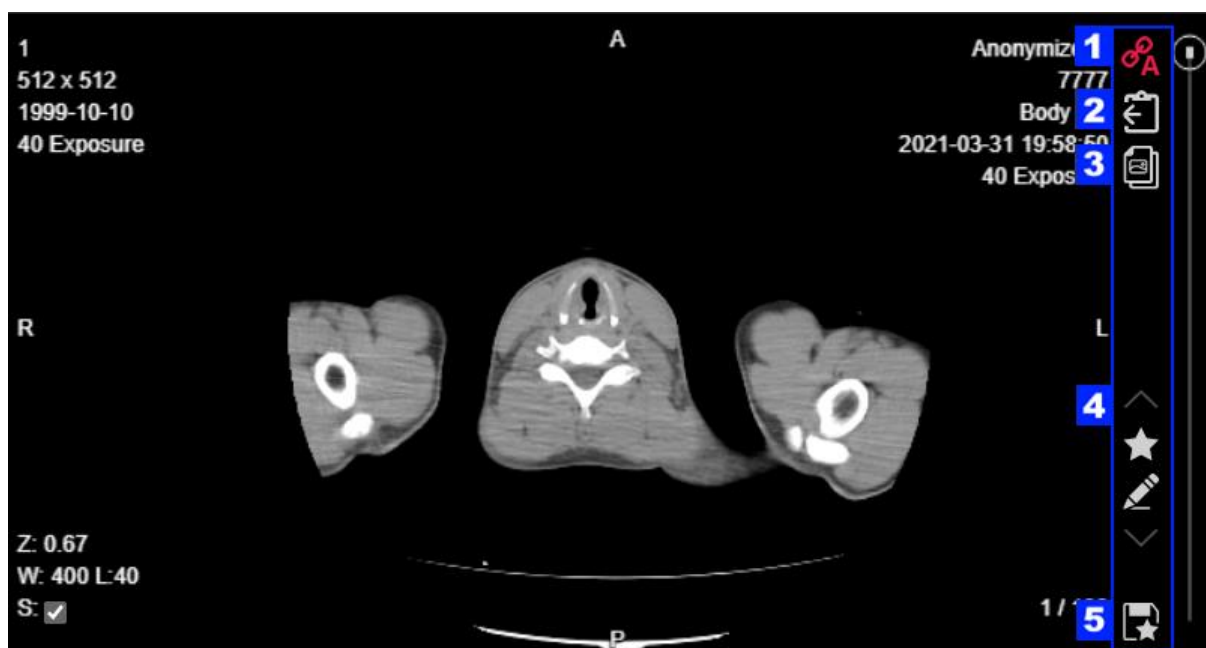


Figure 19. Viewport toolbar

The following tools are accessible from the Viewport toolbar (see control numbers in Figure 19):


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

- Paste the copied measurement on the image by tapping the Paste measurement button (number 2) in the Viewport toolbar. See detail functionality description in section [Copy and paste measurement](#).
- Copy the image and other content, that is displayed in the viewport, to the clipboard by tapping Copy image to the clipboard button (number 3) in the Viewport toolbar. See detail functionality description in section [Copy the viewport content to the clipboard](#).
- View the additional data of the image using the Quick access to additional data buttons (number 4) in the Viewport toolbar. See detail functionality description in section [Quick access to additional data](#).
- Quickly save the key object and annotations by tapping Quick save button (number 5) in the Viewport toolbar. See detail functionality description in sections [Annotations](#) and [Key Objects](#).



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

Copy the viewport content to the clipboard

If image, video or multi-frame is viewed in the viewport, the Copy image to clipboard  button is displayed in the Viewport toolbar. Clicking the button copies the viewport content to the clipboard:

- The png format is used for clipboard image;
- The size of the clipboard image is the same as the size of the viewport's area;
- The viewport's pixels are copied as follows:
 - The currently viewed image or frame, as it is displayed in viewport after all the transformations, like rotation, zoom, windowing, is copied;
 - The fused PET image pixels are copied;
 - All the viewport labels, as displayed in the viewport, are copied;
 - All the measurements with labels, annotations, as displayed in the viewport, are copied;
- The following viewport's elements are not copied:
 - Scroll bar is not copied;
 - Viewport toolbar tools (icons) are not copied;
 - Other toolbars (like fusion toolbar, multi-frame toolbar) are not copied;
 - Viewport controls (like smooth check box) are not copied.

When copied, the clipboard content may be pasted to any source, that supports png format.

Quick access to additional data



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

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

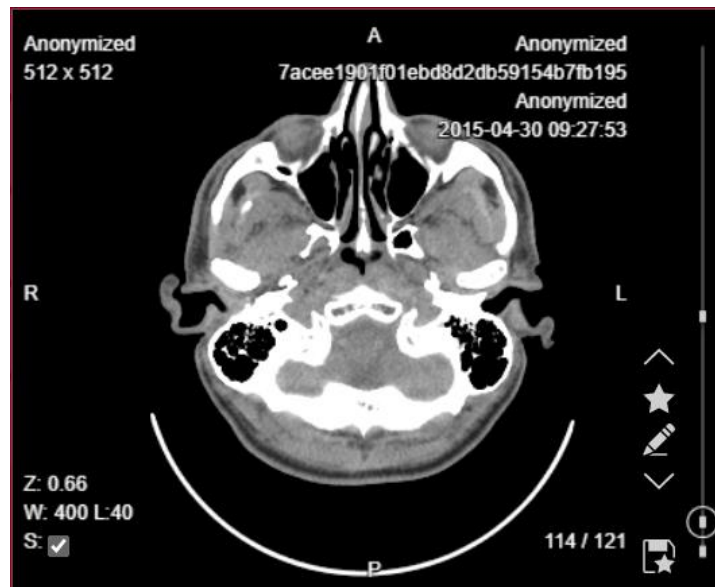







Figure 20. Quick access to additional data controls

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

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

Quick menu

A **quick menu** appears with a right-click mouse operation on the viewports' area. A quick menu offers tools that have been chosen to be included in a quick menu via Settings (refer to the [Settings](#) chapter for more information).

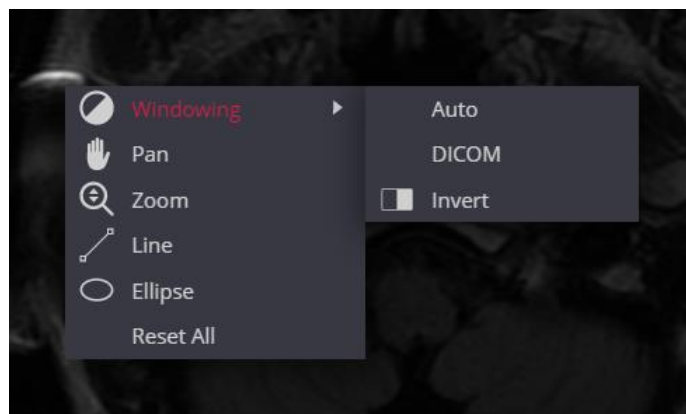


Figure 21. Quick menu

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

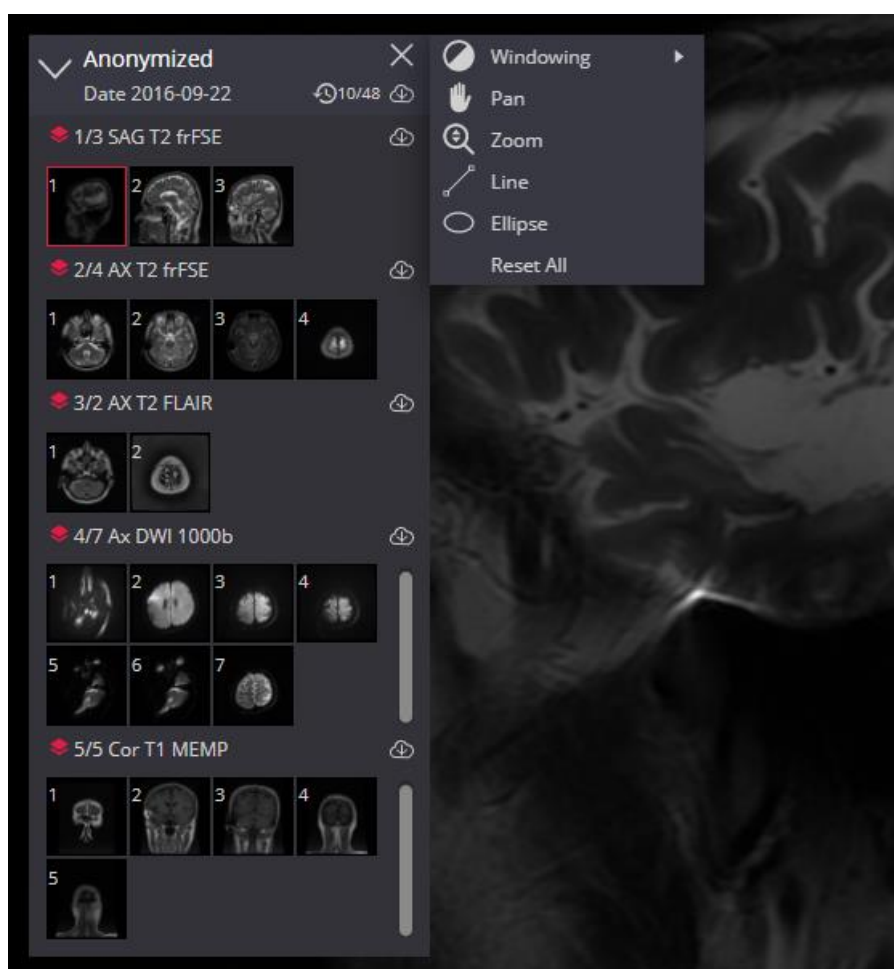


Figure 22. Quick menu with thumbnail zone

Opening studies



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



NOTE! See sections [Patient studies window](#) and [Patient history](#) for detail description how to open the studies from the Patient studies list.



NOTE! To view the image of the study that is already opened in Viewer's window, drag the image picture from thumbnail or use the Series menu (see [Series](#)).

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

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

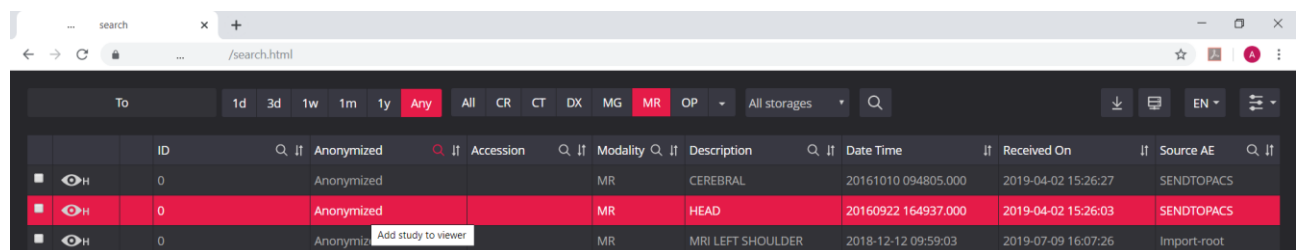


Figure 23. Study selection in the search results list

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

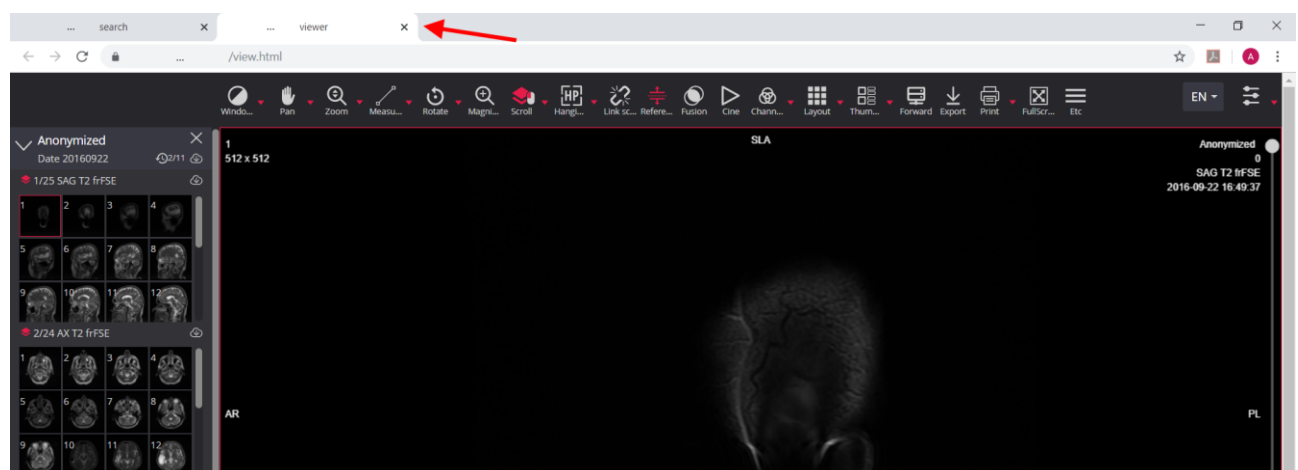


Figure 24. Viewer window in new tab



WARNING! The first image opens, if AutoOpen First Image conditions are met (see description in [Settings](#)).

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

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

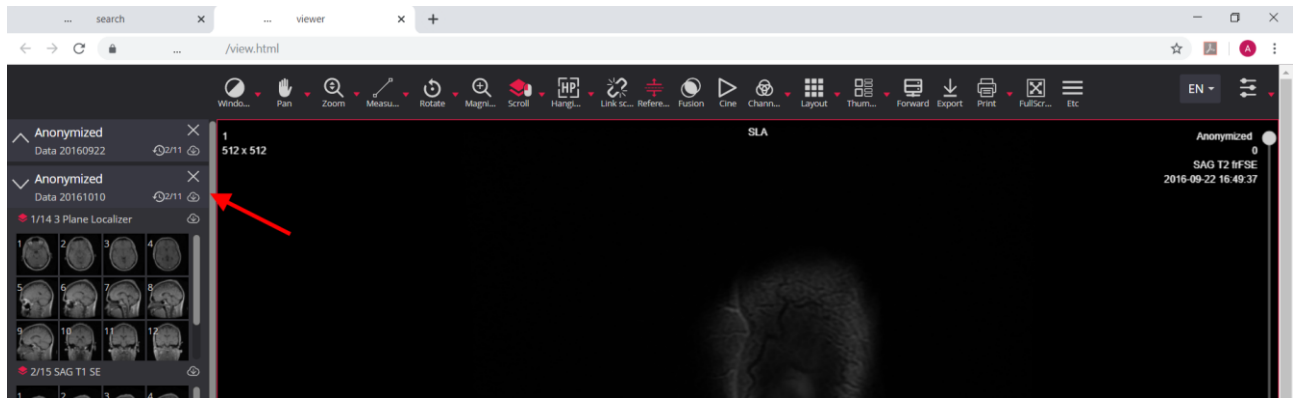


Figure 25. New study opened in the same Viewer window



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



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

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

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

Patient studies window

Patient studies window is displayed in the following conditions:

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

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

PATIENT STUDIES

Anonymized — 0[STOWRS-10.2.29.30-20190805100743]

	ID	Name	Modality	Description	Date Time	Source AE
■	0[STOWRS-10.2.29.30-20190805100	Anonymized	CR, KO, PR	Chest AP	2020-11-16 10:22:49	
■	0[STOWRS-10.2.29.30-20190805100	Anonymized	KO, PR, US		2020-10-15 13:21:42	
■	0[STOWRS-10.2.29.30-20190805100	Anonymized	MG, PR	MG Unknown	2020-10-08 16:33:59	
■	0[STOWRS-10.2.29.30-20190805100	Anonymized	CR, KO, PR	Fémur	2020-09-27 08:49:32	
■	0[STOWRS-10.2.29.30-20190805100	Anonymized	CT, KO, PR	Cerveau_SAN S(Adulte)	2020-09-03 13:34:49	
■	0[STOWRS-	Anonymized	DX, PR	PELVIS	2020-08-18	

Figure 26. Patient studies window

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



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



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

Patient history

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

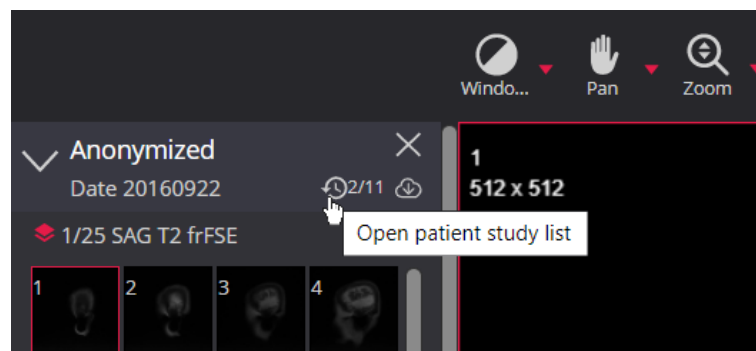


Figure 27. Opening the Patient history window from the header of viewed studies



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

Patient history window displays the patient studies:

The screenshot shows a window titled "PATIENT HISTORY" with a close button (X) in the top right. Below the title bar, it says "Anonymized — 0[STOWRS-10.2.29.30-20190805100743]" and has two filter buttons: "MG" and "All". The main area contains a table with columns: ID, Name, Modality, Description, Date Time, and Source AE. Each row has a small icon to its left, representing a study. The table lists five studies with details like ID, Name (Anonymized), Modality (CR, KO, PR), Description (Chest AP, Fémur, Cerveau_SAN S(Adulte)), Date Time, and Source AE (MEDDREAM).

ID	Name	Modality	Description	Date Time	Source AE
0[STOWRS-10.2.29.30-20190805100	Anonymized	CR, KO, PR	Chest AP	2020-11-16 10:22:49	MEDDREAM
0[STOWRS-10.2.29.30-20190805100	Anonymized	KO, PR, US		2020-10-15 13:21:42	MEDDREAM
Added 0[STOWRS-10.2.29.30-20190805100	Anonymized	MG, PR	MG Unknown	2020-10-08 16:33:59	MEDDREAM
0[STOWRS-10.2.29.30-20190805100	Anonymized	CR, KO, PR	Fémur	2020-09-27 08:49:32	MEDDREAM
0[STOWRS-10.2.29.30-20190805100	Anonymized	CT, KO, PR	Cerveau_SAN S(Adulte)	2020-09-03 13:34:49	MEDDREAM

A "Close" button is located at the bottom right of the window.

Figure 28. Patient history window



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

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

The following study information is provided in **Patient studies list**:







- **ID** - patient's identification number,
- **Name** - patient's name and surname,
- **Modality** - the method which was used to obtain the study images (modality),
- **Description** – the study description,
- **Date Time** – study date and time,
- **Source AE** – device from where the study was sent to the PACS.

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

- The modality of the study from which the Patient history window was opened (**IO** in the figure);

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

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

- Sort the patient studies list. Sorting is possible by all columns. The sort-related functionality:
 - By default, the list is sorted in descending order by **Date Time** when patient studies list is displayed;
 - To sort the list according to the selected column, or to change the sorting order, you need to click the sort button in the in the heading of the selected column. The action performs the sort and changes the sort icon as follows:  sorted ascending,  sorted descending,  unsorted;
 - It is allowed to sort only by one column at a time. Sorting by another column automatically cancels the previous sort.
- Perform the search in the patient study list. Search is possible by all columns with a search icon . The search-related functionality:
 - To perform a search, click on the column name – the system highlights the search icon and search criteria input field. Enter a search phrase in the highlighted input field - the system automatically filters the list based on the text you enter;
 - It is allowed to have filter applied in several columns at a time. The columns with an active filter have highlighted search icon  in the column header.
- Open the patient study for viewing:
 - To open one study, click on the eye icon  in the first column of the studies list;
 - To open multiple studies at once, mark the tick-box next to the studies you want to open and click the **Add studies to viewer** button. All the studies, that currently displayed in the list, may be marked or unmarked at once by clicking the tick-box in the header of the first column;
 - All the studies, that are already opened in Viewer, are highlighted as **Added** and haven't controls for opening.

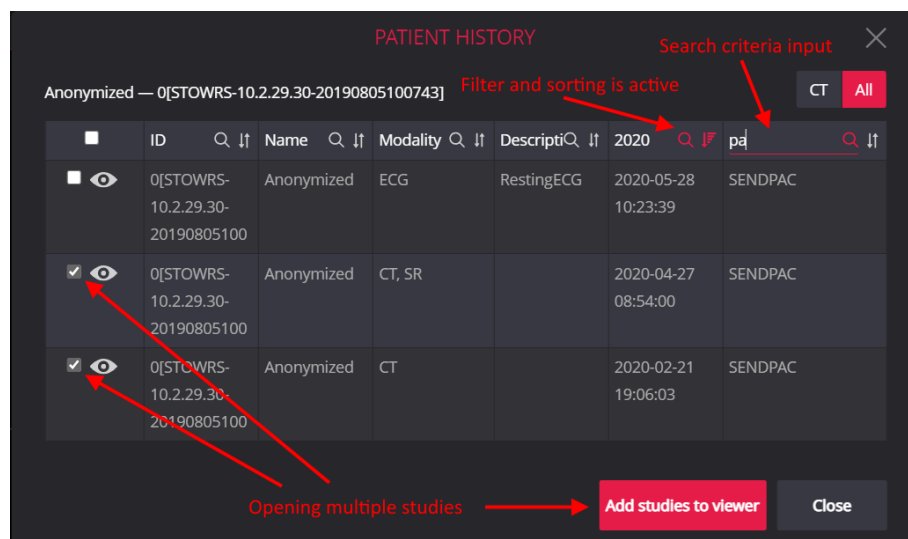


Figure 29. Searching and opening several studies from Patient history window



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



WARNING! Patient history search is performed according to the *Patient ID*. Contact your system administrator, if multiple patients ID are displayed.

Tools for image manipulation and analysis



NOTE! In section [Toolbar Properties](#) you can configure, what buttons and in what order are shown in toolbar.

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

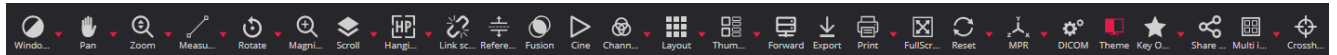



Figure 30. Image manipulation tools

Windowing



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

For changing the brightness with mouse, assign the mouse button to Windowing function . Hold down the assigned button and drag the mouse upwards or downwards (to change Level values), and right or left to change Window values.

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

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

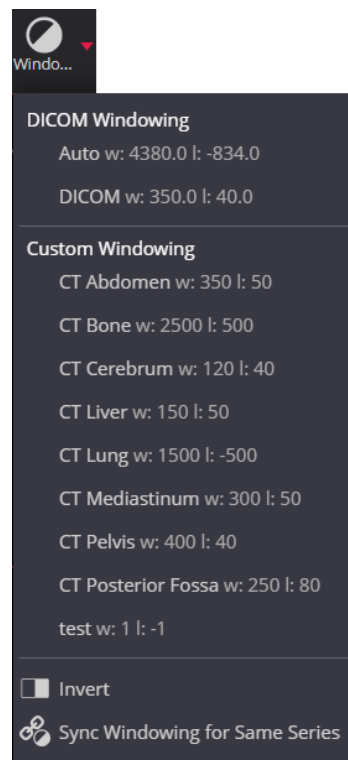



Figure 31. Window button menu example

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

The description of Windowing menu elements:


- Static group **DICOM Windowing**. Group contains the following options:
 - **Auto** – the system analyses the image and adjusts the brightness and contrast automatically. Static menu option. Auto windowing is applied, if no other options available in DICOM Windowing group.
 - Dynamic menu options - all the Window and Level value pairs from image DICOM data: windowing title, w value, and l value are displayed. The first option is automatically applied, if available.
- **VOI LUT (Value Of Interest Look-Up Table)** dynamic group is displayed only if VOI LUT configurations are found in image DICOM file. This transformation gives greater weight to the range of values of interest. The DICOM Standard Window Center and Window Width are linear VOI LUT where only 2 parameters are specified - center and width of the interval. Meanwhile, the non-linear VOI LUT uses a free shape curve in the form of a table. In MedDream user environment VOI LUT is called non-linear transformation.
 - The VOI LUT group displays all VOI LUT configurations that are available in the active image DICOM file. The names of VOI LUT configurations specified in the DICOM file are displayed. If VOI LUT configurations exist, the first VOI LUT configuration is automatically applied, along with Auto w and l values.
- The **Color LUT** group displays the **COLOR PALETTE** menu, if COLOR PALETTE is found in image DICOM file. If there is a Color Palette, it will be applied during the study loading process. After applying another Window Leveling perfusion, the Color palette will not be applied automatically. To apply the color palette after changing the windowing level, click the **COLOR PALETTE** menu.
- **Custom Windowing** dynamic group holds the custom windowing options that are define in settings (see section [Windowing settings](#)), if the active image modality adheres to settings.
- **Invert** – the static option that is used to invert the image.
- **Sync Windowing for Same Series** – static option that allows applying windowing values for the for the same series displayed in different viewports, if windowing is changed with mouse. Windowing

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

Pan



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

For changing the image position with mouse, assign the mouse button to Pan function . To move an image within the pane:

Press the selected mouse button on the image and drag the cursor to desired place or position.

Release the mouse button to leave the image in its new position.

You can use the Pan menu for changing the image alignment:

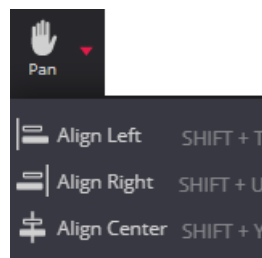



Figure 32. Image alignment options in Pan menu

Zoom



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

For changing the image size with mouse, assign the mouse button to Zoom function . To zoom the image, do the following:

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

Zoom button menu is used to choose between **Fit to Screen** or **Original resolution**:

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

- Clicking **Original resolution** button, the size of the image changes into original size.

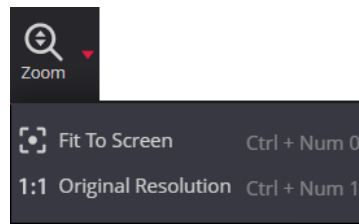


Figure 33. Zoom button menu

Channels



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

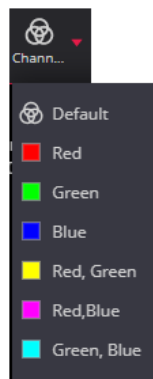


Figure 34. Color selection in Channels button menu

To remove the color highlighting, select the **Default** menu option in Channels button menu.

Scroll



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

For scrolling the series images with mouse without wheel function, assign the mouse button to Scroll function. Once tapped it enables you to scroll through the series of images by using a vertical drag gesture: drag upwards to scroll towards the series beginning, and drag downwards to scroll towards the series ending.

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



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

Scroll button can be extended:

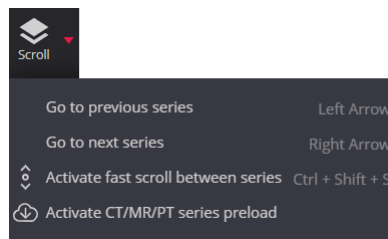




Figure 35. Scroll button menu


- To change the active series, use menu option **Go to previous series** (shortcut - Left Arrow in keyboard) or **Go to next series** (shortcut - Right Arrow in keyboard). In settings this functionality can be included in quick menu, for faster browsing through study series.
- To activate/deactivate of fast scrolling between series with mouse, use **Activate fast scroll between series** option. Series scrolling is enabled if the scroll icon on the left side of the menu is highlighted . Series scrolling settings are stored in your browser's local storage and only apply to the same browser.
- To automatically start series images preload on CT/MR/PT series opening, use **Activate CT/MR/PT series preload** option. Menu option is displayed, only if the not displaying series images thumbnails and automatic preload is configured for CT/MR/PT series. Automatic series preload is enabled if the preload icon on the left side of the menu is highlighted . Automatic preload settings are stored in your browser's local storage and only apply to the same browser.

Magnifier



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



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

You can change magnification in this area with the help of mouse wheel from 1 time (no enlargement) to 50 times. In order to enlarge, press the selected mouse button and scroll the mouse wheel until the desired magnification is reached. The actual magnification value is displayed on the bottom left corner of the active viewport (M x [magnification coefficient]):



Figure 36. Magnification coefficient of Magnifier tool

Layout and Multi image

Layout and **Multi image** functions allow dividing the view zone of the Viewer window for displaying the separate images in each division. It helps in analyzing and comparing the images.



Layout button divides the Viewers' view zone into viewports. Select the desired layout under the extendible **Layout** menu and the view zone will be divided in the selected number of identical size viewports. To change the viewports size, point the mouse cursor to division line (the cursor should obtain the divider look), hold the mouse button down and drag the line:

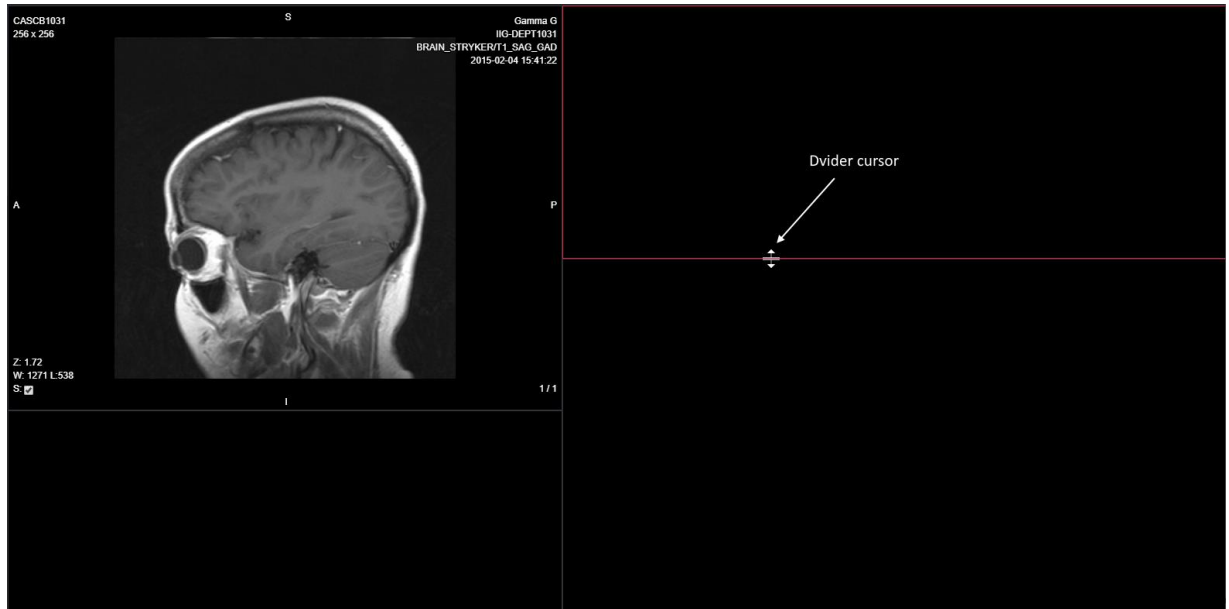
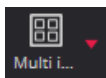


Figure 37. 2x2 layout view with manual viewports' size adjustment



NOTE! Double-click the left mouse button on the image for temporary viewing it on top of layout. Double-clicking the right mouse button on the enlarged image, returns to the previous layout.

NOTE! The layout selection is saved in browser's local storage. If local storage does not contain the layout value, the layout is displayed according the system settings.



Select the menu from **Multi image** button drop down list to open the selected number of series images in the active viewport. The viewport is automatically divided to required number of sections. Each section has the same size and shows the separate image, starting from the active image and following towards the end of the series.

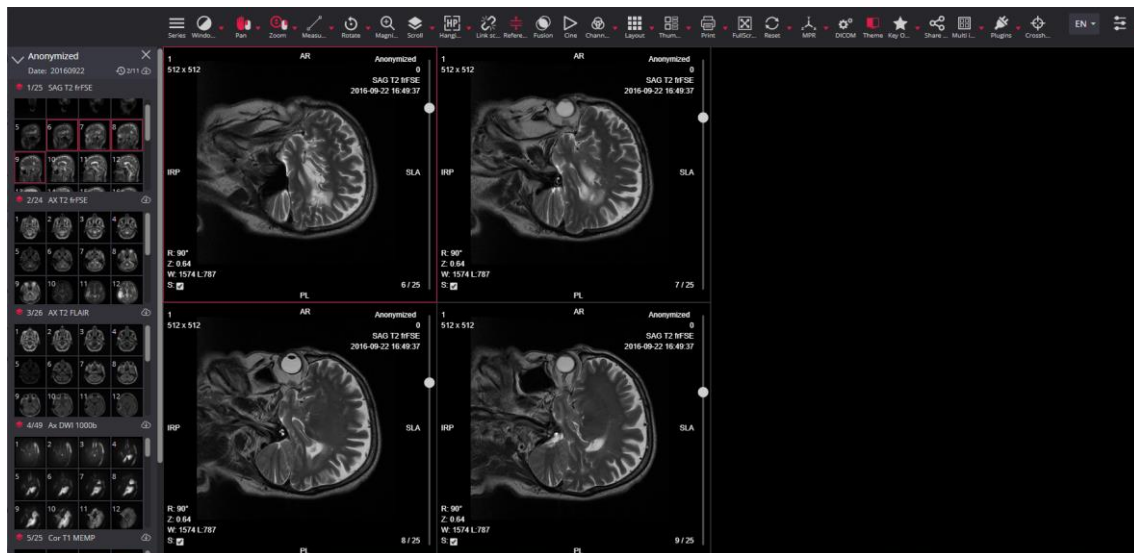


Figure 38. 2x2 multi image menu applied in the first viewport of 1x2 layout

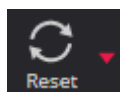


WARNING! You cannot change the size of particular image that is opened as one of multi images. If the viewport size is changed, the size of multi images is automatically adjusted.



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

Reset



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

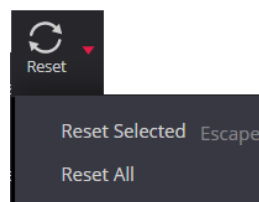


Figure 39. Reset button menu

MPR



NOTE! Multi-planar reconstruction (MPR) may be applied for CT, PT and MR series having more than 2 images in series.



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

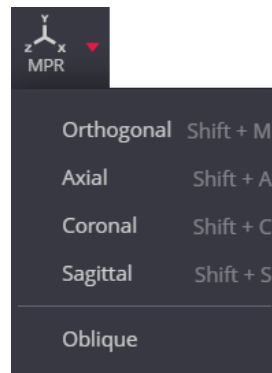


Figure 40. MPR button menu

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

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

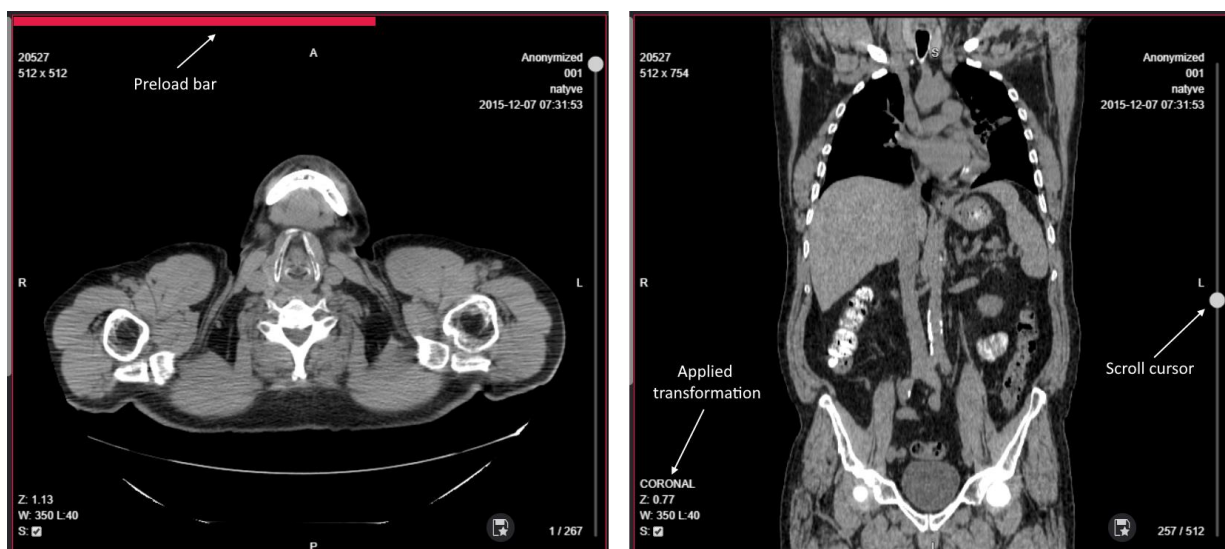


Figure 41. Steps of Coronal image reconstruction from axial series of images: axial series preload and calculated coronal view

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

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

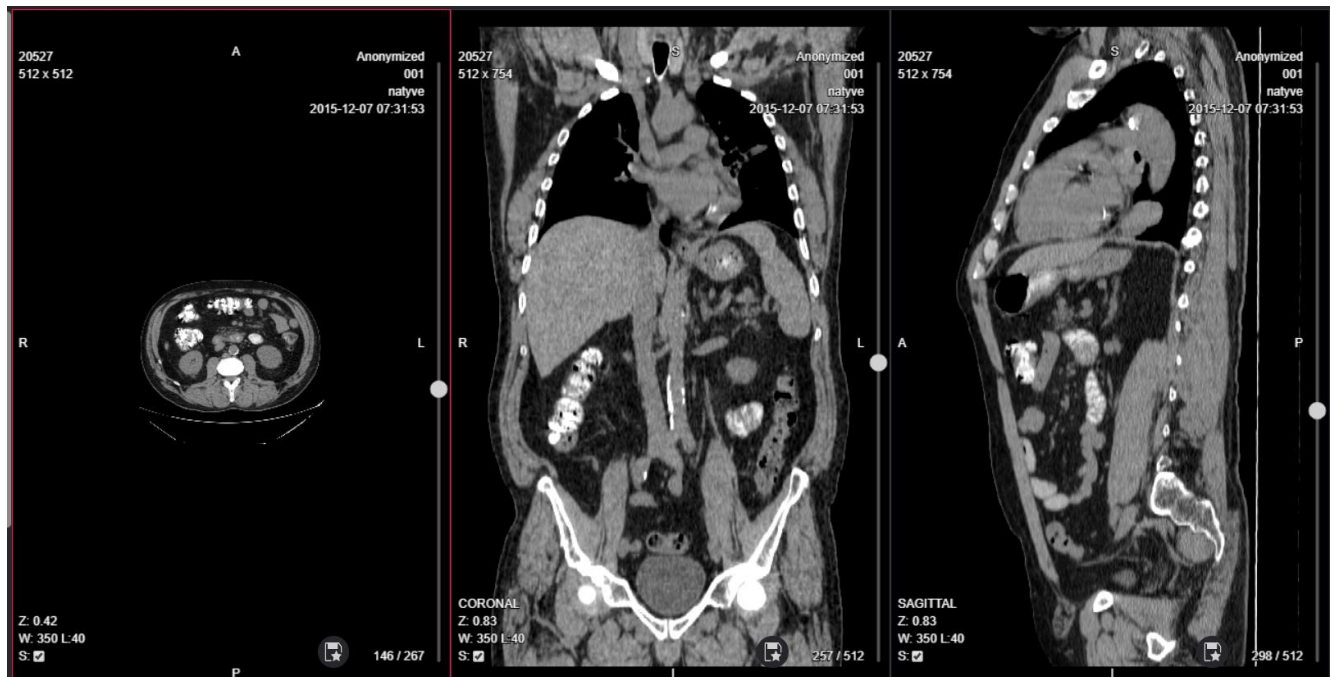


Figure 42. Orthogonal reconstruction from axial series of images



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

The **Oblique** menu launches 3D view reconstruction of series images.



NOTE! The 3D reconstruction module is an additional module and should be granted by license.

Images of one selected series are used for 3D reconstruction. To start the 3D reconstruction, open the series image in the selected viewport and click the **Oblique** menu. The system divides the active viewport into four sections, and start the series preload and reconstruction process:

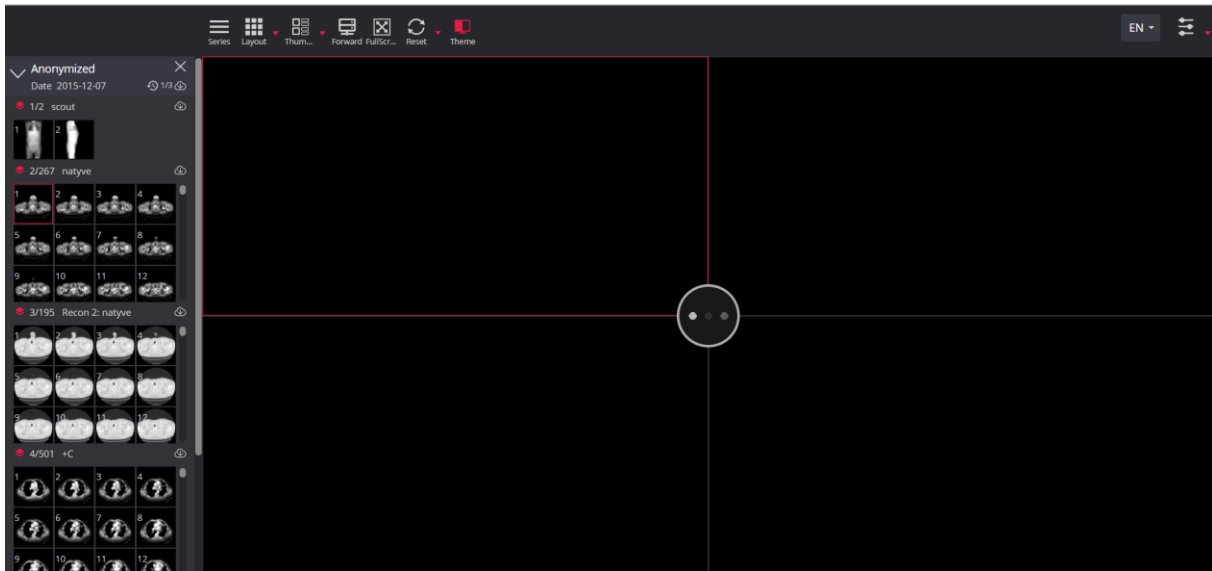


Figure 43. 3D reconstruction in progress

Once the reconstruction process is done, you will see the 3D and three orthogonal planes view in viewports' divisions:

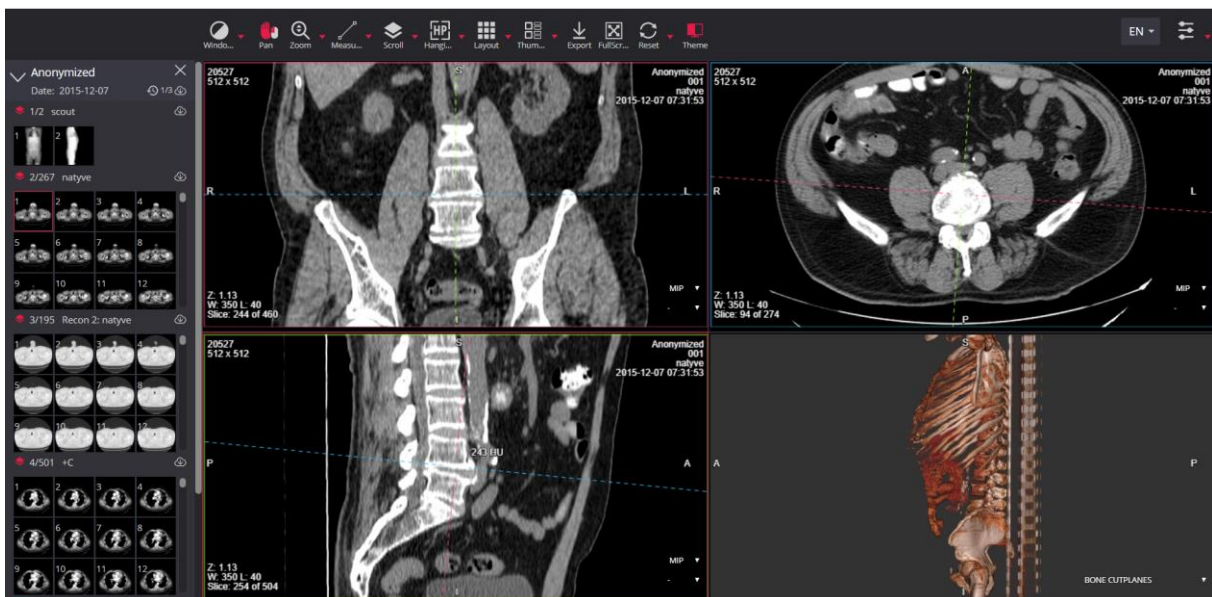


Figure 44. Oblique reconstruction

The value of the slab thickness in millimeters and the rendering mode are displayed in the bottom right corner of each orthogonal view. By default, the orthogonal planes display the image of single slice, and the slab thickness value is undefined: "-". To render the orthogonal view from several image slices, do the following:

- Specify the slab thickness from which you want to generate the image. You can do this in two ways:
 - Expand the slab thickness selection list by clicking the arrow on the right and select the slab thickness:

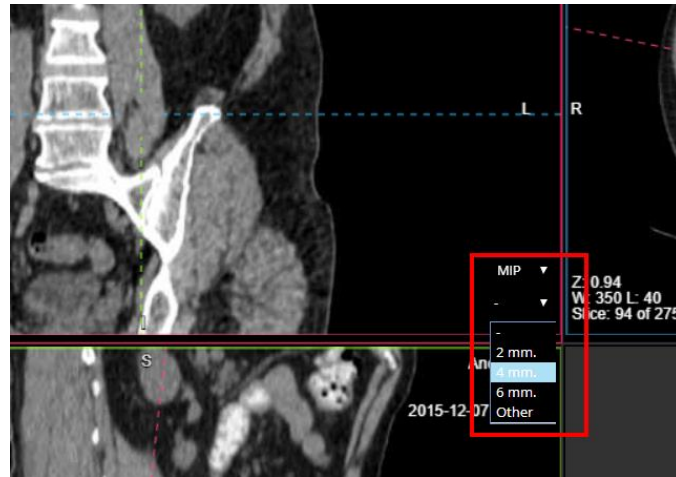


Figure 45. Slab thickness selection in oblique MPR view

- Or, If the required value is not in the list, select **Other** in drop-down list, enter the value in Slab Thickness entry window, and press **Apply** button:

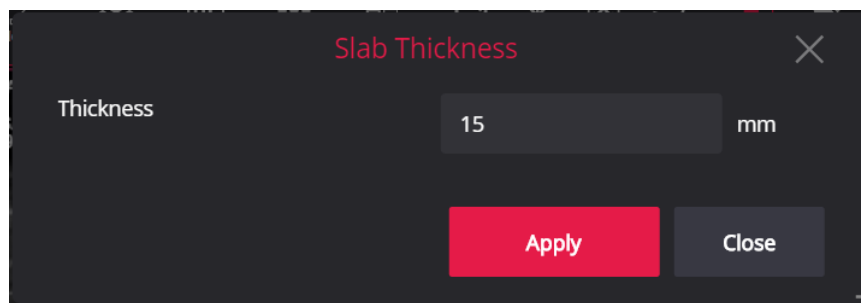


Figure 46. Slab thickness entry window

The entered slab thickness is displayed on image. All the images (slices) that get in the slab are used for rendering the displayed resulting image.

- Select the rendering method from drop-down list:



Figure 47. Rendering method selection in oblique MPR view.

The following rendering methods may be used:

- **MIP** (Maximum Intensity Projection): the pixel gray value in rendered image is the maximum value of all images (slices) of the slab;
- **AVG** (Average Intensity Projection): the pixel gray value in rendered image is the average value of all images (slices) of the slab;

- **MinIP** (Minimum Intensity Projection): the pixel gray value in rendered image is the minimum value of all images (slices) of the slab.
- The system automatically renders images of orthogonal planes according the specified slab thickness and rendering method values:



NOTE! The same slab thickness and rendering method values are applied in all orthogonal planes views.

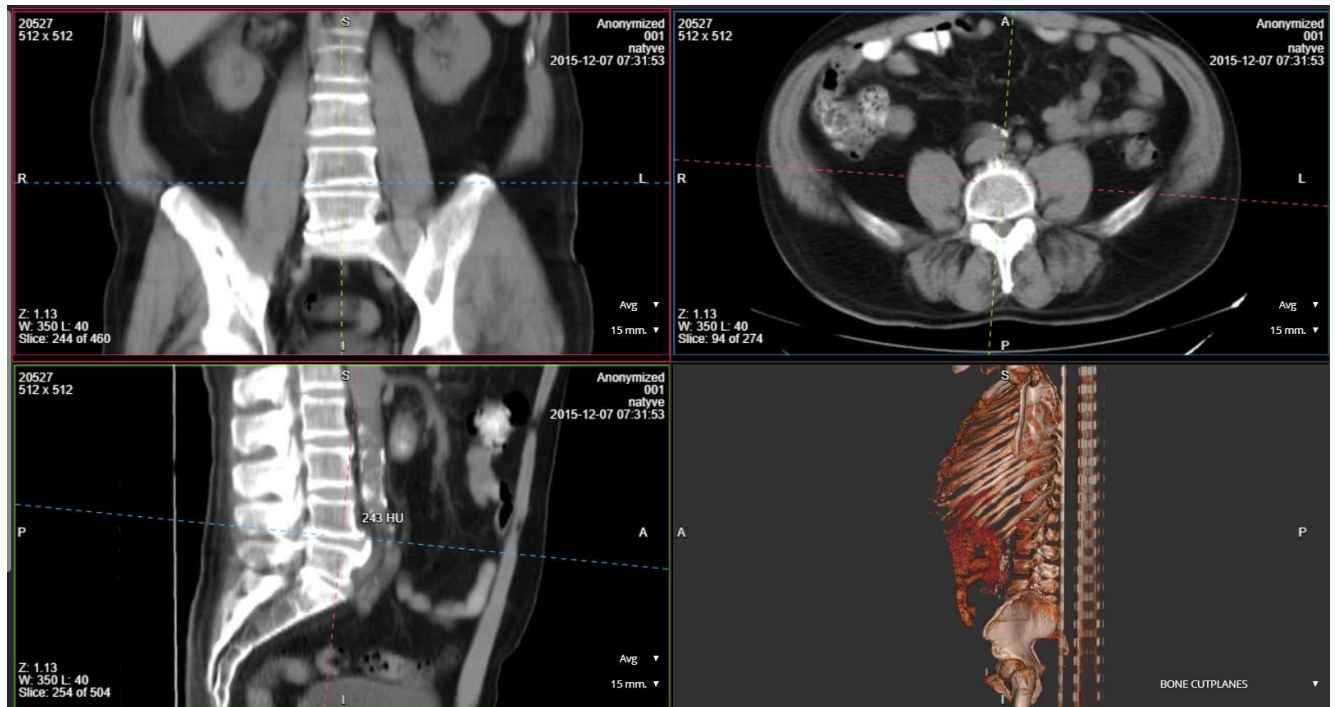


Figure 48. Oblique MPR view with adjusted slab thickness and rendering method



NOTE! To analyze images of the reconstructed series, use tools: **Windowing, Zoom, Pan, Scroll, Measure.** functions are available during MPR Oblique mode. The **Crosshair** function is automatically applied in orthogonal planes and may be rotated.

The 3D view and orthogonal planes views are displayed in separate divisions of the same viewport (as in multi-image case). You cannot manually adjust the size or position of oblique view divisions, but you can add additional viewports using Layout function and open the other studies or series images in them.

Reconstructed 3D studies comparison:

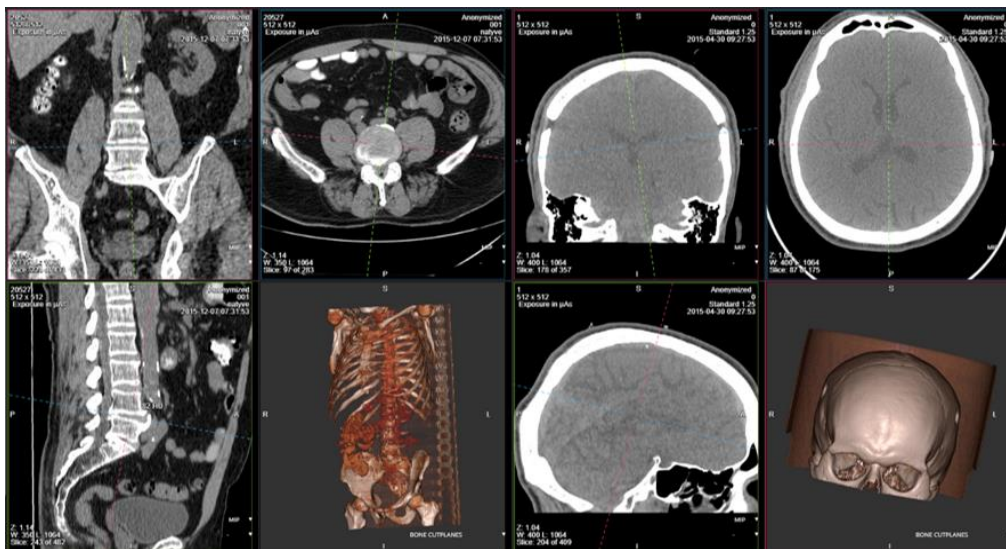


Figure 49. Comparison of two reconstructed 3D studies

Multi-Modality comparison:

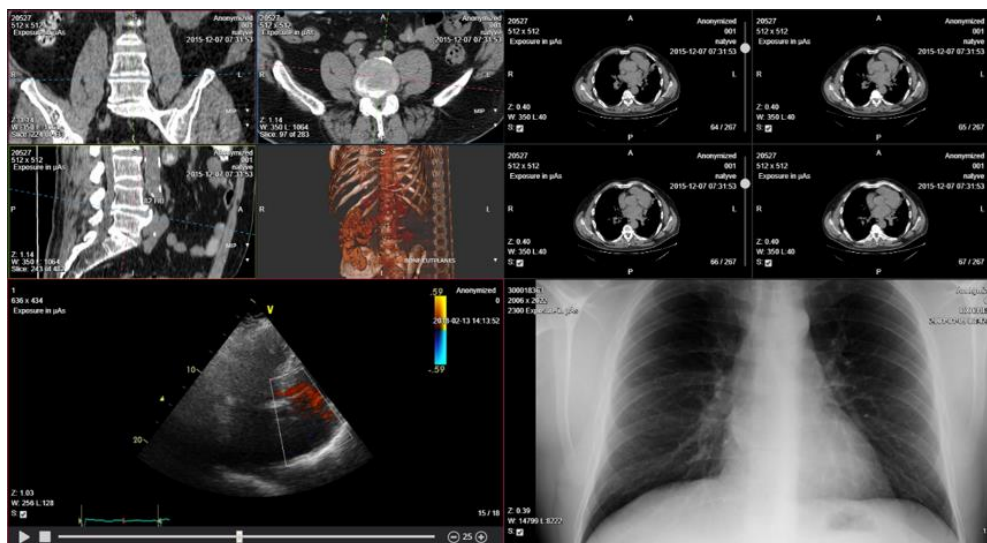


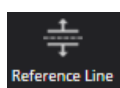
Figure 50. MPR 3D Oblique view and Multi-Modality comparison

Reference Line and Crosshair


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



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



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

- Prepare Layout for image comparison. Move into viewports the images that you want to compare.
- Activate viewport with the image you want to know the location of in regard to other images.
- Click the button **Reference Line**. The button highlights  that indicates activation of reference line function in all the opened viewports.
- Yellow lines, indicating the location of the active image, appear in the images that are in the planes intersecting with an active image plane:

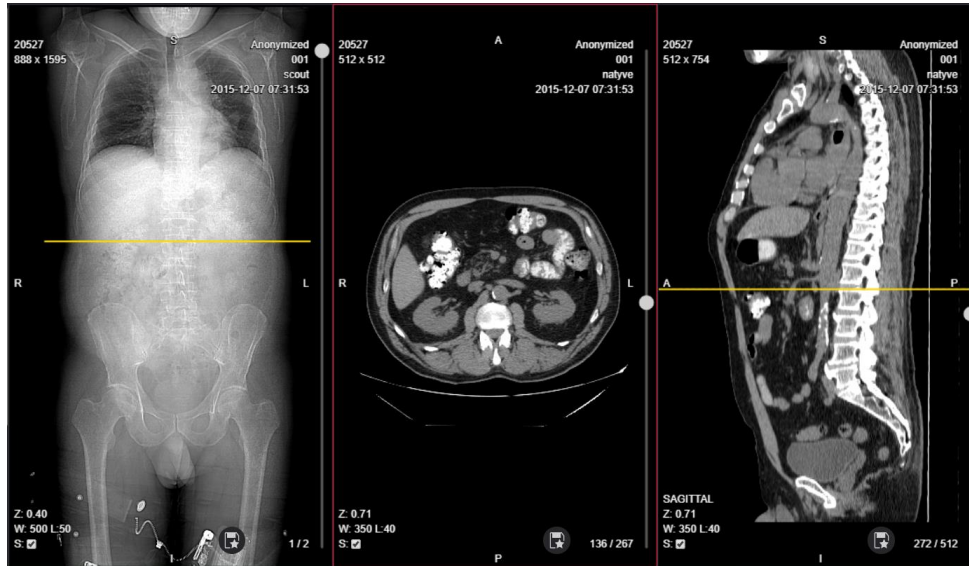


Figure 51. Image reference line in intersecting planes

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



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


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



Figure 52. Not orthogonal intersecting plane view



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

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

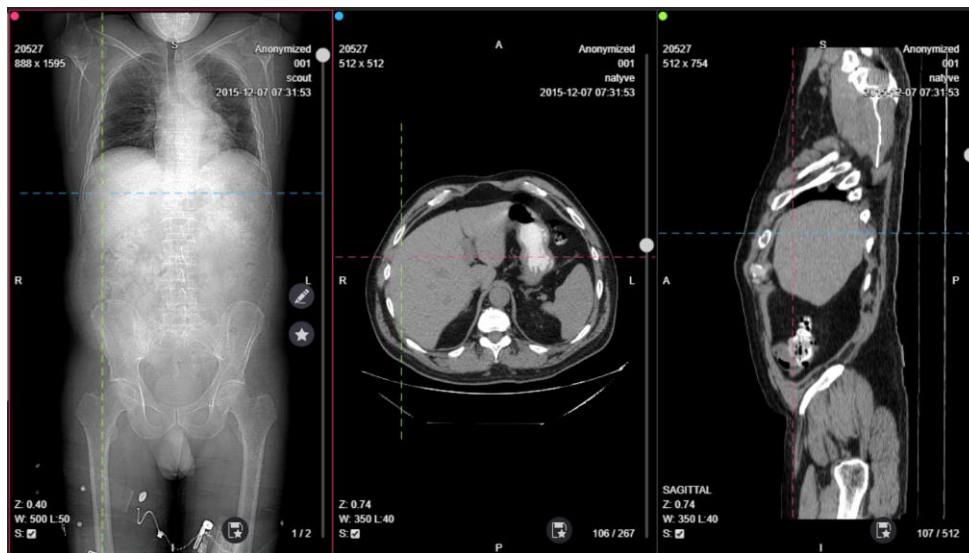


Figure 53. Crosshair tool

- Hold the mouse button pressed and drag the crosshair through the image to see the slices changing in intersecting planes.




NOTE! In Oblique views, you can rotate the crosshair by holding the mouse button pressed and dragging one of the lines.

Rotate



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

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

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

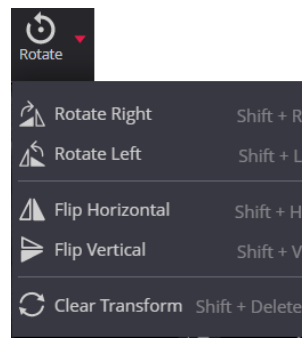


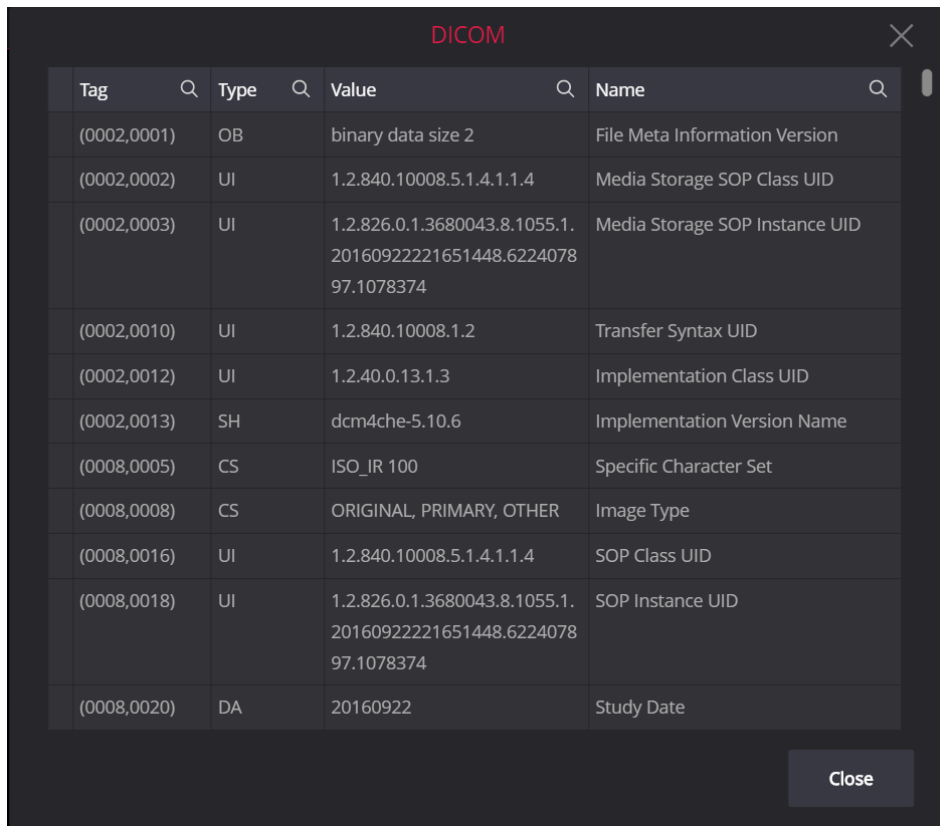
Figure 54. Rotate button menu

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

DICOM



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

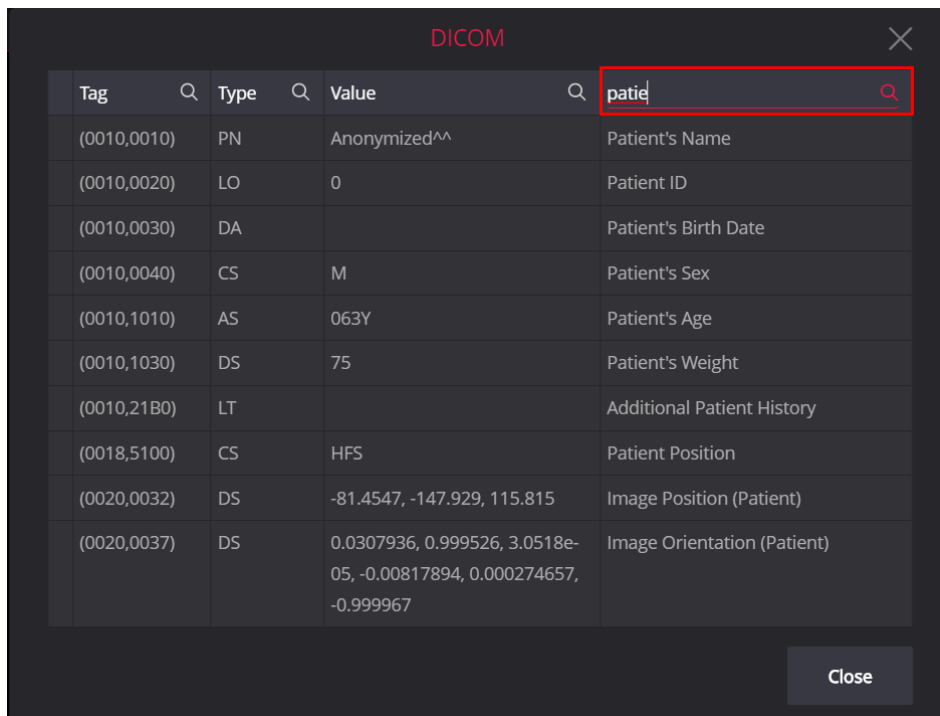


The image shows a window titled "DICOM" with a close button (X) in the top right corner. Below the title bar is a table with four columns: Tag, Type, Value, and Name. Each column has a magnifying glass icon next to it, indicating a search filter. The table contains 12 rows of data. At the bottom right of the window is a "Close" button.

Tag	Type	Value	Name
(0002,0001)	OB	binary data size 2	File Meta Information Version
(0002,0002)	UI	1.2.840.10008.5.1.4.1.1.4	Media Storage SOP Class UID
(0002,0003)	UI	1.2.826.0.1.3680043.8.1055.1.20160922221651448.622407897.1078374	Media Storage SOP Instance UID
(0002,0010)	UI	1.2.840.10008.1.2	Transfer Syntax UID
(0002,0012)	UI	1.2.40.0.13.1.3	Implementation Class UID
(0002,0013)	SH	dcm4che-5.10.6	Implementation Version Name
(0008,0005)	CS	ISO_IR 100	Specific Character Set
(0008,0008)	CS	ORIGINAL, PRIMARY, OTHER	Image Type
(0008,0016)	UI	1.2.840.10008.5.1.4.1.1.4	SOP Class UID
(0008,0018)	UI	1.2.826.0.1.3680043.8.1055.1.20160922221651448.622407897.1078374	SOP Instance UID
(0008,0020)	DA	20160922	Study Date

Figure 55. DICOM tag window

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



The image shows the same "DICOM" window as Figure 55, but with a search filter applied to the "Name" column. The filter text "patie" is entered in the search field, and the table is filtered to show only tags whose names contain "patie". The "Name" column search field is highlighted with a red box.

Tag	Type	Value	Name
(0010,0010)	PN	Anonymized^^	Patient's Name
(0010,0020)	LO	0	Patient ID
(0010,0030)	DA		Patient's Birth Date
(0010,0040)	CS	M	Patient's Sex
(0010,1010)	AS	063Y	Patient's Age
(0010,1030)	DS	75	Patient's Weight
(0010,21B0)	LT		Additional Patient History
(0018,5100)	CS	HFS	Patient Position
(0020,0032)	DS	-81.4547, -147.929, 115.815	Image Position (Patient)
(0020,0037)	DS	0.0307936, 0.999526, 3.0518e-05, -0.00817894, 0.000274657, -0.999967	Image Orientation (Patient)

Figure 56. Search according DICOM tag name in DICOM tag window

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

	(0038,0010)	LO	Urgent	Admission ID
-	(0040,0555)	SQ		Acquisition Context Sequence
	(0040,A040)	CS	CODE	Value Type
-	(0040,A043)	SQ		Concept Name Code Sequence
	(0008,0100)	SH	5.4.5-33-1	Code Value
	(0008,0102)	SH	SCPECG	Coding Scheme Designator
	(0008,0103)	SH	1.3	Coding Scheme Version
	(0008,0104)	LO	Electrode Placement	Code Meaning
+	(0040,A168)	SQ		Concept Code Sequence
+	(0040,B020)	SQ		Waveform Annotation Sequence

Figure 57. Expanding the SQ tags in DICOM tag window

Link scrolled series



Link scrolled series button is intended for making comparison on image slice location. Linking may be applied to currently viewed CT or MR series with more than one image in series. There are three types of this button: **Automatic**, **Manual** and **Disabled**.



Tap the icon once in order to enable the **Automatic** mode. The active series and all the other series with identical modality, frame of reference UID, and image orientation (patient) values and having multiple images are linked for scrolling. System displays automatic series link button in the top right corner of the viewport and switches scrolling on for all series by default.



Tap the icon twice in order to enable the **Manual** mode. The active series and all the other series with identical modality and having multiple images are linked for scrolling. System displays manual series link button in the top right corner of the viewport. The scrolling for the series with the identical image orientation (patient) is switched on by default.



Disabled mode disables synchronization modes.

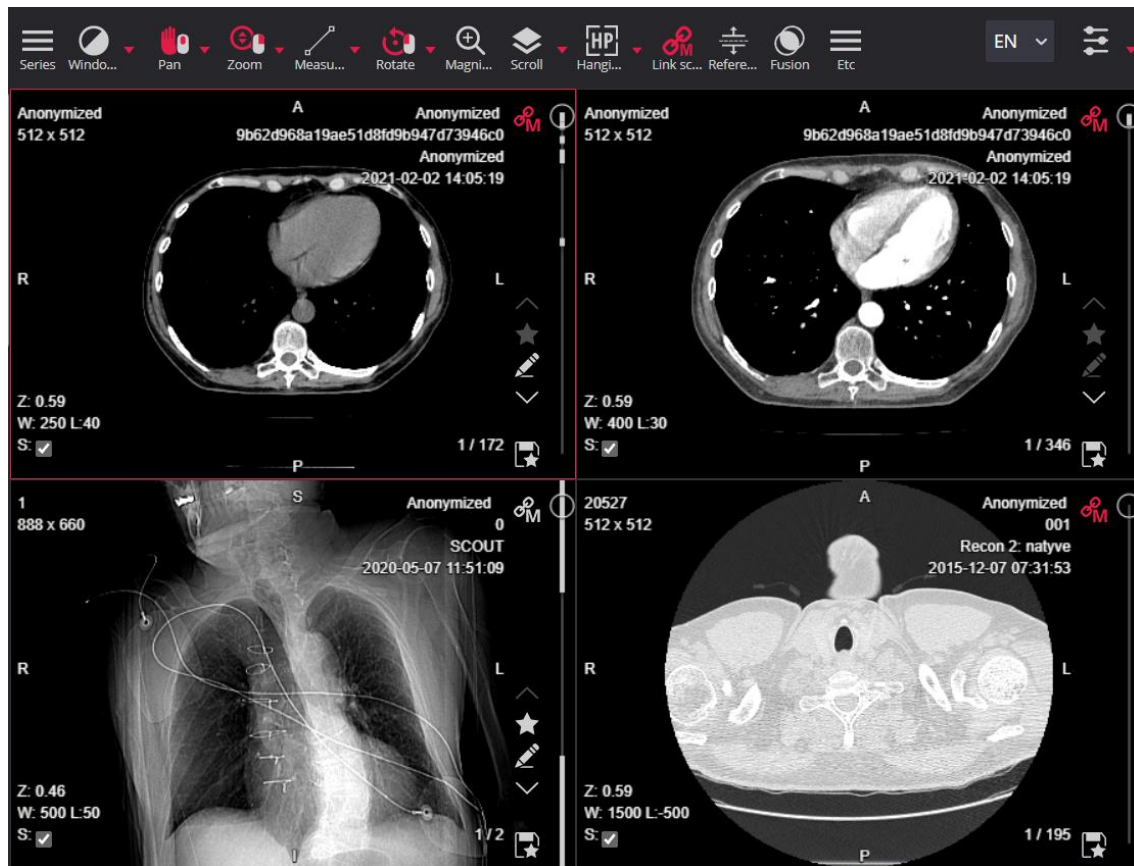


Figure 58. Manual link mode in Viewer with the disabled linked scrolling for one of the series

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

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



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

Tools for measuring, and annotation saving

Measuring images



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

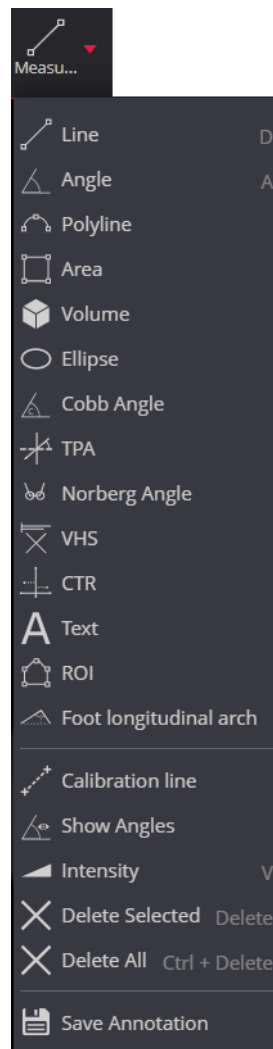




Figure 59. Measure button menu





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

- **Measure** button is not displayed for structure reports (SR).
- ECG studies has different set of Measure tools (see [Special views](#)).
- **Cobb Angle**, **TPA**, **Norberg Angle**, and **VHS** measuring is intended for veterinary usage. By default settings these tools are not shown in Measure menu for other than VET license types.

- **VTI** measuring is applicable and displayed only for US modality.

The top group of **Measure** menu contains the measuring tools. To use the measuring tool, assign mouse button to measure function: the mouse pictogram with assigned button is displayed . The highlighted tool pictogram indicates that tool is ready for measuring. You can change the active measuring tool by selecting the other tool in menu – the selected tool icon is displayed in Measure button: .



NOTE! The measuring tools is automatically deactivated after one measurement is finished: . Click the mouse button on **Measure** icon to use the same tool once more: .



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

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

Line



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

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

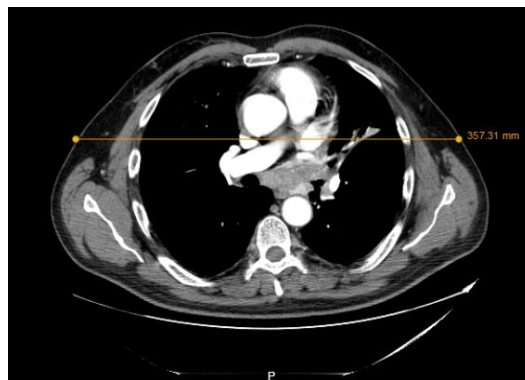
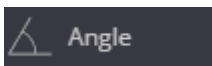


Figure 60. Distance measurement

Angle



Angle tool is used to measure the angle:

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

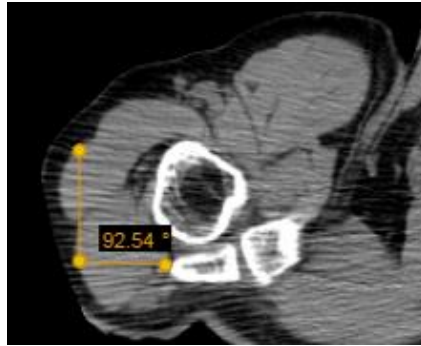


Figure 61. Angle measurement

Polyline



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

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

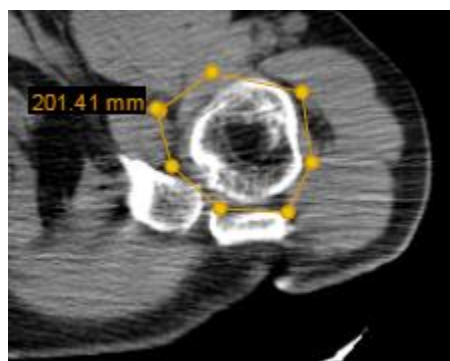


Figure 62. Perimeter measurement

Area



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

- select **Area** tool in **Measure** menu;
- mark points around the area of interest, as described in Polyline tool section;
- when you reach the last point, double click the selected mouse button twice - the area (in square millimeters) will be displayed:

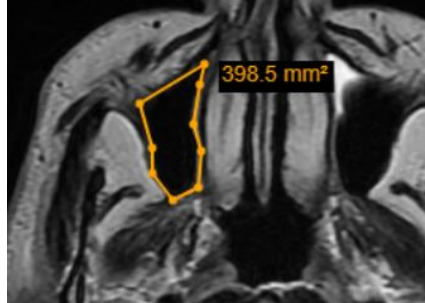


Figure 63. Area measurement

Volume



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

- select **Volume** tool in **Measure** menu;
- place the mouse cursor on the start point of the rotation axis, click and release the selected mouse button;
- then move the cursor to the second, third, fourth, etc. points and each time click the selected mouse button once and release it;
- when you reach the end point of the rotation axis, double click the selected mouse button – program fixes the rotation axis;
- continue marking points on the other side of rotation axis, clicking the selected mouse button once and releasing it at each point;
- when you reach the last point, double click the selected mouse button, and the perimeter (mm), area (mm²), and volume (mm³) of marked object are displayed.

The spatial pattern is created by rotation: the vertical line is the rotation axis, around which the left and the right curves are rotated half of the circle.

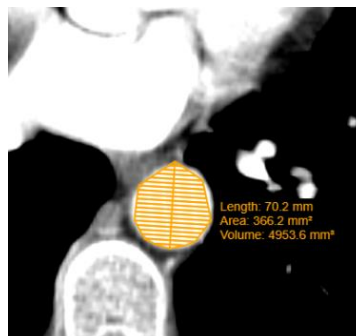


Figure 64. Volume measurement

Velocity Time Integral (VTI)



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

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

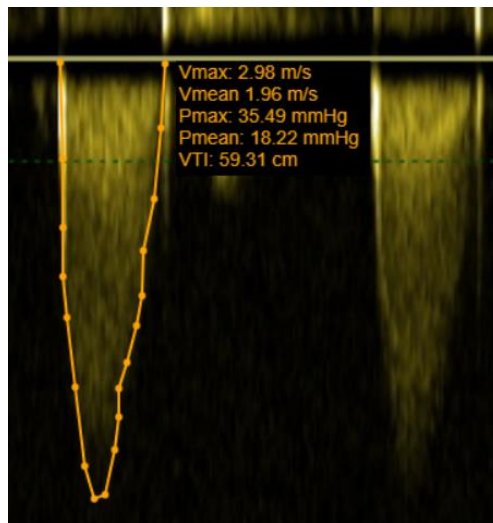
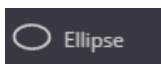


Figure 65. VTI measurement



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

Ellipse

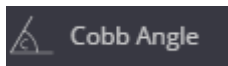


Ellipse is used to measure area, length, width, Min and Max brightness in HU units and STD measurement in cm.



Figure 66. Ellipse measurement

Cobb Angle



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

- select **Cobb angle** tool in **Measure** menu;
- click on image and draw two lines, parallel to the most tilted vertebrae,
- the Cobb angle (angle between lines) measure will appear:

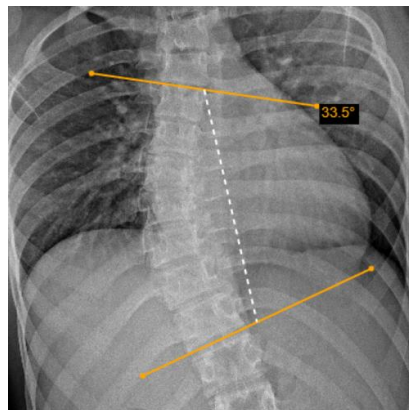


Figure 67. Cobb angle measurement

- you can drag lines and line points, or the whole measurement object by dragging the white dotted line.

Tibial Plateau Angle



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

To measure angle:

- select **TPA** tool in **Measure** menu;
- click on image and draw two lines: first, the tibia axis line (A) and then the tibial plateau slope line (B);

- through lines intersection point the program draws the line (dashed line C), that is perpendicular to the tibia axis line A, and displays the angle between the line C and tibial plateau slope line B:



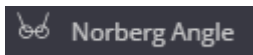
Figure 68. Tibial Plateau Angle (TPA) measurement

- you can drag the line points or the whole measurement object simultaneously.



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

Norberg Angle



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

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

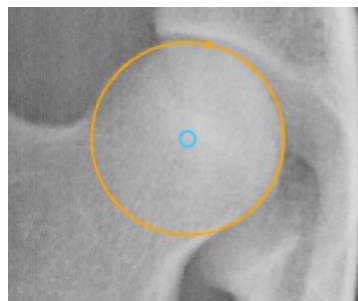


Figure 69. Norberg angle circle with the center in femoral head

- repeat the same process on other femoral head – draw the second circle of the Norberg angle;
- actions with other click the selected mouse button over the selected image point to place the first circle of the Norberg angle,
- the program joins the circle centers with a line and draws a line from each center at 105.0 degrees - the Norberg angle for good hip:

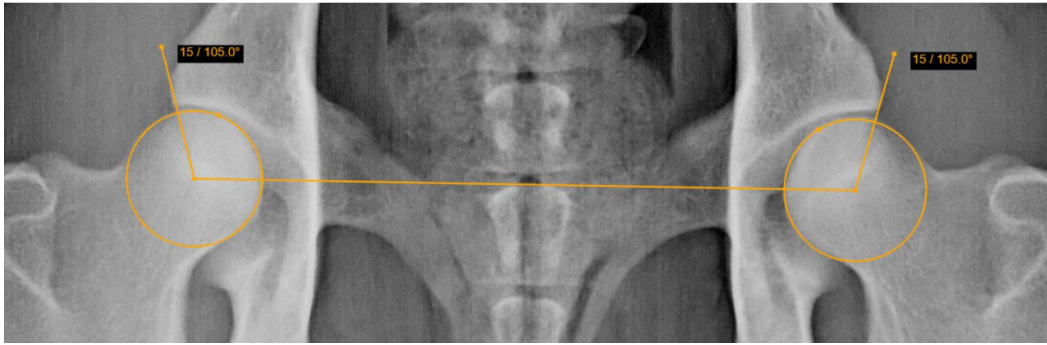


Figure 70. Norberg angle measurement

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



Figure 71. Adjusted Norberg angle measurement

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



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

Verbal Heart Scale



The **VHS** (Vertebral Heart Scale) button is used to measure heart size and provide an accurate assessment of true cardiac enlargement. To perform a VHS measurement:

- select **VHS** tool in **Measure** menu;
- place the mouse cursor and click the selected mouse button on the point from which you want to start measuring Long Axis (L),
- move the cursor to the end point of long axis and click the selected mouse button again - the Long Axis line will appear:

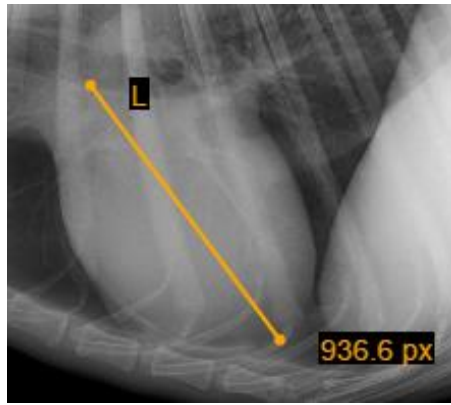


Figure 72. Long axis of VHS measurement

- place the mouse cursor and click the selected mouse button on the point from which you want to start measuring Short Axis (S);
- move the cursor to the end point of short axis and click the selected mouse button again – the Short Axis line will appear:

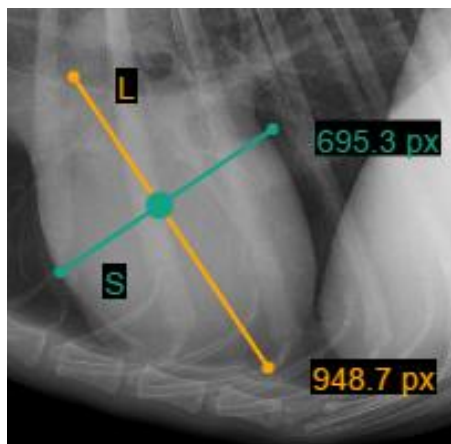


Figure 73. Short Axis of VHS measurement

- In order to define SL point, place your mouse cursor and click the left mouse button on the point from which you want to measure S and L lines - S and L lines will appear:

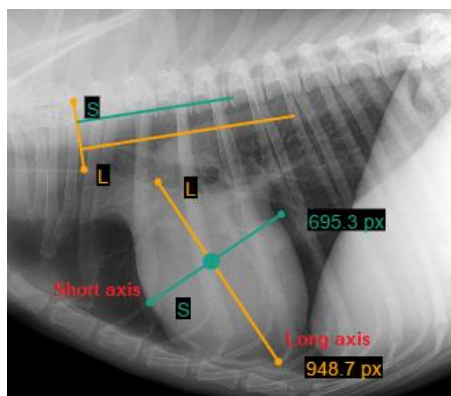


Figure 74. VHS measurement

You can rotate lines by dragging the ends of the line (dots) according to your needs. Click the left mouse button on the yellow dot (highlighted in red) and drag the line into a position where you want it to be. Middle vertical line (S and L line intersection point) allows to move S and L lines at the same time:

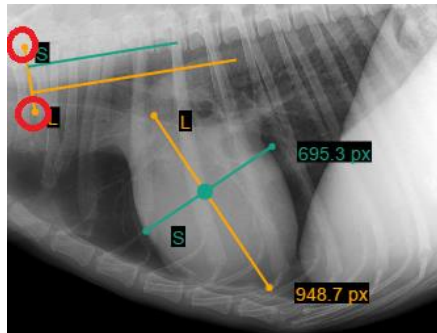


Figure 75. S and L lines rotation



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

Cardiothoracic ratio



The **CTR** (Cardiothoracic ratio) button is used to measure the ratio of maximal horizontal cardiac diameter to maximal horizontal thoracic diameter and aids in the detection of enlargement of the cardiac silhouette. To perform a CTR measurement:

- select **CTR** tool in **Measure** menu,
- place the mouse cursor and click the selected mouse button on the point at the inner border of rib in the widest place of thoracic cavity to start measuring thoracic diameter,
- move the cursor to the inner border of the same rib on the other side of thoracic cavity and click the selected mouse button again - the thoracic diameter line and measurement description with length of the line will appear while drawing:

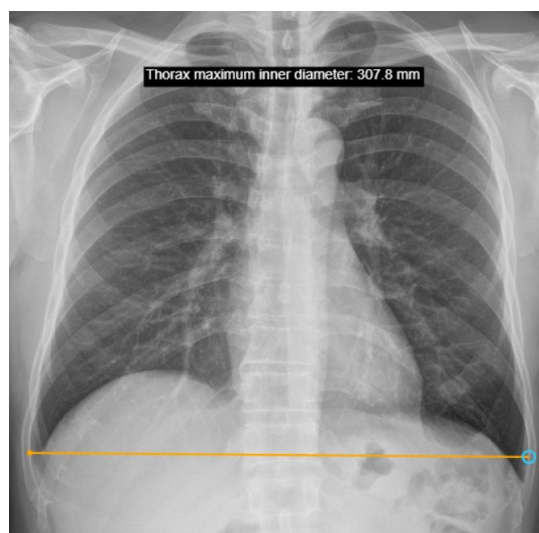


Figure 76. Drawing the maximal inner thoracic diameter line of CTR measurement

- place the mouse cursor and click the selected mouse button at the most left point of the cardiac shadow,
- move the cursor towards the right edge of the cardiac shadow - the cardiac shadow transverse line and processing note in measurement description will appear while drawing:

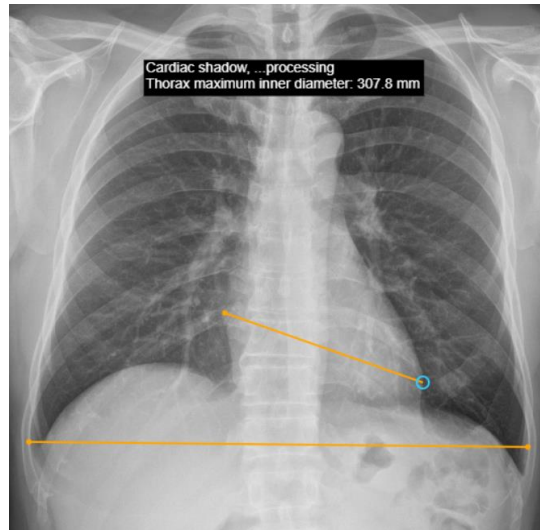


Figure 77. Drawing cardiac shadow transverse line of CTR measurement

- click the selected mouse button at the most right point of the cardiac shadow to finish the cardiac shadow transverse line to finish the CTR measurement,
- the system draws the midline of the thorax, and cardiac shadow diameter as two perpendiculars from the ends of the cardiac shadow transverse line to the midline. The cardiothoracic ratio is calculated as the percentage ratio of cardiac shadow diameter to maximal inner thoracic diameter, and displayed in the measurement description:

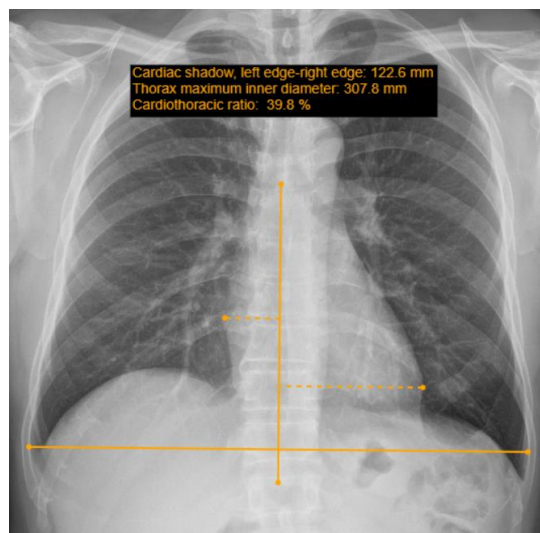
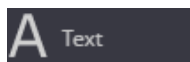


Figure 78. CTR measurement

You can adjust the measurement according to your needs by dragging the ends of the lines, or the whole thoracic diameter line, or the midline.

Text annotations



The **Text** tool is used to save the annotations of the measurements.

select **Text** tool in **Measure** menu;

to insert text box with arrow pointing to an object or image location, click the mouse button at the arrow end and drag the mouse to the place of text box;

to insert only text box, simply click at the desired image place;

an annotation text window with an arrow (if selected) will appear on the selected image place and the text entry field (white field) will appear at the bottom of the image;

enter the text in the text entry field and press **Enter** button;

the entered text will appear in the text box and the box will be resized accordingly.

yellow arrow can be pointed to any place of the image by dragging its end point.

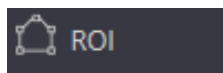
yellow-border text window can be placed with a drag and drop motion anywhere on the image, for example, next to the measurement you want to add text to;

double-click the text box for opening the text entry field and changing the entered text.



Figure 79. Text entry field

Region Of Interest



The **ROI** (Region Of Interest) is the same as area measurement only without measurements.

Foot longitudinal arch



The **Foot longitudinal arch** button is used to measure the angle and height of the foot medial longitudinal arch and aids in the detection of the longitudinal flatfoot. To perform a foot medial longitudinal arch measurement:

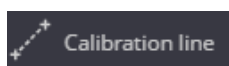
- open the foot radiograph image,
- select **Foot longitudinal arch** tool in **Measure** menu,
- place the mouse cursor on the point at the lower margin of calcaneus and click the selected mouse button,
- move the cursor to the lowest margin of cuneonavicular join and click the selected mouse button again – the line connecting the point and cursor will appear while moving the cursor,
- move the cursor to the lowest margin of the first metatarsal and click the selected mouse button to finish the foot medial longitudinal arch measurement - the line connecting the second and third points will appear,
- the system measures and displays arch angle on the image,
- the system draws the line through the angle's end points and measures the distance from the angle vertex to this line.



Figure 80. Foot medial longitudinal arch angle and height measurement

You can adjust the measurement according to your needs by dragging the vertices of the angle.

Calibration line



The **Calibration line** button is used to change the scale of measurement:

- select **Calibration line** tool in **Measure** menu;
- draw a line between two points at a known distance:

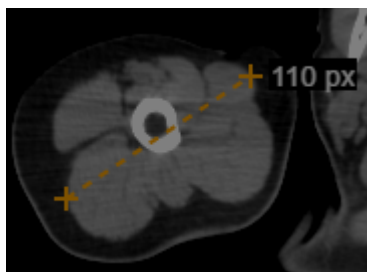


Figure 81. Calibration line

- indicate line length in millimeters in a pop-up window:

A dark-themed pop-up window titled "Calibration" with a close button (X) in the top right. Inside, there is a text input field with the placeholder "Enter new distance" and a unit label "mm". Below the input field are three buttons: "Use default", "Apply", and "Close".

Figure 82. Entering the Calibration line length

- once the data is entered, click **Apply** button— data will appear on the left bottom corner of the screen:

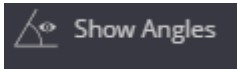
CAL: 1 mm. = 0.5 px

Figure 83. Calibration ratio result

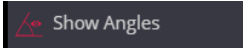


NOTE! Use **default** button resets to default calibration settings.

Show Angles



Use the **Show Angles** function to see the angles between any intersecting lines. To display the angle measurements:

- select **Show Angles** tool in **Measure** menu to activate the function: the highlighted icon indicates that function is activated ;
- if **Show Angles** function is active, the angles between intersecting lines are displayed:

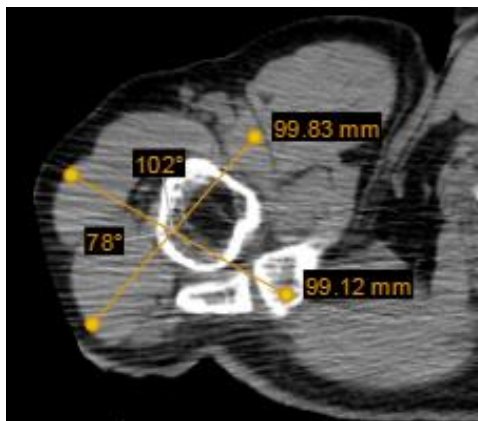
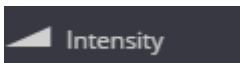


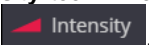
Figure 84. Angle measurement between intersecting lines

- Click the activated **Show Angles** menu once more to deactivate the function.

Intensity



The **Intensity** button is used to measure the density of a CT image. To measure the density:

- select **Intensity** tool in **Measure** menu to activate the function: the highlighted icon indicates that function is activated .
- move the mouse cursor over the point you want;
- the density of the point (in Hounsfield units, HU) and its coordinates are displayed at the bottom left corner:

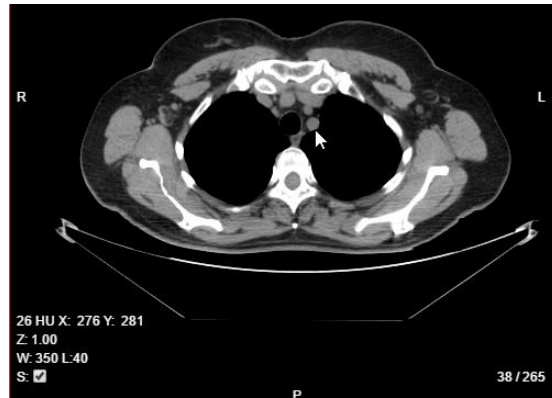


Figure 85. Intensity measurement

- click the activated **Intensity** menu once more to deactivate the function.

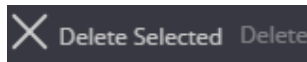
Delete measurements



The **Delete All** menu is used to remove all measurements of an active image at once.

To remove the measurements:

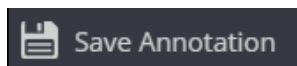
- select the image from which you want to remove all measurements;
- select **Delete All** in **Measure** menu – all measurements will be deleted from the active image.



The **Delete Selected** menu is used to remove only selected measurements:

- select the image from which you want to remove some measurement;
- select the measurements on the image;
- select **Delete Selected** in **Measure** menu – the selected measurement will be deleted.


Save Annotation





The **Save Annotation** menu allows to save the measurements for later usage and sharing. All measurements including text can be saved as annotation. See description how to save and to review saved annotations in section Annotations.

Copy and paste measurement

Copy and paste measurement actions allows you to have the same measurement displayed in the same place on the different images, and so compare and analyze the difference among the images. The copy and paste measurement actions sequence is as follows:

1. The Copy measurement button  is displayed in measurement's label, if the copy and paste actions are available for this measurement. The measurements, that may be copied and pasted, are listed in subsections of this section.

2. Clicking the Copy measurement button starts the copy and paste measurement actions sequence, and system performs the following actions:

- The copied measurement is highlighted;
- The Stop actions button  is displayed in label of the copied measurement instead of the Copy measurement button;
- The Paste measurement button  is displayed in all viewports with images, on which the measurement can be pasted.



WARNING! Only one Copy and paste measurement actions sequence is allowed at a time.

3. Clicking the Paste measurement button draws the copied measurement on the image:

- The pasted measurement is displayed exactly at the same place of the image where the copied measurement is displayed;
- The Stop actions button is displayed in the pasted measurement description.

4. You can locate the image for pasting the measurement in following ways:

- Locate the required image in the viewport with Paste measurement button by scrolling the series;
- Open image or series, and the system automatically displays the Paste measurement button in the viewport, if the measurement may be pasted on this image.

When done with pasting measurement, you can stop the copy and paste measurement actions sequence in following ways:

- By clicking the Stop actions button in the label of the pasted measurement;
- By starting a new copy and paste actions sequence;
- The system automatically stops the copy and paste measurement actions sequence when the last Paste measurement button is removed either because of changing Viewer layout, or because of opening another image in the viewport.



NOTE! Stopping the copy and paste measurement action sequence does not delete the pasted measurements.

Copy and paste ellipse

Copy and paste ellipse actions allows comparing the image statistics in different computer tomography series and images. The copied ellipse may be pasted on CT images, that have the same frame of reference identifier, patient orientation and scan direction.

The ellipse may be copied and pasted on CT images with fusions. In case of fused series, the PET image statistics is displayed in pasted ellipse label as well.

Annotations

Annotations can be created, saved, and viewed.



WARNING! Annotations functionality may be disabled in configuration.

To **create** and **save** annotation:

- Open the image that you want to annotate.
- Do the required manipulations, for example, change windowing, rotate, or other (see description of manipulation tools in section [Tools for image manipulation and analysis](#)).
- Add the measurements, text annotations (see description in section [Tools for measuring, and annotation saving](#)).
- Measuring images).
- Save actual presentation state either with **Save Annotation** menu, or with **Quick save KO, PR** button, as described below:
 - select **Save Annotation** in **Measure** menu - save presentation state window will appear:

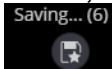

Figure 86. Save presentation state window

Enter the required description, creator name, if desired, and click **Save** button.

- Click the **Quick save KO, PR** button  at the bottom right side of the image. The current date and time are used as description of presentation state.



NOTE! Please notice, that **Quick save KO, PR** button initiates double action: saves the presentation state and saves key objects.

NOTE! To prevent the repeated clicks, system deactivates the **Quick save KO, PR** button and displays the notification about ongoing saving process on top of the button . Saving success notification  is displayed on successful saving process completion. The number in parentheses is the serial number of the image in the series

- System saves annotation with the following information:
 - the date and time of annotation saving;
 - the annotation description, creator name, if entered;
 - any drawn measurements;
 - written text.



WARNING! Annotation saving is implemented according to DICOM standard. The function is available only if the used study storage provides DICOM saving functionality.

NOTE! Several annotations may be saved for the same image. Each annotation is saved as separate series of PR modality.

Once the annotation has been saved, the annotation icon (pencil) will appear on image thumbnail:



Figure 87. Annotation icon on image thumbnail

To **view** saved annotation:

- drag and drop the annotated image (the one that has the annotation icon) to the viewport, or use quick access controls (see section [Viewport toolbar](#)). - the active annotation button is displayed on the image in quick access controls group:

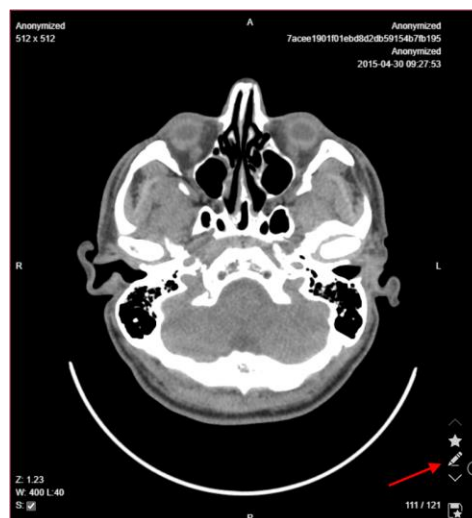


Figure 88. Annotation button on image

- move your mouse cursor to the **Annotation** button and click it. If there are several annotations, you can choose which one to review from the list. Hold the cursor over the menu item to see the tooltip with annotation description, creator name and saving date and time:

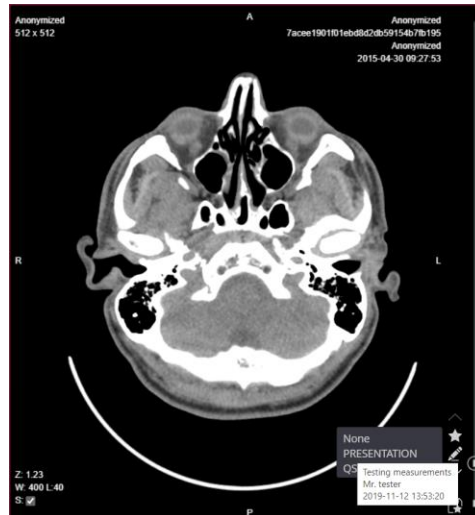


Figure 89. List of annotations and annotation description



NOTE! QS_PRESENTATION indicates annotations saved with **Quick Save KO, PR** button. PRESENTATION indicates annotations saved with **Save Annotation** menu.

- click on the annotation you have chosen to view and the saved annotation will appear on the screen with an information that has been saved previously:

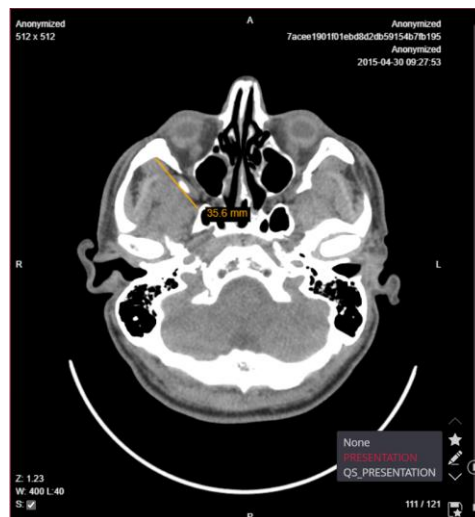


Figure 90. View annotation.



WARNING! Saved Annotations can only be viewed.



NOTE! Currently viewed annotation is highlighted. Select option **None** to return to the image.

Key Objects



Key Objects concept is used in order to mark most interesting instances and save them for later review. Marked instances as Key Objects are stored in DICOM file of KO modality. Instances from different series can be stored in one Key Object selection. All instances marked as key objects are annotated with small star symbol.



WARNING! Key objects functionality may be disabled in configuration.

To **create** key object:

- Open the image that you want to include in key object.
- Expand the **Key objects** menu and select “**Mark image as KO**” from the list.
- The image marking as key object window will appear:

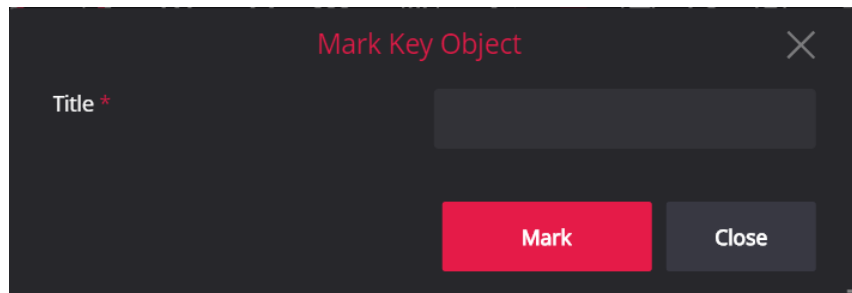


Figure 91. Mark image as key object window

- Enter the key object title or select the one from dropdown list of not saved key objects in the **Title** field, and click the **Mark** button.
- System adds the active image into selected key object. The unsaved key object (star filled with grey background) button is displayed on the active image in viewport and thumbnail. The key object title is displayed in extendable menu of **Key Objects** tool.

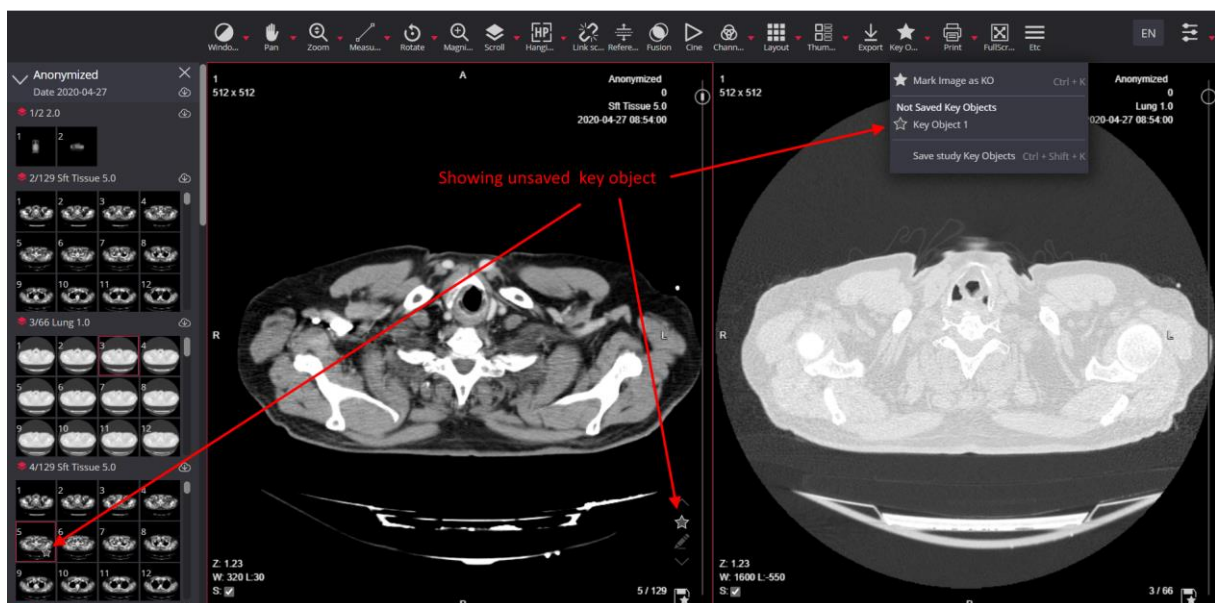


Figure 92. Not saved Key Object



NOTE! You can have several unsaved key objects at a time.

To **save** created (marked) key object:

- Expand the **Key objects** menu and select “**Save study key objects**” from the list. The key object saving window with all unsaved key objects listed will appear:

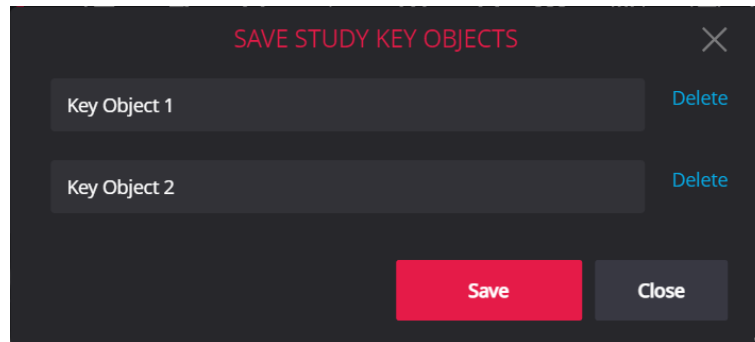


Figure 93. Save study key object window

- You can do the following actions in the window:
 - change the name of Key object by clicking the entry field and editing text in it,
 - delete the not needed Key object clicking **Delete** button on the right of the key object title,
 - After making the desired changes, save the Key objects by clicking the **Save** button.
- System saves the key objects with all the marked images in it. The saved key object icon (star filled with white background) is displayed on the image in viewport and thumbnail. The key object title is displayed in Saved key objects group of extendable **Key Objects** button's menu.

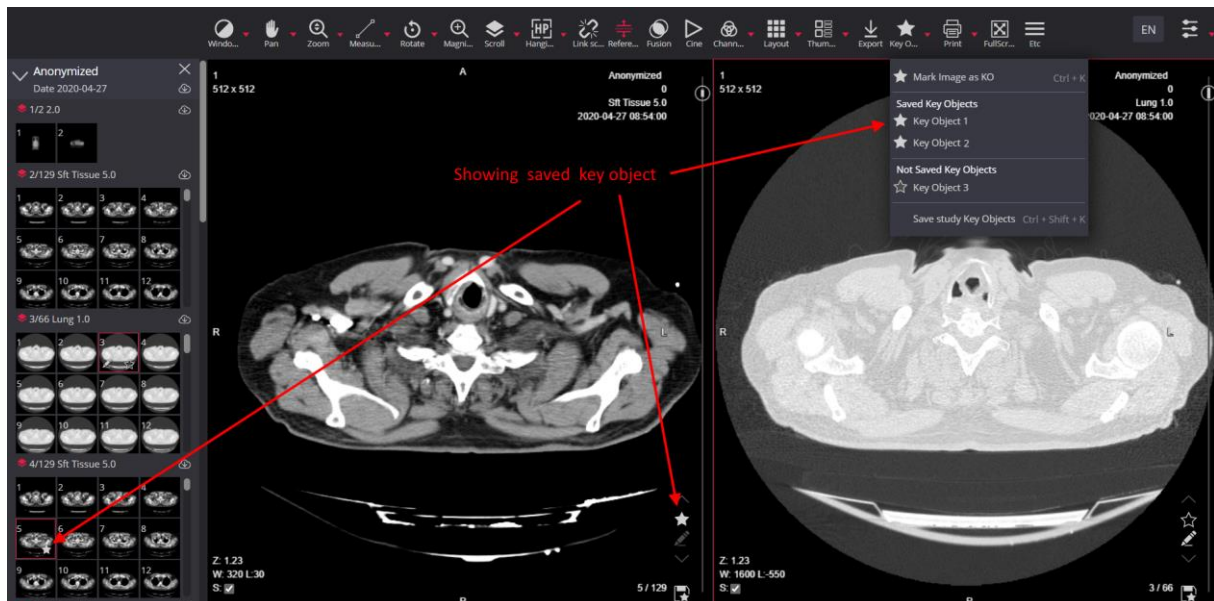


Figure 94. Saved Key Object



WARNING! Key object saving is implemented according to DICOM standard. The function is available only if the used study storage provides DICOM saving functionality.



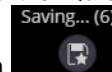
You can use **Quick save KO, PR** button at the bottom right of the image to save the current image as key object. In this case, the current date and time are used as title of key object.



NOTE! Please notice, that **Quick save KO, PR** button initiates double action: saves the presentation state and saves key objects.

NOTE! Quick save can be used only one time per image and saves key object only if the image is not included in any other saved or unsaved key object.

NOTE! To prevent the repeated clicks, system deactivates the **Quick save KO, PR** button and



displays the notification about ongoing saving process on top of the button . Saving success notification



is displayed on successful saving process completion. The number in parentheses is the serial number of the image in the series.

To **view** not saved key object or saved key object:

- Open the key object's image in viewport. You can do this either by selecting the title of the Key object from the drop-down menu of the **Key Objects** tool, or by dragging a key object image, that is marked with star icon, from thumbnail bar to viewport, or with quick access controls (see section [Viewport toolbar](#)).



NOTE! Use the drop-down menu of the **Key Objects** tool, to see the key object's images from several series of the study. If Key object, that contains images from several series, is opened from menu, each series is opened in a separate viewport, starting from the first viewport. Key object filter is automatically activated in each viewport. If the number of series exceeds the maximum possible number of viewports, the warning is displayed.



WARNING! If Key object image is opened from thumbnail or with quick access controls, Key object filter is not activated. To activate the filter, expand the key objects filter menu by clicking the key object icon on the right of the image, and click the Key object title in filter menu.

- Scroll through the images of the activated key object with mouse as described in section [Scroll](#).



NOTE! The scroll is performed only in one series.

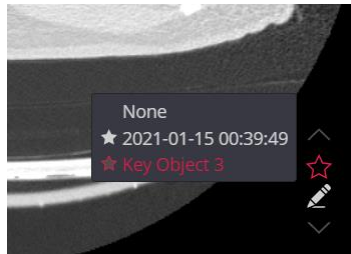


Figure 95. Selection of Key object filter in context menu



NOTE! Key object filter displays all key objects that contain the active image. The star with transparent background indicates that image is included in both, saved and unsaved, key objects. If filter is applied, the title of active key object and the star icon are highlighted.

Segmentation



Segmentation provides the tools for marking the regions of interest in medical images, saving these regions as segment, and share with other interested parties, or use in artificial intelligence modules. The system also provides the user possibility to measure and to copy to the clipboard the statistics of the segments.

To start working with segmentation tools, expand the **Segmentation** menu in the main menu group, and select the tool from the list:

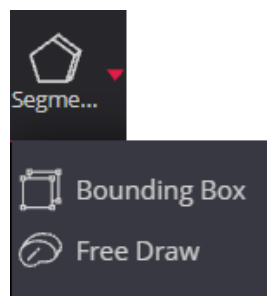


Figure 96. Segmentation button menu



WARNING! Any or all segmentation tools may be disabled in configuration, or by user rights.



NOTE! The system automatically starts orthogonal multi-planar reconstruction, if the Bounding Box segmentation is selected for CT or MR series with multiple images. The layout may be changed, or the reconstructed series may be displayed on the top of the previously viewed series.

System opens the Segmentation window, and activates the tab of the selected segmentation tool:

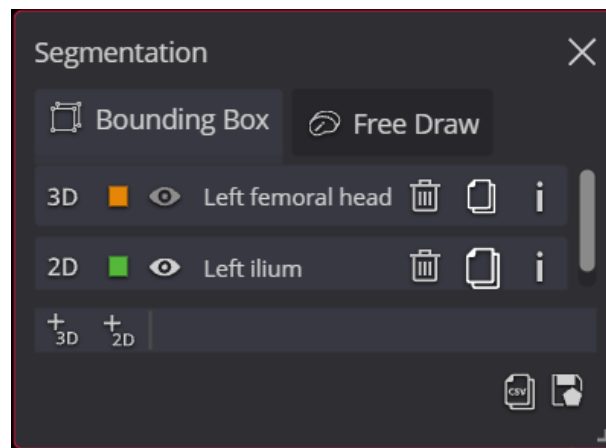


Figure 97. Segmentation window



NOTE! You can change the segmentation tool by selecting the tool's tab directly in the Segmentation window.

NOTE! The sections [Bounding Box](#), and [Free Draw](#) describe how to perform the segmentation, or edit the created segments using a particular segmentation tool. How to view or measure the segments, see in section [Viewing and measuring segments](#).

Bounding Box



The **Bounding Box** tool allows marking the region of interest by drawing the bounding rectangular around it. The 2D bounding box option may be used to mark the region on one image. The 3D bounding box option may be used to mark the 3D region in series of images.




WARNING! Performing the Bounding Box segmentation, or viewing Bounding Box segments may be disabled by user rights.



NOTE! The bounding box segment consists of only one 2D rectangle region or one 3D cube region.

To **create** a new 2D bounding box segment:

- Open the image, in which you are going to mark the region.
- Open the Segmentation window and select the Bounding Box tool tab in it.
- Press the new 2D segment icon , which is displayed on the left of the tools bar at the bottom of the Segmentation dialog. The icon is highlighted and drawing is activated.
- Draw the 2D bounding box:
 - place the mouse cursor in the center of the region of interest,

- click the left mouse button,
 - move the mouse cursor to the corner of the region of interest,
 - the system draws the rectangle that expands from the center to the cursor position,
 - when the rectangle has the required size, click the left mouse button to finish the drawing.
- The system adds the 2D bounding box segment record in the Bounding Box tab of the Segmentation dialog. The default name and color, that was assigned to the segment, are displayed in the list and on the image:

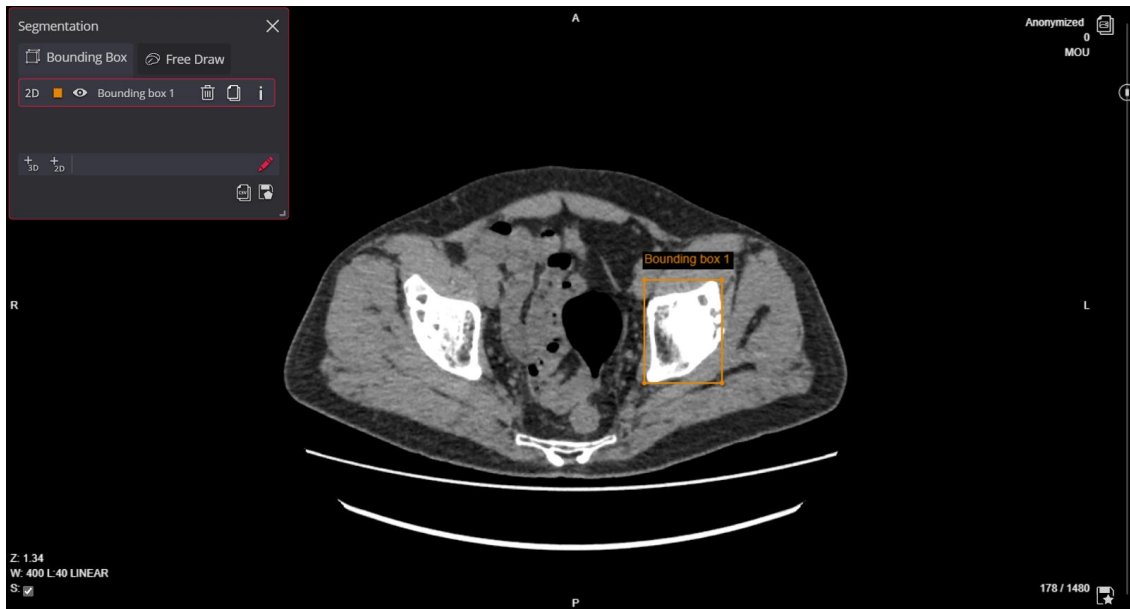



Figure 98. New 2D bounding box segment created



modality.

WARNING! 2D bounding box segmentation may be done only on images of CT, MR, PT, or MG



NOTE! The system selects created 2D bounding box segment record in the list and activates its editing. Click the highlighted edit tool  to deactivate editing, if adjustment of the segment region is not needed.

To mark the volumetric region using 3D bounding box tool, it is recommended to have the intersecting original or reconstructed series displayed in the viewports of the Viewer window for locating the region of interest:

- The system automatically starts orthogonal multi-planar reconstruction, if the Bounding Box tool is selected in Segmentation menu for CT or MR series with multiple images.
- Select the orthogonal reconstructions from MPR tool menu, if the Segmentation window is already opened.
- Adjust Viewer layout and open the intersecting series in the viewports.
- Use reference line or crosshair tools to locate the region of interest in the intersecting series.




Figure 99. Left femoral head located in reconstructed series using crosshair tool



WARNING! 3D bounding box segmentation may be done only on images of CT, MR, or PT with more than two images in series.

To **create** a new 3D bounding box segment:

- Open the Segmentation dialog and select the Bounding Box tool tab in it.
- Open the image, in which you are going to mark the region. Scroll images in the series, or use crosshair to open the image, that is located in the middle of the region of interest, because the system expands the box to both sides from the current image.
- Press the new 3D segment icon , which is displayed on the left of the tools bar at the bottom of the Segmentation window. The icon is highlighted and drawing is activated.
- Draw the 3D bounding box:
 - select the image in original or reconstructed series,
 - place the mouse cursor in the center of the region of interest,
 - click the left mouse button,
 - move the mouse cursor to the corner of the region of interest,
 - the system draws the rectangle that expands from the center to the cursor position,
 - when the rectangle has the required size, click the left mouse button to finish the drawing.



NOTE! The saved 3D bounding box refers to the images of the original series on which the 3D Bounding Box segment is created. If 3D bounding box is created in reconstructed series, the original series, that was used to create the reconstructed series, is referred.

- The system creates 3D bounding box:

- The 3D bounding box segment record is placed in the Bounding Box tab of the Segmentation dialog
- The system creates the 3D right-angle box based on the rectangle, that was drawn by the user. The 3D box is expanded in perpendicular direction to both sides from the current image, and the width of the box is calculated by dividing the perimeter of the rectangle by 4.
- The 3D bounding box and image plane intersection contours are displayed on all the images in original or reconstructed series, that intersects the 3D bounding box:

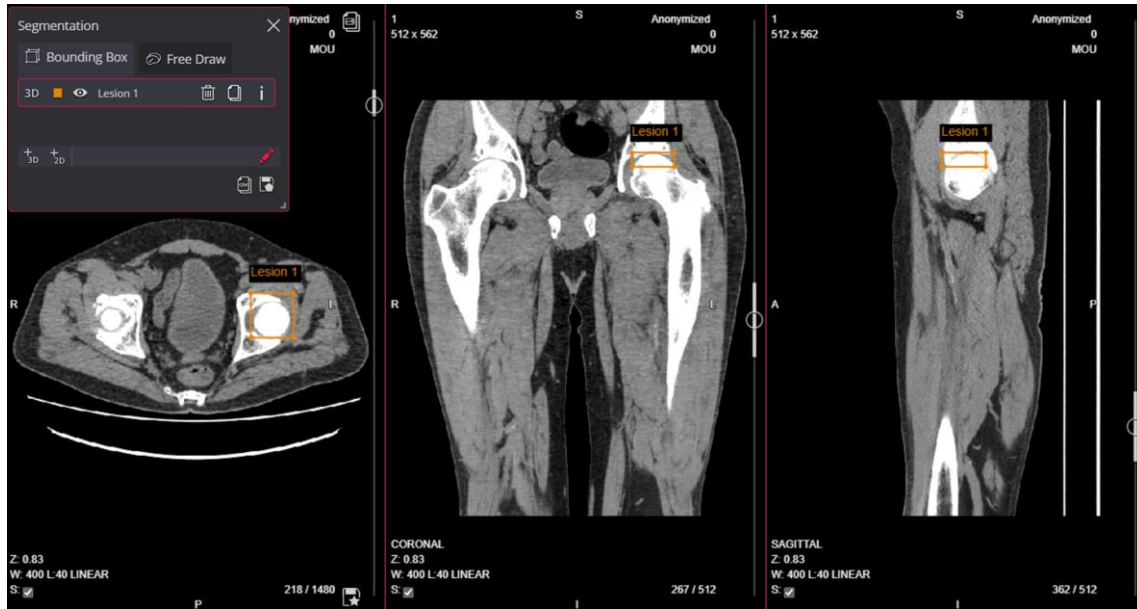




Figure 100. New 3D bounding box segment created



NOTE! The system selects created 3D bounding box segment and activates its editing. Click the highlighted edit tool  to deactivate editing, if adjustment of the segmented region is not needed.

To **create** a new bounding box as a copy of existing 2D bounding box, or 3D bounding box:

- Open the Segmentation dialog and select the Bounding Box tool tab in it.
- Find in the list the 2D or 3D bounding box, that you want to duplicate.
- Press the Duplicate icon , which is displayed on the right side of the record.
- The system creates the copy of the selected 2D or 3D bounding box, assigns the label and the color to it, and displays contours on image. The new bounding box segment record is added to the Bounding Box tab of the Segmentation window:

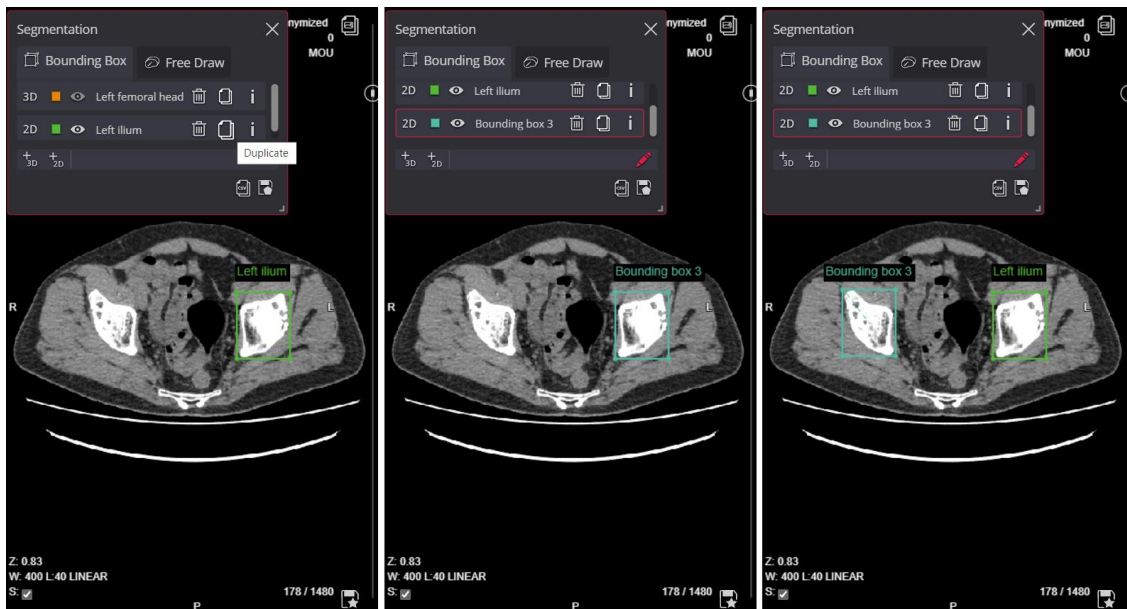



Figure 101. Left ilium segmentation duplicated and created Bounding box 3 copy moved





NOTE! The system selects created bounding box segment record in the list and activates its editing.


Edit the copied segment, if needed, or click the highlighted edit tool  to deactivate editing.

To **work with existing** 2D bounding box segment, or 3D bounding box segment, activate it by clicking on the record:

- the active record is highlighted with red border,
- and the tools for editing the bounding box are displayed in the tools bar at the bottom of the Segmentation window.

You can change the segment name and color:

- To change the segment name, click on the name in segment record, and enter a new name in the activated entry field: .
- To change the segment color, click on the color box  in segment record, and select the other color in the opened Choose Color dialog.

You can change the bounding box size and rotation for the selected segment. Press the edit segment icon  in the tools bar at the bottom of the Segmentation window. The icon is highlighted and the bounding box editing is activated:



NOTE! 3D bounding box contours are displayed on all intersecting original and reconstructed images. Scroll the images in the series, view the contours, and select the image for 3D bounding box adjustment.

- To move the bounding box, hover the mouse cursor over the center of the rectangle until the center of the figure is marked, then press the left mouse button, drag the box to the desired position, and release the mouse button, when done:

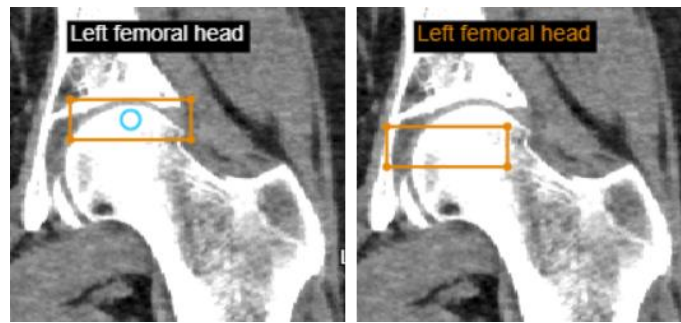


Figure 102. The bounding box moved to the center of the femoral head

- To rotate the bounding box, hover the mouse cursor over the corner of the rectangle until the corner is marked, then press the ALT key and the left mouse button, and, holding the keys pressed, drag the corner. Release the mouse button, when the box is rotated to the desired position:

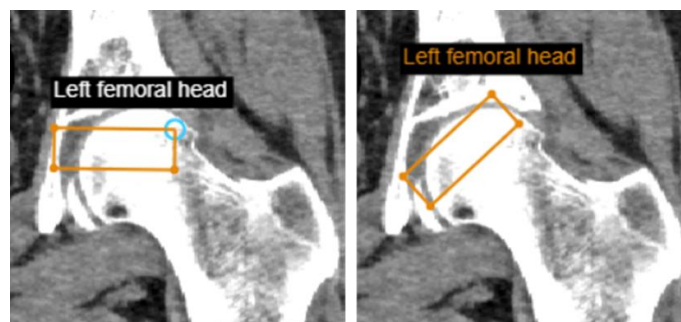


Figure 103. The bounding box rotated to better match the femoral head

- The bounding box may be resized by dragging the corner of the box, or by dragging the edge of the box. To resize the bounding box, hover the mouse cursor over the corner or the edge until the object is marked, then press the left mouse button, and, holding the button pressed, drag the corner or the edge. Release the mouse button, when the box reaches the desired size:

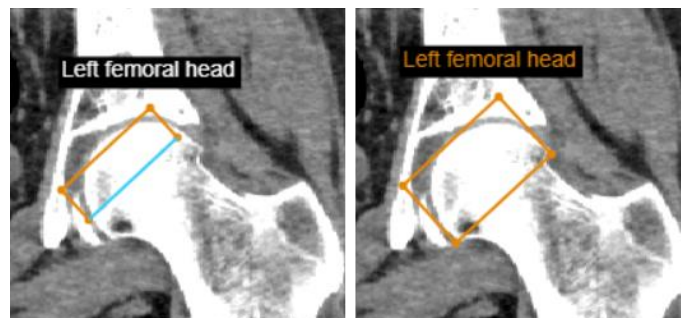


Figure 104. The bounding box is resized to fit the femoral head



NOTE! You can edit the 3D bounding box on any image in original or reconstructed series, that intersects the box and has the tetragonal intersection contour. The changes apply to the whole box and all the contours of the 3D bounding box on the other images are automatically updated.


NOTE! The shape of the image and 3D bounding box intersection contour may vary from triangle to hexagon, if 3D bounding box is rotated in more than one perpendicular plane.




WARNING! The 3D bounding box editing actions (move, rotate, resize) are not allowed in the images, that has other than tetragonal intersection contour.



Figure 105. The 3D bounding box contours after rotating the box in axial and coronal planes



When done with bounding box editing, press the active edit icon  once more to stop the editing. The icon highlighting is switched off.

To **delete** the bounding box segment:

- Open the Segmentation dialog and select the Bounding Box tool tab in it.
- Find in the list the 2D or 3D bounding box, that you want to delete.
- Press the Delete icon , which is displayed on the right side of the record.
- The system removes the segment contours from all images and segment record from the list.



WARNING! Until not saved, the created, deleted or edited segments are held in program temporary storage and will be lost, if closing the Viewer or closing the study, that has segmentations with unsaved changes.

To **save** the created or edited segments, press the save button  in the right bottom corner of the Segmentation window. The system converts segments data to DICOM format and sends it to PACS. If successfully saved, the notification is displayed, and the saving icon shows empty segment , indicating that no unsaved changes are available.



NOTE! Pressing the save button, saves the segments of all tabs of the Segmentation window.



WARNING! Segments are saved in DICOM format. The function is available only if the used study storage provides DICOM saving functionality.

Free Draw



The **Free Draw** tool allows marking the region of interest by drawing the contour on the image. The area inside the contour is assigned to segment. Several contours may be assigned to one segment. Drawing the contour inside the other contour removes the overlapping area from the segment. Drawing contours on sequential images in the series allows marking the volumetric segment.




WARNING! Performing the Free Draw segmentation, or viewing Free Draw segments may be disabled by user rights.



NOTE! The free draw segment may consist of multiple contours on the same or different images in the same series.

To **create** a new free draw segment:

- Open the image/series, in which you are going to draw the contour.
- Open the Segmentation dialog and select the Free Draw tool tab in it.
- Press the new segment icon , which is displayed on the left of the tools bar at the bottom of the Segmentation window. The icon is highlighted and drawing is activated.
- Draw the contour:
 - place the mouse cursor on the edge of the contour to be drawn,
 - press and hold the left mouse button,
 - draw the contour around the region of interest by holding the button pressed and dragging the mouse,
 - release the mouse button, when the drawing is finished.



NOTE! The system automatically connects the contour endpoints.

NOTE! The intersection of contour line is handled as separate contours. You can remove the wrong contour with contour erase tool.

- The system colors the area inside the contour, and adds the segment record in the Free Draw tab of the Segmentation window. The default name for segment is generated:

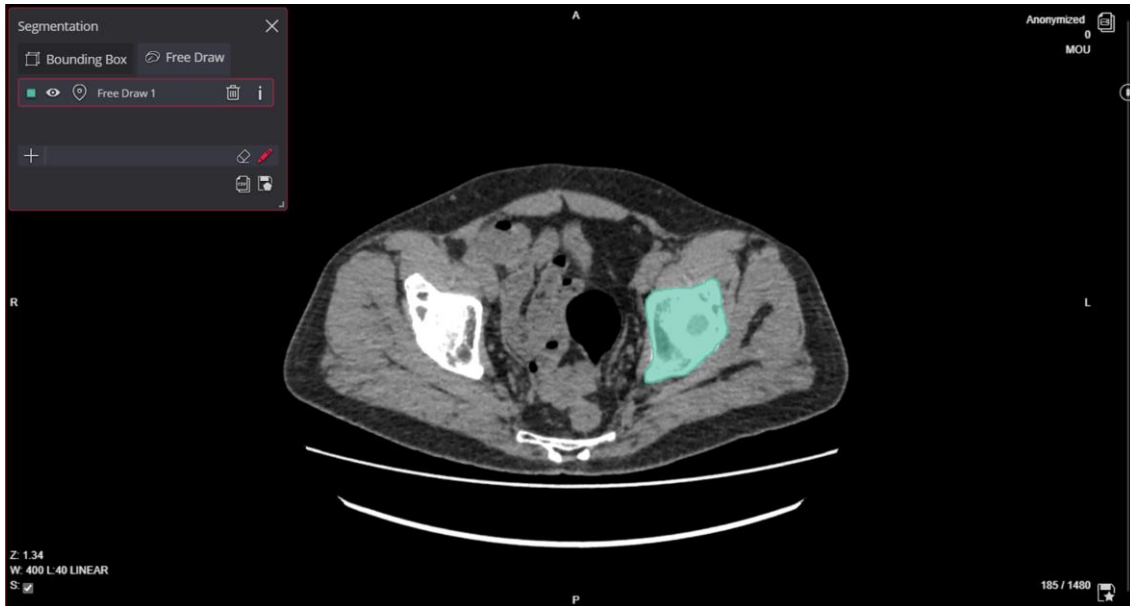



Figure 106. New free draw segment created



WARNING! Free draw segmentation may be done only on images of CT, MR, PT, or MG modality.





NOTE! The system selects created free draw segment record in the list and activates its editing. Click the highlighted edit tool  to deactivate editing, if adjustment of the segment region is not needed.


NOTE! You can use the viewer tools, like zoom, pan, windowing to arrange the image for contour drawing.

To work with existing free draw segment, activate it by clicking on the record:

- the active record is highlighted with red border,
- and the tools for editing the free draw segment are displayed in the tools bar at the bottom of the Segmentation window.

You can change the segment name and color:

- To change the segment name, click on the name in segment record, and enter a new name in the activated entry field: .
- To change the segment color, click on the color box  in segment record, and select the other color in the opened Choose Color dialog.

You can change the region of the active free draw segment. Press the edit icon  in the tools bar at the bottom of the Segmentation dialog. The icon is highlighted and the contours editing is activated:



NOTE! The label with segment name is not displayed on the image while contour editing is active for the segment.

- To remove the inner area from the segment, draw the contour inside the existing contour:

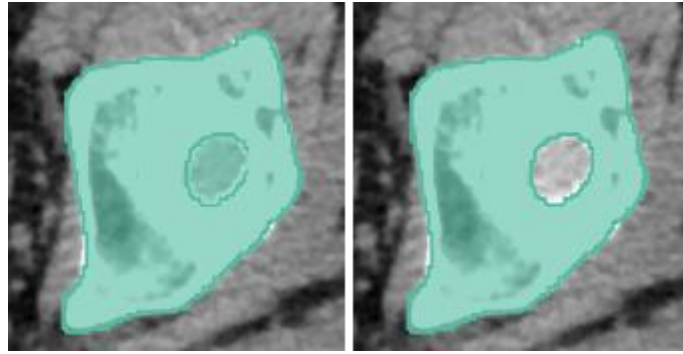


Figure 107. Inner femoral head area marked inside the ilium segment



NOTE! The same result is achieved by drawing the inner contour first, and then the outer contour around it.

- To remove the area from the side of the segmented region, hold the ALT key pressed and draw the contour intersecting the segment border:

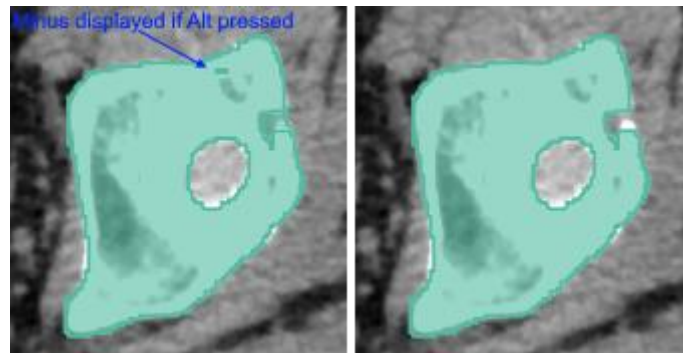


Figure 108. The area removed from the side of the ilium segment

- To add the area to the side of the segmented region, hold the SHIFT key pressed and draw the contour that intersects the segment border:

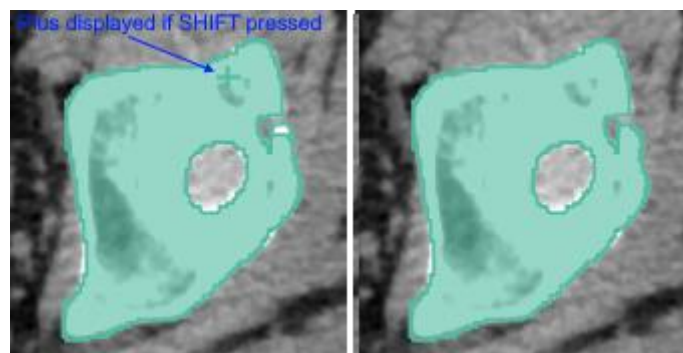


Figure 109. The area added to the side of the ilium segment

- To add additional region to the active segment, draw a new contour. You can draw a new contour either on the same image, or to scroll the mages in the series and use the other image:

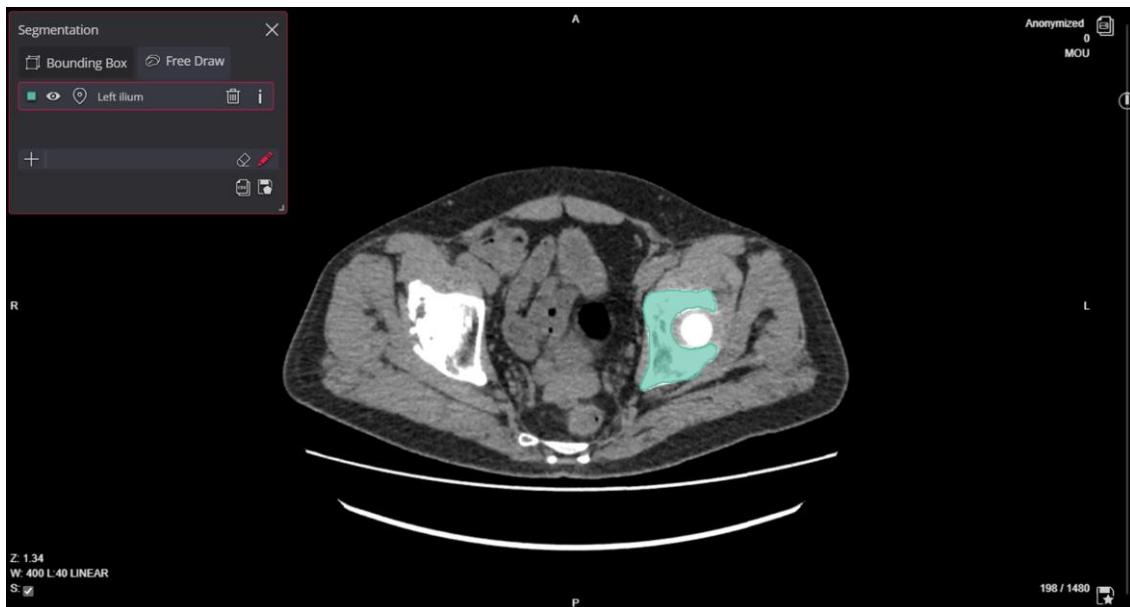




Figure 110. The region added to Left ilium segment by drawing ilium contour on the other image of the series

When done with segment editing, press the active edit icon  once more to stop the editing. The icon highlighting is stopped, and the segment label is displayed on image.

It is possible to erase the contour from the free draw segment, or to delete the whole segment.

To **erase the contour** from the free draw segment:

- Open the image that has the wrong contour on it.
- Select the segment in the Free Draw tab, and activate the Contour erase tool  for the segment. The tool icon is highlighted, if the tool is active.
- Hover the mouse cursor over the region inside the contour until the contour is highlighted.
- Press the left mouse button to erase the highlighted contour.

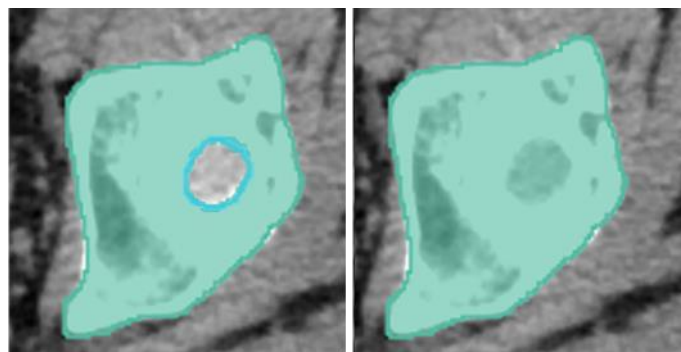




Figure 111. Inner femoral head contour deleted from the ilium segment

- When all not needed contours are deleted, press the active Contour erase icon  to deactivate contour erasing. The icon highlighting is switched off.





NOTE! The system deletes the whole free draw segment, if the last contour of this segment is erased.

To **delete** the free draw segment:

- Open the Segmentation window and select the Free Draw tool tab in it.
- Find in the list the free draw segment, that you want to delete.
- Press the Delete icon , which is displayed on the right side of the record.
- The system removes the segment contours from all images and segment record from the list.



WARNING! Until not saved, the created, deleted or edited segments are held in program temporary storage and will be lost, if closing the Viewer or closing the study, that has segmentations with unsaved changes.

To **save** the created or edited segments, press the save button  in the right bottom corner of the Segmentation window. The system converts segments data to DICOM format and sends it to PACS. If successfully saved, the notification is displayed, and the saving icon shows empty segment , indicating that no unsaved changes are available.



NOTE! Pressing the save button, saves the segments for all segmentation tools.



WARNING! Segments are saved in DICOM format. The function is available only if the used study storage provides DICOM saving functionality.


Viewing and measuring segments

If stored in DICOM, the segments data for the study is loaded to the Viewer, and contours are displayed on the images without any additional action needed.



WARNING! Viewing any or all segments may be disabled in configuration, or by user rights.

To view the images with segments data in series:

- Open the series in the viewport and preload the series data, if not preloaded automatically. When series data is preloaded, the marks on scrollbar  indicates the place of images with segment contours.
- Press at the mark on the scrollbar to navigate to the image. The image is displayed in the viewport, and the segments contours are displayed on the image.
- Use the mouse wheel to scroll the image one by one and see the segments on nearby images:

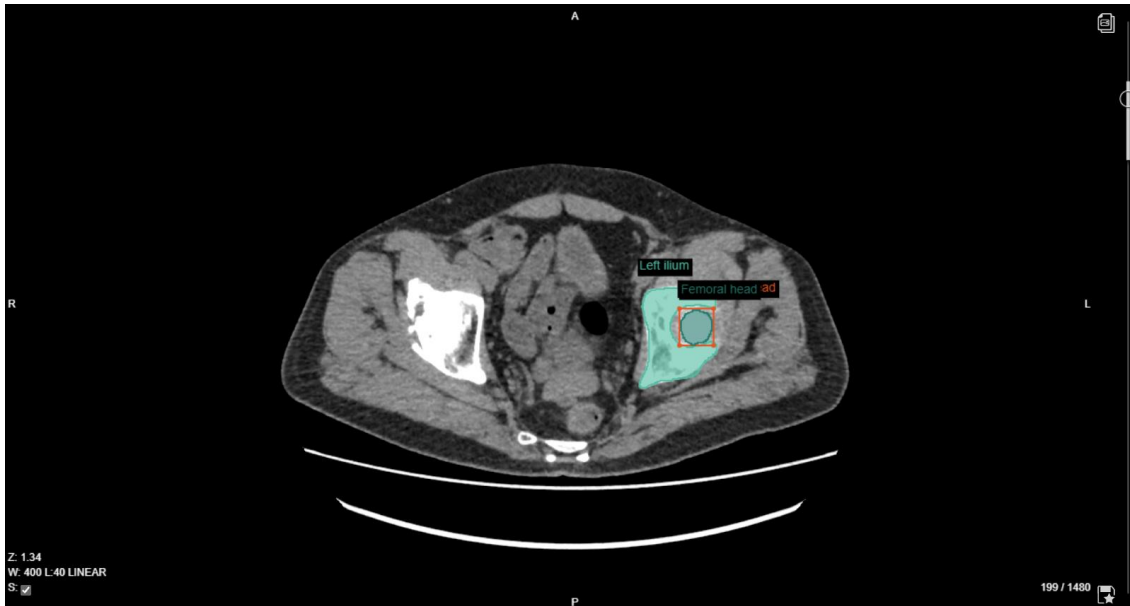




Figure 112. Viewing the image with free draw and bounding box segments

Location function of free draw segment may be used to open the first image with the contour of this segment in series:

- open the Segmentation window,
- select Free Draw tab and find the segment record in the list,
- press the location icon  for the segment.
- The system opens the first image in series with the contour of this segment in the active viewport.

If segments viewing or editing is complicated because of contours overlap, use the segment hide function:

- open the Segmentation window,
- select the appropriate tab and find the segment record in the list,
- press the eye icon  for the segment, which contours you want to hide.
- The system hides the contours and label of the selected segment. The greyed eye icon indicates, that segment contours are not displayed:

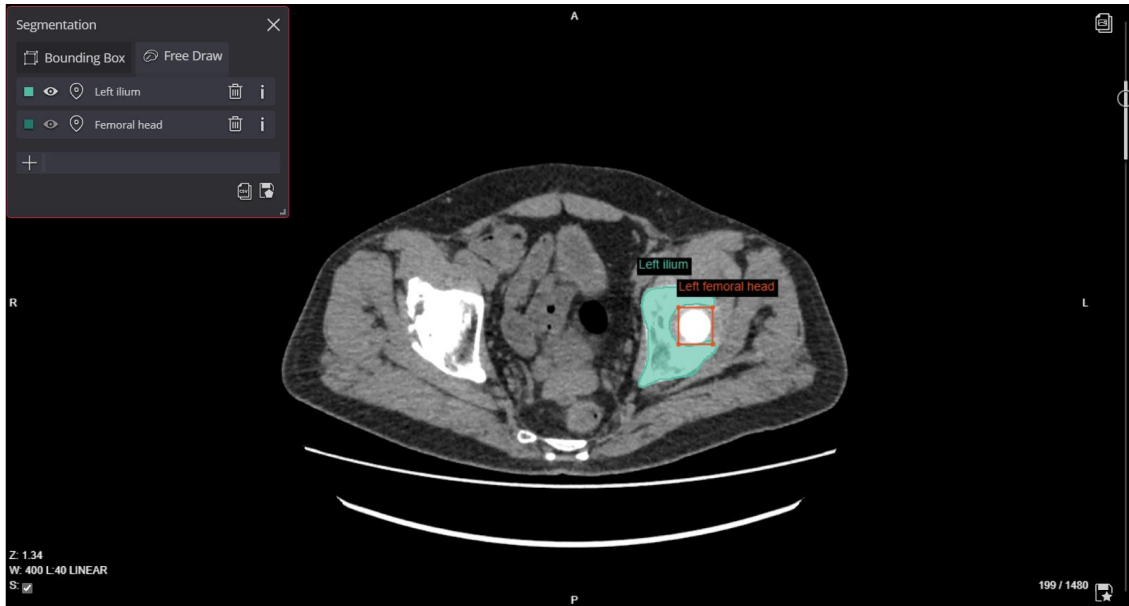


Figure 113. Contours of Femoral head segment not displayed on the image



NOTE! Location marks on the scrollbar are not displayed for the hidden segments.

The system provides possibility measure the area, volume and pixel intensity statistics for the segment. The measurements values are calculated per image. The volume is also measured for the whole segment. The user can view the segment measurements, or copy the measurements to the clipboard.



NOTE! The segment is measured and values are calculated on request, and is not saved in DICOM when saving segments.



WARNING! The segment measurements may be disabled.

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

The following values are measured and displayed per image, that contains the region of the segment:

- The Slice thickness value from DICOM file is displayed for the image, if available.
- The Calculated slice thickness is measured based on the position and orientation of the image itself and neighboring images. The value is calculated for parallel slices, and only if the image position and orientation in patient coordinates system data is available in DICOM.



NOTE! The Slice thickness value and Calculated slice thickness measurement are applicable for CT, MR and PET modalities, and not applicable for MG modality.

NOTE! The Slice thickness value and Calculated slice thickness measurement are applicable for Free Draw segments, and not applicable for Bounding Box segments.

- Voxel count is the number of voxels, that are counted as belonging to segment on this image. The voxel belongs to the segment if the center of the voxel (pixel in 2D image) is in the contour or inside the segmented region.
- Intensity values for the voxels, that belongs to segment on the image: minimum intensity, maximum intensity, mean intensity, standard deviation, and sum.



NOTE! The radiodensity in Hounsfield units (HU) is calculated for images of CT modality. The Body Weight standard uptake value (SUVBW) in g/ml is calculated for images of PT modality. For other modalities, or in case the data required for HU or SUVBW calculation is not available in DICOM file, the pixel intensity values are used.

- Voxels area is calculated by multiplying the row spacing, the column spacing, and the voxel count. The value is calculated only if the pixel spacing information is available in the DICOM file.



NOTE! Voxels area may be not equal to geometric area inside the contours of the segment.

- Voxels volume is calculated by multiplying the voxels area and calculated slice thickness, if these were measured.



NOTE! The Voxels volume measurement is applicable for Free Draw segments, and not applicable for Bounding Box segments.

The total volume measurement per whole segment is also available:


- The total volume for the free draw segment is calculated as sum of the voxels volume per each image, that contains the regions of this segment.
- The total volume of 3D Bounding Box segment is calculated as geometric volume of 3D cube, by calculating the length of the three cube edges (length, width, and height) from the coordinates of the corner points in patient coordinates system, and then multiplying these lengths.



NOTE! The total volume measurement is not applicable for 2D Bounding Box segment.

NOTE! The volume is not measured, if the data, that is required for calculations, is not available in DICOM file.

To **view** measured values for segment:

- Open the Segmentation window, select the tab and find the segment record in the list.
- Press the Show/Hide measurements icon , which is displayed on the right side of the record.
- The system opens the measurement window below the segment record, and displays the measured values for the segment in it:

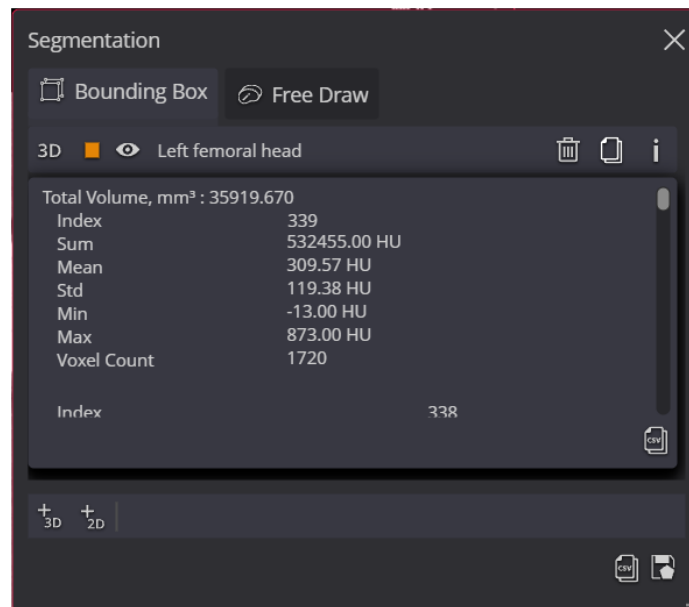




Figure 114. Measurement window displayed for Left femoral head segment


- The Total volume, if applicable, is displayed on the top of the window. The measured values per each image, that contains the regions of this segment, is displayed bellow.



NOTE! The 3D bounding box measurement values are always calculated for the referred series.

NOTE! Press the Show/Hide measurements icon  once more, to close the Measurement window for segment.

To copy to the clipboard the measured values of the segment, press the Copy measurements as CSV icon , which is displayed in the bottom right corner of the Measurement window. The system copies the values, that are displayed in the Measurement window, to the clipboard.

To copy to the clipboard the measured values of all segments, that are currently displayed in all tabs of the Segmentation window, press the Copy measurements as CSV icon , which is displayed in the bottom right corner of the Segmentation window. The system calculates the values for all segments, and copies the values to the clipboard.

Tools for study exchange

Share files via DICOM Library



Share via DICOM Library tool is used to send files to DICOM Library.

Select the images you want to share:

- To send several images from different series or studies:

- select the layout to fit the images you want to send,
- and open the required images in separate viewports;
- To send one image, or series of images, or the whole study
 - open the required image, or any image of the required series/study in the viewport,
 - or activate the viewport with such an image.

Press **Share via DICOM Library** button, and dialog window will appear on the screen. Please indicate, what are you going to send in expandable list of available **Scope** selection:

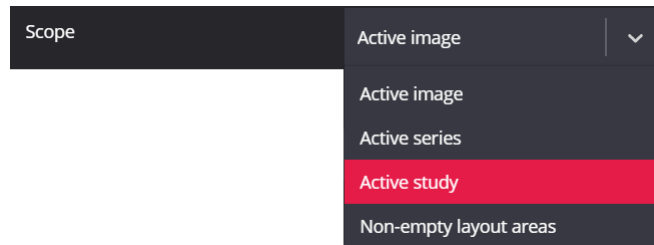


Figure 115. Selecting scope for sharing via DICOM Library

Please enter e-mail of the sender and recipient, subject, and message for recipient. When done with data entry, click **Send** button.



NOTE! You can resize the message entry field to fit the message by dragging the bottom right corner of the field.



CAUTION! The system does not anonymize the content of shared images and entered message. You take responsibility for sensitive data in shared information.

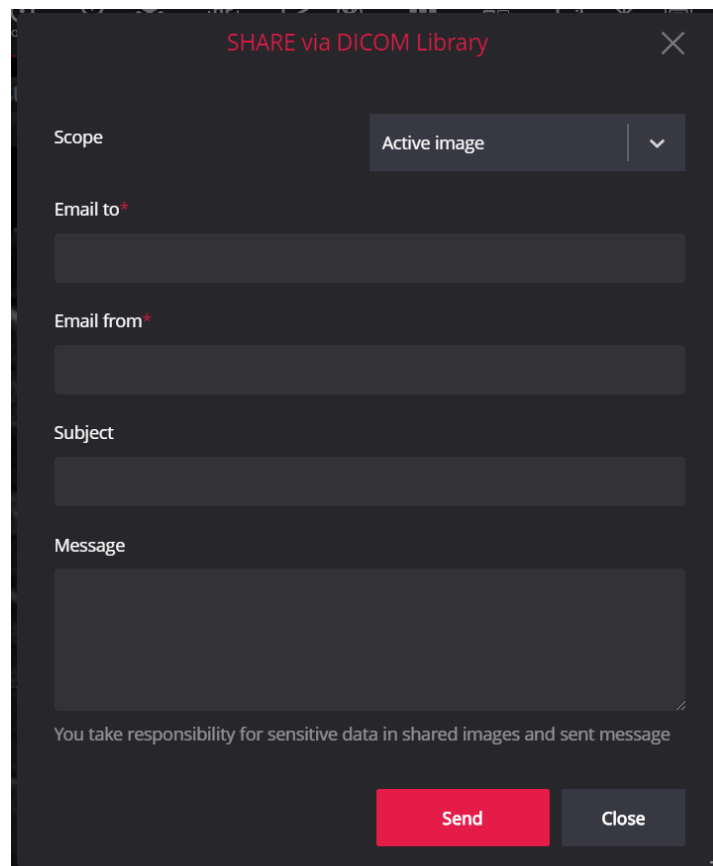


Figure 116. Share via DICOM Library dialog window



WARNING! Share files via DICOM Library function should be enabled and the required parameters should be set in configuration.

Forward



The tool **Forward** is used to send the studies, that are currently opened in viewer, to the remote device.

Clicking the **Forward** button opens the forward window with the list of forwarded studies in it:

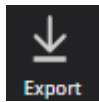
- The study with currently viewed image is marked in list of forwarded studies, if the active viewport contains image;
- All the studies are marked in list of forwarded studies, if the active viewport is empty.

You can change the studies marking in forwarded studies list in forward window. See detail forward window description in section [Export and Forward](#).



WARNING! Forward function should be enabled and the required parameters (list of forward destination machines) should be set in configuration.

Export



The **Export** tool lets you save an active image, series, or entire study as an archive or as an ISO image for recording on CD / DVD media.

Please, select the studies for export:

- To export one currently viewed image, series, or study, activate the viewport with series/studies image and click **Export** tool's button;
- To export all the studies, that are currently opened in viewer, activate the empty viewport and click **Export** tool's button.

Clicking the **Export** button opens the export window with the list of exported studies in it. See detail export window description in section [Export and Forward](#).



WARNING! **Export** function should be enabled and the required parameters (path to DICOMDIR viewer and size of ISO archive) should be set in configuration.

LiveShare



LiveShare tool is used to share the content of user's (further named as host) Viewer window with one or more other users (further named as guests).

First, prepare the Viewer window for content live sharing:

- Open the studies you are going to share in the Viewer window, and close the studies, that are not supposed to be shared.



WARNING! The system grants to the guests the access to all the studies, that are opened in host's Viewer window when starting live sharing, and these studies will be displayed in the thumbnail panel of the guests' Viewer window. Opening or closing the studies, while sharing is on, is not supported.

- Select preferred layout and open images in viewports.



WARNING! Live sharing is dedicated for images. Multiframe, video, ECG, PDF, SR documents is not supposed to be live shared.

To start live sharing, do the following:

- Press the **LiveShare** button to open the LiveShare host window:

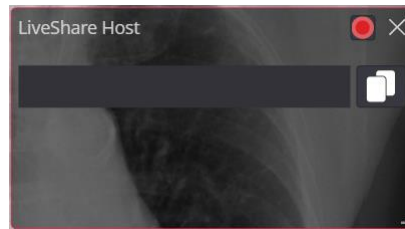




Figure 117. LiveShare host window when live sharing not started



NOTE! You can change the shared studies list, while liveShare session is not started and guest URL is not generated by system.

- Press the Start LiveShare button  in the LiveShare host window to start live sharing session. The system warns about limited live share functionality, and you should confirm the action. The system generates the guest URL and shows it in the LiveShare host window.
- Deliver the guest URL to session attendees:
 - Copy the guest URL to the clipboard by clicking Copy LiveShare link button , or using keyboard shortcuts in URL field: CTRL+A for selecting the link text, and CTRL+C for copying the selected text to clipboard;
 - Paste the copied link and send it to session attendees.
- When remote attendee launches the guest URL, the guest Viewer window with the live shared studies is opened and connected to your liveShare session, and the Viewers count is updated in the LiveShare host window:

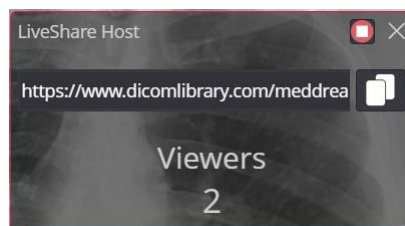


Figure 118. LiveShare host window with liveShare session running and two guests connected



NOTE! The non-modal LiveShare host window should not be closed, while liveShare session is running. Closing the window ends the liveShare session.

The guest URL may be copied, send to guest user, and guest may connect at any time during the session. The number of guests is not limited.



NOTE! Separate license connection is used per host, and per each connected guest.

Do the work you want to share with session attendees, after guests are connected. The live sharing of the following actions is supported:

- Changing the appearance of the Viewer window (layout, thumbnail panel position, multi-image);

- Opening images in viewports;



WARNING! Live sharing is dedicated for images. Multiframe, video, ECG, PDF, SR documents is not supposed to be live shared.

- Changing windowing values;
- Image spatial transformations (pan, scale, rotate, flip);
- Image scrolling (scroll menu actions, scrollbar actions);
- Location functions (reference line, crosshair);
- Measurements (except the calibration line);
- Resetting changes in viewport (applied measurements, spatial transformations);
- Multiplanar reconstruction (orthogonal planes).

The guest Viewer window repeats the host Viewer window content and host's actions:

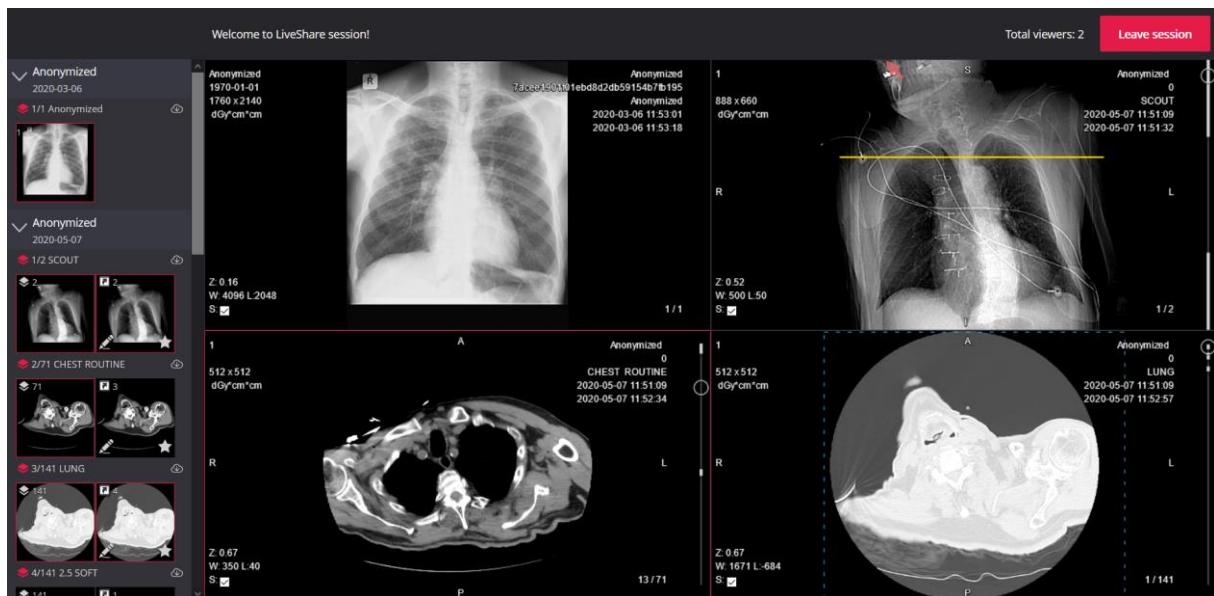




Figure 119. Guest Viewer window

LiveShare session guest is not allowed to perform any action with studies and images in the guest Viewer window.

Guest may leave the liveShare session by pressing the Leave session button in Guest Viewer window. If guest has left the session, the Viewers count is automatically updated in the LiveShare host window.

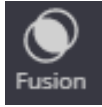
Stop the liveShare session, when done:

- Press the Stop LiveShare button  in the LiveShare host window, or
- Close the LiveShare host window with Close button , and the liveShare session will be stopped.



WARNING! LiveShare function should be enabled in configuration, and sockets connection to MedDream server from host's and guests' workplace should be allowed.

Fusion function for Positron Emission Tomography (PET CT)



The **Fusion** function allows you to combine the series of PET and CT types (attach the selected PET series to the displayed CT series), thus linking the sites of radioactive drug concentrations with the anatomical patient structure. The series fusion function can be selected only after loading the series into the active window. The **Fusion** function is achieved by selecting the Fusion icon in the main toolbar or by pressing the **F** keyboard shortcut button.



NOTE! If there is no PET series in the open study (-ies), notification will appear on the screen:

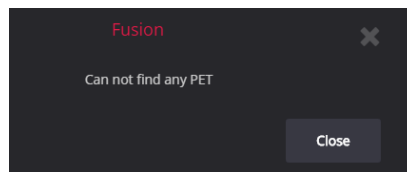


Figure 120. PET series not found notification



NOTE! The ability to choose a PET series from another study allows the user to combine series of different studies. This function also allows the user to combine magnetic resonance imaging (MR) series with PET series.

To start fusion:

- Select or open the image from CT series that you want to combine with PET series.
- Click **Fusion** button and the following pop-up window with positron emission tomography (PET) will appear on the screen:

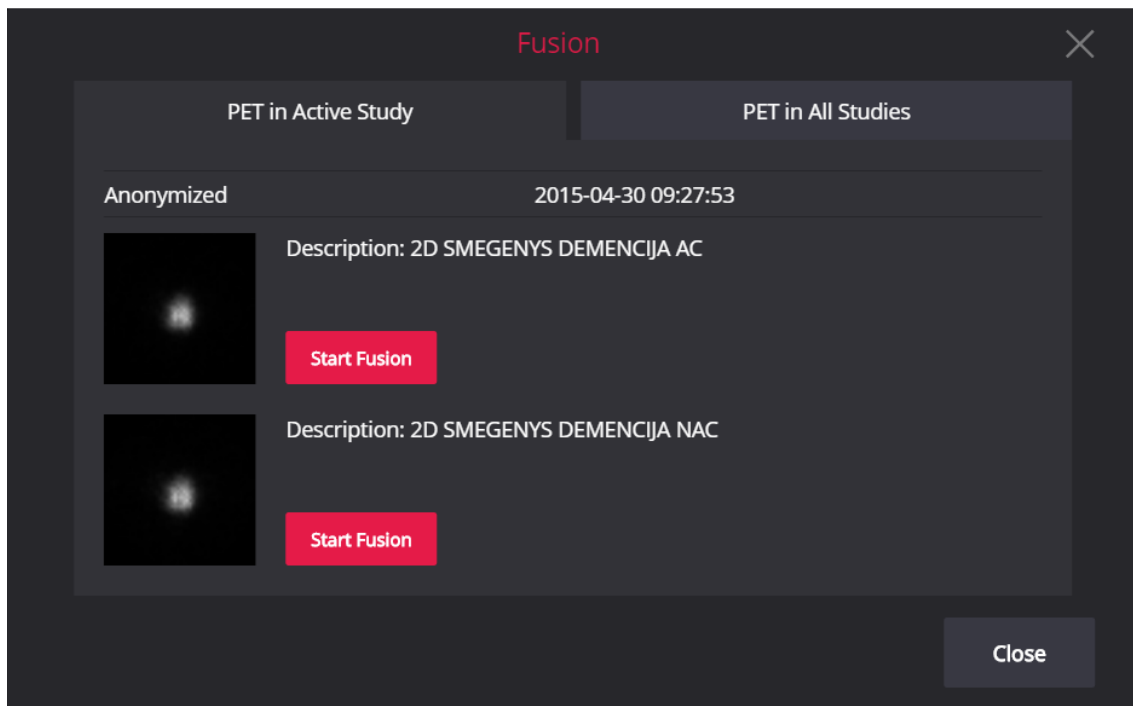


Figure 121. PET series selection window

- The PET series selection dialog allows the user to select PET series from an active study (a study that has a CT series open in the active viewport) or from a series of PET in other open studies. Select the PET series you want to combine with an active CT series and click the **Start Fusion** button.
- The program preloads CT series, if not loaded earlier, and then fuses them. The preload process progress is seen on the screen:

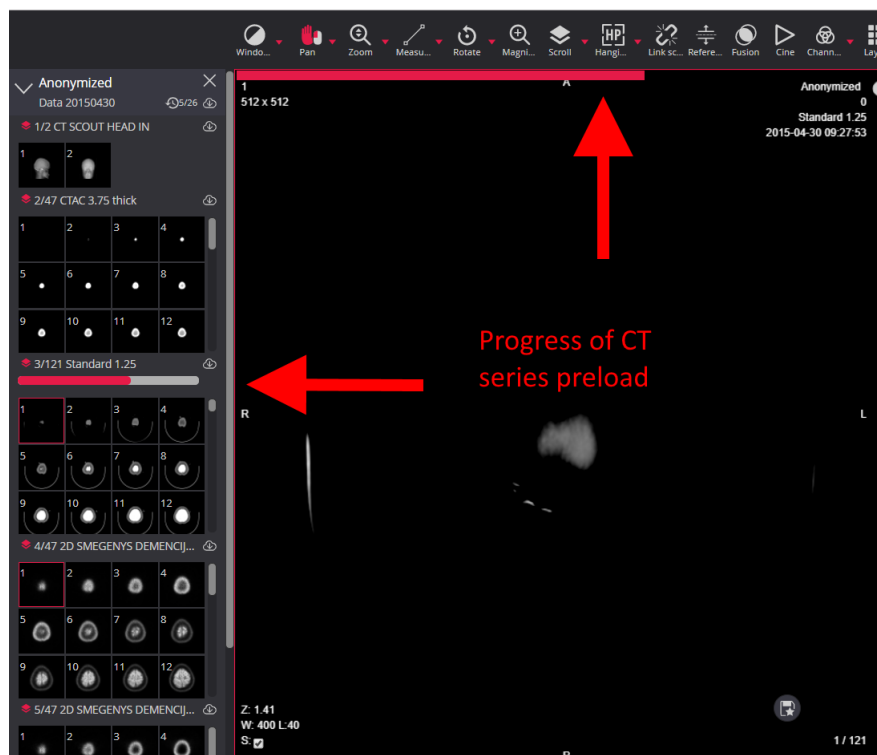


Figure 122. Fusion process

- Once the fusion process is finished, the fusion series and the toolbar of fusion series are displayed in the active viewport:

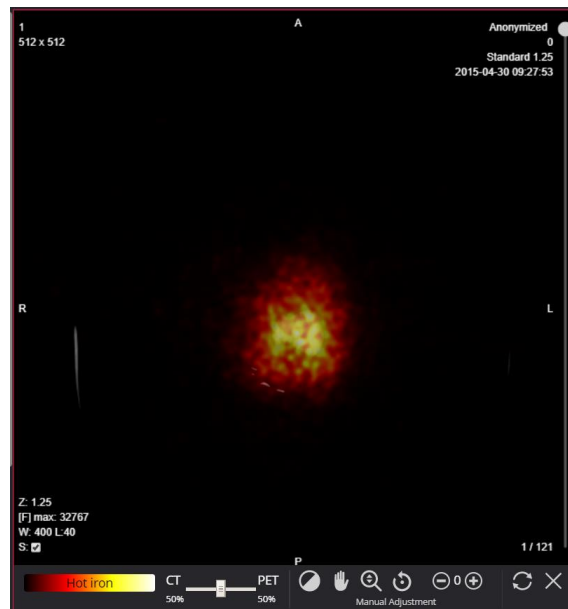


Figure 123. Fusion series



NOTE! The time of selected CT and PET series preload process depends on the size of series and the connection speed.

Manipulating fusion series

The functionality of the fusion series toolbar is described below.

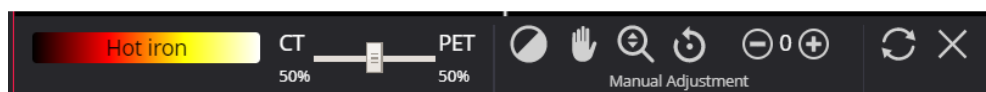


Figure 124. The toolbar of the fusion series

1. Changing the color range

By default, the **Hot iron** color range is applied to the PET series of fusion series. However, according to the specificities of the anatomical body sections analyzed, different color range can be used. The choice of the color selection is performed by expanding the list of color schemes and choosing the desired color range. The selected color range is automatically applied for the fusion PET series immediately after selection.

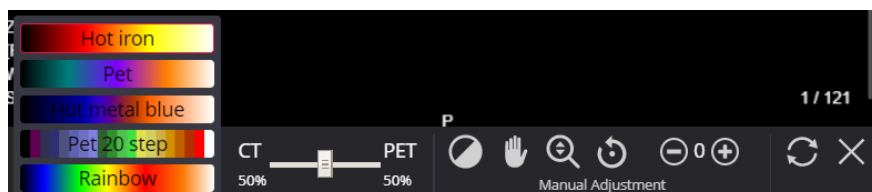


Figure 125. Changing color range of the fusion PET series

2. Changing the fusion ratio

In the analysis of fusion series, it is important to have the ability to change the fusion ratio. You can change the ratio in fusion ratio bar by dragging the marker to the PET or CT series side. In this way, one or the other series is highlighted and a clearer view is provided. By default, the 50% to 50% ration is applied.



Figure 126. Fusion ratio bar in fusion series toolbar

3. Upper layer data adjustment

If the fusion of the series is not completely symmetrical, then the **Pan** tool in the fusion series toolbar can be used. This tool allows you to change position of the upper fusion series (PET) and visually anatomically link the fusion series.

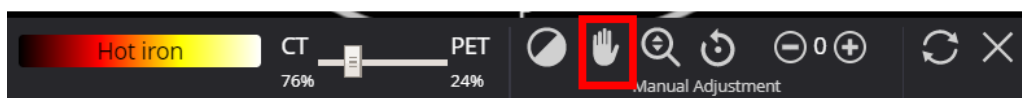


Figure 127. Pan tool in fusion series toolbar



NOTE! To change the position of the whole fusion images, use the **Pan** tool located on the main Viewer's toolbar.

4. Adjust the contrast and brightness of the upper layer

By choosing the **Windowing** tool in the fusion toolbar, the user can change the contrast and brightness of the upper fusion series (PET). If the **Windowing** tool is selected from the Viewer's main toolbar, then the overall brightness level (PET and CT series) is changed.

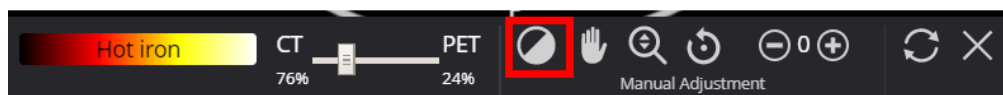


Figure 128. Windowing tool in fusion series toolbar

5. Upper layer zoom function

By choosing the **Zoom** tool in the fusion toolbar, the user can change the scale of the upper fusion series (PET). If the Zoom tool is selected from the Viewer's main toolbar, in this case the overall (PET and CT series) scaling is changed.



Figure 129. Zoom tool in fusion series toolbar

6. Upper layer rotation

By choosing the **Rotate** tool in the fusion toolbar, the user can rotate the image of the upper fusion series (PET). If the **Rotate** tool is selected from the Viewer's main toolbar, in this case the whole fusion image (PET and CT series) is rotated.

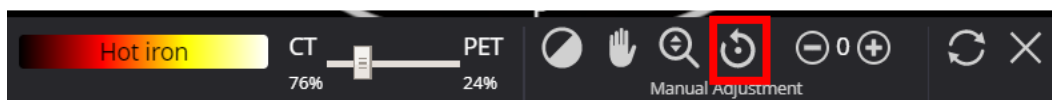


Figure 130. Rotate tool in fusion series toolbar

7. Upper layer image overlay

If there is a mismatch between the fusion series, the series images can be overlaid with the **Manual Adjustment** tool in the fusion series toolbar. The overlay is possible by changing the image of the upper fusion series (PET) to the next (by clicking the + button) or by changing the image of the upper fusion series (PET) to the previous one (by clicking the – button).

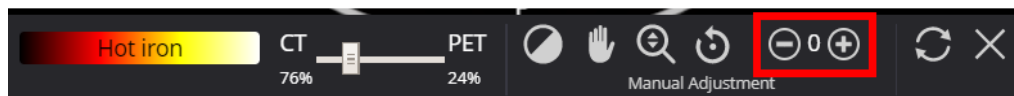


Figure 131. Upper layer Manual Adjustment tool in fusion series toolbar

8. Standard Uptake Value (SUV)

The main measurement used in the fusion series is the standard uptake value (**SUV**). The standard uptake value is calculated according to the formula:

$$SUV_{bw} = \frac{\text{weight in grams}}{\text{injected dose}}$$

The **Standard Uptake Value** is calculated by choosing **Ellipse** measurement (see description in section Ellipse) from the **Measure** expandable menu in the Viewer's main toolbar and marking the location in the fused image. Three standard uptake values (average, minimum and maximum) are calculated:

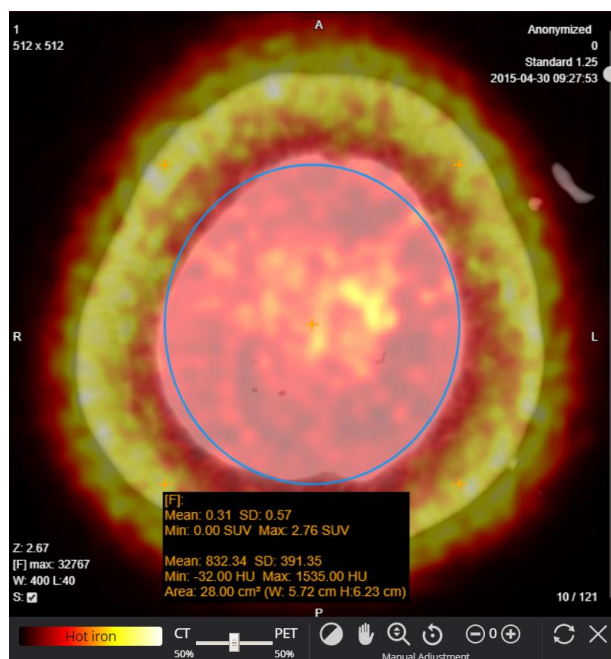


Figure 132. Standard uptake value measurement in fusion series

9. Reset PET manipulations

Reset button in fusion series toolbar cancels all the manual adjustments that were done with the upper fusion series (PET) and restores the fused series to the original state.



Figure 133. Reset button in fusion series toolbar

10. Closing fusion series

To close the fusion series, click on **Close** button (X icon) at the end of the fusion series toolbar.



Figure 134. Close button in fusion series toolbar

Cine mode



Using **Cine mode**, you may put all series images into one movie. Click on the **Cine mode** tool in Viewer's main toolbar wait until the series images preload is done, if not loaded earlier:

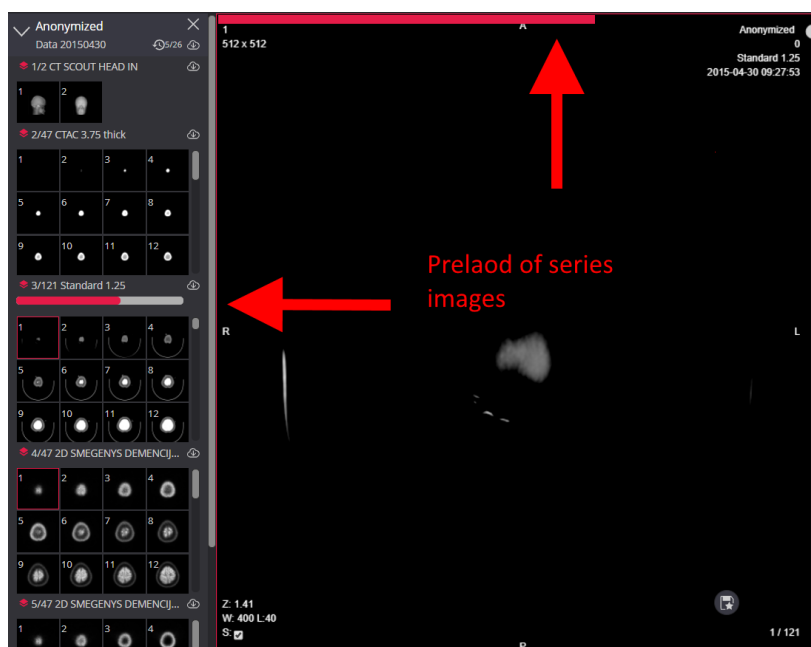







Figure 135. Preload of series data for cine mode

When images are preloaded, the function allows you to play series images as movie (one image corresponds to one frame):



Figure 136. Cine mode movie playing

Toolbar for controlling the movie playing is displayed at the bottom of the viewport:

- To switch the movie playing off or on, click Pause  or Play  button. The button icon changes correspondingly to the current play status;
- To increase or decrease the movie frame rate, click '+' or '-' button correspondingly. The changed number of frames per second is displayed in toolbar , and immediately applied;
- To view the movie frame by frame, use the Previous Instance  and Next Instance  buttons. If movie was playing, clicking the Previous Instance or Next instance button pause movie and then navigates to the previous or next frame from the stopped frame until movie beginning or end is reached.

To turn the Cine mode off, just open an image from a different series in the same viewport, or click the **Cine** button once more time.



WARNING! Windowing, Pan and Zoom functions are available during cine mode (see [Manipulating and analyzing images](#)).

Other Viewer tools

Series



Series button opens the **Study** window:

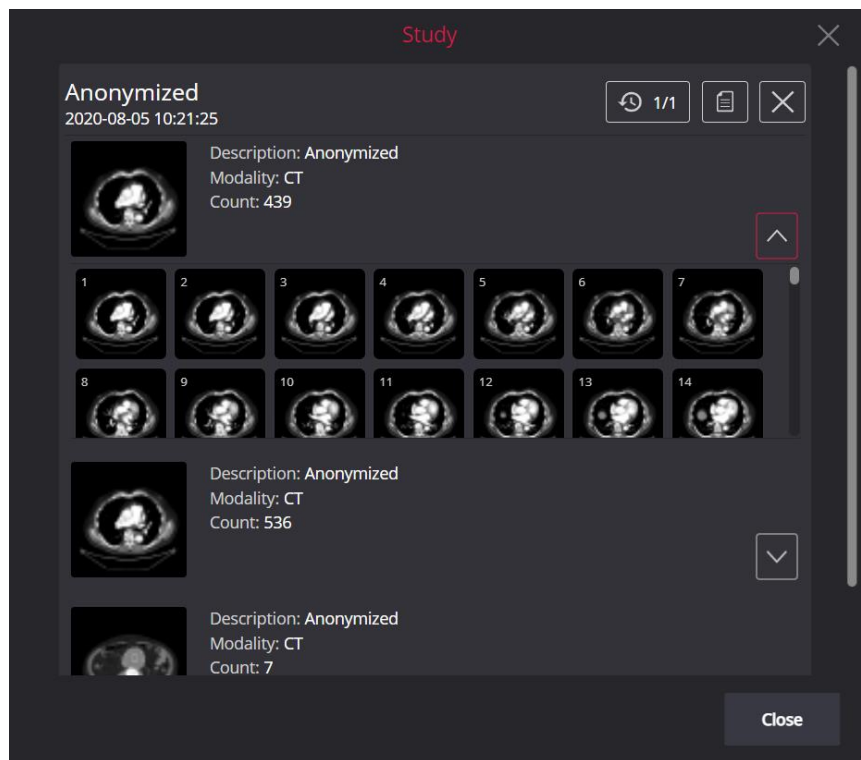





Figure 137. Study window

At the top of the window the patient name and study date are displayed. The study information is followed by the list of study's series. The series description displays the following: the thumbnail of the first image, series description, modality and number of images in series.

In Study window you can perform the following:

- Expand or collapse the series images list by clicking the chevron icon at the right of the series description;
- Open the image in viewer window by clicking the image thumbnail in series description or expanded series image list;
- Open patient's studies modal by clicking the patient's history icon  on the right side of the study description. See detail description in section [Patient history](#);
- Open the study report form (see [Report module](#) section for detail description) by clicking the Create report  icon, or Edit report  icon at the right of the study description;
- Delete the study from the viewer's window and study window by clicking the **Close** button (icon **X**) at the right of the study description.

Plugins



Plugins button extendable menu holds links to external systems and services. The plugins are displayed in expandable menu of **Plugins** button, if configured by system administrator.



NOTE! Third party plugin for DICOM print may be integrated for some PACS. For details, contact to Softneta support at this email: support@softneta.com.

Full Screen



Full Screen button is used to turn on the full screen mode. Move mouse cursor on **Full Screen** icon and click it - the Full Screen mode will be enabled. Click either the icon once again or ESC button in the keyboard in order to exit the Full Screen Mode.

Theme

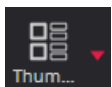


Theme changes MedDream default color (red color in standard product version) to the blue color that is clearly visible on black and white monitors.



NOTE! The default color may be different if the product is used in an integrated solution and rebranded to meet the colors of the integrating system.

Thumbnails



Thumbnails button enables changing the thumbnail place in viewer window. You can select the desired place from dropdown menu: Left; Top; Bottom; Right; Quick menu.



NOTE! The user selection is saved in browser's local storage and used when starting the viewer. If local storage does not contain the thumbnail position value, the position is set according the system settings.

NOTE! The default thumbnail place is configured in [Settings](#).

Preload Series



The **Preload Series** button preloads the series images, so scrolling the images with mouse wheel works much faster. Once you click the preload icon, preloading starts and preload progress bar appears in the viewport:

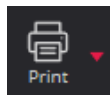


Figure 138. Series preload process progress bar



NOTE! The **Preload series** button is not displayed if the series data is already loaded.

Print



To print images, click **Print** button (enabled for images, videos, and multi-frame, and disabled for ECG, SR and pdf documents). There are two print options:

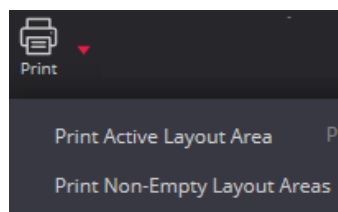


Figure 139. Print options

Click on one of Print options (**Print Active Layout Area** or **Print Non-Empty Layout Areas**) in order to print the view of selected viewport.

Hanging protocols



NOTE! Hanging protocol is automatically applied only to the first study that is opened in the viewer.



Clicking the **Hanging protocol** button opens Hanging protocol options window.

Figure 140. Hanging protocol options window

You can see the currently applied hanging protocol and apply the other hanging protocol in **Manual hanging protocol selection** section.

To apply other hanging protocol:

- select the hanging protocol group from **Hanging protocol group** drop-down list;
- select the hanging protocol from **Hanging protocol** drop-down list;
- click **Apply** button.



NOTE! Manual hanging protocol selection section is shown only for the studies with automatically applied hanging protocol.

NOTE! Only the hanging protocol groups and the hanging protocols that can be applied to the active study according to the group and study conditions are available for manual selection.

In **Current workspace settings** section, you can see and change the setting of automatic apply in workspace:

- to change device setting select the device from **Current device** drop-down list;
- to change the **Automatically apply hanging protocol** setting select **Enable** or **Disable** button;
- click **Apply** button to save the settings.



NOTE! The workspace settings are saved in browser's storage and are applicable only for the same browser.

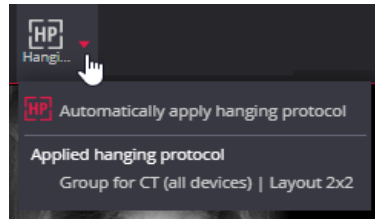



Figure 141. Hanging protocol menu options

Hanging protocol button's pop-up menu provides quicker access to some information and functions of Hanging protocol options window:

- menu **Automatically apply hanging protocol** shows the current property value – highlighted icon  means that that automatic apply is enabled. Clicking the menu inverts the value and highlighting;
- menu **Applied hanging protocol** show the currently applied hanging protocol. Clicking the menu opens Hanging protocol options window.

Shortcuts ALT+V and ALT+C can be used to apply correspondingly the next and the previous hanging protocol from current hanging protocol group.

Report



Clicking the **Report** button opens the report form. See detail requirements for report module accessibility and report form description in section [Report module](#).

Special views

The section describes the image types that may be included in DICOM file and that needs the special handling when opened in viewer's window.

ECG module

This module allows you to view DICOM ECG wave data.

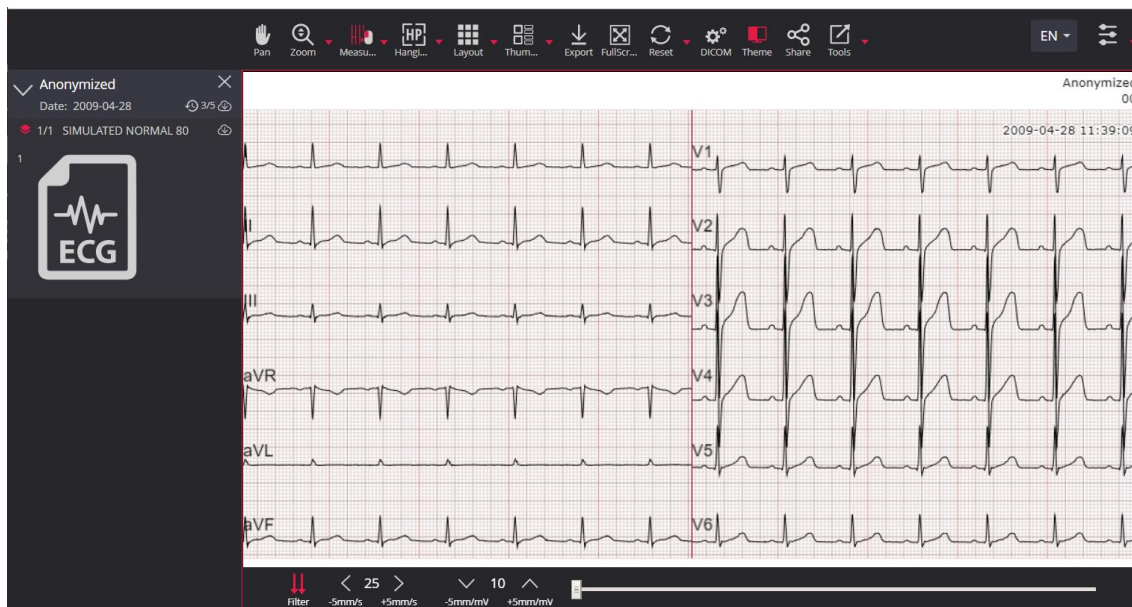


Figure 142. ECG viewer window

The section describes ECG measurements and ECG viewport toolbar. See the description of main Viewer window toolbar for other tools.

ECG Viewer window has different **Measure** menu:

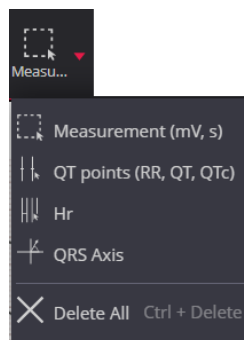
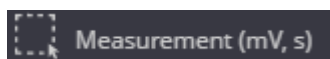


Figure 143. ECG measure tools



The **Measurement** button is used to measure the duration (first number, 0.75 s in the example) and amplitude (second number, in this case 1.18 mV) of the selected ECG segment, and to calculate the heart rate per minute (third number in the example, 80 bpm). To measure the values:

- select **Measurement** tool,
- hover the mouse cursor on the point where you want to start the measuring,
- press the selected mouse button and drag the cursor to desired position,
- release the mouse button when the cursor is on the point where you want to end measuring.



Figure 144. Using Measurement (mV, s) tool

QT points (RR, QT, QTc)

The **QT points** tool (duration of the electrical systole) is used to measure the QT intervals (RR, QT, QTc) of a selected ECG fragment. To measure the intervals:

- select **QT points** tool,
- hover the mouse cursor over the start-point of the Q wave and click the selected mouse button,
- hover the mouse cursor over the end-point of the T wave and click the selected mouse button,
- hover the mouse cursor over the start-point of the next Q wave and click the selected mouse button.

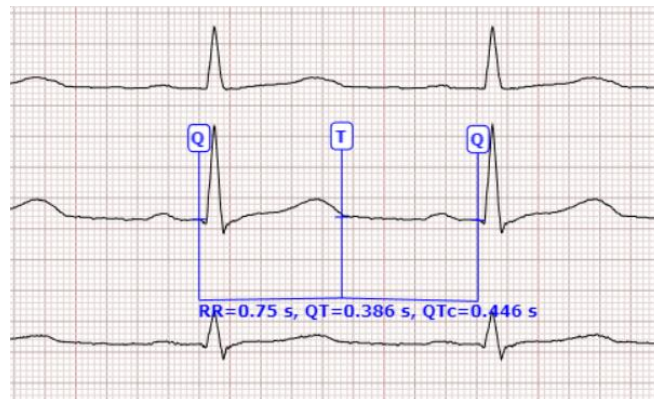


Figure 145. Using QT points tool

HR

The button **HR** is designated to measure heart rate and visually estimate its irregularity. To measure:

- select **HR** measurement tool;
- hover the mouse cursor over the peak of the R wave and click the selected mouse button,
- hover the mouse cursor over the peak of next R wave and click the selected mouse button,
- now you can compare given interval with other R waves.



Figure 146. Using HR measurement tool



The **QRS Axis** is used to measure cardiac interventricular partition and ventricular depolarization spreading. Measurement is performed on one or more complete segments of lead I and aVF lead. To measure:

- select **QRS axis** measurement tool,
- hover the mouse cursor over the isoelectric line before P wave and click the selected mouse button,
- hover the mouse cursor over the isoelectric line after T wave and click the selected mouse button.

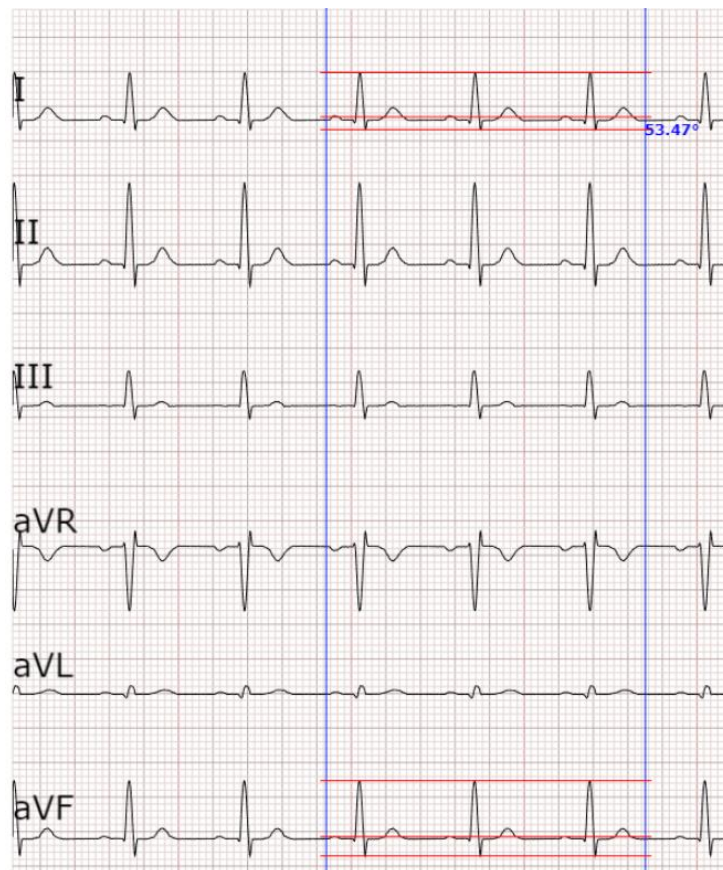


Figure 147. Using QRS Axis tool



The **Delete All** menu is used to remove all measurements.

Description of ECG viewport toolbar's tools:

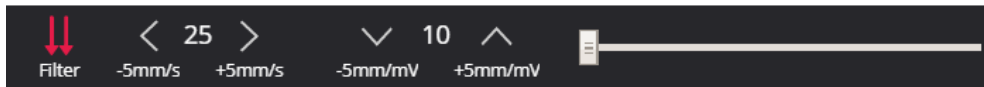
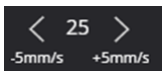


Figure 148. ECG viewport toolbar

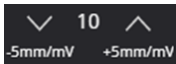


Filter function is used for the following:

- to trim the edges of unnecessary points (points to the first spike that has no importance);
- to trim high and low frequency signals applying low-pass and high-pass frequency filters under the "Filter Low Frequency" (003A,0220) and "Filter High Frequency" (003A,0221) tags;
- to eliminate baseline wandering interference;
- filters out specified frequency signals adjusting band-stop filter by **Notch Filter Frequency** (003A, 0222) tag.



Change horizontal scale (mm per second).



Change vertical scale (mm per mV).



ECG view scrollbar.

SR view

SR view enables to view structured reports.

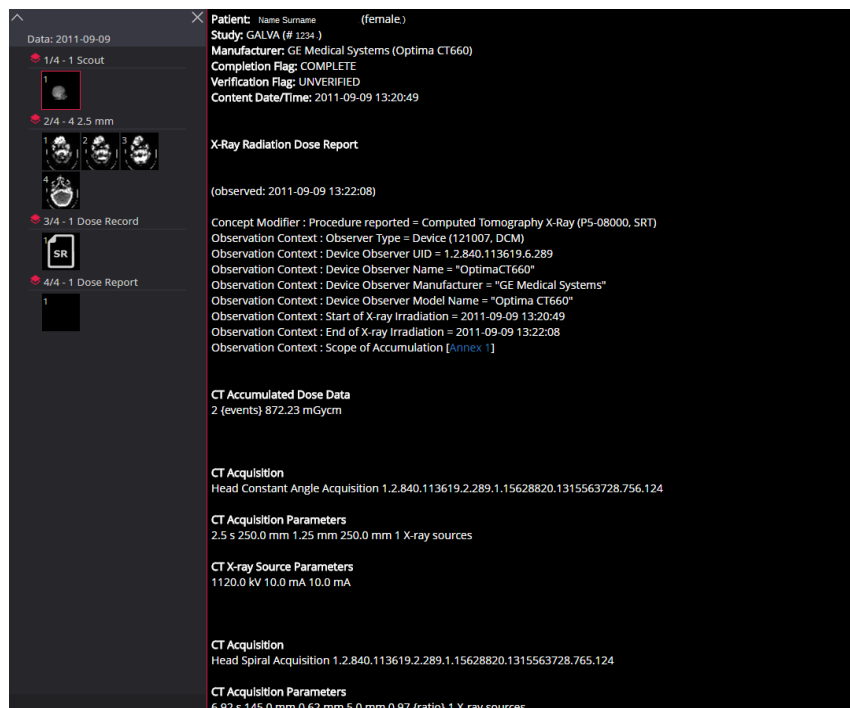


Figure 149. SR viewer window

SR window displays standard DICOM Structured Reports.

PDF view

PDF view enables to view PDF files encapsulated in DICOM format.

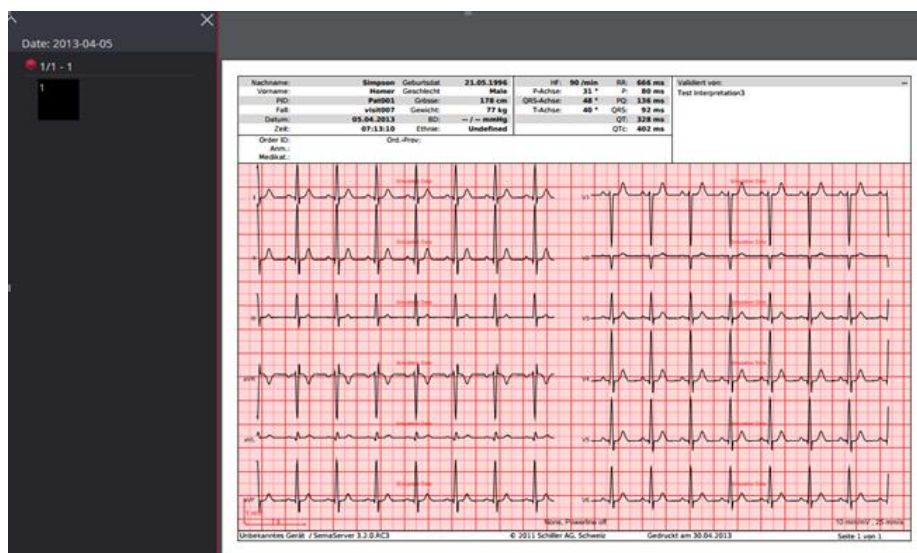


Figure 150. PDF display



WARNING! PDF file is opened with default PDF reader. Some Web browsers have built-in readers. In other cases, the additional software for pdf reading and displaying, like Adobe Acrobat Reader, should be deployed in user workplace.

Video view

Software enables to view video files, MPEG2 and MPEG4 (H.264), encapsulated in DICOM format.

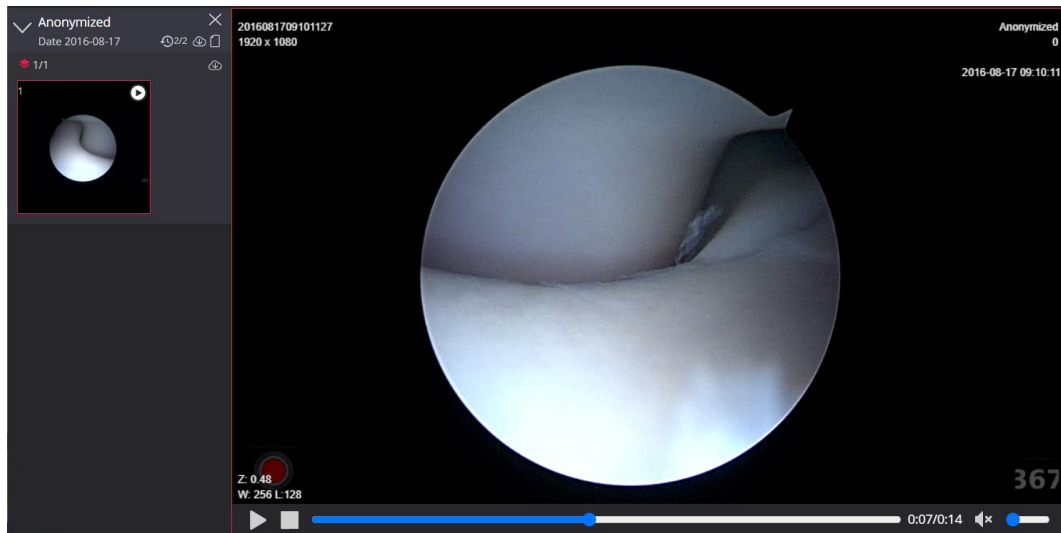










Figure 151. Video player

The play icon  is displayed on the thumbnail of video image. The standard video player is used for opening and playing video.

Toolbar for controlling the video playing is displayed at the bottom of the viewport:

- To switch the video playing off or on, click Pause  or Play  button. The button icon changes correspondingly to the current play status;
- To navigate quickly to the particular place in the video file, click on timeline, or drag the timeline cursor , or hover the mouse pointer over the timeline and scroll the mouse wheel. If timeline is used to view video by instance, the video playing is paused, if it was switched on. After finishing the actions with timeline, the video playing is automatically switched on. The time played from the beginning of the video and full time of video is displayed on the right of the timeline **0:29/4:00**;
- To stop playing and set the player to the beginning of video file, click the Stop playback  button;
- To switch the volume Off , or On , click the volume icon. To change the volume of the played video, drag the volume bar cursor or click on the volume bar .

Multi-frame view


Software enables to view multi-frame images, encapsulated in DICOM format.




NOTE! The system displays CT or MR type enhanced multi-frame image as a series of images.









Figure 152. Viewing multi-frame image

The play icon  is displayed on the thumbnail of multi-frame image.

System automatically starts loading of instances, when the multi-frame image is opened in the viewport. The loading progress bar is displayed as red line on top of the timeline .

Toolbar for controlling the multi-frame playing is displayed at the bottom of the viewport:

- To switch the multi-frame playing off or on, click Pause  or Play  buttons. The button icon changes correspondingly to the current play status;
- To navigate through the multi-frame image by instance, use the Previous Instance , or Next Instance  buttons;
- To navigate quickly to the particular place in the video file, click on timeline, or drag the timeline cursor , or hover the mouse pointer over the timeline and scroll the mouse wheel. If timeline is used to view multi-frame image instances, the multi-frame playing is automatically switched off;
- To increase or decrease the frame rate, click '+' or '-' button correspondingly. The changed number of frames per second is displayed in toolbar , and immediately applied.

MedDream DICOM Viewer Chrome browser extension for multi-monitors

Requirements

- MedDream DICOM Viewer multi display browser extension requires Google Chrome browser version 52 or newer.
- Multi display requires more than one display.
- Recommended to have monitors with the same resolution (and Windows PC - the same scale), to expand browser content to correct size and position.

Extension installation

1. Extension can be found here:
 - Open Google Chrome Properties -> More tools -> Extensions:

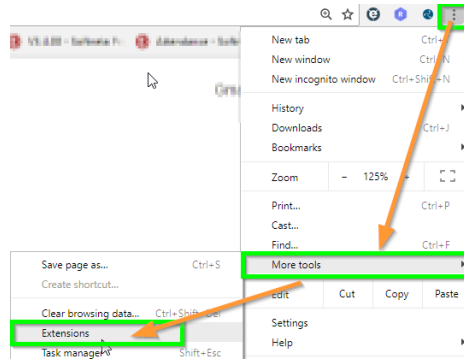


Figure 153 Chrome properties

In opened window select Extensions (in the left upper corner) -> Open Chrome Web Store

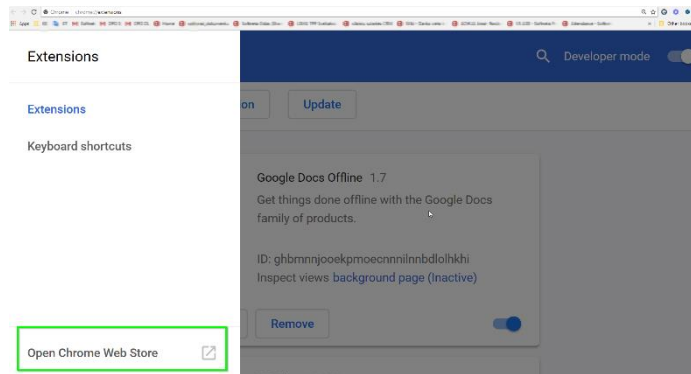


Figure 154 Chrome web store

- Go directly to Google Chrome extensions website -> <https://chrome.google.com/webstore/category/extensions>
- 2. Search for MedDream browser extension: type “meddream” or “multi-monitors” in the search field.

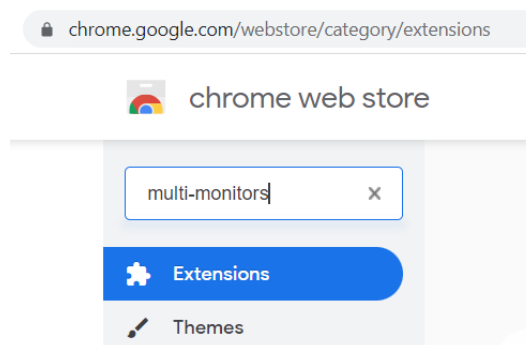




Figure 155 Filtering MedDream extension

3. Find the “MedDream extension for multi-monitors” in Extensions list, select to add the extension by pressing the **Add to Chrome** button, and confirm the installation.
4. The extension is added to the Chrome browser:
 - the extension icon  is displayed in the browser's extensions toolbar,
 - the notification about possibility to manage the extension by clicking on the icon, or by finding the extension in the extensions list under Extensions menu, is displayed.

Extension configuration

1. Open the extension options window by clicking the extension icon  the In Google Chrome browser's extension toolbar in the right upper corner, or by opening the extension from extensions list, and selecting the extension options.

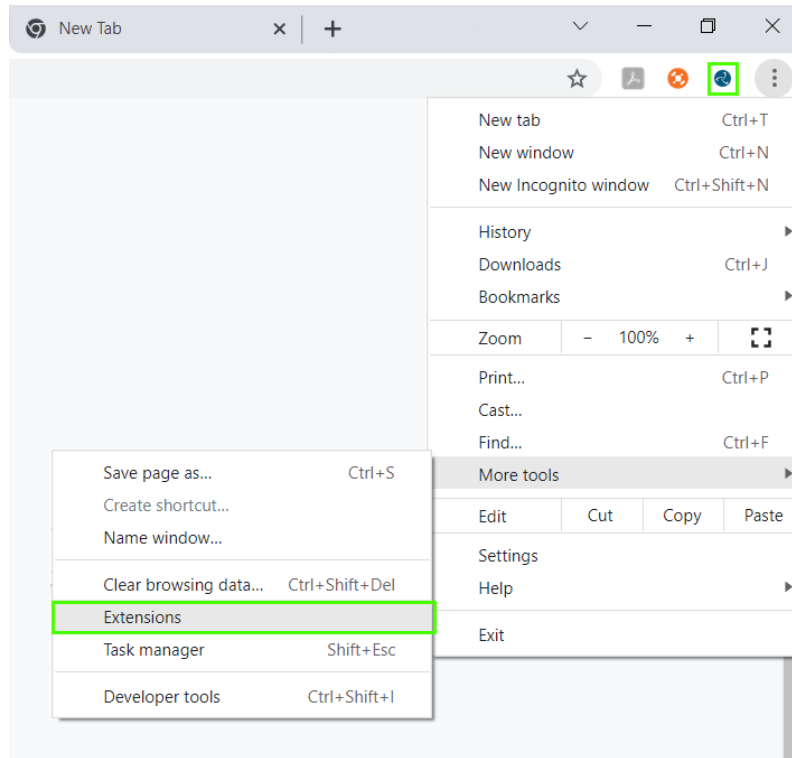


Figure 156 Accessing the options of the added MedDream extension



Please note, that parameters are stored in browser local storage, thus after deleting temporary files should be set up again.

2. The user has to set up:
 - 2.1. Appropriate URL context path for version 7.5 and later should be "/view";



NOTE! If user will leave empty URL context path, it will be filled by default value "/md5/index" that is used for versions earlier than v7.5.

- 2.2. Specify desired monitors which will be used for MedDream DICOM Viewer and click save button.
- 2.3. Example of configured extension:

Debug(extension console output): ☐

Url part to search(index, search/index,...):

Select monitors to display/expand content

Select 1 display

Select 2 display

Figure 157 Configured extension's example



NOTE! Parameters are stored in browser local storage, thus should be set up again if deleting temporary files.

2.4. When MedDream DICOM Viewer will be opened, the extension detects context path and automatically seizes web browser window in specified displays. It is recommended to use appropriate thumbnail layout like Thumbnail Top or Thumbnail Down.



Figure 158 MedDream DICOM Viewer on 2 displays



Figure 159 MedDream DICOM Viewer on 3 displays

Size and position of modal dialog window

Each modal dialog in the system is designed to fit one of the widths:

- either narrow dialog with a width of 570 pixels,
- or medium dialog with a width of 750 pixels.

By default, system opens the dialog in designed narrow or medium width and aligns it horizontally in the center of the parent window, and vertically at the top of the parent window. If the default width or position is inconvenient, for example in large monitors, or when multiple monitors are used, the user can change it.

To change the width of the dialog window, perform the following:

- hover the mouse pointer over the grey triangle at the bottom right corner of the dialog window (the cursor should obtain the resize cursor look),
- press the right mouse button, and drag the mouse right or left to change the width of the dialog window,
- release the mouse button when the dialog has the preferred width.



NOTE! The new width is saved in browser local storage and is applied instead of default 570 pixels narrow width, if the width of the narrow dialog was changed, or default 750 pixels medium width, if the width of the medium dialog was changed.

To change the horizontal alignment of the dialog window, perform the following:

- hover the mouse pointer over the title of the dialog window (the cursor should obtain the move cursor look),
- press the right mouse button, and drag the mouse right or left to move the dialog window,
- release the mouse button when the dialog is in the preferred position.



NOTE! The system saves the distance from the left side of the parent window in browser local storage and opens modal dialogs at this position instead of the default horizontal alignment in the center of the parent window.

Export and Forward



Clicking the export **Export** menu in Search window or Viewer window opens the Export window. Clicking the forward



Forward menu in Search window or Viewer window opens the Forward window.



WARNING! Forward and Export functions are not available in Search results window if working in mobile mode.

You should select the studies that you are going to export or forward in advance. The study selection in Search window is done by marking the tick-box as described in section [Search of studies](#). The study selection in Viewer window is done by activating the required viewport as described in sections [Forward](#) and [Export](#). The selected studies are displayed in export or forward window. The studies list contains the following information about the study:

- **ID** - patient's identification number,
- **Name** - patient's name and surname,
- **Modality** - the method which was used to obtain the study images (modality),
- **Description** – the study description,
- **Date Time** – study date and time,
- **Source AE** – device from where the study was sent to the PACS.

Forward window

To send the selected studies to the remote DICOM device, click the **Forward** button. The Forward window is displayed:

<input checked="" type="checkbox"/>	ID	Name	Modality	Description	Date Time	Source AE
<input checked="" type="checkbox"/>	00	Anonymized	KO, OT, PR		2014-11-27 12:54:44	MEDDREAM
<input checked="" type="checkbox"/>	00	Anonymized	US		2013-12-19 11:22:21	Import-root

Forward to: ▼

Recently forwarded... Forward Close

Figure 160. Forward window

Studies list at the top of the window contains the studies that are available for forwarding. If no studies are available, the "Empty list" message is displayed. The checked tick-box in the first column indicates the studies, that are marked for forwarding:

- All the studies are marked for forward, if the Forward window is opened from Search window;

- Either one, or all the studies may be marked for forward, if the Forward window is opened from Viewer window (see detail description in section [Forward](#)).

To change selection for the particular study, click the tick-box next to the study. The selection all the studies, that currently displayed in the list, may be changed at once by clicking the tick-box in the header of the first column.

The forward destination devices are listed below the studies list in **Forward to** expandable list:

- The list contains all the devices that are configured as forward destinations in system settings.
- To expand and view the list, click the chevron icon on the right.
- To search for specific device, enter the text in recipient search entry field above the devices list: the list is expanded and automatically filtered according to the entered text:

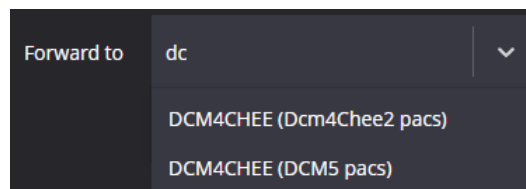


Figure 161. Searching for the forward destination

- To select the device, click on it in the expanded list.



WARNING! For proper forward functioning the forward destination should be properly configured and the device should support DICOM saving functionality.

Click the **Forward** button in forward window to start the study forwarding process:

- if either studies, or device list is empty, the process is not started and the error is displayed;
- if the forward is started, the information message about initiated forward process is displayed:

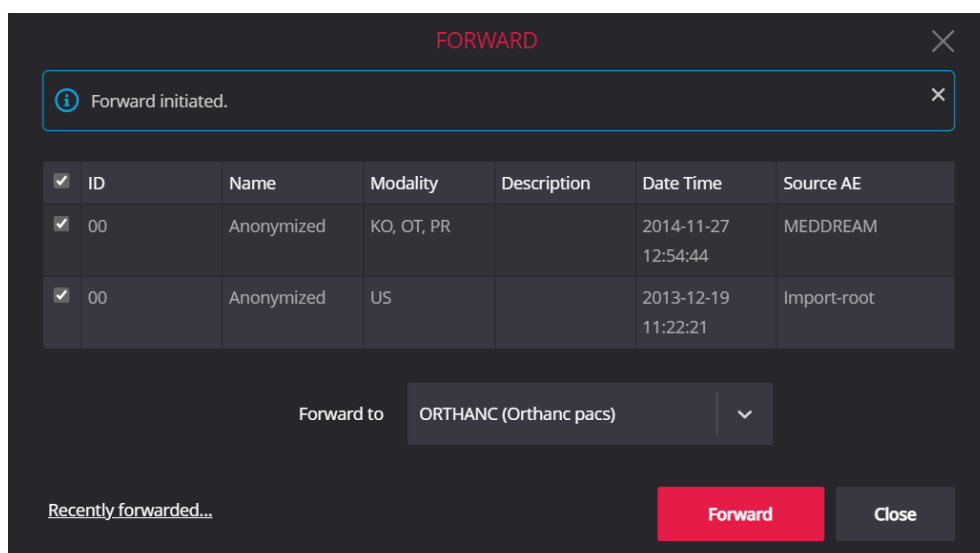


Figure 162. Information about initiated forward process

Click **Recently forwarded...** link in Forward window to see the status of the initiated forward processes:

RECENTLY FORWARDED				
Name	Initiated At	From	To	Status
****	Moments ago	BUNNY	DCM4CHEE	Processing
Anonymized	Less than 5 mins ago	BUNNY	DCM4CHEE	Finished
Anonym, ****, Anonymized	Less than 5 mins ago	ORTHANC, BUNNY	DCM4CHEE	Finished
Anonymized, ****	2021-01-07 16:43:27	BUNNY	ORTHANC	Aborted with error
Anonymized	2021-01-07 16:43:05	Dcm4chee5	ORTHANC	Finished

Close

Figure 163. Forward processes list in Recently forwarded window

The forward processes list contains the following information about each forward process:

- **Name** - patient's name. Multiple commas separated names are displayed, if several studies for different patients are forwarded;
- **Initiated at** - date time, when the forward process was initiated. For processes, that are initiated less than 1 minute ago, the value *Moments ago* is displayed;
- **From** – the name of storage from which the study is forwarded. Multiple commas separated names are displayed, if several studies from different storages are forwarded;
- **To** – forward destination;
- **Status** – status of the forward process. The possible values:
 - *Waiting to be picked up* – waiting for response from forward service;
 - *Preparing* - forward process initialization, that might take a long time in some cases, is in progress;
 - *Processing* - forward process is in progress;
 - *Finished* – forward process is finished;
 - *Aborted with error* - error occurred during forward process.

Click **Close** button to close the Recently forwarded window and return to the Forward window.

Click **Close** button in the Forward window, if you initiated all wanted forwarding.

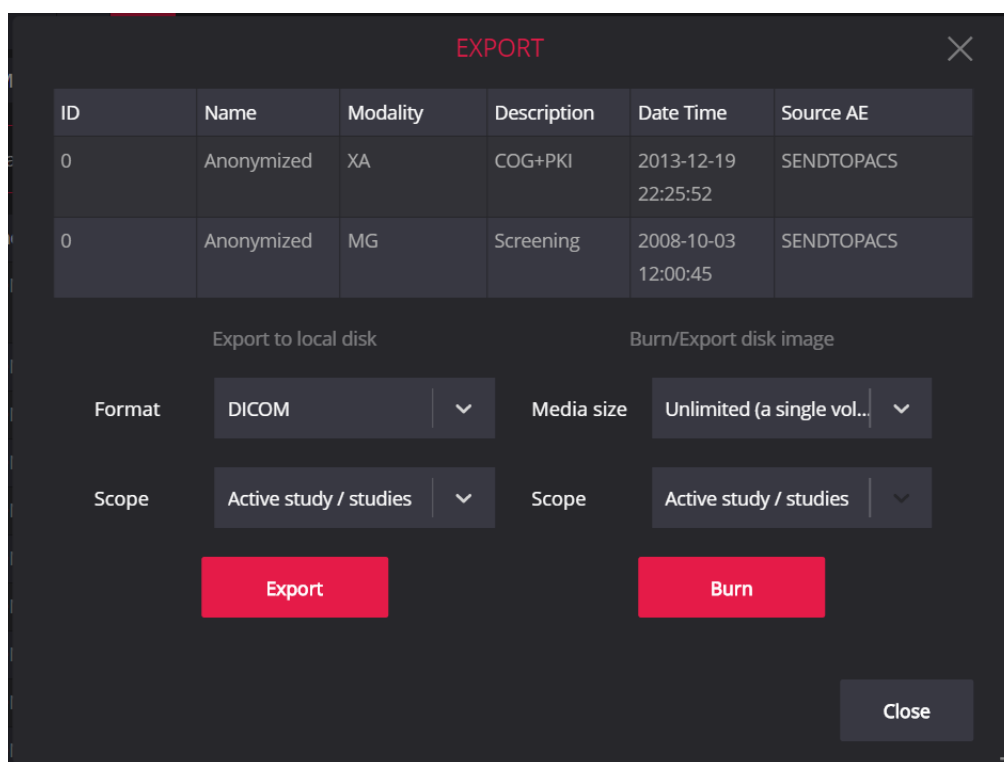


NOTE! The Recently forwarded window shows the last ten forward processes, that were initiated from the current browser window. You can access the forward processes list from the Forward window until the browser window is not closed.

NOTE! The Viewer windows don't share the forward processes list, and each browser window or tab has separate list in Recently forwarded window.

Export / Burn to CD/DVD window

To export the selected studies, click the **Export** button. The system displays the Export window:



The screenshot shows the 'EXPORT' window with a table of studies and export options.

ID	Name	Modality	Description	Date Time	Source AE
0	Anonymized	XA	COG+PKI	2013-12-19 22:25:52	SENDTOPACS
0	Anonymized	MG	Screening	2008-10-03 12:00:45	SENDTOPACS

Below the table, there are two main sections: 'Export to local disk' and 'Burn/Export disk image'.

Export to local disk:

- Format: DICOM (dropdown)
- Media size: Unlimited (a single vol...) (dropdown)
- Scope: Active study / studies (dropdown)
- Export button

Burn/Export disk image:

- Media size: Unlimited (a single vol...) (dropdown)
- Scope: Active study / studies (dropdown)
- Burn button

At the bottom right is a 'Close' button.

Figure 164. Export window

Studies list at the top of the window contains the studies that you have selected for export. If no studies were selected, the "Empty list" message is displayed.

I. Export to local disk

To save the selected for export studies in the archive file on the local disk, do the following:

- Select the file saving format in the **Format** field:
 - if **DICOM** format is selected, the output archive contains DICOM files;
 - if **JPEG/MP4/pdf** format is selected, the output archive contains jpg, mp4(mpg) or pdf files, depending on image format;
 - if **TIFF/MP4/pdf** format is selected, the output archive contains tiff, mp4(mpg) or pdf files, depending on image format;
 - if **PNG/MP4/pdf** format is selected, the output archive contains png, mp4(mpg) or pdf files, depending on image format;
 - if **BMP/MP4/pdf** format is selected, the output archive contains bmp, mp4(mpg) or pdf files, depending on image format.



WARNING! JPEG/MP4/pdf, TIFF/MP4/pdf, PNG/MP4/pdf, and BMP/MP4/pdf formats are disabled in the following conditions:

- At least one study contains object of SR or ECG type, if study export (**Active study / studies**) is selected.
- The active series contains object of SR or ECG type, if series export (**Active series**) is selected.
- The active image is SR or ECG type, if image export (**Active image / video**) is selected.

- Select the export scope in the Scope field:

- selecting the **Active image / video**, exports the image from the active viewport;
- selecting the **Active series**, exports the series of the active image;
- selecting **Active study / studies**, exports all the selected studies.



WARNING! **Active image / video** and **Active series** scopes are enabled only for active study export from Viewer window.

3. Click the **Export** button.

The system launches export process and displays the export progress window:

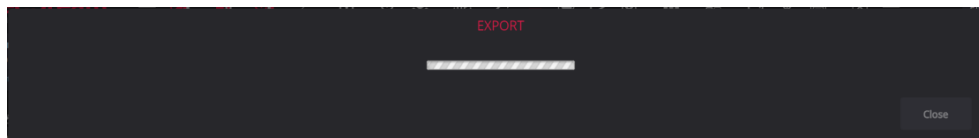


Figure 165. Export progress window

Any other user actions are disabled until the export process is in progress. If the export to file is ended, the export progress window automatically closes and returns to export window. In case of export process failure, the error message is displayed. In case of export process success, the created archive (.zip file) is saved in browser's download catalog.

II. Burn/Export disk image

To burn the selected for export studies in CD or DVD, do the following:

1. Select media in the **Media size** field. The following media sizes are provided in default system configuration:
 - select **Unlimited (a single volume)** format for image saving in a single file;
 - select **CD** format for image split to 650 MB volumes;
 - select **DVD** format for image split to 4.7 GB volumes;
 - select **Dual-Layer DVD** format for image split to 8.5 GB volumes.



WARNING! The media sizes may be supplemented or replaced with other values by system administrator.



NOTE! Scope selection is disabled for burn, and all the selected studies are exported.

2. Click the **Burn** button.

The system launches export process and displays the export progress window:

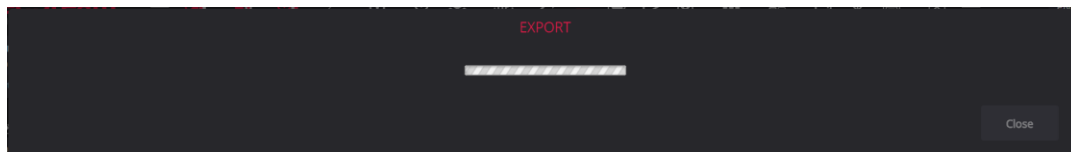


Figure 166. Export progress window

Any other user actions are disabled until the export process is in progress. If the export is ended, the export progress window automatically closes and returns to export window. In case of export process failure, the error message is displayed. In case of export process success, the list of created volumes and controls for saving them are displayed in Export window:

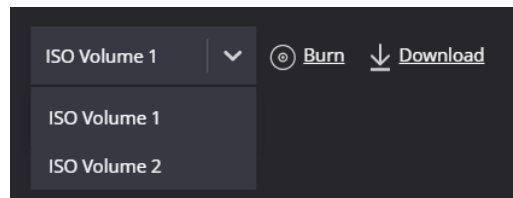


Figure 167. ISO volumes list and saving buttons

3. To burn the created volume, select the volume from the expandable list of created volumes and click the **Burn** link. The system creates the '*.burn' archive and the downloaded file is saved in browser's download catalog. The automatic burning software launch must be configured on user's machine.
4. To save the created volume as '*.iso' file, select the volume from the expandable list of created volumes and click the **Download** link. The system creates the '*.iso' archive and the downloaded file is saved in browser's download catalog. The automatic start of the recording software must be configured on the user's computer.



NOTE! Do not close the export dialog until each created volume is not downloaded or burned. The exported volumes could not be saved, if the export dialog is closed.






WARNING! The viewer may be included in ISO archive, if the appropriate viewer software is provided and system administrator configures to enclose it in export archive.

Report module



NOTE! The Report module is an additional module and should be granted by license.

The Report window is opened by clicking the displayed report icon in the results list of the Search window, or in thumbnail zone, Series modal, or toolbar of the Viewer window:

- Create report  icon is displayed, if the study does not have saved report and the user has right to edit reports.
- Edit report  icon is displayed, if the study has saved report and the user has right to edit reports.
- Open report  icon is displayed, if the study has saved report and the user has right to view reports.



WARNING! The **Report** icon is visible only if the Report module is allowed by license, system configuration, and the user has right to view or edit reports.

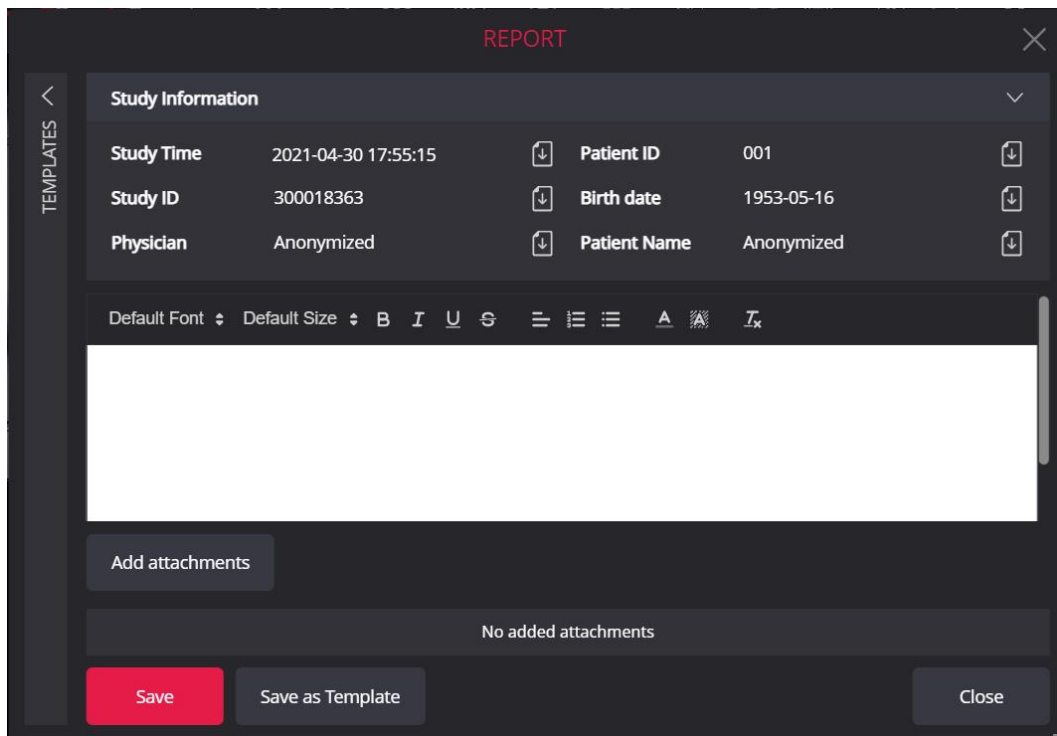


Figure 168. Report window in edit mode is opened after clicking the Create report icon



NOTE! By default, the Report window is opened as modal window. Opening Report window in separate browser tab may be configured in Reports settings (see [Settings](#)).

NOTE! The fields in the Study information may not be displayed, if the corresponding data is not obtained from the DICOM file.

By default, the Report window size is adjusted to the screen size, Study information is expanded, and Templates group is collapsed and displayed either on top, or at the left of the main report fields. You can adjust the report's window view and size.





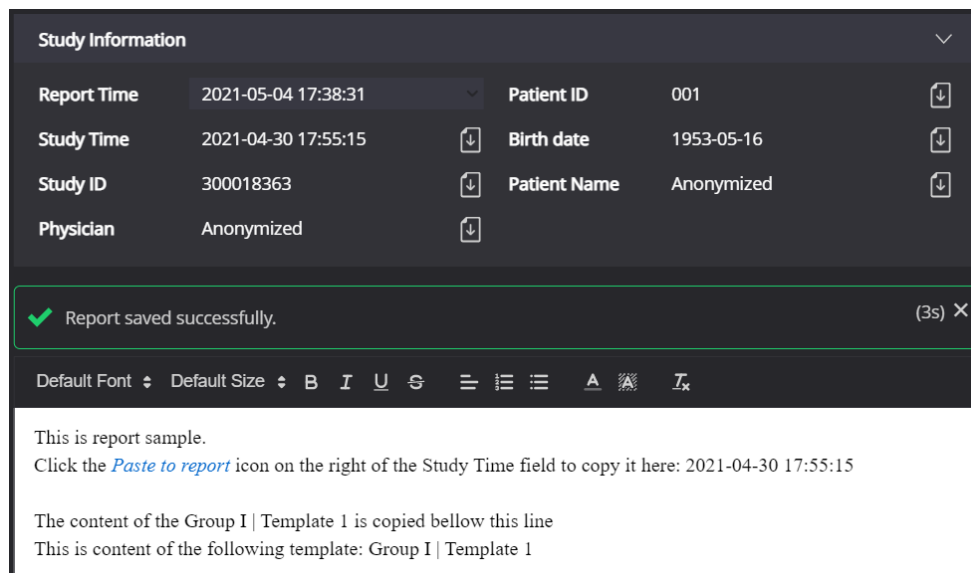
NOTE! The changes in report window size, expand/collapse status of Templates, template group, and Study information are saved in browser local storage and are restored next time the report window is opened by the user.

You can perform the following in the Report window:

- To use and manage the report templates:
 - To expand or collapse Templates section, click the chevron icon above the Template label;
 - To open the Template window with the content of current report to be saved as template, click the **Save as Template** button.
- To view or collapse the study information by clicking the chevron icon on the right of the field.
- To enter and save the report for the study.
- To view and restore the previous report version.
- To print the saved report.

Creating or editing the report content:

- You can enter the report content in editor field. The text and image copy (Ctrl+C), cut (Ctrl+X), and paste (Ctrl+V) is allowed. Use the toolbar above the editor to format text.
- You can copy the Study Time, Study ID, Patient ID, Patient name, Birthday, and Physician data from the Study information to report content:
 - place the cursor in the text editor at the position where the data should be copied,
 - click the Paste to report  icon on the right of the appropriate field,
 - and the system copies the field value to the specified place.
- You can copy the content from the selected report template to the report:
 - place the cursor in the text editor at the end of the line below which you want the template content to be copied,
 - find the template in the templates list, and click the Load template to report  icon on the left of the template name,
 - and the system copies the content of the template in a new line.
- To save the report content, click the **Save** button at the bottom of the Report window. The system saves the report content – the notification about saved report is displayed above the editor, and report saving time is displayed in the first row of Study information:



Study Information

Report Time	2021-05-04 17:38:31	Patient ID	001
Study Time	2021-04-30 17:55:15	Birth date	1953-05-16
Study ID	300018363	Patient Name	Anonymized
Physician	Anonymized		

✓ Report saved successfully. (3s) ✕

Default Font ▾ Default Size ▾ B I U

This is report sample.
Click the [Paste to report](#) icon on the right of the Study Time field to copy it here: 2021-04-30 17:55:15

The content of the Group I | Template 1 is copied bellow this line
This is content of the following template: Group I | Template 1

Figure 169. Report content successfully saved

- You can apply all the above-described action to edit the content of the saved report either directly after saving, or if opening the previously saved report window with Edit report button. Each time you save the report content by clicking the **Save** button, the system creates a new report version and updates the saving time in the Report time field. All the attachments that were added to the previous report version are automatically added to the new report version.



NOTE! All the unsaved report content changes are discarded if the Report window is closed with **Close** button.

Managing report attachments:



NOTE! Attachment can be added only to the saved report, and only to the last report version.

- You can add attachments to the saved report:
 - click the **Add attachments** button,
 - select one or more files in the displayed file open dialog and close the dialog with Open button,
 - system saves attachments, and adds to the last saved report version – the notification about saved attachments is displayed above the editor, and added attachments are listed below the Add attachment button:

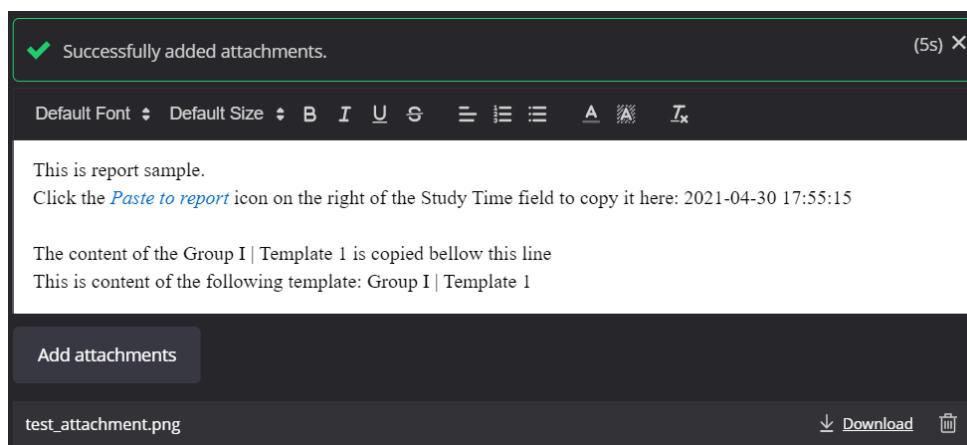


Figure 170. Report attachments successfully added



WARNING! The size limits for one attachment file and one-time upload package, that are defined in system configuration, cannot be exceeded.

- You can remove the report attachment by clicking the Remove button on the right of the attachment – system removes the attachment and displays notification above the editor.
- You can download the attachment to your computer by clicking the Download [Download](#) link on the right of the attachment.

Viewing and restoring the previous report version:

- You can view the previous report version, if more than one report version is saved. Click the chevron icon at the right of the Report Time field and select the report version that you want to view from the report versions drop-down list:

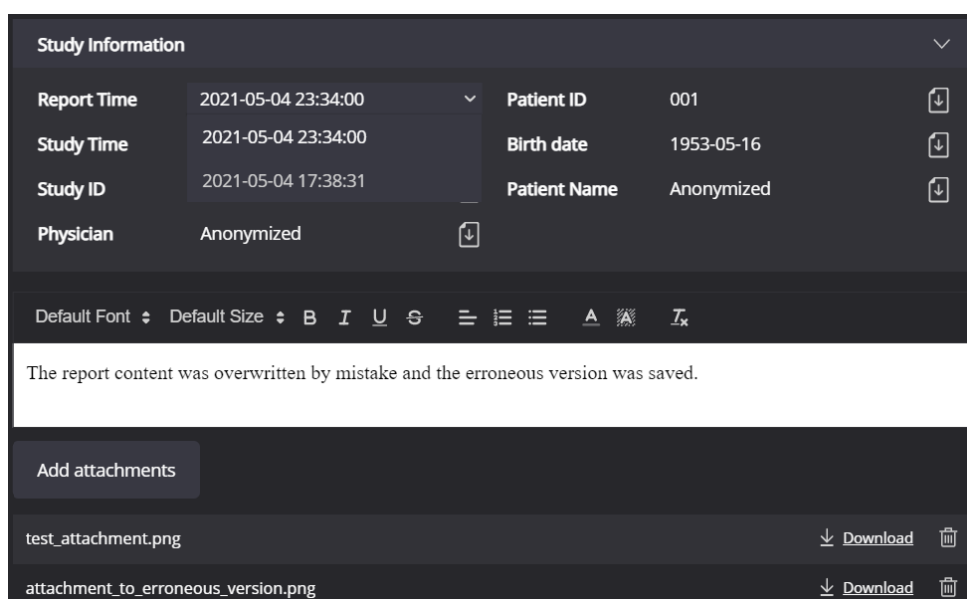


Figure 171. Selecting the report version

- System loads and shows the content of the selected report version. The attachment list displays all the attachments, that were either automatically attached when saving the version, or added to the version by the user after saving.
- You can download the attachments of the report version, view and print the report version. It is not allowed to change the content and attachments of the historical report version.

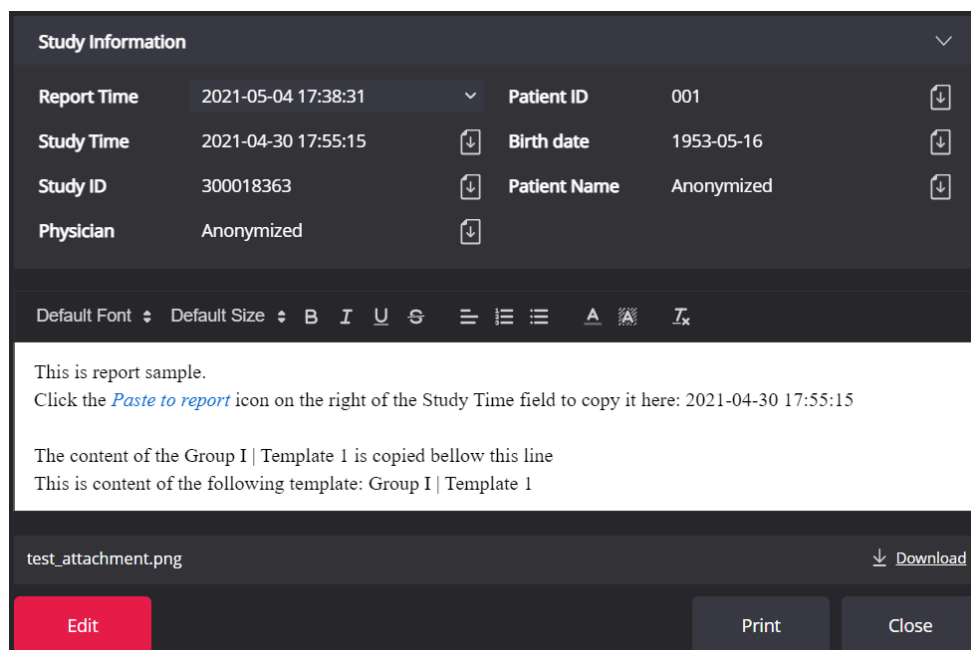


Figure 172. Viewing historical report version

- You can restore the historical report version by clicking the **Edit** button. If action is confirmed, the historical report versions is be saved as the latest.



NOTE! Attachment of the historical report version will be attached to the latest report version, if the historical report version is saved as the latest.

Printing report:



NOTE! The system prints the historical or latest saved report version. You should save the changes you have done, if you want to print them.

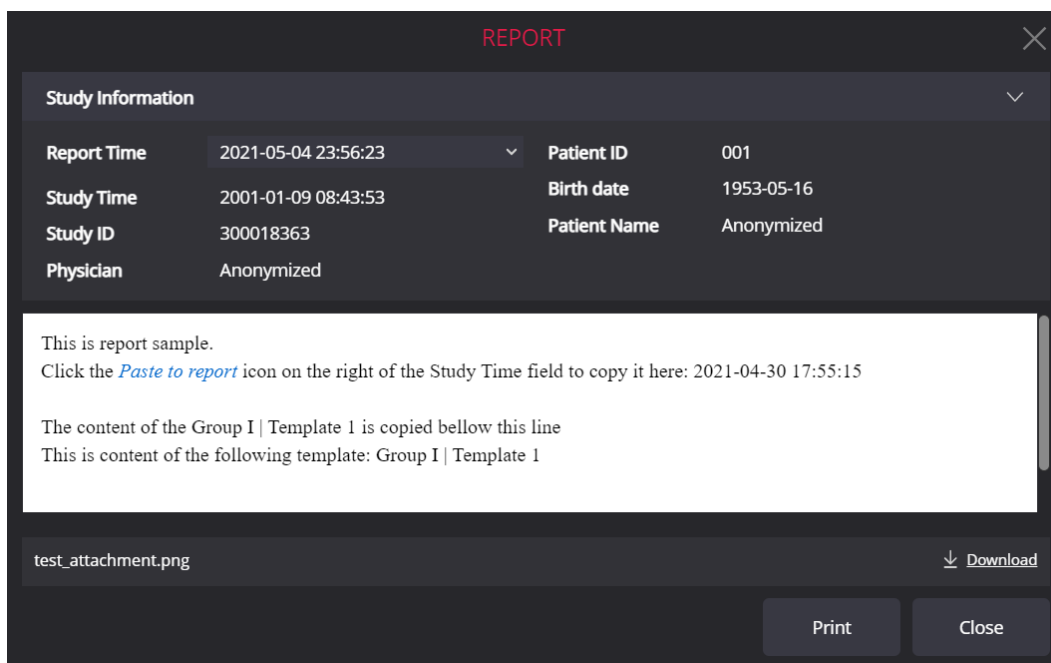
To print the report content, click the **Print** button at the bottom of the Report window. The system opens the report print preview in a new browser tab with the report content wrapped in the print template. The print template may include the additional data, such as company logo, users' signature, data from studies DICOM file.



NOTE! Report print template is configured by system administrator.

Viewing report:

If the user does not have right to edit report, but has right to view reports, the system opens Report window in view mode:



REPORT

Study Information

Report Time	2021-05-04 23:56:23	Patient ID	001
Study Time	2001-01-09 08:43:53	Birth date	1953-05-16
Study ID	300018363	Patient Name	Anonymized
Physician	Anonymized		

This is report sample.
Click the [Paste to report](#) icon on the right of the Study Time field to copy it here: 2021-04-30 17:55:15

The content of the Group I | Template 1 is copied bellow this line
This is content of the following template: Group I | Template 1

test_attachment.png [Download](#)

[Print](#) [Close](#)

Figure 173. Report window in view mode

The user with report viewing rights can perform the following in the Report window:

- View the content of the historical or latest report version;
- Print the content of the viewed report version;
- Save attachments of the viewed report version in users computer.

Managing report templates



NOTE! The report templates are assigned to the system user and are visible only for this user.

NOTE! The report templates section in Report window is visible only if the user has rights to edit reports.

User's report templates are displayed in Templates section of the Report window. You should expand the Templates section to view the list of available templates:

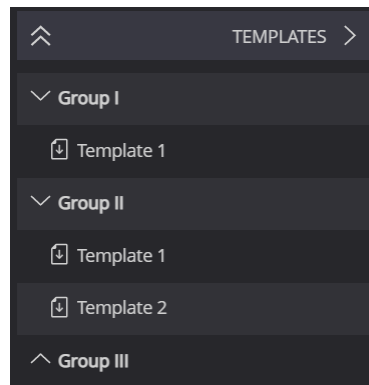





Figure 174. Templates section of the Report window

The templates are grouped by group name, and sorted in a group alphabetically by template name. You can expand and collapse the template group by clicking the chevron icon on the left of the group name. You can expand or collapse all template groups at once by clicking double chevron  icon in the templates' header row.

Hover mouse cursor over the group row to see the group management buttons. You can do the following actions:




- Press the Edit  button, or double-click group name to turn the group name to entry field and edit it directly in templates list;
- Press the Remove  button, and confirm the action to remove the templates group with all the templates in this group.

Hover mouse cursor over the template row to see the template management buttons




. You can do the following actions:

- Double-click template name to turn the template name to entry field and edit it directly in templates list;
- Press the Remove  button to delete the template. The system shows action confirmation message and deletes the template, if confirmed.



NOTE! The template group will not be displayed, if the last template with this group name is deleted.

- Press the Edit  button to view and edit the template's data in Template window:

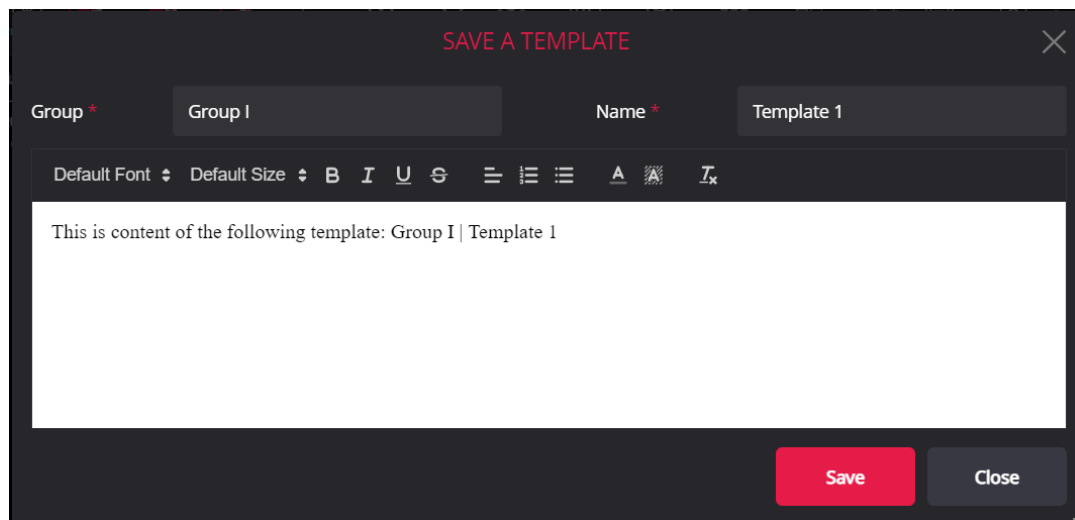


Figure 175. Report template window



NOTE! To create a new template, click the **Save as Template** button at the bottom of the Report window. The system opens Report template window and copies the text displayed in the Report window to it.


You can perform the following in the Report template window:

- To enter or edit group name in Group entry field. If the entered group name equals to the already existing group name, the saved template is displayed in this group. Otherwise, a new group is displayed in template list.
- To enter or edit template name in Name entry field.
- To save the template by clicking the **Save** button. The system saves the template, closes the Template window, and displays the new or updated template in templates list.



NOTE! The changes are not saved, if the Template window is closed with **Close** button.

System menu functions

The section describes all the options that may be displayed under expandable **System** menu .

The system menu in the Search window contains options: **About**, **License Agreement**, **Help**, **Settings** and **Log Off**. The system menu in the Viewer window contains options: **About**, **License Agreement**, **Help**, **Shortcuts**, **Settings** and **Log Off**. Read the conditions, under which the one or more options are not shown, in the Search window and the Viewer window description.

About

Clicking **About** menu opens the information window:

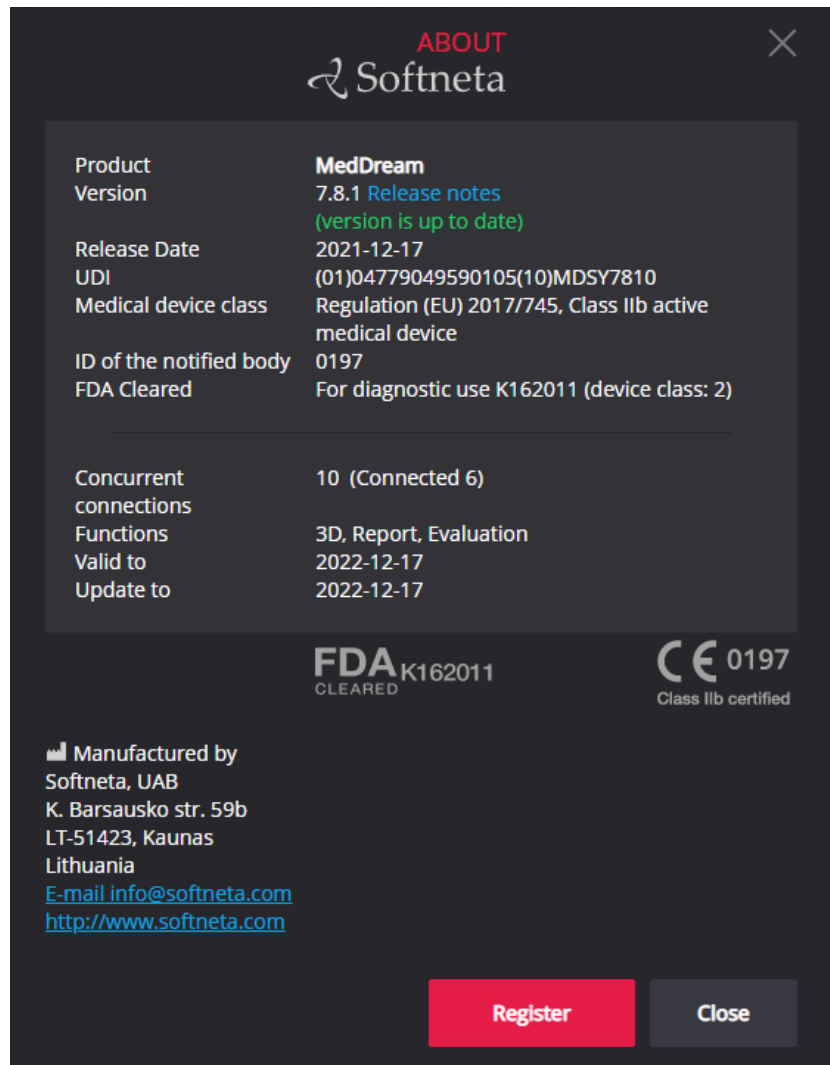


Figure 176. Information window

The description of displayed information:

- **Product** provides the official product name.
- Fields **Version**, and **Release date** holds information about the installed version. The versions' release notes are accessible by clicking the **Release notes** link. If updates are available, the notification is displayed in place of '(version is up to date)'.
- **UDI** – Unique Device Identification number.

- Fields **Medical device class**, **ID of the notified body**, and **FDA cleared mark** holds the products' certification data. The certification information is not applicable for VET installation.
- **License to** contains the information about organization that owns the license of current product installation.
- **Concurrent connections** describe the number of concurrent connections that is issued for the license and the number of currently used connections. The text 'unlimited' indicates that number of connections is unlimited.
- Field **Modules** shows the software modules that are granted by the license (for example, 3D module).
- Fields **Valid to** and **Updates to** indicates dates, until the current license is valid and will receive updates.
- Contacts of product manufacturer.

You can open the release notes modal by clicking the **Release notes** link near the version number:

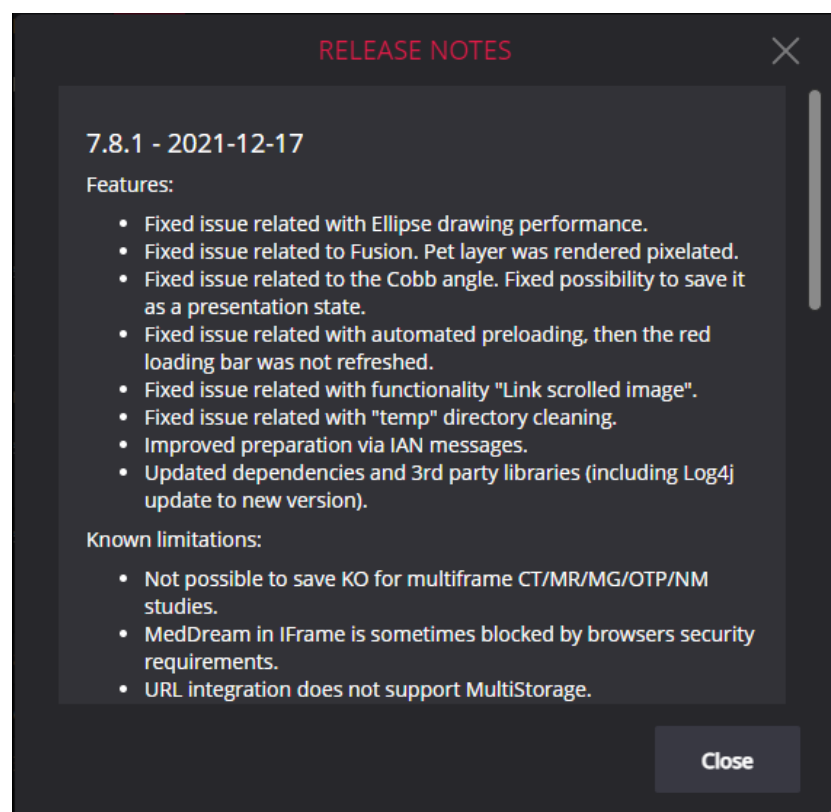


Figure 177. Release notes window

You can initiate the license registration or update by clicking the **Register** button (see description in section [License registration](#)).



WARNING! The **Register** button is visible only if user has administrator right granted by user rights and Settings menu is enabled in system settings.

License Agreement

License Agreement menu opens the **Software License Agreement (EULA)** modal:

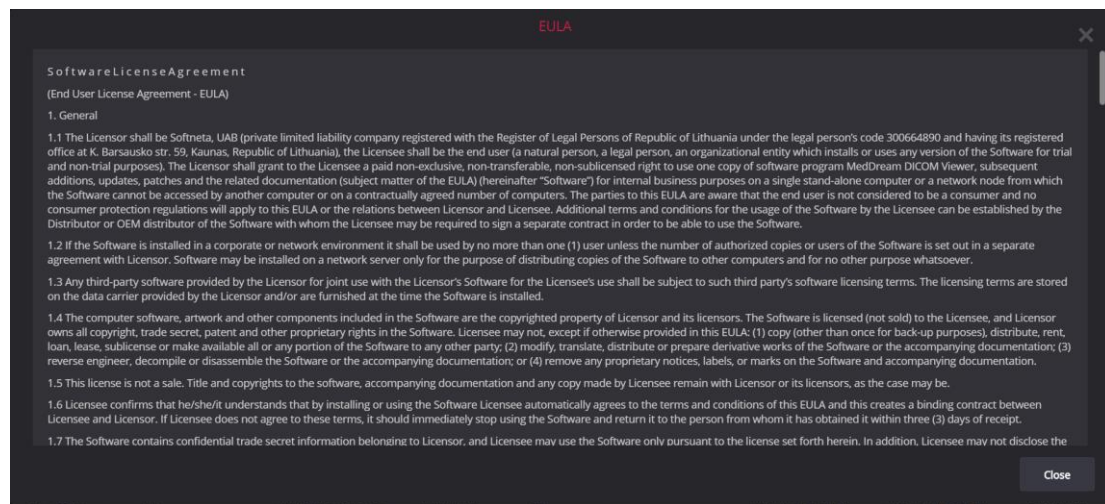


Figure 178. EULA window

Help

Help menu forwards you to the user manual of MedDream WEB DICOM Viewer.

Shortcuts

Shortcuts menu will display modal with keyboard shortcuts. A *keyboard shortcut* is a sequence or combination of keystrokes on a computer keyboard which invokes commands in a software.

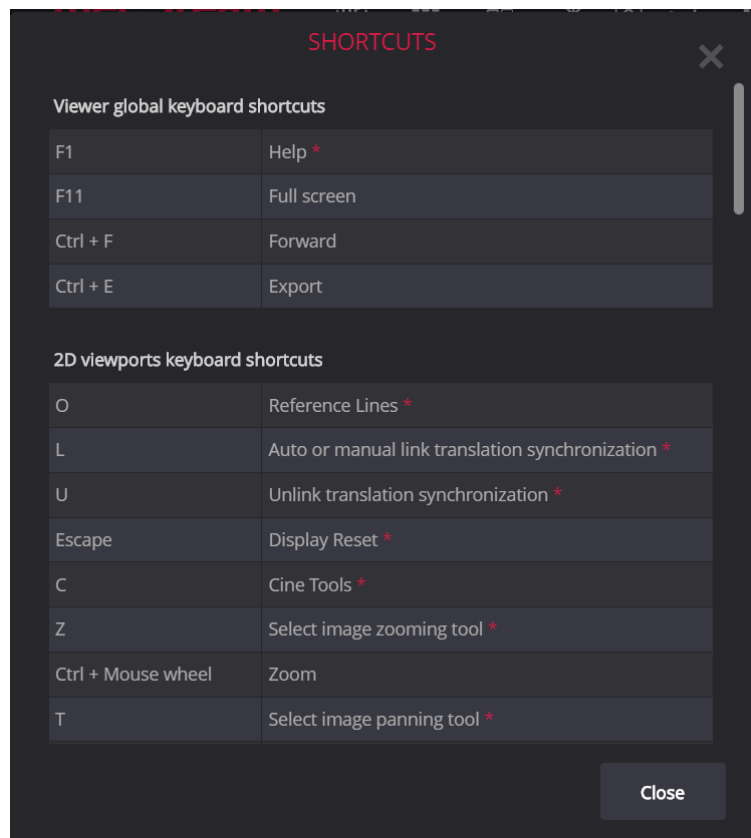


Figure 179. Shortcuts window

Settings

To change MedDream viewer's settings, click button **Settings** and it will lead you to the settings window. For more information see Settings.



NOTE! The **Settings** menu is visible only if user has administrator right granted by user rights and Settings menu is enabled in system settings.

Log Off

Use **Log Off** option, if you finished working with the program. Logging off from the Search window, closes all the Viewer windows that were opened from Search window and destroys the browser session.

In case the integrated solution is used and the Search window is disabled, **Log Off** is available under the System menu in Viewer window.



CAUTION! Please notice, that closing the program without Log Off (using browser window close 'x' button) is not safe and may lead to unauthorized access to medical data.

License registration



WARNING! License registration is required for legal software use. The license registration function is accessible only for users having administrator rights.

You can open the license registration window in such ways:

- By clicking the **Register** button in demo notification window. The demo notification window is displayed, if the system runs without registered license (in demo mode):

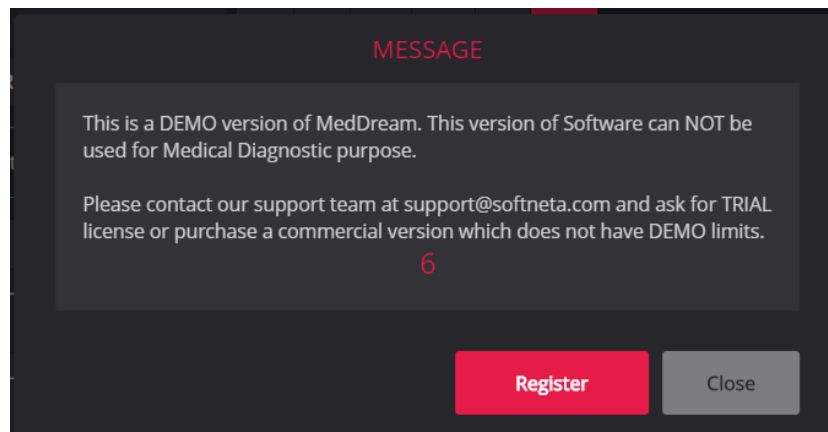


Figure 180. Demo version notification

- By click the **Register** button in About window (see description in section About).

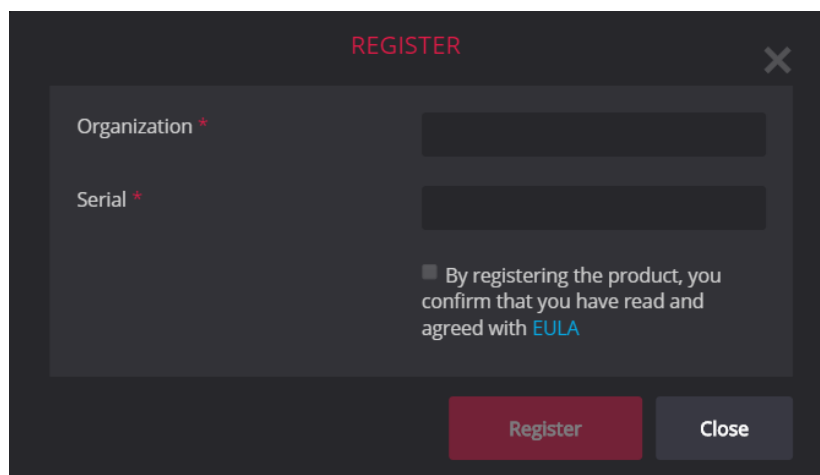


Figure 181. Registration window, if EULA is not read

You should enter the organization and license number that you were given by system administrator or system provider in license registration window. To start registration, you should read the end user license agreement. Click EULA link to open and read the end user license agreement, and check the confirmation box after the reading - the **Register** button is activated:

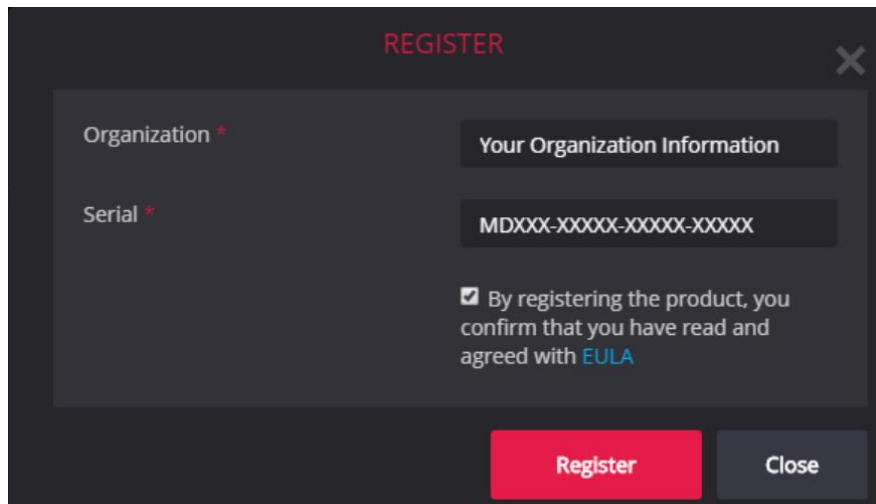
A screenshot of a software registration window titled "REGISTER" in red text. The window has a dark gray background and a close button (X) in the top right corner. It contains two input fields: "Organization *" and "Serial *". The "Organization" field has a placeholder text "Your Organization Information". The "Serial" field has a placeholder text "MDXXX-XXXXX-XXXXX-XXXXX". Below these fields is a checkbox that is checked, with the text "By registering the product, you confirm that you have read and agreed with [EULA](#)". At the bottom right, there are two buttons: a red "Register" button and a gray "Close" button.

Figure 182. Registration window – registration activated

After the **Register** button is clicked, the system connects to the license server, verifies the entered license data, and registers the license. You can view the registered license data in About window.



WARNING! The internet connection and access to license server should be ensured for successful license registration.

Settings

System settings allow you to customize the appearance and functionality of the system according the user's needs. To change your MedDream settings, select **Settings** from the system drop-down menu (this menu is available only to users who has system administrator rights). The settings window is opened in a separate browser tab or window.

System settings are grouped by system windows and / or functions. Each set of settings is in a separate tab, which is opened by clicking on the tab name.

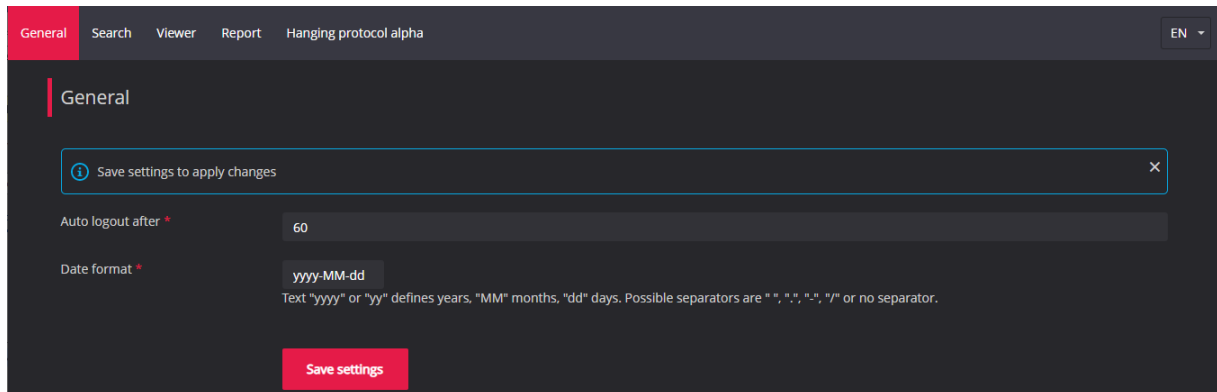


Figure 183. Settings window

The **Save settings** button at the bottom of each tab saves the settings' values into the settings storage. The saved settings are applied after the system restart.



NOTE! You will lose the changes that you've made if you exit the tab or close the settings window without clicking Save Settings at the bottom of the tab.

NOTE! Note that system settings are shared by all users. If you save your changes, the setting, that you or other users have previously saved, will be lost and cannot be restored.

NOTE! Note that user can change some of settings and these changes are saved in browser's local storage. If the browser's local storage contains setting values, the system used these values instead of settings file. To use the settings file, you should clean the browser's local storage on user machine.

A detailed description of each tab is provided in the subsections of this section.

General settings

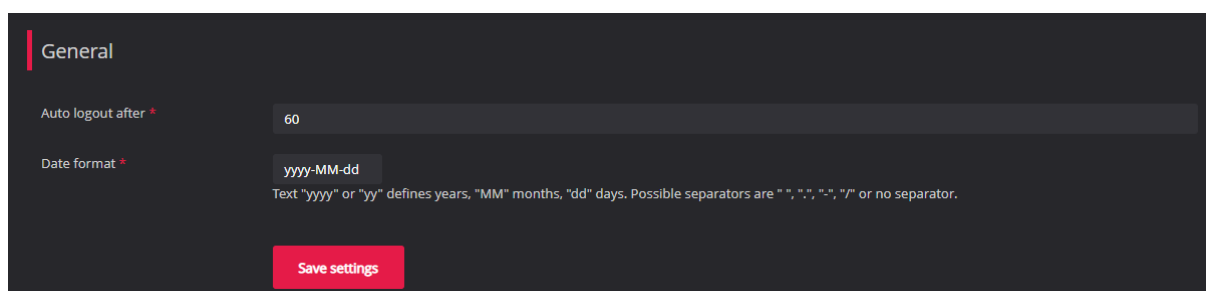


Figure 184. Settings window: general settings

On **General** tab you can modify the following settings:

- **Auto logout after** – you can enter the time frame in minutes when the system will logout automatically in case you forget to logout and close the system window. The default value is 60 minutes.
- **Date format** – you can specify the date display format. The default value is yyyy-mm-dd.

Search window settings

Figure 185. Settings window: search setting

On **Search tab** you can modify the following settings:

Day Filter – you can create day filter that will be applied by default when Search window opens. The filter options are: **any, 1d, 3d, 1w, 1m, 1y**. The default day filter is **3d**.



NOTE! This filter is for compatibility with some PACSes (in MedDream "DICOM" PACS integration mode) that require a date range in all queries. It can also be used in direct integration modes if the database is too slow and accidental activation of the "Any" date choice results in unexpectedly long response times that disrupt the ordinary workflow.

Default modalities – you can select modalities which buttons will be shown on the main search window for quick access. Click the modality button and it is highlighted. To change the selections status, click the modality button once more. The default selection is: CR; CT; DX; MR.



NOTE! The user can change the default modalities in Search window. The changes are saved in browser's local storage and will be applied when the user opens the Search window in the same browser.

NOTE! The default modalities setting is not applicable in mobile mode. In hist all modalities are displayed in Search criteria window and this list cannot be configured.

Study paging – this setting allows you to set the number of studies shown on the page of the main search window. Select the studies per page that you wish to be shown as a default setting from the drop-down list values: 10, 20, 30, 40, 50, 100. The default value is 20 records per page.

Viewer window settings

In **Viewer tab** you can edit general Viewer settings, info label settings, toolbar settings and custom windowing settings.

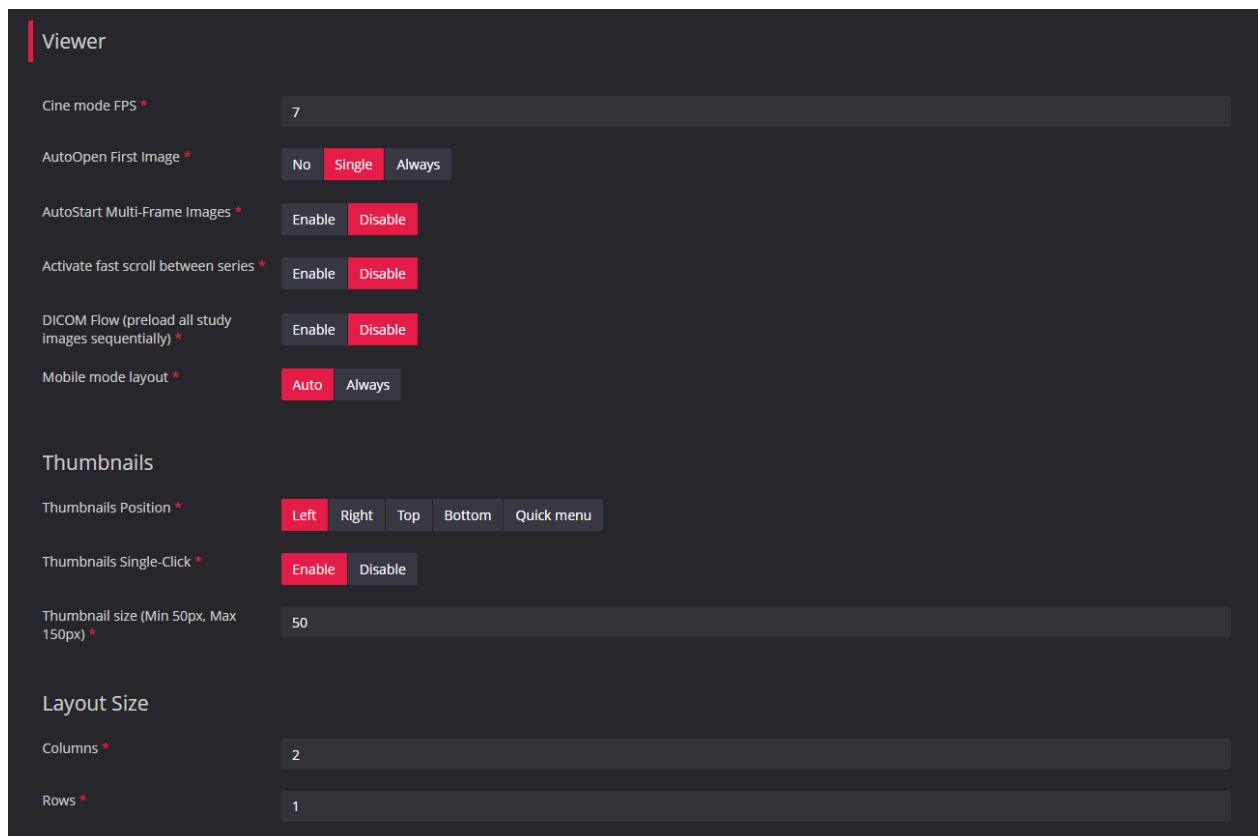


Figure 186. Settings window: general Viewer window settings

In Viewer tab of the Settings window, you can change the following Viewer settings:

Cine mode FPS – number of frames per second when playing multi-frame images. The default value is 7 fps.

AutoOpen First Image – automatically opens the first image according to your choices:

No The first image does not open automatically when the study is opened in Viewer.

Single The first image is opened automatically only if the study consists of one image.

Always The first image is always opened automatically.

The default selection is **Single**.



NOTE! Automatic image opening is applied only if opening study in new Viewer window and in desktop mode.

- **AutoStart Multi-Frame Images** - automatically start playing multi-frame images, if enabled. The default selection is **Disabled**.
- **Activate fast scroll between series** – if option is enabled, the fast scroll function scrolls throughout all the series of the study, that is the first image of the next series is opened when the end of the current series is reached. The default selection is **Disabled**.



NOTE! The user can activate or deactivate the fast scroll between series in Viewer window. The changes are saved in browser's local storage and will be applied when the user opens the Viewer window in the same browser next time.

- **DICOM flow (preload all study images sequentially)** – cache all images in advance. After an image is cached, scrolling through adjacent images takes very little time, but the entire study must fit into browser's memory. The default selection is **Disabled**.
- **Mobile mode layout** forces mobile view used in desktop mode. The **Auto** options applies the mobile layout if working in mobile mode. The software automatically switches to mobile mode, if detects the mobile device on startup or desktop window resolution is resized to less than 992 pixels. If you need the Viewer's window mobile layout in desktop mode, use **Always** option. The default selection is **Auto**.
- **Thumbnails position** – allows to modify position of thumbnails with five possible options: Left, Right, Top, Bottom, Quick menu. The default selection is **Left**.
- **Thumbnails Single-Click** - once the option is enabled, a single click on an image icon will open the image (otherwise a double click is required). The default selection is **Enable**.
- **Thumbnail size** - indicates the size of the thumbnail image from minimum size equal to 50px to maximum size equal to 150px. The default value is 50 px.
- **Layout Size** – indicates the number of viewports in the Viewer window:

Columns - indicates the layout's number of columns. The values from 1 to 6 are allowed. The default value is 2.

Rows - indicates the layout's number of rows. The values from 1 to 3 are allowed. The default value is 1.



NOTE! The user can change the layout size in Viewer window. The changes are saved in browser's local storage and will be applied when the user opens the Viewer window in the same browser next time.

Info Label Properties

The **Info Label properties** section of Viewer tab in Settings window is used to indicate DICOM tags containing the information that should be displayed over the image.

Section	DICOM Tag	Action
Left Side Information	(0020,0010)	Remove
	(0028,0011) x (0028,0010)	Remove
	Add Field	
Right Side Information	(0010,0010)	Remove
	(0010,0020)	Remove
	(0008,103E)	Remove
	(0008,0020) (0008,0030)	Remove
	Add Field	

Figure 187. Setting window: Info Label properties in Viewer tab

In order to add new info label:

- Select the label place (**Left Side Information** or **Right Side Information**) and click **Add Field** in the appropriate section. The system shows the entry field:

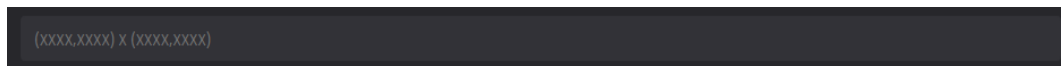


Figure 188. Info Label entry field

- Enter the label. The DICOM tag should be enclosed in parentheses using format (xxxx,xxxx). Label example: Patient position (0018,5100): (0020,1040).
- Save settings.



NOTE! Only first level DICOM tags may be used in labels.

After restart the system loads the new settings and shows the label on the image:

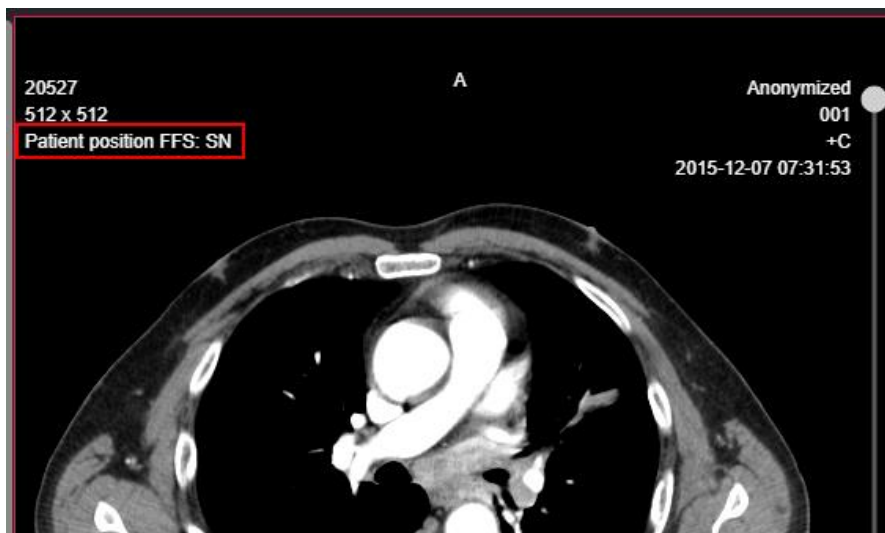


Figure 189. Showing Info Label on image

The default info labels are (see labels' view in the picture above):

- **Left Side Information**
 - (0020,0010) Study ID
 - (0028,0011) x (0028,0010) Image size in pixels Columns x Rows
- **Right Side Information**
 - (0010,0010) Patient's name
 - (0010,0020) Patient's ID
 - (0008,103E) Series Description
 - (0008,0020) (0008,0030) Study date Study time

To remove the label:

- click **Remove** on the right side of the label entry field,
- confirm the action,

- save settings.

Toolbar Properties

In the **Toolbar properties** section of Viewer tab in Settings window you can customize the Viewer toolbar's tools and the order in which they are displayed.

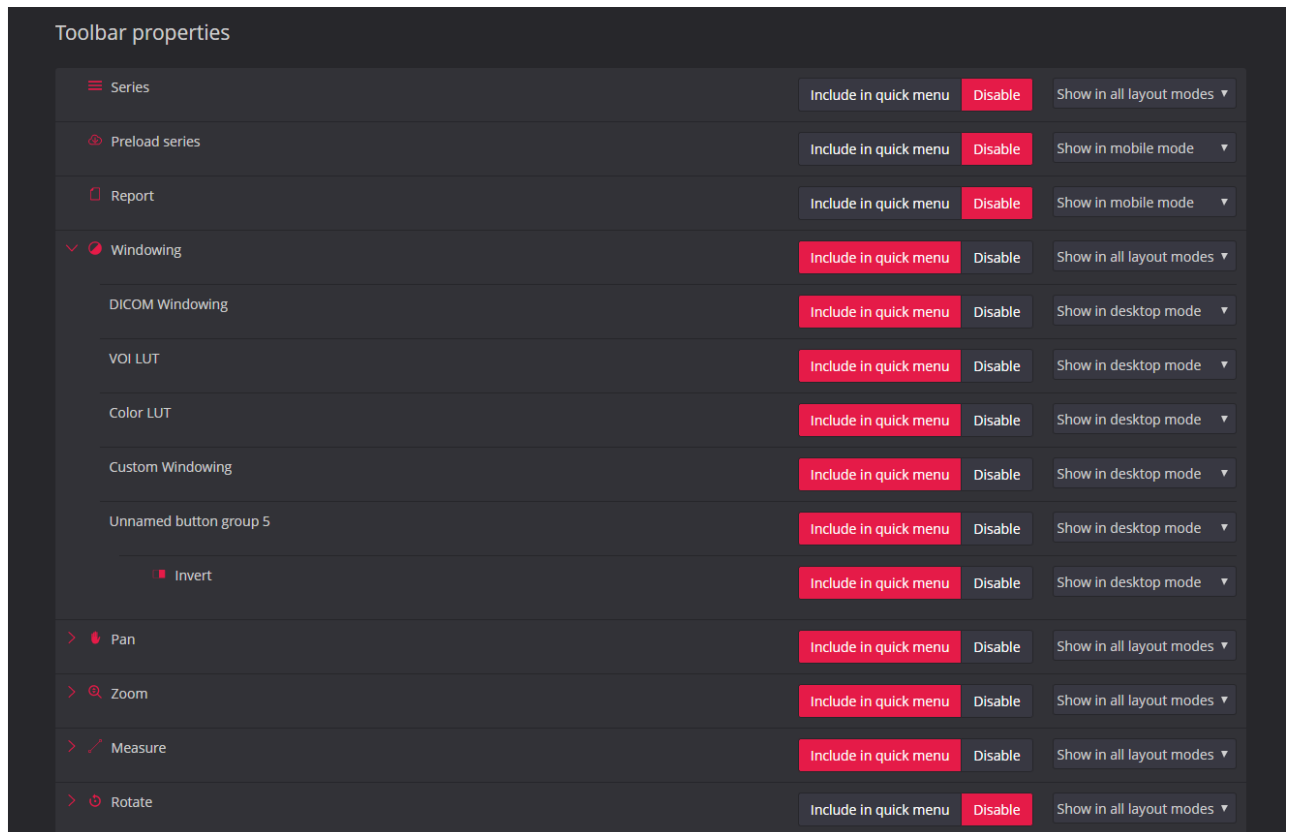


Figure 190. Setting window: Toolbar properties in Viewer tab

Use toolbar properties for:

- Changing the order of toolbar's tools.
- Showing or hiding the tool.
- Customizing the quick menu.

To change the place of tool (or tools group) in toolbar, press the right mouse button on the tool and drag the tool on top of the desired place (line). After releasing the mouse button, the tool will be inserted above the line.

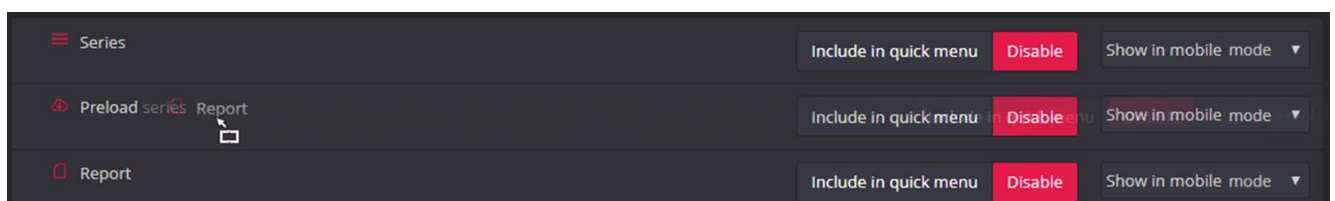


Figure 191. Changing the tool's position in toolbar



NOTE! You can change the tool (or tools group) place in toolbar. You cannot change the item place in tool group (tool's expandable menu).

To customize the toolbar view for different modes, select in what mode the tool should be shown in toolbar:

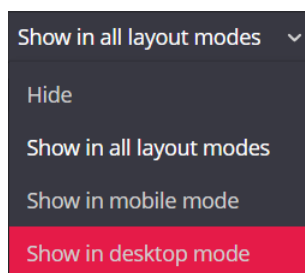


Figure 192. Selecting the tool's showing mode

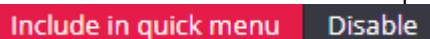
- **Show in all layout modes** – the tool is always shown in toolbar.
- **Show in desktop mode** – the tool is shown in toolbar only if working in desktop mode.
- **Show in mobile mode** – the tool is shown in toolbar only if working in mobile mode.
- **Hide** – the tool is never shown in toolbar.



NOTE! If working in desktop mode with mobile layout (Mobile mode layout set to Always), the desktop toolbar is used.

NOTE! You can change the display mode selection for all levels: the toolbar's tool, options group and menu option in tool's expandable menu. Verify the visibility of higher hierarchy items (like tool's group, or tool's) when changing the item's visibility mode: the option in expandable menu is displayed only if the tool group and tool are visible in the selected mode.

To include the item in quick menu, use the quick menu customization settings



Include in quick menu selection adds the item in quick menu, and **Disable** selection removes it from quick menu. You can include in quick menu the following:

- the menu option from expandable tool's menu, for example the **Line** option from **Measure** tool's menu;
- the group of generated menu options – all the generated menu options will be included in quick menu. For example, the **DICOM Windowing** menu group from **Windowing** tool's menu.



NOTE! The system generates two-level quick menu, if you specify to include the tool itself in the quick menu. Otherwise (the tool (for example, **Measure**) include in quick menu is disabled, and its menu option (for example, **Line**) include in quick menu is enabled) the **Line** option is included in first level quick menu.

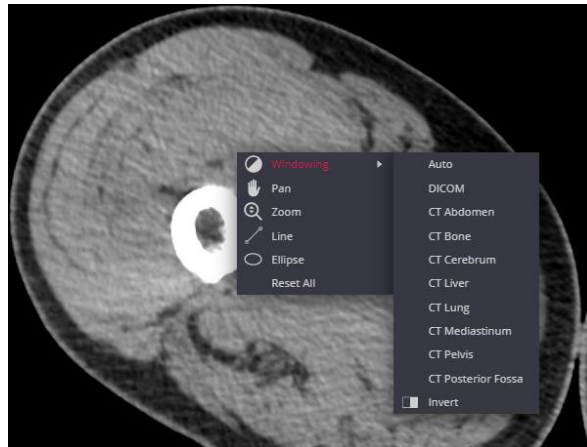


Figure 193. Quick menu: default settings

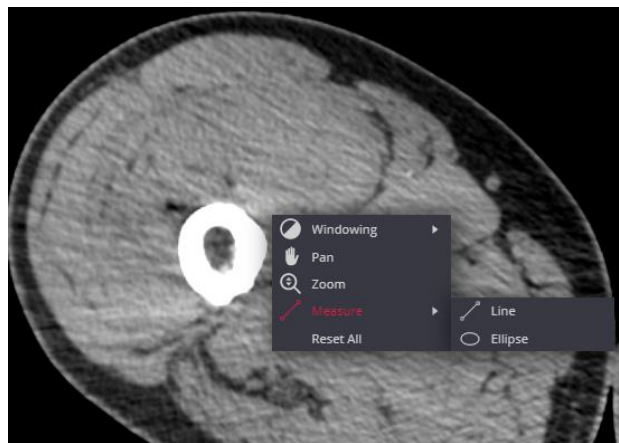


Figure 194. Quick menu: Measure tool included in quick menu and measure option moved to second quick menu level

Windowing settings

The Windowing settings of Viewer tab in Settings window allows users to create a custom window level preset for a selected modality list. The custom windowing options will be shown in expandable **Windowing** menu under **Custom Windowing** group.

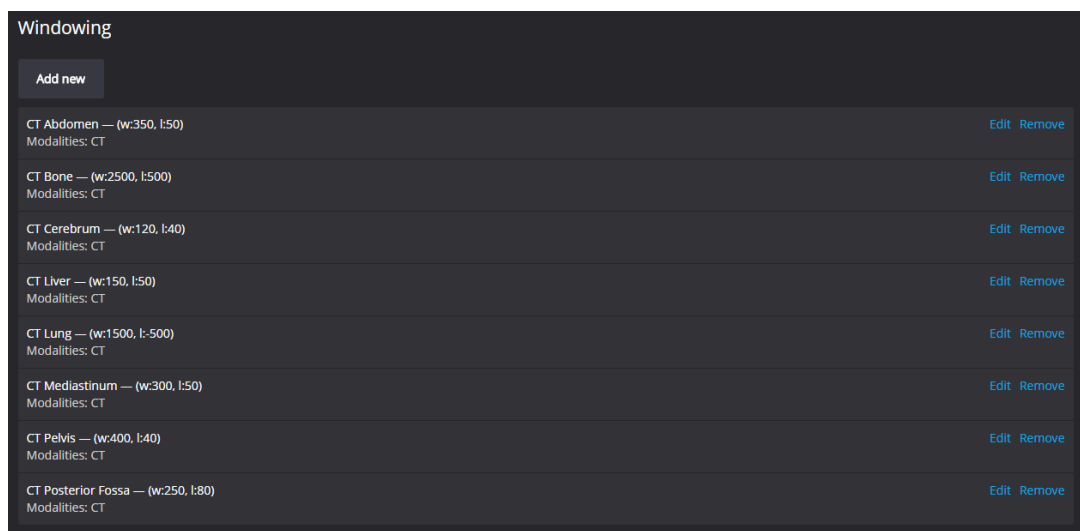


Figure 195. Custom windowing options: default values

The default settings after system deployment contain the following options for CT modality:

- **CT Abdomen** – a preset setting for abdomen studies.
- **CT Bone** – a preset setting for bone studies.
- **CT Cerebrum** – a preset setting for cerebrum studies.
- **CT Liver** - a preset setting for the liver studies.
- **CT Lung** – a preset setting used for studying the images of the lungs.
- **CT Mediastinum** - a preset setting for mediastinum studies.
- **CT Pelvis** – a preset setting for pelvis studies.
- **CT Posterior Fossa** - a preset setting for Posterior Fossa studies.

To create custom windowing option:

- click **Add new**;
- enter values for the custom windowing option: **Label**, **Width**, and **Center**. Select modalities of your choice in order to assign the new window level function to certain modality (-ies). All four fields are mandatory:

The 'Create windowing' dialog box is shown with the following details:

- Title:** Create windowing
- Label *:** Test
- Width *:** 150
- Center *:** 150
- Modalities *:** A grid of buttons including CR, CT (highlighted), DX, ECG, ES, IO, MG, MR, NM, OT, OP, PT, PX, RF, RG, XA, US, XC, and LIVE.
- Buttons:** Create (red), Close (grey).

Figure 196. Custom Windowing creation window

- once done that, click on **Create** button.

New predefined Windowing level will appear on the Windowing menu, if the modality of the active image corresponds to the custom windowing modalities. To apply the custom windowing, click its title in drop-down menu.



Figure 197. Custom windowing in the drop-down Windowing menu

You can remove the custom windowing by clicking the **Remove** button on the right of the record. You can **Edit** the custom windowing values, if desired.

Report settings



Figure 198. Settings window: report settings

On **Report** tab you can modify the following settings:

- **Open in new window** – selecting the **Enable** option opens the study Report in a new browser tab. The default selection is **Disable** and the Report is opened in modal window.

Hanging protocol settings

On **Hanging protocol** tab, you can create new hanging protocols, review and modify existing hanging protocols.

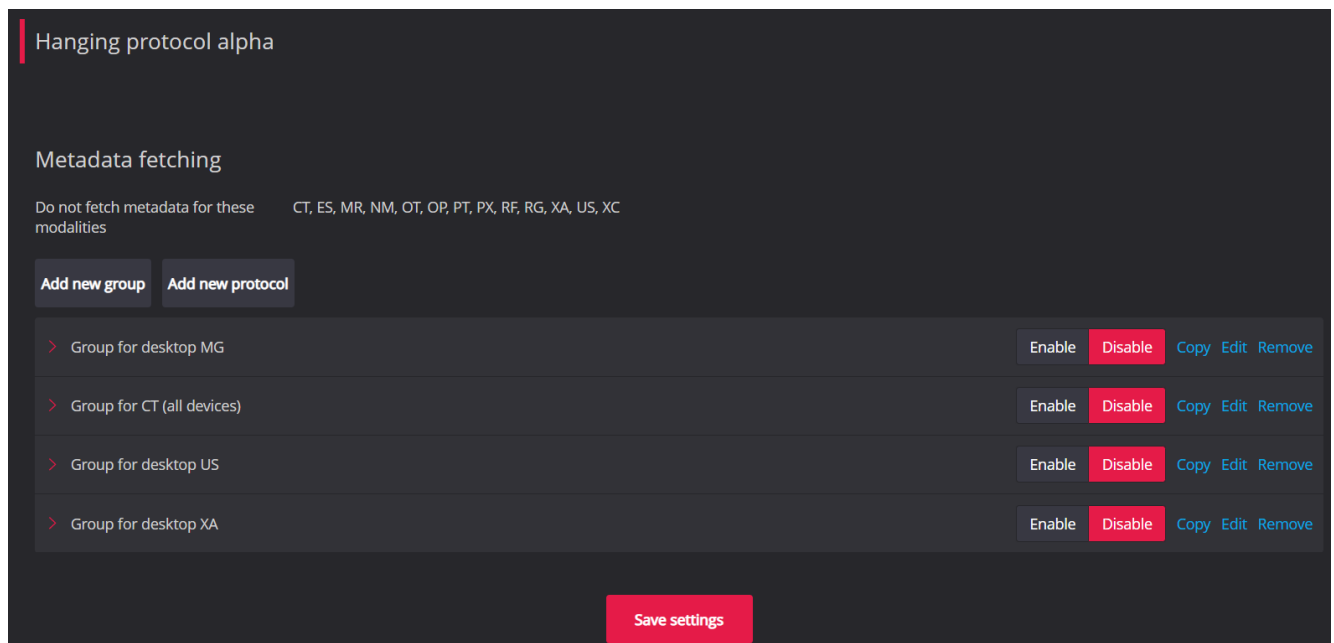


Figure 199. Hanging protocol settings



NOTE! All the data changes that are done in Hanging protocol list, group and protocol child windows (like create group window, create protocol window) are saved in the temporary storage. That means the changes are not accessible to the other users and would be lost in case of program accidental close. The permanent data saving is done only when the **Save settings** is done.

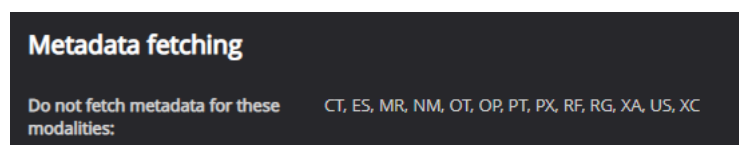


Figure 200. Modality filter for metadata fetching

By default, “Do not *fetch metadata for these modalities*” are set for modalities CT, ES, MR, NM, OT, OP, PT, PX, RF, RG, XA, US, XC. If metadata is not used, only the conditions with following tags are executed:

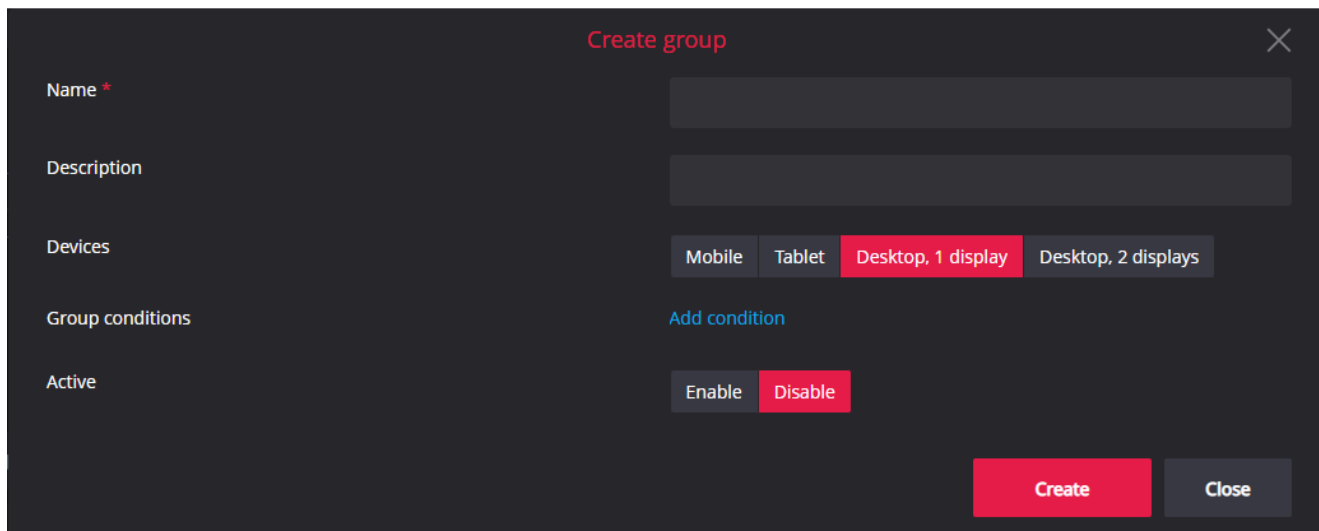
- Special tags: series_count, instances_count, no.
- DICOM tags: (0008,0016) SOPClassUID, (0002,0010) TransferSyntaxUid, (0008,0060) Modality, (0010,0010) PatientName, (0008,1030) StudyDescription, (0008,103E) SeriesDescription.
- In conditions with DICOM tags (0020,0011) SeriesNumber and (0020,0013) InstanceNumber, the system correspondingly uses the series or image serial number, starting from 0, instead of the tag's value from DICOM file.

If the Hanging protocol includes conditions with tags other than those listed above, such conditions are ignored.



WARNING! In Hanging protocol alpha version, the setting **Do not fetch metadata for these modalities** can only be modified in settings file. Note that for large-scale studies (for example CT, MRI) it is recommended not to use metadata due to long loading time.

Clicking the **Add new group** button on Hanging protocol tab opens the **Create group** window:



The 'Create group' window is a dark-themed dialog box with a close button (X) in the top right corner. It contains the following fields and controls:

- Name ***: A text input field.
- Description**: A text input field.
- Devices**: A row of four buttons: 'Mobile', 'Tablet', 'Desktop, 1 display' (highlighted in red), and 'Desktop, 2 displays'.
- Group conditions**: A blue link labeled 'Add condition'.
- Active**: A row of two buttons: 'Enable' and 'Disable' (highlighted in red).
- At the bottom right are two large buttons: 'Create' (red) and 'Close' (dark gray).

Figure 201. Create hanging protocol group window

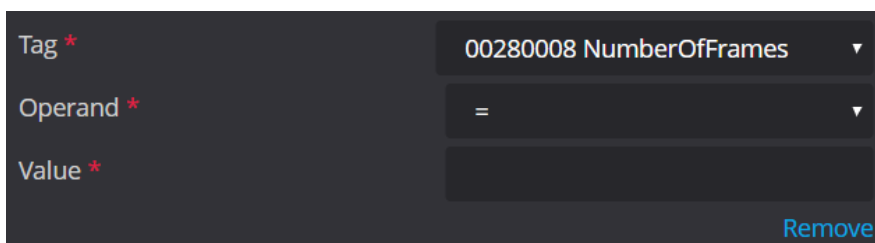
To create a new hanging protocol group:

- Enter the required group name in **Name** field. The group name is used for protocol identification and is shown to the users in MedDream viewer.
- If you need, enter the group description in **Description** field. The group description is only visible in settings.
- Select the **Devices** for which the group's protocols should be applied. Clicking the button with device name enables or disables selection.
- Specify the **Group conditions**.

Entering the Hanging protocol condition

Condition is an expression that could be evaluated as true or false and is used for automatic applying of Hanging Protocol. Condition consist of special tag or DICOM tag that is evaluated against static value according the specified 'operand'. An example of condition: 'Modality equals to 'XA''. Several conditions are joined using AND operand, that means all conditions in the group should be met.

A **Tag**, **Operand** and **Value** fields for new condition entry is displayed if **Add condition** is clicked:



The 'Hanging protocol condition's entry fields' form is a dark-themed dialog box with the following fields and controls:

- Tag ***: A dropdown menu showing '00280008 NumberOfFrames'.
- Operand ***: A dropdown menu showing '='.
- Value ***: A text input field.
- A blue 'Remove' button is located at the bottom right.

Figure 202. Hanging protocol condition's entry fields

To enter the condition:

- select DICOM or special tag in **Tag** drop-down list. In group conditions the special tags **series_count** (number of series in study) and **instances_count** (number of images in study) can be used;
- select the evaluation operand in **Operand** drop-down list. The operands list is automatically adjusted to the type of selected tag. The operands list for numeric tags: "=", ">", "<", ">=", "<=", "!=". The operands list for string tags: "match", "not_match", "begins_with", "end_with", "contain";
- enter the value in **Value** field. The string value should be entered for string tag, and the numeric value should be entered for numeric tag.

To remove the entered condition, click the **Remove** button below the condition entry fields.

- Activate hanging protocol group by selecting Enable or Disable buttons in the **Active** field. The disabled groups and its protocols are not used for automatic or manual apply.
- Click the **Create** button when all the group data is entered. The **Create group** window is closed, the entered group data is saved in temporary storage and is shown at the end of hanging protocol list on Hanging protocol setting tab.

Clicking the **Add new protocol** button on Hanging protocol tab opens the **Create protocol** window:

Figure 203. Create protocol window

To create a new hanging protocol:

- Select the group of the hanging protocol in **Group** drop-down list.
- Enter the required protocol name in **Name** field. The protocol name is used for protocol identification and is shown to the users in MedDream viewer.
- If needed, enter the protocol description in **Description** field.
- Define the layout by entering the number of columns in **Layout columns** field and the number of rows in **Layout rows** field.
- Specify the **Study conditions**, that will be used to select whether the protocol should be applied to the study. See description of condition entering on page 171.
- Specify the image selection and display data for each view:



NOTE! The view is identified by number [row number]x[column number], that is identifier “1x2” indicates the view in the first row and second column. The arrow near the view indicator can be used to expand or collapse the data entry fields for the view.

Figure 204. Entering View settings in hanging protocol

- specify the **Prior conditions** if you want the image from other study in patient history to be loaded in the view. The special tag **no** (the number of prior study from patient's history, starting from the most recent as "1") can be used. If **no** not specified, the most recent prior study that meets the other conditions is taken. See description of condition entering on page 171;
- specify the **Instance condition** for selecting the image from the study, that you are opening (or prior study, if prior study conditions are entered), to display in the view. See detail description of condition entering on page 171;
- enter the values for image display: windowing, rotation, scale, alignment.
- Click the **Create** button when all the protocol and views data is entered. The Create protocol window is closed, a new protocol is saved in temporary storage and is shown as the last protocol of selected group in protocols list on Hanging protocol setting tab.

The Hanging protocol list is two level expandable list with the hanging protocol group in the first level and the hanging protocols of the group in the second level.

Figure 205. Hanging protocols list

You can perform the following in the hanging protocols list:

- To expands or collapse the list of group's protocols with chevron icon at the left of group's name.
- To enable the group's protocols by selecting the Enable/Disable buttons. The disabled groups and its protocols are not used for automatic or manual apply.
- The controls at the end of each group's and protocol's line provides access to group's or protocol's data review and edit:

- clicking the **Copy** button makes the copy of hanging protocol or group of protocols. The protocol is placed at the end of the group protocols list and postfix “-copy” is added to the name of the copied protocol. The group is placed at the at the end of the group list and postfix “-copy” is added to the name of the copied group and all its protocols;
 - Clicking the **Edit** button at the end of group line opens the **Edit group** window with group data filled in the entry fields. You can review and edit the group's data. See detail fields description on page 170;
 - Clicking the **Edit** button at the end of protocol line opens the **Edit protocol** window with protocol data filled in the entry fields. You can review and edit the protocol's data. See detail fields description on page 172;
 - Clicking the **Remove** button at the end of group or protocol line deletes the item. If the group is removed, all the protocols of this group are also deleted.
- The drag-and-drop functionality for changing the order of group in the list and for changing the order of protocols in the group. To change the place of the group or protocol item, press the right mouse button on the item and drag the item to the desired place. The items order is important in automatic hanging protocol apply: the first group, that meets the group conditions, is chosen and the first protocol of this group, that meets the study conditions, is applied.

MedDream Mobile mode

You do not need a separate MedDream software version to use it on mobile devices. MedDream software automatically switches to mobile mode, if detects the mobile device on startup or desktop window resolution is resized to less than 992 pixels.



WARNING! Note, that browser's zoom function changes resolution and the software may automatically switch to mobile mode.

Features of MedDream mobile mode:

- Adjusted Search window layout;
- Adjusted Viewer window layout;
- Adjusted Settings window menu;
- Some functional limitations.

Further subsections describe Search window, Viewer window, and Settings window mobile layout and mobile mode functional limitations. For detail functionality and usage description see [Logging on to MedDream](#), [Search of studies](#), [MedDream DICOM Viewer](#), and [Settings](#) sections of this manual.

Search of studies in mobile mode

Search for studies mobile layout consist of two windows:

- Search criteria window;
- Search results window.

If successfully logged in, the **Search criteria** window opens:

Figure 206. Search criteria window in mobile mode

The following search criteria are supported in mobile mode:

- **ID** – patient's ID,
- **Name** - patient's name and/or surname,
- **Description** –study description,
- **Date Time** - date interval, selected in pick list,
- **Modality** – modalities selected in pick list,
- **Storage** – the PACS or other configured storage., selected in drop-down list.

See the detail description of search criteria in section Search of studies.



WARNING! The mobile mode has the following search limitations comparing to desktop version:

- search according accession number and source AE title is not allowed;
- search according custom date interval is not allowed;
- the customization of modalities pick list and search according custom modality is not allowed.

To find the study, enter **search criteria** and press the **Search** button. System displays the studies list in the **Search results** window:

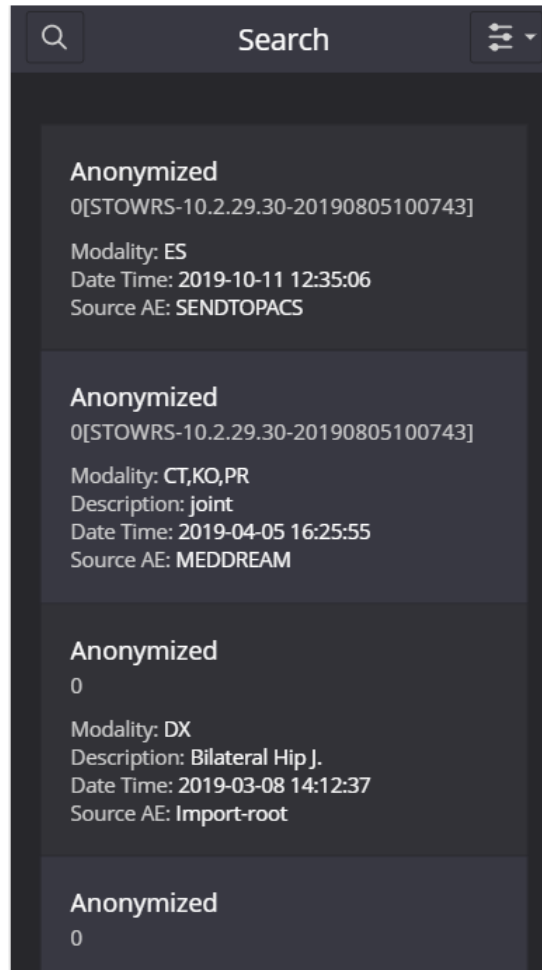


Figure 207. Search results window in mobile mode

The results list displays the following study information:

- Patient's name and surname in the first line.
- Patient's ID number in next line.
- **Modality** – field shows method which was used to obtain the study images (modality).
- **Description** – field shows study description
- **Date Time** – field shows study date and time
- **Source AE** – field shows title of the device from where the study was sent to the PACS.



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

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

1. To navigate through result list, use scrolling or dragging up and down. The number of currently loaded studies and total number of search results are displayed at the bottom of the list:

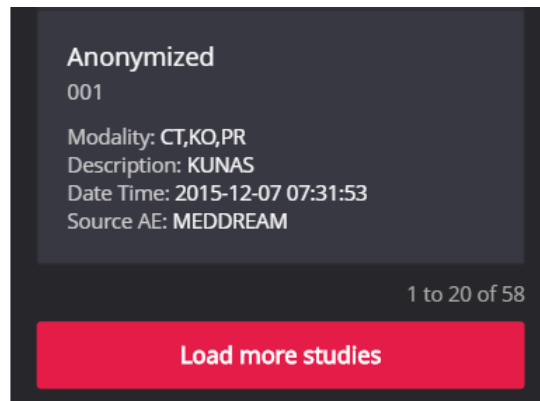


Figure 208. Page navigation in the search results in mobile mode


2. To load more studies, press **Load more studies** button – next page is loaded.




NOTE! The number of studies per page is defined in system settings.


NOTE! The **Load more studies** button is not displayed if all the studies are loaded.

3. To open the study in viewer, press at any place of study description. The selected study opens in Viewer (see Opening studies in MedDream Mobile mode section for detail description).

4. To return to the Search criteria window, press the search button  at the top left corner of the search results window.

The description of the other buttons in the **Search criteria** window and **Search results** window:

1. To change the language, press the **Language** button  at the top left corner of the **Search criteria** window and press the language option in drop-down menu.

2. **System** menu  at the top left corner of the **Search criteria** window and **Search results** enables access detailed system information and functionality description (see System menu functions section for detail description).



WARNING! Systems menu options may be disabled in Settings. The Settings options may also be not allowed by user rights.

WARNING! The Forward and Export functions in search results list are not available in mobile mode.

Viewer window in mobile mode

The Viewer window mobile layout contains the following zones:

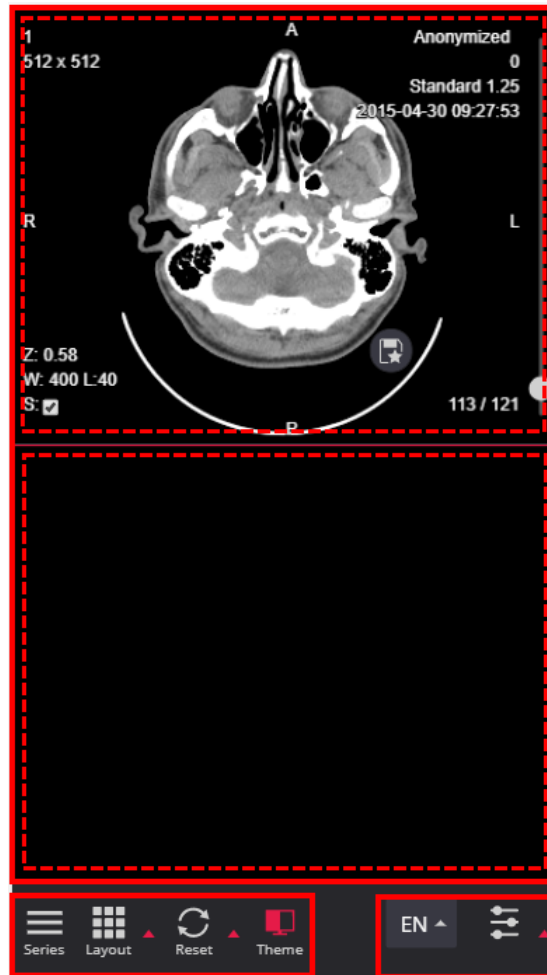


Figure 209. Viewer window zones in mobile mode

1. Image manipulation tools zone is shown at the bottom left side of the window. What buttons and in what order are shown in toolbar is described in system settings (see section Toolbar Properties).



NOTE! The tools set may vary depending on content of the active viewport.

If there is not enough space for all toolbar buttons, the toolbar is extended and horizontal scroll bar is displayed under the toolbar:

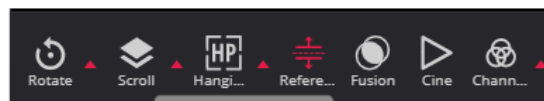



Figure 210. Toolbar's scrollbar in mobile mode.

Drag the toolbar to get the required tools.

In toolbar you can activate tool usage, if the tool can be operated on the touch screen. To activate the tool, follow these steps:


- Press on the icon of inactive tool



- The tool is activated and tool icon is highlighted . In the example, the activated Windowing tool can be used on the touch screen: dragging upwards or downwards changes Level values, and dragging right or left changes Window values.

The tool activation is deleted by pressing the tool icon once more or by activating another tool.



NOTE! Mobile mode does not support middle and right mouse button actions and only the tool, that is associated with the left mouse button (indicated by mouse icon ) , is activated.

For a description of image manipulation tools in mobile mode, see the section Manipulating images in MedDream Mobile .

Press the triangle on the left of tool icon or long press tool icon to open the modal with tool's menu:

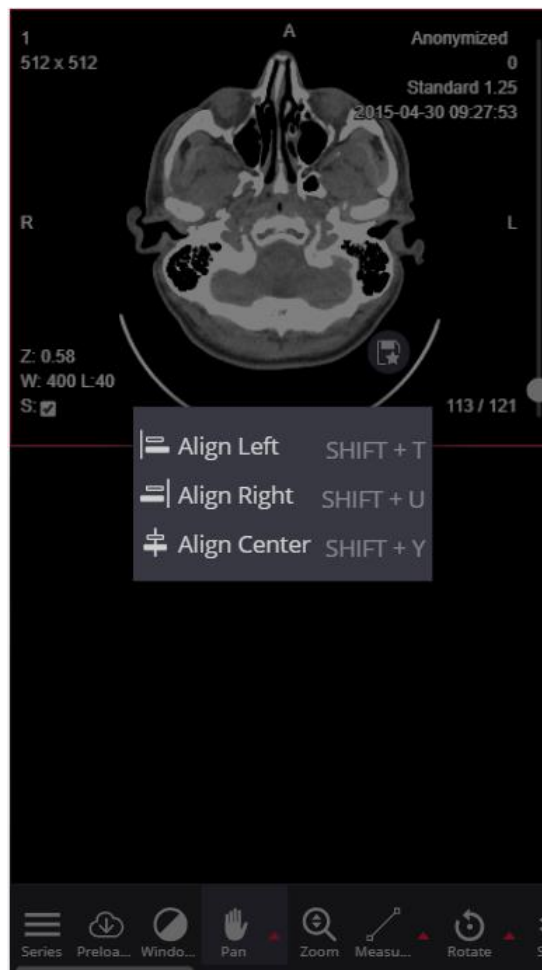


Figure 211. Tool's menu in Viewer window in mobile mode

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

2. The system tools zone at the bottom right corner of the window contains language selection button and system menu button, that function identically as in desktop mode (see description on page 41).

3. The view zone takes the largest part of the Viewer window and is designated to view and analyze the images. The view zone may be divided to several sections, each section (dashed line in figure) working as separate viewport for image viewing. The manipulation is allowed in one active viewport at a time. To activate the viewport, press on the viewport area – the active viewport is highlighted. The image manipulation toolbar is automatically adjusted according the content of the active viewport.

At the right side of the viewport the scroll bar with the scroll cursor, that is scrolled respectively to the position of the active image in the series, is shown. At the bottom of the scroll bar is the total number of images in the series and the number of the active image. Dragging the cursor along the scroll bar or pressing on the desired scroll bar position changes the image.



NOTE! Viewer window mobile layout does not support thumbnail. To open the image use toolbar's button **Series** (see description in section [Series](#)). To preload the series images, use toolbar's button **Preload Series** (see description in section [Preload Series](#)).

NOTE! The quick menu is not supported in mobile mode.

Opening studies in MedDream Mobile mode



NOTE! See section [Patient studies list in mobile mode](#) for detail description how to open the studies from the Patient studies list.

To open the study from MedDream Search window, please do the following:

1. Find the required study in Search results window and press on the study description area:

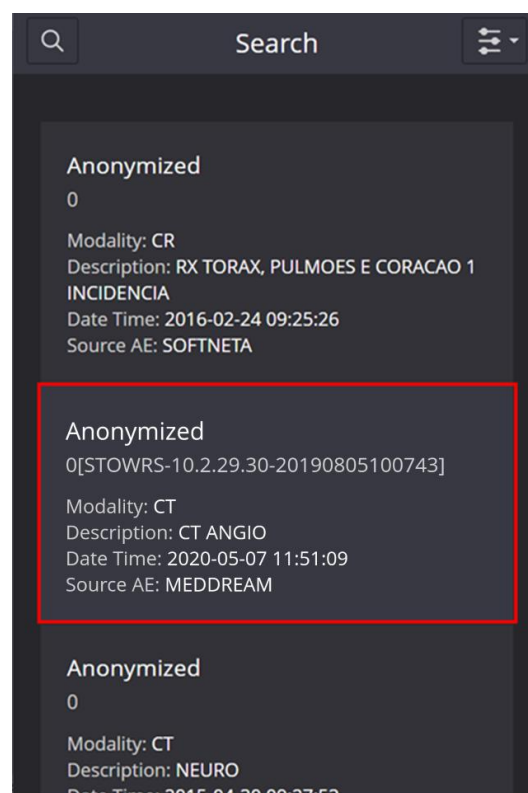


Figure 212. Study description area in Search results window in mobile mode

2. A new browser tab with a Viewer window will pop up and the Study window automatically opens in it:



Figure 213. Selecting the study image in mobile mode



NOTE! The first image automatically opens, if the first image opening conditions are met (see description in [Settings](#)).

3. Find and press the image in the Study window (see detail description in section [Series](#)) to open it in Viewer. Or close the Study window by pressing **Close** button to the first study image, that was opened in background.



Figure 214. Viewing selected image in mobile mode

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

- Change the Viewer window layout (see description in [Layout and Multi image](#)) and press on the viewport in which you want to open other study. The viewport is activated:

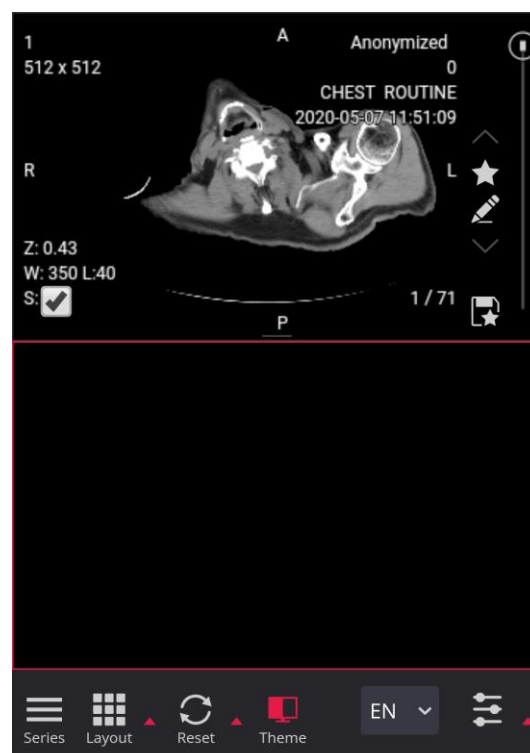


Figure 215. 2x1 Screen layout with active bottom viewport in Viewer window mobile mode

- Go back to the search results window by pressing MedDream search browser's tab.
- Find and select the study in search results, as described in step 1.
- The program navigates to MedDream viewer browser's tab and pop-ups the Study window. The Study window contains all the studies that were opened in Viewer's window. The selected study is displayed in the first position of studies list:

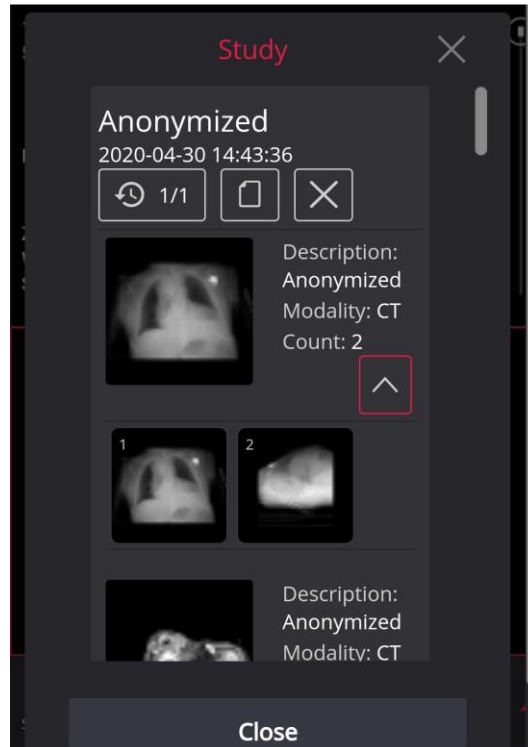


Figure 216. New study added at the top of the studies list of the viewer window



NOTE! Use Series button to open the Study window and select the other image from the studies that are already opened in Viewer's window.



NOTE! Use patient history button in Study window to open the study from patient historical studies list.

- Find and press the image thumbnail to open it in an active viewport:

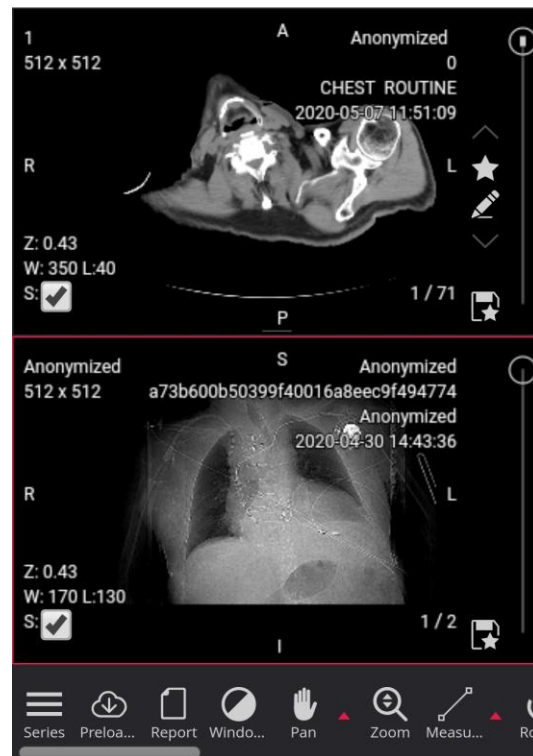


Figure 217. Multiple images opened in mobile mode

Patient studies list in mobile mode

The Patient studies list may be viewed in Patient studies window, and Patient history window. See sections [Patient studies window](#) and [Patient history](#) for detail conditions when and how these windows may be opened.

In mobile mode the list view is used for patient studies list:

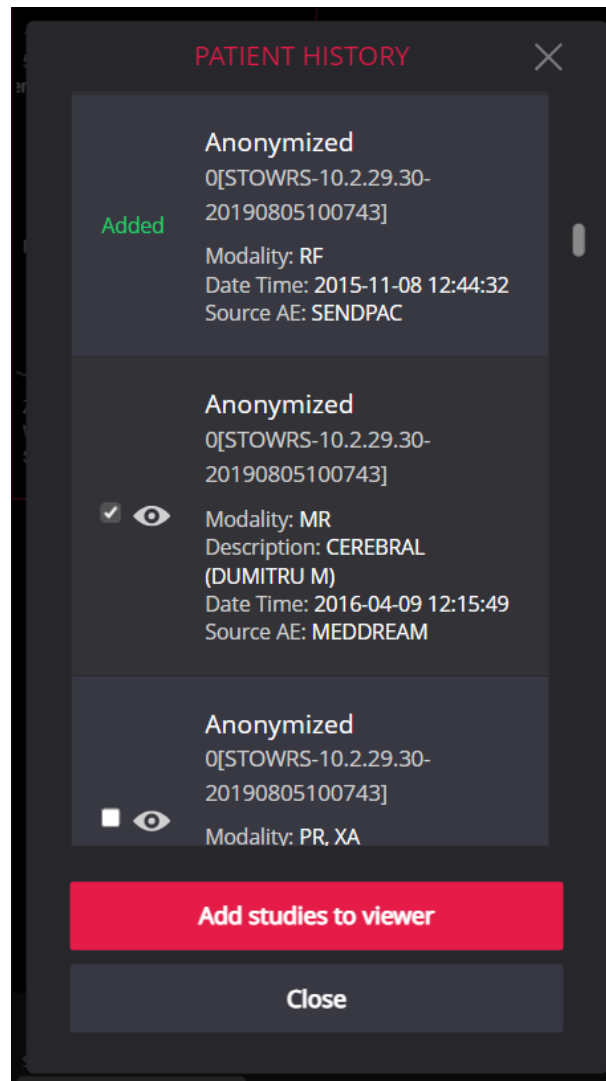



Figure 218. Patient studies list in mobile mode

You can scroll the list and open the patient studies for viewing:

- To open one study, press on the eye icon  at the left of the study description;
- To open multiple studies at once, press and mark the tick-box next to the studies description and press the **Add studies to viewer** button, when all the required studies are marked;
- All the studies, that are already opened in Viewer, are highlighted as **Added** and haven't controls for opening.

Manipulating images in MedDream Mobile mode




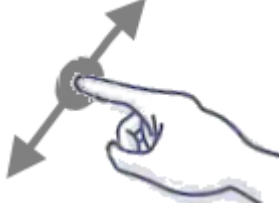
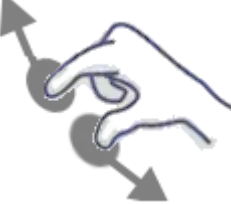

The section describes the specifics of using the image manipulation tools with touch screens. See detail description of particular tool in the following sections:

- [Tools for image manipulation and analysis](#) section describes tools: Windowing, Pan, Zoom, Channels, Scroll, Magnifier, Layout, Multi image, Reset, MPR, Reference Line, Crosshair, Rotate, DICOM, and Link;
- [Tools for measuring, and annotation saving](#) section describes Annotations, Key Objects, and measure menu tools: Line, Angle, Polyline, Area, Volume, Velocity Time Integral (VTI), Ellipse, Cobb Angle, Tibial

Plateau Angle, Norberg Angle, Verbal Heart Scale, Text annotations, Region Of Interest, Calibration line, Show Angles, Intensity, Delete measurements, Save Annotation;

- [Tools for study exchange](#) section describes Share files via DICOM Library, Forward, Export, and LiveShare tools;
- [Fusion function for Positron Emission Tomography \(PET CT\)](#) section describes the fusion tool;
- [Cine mode](#) section describes the playing as video tool;
- [Other Viewer tools](#) for tools Series, Plugins, Full Screen, Theme, Preload Series, Print, and Hanging protocols;
- [ECG module](#) for ECD manipulation toolbar and measure tools.

The table below describes what finger actions should be used on touch screens instead of mouse actions.

Touch action description	Corresponding mouse action
 <p>Press</p> <p>Briefly touch the screen with finger</p>	Mouse left button click action
 <p>Double press</p> <p>Rapidly touch the screen twice with finger</p>	Mouse right button double click action
 <p>Long press</p> <p>Touch the screen with finger for longer period of time</p>	Used only in mobile layout to open tool's expandable menu.
 <p>Drag</p> <p>Touch the screen and move finger towards required direction without losing contact</p>	Mouse drag
 <p>Zoom</p> <p>Touch the screen with two fingers and move them closer or further each other without losing contact</p>	Used only in mobile layout to zoom image in or out.
 <p>Scroll</p> <p>Touch the screen with the finger and quickly slide up or down, releasing the finger</p>	Used only in mobile layout to scroll the list.



NOTE! Two fingers zoom is not working if any of Measure tools is activated.

Setting window in mobile mode

The Settings in mobile mode are grouped by system windows and / or functions as in desktop mode.

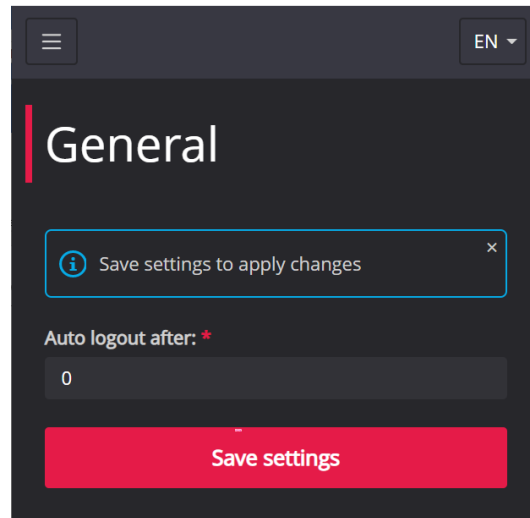



Figure 219. Settings window in mobile mode: General settings

To open the required setting group, do the following:

- Press the menu button  on the top left corner of the Settings window. The system displays the settings window menu:

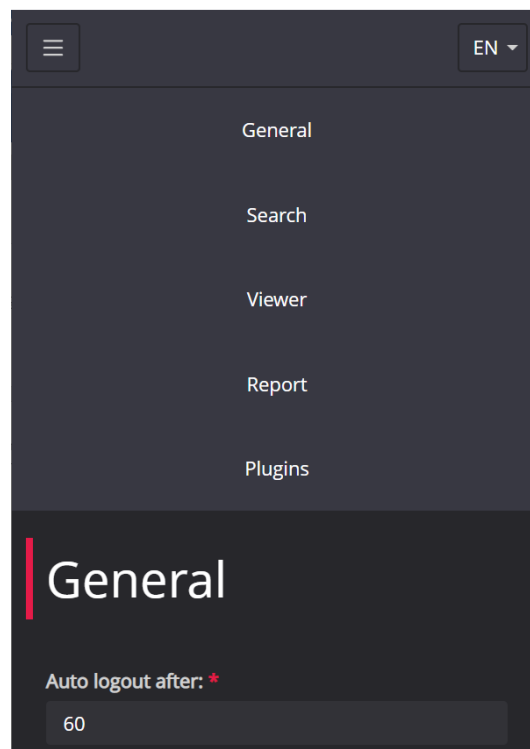


Figure 220. Settings window menu in mobile mode

- Press the menu item. The selected settings tab is opened:

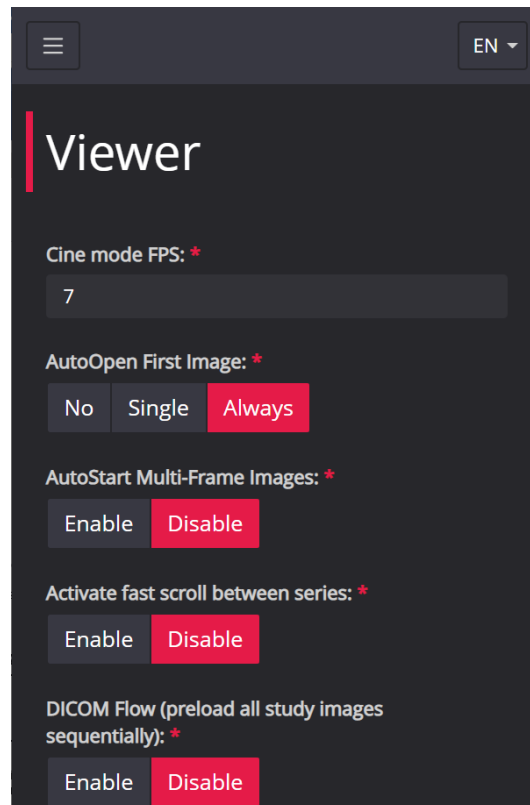


Figure 221. Settings window in mobile mode: Viewer settings

See detail settings groups and fields description in section [Settings](#).

Table of Figures

Figure 1. Log in window	33
Figure 2. Language selection in a log in window	33
Figure 3. Search window	34
Figure 4. Search criteria entry fields in search results list	34
Figure 5. Quick pick list for choosing the study date interval	35
Figure 6. Study date interval entry fields	35
Figure 7. Pick list for choosing modality: CT is chosen	35
Figure 8. Customization of modalities pick list	36
Figure 9. Picking the storage	37
Figure 10. Page navigation in the search results list	37
Figure 11. Marking the study	38
Figure 12. The other menu in Search window	38
Figure 13. Viewer window zones	39
Figure 14. Expanded toolbar	40
Figure 15. Action controls in Thumbnail	42
Figure 16. Preload progress bar	43
Figure 17. CT series default view without images thumbnails, and with phase filter	43
Figure 18. Image scroll bar	45
Figure 19. Viewport toolbar	45
Figure 20. Quick access to additional data controls	47
Figure 21. Quick menu	48
Figure 22. Quick menu with thumbnail zone	48
Figure 23. Study selection in the search results list	49
Figure 24. Viewer window in new tab	49
Figure 25. New study opened in the same Viewer window	50
Figure 26. Patient studies window	51
Figure 27. Opening the Patient history window from the header of viewed studies	51
Figure 28. Patient history window	52
Figure 29. Searching and opening several studies from Patient history window	53
Figure 30. Image manipulation tools	54
Figure 31. Window button menu example	55
Figure 32. Image alignment options in Pan menu	56
Figure 33. Zoom button menu	57
Figure 34. Color selection in Channels button menu	57
Figure 35. Scroll button menu	58

Figure 36. Magnification coefficient of Magnifier tool.....	58
Figure 37. 2x2 layout view with manual viewports' size adjustment	59
Figure 38. 2x2 multi image menu applied in the first viewport of 1x2 layout	60
Figure 39. Reset button menu	60
Figure 40. MPR button menu	61
Figure 41. Steps of Coronal image reconstruction from axial series of images: axial series preload and calculated coronal view	61
Figure 42. Orthogonal reconstruction from axial series of images	62
Figure 43. 3D reconstruction in progress	63
Figure 44. Oblique reconstruction	63
Figure 45. Slab thickness selection in oblique MPR view	64
Figure 46. Slab thickness entry window	64
Figure 47. Rendering method selection in oblique MPR view	64
Figure 48. Oblique MPR view with adjusted slab thickness and rendering method	65
Figure 49. Comparison of two reconstructed 3D studies	66
Figure 50. MPR 3D Oblique view and Multi-Modality comparison	66
Figure 51. Image reference line in intersecting planes	67
Figure 52. Not orthogonal intersecting plane view	68
Figure 53. Crosshair tool	68
Figure 54. Rotate button menu	69
Figure 55. DICOM tag window	70
Figure 56. Search according DICOM tag name in DICOM tag window	70
Figure 57. Expanding the SQ tags in DICOM tag window	71
Figure 58. Manual link mode in Viewer with the disabled linked scrolling for one of the series	72
Figure 59. Measure button menu	73
Figure 60. Distance measurement	74
Figure 61. Angle measurement	75
Figure 62. Perimeter measurement	75
Figure 63. Area measurement	76
Figure 64. Volume measurement	76
Figure 65. VTI measurement	77
Figure 66. Ellipse measurement	78
Figure 67. Cobb angle measurement	78
Figure 68. Tibial Plateau Angle (TPA) measurement	79
Figure 69. Norberg angle circle with the center in femoral head	79
Figure 70. Norberg angle measurement	80
Figure 71. Adjusted Norberg angle measurement	80

Figure 72. Long axis of VHS measurement.....	81
Figure 73. Short Axis of VHS measurement	81
Figure 74. VHS measurement	81
Figure 75. S and L lines rotation	82
Figure 76. Drawing the maximal inner thoracic diameter line of CTR measurement.....	82
Figure 77. Drawing cardiac shadow transverse line of CTR measurement	83
Figure 78. CTR measurement	83
Figure 79. Text entry field	84
Figure 80. Foot medial longitudinal arch angle and height measurement	85
Figure 81. Calibration line.....	85
Figure 82. Entering the Calibration line length	85
Figure 83. Calibration ratio result.....	85
Figure 84. Angle measurement between intersecting lines.....	86
Figure 85. Intensity measurement.....	87
Figure 86. Save presentation state window.....	89
Figure 87. Annotation icon on image thumbnail	90
Figure 88. Annotation button on image.....	90
Figure 89. List of annotations and annotation description	91
Figure 90. View annotation	91
Figure 91. Mark image as key object window	92
Figure 92. Not saved Key Object	92
Figure 93. Save study key object window	93
Figure 94. Saved Key Object	93
Figure 95. Selection of Key object filter in context menu.....	95
Figure 96. Segmentation button menu	95
Figure 97. Segmentation window	96
Figure 98. New 2D bounding box segment created.....	97
Figure 99. Left femoral head located in reconstructed series using crosshair tool	98
Figure 100. New 3D bounding box segment created.....	99
Figure 101. Left ilium segmentation duplicated and created Bounding box 3 copy moved.....	100
Figure 102. The bounding box moved to the center of the femoral head	101
Figure 103. The bounding box rotated to better match the femoral head	101
Figure 104. The bounding box is resized to fit the femoral head	101
Figure 105. The 3D bounding box contours after rotating the box in axial and coronal planes	102
Figure 106. New free draw segment created	104
Figure 107. Inner femoral head area marked inside the ilium segment.....	105

Figure 108. The area removed from the side of the ilium segment	105
Figure 109. The area added to the side of the ilium segment	105
Figure 110. The region added to Left ilium segment by drawing ilium contour on the other image of the series	106
Figure 111. Inner femoral head contour deleted from the ilium segment	106
Figure 112. Viewing the image with free draw and bounding box segments	108
Figure 113. Contours of Femoral head segment not displayed on the image	109
Figure 114. Measurement window displayed for Left femoral head segment	111
Figure 115. Selecting scope for sharing via DICOM Library	112
Figure 116. Share via DICOM Library dialog window	113
Figure 117. LiveShare host window when live sharing not started	115
Figure 118. LiveShare host window with liveShare session running and two guests connected.....	115
Figure 119. Guest Viewer window	116
Figure 120. PET series not found notification	117
Figure 121. PET series selection window	118
Figure 122. Fusion process	118
Figure 123. Fusion series	119
Figure 124. The toolbar of the fusion series	119
Figure 125. Changing color range of the fusion PET series.....	119
Figure 126. Fusion ratio bar in fusion series toolbar	120
Figure 127. Pan tool in fusion series toolbar	120
Figure 128. Pan tool in fusion series toolbar	120
Figure 129. Zoom tool in fusion series toolbar	120
Figure 130. Rotate tool in fusion series toolbar	120
Figure 131. Upper layer Manual Adjustment tool in fusion series toolbar	121
Figure 132. Standard uptake value measurement in fusion series	121
Figure 133. Reset button in fusion series toolbar	121
Figure 134. Close button in fusion series toolbar	122
Figure 135. Preload of series data for cine mode	122
Figure 136. Cine mode movie playing	123
Figure 137. Study window	124
Figure 138. Series preload process progress bar	126
Figure 139. Print options.....	126
Figure 140. Hanging protocol options window	127
Figure 141. Hanging protocol menu options	128
Figure 142. ECG viewer window	129
Figure 143. ECG measure tools.....	129

Figure 144. Using Measurement (mV, s) tool.....	130
Figure 145. Using QT points tool	130
Figure 146. Using HR measurement tool	131
Figure 147. Using QRS Axis tool	131
Figure 148. ECG viewport toolbar.....	132
Figure 149. SR viewer window.....	133
Figure 150. PDF display	133
Figure 151. Video player.....	134
Figure 152. Viewing multi-frame image	135
Figure 153 Chrome properties	136
Figure 154 Chrome web store	136
Figure 155 Filtering MedDream extension	136
Figure 156 Accessing the options of the added MedDream extension	137
Figure 157 Configured extension`s example.....	138
Figure 158 MedDream DICOM Viewer on 2 displays	138
Figure 159 MedDream DICOM Viewer on 3 displays	139
Figure 160. Forward window	140
Figure 161. Searching for the forward destination	141
Figure 162. Information about initiated forward process.....	141
Figure 163. Forward processes list in Recently forwarded window	142
Figure 164. Export window	143
Figure 165. Export progress window	144
Figure 166. Export progress window	145
Figure 167. ISO volumes list and saving buttons	145
Figure 168. Report window in edit mode is opened after clicking the Create report icon.....	146
Figure 169. Report content successfully saved	148
Figure 170. Report attachments successfully added.....	149
Figure 171. Selecting the report version.....	149
Figure 172. Viewing historical report version	150
Figure 173. Report window in view mode.....	151
Figure 174. Templates section of the Report window	152
Figure 175. Report template window	153
Figure 176. Information window	154
Figure 177. Release notes window	155
Figure 178. EULA window	156
Figure 179. Shortcuts window	156

Figure 180. Demo version notification	158
Figure 181. Registration window, if EULA is not read	158
Figure 182. Registration window – registration activated	159
Figure 183. Settings window	160
Figure 184. Settings window: general settings.....	160
Figure 185. Settings window: search setting	161
Figure 186. Settings window: general Viewer window settings.....	162
Figure 187. Setting window: Info Label properties in Viewer tab	163
Figure 188. Info Label entry field.....	164
Figure 189. Showing Info Label on image	164
Figure 190. Setting window: Toolbar properties in Viewer tab	165
Figure 191. Changing the tool's position in toolbar	165
Figure 192. Selecting the tool's showing mode.....	166
Figure 193. Quick menu: default settings	167
Figure 194. Quick menu: Measure tool included in quick menu and measure option moved to second quick menu level	167
Figure 195. Custom windowing options: default values.....	168
Figure 196. Custom Windowing creation window	168
Figure 197. Custom windowing in the drop-down Windowing menu	169
Figure 198. Settings window: report settings	169
Figure 199. Hanging protocol settings	170
Figure 200. Modality filter for metadata fetching	170
Figure 201. Create hanging protocol group window	171
Figure 202. Hanging protocol condition's entry fields	171
Figure 203. Create protocol window	172
Figure 204. Entering View settings in hanging protocol.....	173
Figure 205. Hanging protocols list.....	173
Figure 206. Search criteria window in mobile mode	176
Figure 207. Search results window in mobile mode	177
Figure 208. Page navigation in the search results in mobile mode	178
Figure 209. Viewer window zones in mobile mode	179
Figure 210. Toolbar's scrollbar in mobile mode.	179
Figure 211. Tool's menu in Viewer window in mobile mode	180
Figure 212. Study description area in Search results window in mobile mode	181
Figure 213. Selecting the study image in mobile mode	182
Figure 214. Viewing selected image in mobile mode.....	183
Figure 215. 2x1 Screen layout with active bottom viewport in Viewer window mobile mode	183

Figure 216. New study added at the top of the studies list of the viewer window	184
Figure 217. Multiple images opened in mobile mode	185
Figure 218. Patient studies list in mobile mode	186
Figure 219. Settings window in mobile mode: General settings	188
Figure 220. Settings window menu in mobile mode	188
Figure 221. Settings window in mobile mode: Viewer settings	189

Index

A

About.....	154
Angle.....	74
Annotations.....	89
Area.....	75

B

Bounding Box.....	96
-------------------	----

C

Calibration line	85
Cardiothoracic ratio (CTR)	82
Channels	57
Cine mode.....	122
Cob Angle.....	78
Copy and paste ellipse	88
Copy and paste measurement.....	87
Copy the viewport content to the clipboard	46
Crosshair	68

D

Delete all measurements	87
Delete selected measurement.....	87
DICOM	69
DICOM print plugin	125

E

ECG module.....	128
Ellipse.....	77
Entering the Hanging protocol condition	171
Export	114
Export and Forward	140
Export window	142

F

Foot longitudinal arch	84
Forward.....	113
Forward window.....	140
Free Draw	103
Full Screen.....	125
Fusion function for Positron Emission Tomography (PET CT)	117

G

General settings.....	160
-----------------------	-----

H

Hanging protocol settings	169
Hanging protocols	126
Heart rate (HR) measurement	130
Help	156

I

Info Label Properties	163
Intensity	86

K

Key Objects	92
-------------------	----

L

Layout	59
License Agreement	155
License registration	158
Line	74
Link scrolled series	71
LiveShare	114
Log Off	157
Logging on to MedDream	33

M

Magnifier	58
Manipulating fusion series	119
Manipulating images in MedDream Mobile mode	186
Measurement (mV,s)	129
Measuring images	73
MedDream DICOM Viewer	39
MedDream DICOM Viewer Chrome browser extension for multi-monitors	135
MedDream Mobile mode	175
MPR	61
Multi image	59
Multi-frame view	134

N

Norberg Angle	79
---------------------	----

O

Opening studies	49
Opening studies in MedDream Mobile mode	181

P

Pan	56
Patient history	51
Patient studies list in mobile mode	185
Patient studies window	50
PDF view	133
Plugins	124

Polyline	75
Preload Series.....	42, 125
Preload Study	42, 58
Print	126

Q

QRS measurement.....	131
QT points (PR, QT, QTs)	130
Quick access to additional data	46
Quick menu	47
Quick save KO, PR	89, 94

R

Reference Line.....	66
Region Of Interest.....	84
Report.....	128
Report module	146
Report settings	169
Reset.....	60
Rotate	68

S

Save Annotation	87
Scroll	57
Search of studies	33
Search of studies in mobile mode	175
Search window settings	161
Segment measuring.....	107
Segment viewing.....	107
Segmentation.....	95
Series	123
Settings	157
Settings	160
Settings window in mobile mode.....	188
Share files via DICOM Library	111
Shortcuts.....	156
Show Angles.....	86
System menu functions.....	154
System tools in the Viewer window.....	41
Size and position of modal dialog window	139
SR view.....	132

T

Table of Contents	3
Table of Figures	190
Text annotations.....	83
Theme.....	125
Thumbnails.....	125
Thumbnails bar in the Viewer window.....	41
Tibial Plateau Angle	78
Toolbar in the Viewer window.....	39
Toolbar Properties	165

V

Velocity Time Integral (VTI)	76
Verbal Heart Scale	80
Video view.....	134
View zone in the Viewer window.....	44
Viewer window.....	39
Viewer window in mobile mode	178
Viewer window settings	161
Viewport toolbar	45
Volume.....	76

W

Windowing	54
Windowing settings	167

Z

Zoom.....	56
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