The information contained in this User Manual belongs to Inobitec, LLC (Voronezh, Russia). The Manual is delivered to the users of Inobitec DICOM Viewer software product exclusively for the purpose of working with this product. No part of the information contained herein can be modified, used for any other purpose or delivered to any third party without the prior written consent of Inobitec, LLC (Voronezh, Russia). Inobitec, LLC reserves the right to alter this Manual without prior notice. Screenshots are made in Windows for the Dark style of the Viewer. Certain visual differences between the Viewer interface and the images in the screenshots are allowable.
## Contents

### About this Manual
- Accepted Conventions .......................................................... 15
- Warnings .................................................................................. 15

### Technical Support ................................................................ 16

### About the Product ................................................................ 17
- DICOM Viewer Functionality .................................................... 18
- New Functions in Version 2.12 .................................................. 24

### Installing, Uninstalling and Launching the Program .............. 25
- System Requirements ................................................................ 25
- Installing and Uninstalling the Program ..................................... 26
  - Installing the Program on Windows ......................................... 26
  - Silent Installation on Windows ............................................... 34
  - Uninstalling the Program on Windows ..................................... 35
  - Silent Uninstallation on Windows ........................................... 37
- Installing and Uninstalling the Program on Mac OS .................. 37
- Installing and Uninstalling the Program in AppImage Format on Linux ................................................................. 38
- Launching with Shortcuts .......................................................... 39
- Launch multiple instances of the program ............................... 39
- Service files ............................................................................. 40
- Import CLUTs .......................................................................... 40
- Getting Started ................................................................. 40
- First run of the Program ......................................................... 41
- Launching the Web Viewer ....................................................... 46

### Program Window Elements .................................................. 47
  1. Main Menu ........................................................................ 48
    1.1 File ........................................................................ 48
    1.2 Network ..................................................................... 48
    1.3 Storage ....................................................................... 49
    1.4 View .......................................................................... 49
    1.5 Studies ....................................................................... 50
    1.6 Series .......................................................................... 50
## CONTENTS

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.7 Options</td>
<td>51</td>
</tr>
<tr>
<td>1.8 Help</td>
<td>51</td>
</tr>
<tr>
<td>1.2 Window Management</td>
<td>51</td>
</tr>
<tr>
<td>1.3 Tab Panel</td>
<td>52</td>
</tr>
<tr>
<td>1.3.1 General</td>
<td>52</td>
</tr>
<tr>
<td>1.3.2 Manage a Tab</td>
<td>53</td>
</tr>
<tr>
<td>1.4 Toolbar</td>
<td>55</td>
</tr>
<tr>
<td>1.5 Select Data Source</td>
<td>57</td>
</tr>
<tr>
<td>1.5.1 Select a CD, DVD or Local Folder as the Data Source</td>
<td>57</td>
</tr>
<tr>
<td>1.5.2 Opening Zipped DICOM Studies</td>
<td>57</td>
</tr>
<tr>
<td>1.5.3 Opening DICOM studies by dragging and dropping</td>
<td>58</td>
</tr>
<tr>
<td>1.5.4 Select a PACS Server or Local Storage as the Data Source</td>
<td>59</td>
</tr>
<tr>
<td>1.6 Save Studies and Series to the folder</td>
<td>60</td>
</tr>
<tr>
<td>1.6.1 Save Studies to the folder</td>
<td>60</td>
</tr>
<tr>
<td>1.6.2 Save Series to the folder</td>
<td>62</td>
</tr>
<tr>
<td>1.7 Search Panel</td>
<td>63</td>
</tr>
<tr>
<td>1.7.1 Saving the Search Parameters</td>
<td>64</td>
</tr>
<tr>
<td>1.7.2 Searching for Studies by Preset Parameters</td>
<td>65</td>
</tr>
<tr>
<td>1.8 Select Server Panel</td>
<td>65</td>
</tr>
<tr>
<td>1.9 Study Panel</td>
<td>66</td>
</tr>
<tr>
<td>1.9.1 Customize Study Panel</td>
<td>66</td>
</tr>
<tr>
<td>1.9.2 Sort Studies</td>
<td>67</td>
</tr>
<tr>
<td>1.9.3 Edit Patient Name and Description in a Study</td>
<td>68</td>
</tr>
<tr>
<td>1.9.4 Study List Export</td>
<td>69</td>
</tr>
<tr>
<td>1.10 Series Panel</td>
<td>71</td>
</tr>
<tr>
<td>1.11 Studies and Series Download/Upload Panels</td>
<td>71</td>
</tr>
<tr>
<td>1.12 Information Panel</td>
<td>73</td>
</tr>
<tr>
<td>1.13 Uncompress series</td>
<td>73</td>
</tr>
<tr>
<td>1.14 Tool Control Buttons</td>
<td>74</td>
</tr>
<tr>
<td>2 View Flat Images</td>
<td>75</td>
</tr>
<tr>
<td>2.1 Open Series</td>
<td>75</td>
</tr>
<tr>
<td>2.2 Open Series with Current Settings</td>
<td>77</td>
</tr>
<tr>
<td>2.3 Working with Several Monitors and Split Screen</td>
<td>77</td>
</tr>
<tr>
<td>2.4 Resampling filter</td>
<td>79</td>
</tr>
<tr>
<td>2.5 View Images in a Series</td>
<td>80</td>
</tr>
<tr>
<td>2.6 Switch between Series</td>
<td>81</td>
</tr>
<tr>
<td>2.7 View Several Studies at a Time</td>
<td>81</td>
</tr>
<tr>
<td>2.8 View Multiple Series</td>
<td>83</td>
</tr>
<tr>
<td>2.8.1 Auto Mode</td>
<td>85</td>
</tr>
<tr>
<td>2.8.2 Stacked Mode</td>
<td>85</td>
</tr>
<tr>
<td>2.8.3 Grid Mode</td>
<td>86</td>
</tr>
<tr>
<td>2.8.4 Custom Mode</td>
<td>86</td>
</tr>
<tr>
<td>2.9 View Multiple Images in the Same Series Simultaneously</td>
<td>88</td>
</tr>
<tr>
<td>2.10 Viewing Several Series as a Single Multiphase Series</td>
<td>90</td>
</tr>
<tr>
<td>2.11 Viewing Orthogonal Projections of Images</td>
<td>91</td>
</tr>
<tr>
<td>2.12 Play images</td>
<td>92</td>
</tr>
<tr>
<td>2.13 Video recording</td>
<td>93</td>
</tr>
</tbody>
</table>
2.14 Zoom, Pan, Rotate ......................................................... 95
  2.14.1 Zoom .................................................................................. 95
  2.14.2 Pan ...................................................................................... 96
  2.14.3 Rotate .................................................................................. 96
2.15 Set Window Level and Width .................................................. 96
  2.15.1 User Presets for Window Width and Level ....................... 99
  2.15.2 Actions with presets ............................................................. 100
  2.15.3 Additional Width and Level Settings ............................... 101
  2.15.4 Setting the Window Width and Level for Merged Series ... 102
2.16 Magnifier ................................................................................. 103
2.17 Measurements .......................................................................... 103
  2.17.1 Ruler ................................................................................... 104
  2.17.2 Polygonal Ruler ................................................................. 105
  2.17.3 Angle .................................................................................. 106
  2.17.4 Cobb angle meter ............................................................... 106
  2.17.5 Measure Intensity at a Point .............................................. 107
  2.17.6 Measure the Intensity Average and Standard Deviation in an Area ................................................... 108
  2.17.7 Drawing Parameters .......................................................... 109
  2.17.8 Move Measurements .......................................................... 110
  2.17.9 Move Measurement Results .............................................. 110
  2.17.10 Delete all Annotations and Measurements ................... 110
  2.17.11 Measuring Dimensions and Area during Ultrasound Imaging .......................................................... 110
  2.17.12 Measuring the Time Interval and the Blood Flow Velocity during Ultrasound Imaging ....................... 111
2.18 Perfusion Parameters Estimation ............................................. 111
  2.18.1 Open series in Perfusion Parameters Estimation mode .... 112
  2.18.2 Setting the Time Interval on the Perfusion Panel .......... 113
  2.18.3 Brain Perfusion Parameters Estimation ......................... 115
  2.18.4 Map mode ........................................................................ 119
  2.18.5 Advanced Settings for Bayesian Estimation Algorithm .... 122
  2.18.6 Deconvolution Advanced Settings ................................. 126
2.19 Evaluation of Blood Flow Parameters ..................................... 127
  2.19.1 Opening a Series in the Blood Flow Parameters Evaluation Mode .................................................. 128
  2.19.2 Changing the Configuration Parameters for a PC MRI Series .................................................. 132
  2.19.3 Building and Editing Vessels ROI ................................. 132
  2.19.4 Blood Flow Analysis Panel. Displaying the Results of General Blood Flow Analysis ....................... 134
  2.19.5 Evaluating the General Blood Flow Analysis Parameters .................................................. 137
  2.19.6 Designing a Trajectory for the Pulse Wave ................. 139
  2.19.7 Getting the Results of Advanced Blood Flow Analysis without Building a Pulse Wave Trajectory .......... 142
  2.19.8 Blood Flow Analysis Panel. Displaying the Results of Advanced Blood Flow Analysis ....................... 143
  2.19.9 Evaluation of the Parameters for Advanced Blood Flow Analysis .................................................. 145
  2.19.10 Blood Flow Parameters Evaluation for Two Slices ........ 146
2.20 Visualize Images ...................................................................... 149
  2.20.1 Select CLUT ................................................................. 149
  2.20.2 Edit CLUTs List ................................................................. 150
CONTENTS

2.20.3 CLUT Parameters ........................................... 153
2.20.4 Create and Edit CLUT ..................................... 155
2.20.5 User CLUTs Import ........................................ 157

2.21 SUV Measurement ............................................. 157

2.22 Calcium Scoring .............................................. 160
2.22.1 Selection of measurement areas ......................... 160
2.22.2 Actions with measurement areas ....................... 162
2.22.3 Measurement results ...................................... 163

2.23 Scout Lines ..................................................... 165
2.23.1 The Tool Menu ............................................ 165
2.23.2 Line Settings .............................................. 166

2.24 Set Up Viewer Workspace ................................... 167

2.25 Export Images .................................................. 168
2.25.1 Export to DICOM ......................................... 168
2.25.2 Export to Image ........................................... 170

2.26 DSA Mode ....................................................... 172
2.26.1 Single-image subtraction view ......................... 172
2.26.2 Series subtraction view .................................. 173
2.26.3 Viewing Several Series of the Same Study Fused in One Multiphase Series with Subtraction ................................. 174

2.27 Image Information in the Series Window .................. 174
2.27.1 Orientation Cube ......................................... 174
2.27.2 Scale ....................................................... 175
2.27.3 Image Information ....................................... 175
2.27.4 Patient Information ...................................... 176

2.28 View DICOM Tags ............................................. 176

2.29 Viewing Structured Reports ................................ 176

2.30 Graphic Label Tool ............................................ 177
2.30.1 General .................................................... 177
2.30.2 Create Labels ............................................. 178
2.30.3 Actions with Labels ..................................... 181

2.31 Synchronize Images ........................................... 182
2.32 Synchronization by a Point ................................ 183
2.33 Mirror Image Horizontally/Vertically ..................... 184
2.34 Calibration sizes .............................................. 184
2.35 Apparent diffusion coefficient ............................. 185

3 Volume Reconstruction .......................................... 186
3.1 View Images .................................................... 186
3.2 Model Projection .............................................. 187
3.3 Actions with Model .......................................... 188
3.4 Model Positioning Tools ..................................... 189
3.4.1 Model Shift ............................................... 189
3.4.2 Model Rotation .......................................... 190
3.4.3 Model Scaling ........................................... 190
3.5 «Select Model Point» Tool .................................. 190
3.6 The Play Tool .................................................. 190
3.7 Video recording ............................................... 191
5.4.1 View Modes .......................................................... 233
5.4.2 Working with Planes in 3D Cursor Mode .................... 233
5.4.3 Working with Planes in the Cutting Plane Mode .......... 234
5.5 Series Synchronization in MPR Reconstruction Tabs .......... 235
5.6 Curvilinear Reconstruction ....................................... 237
5.6.1 Build Surface .................................................. 237
5.6.2 Choosing a Display Mode for an Involute of a Curve .... 239
5.6.3 Curve settings .................................................. 241
5.6.4 Actions with a Curve ......................................... 242
5.6.5 Position of a Curve, Its Nodes and Surface in Space .... 243
5.6.6 Curved Reconstructions Cross Sections Mode ............ 244
5.7 Displaying Section Planes on 3D Models ...................... 248
5.8 «Render settings» Tool .......................................... 251
5.9 The Play Tool ..................................................... 251
5.10 Video recording .................................................... 251
5.11 Markers ............................................................ 252
5.11.1 General ....................................................... 252
5.11.2 Add Markers .................................................. 252
5.11.3 Add Line Markers ............................................ 253
5.11.4 Polylgonal Marker line ...................................... 253
5.11.5 Actions with Markers ....................................... 254
5.11.6 Marker Properties ............................................ 254
5.11.7 Position of Markers in Space ............................... 255
5.12 Reconstruction Modes. Slice Thickness ....................... 255
5.12.1 Render Modes ................................................ 255
5.12.2 Slice Thickness .............................................. 255
5.13 Rotate Image in the Section Plane .............................. 256
5.14 Mirror Image Horizontally/Vertically ........................... 257
5.15 Show labels tool .................................................. 257
5.16 Export Images .................................................... 258
5.17 Reslice ........................................................... 258
5.18 Measurements ..................................................... 260
5.19 Annotations ....................................................... 261
5.20 Volume Reconstruction window ................................. 261
5.21 Diffusion Tensor Imaging (DTI) Mode ......................... 261
5.21.1 Open series in DTI Mode .................................... 262
5.21.2 Select Visible Fibers ........................................ 263
5.21.3 Fiber Color ................................................... 265
5.21.4 Scalar Maps .................................................. 265
5.21.5 Building a Surface ......................................... 266
5.21.6 Creating a Voxel Model of Fibers ......................... 267
5.21.7 Saving data in a file ........................................ 267
6 Segmentation .......................................................... 268
6.1 The Segmented Structures Panel ................................. 271
6.2 The Mask .......................................................... 275
6.2.1 Creating a new structure and mask ....................... 275
6.2.2 Changing the structure mask using CLUTs ............... 276
6.2.3 The Editing mask ......................................................... 277
6.2.4 Set Mask Tool ......................................................... 278
6.3 Creating segmented structure ........................................... 279
  6.3.1 Creating a structure by copying ..................................... 279
  6.3.2 Creating a Structure with a Empty Mask ......................... 280
6.4 Actions with structure .................................................. 280
6.5 Building surface ......................................................... 282
6.6 Copying a Surface ........................................................ 284
6.7 Import and Export ........................................................ 286
  6.7.1 Export surface ....................................................... 286
  6.7.2 Import surface ....................................................... 289
  6.7.3 Export a structure to the current study ......................... 290
  6.7.4 Export a structure to DICOM RT .................................. 291
  6.7.5 Importing a Structure from DICOM RT ......................... 293
6.8 Changing the structure mask with segmentation tools ............... 294
  6.8.1 Tools for automatic segmented structure mask filling ......... 296
  6.8.2 Brush restore tool .................................................. 297
  6.8.3 Region growing tool ................................................. 298
  6.8.4 Vessel tree segmentation tool ..................................... 300
  6.8.5 Watershed segmentation tool ....................................... 302
  6.8.6 Multi-segment growing tool ....................................... 304
  6.8.7 Segmented structures regions growing Tool ................. 306
6.9 Union, subtraction and intersection of structures .................... 307
  6.9.1 Union ............................................................... 307
  6.9.2 Subtraction .......................................................... 308
  6.9.3 Intersection ........................................................ 309
  6.9.4 «Subtract dilated» Tool ........................................... 310
6.10 Building Mask with Contours .......................................... 311
  6.10.1 General Information ............................................... 311
  6.10.2 Building a Structure Mask with Contours ....................... 312
  6.10.3 Work with Contours .............................................. 314
  6.10.4 Setting the Contour Display Parameters ......................... 314
6.11 Saving and Opening Segmentation Projects and DTI Projects ...... 316
  6.11.1 Saving a Project .................................................. 316
  6.11.2 Saving Projects Automatically .................................. 318
  6.11.3 Resuming Work with Segmentation Projects ................. 320
  6.11.4 Opening a Project with Source DICOM Data .................. 321
  6.11.5 Opening a Project without Source DICOM Data ............... 323
6.12 Histograms .................................................................... 324
  6.12.1 Rendering a Histogram for a Structure ......................... 324
  6.12.2 Histogram for a ROI ............................................... 326

7 Vessel analysis module ..................................................... 327
  7.1 Open Studies in Vessel Analysis Module .................................. 327
    7.1.1 Vessels list ........................................................ 330
  7.2 «Render settings» Tool ................................................ 331
  7.3 The Play Tool .......................................................... 331
  7.4 Video recording .......................................................... 331
# The Local Storage

13.1 View Storage Status ................................................. 400
13.2 Verify Storage ....................................................... 401
13.3 Clear Storage ......................................................... 401
13.4 Automatic Local Storage cleaning ................................. 401

# Disk Creator

14.1 General information .................................................. 402
14.2 Add Data to Disk Creator ........................................... 404
  14.2.1 Automatically Add Data to a Disk Image ...................... 404
  14.2.2 Manually Add Data to a Disk Image .......................... 404
  14.2.3 Adding the DICOM Viewer to the Disk Image ................. 404
14.3 Burn image .......................................................... 405
  14.3.1 Write to Disk .................................................... 405
  14.3.2 Write to Memory Card or Folder .............................. 406
  14.3.3 Burn an image to CD / DVD in Linux and macOS operating systems .......................... 407
14.4 View studies written on disk ...................................... 407

# DICOM Viewer Settings

15.1 General ............................................................. 409
15.2 User interface ....................................................... 410
15.3 DICOM .............................................................. 410
15.4 Screen .............................................................. 411
  15.4.1 Setting an Additional Monitor ............................... 411
  15.4.2 Customizing the Screen Parameters ......................... 412
  15.4.3 High resolution monitor support ............................. 414
15.5 Skins ................................................................. 414
15.6 Modules ............................................................ 415
  15.6.1 Set Up Image Viewer Module ................................ 415
  15.6.2 Set Up Study List Module .................................... 417
  15.6.3 Set Up 3D Reconstruction Module ......................... 417
  15.6.4 Set Up Vessel Analysis Module .............................. 419
  15.6.5 Set Up Network Support Module ............................. 419
  15.6.6 Set Up Local Storage Module ............................... 419
  15.6.7 Set Up «DICOM CD/DVD Creator» .......................... 419
  15.6.8 Set Up PET Analysis Module ................................. 420
15.7 Set Up Hotkeys Module ............................................ 420
15.8 Import and Export Settings ....................................... 422
  15.8.1 Export Settings ................................................. 422
  15.8.2 Import Settings ................................................ 423

# DICOM Tag Viewing

16.1 DICOM Tags. General Information ............................... 424
16.2 DICOM Tag Viewer Window ....................................... 425
  16.2.1 Toolbar ........................................................ 425
  16.2.2 Tag Tree ....................................................... 426
  16.2.3 Search ......................................................... 427
16.3 Anonymize studies and series ................................... 427
<table>
<thead>
<tr>
<th>CONTENTS</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>“Hotkeys”</td>
<td>459</td>
</tr>
<tr>
<td>Index</td>
<td>465</td>
</tr>
<tr>
<td>Glossary</td>
<td>465</td>
</tr>
</tbody>
</table>
About this Manual

This User Manual describes the functionality of Inobitec DICOM Viewer (version 2.12) and provides instructions on how to use this software product.

Accepted Conventions

Names of program interface elements, key names and important notes are printed in **bold**. Image captions are printed in *italics*. The page numbers which contain a detailed description of the subject are printed in **bold** in the Index.

Warnings

Warnings are used to attract attention to important information. Warnings may be marked with the following symbols:

- **Notifies the user that there is a great chance of unexpected and potentially hazardous effect.**

- **Is used to attract the user’s attention to important notes, advice and recommendations.**
Technical Support

Technical support of Inobitec DICOM Viewer users is provided by the Inobitec, LLC team. If you apply for technical support, please include the following information in your message:

- your computer OS name, version and bitness (you can get this information from your system administrator);
- DICOM Viewer version (e.g. 2.3.0.6631). To get your version number, select the About... item from the main Help menu;
- product code. To find out the product code, select the License... item from the main Help menu.

To apply for technical support, or if you have any further questions or comments, please email us at support@inobitec.com
About the Product

Inobitec DICOM Viewer software is intended for visualization, analysis and printing of medical data obtained from various DICOM equipment (modality). The program can be installed on a diagnostic workstation and integrated with PACS. Inobitec DICOM Viewer brings the capabilities of diagnostics to the new level and makes it possible to detect an abnormality in due time, effectively predict its development and carefully plan the treatment.

To diagnose the Inobitec DICOM Viewer software should only be used by specialists who have the necessary qualifications in the relevant field.

Inobitec DICOM Viewer software product and installer does not:

- collect and transfer confidential user information;
- intercept network traffic;
- show ads;
- send spam;
- show messages not related to work;
- automatically update itself without notifying the user.

After uninstalling you do not need to restore your operating system and browser settings. Uninstalling is free of charge. Uninstalling does not adversely affect the operation of the computer and installed software. Files not related to the DICOM Viewer are not removed and changed after uninstalling. The DICOM Viewer functionality, installing, uninstalling, licensing are fully described in this User Manual on the website inobitec.com. License Agreement is available from the link https://inobitec.com/eng/about/viewerLic/.

The DICOM Viewer is available in two editions:

- **Lite**: contains sufficient functionality for high-grade work, including storage and transfer of information on a network. This edition does not contain tools for conducting highly specialized studies. Its cost is much lower than the cost of the Pro edition.

- **Pro**: contains all the functionality which is currently available. In the User Manual the description of the functionality is marked with the symbol \(^{\text{PRO}}\).

The edition of the DICOM Viewer which is recorded on the disk and the memory card contains minimal functionality for viewing studies by patients.

Starting from version 1.11.0, specialized modules can additionally be connected to the Pro edition. Such modules are licensed and paid for separately. The main functionality remains...
available in the Pro edition. In the User Manual the description of additional functionality is marked with the symbol «ADD».

If the functionality is not available in the current edition, then a corresponding warning appears. It indicates in which edition the functionality is available.

32-bit and 64-bit builds are available for Windows operating systems. 64-bit builds are available for Linux and macOS. You can install only a 32-bit build of the program on a computer with a 32-bit operating system, and any build on a computer with 64-bit one, but it is recommended to install 64-bit, since it uses computer resources more efficiently. The functionality that requires a large amount of RAM is available only in 64-bit builds.

**DICOM Viewer Functionality**

**INOBITEC Products Comparison Table**

<table>
<thead>
<tr>
<th>Function</th>
<th>Lite</th>
<th>Pro</th>
<th>Web</th>
</tr>
</thead>
<tbody>
<tr>
<td>View flat images with the following options:</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>rotate, pan, zoom, mirror</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>change window width and level</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>change the window width and level based on the image parameters (Full dynamic W/L)</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>customization of WL presets</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>opening DICOM studies from zip archives</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>opening several DICOM studies at the same time</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>automatic filling tab windows with the series</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>synchronization of series windows in case of window level/width alteration, movement, scaling, and scrolling</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>calibrate image size</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>show image scout lines on other series images</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>flat image view with orthogonal projections</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>merge series into phases</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>measure length, angles</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>play series images subsequently as a movie</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>choose image resampling filter in the Flat Images View window</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Function</td>
<td>Lite</td>
<td>Pro</td>
<td>Web</td>
</tr>
<tr>
<td>-------------------------------------------------------------------------</td>
<td>------</td>
<td>-----</td>
<td>-----</td>
</tr>
<tr>
<td>build freeform contours with the Pencil tool</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>add comments, labels and various graphic elements on images</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>moving comments, measurements, measurement results and various graphic elements on images</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>measure Cobb angles and intensity at a certain point or in a certain area</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>export images to a graphic file</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>export images to a new series of DICOM images</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>DSA (Digital Subtraction Angiography)</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>measurement of speed and time interval for dopplergram</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>distance measurement on ultrasound studies</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>support for color lookup tables (CLUTs) embedded in DICOM data</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>applying different CLUTs to images</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>edit CLUTs</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>cerebral Perfusion</td>
<td></td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>blood flow parameters evaluation on the basis of phase-contrast images</td>
<td></td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>calcium scoring</td>
<td></td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>measurement of apparent diffusion coefficient (ADC)</td>
<td></td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>View three-dimensional tissue reconstruction with the following options:</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>rotate, pan and zoom the model</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>view scaled-down multiplanar reconstruction of the series simultaneously (with automatic synchronization)</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>cut the outside and inside parts of the model</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>MIP (Maximum Intensity Projection)</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>measure length, angles</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>export the model to a graphic file</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>export the model to a new series of DICOM images</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>export of several images obtained by rotating the model to a graphic file</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Function</td>
<td>Lite</td>
<td>Pro</td>
<td>Web</td>
</tr>
<tr>
<td>-------------------------------------------------------------------------</td>
<td>------</td>
<td>-----</td>
<td>-----</td>
</tr>
<tr>
<td>export of several images obtained by rotating the model to a new series of DICOM images</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>switching projection</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>add markers and line markers</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>delete bone tissue in the manual mode (interactively and automatically)</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>delete bone tissue for merged series</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>build the surface by the model</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>surface construction for the main volume</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>surface building for each phase of the main volume in multiphase series</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>individual change of parameters for each constructed surface</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>measure the shortest path on the surface of a visible volume with the Surface Ruler tool</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>import of multiple surfaces</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>segmentation</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>View multiplanar reconstruction with the following options:</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>view axial, frontal and sagittal sections of tissue</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>rotate cutting planes in space</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>3D view</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>measure length, angles</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>add markers and line markers</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>build freeform contours with the Pencil tool</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>setting modes MIP, MinIP, AIP</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>set slice thickness</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>MPR view sync on several monitors</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>display of MPR planes on 3D view</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>building a curvilinear reconstruction</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>build a section of a spatial model by a random surface</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>cross-section view for curvilinear reconstruction</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>export sections of any of the planes with a selectable increment to a series</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Function</td>
<td>Lite</td>
<td>Pro</td>
<td>Web</td>
</tr>
<tr>
<td>-------------------------------------------------------------------------</td>
<td>------</td>
<td>-----</td>
<td>-----</td>
</tr>
<tr>
<td>segmentation</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>surface construction for the main volume</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>surface building for each phase of the main volume in multiphase series</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>individual change of parameters for each constructed surface</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>import of multiple surfaces</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>contour based segmentation</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>showing the mask outline</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>histogram display for ROI</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>mixed RGB colors Fusion</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Diffusion Tensor Imaging (DTI) support</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Virtual endoscopy (viewing the inner surfaces of cavities in tissues)</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>automatically and manually navigate the inside a cavity</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>build cavity surfaces</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>view scaled-down multiplanar reconstruction of the series simultaneously (with automatic synchronization)</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Merge series with the following options:</td>
<td>✓</td>
<td></td>
<td></td>
</tr>
<tr>
<td>remove bone tissue for DualScan and DualEnergy studies</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>build three-dimensional models based on multiple series of images of the same tissue in different modes</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>quickly switch to a full-scale view of three-dimensional reconstruction, multiplanar reconstruction and virtual endoscopy of the model built by merging series</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>stitch images</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>export of volume stitching</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>View electrocardiogram with the following options:</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>measure time intervals and values on graphs</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>using filters</td>
<td></td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>export images to a new series of DICOM images</td>
<td></td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Print images on paper or film using a DICOM printer with the following options:</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Function</td>
<td>Lite</td>
<td>Pro</td>
<td>Web</td>
</tr>
<tr>
<td>-------------------------------------------------------------------------</td>
<td>------</td>
<td>-----</td>
<td>-----</td>
</tr>
<tr>
<td>adding reference images</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>exporting pages to the PACS server for printing</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>adding logo</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Open studies by dragging and dropping on the program icon and program window</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Open studies in the background</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Transformation indicators in the series window with an opportunity to undo the transformations</td>
<td></td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>Open/save file using Native OS dialogs</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Voxel and polygon rendering support on Metal for macOS starting with Version 10.15</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Set up the interface and the DICOM Viewer functionality with the capability to export and import the settings configuration</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Tool control with the left, the right and the middle mouse buttons</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>High resolution monitor support</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>View DICOM tags</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>The support of secure connection with TLS</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>PDF data support and presentation in DICOM files</td>
<td>✓</td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>Support for structured reports (SR)</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>The opportunity to view several types of data in one window simultaneously: flat images, volume reconstructions, MPR, ECG, video, PDF documents and structured reports</td>
<td>✓</td>
<td></td>
<td>✓</td>
</tr>
<tr>
<td>Minimize application window to system tray</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Integrated help system</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Create series display templates for various modalities</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Write data to CD, DVD and flash cards</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Integration with PACS servers</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Store data in a local storage</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Work as a PACS server, support C-FIND and C-MOVE</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Saving studies to a folder</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Saving selected series to a folder</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Integration with third-party systems</td>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
</tbody>
</table>
DICOM Viewer Functionality

<table>
<thead>
<tr>
<th>Function</th>
<th>Lite</th>
<th>Pro</th>
<th>Web</th>
</tr>
</thead>
<tbody>
<tr>
<td>Edit patient name and study description on the Local Storage</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Anonymize studies and series with the ability to change DICOM tags</td>
<td>✓</td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>PLY, OBJ, STL, GLB formats surface export</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>PLY, OBJ, STL formats surface import</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Saving the model orientation and projection in spj-projects</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Embedded WebViewer</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Register images</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Record video from viewing windows</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
<tr>
<td>Play video contained in DICOM files</td>
<td></td>
<td>✓</td>
<td></td>
</tr>
</tbody>
</table>

«Web» is the Inobitec Web DICOM Viewer, an individual product with the functions comparable to those of the desktop DICOM Viewer version. More information can be found in the Products and Downloads pages.

Additional modules to the Pro edition, purchased separately:

<table>
<thead>
<tr>
<th>Name</th>
<th>Short Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vessel Analysis</td>
<td>Virtual endoscopy of vessels</td>
</tr>
<tr>
<td>Coronary Arteries Analysis</td>
<td>Virtual endoscopy of coronary arteries</td>
</tr>
<tr>
<td>PET Analysis</td>
<td>Analysis of one or several studies containing the PET series with the capability to view the MIP of the PET series, CT and PET fusion, CT and PET series separately, measuring SUV</td>
</tr>
<tr>
<td>Extended Segmentation</td>
<td>The opportunity to save and open segmentation projects from file and DICOM RT series</td>
</tr>
<tr>
<td>Image Annotation</td>
<td>The module is designed to prepare data for training neural networks to recognise various pathologies automatically</td>
</tr>
</tbody>
</table>
## About the Product

### New Functions in Version 2.12

<table>
<thead>
<tr>
<th>Function</th>
<th>Available in edition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Command execution via URL using <em>inobitec://</em> protocol</td>
<td>✓ ✓</td>
</tr>
<tr>
<td>Support of Structured Report (SR)</td>
<td>✓ ✓</td>
</tr>
<tr>
<td>The program operation on several monitors has been improved</td>
<td>✓ ✓</td>
</tr>
<tr>
<td>Display of additional tags on US studies</td>
<td>✓ ✓</td>
</tr>
<tr>
<td>Language selection menu for integrated user manual</td>
<td>✓ ✓</td>
</tr>
<tr>
<td>Export of volume stitching</td>
<td>✓</td>
</tr>
</tbody>
</table>

✓ — Functionality is available in this edition  
+ — Functionality is available in an additional module to the Pro edition
Installing, Uninstalling and Launching the Program

System Requirements

Minimum System Requirements

Operating system:

- Windows 7 32-bit;
- macOS version 10.13;
- Ubuntu version 18.04;
- Ubuntu version 20.04;

**RAM**: 2 GB;
**free disk space**: 300 MB;
**CPU**: 1.5 GHz;
**video card**: without hardware acceleration support;
**keyboard**: standard;
**mouse**: two-button with a scroll wheel;
**display**: resolution 1024x768;
**network card**.

Recommended System Requirements

Operating system:

- Windows 7 64-bit and greater;
- macOS version 10.15 and greater;
- Ubuntu version 18.04;
- Ubuntu version 20.04;
Installing, Uninstalling and Launching the Program

RAM: 16 GB (for full-fledged 3D and 4D reconstruction);
free disk space: 500 MB;
CPU: 3 GHz (4 or more cores);
video card: GeForce GTX 700 series with embedded memory of 4 GB (with CUDA support). For optimal performance, when working with segmentation functions, we recommend to run the program on a hardware with GeForce GTX 1070 and up with minimum 8GB VRAM;
keyboard: standard;
mouse: two-button with a scroll wheel;
display: two displays, resolution HD 1920x1080;
network card.

Installing and Uninstalling the Program

Installing the Program on Windows

To install the program:

1. Run the installer by double-click.
2. Click CONTINUE in the window shown in Fig. 1.
3. It is strongly recommended to update graphics adapter drivers (integrated or discrete) from the official manufacturer's website, in order to prevent possible failure in operation of DICOM Viewer. If you are sure that drivers are up to date check the The drivers on
Installing and Uninstalling the Program

This device have been updated box in the window shown in Fig. 2, and click CONTINUE. Otherwise stop installation (click CANCEL and in the confirmation dialog click Yes) and update drivers. To return to the previous installation step click GO BACK.

Figure 2: Software recomendation

4. Read the License Agreement carefully. Its text is also available from the link inobitec.com/eng/about/viewerLic/. If you agree the terms and conditions, check the item I accept the license and click CONTINUE (Fig. 3). Otherwise click CANCEL and in the confirmation dialog box that appears click Yes.
Installing, Uninstalling and Launching the Program

Figure 3: License Agreement

Figure 4: Select users
5. Select for whom you want to install the program (Fig. 4). If you select **Anyone who uses this computer (all users)**, then the program will be installed to the system folder, and you will need administrative privileges.

6. If necessary, change the Installation Folder (Fig. 5). We recommend leaving the default value. Click **CONTINUE**.

   **Attention:**
   - it is prohibited to specify a path with only the disk root (e.g. D:\);
   - it is prohibited to specify folders created by other users and third-party software;
   - when the program is being installed for all the users, specify a folder that can be accessed by all the users.

   ![Installation Folder](image)

   **Figure 5: Installation Folder**

7. If another version of the program is already installed in the selected folder, then the message **The directory you selected already exists and contains an installation. To install the product the installation will be uninstalled first** will be displayed.

   To uninstall, click **Yes**. The uninstaller will start (see the Section **Uninstalling the Program on Windows**). After the uninstall the installation will continue.

   To leave the already installed version of the program and select a new folder to install, click **No** and in the window shown in Fig. 5, specify another folder.
8. If you select installation for all users, then you need to specify the Common Directory to store the program service information (Fig. 6). If necessary, change the path to the Common Directory. We recommend leaving the default value. Click **CONTINUE**.

![Figure 6: Common Directory for service information](image)

9. If the DICOM Viewer is meant to be integrated with third-party systems, activate the program launch with the help of URL commands by checking the **Register the schema «inobitec» to launch a viewer with parameters from browser** box in the **Launch by browser** window (Fig. 7). The box is unchecked by default. For details on how to launch the program with URL commands, see Section 18.2.
10. In the **Select Components** window, (Fig. 8) select the required components by check the boxes. To expand or collapse the component tree, click on the symbols to the left of the component group name (highlighted in red and green in the Fig. 8):

- **the Help group:**
  - **Slideshow tips:** Compact movies for tooltips;
  - **Assistant (English):** English integrated help system;
  - **Assistant (Russian):** Russian integrated help system;
  - **User manual PDF (English):** English user manual in PDF format;
  - **User manual PDF (Russian):** Russian user manual in PDF format.

- **the Languages group** contains available languages.

For detailed information about a component select it with the mouse.
Installing, Uninstalling and Launching the Program

Figure 8: Select Components Window

Figure 9: Start Menu Shortcuts
11. If necessary, change the folder for the program’s shortcuts in the **Start** menu (Fig. 9). We recommend leaving the default value. Click **CONTINUE**.

![Image of the installer screen](image.png)

*Figure 10: Confirm installation*

12. In the confirmation window click the **INSTALL** button (Fig. 10).

13. Wait until the installation process is complete (Fig. 11). Click the **DONE** button.
Silent Installation on Windows

Silent installation allows you to speed up and automate the process of installing the program by submitting the installation parameters to the installer through the file. Such installation can be launched automatically on domain computers using Microsoft Active Directory.

To prepare the installer for a silent installation:

1. Unpack the installer to a folder using an archiver (for example, 7-zip).
2. Go to the folder where the installer is unpacked.
3. Edit the following parameters in the autoinstall.qs file:

   (a) **AllUsers** = false to install only for current user (by default) or **AllUsers** = true to install for all users;

   (b) **TargetPathName**: path to folder to install the DICOM Viewer. If **AllUsers** = true then the default value is `C:\Program Files\InobitecDICOMViewer<Edition><Version>`, if **AllUsers** = false then default value is `C:\Users\<CurrentUserName>\InobitecDICOMViewer<Edition><Version>`. If necessary, specify another value.

   (c) **CommonPath**: path to the common folder (only if **AllUsers** = true). The default value is `C:\ProgramData\InobitecDICOMViewer<Edition><Version>`. If necessary, specify another value. All users must have write access to the specified folder.

   (d) **LocalStoragePath**: path to the local storage. The default value is `C:\Users\<username>\InobitecDICOMViewerWorkspace`. 
Installing and Uninstalling the Program

(e) **OptionsFilePath**: path to the file with settings exported from an already installed DICOM Viewer. For details on how to export settings see Section 15.8. The settings file should be in the current folder. If the file is not specified, the default settings are used.

(f) **ForceInstall = false** to remove the previously installed version of the DICOM Viewer in the folder selected for installation.

If national characters are used save the `autostart.qs` file in utf-8 encoding.

To install the DICOM Viewer run the `silent_install.bat` file. Log is written to file `%temp%\install\%DATE%.log`, where `%temp%` and `%DATE%` are Windows system variables.

**Uninstalling the Program on Windows**

To uninstall the program:

1. Run the uninstaller using one of the following methods:
   
   (a) select **Inobitec Dicom Viewer -> Uninstall** in the **Start** menu or
   
   (b) use **Programs and Features** in the **Control Panel**.

2. Make sure that the item **Remove all components** is selected in the window shown in Fig. 12 and click the **CONTINUE** button.

![Figure 12: Beginning of the uninstallation](image-url)
3. In the confirmation window click the **UNINSTALL** button (Fig. 13).

![Figure 13: Confirm uninstallation](image)

4. In the confirmation window click the **DONE** button (Fig. 14).
Silent Uninstallation on Windows

Silent uninstallation allows you to automate the process of uninstalling of the program similar to silent installation.

To prepare the installer for a silent uninstallation:

1. Unpack the installer to a folder using an archiver (for example, 7-zip).
2. Go to the folder where the installer is unpacked.
3. Change the text for the path to the folder with the DICOM Viewer to uninstall in the silent_uninstall.bat file.

To uninstall the DICOM Viewer run the silent_install.bat file. Log is written to the %temp%\uninstall\%DATE%.log, where %temp% and %DATE% are Windows system variables.

Installing and Uninstalling the Program on Mac OS

To install the program uncompress the dmg file and drag DICOMViewer.app into the open Applications folder. The icon is displayed on the file while dragging. Release the mouse button and wait for the program installation to complete.

To uninstall the program remove the DICOMViewer.app from the Applications folder.
Installing and Uninstalling the Program in AppImage Format on Linux

Inobitec DICOM Viewer software for Linux OS is comprised of only one file in `<InobitecDICOMViewer><Bitness><Edition><Version>` format with AppImage extension. The file contains the program with all the libraries required for its functioning. Example: `InobitecDICOMViewer-linux-64-bit-pro-2.7.0.AppImage`.

To install and run the program in AppImage format, proceed as follows (for Ubuntu):

1. **We advise you to transfer** the downloaded Inobitec DICOM Viewer file from the `Downloads` file directory to the directory you need.

2. **Provide the AppImage file a permission to be executed.** For that purpose, mouse over the file and click the right mouse button. In the context menu, select **Properties**. When the Properties menu (Fig. 15) pops up, go to the **Permissions** tab and check the **Allow executing file as program** box. Close the Properties menu.

3. **To run the program file,** double-click on it with the left mouse button.

   ![Figure 15: «Properties» menu](image)

To uninstall the program in AppImage format remove the file from the directory.

**If to run the AppImage you need to install FUSE**

On Linux OS, **FUSE** (filesystem in userspace) software is required to work with AppImage files.

The Inobitec DICOM Viewer distribution for Linux OS in AppImage format requires **FUSE 2** functionality.

If the **FUSE 2** is not installed in your operating system, install and configure it manually. You will find detailed instructions on how to install and set up **FUSE 2** together with command...
Installing and Uninstalling the Program

examples at https://docs.appimage.org/user-guide/troubleshooting/fuse.html.
The resource may not be available. In this case you will have to find the information on in-
stalling and setting up FUSE 2 on your system for yourself.

Launching with Shortcuts

Starting from version 2.6 the DICOM Viewer shortcut in Windows operating systems is dis-
The editions available are:

- **PRO** — professional;

- **LITE** — simplified;

For example Inobitec PRO 2.6.0.

Each version and edition of the DICOM Viewer installed in Windows has their own shortcuts on the Desktop and the Start Menu to ensure the convenience of launching.

To launch the program, double-click on the desktop shortcut or click on the shortcut from the Start menu.

On Windows and macOS, the DICOM Viewer may be launched by dragging and dropping the data folder on the program icon. The studies contained in the folder will be opened in a new tab DICOM data in the folder, and, depending on the data type, the first series of the first study on the list will be opened:

- In the Flat image viewing tab;

- In the ECG viewing tab;

- With the PDF viewer (if installed), by default;

- In the DICOM Tag Viewing tab, if the series cannot be opened in the above mentioned tabs/by the above mentioned programs.

If the DICOM Viewer has already been launched, the data will be opened in it. If there are no data in the folder to be displayed, an empty tab DICOM data in the folder will pop up.

Launch multiple instances of the program

If one instance of editions Pro or Lite is already launched, then other instances of editions Pro or Lite exit and activate the first instance. If another instance is launched from the command line, then the command line options are sent to the first instance (see Sections 18.1 and 18.2).

Note that sometimes the program cannot exit immediately when the main window closes (e.g. if data is being transferred over the network, or if information is being written to a disk or flash card). In this case, if you try to launch the program, the main window of the launched instance does not open and you should wait until the launched instance exits and then launch the program again.
Service files

Service files are located in the following folders, depending on the operating system:

<table>
<thead>
<tr>
<th>Operating System</th>
<th>Service File Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>Windows</td>
<td>C:\Users&lt;Username&gt;\AppData\Local\Inobitec&lt;program name&gt;</td>
</tr>
<tr>
<td>Linux</td>
<td>~/.local/share/Inobitec/&lt;program name&gt;</td>
</tr>
<tr>
<td>macOS</td>
<td>~/Library/Application Support/Inobitec/&lt;program name&gt;</td>
</tr>
</tbody>
</table>

The following files are service ones:

- log files (are located in the subfolder **Logs**);
- memory dumps, written if the program crashed (are located in the subfolder **Dumps**). Only for Windows;
- configuration files (are located in the subfolder **Configs**);
- CLUTs (are located in the subfolder **Configs**);
- 3D image renderer files (are located in the subfolder **OpenCL**).

E.g. *Smith* user’s log files for *Inobitec DICOM Viewer Pro* version 1.9.1 installed in *Windows* are located in *C:\Users\Smith\AppData\Local\Inobitec\Inobitec DICOM Viewer Professional Edition 1.9.1\Logs* folder.

Path to log files can be changed (see Section 15.1).

Import CLUTs

The CLUTs import option provides an opportunity to use customized CLUTs (e.g. CLUTs created by other users or CLUTs from previous DICOM Viewer versions).

CLUTs are saved in *vt_config.xml* file.

To import CLUTs, copy the *vt_config.xml* file to the **Configs** folder. The location of the **Configs** folder depends on the operating system (see Section Service files).

For example, a user named *Smith* working on *Windows* will find the CLUTs for *Inobitec DICOM Viewer Pro 2.7.0* in the following folder:

*C:\Users\Smith\AppData\Local \Inobitec \Inobitec DICOM Viewer Professional Edition 2.7.0\Configs*

Getting Started

To avoid problems with the DICOM Viewer, do the following before you start working with the program:

1. Limit the access to the computers with the program installed in order to protect the patients’ personal data.
2. If you need to print images on a DICOM printer, make sure that the printer is available and print a test page.

3. If you need to record data on a CD/DVD, make sure that the disk drive is available and make a test record.

4. If you need to download data from the modality to the local storage, check the modality connection settings by downloading test data. Errors may occur when studies are opened, depending on the modality settings (e.g. the modality may make an error in recording the width and the level of the window; in this case you will need to change the window width and level settings manually while viewing the images).

5. Make sure that the data downloaded from the modality can be viewed in the modes chosen (e.g. a study contains several phases for viewing images in the digital subtraction angiography mode).

Before starting a procedure that requires flawless operation of the DICOM Viewer, do the following:

1. If there is an uninterruptible power supply unit, make sure it is in working order.

2. Check the DICOM servers availability; depending on the tasks to be performed, check the ability to upload, download and search for data.

3. If you need to download studies in the local storage, check the amount of free space on the hard disk drive where this storage is placed.

**First run of the Program**

When you first start the DICOM Viewer, the welcome panel opens (Fig. 16). The welcome panel may also be displayed at the first startup after the upgrade the DICOM Viewer. Initialization of the DICOM Viewer is performed in the welcome panel.
Installing, Uninstalling and Launching the Program

The following information is displayed in the welcome panel:

- **Link More.** Download page Inobitec DICOM Viewer is available at this link.

- **Link Documentation.** Clicking the link brings up the help system of the DICOM Viewer. If the help system for the current language is not installed, a dialog box is displayed with a warning and a link to online help.

To cancel the DICOM Viewer launch and initialization, press **Esc** on the keyboard. Select **YES** in the dialog box for cancelling initialization and launch (Fig. 17). If you do not want to cancel initialization and launch the DICOM Viewer click the **NO** button.

![Figure 16: Welcome panel](image)

To complete initialization and launch of the DICOM Viewer main window, you need to follow all the setting up steps provided in the welcome panel. If the user cancels the DICOM Viewer initialization, the welcome panel will pop up the next time the program is launched.

To go to the next page, click the **CONTINUE** button.

1. On the page **Local Storage** (Fig. 18) change the path to the Local Storage DICOM data. We recommend leaving the default value.
The path to the Local Storage can be changed by the user after initialization of DICOM Viewer. For more information see Section 15.1.

![Local Storage](image)

*Figure 18: Path to the Local Storage*

To make the Lokal Storage for all the users of this PC, check the **Shared settings (for all users)** box. This mode is disabled by default. It can only be done if the DICOM Viewer was launched by a user with administrator privileges. The users who do not have administrator privileges cannot check or uncheck this box. In this case, an informational message is displayed (Fig. 19).

![Dialogue warning](image)

*Figure 19: Dialogue warning about lack of administrative privileges*

To continue initialization the DICOM Viewer click on the **NO** button. To close the welcome panel without saving parameter values, click on the **YES** button. The DICOM Viewer does not start in this case. The welcome panel will be launched at the next the DICOM Viewer start.

Click on the **Next** button to go to the next page, or **Back** to return to the previous page.

2. On the page **DICOM Listener** (Fig. 20) set the parameters of the DICOM listener service.
Installing, Uninstalling and Launching the Program

**Figure 20: DICOM Service**

- Enter the computer name (AE Title) in the field. The length of AE Title value shall not exceed 16 characters. Cyrillic letters and «\» symbols in AE titles are not allowed.

- Enter the port. Default value 3000.

This functionality is described in Section 12.1.1 and can be configured later. If this functionality has already been configured in this computer, then the window shown in Fig. 20 will contain the values specified earlier. Parameters specified earlier for a specific user will not be changed if you install the program for another user or for all users.

To save the current settings for all the users of this PC, check the **Shared settings (for all users)** box. This mode is disabled by default. It can only be done if the DICOM Viewer was launched by a user with administrator privileges. The users who do not have administrator privileges cannot check or uncheck this box. In this case, an informational message is displayed (Fig. 19).

To continue initialization the DICOM Viewer click on the **NO** button. To close the welcome panel without saving parameter values, click on the **YES** button. The DICOM Viewer does not start in this case. The welcome panel will be launched at the next the DICOM Viewer start.

Click the **NEXT** button to go to the next page or the **BACK** button to return to the previous page.

3. Take part in the survey by answering the two questions on the **Survey** pages (Fig. 21 and 22).
To answer a question, choose one of the options provided by selecting the respective radio button. The NEXT button will be activated as soon as the user chooses one of the options. To go to the previous step, click BACK.

The DONE button will be activated as soon as the user chooses one of the options. Click the DONE button, to complete the initialization of the DICOM Viewer, or BACK to return to the previous page. If you return to the previous step, the current survey results are saved.
Launching the Web Viewer

Functionality is available in the Pro edition

To use the Web Viewer, you should enable web access (see Section 12.1.3). To open the Web Viewer:

1. Open any Web browser.

2. Enter the link in the address bar to access to the Web Viewer. You can see this link in the services settings dialog (see Section 12.1.3). The link looks like http://youraddress:port. Replace youraddress with the ip address or the computer name on which the DICOM Viewer is installed and replace port with the web access port specified in the Services dialog.

3. Go to the entered link.

4. Enter the user name and user password specified in the services settings dialog.
Chapter 1

Program Window Elements

The main application window looks as follows (Fig. 1.1).

![Figure 1.1: Main application window](image)

The DICOM Viewer window consists of several elements.
1.1 Main Menu

The Main menu is shown in Fig. 1.2 (highlighted in red).

![Figure 1.2: Location of the main menu in the DICOM Viewer window](image)

The main menu includes several items.

1.1.1 File

The File menu item contains the following sub-items:

- **Study list** opens a new tab in the program window;
- **Open image annotation results...** opens a dialog box for selection of a JSON-file with annotation results that were saved earlier (Chapter 11);
- **Open project...** opens a dialog box for selection of a segmentation project or DTI file containing source DICOM data. The project will be opened in the default tab (see Section 6.11.4);
- **Open project as...** opens a dialog box for selection of a segmentation project or DTI file containing source DICOM data. This option allows the user to open a part of the project and select the tab where it will be opened (see Section 6.11.4);
- **Preview** opens the image preview tab for printing on paper;
- **DICOM preview** opens the image preview tab for DICOM printing;
- **Page layout** opens the settings for printing on paper;
- **Print** opens the system dialog for printing on paper;
- **Exit** shuts down the program.

1.1.2 Network

The Network main menu item contains the following sub-items:

- **Network status...**;
- **Servers...**;
- **Services**;
1.1. MAIN MENU

- DICOM printer setup...

For details on how to work with the network, see Chapter 12. The DICOM printer settings are described in Chapter 17.

1.1.3 Storage

The Storage main menu item contains the following sub-items:

- Storage status...;
- Check storage...;
- Clear storage...

For details on how to work with the storage, see Chapter 13.

1.1.4 View

The View main menu item contains the following sub-items:

- Image viewer;
- Volume reconstruction;
- MPR reconstruction;
- Vessel Analysis\textsuperscript{ADD};
- Coronary Artery Analysis\textsuperscript{ADD};
- Virtual endoscopy\textsuperscript{PRO};
- Series fusion\textsuperscript{PRO};
- PET Analysis\textsuperscript{ADD};
- Open pdf document;
- ECG viewer.

If a sub-item name is displayed in grey, it means that the command is unavailable for the selected study. If all sub-item names are displayed in grey, it means that no study has been selected from the study panel. Section 1.5 describes how to select studies. Three display modes are available for each sub-item

- Show at window 1 opens images in a new tab;
- Show as detached window opens images in a separate window;
- Show fullscreen opens images in the full screen mode. To exit the full screen mode, press Esc or F11 on the keyboard.

If the DICOM Viewer is set up for working with two displays, and/or if the screen is split, there are up to four options for displaying a tab. The monitor settings are described in Section 15.4.
1.1.5 Studies

The Studies main menu item contains the following sub-items:

- Open DICOM CD/DVD...
- Scan DICOM folder...
- Open zip archive... (see Section 1.5.2)
- Search
- Download selected studies to Local Storage
- Upload selected studies to remote server
- Add selected studies to Local Storage
- Remove selected studies from Local Storage
- Add the selected studies to DICOM CD/DVD image
- Save studies to folder
- Create anonymized copies of selected studies... (see Section 16.3)
- Export study list to CSV... (see Section: Study Panel)
- Edit patient name (see Section 1.9.3)
- Restore patient name
- Edit description (see Section 1.9.3)
- Restore description

For details on how to select data source, see Section 1.5. Sub-items Server search and Local storage search are available for the sub-item Search. For details on how to work with studies, see Section 1.11.

1.1.6 Series

The Series main menu item contains the following sub-items:

- Download selected series to Local Storage
- Upload selected series to remote server
- Add selected series to Local Storage
- Remove selected series from Local Storage
- Add selected series to DICOM CD/DVD image
- Save series to folder (see Section 1.6.2)
1.2. WINDOW MANAGEMENT

- Create uncompressed copy of series (see Section 1.13);
- Create anonymized copy of series... (see section 16.3);
- Sort.

Sub-items Sort by description, Sort by time and Sort by series number are available for the sub-item Sort.
For details on how to work with series, see Section 1.11.

1.1.7 Options

The Settings main menu item contains the following sub-items:

- Settings...;
- Export settings...;
- Import settings....

The DICOM Viewer settings are described in Chapter 15.

1.1.8 Help

The Help menu item contains the following sub-items:

- Contents... opens the Help System;
- License... opens a window to enter the license key;
- License from file... opens a window to load a trial version activation key file;
- About... displays a window with the information about the DICOM Viewer.

The Help System is described in Chapter 20.

1.2 Window Management

To the DICOM Viewer does not shut down but closed to the system tray, when you close it, check the box Show system tray icon (see Section 15.2). To restore the main window from the tray, double-click on the tray icon in the system tray or right-click on the tray icon and select the Restore item. To shut down the application right-click on the tray icon and select the Exit item (Fig. 1.3).

To enable the DICOM Viewer to minimize to the system tray, check the box Minimize to tray.
When you shut down the DICOM Viewer click **OK** to shut down the DICOM Viewer in the dialog box that appears, or **Cancel** to continue to work with the program. If you want the DICOM Viewer to always shut down without this confirmation, check the box **Don’t show this dialog again** and click **OK**. If you want the DICOM Viewer to show the confirmation dialog, check the box **Confirm on exit** (see Section 15.2).

### 1.3 Tab Panel

#### 1.3.1 General

A tab is a window fixed in the main program window. You can switch from tab to tab using buttons on the tab panel. The tab panel is highlighted in red in Fig. 1.4.

Each tab opened in the DICOM Viewer window corresponds to a button on the panel. To switch to a particular tab, click the corresponding button (Fig. 1.5). The file path or other information about the tab content is displayed on the tab button.
1.3. TAB PANEL

1.3.2 Manage a Tab

To manage a tab, use the buttons in its top right-hand corner (highlighted in red in Fig. 1.6).

Figure 1.6: Tab management buttons

Tab management buttons:

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The <strong>Full screen</strong> button displays the tab in the full screen mode. The tab management buttons are unavailable. To exit, press <strong>Esc</strong> or <strong>F11</strong>.</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>The <strong>Separate window</strong> button displays the tab in a separate window.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

To switch to the full screen mode, you may as well press **F11**, and to go back, you can use **F11** or **Esc**. If the tab is displayed in a separate window, the DICOM Viewer workspace looks as shown in Fig. 1.7.

Figure 1.7: A tab opened in a separate window
The window management buttons are located in the top right-hand corner of the window (highlighted in red in Fig. 1.7). Window management buttons:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Fix window" /></td>
<td>The <strong>Fix window</strong> button embeds the window as a tab in the main DICOM Viewer window.</td>
</tr>
<tr>
<td><img src="image" alt="Full screen" /></td>
<td>The <strong>Full screen</strong> button displays the window in the full screen mode. The window management buttons are unavailable. To exit the full screen mode, press <strong>Esc</strong> or <strong>F11</strong>.</td>
</tr>
<tr>
<td><img src="image" alt="Minimize window" /></td>
<td>The <strong>Minimize window</strong> button reduces the window to an icon located at the bottom of the screen (highlighted in red in Fig. 1.8). The window title is written on the icon.</td>
</tr>
<tr>
<td><img src="image" alt="Expand" /></td>
<td>The <strong>Expand</strong> button expands the window to the full screen. Unlike the full screen mode, the window management buttons will be available.</td>
</tr>
<tr>
<td><img src="image" alt="Close" /></td>
<td>The <strong>Close</strong> button closes the window.</td>
</tr>
<tr>
<td><img src="image" alt="Restore down" /></td>
<td>The <strong>Restore down</strong> button restores the initial window size.</td>
</tr>
</tbody>
</table>

*Figure 1.8: Window reduced to an icon*

To unfold a window from an icon, double-click the left mouse button on the icon.
1.4 Toolbar

The Toolbar is shown in Fig. 1.9 (highlighted in red).

![Toolbar location in the DICOM Viewer window](image)

**Figure 1.9: Toolbar location in the DICOM Viewer window**

Data source selection buttons on the toolbar:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="CD icon" /></td>
<td>The <strong>Open DICOM CD/DVD, which contains DICOMDIR metatile</strong> button sets a CD or DVD as the source of DICOM data and opens the folder selection dialog.</td>
</tr>
<tr>
<td><img src="image" alt="Folder icon" /></td>
<td>The <strong>Scan a folder for DICOM data</strong> button sets a folder as the DICOM data source and opens the folder selection dialog.</td>
</tr>
<tr>
<td><img src="image" alt="Archive icon" /></td>
<td>The <strong>Open a zip archive with DICOM data</strong> button provides a folder with zipped studies as the DICOM data source and opens the folder selection dialog.</td>
</tr>
<tr>
<td><img src="image" alt="Server icon" /></td>
<td>The <strong>Search data on the remote PACS Server</strong> button sets a PACS server as the DICOM data source and opens the search panel.</td>
</tr>
<tr>
<td><img src="image" alt="Storage icon" /></td>
<td>The <strong>Search data in the Local Storage</strong> button sets a local storage as the DICOM data source and opens the search panel.</td>
</tr>
</tbody>
</table>

For details on how to work with the search panel, see Section 1.7. The button corresponding to the selected data source is displayed on a light background.

Image view buttons on the toolbar:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Flat View icon" /></td>
<td>The <strong>Image viewer</strong> button opens images in the flat image view window.</td>
</tr>
<tr>
<td><img src="image" alt="Volume icon" /></td>
<td>The <strong>Volume Reconstruction</strong> button opens images in the volume reconstruction window.</td>
</tr>
<tr>
<td><img src="image" alt="Multiplanar icon" /></td>
<td>The <strong>Multiplanar Reconstruction</strong> button opens images in the multiplanar reconstruction window.</td>
</tr>
<tr>
<td><img src="image" alt="Vessels icon" /></td>
<td>The <strong>Vessels Analysis</strong> opens images in the Vessels Analysis window.</td>
</tr>
</tbody>
</table>

55
### Chapter 1. Program Window Elements

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Coronary Arteries Analysis" /></td>
<td>The <strong>Coronary Arteries Analysis</strong> button opens images in the Coronary Arteries Analysis window.</td>
</tr>
<tr>
<td><img src="image" alt="Virtual Endoscopy" /></td>
<td>The <strong>Virtual Endoscopy</strong> button opens images in the virtual endoscopy window.</td>
</tr>
<tr>
<td><img src="image" alt="Series fusion" /></td>
<td>The <strong>Series fusion</strong> button opens images in the series fusion window.</td>
</tr>
<tr>
<td><img src="image" alt="PET Analysis" /></td>
<td>The <strong>PET Analysis</strong> button opens images in the PET Analysis window.</td>
</tr>
<tr>
<td><img src="image" alt="Show image tags" /></td>
<td>The <strong>Show image tags</strong> button opens DICOM tags for the selected series of the selected study (see Section 16).</td>
</tr>
<tr>
<td><img src="image" alt="Open pdf document" /></td>
<td>The <strong>Open pdf document</strong> button opens the pdf document contained in the study in the default pdf viewer.</td>
</tr>
<tr>
<td><img src="image" alt="ECG Viewer" /></td>
<td>The <strong>ECG Viewer</strong> button opens images in the ECG view window.</td>
</tr>
</tbody>
</table>

If the action corresponding to a button is not available, the button looks pale and cannot be pressed (inactive).

All the buttons in this group are made up of two parts (Fig. 1.10).

*Figure 1.10: Button with location options*

If you click on the arrow (right side of the button highlighted in green), a menu with options for displaying the information on the screen will pop up.

- **display at monitor1** opens images in a new tab;
- **show as detached window** opens images in a separate window;
- **show fullscreen** opens images in the full screen mode.

To open an image in a new tab, click on the button (highlighted in red).

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="DICOM CD/DVD Creator" /></td>
<td>The <strong>DICOM CD/DVD Creator</strong> button opens the creator for disks containing DICOM data. The disk write is described in Chapter 14.</td>
</tr>
<tr>
<td><img src="image" alt="Advanced search" /></td>
<td>The <strong>Advanced search</strong> button opens the advanced search panel at the top of the tab. To hide the panel, click the button again. If the search panel is open, the search button will be displayed against a light background. For details on how to work with the search panel, see the next section.</td>
</tr>
</tbody>
</table>
1.5 Select Data Source

If the DICOM data contains text in national coding that does not match the coding of the main data, then a meaningless sequence of characters in the names of studies, series, etc may be displayed. In this case, to display the text correctly, you must select the target encoding in the settings (see Section 15.3). By default, the encoding of the data source is set. It is the one that is specified in the DICOM files.

1.5.1 Select a CD, DVD or Local Folder as the Data Source

To open studies stored on a CD, DVD or in a local folder:

1. Select a CD or DVD as the data source by clicking the button on the toolbar, or a local folder by clicking on the button. Commands Open DICOM CD/DVD... and Scan DICOM folder... are available as well from the Studies menu.

2. In the window that appears, select the folder containing the images, and click Select. To cancel the action, click Cancel.

The studies stored in the selected location will be displayed on the study panel.

The studies being transferred from the local folder may be opened in the Image viewer, ECG viewer, and DICOM tag viewer tabs before all the files have been read. PDF documents are also available to work with.

You will be able to open studies in other tabs, save them, record or send to the server after all the study directories have been read. If there are several series in a folder with a study, a complete list of such series will be displayed only after all the files have been read.

The process of uploading studies from a local folder is reflected on the information panel in the form of a progress bar. If you close the tab before the files have been read, the process of reading files is stopped.

Attention! If you switch to a different data source and then return to the current one, the study list will be cleared.

1.5.2 Opening Zipped DICOM Studies

The DICOM Viewer provides an opportunity to open and view zipped studies.

To open a zipped study from a local folder, proceed as follows:

1. Choose a local folder with zipped files as the data source by pressing the Open a zip archive with DICOM data button on the toolbar. Command Open zip archive... is also available from the Studies menu.
2. Choose one or several archives in the box that pops up and click **Open**. Click **Cancel** to cancel.

The studies stored in the selected location will be displayed on the study panel. The work with zipped studies is performed in the same way as the work with the studies from a local storage.

The thumbnails for the series from ZIP archives are provided with pictograms. Damaged ZIP archives and damaged files from ZIP archives are ignored by the DICOM Viewer.

If an encrypted ZIP archive is opened, a dialog box (see Fig. 1.11) pops up. Enter the password and click **OK** to open the encrypted ZIP archive or **Cancel** to cancel.

![Zip archive password dialog box](image)

*Figure 1.11: Entering the ZIP archive password dialog box*

**Attention!** If you switch to a different data source and then return to the current one, the study list will be cleared.

### 1.5.3 Opening DICOM studies by dragging and dropping

You can open DICOM studies in several ways:

1. **Dragging and dropping studies on the DICOM Viewer shortcut.** Drag and drop one or more folders with DICOM studies or ZIP archives from the explorer window to the DICOM Viewer shortcut (this option is only available on Windows and macOS). The list of studies will be opened in a new tab **DICOM data in the folder** or **DICOM data in the zip archive**. Besides, the **Image viewer** tab with the first series of the first study will be opened.

   The opportunity to drag and drop both, ZIP archives and unzipped data folders with DICOM data, to the DICOM Viewer shortcut is supported. In this case, the study lists are opened in new tabs **DICOM data in the zip archive** and **DICOM data in the folder**. New **Image viewer** tabs with the first series of the first studies from each list will be opened.

2. **Dragging and dropping studies to the DICOM Viewer study list.** Drag and drop one or more folders with DICOM studies or ZIP archives from the explorer window to the DICOM Viewer study list. The list of studies will be opened in a new tab **DICOM data in the folder** or **DICOM data in the zip archive**. Besides, the **Image viewer** tab with the first series of the first study will be opened.

   Dragging and dropping of ZIP archives and unzipped data folders with DICOM data to the DICOM Viewer study list is supported. In this case, the study lists are opened in new
1.5. **Select Data Source**

Tabs **DICOM data in the zip archive** and **DICOM data in the folder**. New **Image viewer** tabs with the first series of the first studies from each list will be opened.

3. **Dragging and dropping studies to the Image viewer window of the DICOM Viewer.** Drag and drop one or more folders with DICOM studies or ZIP archives from the explorer window to the **Image viewer** window of the DICOM Viewer. The study and its series are added to the series panel. The first series of the study will be opened in a new **Image viewer** window.

   Dragging and dropping of ZIP archives and unzipped data folders with DICOM data to the **Image viewer** window of the DICOM Viewer is supported. Studies and their series are added to the series panel. The first series of the study will be opened in a new **Image viewer** window.

4. **Dragging and dropping studies on the Image viewer window tab button of the DICOM Viewer.** Drag and drop one or more folders with DICOM studies or ZIP archives from the explorer window on the **Image viewer** tab button of the DICOM Viewer. The study and its series are added to the series panel. The first series of the study will be opened in a new **Image viewer** window.

   Dragging and dropping both, ZIP archives and unzipped data folders with DICOM data to the **Image viewer** tab button of the DICOM Viewer is supported. Studies and their series are added to the series panel. The first series of the studies will be opened in a new **Image viewer** window.

### 1.5.4 Select a PACS Server or Local Storage as the Data Source

To open studies stored on a PACS server or in a local storage:

1. Select the PACS server as the data source by clicking the **Search data at remote PACS server** button on the toolbar, or the local storage by clicking **Search data in the local storage**. These commands are available as well from the **Study** context menu.

2. Search for data using the search panel that opens. For details on how to work with the search panel, see Section 1.7. The studies that satisfy the search criteria will be displayed on the study panel. The series panel will display the series of the first retrieved study.

   **Attention! If you switch to a different data source and then return to the current one, the study list will be cleared.**

   To automatically open a Local Storage when you start the DICOM Viewer check this option (Section 15.6.2) and set up a default search period.

   If you open a study from the PACS server, it will be downloaded to the Local Storage. When you close this study the message like **1 series have been downloaded automatically from server. Would you like to keep them on your local storage?** will be displayed. To keep the study in the Local Storage, click **Yes**, to remove, click **No**. If you want to always perform the selected action, check the box **Remember my choice and do not show this dialog again**. For details on how to change your choice, see Section 15.6.2.
CHAPTER 1. PROGRAM WINDOW ELEMENTS

For the study, added to the Local Storage at least partially, the import date is displayed on the Study Panel.

When the DICOM Viewer is used as the PACS server, data from remote devices are added to the local storage. Data transfer may be initiated by a transmitting device, such as a CAT scanner, DICOM Server, or DICOM Viewer installed on another computer.

The list of the studies in the local storage is automatically updated each time data are received from a supported source.

New studies that were transferred to the local storage from other sources are marked on the study list with ➤. This icon will be deleted after the new study is selected or after a search is performed (i.e. the SEARCH button on the search panel is clicked). The new studies that were received from third-party devices but do not comply with the search parameters will not be shown on the study list (for details see Section 1.7).

1.6 Save Studies and Series to the folder

1.6.1 Save Studies to the folder

The DICOM Viewer allows you to save one or more studies from the Local Storage, from a folder, from a Compact Disk or from a PACS Server to a folder.

Attention! Saving studies from a PACS server in C-MOVE mode is not possible. To do it, connect to PACS Server using C-GET mode or first download the studies to the Local Storage and save them to a folder from the Local Storage.

When you try to save studies from the server in c-move, the error «Unsupported server mode» appears.

The PACS Server connection settings are described in Section 12.2.

If you compress data, then the studies are saved to a zip file.

To save studies:

1. Select data source (Local Storage, Folder, Compact Disk, PACS Server to which the DICOM Viewer is connected in C-GET mode). For details on how to select data source, see Section 1.5.

2. Search for data using the search panel that opens. For details on how to work with the search panel, see Section 1.7. The studies that satisfy the search criteria will be displayed on the study panel.

3. Select one or more studies on the Study Panel. For details on how to work with the Study Panel, see Section 1.9.

4. Click the Save studies to the folder button.

5. In the dialog that opens (Fig. 1.12) set up the following parameters:

- Path to save: path to the folder to save studies;
- Folder name (File name): if only one study is selected for saving, this parameter is editable. Otherwise the DICOM Viewer generates a folder name (archive file name) and the Folder name (File name) field is empty. If an archive file with the same name already exists, the DICOM Viewer offers to overwrite it;
1.6. SAVE STUDIES AND SERIES TO THE FOLDER

- the **Compress files** check box: if set, the saved data is compressed into a zip archive;

- if several studies are selected, then the **Save each study into separate folder (file)** check box appears. It allows to save each study into separate folder (archive file);

- the **Anonymize** check box allows to anonymize saving data. For details, see Section 16.3.

- to restore default settings, click the **DEFAULTS** button.

6. Click the **OK** button to save or **CANCEL** to cancel.

![Figure 1.12: Saving studies to the folder dialog](image)

The data saved into the folder is supplied for later recording onto a Compact Disk using the operating system. The Compact Disk opens in the same way as if it were recorded using the DICOM Viewer (without adding the DICOM Viewer to the disk image).
CHAPTER 1. PROGRAM WINDOW ELEMENTS

1.6.2 Save Series to the folder

The DICOM Viewer allows you to save one or more series of a single study from the Local Storage, from a folder, from a Compact Disk or from a PACS Server to a folder.

Attention! Saving DICOM data from a PACS server in C-MOVE mode is not possible. To do it, connect to PACS Server using C-GET mode or first download the studies to the Local Storage and save them to a folder from the Local Storage.

When you try to save studies from the server in c-move, the error «Unsupported server mode» appears.

The PACS Server connection settings are described in Section 12.2.

To save series:

1. Select data source (Local Storage, Folder, Compact Disk, PACS Server to which the DICOM Viewer is connected in C-GET mode). For details on how to select data source, see Section 1.5.

2. Search for data using the search panel that opens. For details on how to work with the search panel, see Section 1.7. The studies that satisfy the search criteria will be displayed on the study panel.

3. Select a study on the Study Panel. For details on how to work with the Study Panel, see Section 1.9.

4. Select one or more series on the Series Panel. For details on how to work with the Study Panel, see Section 1.10.

   Fused series cannot be saved in a folder.

5. Select the Save series to folder option in the Series section of the main menu. If among the selected series there are no series that can be saved in a folder, the Save series to folder button will be unavailable. If there is such a series among the selected series, the Save series to folder button will be available. When series are saved in a folder, the fused series will be skipped.

6. In the Saving series to the folder dialog box that pops up, provide the required parameters. The interface of the dialog box is identical with the interface of the dialog box for saving studies to a folder (see Fig. 1.12).

7. Click the OK button to save or CANCEL to cancel.

The series saved in a folder can be viewed and then recorded on a CD with the OS software.
1.7 Search Panel

The search panel is shown in Fig. 1.13.

To open or close the panel, click the button on the toolbar.

A search query is executed in the text field (see «2» in Fig. 1.13). From the drop-down list («1» in Fig. 1.13), select one of the following search parameters:

- **patient name** (to search for a name that does not start with the entered characters, put an asterisk at the beginning: «*John»);
- **patient ID** (similar to search by name);
- **body part** (Enter the name of a body part in the text field. Under the text field, you will see some options that may be used for searching by body parts);
- **accession number** (similar to search by name);
- **description**.

To search for studies by modality, press the button for the respective modality. The buttons for the selected modalities are highlighted. You can choose any modalities combination. To delete a selected modality, press the button again.

The search panel also provides for search by date of birth, search by the date of study performance or study import. Select one of the following options from the drop-down list (see «3» in Fig. 1.13):

- **by study date**;
- **by import date**;
- **by date of birth**. In the search period drop-down list (see «4» in Fig. 1.13) only the *Exact date* option is available.

You can perform search by the exact date, by the time interval specified or by the period selected from the drop-down list. Choose a period from the drop-down list (see «4» in Fig. 1.13):

- **all time**;
- **today**;
- **yesterday**;
- **last week**;
CHAPTER 1. PROGRAM WINDOW ELEMENTS

- last month;
- last year;
- exact date;
- interval.

To search by date and interval enter the year: YYYY-**-**, year and month: YYYY-MM-**, or the full date. The date can also be selected using the calendar.

After filling in the required fields, click the SEARCH button or press the Enter key on the keyboard. If the SEARCH button is inactive, it means that the selected data source is not available. To clear the search criteria, click CLEAR.

The search for studies on the PACS server with no period specified (option All time) may take some time and increase the server load. Therefore, when you click the SEARCH button, the warning dialog Search for all time. It may take some time. Would you like to continue? will be displayed. To perform a search, click Yes, to cancel, click No.

If four or more characters are entered in the search field, the long search on the PACS server warning message is not displayed, regardless of the specified search date.

The PACS Server may not support the search by some of the selected options and criteria.

1.7.1 Saving the Search Parameters

To simplify study search by commonly used parameters, the DICOM Viewer provides for an opportunity to save study search parameters (presets).

To create a new preset with commonly used parameters, proceed as follows:

1. Open the search panel and specify the search parameters (for details see Section 1.7).
2. Click the arrow on the right-hand side of the SEARCH button and select Save preset.
3. In the Preset creation dialog box (Fig. 1.14), enter the name of the new preset.

![Figure 1.14: The Preset creation dialog box](image)

Click OK, to create new preset, or CANCEL to cancel.

All the current search panel parameters will be saved as the preset.

To delete a preset, click the arrow on the right-hand side of the SEARCH button. Choose the Remove preset option and select the preset to be deleted.
1.7.2 Searching for Studies by Preset Parameters

To search for studies by preset parameters, choose the preset you need in the SEARCH button menu. The search will be performed automatically after you have selected the preset.

The current preset parameters are displayed on the search panel. The preset parameters are specified with consideration for the storage selected. For example, if the search is performed in a storage different from the local storage, it will be impossible to search by the date of import. In this case, a warning will pop up (Fig. 1.15). The search panel does not display the current preset parameters and the search will not be performed.

![Warning that a search cannot be performed](image)

Figure 1.15: Warning that a search cannot be performed

1.8 Select Server Panel

The server selection panel is shown in Fig. 1.16.

![Server selection panel in the DICOM Viewer window](image)

Figure 1.16: Server selection panel in the DICOM Viewer window

The server selection panel specifies the server server on which the search for data is carried out.
1.9 Study Panel

The study panel is shown in Fig. 1.17 (highlighted in red).

![Figure 1.17: Study panel in the DICOM Viewer window](image)

The study panel displays the list of studies stored in the selected location (folder, disk, local storage or PACS server).

To select multiple studies that are contiguous (next to each other):

1. click on one study and then holding Shift click the last study or
2. move the cursor from one study to the last study holding the left mouse button.

To select multiple studies that are anywhere on the study list, click on each one holding the Ctrl button.

1.9.1 Customize Study Panel

The DICOM Viewer allows you to customize columns and the font for the list of studies.

To select columns, right-click on the table header, a menu with a list of columns will be displayed (Fig. 1.18). The displayed columns are marked with a flag. To check/uncheck a column, left-click on its name in the context menu.
1.9. STUDY PANEL

Set size, family and font style to bold and/or italic (see Section 15.6.2).

1.9.2 Sort Studies

If two or more studies are displayed, they can be sorted by a certain parameter. To do this, click on the header of the column the parameter is located in. For instance, to sort by date and time, click on the area highlighted in red in Fig. 1.19.

Next to the column name, there is an arrow showing the sorting order (down arrow — descending 🈶️, up arrow — ascending 🈷️). To change the sorting order, click on the column header again. Studies can be sorted only by one parameter at a time. The default sorting order is ascending.
1.9.3 Edit Patient Name and Description in a Study

Editing the displayed patient name the description for this study are possible only for the studies in the Local Storage or for those that are opened from a folder or from a CD. The data itself will remain unchanged, and this information will not be saved on the PACS server. By default, editing is disabled. To enable it, check the box **Allow to edit patient name and description** (Section 15.6.2).

If you change the patient's name, another patient's study may be mistakenly used for establishing a diagnosis.

To edit the patient name or study description:

1. Right-click on the study on the study panel. The context menu shown in Fig. 1.20 will pop up.

2. Select one of the menu items **Edit Patient Name** and **Edit Description**. The corresponding field will become available for editing, and the cursor will be located in it.

3. Edit the text.

4. Press **Enter** key on the keyboard or click the mouse in the DICOM Viewer window in any area except the edited text to apply the changes.

These commands are available as well from the **Study** context menu. The commands from the context menu (Fig. 1.21) are available during editing. To open the context menu, right-click on the edited text.

![Study context menu](image)

*Figure 1.20: Study context menu*
The following commands are available:

- **Undo**: undo the changes;
- **Redo**: redo the last canceled action;
- **Cut**: delete the selected text and copy it to the exchange buffer;
- **Copy**: copy the selected text to the exchange buffer;
- **Paste**: paste the text from the exchange buffer;
- **Delete**: delete the selected text;
- **Select all**: select all edited text.

To restore a patient name or description, right-click on the study and select the **Restore patient name** or **Restore description** item.

If a command is unavailable, it is displayed in grey in the menu.

The edited patient name and description are displayed in italics after you select it on the Study Panel.

### 1.9.4 Study List Export

To save the list of studies displayed in the Study Panel to a CSV file:

1. Select the **Studies** menu and the **Export study list to CSV...** item.

2. In the dialog (Fig. 1.22) that opens, check columns from which you want to export data and click **OK** to confirm or **CANCEL** to cancel.

3. In the dialog that opens choose the folder and file name. Click **Save** to save data or **Cancel** to cancel.
A study list file in CSV format is a text file with a table. The columns of the table are separated by commas. The file may be opened in any text editor.

The software intended for working with spreadsheets (Microsoft Excel, LibreOffice Calc etc.) is better suited for viewing and analyzing CSV files data.

To open a CSV file in a spreadsheet application undistorted, proceed as follows (as exemplified by LibreOffice Calc):

1. Run the spreadsheet application.

2. In the dialog box for opening a document, select the CSV file and click **Open**.

3. In the **Text Import** dialog box, provide the following parameters:

   - in the **Separator options** section, select the field separator. In our case, it is a comma;
   - in the **Fields** section, highlight all the columns in the imported data view window and select the text column type from the dropdown list.

4. Click **OK** to open the document or **Cancel** to cancel.
1.10 Series Panel

The panel is shown in Fig. 1.23 (highlighted in red). Select the study from the study panel to see the list of series for it. The first series is highlighted automatically.

![Series panel in the DICOM Viewer window](image)

Figure 1.23: Series panel in the DICOM Viewer window

Selecting series is analogous to the studies selecting (see Section 1.9). But if you want to select multiple series by moving the mouse, start moving when cursor is not on the series thumbnail.

1.11 Studies and Series Download/Upload Panels

The panels are shown in Fig. 1.24 (Studies Download/Upload Panel highlighted in green, Series Download/Upload Panel highlighted in red). These panels are identical except that the former is designed to work with studies, and the latter is for series.
CHAPTER 1. PROGRAM WINDOW ELEMENTS

Figure 1.24: Studies and Series download/upload panels in the DICOM Viewer window

Series import/export panel buttons:

<table>
<thead>
<tr>
<th>Action</th>
<th>Button Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="download.png" alt="Download" /></td>
<td>The <strong>Download selected series to Local Storage</strong> button downloads the selected series to the local storage.</td>
</tr>
<tr>
<td><img src="upload.png" alt="Upload" /></td>
<td>The <strong>Upload selected series to remote server</strong> button uploads the selected series to the remote PACS server.</td>
</tr>
<tr>
<td><img src="add.png" alt="Add" /></td>
<td>The <strong>Add selected series to Local Storage</strong> button adds the selected series to the local storage.</td>
</tr>
<tr>
<td><img src="remove.png" alt="Remove" /></td>
<td>The <strong>Remove the selected series from the Local Storage</strong> button deletes the selected series from the local storage.</td>
</tr>
<tr>
<td><img src="cd.png" alt="CD" /></td>
<td>The <strong>Add selected series to DICOM CD/DVD image</strong> button adds the selected series to the CD/DVD Creator. For details on how to work with the creator, see Chapter 14.</td>
</tr>
</tbody>
</table>

If the action corresponding to a button cannot be performed, the button looks pale and cannot be pressed (inactive).

Managing the Studies Download/Upload Panel is completely analogous to the Series Download/Upload Panel.

These actions are available as well from the context menu and the Studies menu item for studies and from the Series menu item for series. To open it from the context menu, click the right mouse button on the study.
1.12 Information Panel

The panel is displayed in Fig. 1.25 (highlighted in red) and Fig. 1.26. Its left part displays the status of the last operation performed. The right part displays the progress bar for the current action and the data download/upload indicator while working with the PACS server or another DICOM Viewer. Fig. 1.26 illustrates data download from the server.

When data are downloaded, an animated ↓ icon is displayed. When data are uploaded, an animated ↑ icon is displayed. When no data are being downloaded or uploaded, no icons or progress bar are displayed.

1.13 Uncompress series

The following functionality allows to uncompress data and save it. This makes it possible to solve the problems with viewing and uploading compressed data on some remote servers. Uncompressing is possible only for studies in the Local Storage.

To uncompress data:
1. Open a study containing compressed data;

2. Select the series that you want to uncompress. For details on how to work with series, see Section 1.10.

3. Select the Series menu and Create uncompressed copy of series item. The selected series will be uncompressed, saved to the Local Storage and marked uncompressed.

1.14 Tool Control Buttons

Starting with the version 2.0, you can use the left, the right and the middle mouse button, which allows you to activate up to three tools at the same time. To activate a tool, click on the tool button with the mouse button. There are two ways to deactivate a tool:

1. Activate another tool with the same button or

2. Click on the tool button with the same mouse button.

On the tool button, you will see a symbol representing the mouse with the respective button selected (see Fig. 1.27).

Figure 1.27: The tools activated with the left, the middle and the right mouse button respectively (from left to right)

If a tool is activated from the main menu, from the context menu or with a hot key, it is automatically assigned to the left mouse button.

If a limited number of clicks is needed to create a graphic object (e.g. two clicks for a ruler, three clicks for corner measurements), then the creation process will be completed after these clicks. If you need an unlimited number of points to create a graphic object (e.g. a polygon or an MPR curve), you have to double-click the button with which the tool was activated to complete the creation process. The objects may be activated by mouse-over. When activated, they may be moved or edited.

The objects created with a certain tool can be edited:

- with the button to which this tool is assigned;
- with the left mouse button, no matter whether the tool is activated or not.

If you mouse over the object and click the right button, the right-click menu will pop up. The measurements and markers are activated if you mouse over them. It allows you to move the marker or edit the measurement.
Chapter 2

View Flat Images

256 gray shades are used to show tissue density. As there are more than 256 density values, similar values are represented by the same colour. To be able to distinguish between similar values, you need to decrease the window width. In this case, a smaller range of values will be represented by 256 gray shades. If necessary, set the desired the window level value.

In Image Viewer window, diagnosis can only be established on the basis of CT, MR, MG, and XA series.

2.1 Open Series

Select a study from the study panel. There are five ways to open a series:

- Click the Image viewer button on the toolbar.
- Double-click the left mouse button on the study title on the toolbar.
- Double-click the left mouse button on the series icon on the series panel.
- Drag the series icon to the study panel holding the left mouse button.
- Right-click the mouse to call the context menu for the series icon, and select one of the options in the Image viewer item.

The series will open in a new tab.

There are two ways to open a series from the explorer window:

- By dragging and dropping the folder with the series from the explorer window to the study list tab. A new study list tab will be opened. The first series of the study will be opened in the new flat image viewer tab.
- By dragging and dropping the folder with the series from the explorer window to the flat image viewer tab button. The first series of the study will be opened in a new window of the current tab.
If necessary, change the sorting order of images. To do it, right-click on the image to open context menu, select the **Image sorting** item, and then select one of the displaying modes:

- **No sorting**;
- **Sort by image number**;
- **Sort by image position and phase**.

The current order is marked with flag. The default sorting order is defined by the **Sort by** parameter (see Section 15.6.1).

The series panel will be displayed on the left. To hide/show it select the main menu Image and the **Quick series list** item or move the cursor to the panel border so that it would look like this: ![Cursor](image) and drag the border holding the left mouse button. The series panel is shown in Fig. 2.1.

![Figure 2.1: Series panel](image)

The DICOM Viewer allows you to open multiple series at a time or the same series multiple times. All series are opened in separate windows of the same tab, and their position will depend on the settings described in Section 2.8.

To open the selected series in the Volume Reconstruction or Multiplanar Reconstruction window, click the **Volume Reconstruction** or **MPR Reconstruction** button on the toolbar respectively.
2.2 Open Series with Current Settings

The DICOM Viewer allows you to open series of the opened study with the window level and width set for the previously opened series. To do this:

1. Open any series and set the window level and width.

2. Select the study view window by clicking the left mouse button on the window header (marked by the arrow in Fig. 2.2).

3. Open another series of this study. The series will be opened with the parameters of the window level and width specified earlier.

4. Repeat Steps 2 and 3 if necessary. The settings for the first opened series will be used.

5. Change the window level and width for the first opened series if necessary.

![The window header is marked by the arrow](image)

Figure 2.2: The window header is marked by the arrow

2.3 Working with Several Monitors and Split Screen

The DICOM Viewer allows you to split the screen into two parts or work with two monitors connected to the same computer. For details on how to set up your monitor, see Section 15.4.

Let us assume that both displays are used, and each one is split (Fig. 2.3). In this case, the DICOM Viewer will be running in four autonomous windows. To close the DICOM Viewer just close any of its windows.
CHAPTER 2. VIEW FLAT IMAGES

Figure 2.3: DICOM Viewer with two split screens. The right display is the main one

In the illustration above, the right monitor is the main one, so the Study list tab is open in its left window. To open this tab in any of the three remaining windows, select the File menu and the Study list item in this window. The series panel on the right side displays the window panel (Fig. 2.4).

Figure 2.4: Window panel

Each window has a display icon corresponding to it.

- the first icon corresponds to the left window of the main display;
- the second icon corresponds to the right window of the main display;
- the third icon corresponds to the left window of the additional display;
- the fourth icon corresponds to the right window of the additional display.

The OS settings determine which display is the main one. The icon corresponding to the current window is displayed against a light background. In Fig. 2.5, the Study list tab is open in each window, and you can see the correspondence between the windows and the display icons. The right display is the main one.
2.4. Resampling filter

To change the Resampling filter, open the Image main menu, select the Resampling filter menu item and in the submenu that opens, select a filter. The active filter is marked with a flag (Fig. 2.6)

![Resampling Filter menu](image)

Figure 2.6: The Resampling Filter menu
The following filters are available:

- Bilinear;
- B-spline;
- Mitchel;
- Catmull-Rom;
- Lanczos3;
- Lanczos5;
- Lanczos7.

By default the Mitchel filter is active.

When filters are used (except for the Bilinear filter), distortions may occur. If you see any dubious artifacts, select the Bilinear filter.

### 2.5 View Images in a Series

When a series is opened, its first image is displayed in the series window. The window for viewing series is shown in Fig. 2.7.

![Series window](image)

**Figure 2.7: Series window**

On the right-hand side of the window, you can see a scroll bar for scrolling images of the series (marked by the green arrow). If the series contains several phases or is a multiframe
series, at the top of the window you will see an additional scroll bar (marked by the red arrow) for switching between phases or frames. In the window, you will find the information on the current image (see Section 2.27).

There are six ways to switch to other images:

- Roll the mouse wheel up to switch to the previous image or down to go to the next one. One click of the wheel changes the position by one image.

- Use the scrollbar on the right side of the series window to move to the target image. To change the position by one image, click the left mouse button on the arrow or the bar above or below the scroll.

- Click the left mouse button holding the Shift key. If the current image is the last in the series, a click will switch you to the first image. Similarly, click the left mouse button holding the Ctrl key to move to the previous image.

- Use the Scrolling tool. Activate the tool on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

If it is impossible to switch between images, the tool may be used for scrolling frames.

- Use the arrow buttons on the toolbar: ←, →.

- Use the context menu: right-click the mouse on the image and select Next image or Previous image.

2.6 Switch between Series

There are two ways to switch between series in the series window:

- Use the arrow buttons on the toolbar: ←, →.

- Use the context menu: right-click on the image and select Next series or Previous series.

2.7 View Several Studies at a Time

To open several studies simultaneously:

1. Open a study by opening any of its series.

2. Switch to the tab containing the study list.

3. Select another study and drag one of its series to the tab with the opened study (highlighted in red in Fig. 2.8).
CHAPTER 2.  VIEW FLAT IMAGES

The series are opened in the same tab but in different study view windows. To maximize any window of the series and restore its size, proceed as follows:

- double-click with the left mouse button on the series window;

- double-click with the left mouse button on the title of the series window;

- click on the **Expand** button in the right-hand upper corner of the series window.

If some tool, such as the tool for measurements or render annotations, has been activated with the left mouse button, you can expand a window or restore its size in two ways:

- double-click with the left mouse button on the title of the series window;

- click on the **Expand** button in the right-hand upper corner of the series window.

The series panel is displayed on the left, and the series are grouped by study (Fig. 2.9). The arrows point to series panel stubs. The series panel at the top of the picture is expanded, and the bottom series panel is folded. To unfold it, just click the left mouse button on the header (marked by the arrow below). Only one series panel may be unfolded at a time, the rest will be folded.
2.8 View Multiple Series

There are several modes for positioning series windows in the study window.

You can choose the mode for arranging series in the study window in the Series arrangement button menu. There are three ways to open this menu:

1. Click the arrow on the right-hand side of the Series arrangement button on the toolbar and select the arrangement mode from the drop-down menu (Fig. 2.10).
2. Move the cursor to the window with the open series, right-click and select **Series arrangement** command from the shortcut menu.

3. Select **Series arrangement** from the **Image** section of the main menu.

You can choose from the following series arrangement modes:

- **Automatic** — the default series arrangement mode (see Section 2.8.1);
- **Stacked** — only one series window may be opened in the study window (see Section 2.8.2);
- **2 near** — the study window is divided into two parts (see Section 2.8.3);
- **2x2** — the study window is divided into four parts (see Section 2.8.3);
- **2x3** — the study window is divided into six parts (see Section 2.8.3);
- **Custom arrangement...** — the user customizes the arrangement of series windows (see Section 2.8.4)

The current series arrangement mode is highlighted in blue on the toolbar and on the menu.

To maximize any window of the series and restore its size, proceed as follows:

- double-click with the left mouse button on the series window;
- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.

If some tool, such as the tool for measurements or render annotations, has been activated with the left mouse button, you can expand a window or restore its size in two ways:

- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.
2.8. VIEW MULTIPLE SERIES

2.8.1 Auto Mode

This mode is active by default. If two or more series are open, they will be located in the window and scaled automatically, occupying the entire window. Five series are displayed in Fig. 2.11.

![Automatic display of series](image)

*Figure 2.11: Automatic display of series*

There are three ways to activate this mode:

- select the **Automatic** item in the Series arrangement button menu on the toolbar;
- locate the cursor to the window with the open series, right-click and select command Series arrangement->**Automatic** in the context menu;
- in the main menu, select **Image->Series arrangement->Automatic**.

2.8.2 Stacked Mode

This mode allows you to open only one series in the study window. If you try to open another series, the current series will be closed.

Activate this mode in several ways:

- select the **Stacked** item in the Series arrangement button menu on the toolbar;
- locate the cursor to the window with the open series, right-click and select command Series arrangement->**Stacked** in the context menu; in the main menu, select **Image->Series arrangement->Stacked**.
2.8.3 Grid Mode

In this mode the study window is split into parts, and a series window can be opened in each of them.

To set up a 1x2, 2x2 or 2x3 grid, select the \( \begin{array}{c} 2 \end{array} \) near, \( \begin{array}{c} 2x2 \end{array} \) or \( \begin{array}{c} 2x3 \end{array} \) item in the Series arrangement button menu.

These grid configuration types are available from the image context menu. Locate the cursor to the window with the open series, right-click and select command Series arrangement. Selection of 1x2, 2x2 or 2x3 grid is available in the main menu Image->Series arrangement.

If the selected grid configuration has fewer cells than there are open series in the study, a warning dialog box pops up (Fig. 2.12), in which the program asks for a permission to close the open series.

Click OK to close the series, or CANCEL to cancel.

![Warning dialog box](image)

Figure 2.12: Warning dialog box

There are two ways to disable the warning dialog box:

- Check the Don't show this dialog again box in the dialog (Fig. 2.12) and click the OK button.

- In the main menu, select Options->Settings...->Modules->Image Viewer, then choose the Image arrangement tab and uncheck the Confirm series closure on the arrangement changing box. For more information on the module settings see Section 15.6.1.

Click OK to apply the settings or Cancel to cancel.

2.8.4 Custom Mode

A grid may have from 1 to 100 cells. The maximum number of rows and columns is 10. This mode can be set by default (see Section 15.6.1).

Fig. 2.13 illustrates a 2*4 grid with three cells filled.
To define your own grid configuration perform the following:

- select the Custom arrangement... item in the Series arrangement button menu;
- locate the cursor to the window with the open series, right-click and select command Series arrangement->Custom arrangement... in the context menu;
- in the main menu, select Image->Series arrangement->Custom arrangement....

This mode can be set by default (see Section 15.6.1).

In the Row/Column setting dialog box (Fig. 2.14) enter the number of rows and columns of the grid.

For customized grids, the DICOM Viewer allows for auto-fill of the cells with the current study series. The auto-fill function is disabled by default. To enable it, in the main menu,
select **Options**->**Settings...**->**Modules**->**Image Viewer**, then choose the **Image arrangement** tab and check the **Turn on auto-fill in series** box. When a series is opened in a new tab, the other series are opened in the cells available. The cells are sorted by serial number.

When positioning series on the grid, the DICOM Viewer allows you to move the boundary between cells. To do this, move the cursor to the panel border so that it would look like \[\] or \[\] and drag the border holding the left mouse button. Setting the priority of horizontal or vertical separator is described in Section 15.6.1.

### 2.9 View Multiple Images in the Same Series Simultaneously

To select the mode for viewing images of the same study, right-click on the image to open context menu, select the **Image arrangement...** item, and then select one of the displaying modes. In general, they are similar to the modes for displaying series.

**Image displaying modes:**

- **Stacked.** Set by default. A single image is displayed in the window.

- **2 below.** Two images are displayed in the window, one above the other. The image order is downward. The entire screen is scrolled at once (i.e. if Images 1 and 2 of the same series are initially displayed, Images 3 and 4 will be displayed next), or one Image is scrolled at once. Selection of the desired mode is described in Section 15.6.1). To apply a new configuration, you should reopen the Flat Image View Tab.

- **2 near.** This mode is similar to the previous one, but the images are positioned horizontally, and the order is from left to right.

- **2x2.** Two columns and two rows of images are displayed in the window. The order is downward from left to right.

- **2x3, 3x2, 3x3, 4x4.** Similar to the previous item.

- **Custom arrangement.** The number of columns and rows is set manually (from 1 to 10). This configuration can be set by default (see Section 15.6.1).

Fig. 2.15 illustrates a 3x2 grid.
2.9. VIEW MULTIPLE IMAGES IN THE SAME SERIES SIMULTANEOUSLY

Multiple series may be displayed on the screen simultaneously, and each series window may contain multiple images. In Fig. 2.16, three series windows are open, the first one displays a single image, the second contains a 2x2 grid, and the third shows a 4x4 grid.

Figure 2.15: Images in a series displayed in a 3x2 grid

Figure 2.16: Displaying multiple series and multiple images in a series
CHAPTER 2. VIEW FLAT IMAGES

To set default viewing images modes for series of different modalities, add settings for these modalities (see Section 15.6.1). Use only English letters to specify modality. The modality designation should coincide with the designation on the icon of the series (Fig. 2.17).

![Figure 2.17: Series modality designation is marked by the red arrow](image)

2.10 Viewing Several Series as a Single Multiphase Series

Several series of a single study may be merged into a single multiphase series. Such a series may be used for assessment of contrast distribution in tissues at regular time intervals, e.g. for viewing it in the digital subtraction angiography (DSA) or perfusion parameters estimation mode.

The following series may be merged:

- saved in the local storage. If the PACS server has been chosen as the DICOM data source, save the series in the local storage;
- having the same modality;
- having the same FrameOfReferenceUID (0020, 0052) tag value.

To merge several series of the same study in a multiphase series, proceed as follows:

1. Select the study on the study panel to see the list of series.
2. Select several series on the list in one of the following ways:

   - select the first and the last series you need while holding the Shift button;
   - mouse over the series you need while holding the left mouse button;
   - select several series placed in different parts of the list while holding the Ctrl button.

3. Hover over the selected series, click the right mouse button and select the Image viewer (open as a single series) option on the menu. Choose one of the three viewing options:

   - Show at window 1 opens images in a new tab;
   - Show as detached window opens images in a separate window;
   - Show fullscreen opens images in the full screen mode. To exit the full screen mode, press Esc or F11 on the keyboard.
2.11. VIEWING ORTHOGONAL PROJECTIONS OF IMAGES

If the selected study series cannot be merged, a dialog box notifying of an error will pop up. To learn about the cause of the error, click the SHOW DETAILS... button.

The merged multiphase series will be opened in the flat image viewer window. A merged series may be opened from the Image viewer tab in the Volume reconstruction and MPR reconstruction tabs.

The new merged series will be added to the list of series of the current study. The description of the merged series comprises a list of all the series included in it, separated by a space followed by a Merged prefix. The series may be opened in the Volume reconstruction and MPR reconstruction tabs. To delete a merged series from the list of series, click the Remove the selected series from the Local Storage button on the series panel.

The following options are unavailable for a merged series:

- saving in a local storage;
- loading to the PACS server;
- adding to a CD/DVD image;
- viewing tags.

When the list of studies is updated, the merged series is deleted automatically.

2.11 Viewing Orthogonal Projections of Images

The DICOM Viewer provides the user an opportunity to change view for the series shown in the Image Viewer tab.

To choose a view for the selected series, in the study window, press the arrow on the right-hand side of the Orthogonal projection button on the toolbar.

*Figure 2.18: Orthogonal projection button drop-down menu*

The following options are available on the Orthogonal projection button drop-down menu (Fig. 2.18):

- Axial projection;
- Coronal projection;
- Sagittal projection.
CHAPTER 2. VIEW FLAT IMAGES

The active projection for the selected window is highlighted in blue on the toolbar and on the drop-down menu.

The default projection for the series is the same as the one used in which it was received from the medical equipment. The respective option is activated on the Orthogonal projection menu. Other options are available for series that can be images sorted by position and phase.

If only a part of the series has been loaded and the user chooses an orthogonal projection different from the one used in which it was received from the medical equipment, the projection will be built on the basis of the data that have already been loaded. If the number of images in the initial series is changed, a new orthogonal projection will be built the next time. If the number of images in the initial series stays the same, the orthogonal projection that was built earlier will be displayed.

If you choose an orthogonal projection in the same viewer window for a second time, the projection will be opened on the slice that was the last to be viewed.

All the operations available for the projection that was used in which it was received from the medical equipment, e.g. measurements, viewing several series, synchronization etc., may be performed with any orthogonal projection.

Images of series may be sorted and tags may be displayed only for the projections that were used in which it was received from the medical equipment. To change the image sorting type for all the series open in the viewer window, open the context menu by right-clicking on the window header, choose the Image sorting section and one of the sorting options.

When you return to the orthogonal projection that corresponds to what we got from the medical equipment, the image sorting does not change.

The Orthogonal projection menu is not available for series:

- which cannot be sorted by Sort by image position and phase;
- having less than 2 pictures for at least one phase;
- consisting of images based on the RGB color model.

The series that were opened from the Image Viewer tab in the Volume Reconstruction, MPR reconstruction tabs are only displayed in the projection used in which it was received from the medical equipment.

The Calcium scoring tool works independently with each orthogonal projection of the series.

When the window width and level parameters are customized, the thumbnail of the active series in the chosen orthogonal projection is shown in the W/L settings dialog box.

The current series in the chosen orthogonal projection is shown in the histogram and the CLUTs tab.

2.12 Play images

The DICOM Viewer allows you to automatically play back images of a series at a certain speed. To set up playback, click on the right part of the Play button and choose parameters.

1. If the series contains several phases or is multiframe, then the DICOM Viewer allows you to switch between the playback of images, phases and frames. To switch, select the Play images, the Play phases or the Play frames item from the «Play» button.
2.13. VIDEO RECORDING

The selected item is marked with a flag. Only the items suitable for this series are available in the context menu.

2. Select the speed (5, 10, 20 or 25 frames per second). If you want to set a different playback speed, select the User defined... item and in the dialog that opens, set the value from 1 to 100. The selected speed will be marked with a flag.

3. If you want to play images cyclically, select the Loop item. The item will be marked with a flag. To disable the cyclic playback, select this command again. The flag will be removed.

   To play the images click on the ➤ button on the toolbar. The button looks like ▶️. To end playback, click on the Pause button.

2.13 Video recording

Functionality is available in the Pro edition

The DICOM Viewer allows you to record video for the selected image viewing window. If you use the View Multiple Series mode (see Section 2.8), then video will be recorded only from the selected window. If you are viewing multiple images in a series at the same time (see Section 2.9), then video will be recorded only for the left bottom image area (highlighted in red in fig. 2.19). The following objects will be recorded:

- tissues;
- measurements;
- annotations;
- scout lines;
- tags;
- orientation cube;
- ruler;
- synchronization crosshair.

The following objects will not be recorded:

- cursor;
- dialog windows.

Video recording will be stopped if:

- focus is moved to another window within this tab;
• window size is changed.

Figure 2.19: Video recording area is highlighted in green

Video recording can be synchronized with playback (see Section 2.13). To start playback when recording a video and stop it after completing a video recording, click on the arrow on the right side of the button, select the Settings... item and in the dialog that opens (fig. 2.20), check the Start playback after recording starts box. If this box is checked then video recording will stop after the playback is stopped.

Figure 2.20: Video record settings dialog box

Chose one for the following options from the Encoder drop-down list:

• **Auto.** The choice of the encoder depends on the number of pixels in the window recorded. If the number of pixels (width × height) is \( \leq 9437184 \), the H264 encoder...
will be used. For windows with more than 9437184 pixels, the MPEG4 encoder will be used. By default, the encoder is selected automatically;

- **H264.** The encoder is used for recording videos when the number of pixels in the window \((\text{width} \times \text{height})\) is \(\leq 9437184\). If the number of pixels in the window is greater, a window suggesting that the MPEG4 encoder should be selected instead will pop up when the user presses «OK»;

- **MPEG4.** The encoder may be used for recording videos in the windows of any size, but the resulting video file will occupy more space on a disc compared to a file created with the H264 encoder.

To set the frame rate, enter the value into the **Frame per second** field. Click **OK** to apply the settings or **CANCEL** to cancel.

To start recording video:

1. Click on the **Start video record** button. The file save dialog opens.

2. Select the save path and the file name.

3. To start video recording, click **Save** and to cancel, click **Cancel**.

During video recording, the button looks like . To stop video recording, click the button. After the video recording is completed, the **Video record was stopped** message appears.

The video will be saved in a file with .mp4 extension.

### 2.14 Zoom. Pan. Rotate

#### 2.14.1 Zoom

To zoom an image, use one of the following methods:

1. Roll the mouse wheel holding the **Ctrl** key. Roll the wheel up to zoom in or down to zoom out.

2. With the **Zoom** tool. Activate the tool by clicking on the button and zoom the image, moving the cursor up and down. To select scale values, call the drop-down menu, clicking on the arrow on the right side of the button and select the value. To set the scale manually, select the **Custom zoom...** item from the drop-down menu. This tool is also available from the image context menu and from the **Image** main menu item.

Images are scaled relative to the point the cursor is located at.
CHAPTER 2. VIEW FLAT IMAGES

2.14.2 Pan

There are two ways to move the image in the view window:

1. Move the mouse holding the wheel and the **Shift** key on the keyboard. This key combination is set by default. You can disable or change the setting in the **Controllers** tab of the **Image viewer** module (see Section 15.6.1).

2. Activate the **Pan** tool on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. To move an image, move the cursor around the screen while holding down the mouse button.

This tool is also available from the image context menu and from the **Image** main menu item.

2.14.3 Rotate

To rotate an image by an angle multiple of 90 degrees, click on the arrow on the right side of the **Rotate** button on the toolbar, and select one of the four options:

- Set 0°;
- Set 90° clockwise;
- Set 180°;
- Set 90° counterclockwise.

To rotate an image by an arbitrary angle, activate the **Rotate** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. Rotate the image by moving the mouse while holding down the button that activated the tool. When you finish, click the **Rotate** button to deactivate the tool.

These commands are available from the image context menu. To open them, right-click on the image and select the **Rotate** item from the context menu.

This tool is also available from the image context menu and from the **Image** main menu item.

2.15 Set Window Level and Width

The current window level and width values are displayed in the top right-hand corner of the window. If the **Adjust W/L** tool on the toolbar is active, these changes are made holding the button which the tool was activated. To learn more about tool control, see Section 1.14.

In the **Volume Reconstruction** tab or **Multiplanar Reconstruction** tab, you can also activate the tool from the right-click menu of the image. In the **Flat Image Viewer** tab, the tool is available in the **Image** section of the main menu. In the **Multiplanar Reconstruction** tab, the tool is available in the **MPR** section of the main menu. In the **Volume Reconstruction** tab, the tool is available in the **Volume** section of the main menu.
To change the parameters, move the mouse in the study window, holding the button which the tool was activated

- to increase the window level — down;
- to reduce the window level — up;
- to reduce the window width — left;
- to increase the window width — right.

If you haven’t activated any tools with the right mouse button, you can change the window width and level by moving the mouse while holding the right button. In the Controllers tab of the Image viewer module (see Section 15.6.1), you can choose the mouse button which will be used by default to change the window parameters.

The terms «window width» and «window level» in digital images commonly refer to «contrast» and «brightness» respectively on your computer.

For certain types of tissues, the DICOM Viewer has preset width and level values. To change the width and level settings, click the arrow on the right-hand side of the Custom W/L button.

![Figure 2.21: Menu of preset width and level values](image)

The following preset values are available in the drop-down menu (see Figure 2.21):

- **Recommended** — the DICOM Viewer applies the values of the corresponding image tags. They are used by default.

- **Full dynamic** — the mode where the window width and level depends on the image parameters available. This mode is used when the window width and level is not mentioned in the study.
• **Bones** — for viewing bone tissues.
• **Lung** — for viewing lung tissues.
• **Brain** — for viewing brain tissues.
• **Chest** — for viewing chest tissues.
• **Headneck** — for viewing head and neck tissues.
• **Abdomen** — for viewing abdominal tissues.
• **Custom W/L...** — the window width and level parameters are provided by the user in the *Window Level settings* dialog box (see Figure 2.22) and are used for all the images in the series.

To select one of the modes without the preview option, click on the arrow on the right side of the button. You cannot edit the values predefined for specific tissues. To return to the original settings, select the **Recommended** mode.

To customize the window width and level settings, click the **Custom W/L** button. In the *Window Level settings* dialog box (Figure 2.22) that pops up, provide the window width and level parameters or choose the preset values you need from the **Preset** dropdown list. On the **Preset** list, you will find standard preset values, as well as presets saved by the user earlier (see Section 2.15.2). Standard preset values are marked with icons.

In the *Window Level settings* dialogue box, you will see the hotkey and the window width and level settings assigned to the selected preset.

![Image of Window/Level settings dialog box]

*Figure 2.22: Dialog box Window Level settings*

Click **OK** to apply the settings or **CANCEL** to cancel.
2.15. SET WINDOW LEVEL AND WIDTH

2.15.1 User Presets for Window Width and Level

There are two ways to create a user preset for window width and level:

1. Manually specify the values in the Width, Center, Min and Max fields of the Window Level settings dialog box. When a value is changed in one of the fields, the values in the other fields are changed automatically according to the following formulas:

   \[ \text{Width} = \text{Max} - \text{Min}; \]

   \[ \text{Center} = (\text{Max} + \text{Min})/2. \]

   If the window width and level settings provided are different from the existing presets, a <Custom W/L> value will be shown on the Preset dropdown list.

2. Change the window width and level settings with the Adjust W/L tool (see Section 2.15). Open the Window Level settings dialog box by clicking the button on the toolbar.

   If the window width and level settings provided are different from the existing presets, a <Custom W/L> value will be shown on the Preset dropdown list.

   To save the provided window width and level settings as a new preset, click the Save preset button in the Window Level settings window. In the New W/L preset dialog box that pops up (see Fig. 2.23), provide the preset name and assign a hotkey to it. By default, the name assigned is in the W<window width value>/L<window center value> format, and the Hotkey box remains empty.

   ![New W/L preset dialog box](image)

   Figure 2.23: Creating a new preset

   Provide a unique preset name. Assign a hotkey if required (see Section 2.15.2)
   Click SAVE to save the preset or CANCEL to cancel.

   After the new preset has been successfully saved, it will be shown in the Window Level settings dialog box.
2.15.2 Actions with presets

**Actions with hotkeys.** To assign or change a preset hotkey, proceed as follows:

1. Open the *Window Level settings* dialog box by clicking the 📊 key on the toolbar.
2. Choose the preset required from the *Preset* dropdown list.
3. Click the *Set the hotkey* button.
4. In the *Set the hotkey* dialog box that pops up (Fig. 2.24), provide a value in the *Hotkey* field. The permissible values are:
   - any single key on the alphanumeric keyboard or a function key, such as A or F5;
   - combinations of modifier keys (Alt, Ctrl, Shift) and alphanumeric or function keys pressed simultaneously, e.g. Ctrl+H, Shift+F5, or Alt+Ctrl+Shift+Q.

![Figure 2.24: Setting up a hotkey](image)

If the value specified in the *Hotkey* box is already assigned to another action or tool, a notification that the existing hotkey will be reassigned will appear in the dialog box. The user can also reassign hotkeys for standard window width and level settings.

5. Click «OK» to save the hotkey or CANCEL to cancel.

**When a hotkey is reassigned, the user may have to relaunch the program for the changes to take effect. If the reassigned hotkey was assigned to another W/L preset, no relaunch is required.**

**Deleting a user hotkey.** To delete a user hotkey, proceed as follows:

1. Open the *Window Level settings* dialog box by clicking the 📊 key on the toolbar.
2. Choose the preset to be deleted from the *Preset* dropdown list.
3. Click the *Remove the preset* button.
4. In the dialog box that pops up, click REMOVE to delete the preset or CANCEL to cancel.
2.15. SET WINDOW LEVEL AND WIDTH

Only the presets that were created earlier by the user can be deleted. Standard presets cannot be deleted.

After the selected preset has been deleted, the previous preset on the list will be used as the current preset. The hotkey assigned to the deleted preset will be vacant.

User presets import and export. Window width and level presets will be exported and imported with other program settings (see Section 15.8).

2.15.3 Additional Width and Level Settings

To enable additional image viewer settings, proceed as follows:

1. Choose Settings... in the Options menu.

2. Choose Image viewer in the Modules list and click the Settings button.

3. From the Image viewer settings window, go to the W/L settings tab (Figure 2.25).

![Image viewer settings dialog box](image)

Figure 2.25: Image viewer settings dialog box
4. For the Flat Image Viewer mode, select the following options:

- To calculate the Recommended and Full dynamic values and apply them to all the slices in the study, check the box Use the same W/L value for all images in Series. If you do not select this option, the Recommended and Full dynamic values will be calculated for each image separately.

- If the window width and level values provided in the series tags are incorrect, check the box Recalculate recommended W/L. The recommended values are calculated on the basis of the image properties. The values provided in the series tags are ignored.

- To set the default window width and level values for the DSA mode, check the Default DSA W/L. Provide the required numerical values in the Width and Center boxes.

Click OK to apply the settings or CANCEL to cancel.

The options Use the same W/L value for all images in Series and Recalculate recommended W/L impact the window width and level values in the Recommended and Full dynamic modes.

To restore the default settings, click the DEFAULTS button.

### 2.15.4 Setting the Window Width and Level for Merged Series

To use the values provided in the Window Level settings dialog box (Figure 2.22) when viewing merged series, proceed as follows:

1. In the list of layers for the merged series, choose any except the first (base) layer. For details on series fusion, see Chapter 4. In the Window Level settings dialog box (Figure 2.22), provide the window width and level parameters or choose the preset values you need for this layer.

2. Open the merged series in the Volume Reconstruction or Multiplanar Reconstruction tab by pressing the respective button on the toolbar.

The width and level parameters for the first (base) layer are taken from the series tags. For the other layers, the width and level parameters are chosen by the user in the tab for merging layers.
2.16 Magnifier

This tool allows you to increase the tissue with a zoom increment of 2 to 32 (Fig. 2.26).

To magnify the tissue:

1. Activate the Magnifier tool on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Move the cursor to the area you want to make out.

3. The radius and the zoom increment of the tool are set in the context menu of the tool. To set these parameters, click on the arrow on the right side of the button.

4. To increase the value of the zoom increment, click the mouse button with which the tool was activated. To reduce value, click the mouse button with which the tool was activated holding down the Alt key on the keyboard.

![Figure 2.26: Tool Magnifier](image)

2.17 Measurements

To avoid errors caused by the discrepancy between the image size and the real size, Calibration tool should be used when working with projection images (e.g. X-ray images) (see Section 2.34).

The measurement accuracy is up to one screen pixel. As a screen pixel is smaller than a source image pixel, the true linear measurement accuracy is up to one source image pixel. Errors may also occur in density measurements. The most accurate measurements are performed with bilinear interpolation (see Section 2.4).

The following tools are used to measure various parameters: Ruler, Polygonal ruler, Angle, Cobb angle, Point value, ROI rectangle, ROI ellipse, ROI polygon. To select one of
these tools, click on the arrow on the right side of the tool selection button. The button will look different depending on the selected tool:

<table>
<thead>
<tr>
<th>Tool</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ruler</td>
<td>(selected by default)</td>
</tr>
<tr>
<td>Polygonal ruler</td>
<td></td>
</tr>
<tr>
<td>Angle</td>
<td></td>
</tr>
<tr>
<td>Cobb angle</td>
<td></td>
</tr>
<tr>
<td>Point value</td>
<td></td>
</tr>
<tr>
<td>ROI rectangle</td>
<td></td>
</tr>
<tr>
<td>ROI ellipse</td>
<td></td>
</tr>
<tr>
<td>ROI polygon</td>
<td></td>
</tr>
</tbody>
</table>

To activate or deactivate the tool that is currently selected, just click on the tool selection button. If some tool is activated, the button is highlighted. The drawn objects will be displayed in the window while it is open, and you can pan, zoom or rotate them together with the image.

If the series is open in multiple windows or tabs, the measurements made in any window, appear in all the other windows.

2.17.1 Ruler

To measure distance in an image:

1. Activate the **Ruler** tool on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. You can measure the distance in two ways:

   - Mark the first point by clicking the mouse button. Drag the cursor over the screen. The distance from the first point to the current point will be displayed beside the line. To fix the current point, click the mouse button.
   - Click on the mouse button at the starting point and move the cursor to the endpoint while holding the mouse button. The distance from the first point to the current point will be displayed beside the line. To fix the endpoint, release the mouse button.
3. To cancel an incomplete measurement, press **Esc**.

This tool is also available from the image context menu and from the **Image** main menu item. Activation is only possible with the left mouse button.

The measurement results are not saved in the project file. To save the measurement results, export the current image to a file (see Section 2.25) or use marker lines (see Section 5.11.3).

### 2.17.2 Polygonal Ruler

To perform polygonal linear measurements:

1. Activate the **Polygonal ruler** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Mark the first point on the toolbar by clicking the mouse button.

3. Drag the cursor over the screen. The distance from the first point to the current point will be displayed beside the line.

4. To fix the current point, click the mouse button.

5. Repeat Steps 3 and 4 until the last but one point is fixed.

6. Fix the last point by double-clicking the mouse.

7. To cancel an incomplete measurement, press **Esc**.

To move the linear measurement point:

1. Locate the cursor on the point to be moved.

2. Drag the point, holding down the left mouse button or the button to which this tool is assigned;

3. Release the mouse button.

To delete a point:

1. Locate the cursor on the point to be deleted.

2. Right-click the mouse and select the **Remove point** command.

To insert a point:

1. Locate the cursor on the ruler where you want to insert a point.

2. Right-click the mouse and select the **Insert point** command.

This tool is also available from the image context menu and from the **Image** main menu item. Activation is only possible with the left mouse button.

The measurement results are not saved in the project file. To save the measurement results, export the current image to a file (see Section 2.25) or use polygonal marker lines (see Section 5.11.4).
2.17.3 Angle

To measure an angle:

1. Activate the Angle tool from the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Put two points on the image, clicking the mouse button. The second point is the angle apex.

3. Move the cursor over the screen to set the other side of the angle.

4. Click the mouse button to fix the second side of the angle.

5. To cancel an incomplete measurement, press Esc.

The DICOM Viewer allows you to build as many angles as you need. To deactivate the tool, click on the tool selection button.

This tool is also available from the image context menu and from the Image main menu item. Activation is only possible with the left mouse button.

The measurement results are not saved in the project file. To save the measurement results, export the current image to a file (see Section 2.25) or use polygonal marker lines (see Section 5.11.4).

2.17.4 Cobb angle meter

To measure a Cobb angle:

1. Activate the Cobb angle tool from the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Draw a line that runs along the border of one of the vertebrae. To do this, click the mouse button to set two points through which the line must pass.

3. Likewise, construct a line for the second vertebra.

4. To cancel an incomplete measurement, press Esc.

To display additional parameters, hover the mouse over the measurement tool or the measurement value. Right-click the mouse and select the Tool options... item from the context menu.

In the Tool options dialog box, provide the measurement name, as well as the color, the line width, and the font size for the angle value. To join the measurement value to the angle with a dashed line, check the Footnote line box.

To display the value of the adjacent angle, check the Adjacent angle box.

To show the angle value at the intersection of segments, check the Show intersection box. If this function is disabled or the segments do not intersect, the angle value is shown only at the intersection of normals. In Fig. 2.27 the option Show intersection is disabled, and in Fig. 2.28 is enabled.
2.17. MEASUREMENTS

To use these parameters by default, check the box **Set as default**. To apply the settings, click **OK**. To cancel, click **CANCEL**.

To delete measurement, locate the cursor on it, right-click the mouse and select the **Remove object**. For more information see Section 2.17.10.

This tool is also available from the image context menu and from the **Image** main menu item. Activation is only possible with the left mouse button.

The measurement results are not saved in the project file. To save the measurement results, export the current image to a file (see Section 2.25) or use polygonal marker lines (see Section 5.11.4).

### 2.17.5 Measure Intensity at a Point

If non-bilinear interpolation filters are used, significant errors may occur when intensity is measured in a certain point. In this case, the intensity value will be marked by an asterisk. For more accurate measurements, use the bilinear interpolation filter (see Section 2.4).

To measure intensity at some point:
1. Activate the **Point value** tool from the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Click the mouse button on the target point.

The point will be highlighted at the image, and the intensity value will be displayed next to it. It is shown in the «k HU» format for original images and in «k», where k is the intensity value at the point. If the value is inaccurate, you will see a «*» symbol next to it.

To adjust the **Point value** tool, locate the cursor on the point or the measurement results on the image. Right-click the mouse and select the **Tool options...** item from the context menu. In the **Tool options** dialog box enter the measurement name. Set the color and the font size. To connect the block with the measurement results with a dotted line, the **Footnote line** box must be checked. To use these parameters by default, check the box **Set as default**.

To apply the settings, click **OK**. To cancel, click **CANCEL**.

To delete measurement, locate the cursor on it, right-click the mouse and select the **Remove object**.

This tool is also available from the image context menu and from the **Image** main menu item. Activation is only possible with the left mouse button.

The measurement results are not saved in the project file. To save the measurement results, export the current image to a file (see Section 2.25).

### 2.17.6 Measure the Intensity Average and Standard Deviation in an Area

To measure the average intensity value and standard deviation in a particular area:

1. Activate one of the **ROI ...** tools (rectangle , ellipse , or polygon ) from the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. You can draw a rectangle in two ways:

   • Click the mouse button to mark the first corner of the rectangle. Move the cursor to the place where the opposite corner of the rectangle should be located. The rectangle will be displayed on the screen. To fix the second corner of the rectangle, click the mouse button.

   • Click the mouse button to mark the first corner of the rectangle and move the cursor to the place where the opposite corner of the rectangle should be located while holding the mouse button. The rectangle will be displayed on the screen. To fix the point, release the mouse button.

3. To draw an ellipse, just draw the rectangle the ellipse is inscribed in.

4. To draw a polygon, click the mouse button to mark each apex and then double-click the mouse to finish.

5. To cancel an incomplete measurement, press **Esc**.
These tools are also available from the image context menu and from the Image main menu item. Activation is only possible with the left mouse button. The following parameters will be displayed next to the highlighted area:

- minimum intensity value;
- maximum intensity value;
- average intensity value;
- standard deviation;
- area perimeter;
- area space.

### 2.17.7 Drawing Parameters

To set the default drawing parameters for measurement tools:

1. Click on the arrow on the right side of the measurement tool selection button.
2. Select the item Default tool options....
3. In the dialog box that appears, set the color by clicking on the color box.
4. Set the line thickness and the font size.
5. Set length and area units (millimetres or centimetres).
6. To connect the footnote and the measurement of the dotted line, check the box Footnote line.
7. To apply the settings, click OK. To cancel, click CANCEL.

Drawing parameters are available as well from the image context menu and from the Image main menu item. The settings will be applied only to the measurements conducted in the flat image view window. For multiplanar reconstruction, similar settings should be saved separately.

To edit the drawing parameters of an existing measurement:

1. Locate the cursor on the measurement to highlight a line or a point.
2. Right-click the mouse.
3. Select the Tool options... item from the context menu.
4. In the dialog box that appears, set the parameters in the same way as the default drawing parameters.
5. To use these parameters by default, check the box Set as default. Set the measurement name if necessary.
2.17.8 Move Measurements

To move a measurement:

1. Locate the cursor on the measurement to highlight the line or point or to magnify the cross, marking the angular point. Do not locate the cursor on angle points.

2. Move the measurement, holding any mouse button.

2.17.9 Move Measurement Results

To move a measurement result:

1. Locate the cursor on the measurement so that it is highlighted by a dotted frame.

2. Move the measurement result, holding down the left mouse button or the button to which this tool is assigned;

If the cursor is located on the measurement, the corresponding measurement result will be highlighted, and vice versa.

2.17.10 Delete all Annotations and Measurements

To delete annotations and measurements:

1. Locate the cursor on the measurement to highlight a line or a point.

2. Right-click the mouse.

3. Select the Remove object item from the context menu.

To delete all annotations and measurements, click the Delete all annotations and measurements button on the toolbar or select the corresponding item from the image context menu. In the dialog box that appears, Click Yes to delete or No to cancel. If you want the DICOM Viewer to always delete annotations and measurements without this confirmation, check the box Don't show this dialog again and click Yes. If you want the DICOM Viewer to show the confirmation dialog, check the box Ask before deleting all annotations and measurements (see Section 15.6.1).

Please note that all other graphic objects created manually will be deleted as well.

This tool is also available from the image context menu and from the Image main menu item.

2.17.11 Measuring Dimensions and Area during Ultrasound Imaging

The Ruler, Polygonal ruler, ROI rectangle, ROI ellipse and ROI polygon tools may be used for linear and area measurements on ultrasound images (series with US modality).

Ultrasound study series may contain data on the areas of images with a certain pixel size.
2.18. PERFUSION PARAMETERS ESTIMATION

If measuring tools are applied to the area of the image for which the pixel size has been determined, then the measurement units provided for in the tool parameters will be used for linear and area measurements (see Section 2.17.7).

If a line or a part of the measuring area stretches beyond the area for which the pixel size has been determined, linear and area measurements will be performed in pixels.

If the series does not contain any data on the areas for which the pixel size has been determined, linear and area measurements will be performed in pixels.

2.17.12 Measuring the Time Interval and the Blood Flow Velocity during Ultrasound Imaging

The Ruler and Polygonal ruler tools may be used for measuring the time interval and the blood flow velocity when performing ultrasound examination (series with US modality) with dopplergram.

For the Polygonal ruler tool, the values of the time interval and blood flow velocity are only shown when the measurement is made by two points.

When measurements are performed, the measurement value is shown on the dopplergram image next to the segment built, in the \( X: x \ s \ Y: y \ cm/s \) format, where \( x \) is the value of the time interval in seconds (s) accurate up to hundredth; \( y \) is the value of the blood flow velocity in cm/s, accurate up to hundredth.

If the measurement is fully or partly performed beyond the Doppler area, the linear dimension will be shown next to the segment built. In this case, the measurement units depend on the current algorithm and program settings.

If no image areas are suitable for evaluation of the time interval and the blood flow velocity, then when a measurement is made, the linear value will be shown next to the segment built. In this case, the measurement units depend on the current algorithm and program settings.

2.18 Perfusion Parameters Estimation

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

The following series are suitable for perfusion parameters estimation:

- multiphase MR series. The minimal recommended phase number for brain perfusion parameters estimation is 40

- multiphase CT series
2.18.1 Open series in Perfusion Parameters Estimation mode

This function cannot be used for establishing a diagnosis

To open series in perfusion parameters estimation mode:

1. Open a series in the View Flat Images window.
2. Make sure that the series images are sorted by image position and phase (For details on how to sort images see Section 2.1).
3. Select the main menu Image and the Perfusion item.

The perfusion parameters estimation panel will be displayed on the right side of the window (Fig. 2.29).

This panel has two tabs: General and Brain perfusion. The General tab allows for evaluation of the parameters of general perfusion analysis for different types of tissue. The Brain perfusion tab is used for evaluation of the cerebral parameters of brain tissue perfusion.

If the time interval between phases has not been set automatically, when you open the perfusion panel, you will see a dialog box (Fig. 2.30) where you need to specify the time interval between phases (see Section 2.18.2).

If the series is not suitable for Perfusion Parameters Estimation, then the The current series don't fit in perfusion message will be displayed on the Perfusion Parameters Estimation panel.
2.18.2 Setting the Time Interval on the Perfusion Panel

This function cannot be used for establishing a diagnosis

Functionality is available in the Pro edition

The time interval between phases is set automatically on the basis of the DICOM tags for the series. The tags used for determining the time interval are listed below in order of priority:

- AcquisitionDate (0008,0022) and AcquisitionTime (0008,0032);
- AcquisitionDateTime (0008,002A);
- FrameAcquisitionDateTime (0018,9074);
- ContentDate (0008,0023) and ContentTime (0008,0033);
- TriggerTime (0018,1060).

If the time interval between phases has not been set automatically, when you open the perfusion panel, you will see a Perfusion settings dialog box (Fig. 2.30).

Specify the time interval between phases in seconds in the Time interval $\Delta t$ (sec) field. The value provided must be $\geq 0.01$. Click OK to proceed with perfusion parameters estimation or CANCEL to cancel. When you click CANCEL, the perfusion parameters estimation panel becomes unavailable. To make another attempt to specify the time interval, relaunch the perfusion parameters estimation panel.

To see the interval between phases, build a ROI for some tissue or a ROI AIF (see Section 2.18.3). The minimum length of a time axis segment shown in the chart is equal to the time interval between phases (Fig. 2.31).
CHAPTER 2. VIEW FLAT IMAGES

Figure 2.31: The time interval between phases as shown in the chart

To change the given time interval between phases, click the **Settings** button on the perfusion panel. In the **Perfusion settings** dialog box (Fig. 2.32), change the current value shown in the **Time interval** $\Delta t$ (sec) field.

![Perfusion settings dialog box](image)

Figure 2.32: The dialog box for setting the current time interval and the rCBF measurement units

After the time interval between phases has been changed, all the parameters for tissue ROI and maps are reevaluated.

To change the rCBF measurement units, choose the required value from the **Units of rCBF** list (Fig. 2.32) and click **OK**. The default value is $\text{ml/ml}^{-1} \cdot \text{sec}^{-1}$.

Once you have changed the rCBF measurement units, the following parameters will also be changed:

- The legend of the color table scale for the rCBF parameter map;
- The minimum and maximum range values in the **Range of values** section of the rCBF map in the **Map** tab on the perfusion panel;
- The rCBF parameter value for the tissue ROI built;
- The values on the ordinate axis for tissue ROI response charts.
The selected rCBF measurement units are set for all the perfusion panels opened in the DICOM Viewer.

### 2.18.3 Brain Perfusion Parameters Estimation

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

To estimate brain perfusion parameters, go to the Brain perfusion tab.
To add a simulated artery input function (AIF), proceed as follows:

1. Click the Add AIF. To create a simulated AIF, choose Simulated in the drop-down list.

2. Provide the following AIF parameters:
   - Appearance time (time before the commencement of the first bolus passage);
   - Time to concentration peak;
   - Concentration peak value;
   - Sharpness.

The chart shows a simulated AIF built on the basis of the stated parameters. Click OK to create a simulated AIF or Cancel to cancel.

To create an AIF with the help of ROI:

1. Find the image that shows the artery.

2. Click the Add AIF button, and choose ROI in the drop-down list.

3. Activate one of the following tools — ROI rectangle, ROI ellipse, or ROI polygon — on the perfusion parameters estimation panel with the left, right, or middle mouse button. To continue work with the same tool, use the button with which the tool was activated. For details on tool management, see Section 1.14.

4. Build ROI around the artery. Graphs of artery input function for each ROI pixel will be displayed at the bottom of the Perfusion Parameters Estimation panel. A ROI AIF graph is an averaged graph based on the graphs for the selected pixels. By default, all the pixels are selected.

5. To adjust the constructed ROI AIF, highlight several pixel graphs in ROI. To do that, select the graphs by left-clicking on them while holding the Ctrl key, or else you can move the mouse while holding the left mouse button. All the pixel graphs are highlighted by default. If you change the ROI, the selected pixel graphs will be reset. Click OK to build an AIF on the basis of the ROI, or Cancel to cancel.
6. To limit the interval of the phases for which the parameters are calculated, enter the numbers of the first and the last phase in the respective fields, and press Enter key on the keyboard. You may also move the interval limits on the chart. To do that, pause the mouse pointer on the limit so that it appears as ↔ and move the limit while holding the left mouse button.

7. If the peak on the intensity graph is negative, you need to switch the Type of images to T2-weighted (the default value). The other value is T1-weighted. The Type of images setting is only used for MPT study series.

The AIF added will be displayed on the AIF list panel. If the AIF is based on a complete model, its name will start with the word «Simulated», if it is created with the help of ROI, its name will start with «ROI». To choose a name for an AIF, left-click the input box and print the name. All the AIF graphs are shown in dotted line. To apply a certain AIF, click on the respective AIF switch. To show or hide a certain AIF, check or uncheck the Show box. To change the pixels selected in ROI, click Settings for the respective AIF. To go to the image for which the AIF was created, click on the right-hand side of the name. To delete the selected AIF, click the Delete button.

The charts may show:

- The intensity values (for AIF with ROI, tissue ROI);
- The concentration values (for all the AIF, tissue ROI);
- The response function values (for tissue ROI).

Select Intensity, Concentration, or Response in the drop-down list over the chart. The Response chart is built for tissue ROI on the basis of the data for the AIF selected.

The X-axis shows the time, while the Y-axis shows the intensity, concentration, or relative bolus concentration (depends on the chart selected).

To move the chart along the vertical axis, move the mouse up or down while holding the left mouse button and the Shift key. To resize the chart, move the mouse up or down while holding the left mouse button and the Ctrl key. If you check the Fit to plot box, the graph will be fitted to the window size. This box is checked by default. If you check the Show label box, the values will be shown in the point where the cursor is placed. This box is also checked by default.

The concentration graph for ROI objects has the following key points:

- The point showing the commencement of the bolus passage through the tissue ROI (a round point);
- The point showing the bolus peak concentration in the tissue ROI (a round point);
- The point showing the end of the first bolus passage through the tissue ROI (a round point);
- The point showing the steepest slope of the concentration curve (a square point).
2.18. PERFUSION PARAMETERS ESTIMATION

Figure 2.33: The panel Brain perfusion

To build a ROI for evaluating the intensity, concentration, or response values, proceed as follows:

1. Activate one of the following tools — Point value , ROI rectangle , ROI ellipse , or ROI polygon — with the left, right or middle mouse button. To continue work with the same tool, use the button with which the tool was activated. For details on tool management, see Section 1.14.

2. Build a ROI object for the area you need.

3. Configure the settings in the General tab:

   • In the Range of intensities section, set the minimum and the maximum value of the intensity range for pixels. A pixel falls within this range if at least one of the values of the respective graph of intensities built by phases falls within this range. The following requirements must be met:
– The values provided must be integers;
– The intensity value in the left field must be smaller than the value in the right field.

The default values are from 100 to $+\infty$ for MRI-series and from 0 to 300 for CT-series.

If the ROI does not contain any pixels falling within this range, no graph will be built for this ROI.

• In the **Enable filtering** section, you can enable/disable the use of the smoothing filter for pixel intensity distribution graphs in order to set the signal-to-noise ratio. By default, the filter is enabled.
  – Choose the type of filter in the **Filter type** drop-down list. By default, the **Median filter** is enabled. At present, only one algorithm of raw data conversion with the median filter has been implemented. The list of filters will be expanded.
  – Provide the value in pixels in the **Filter radius** field. Only integers $\geq 1$ must be entered. The filter radius determines the degree of smoothing for the graph of intensities (the greater is the value, the higher is the degree of smoothing).

The default value of the filter radius is 1 for MRI series and 3 for CT series.

• In the **Remove skin** section, you can enable/disable the deletion of skin pixels. By default, the filter is enabled. Provide integer values in the **Opening radius** and **Dilation radius** fields. The default values are 10 for **Opening radius** and 2 for **Dilation radius**.

The ROI built will be shown on the **Tissue ROI list**.

At the top of the perfusion parameters estimation panel, the graphs depicting the changes in intensity, concentration, or response values across time are shown. These graphs are presented as a solid line. To switch between the **Intensity**, **Concentration**, and **Response** parameters, choose the value you need from the **Chart name** drop-down list.

You may perform the following actions with the study subjects (AIF with ROI, simulated AIF, or tissue ROI):

1. Rename.

2. Change a color. Click the color button to the right of the AIF or ROI name.

3. Change visibility. To make an AIF or ROI invisible, uncheck the box for the selected AIF or ROI.

4. Move the phases. If the patient moves while scanning is being performed, the tissues for which AIF and ROI are to be built are displaced, and the phases are changed. The DICOM Viewer provides an opportunity to build AIF and ROI separately for each phase. To move an AIF or ROI for the current phase, hold down the **Ctrl** key while moving; for the current and all the following phases hold down the **Shift** key; for the current and all the previous phases hold down the **Alt** key. You cannot resize the ROI for a particular phase. If you try to resize the ROI for a particular phase or phase subset, the ROI for the other phases will be resized accordingly. Tissue ROI resizing and relocation only affects the evaluation of the parameters of the selected tissue area.
5. Move to the next slice. To move an AIF or ROI to the next slice, choose **Move ROI to previous slice** or **Move ROI to next slice** in the right-click menu.

6. Remove. Click the button for selected AIF or ROI.

To go to image containing AIF or ROI, click the button.

The values of the following parameters are shown for ROIs:

- **Time to peak (TTP)**;
- **Cerebral blood flow (rCBF)**;
- **Cerebral blood volume (rCBV)**;
- **Time to peak of response (Tmax)**;
- **Mean transit time (MTT)**.

### 2.18.4 Map mode

**Functionality is available in the Pro edition**

This function cannot be used for establishing a diagnosis

To activate the map display mode, check the **Enable** box on the **Map** tab of the perfusion panel. This box is unchecked by default.

![Map tab of the perfusion panel](image)

**Figure 2.34: The Map tab of the perfusion panel**
In the **Mode** drop-down list, choose one of the preset map display modes. The following map display modes are available:

- **Conventional.** One map for one selected perfusion parameter is displayed in the series window. The option is shown in the **Mode** list as: `<Full parameter name>`, e.g. *Time to peak* (Fig. 2.34a);

- **Multimap.** Several maps for different perfusion parameters of the same slice are displayed simultaneously in the same window. The option is shown in the **Mode** list as: `<Short name of parameter 1>...<Short name of parameter l>_n×m`, where $l=n×m$;
  
  $n$ is the number of lines, and $m$ is the number of columns for displaying images in the series window.

  E.g. *rCBF-rCBV-MTT-Tmax_2x2* (Fig. 2.34b). In the **Map** tab, an additional tab bar with map parameters is displayed.

If you choose the multimap mode, maps are automatically displayed in the series window. If the multimap mode is enabled, you cannot change the arrangement of the images via the context menu. To escape from the multimap menu, choose the Conventional mode or disable the map display function by unchecking the **Enable** box in the **Map** tab.

The following modes are available for the **General** tab:

- **Time to peak**;
- **Area under curve**;
- **Maximal slope**;
- **TTP-Area-Slope_1x3**.

If at least one AIF has been provided, the following modes are available for the **Brain perfusion** tab:

- **Time to peak**;
- **Area under curve**;
- **Maximal slope**;
- **TTP-Area-Slope_1x3**;
- **Cerebral blood flow**;
- **Cerebral blood volume**;
- **Mean transit time**;
- **Time to peak of response**;
- **rCBF-rCBV-MTT-Tmax_2x2**.

If no AIF has been provided, you will only be able to use the modes that are available in the **General** tab.

The following parameters are provided for a map:
2.18. PERFUSION PARAMETERS ESTIMATION

- **CLUTs.** A drop-down list of color tables that determine the map color spectrum. The setting applies to all displayed maps. The «[WL]Map(spectrum)» color table is used by default. Users may create their own color tables with the Perfusion tag. The user’s color tables are added to the drop-down list.

- The **Range of values** table is used for setting the minimum and maximum map values. If the **Automatic selection** box is checked, the input fields for the minimum and the maximum map value percentile ranks are displayed. The minimum percentile rank determines the percentage of pixels for which the parameter value is above the minimum range value. The maximum percentile rank determines the percentage of pixels for which the parameter value is below the maximum range value. When the percentile ranks are set, the entered values are checked. The value range for each field is from 1 to 100. The sum of the minimum and the maximum percentile ranks must be more than 100. If the entered value is invalid, then after you press **Enter** key on the keyboard, the previous valid value will be restored.
  
If the **Automatic selection** box is unchecked, the input fields for the minimum and the maximum map values are displayed. The minimum and the maximum map values are shown at the beginning and the end of the color range. By default, the **Automatic selection** box is checked, with both percentile ranks at 95%.

- **Opacity.** By moving the slider, you can set the map opacity.

In the multimap mode, **Range of values** and **Opacity** settings are provided separately for each map for the selected parameter available in this mode. You can select a map from the tab bar (Fig. 2.34b).

When the map is activated, in the left-hand side of the window you see a color range (Fig. 2.35). Above the range, you will see the short or abbreviated name of the parameter. The parameter units are shown in parentheses.
To hide the range, uncheck the **Show color range** box on the **Range of values** panel. This box is checked by default. In the multimap mode, the range visibility is set individually for each parameter.

To change the range values, move your mouse over the upper or the lower bound, so that it looks like 🔁. Then move the bound outwards to enlarge the range or inwards to shrink it. The bound value will be displayed when moved. When you release the mouse button, the range will be adjusted and the range values will be saved. The **Automatic selection** box on the **Range of values** panel will be unchecked. In the input fields, you will see the minimum and the maximum color range values.

### 2.18.5 Advanced Settings for Bayesian Estimation Algorithm

**Functionality is available in the Pro edition**

**This function cannot be used for establishing a diagnosis**

Select the algorithm by clicking the **Bayesian estimation** radio button in the **Advanced** tab on the **Brain perfusion** panel (Fig. 2.36).
2.18. PERFUSION PARAMETERS ESTIMATION

Figure 2.36: Bayesian estimation algorithm selected in the Advanced tab

To set the algorithm parameters, click on the SETTINGS button. In the Bayesian estimation dialog box (Fig. 2.37) set the following parameters:

- The section Settings of the response function:
  - To enable/disable oscillation amplitude regulation for the function graph, check/uncheck the Physiological box. Regulation is enabled by default.
– Specify the oscillation factor value in the **Oscillation factor** field. Permissible values are all non-negative real numbers. The default value is 0,01; The oscillation factor provides for the maximum permissible ratio of the oscillation amplitude value to the peak value of the response function graph. Figures 2.38 and 2.39 show response function graphs for the same ROI but different oscillation factor values.

![Figure 2.38: Oscillation factor 0,3](image)

**Figure 2.38: Oscillation factor 0,3**

![Figure 2.39: Oscillation factor 0,01](image)

**Figure 2.39: Oscillation factor 0,01**

– The **Finite** option enables/disables transformations used to create response function graphs decreasing to zero over finite time after reaching the peak. The option is enabled by default. Figures 2.40 and 2.41 show response function graphs for the same ROI but different **Finite** option values.

![Figure 2.40: Option Finite is enabled](image)

**Figure 2.40: Option Finite is enabled**
The following parameters are specified in the **Domain parameters** section:

- **The minimum and maximum Range of the T values.** The values provided must be real numbers. The lower bound must be $\leq -4$, while the upper bound must be $\geq 0$. The default range of values is -4 to 40.

- **The minimum and maximum Regularization range values.** The values provided must be real numbers. The minimum range value must be $\geq 1$. The maximum range value must comply to the following formula:

$$\ln\left(\frac{\alpha_{\text{max}}}{\alpha_{\text{min}}}\right)/\ln(\alpha_0) > 10, \quad (2.1)$$

Where $\alpha_{\text{max}}$ is the maximum regularization range value, $\alpha_{\text{min}}$ is the minimum regularization range value, and $\alpha_0$ is the regularization factor.

The default range of value is 1 to 1e6 (1000000);

- **Regularization factor.** The value provided must be a real number more than 1 and complying to the formula 2.1.

The default value of the regularization factor is set to 2;

- **Density factor.** The entered value must be an integer greater than 1. The default setting is 4.

Click the **OK** button to apply the algorithm settings or **CANCEL** to cancel.

If any of the parameters is changed, the following values will be reevaluated in the **Bayesian estimation** dialog box:

- Parameters for the tissue ROI provided.

- Parameters maps for rCBF, rCBV, MTT, and Tmax parameters (if a map display mode with one of the listed parameters has been set).

To enable AIF smoothing, check the **Fit the AIF data with the gamma-variate function** box. If you enable the smoothing function, the ROI and AIF graphs will be smoothed. Besides, the TTP, rCBV, rCBF, MTT, and Tmax parameters for ROI and maps will be re-evaluated. Simulated AIFs are not smoothed as they are initially built with the help of the gamma-variate function.
To enable the smoothing of concentration charts, check the **Fit the AIF tissue concentration data with the gamma-variate function** box. If you enable this function, all the concentration graphs for tissue ROI will be smoothed. Besides, the TTP, rCBV, rCBF, MTT, and Tmax parameters for ROI and maps will be re-evaluated.

In most cases, if you enable AIF or concentration graphs smoothing, it does not affect the TTP parameter value.

### 2.18.6 Deconvolution Advanced Settings

**Functionality is available in the Pro edition**

> **This function cannot be used for establishing a diagnosis**

To choose a deconvolution algorithm on the basis of singular value decomposition (SVD) and set its parameters, go to the **Advanced** tab on the **Brain perfusion** panel. SVD deconvolution algorithm established by default

![Figure 2.42: The Advanced tab of the perfusion panel](image)

To apply one of the SVD deconvolution algorithms and set its parameters, click the respective option:
2.19. EVALUATION OF BLOOD FLOW PARAMETERS

- **sSVD**: a non-circular algorithm. The regularization method is TSVD, the parameters adjustment method is Stationary. The threshold (the default value of 0.2) is provided as the numeric parameter.

- **cSVD**: a circular algorithm. The regularization method is TSVD, the parameters adjustment method is Stationary. The threshold (the default value of 0.2) is provided as the numeric parameter.

- **oSVD**: a circular algorithm. The regularization method is TSVD, the parameters adjustment method is the oscillation method. The oscillation index (the default value of 0.05) is provided as the numeric parameter.

- **Custom SVD** allows for setting individual combinations of regularization methods, parameters adjustment methods, and their values.

The standard **sSVD** algorithm is used by default.

To choose a circular custom algorithm, check the **Circular** box. This box is unchecked by default.

In the **Regularization method** drop-down list, choose the regularization method: **TSVD** or **Tikhonov regularization**. In the **Parameters adjustment method** drop-down list, choose the adjustment method: **Fixed** or **Oscillation method**. The threshold value or the oscillation method depends on the chosen parameters adjustment method. If you do not know what value should be provided, leave the default value. If you change the deconvolution settings, the perfusion parameters (rCBV, rCBF, Tmax, MTT) will be re-evaluated for tissue ROI and maps. The principles of work of the smoothing functions **Fit the AIF data with the gamma-variate function** and **Fit the AIF tissue concentration data with the gamma-variate function** are described in Section 2.18.5. In most cases, if you enable AIF or concentration graphs smoothing, it does not affect the TTP parameter value.

2.19 Evaluation of Blood Flow Parameters

Functionality is available in the **Pro edition**

This function cannot be used for establishing a diagnosis

The evaluation of blood flow parameters based on phase-contrast images provides for:

- obtaining the data concerned with the blood flow velocity and volume on the basis of phase-contrast images;

- calculating the pulse-wave velocity (PWV parameter) on the basis of the data obtained.

To evaluate the blood flow parameters, you can use:

- multiphase series of magnitude images or a magnitude MRI (**MAG MRI**);

- multiphase series of phase-contrast images or a phase-contrast MRI (**PC MRI**).
2.19.1 Opening a Series in the Blood Flow Parameters Evaluation Mode

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

To evaluate the blood flow parameters, proceed as follows:

1. Open a suitable magnitude MRI (MAG MRI) series and the respective phase-contrast MRI (PC MRI) series in the flat image viewer window (Fig. 2.43). Make sure that the images have been sorted by number and phase (for details see Section 2.1). Each pair of series (MAG MRI and PC MRI) that can be used for blood flow analysis represents a separate slice.

![Figure 2.43: The windows for MAG MRI and PC MRI series have been opened in the flat image viewer tab](image)

2. On the Image main menu, choose the Flow analysis item.
2.19. EVALUATION OF BLOOD FLOW PARAMETERS

3. Provide the following parameters in the **Input data for flow analysis** dialog box (Fig. 2.44):

   - the *Available series* list is automatically filled with the series that have been opened in the window of the current tab. The search and the choice of a compatible MAG MRI and PC MRI couple from the list of the series available are performed automatically. The type of each series representing one of the detected slices is specified as `<series type><slice number>`, e.g. PC1 or MAG1. The values in the *Type* column are highlighted in red if:
     - One of the series (MAG MRI or PC MRI) has not been specified for the slice.
     - Not all the phase-contrast slice parameters have been provided.
     - An attempt to read the sequence of phases from the tags of a phase-contrast series has failed.

   A sequence of phases is an ascending sequence of time values determined for each slice separately. The first element of the sequence is the value of the *Trigger-Time (0018, 1060)* tag of the phase-contrast series. If a value in the *Type* column is highlighted in red, an error message will pop up as a balloon tip when you mouse over this value. If a compatible pair has not been determined automatically, select the series manually.
MAG MRI and PC MRI compatibility criteria:

- the same number of phases (obligatory);
- section position and orientation compatibility (obligatory);
- the series must have the MR modality (recommended);
- the series must be multiphase (obligatory);
- the Manufacturer tag must comprise the SIEMENS value (recommended);
- the contents of the ReferencedImageSequence tag sequence must be the same (recommended);
- the ImageType tag must start with ORIGINAL\PRIMARY\P (for PC MRI) or ORIGINAL\PRIMARY\M (for MAG MRI) string expression (recommended).

When automatic search is being performed, all the listed criteria are to be taken into account; if the search is performed manually, only the obligatory criteria must be met. The series that can be selected manually do not belong to any slice (null values are assigned to such series in the Type column). To select a compatible pair of series manually, highlight the PC MRI series and click the PC button. Then select the respective MAG MRI series and click the MAG button. For each slice, an individual pair of PC MRI and MAG MRI series must be specified. The compatibility of the selected series must be tested according to the obligatory criteria.

In the Type column, specify the type in the <series type><slice number> format for each series representing one of the slices determined, e.g. PC1 or MAG1. If the highlighted series belongs to a slice that has already been selected, then the PC and MAG buttons will be unavailable.

If the selected series does not comply with the obligatory criteria for PC MRI and MAG MRI selection, a dialog box is displayed with a message that the selected series cannot be set as PC MRI or MAG MRI.

To delete a slice, select the series corresponding to this slice and click the « — » button. In the Type column, a null value is assigned to each series representing a deleted slice. If the selected series does not belong to any of the slices, the « — » button will be deactivated.

- **Slice parameters** are used to evaluate general blood flow parameters and are set automatically on the basis of PC MRI tags:
  
  - **Maximal intensity**;
  - **Velocity encoding (cm/s)** When you specify the parameter manually, the new value is set for all the slices for which this parameter cannot be taken from the PC MRI series tags;
  - **Heart rate (beats/min)**;
  - **Max number of automatically detected ROI** is used to restrict the maximum number of vessels ROI set by default when the panel is opened. As the algorithm for automatic recognition of vessel contours creates the list in the order of descending accuracy, this parameter allows for excluding odd ROI from consideration. The default value of the Max number of automatically detected ROI parameter is 2 (if only one slice has been selected) or 1 (if two or more slices have been selected). If the value of this parameter has not been provided, then the blood flow parameters will be estimated for all the vessels detected automatically.
2.19. EVALUATION OF BLOOD FLOW PARAMETERS

Not all the required parameters may be set automatically, but only some of them. In such a case, the rest of the parameters specified in the dialog box are to be set manually.

4. Click the **OK** button to provide the data for blood flow analysis. Click the **CANCEL** button to cancel the data input.

If you have not provided all the required parameters in the **Input data for flow analysis** dialog box (Fig. 2.44), the **OK** button will be inactive.

The vessels ROI that are built in the MAG MRI series window are reproduced in the PC MRI series window. The blood flow analysis panel where the obtained results for all the vessels found will be presented as graphs and tables will appear on the right-hand side of the tab (Fig. 2.45).

When one of the windows (MAG MRI or PC MRI) is closed, the blood flow analysis panel is deactivated and all the vessels, as well as the evaluation results, are deleted.

![Figure 2.45: Blood flow parameters evaluation mode](image)

On the **General** tab, general blood flow results are analyzed for each vessel detected. On the **PWV** tab advanced analysis of blood flow results is performed, which includes the calculation of additional parameters, such as: pulse wave velocity (PWV) and pulse transit time (PTT).
2.19.2 Changing the Configuration Parameters for a PC MRI Series

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

To change the configuration parameters for a PC MRI series in the process of work, click the PC MRI parameters button on the blood flow analysis panel. The current values of the parameters are shown in the PC MRI parameters dialog box (Fig. 2.46).

![Figure 2.46: The dialog box for changing the PC MRI parameters](image)

Change the values of the parameters. If you have not provided all the required parameters in the PC MRI parameters dialog box, the OK button will be inactive.

To reevaluate the blood flow parameters for all the vessels considered, click the OK button. To cancel, click the CANCEL button.

2.19.3 Building and Editing Vessels ROI

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

To evaluate general blood flow parameters for each of the vessels detected, go to the General tab.

To add ROI for the vessels that have not been included in the list by default, proceed as follows:

1. With the left, right or middle mouse button, activate the Detect vessel ROI by point tool on the panel for blood flow parameters evaluation. Use the same button to work with the tool. For details on working with tools, see Section 1.14.
2.19. EVALUATION OF BLOOD FLOW PARAMETERS

Attention! The tool works only in the MAG MRI window selected in the “Input data for flow analysis” dialog box (Fig. 2.44). If you choose a window from a different series, you will be notified that the tool is not available for the window selected.

2. Click on a magnitude image (MAG MRI), at a point where you expect to find a vessel. The ROI for the vessel detected will be built for all the phases, with consideration for the position and the size of the vessel section in each phase. A new vessel will be added to the list placed on the blood flow parameters evaluation panel, and the parameters evaluated will be presented as graphs and tables. If no vessel ROI is detected in the point specified, you will be notified that there is no vessel ROI at this point.

The Detect vessel ROI by point tool may be used for restoring the vessels that were deleted earlier.

To build or edit a vessel ROI with contour lines, proceed as follows:

1. With the left, right or middle mouse button, activate the Vessel ROI (contour) tool on the panel for blood flow parameters evaluation. Use the same button to work with the tool. For details on working with tools, see Section 1.14.

2. Press and hold the mouse button to create a contour. Release the button to finish the process and to close the contour. A new vessel will be added to the list placed on the blood flow parameters evaluation panel, and the parameters evaluated will be presented as graphs and tables.

The Vessel ROI (contour) tool provides an opportunity to edit the ROI of automatically detected vessels.

On the PWV tab, the Vessel ROI (contour) tool is only available for editing vessels ROI. Edit the ROI for each phase. The following editing methods are available:

- **changing the ROI shape.** To change the ROI shape, mouse over the contour of the ROI to be edited. The ROI contour line will be highlighted. Press the mouse button at the point where you want to edit the contour and draw a new line while holding the button. Release the mouse button to finish the editing process. All the blood flow parameters for the vessel will be reevaluated. Press Esc on your keyboard while still holding the mouse button to cancel the building or editing operations for the current contour;

- **moving the ROI.** To move a ROI, mouse over the contour of the ROI to be moved. Move the mouse while holding the mouse button and the Shift key on the keyboard.
2.19.4 Blood Flow Analysis Panel. Displaying the Results of General Blood Flow Analysis

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

On the General tab, general blood flow results are analyzed for each vessel detected. The results of general blood flow analysis are presented as graphs and tables.

On the coordinate plane (Fig. 2.47) graphical data for the parameter selected from the drop-down list are presented:

- Mean velocity;
- Velocity dispersion;
- Area;
- Total flow.

Figure 2.47: Mean velocity parameters graphs for the vessels detected

The time values are shown on the x-axis, while the values of the parameter chosen from the drop-down list are shown on the y-axis. The range of values for the time axis is formed by combining the phase sequences for all the slices. The resulting sequence does not contain any matching values and is sorted in ascending order. The current phase position is marked
by a blue slider. In the series window, the phase that is the closest to the time value marked by the slider on the graph is selected as the current phase. To change the current phase, mouse over the slider so that the cursor is displayed as \( \leftrightarrow \). While holding the left mouse button, move the slider to the right or to the left. When you move the slider, the current phase is changed in PC MRI and MAG MRI windows. When you change the current phase, the results presented in the Current phase parameters table are also changed (Fig. 2.49).

To move the graph along the y-axis, move the mouse up and down while holding the left mouse button and the Shift key on the keyboard. To scale the graph, move the mouse up and down while holding the left mouse button and the Ctrl key on the keyboard.

To smooth the graphical data by cubic spline interpolation, check the Use smoothing box. By default, this option is disabled. The Fit to plot box is used to adjust the graph to the size of the window. The box is checked by default. The Show label box is used to show the position of the point where the cursor is placed. By default, this option is disabled.

The Vessels table (Fig. 2.48) is used to adjust the display settings for the vessels ROI and graphs. The table shows the number of the slice with the vessel. When you mouse over a cell with a slice number, a balloon tip with the basic data on the slice pops up.

![Vessels Table](image)

Figure 2.48: The Vessels table on the blood flow analysis panel

You can perform the following actions with the settings for vessels ROI and graphs:

- **renaming.** Double-click on the name of the vessel with the left mouse button. Type the new name and press Enter on the keyboard. The new name of the vessel will be shown in the respective cells of the tables displaying the blood flow parameters;

- **changing the color.** Click on the color icon next to the name of the vessel and select the color in the dialog box. The color icon, the ROI contours for all the phases, and the graphs for the selected vessel will be changed accordingly;

- **adjusting visibility.** To hide/show the ROI contours for all the phases, as well as the graphs for the selected vessel, tick/untick the Show box;

- **inverting the graph.** To invert the graph values (reverse the sign), check the Invert box. By default, this box is only checked for the vessels with backward blood flow volume. The graph values are inverted for Mean velocity and Total flow parameters;

- **deleting.** To delete a selected vessel, click the button. All the data for this vessel will be deleted: the ROI for all the phases, the graph and the evaluation results from the tables, the blood flow parameters.
The deleted vessel may be restored with the Detect vessel ROI by point tool (see Section. 2.19.3).

In the Current phase parameters table (Fig. 2.49), you will find the basic blood flow parameters:

- Mean velocity (\(v_{\text{mean}}\));
- Velocity dispersion (\(\text{Disp}\));
- Area;
- Total flow (\(F_{\text{total}}\)).

Tick the Show extended parameters box to display the following additional parameters in the table:

- Min velocity (\(v_{\text{min}}\));
- Max velocity (\(v_{\text{max}}\));
- Positive flow (\(F_{\text{positive}}\));
- Negative flow (\(F_{\text{negative}}\)).

The parameters shown in the Current phase parameters table are time-dependent and change with the current phase.

In the Integral parameters table (Fig. 2.50), the values of the following parameters are shown:

- Net volume (\(V_{\text{net}}\));
- Forward volume (\(V_{\text{forward}}\));
- Backward volume (\(V_{\text{backward}}\));
- Cardiac output (CO).
2.19. EVALUATION OF BLOOD FLOW PARAMETERS

These parameters are not time-dependent and do not change with the current phase.

![Integral parameters table on the blood flow analysis panel]

Figure 2.50: The Integral parameters table on the blood flow analysis panel

2.19.5 Evaluating the General Blood Flow Analysis Parameters

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

The following parameters are calculated while performing general blood flow analysis:

- **Phase parameters:**
  - **Mean velocity** \( v_{\text{mean}} \) (measured in cm/s). This parameter is calculated as the mean value for all the velocity values evaluated for each point of the ROI. The velocity for a particular ROI point is calculated according to the formula below:

\[
v_{\text{point}} = \left( \frac{2 \times I_{\text{point}}}{I_{\text{max}}} - 1 \right) \times v_{\text{enc}}
\]  

(2.2)

where \( v_{\text{point}} \) is the velocity at a particular ROI point,
\( I_{\text{point}} \) is the intensity at a phase-contrast image point,
\( I_{\text{max}} \) is the maximum intensity for the series,
\( v_{\text{enc}} \) is the velocity encoding;

- **Velocity dispersion** \( (\text{Disp}) \). This parameter is calculated as the velocity variance for each point of the ROI;

- **Area** \( (\text{Area}, \text{measured in cm}^2) \). This parameter is calculated as the area of the ROI;

- **Total flow** \( (F_{\text{total}}, \text{measured in ml/s}) \). The value is calculated according to the formula below:

\[
F_{\text{total}} = v_{\text{mean}} \times \text{Area}
\]  

(2.3)
– **Min velocity** \( (v_{\text{min}}, \text{measured in cm/s}) \). The value is calculated as the minimum velocity among all the points of the ROI;

– **Max velocity** \( (v_{\text{max}}, \text{measured in cm/s}) \). The value is calculated as the maximum velocity among all the points of the ROI;

– **Positive flow** \( (F_{\text{positive}}, \text{measured in ml/s}) \). The value is calculated according to the formula below:

\[
F_{\text{positive}} = v_{\text{mean positive}} \times \text{Area}_{\text{positive}}
\]  

where \( v_{\text{mean positive}} \) is the mean velocity for all the ROI points with positive velocity values,
\( \text{Area}_{\text{positive}} \) is the area of all the points with positive velocity values;

– **Negative flow** \( (F_{\text{negative}}, \text{measured in ml/s}) \). The value is calculated according to the formula below:

\[
F_{\text{negative}} = v_{\text{mean negative}} \times \text{Area}_{\text{negative}}
\]  

where \( v_{\text{mean negative}} \) is the mean velocity for all the ROI points with negative velocity values,
\( \text{Area}_{\text{negative}} \) is the area of all the points with negative velocity values;

• **Integral parameters**:

– **Net volume** \( (V_{\text{net}}, \text{measured in ml}) \). The value is calculated according to the formula below:

\[
V_{\text{net}} = \int_{t_0}^{t_n} F_{\text{total}} dt
\]  

where \( F_{\text{total}} \) is the blood flow,
\( t_0 \) is the time of the first phase,
\( t_n \) is the time of the last phase;

– **Forward volume** \( (V_{\text{forward}}, \text{measured in ml}) \). The value is calculated according to the formula below:

\[
V_{\text{forward}} = \int_{t_0}^{t_n} F_{\text{positive}} dt
\]  

where \( F_{\text{positive}} \) is the positive blood flow,
\( t_0 \) is the time of the first phase,
\( t_n \) is the time of the last phase;

– **Backward volume** \( (V_{\text{backward}}, \text{measured in ml}) \). The value is calculated according to the formula below:

\[
V_{\text{backward}} = \int_{t_0}^{t_n} F_{\text{negative}} dt
\]
2.19. EVALUATION OF BLOOD FLOW PARAMETERS

where \( F_{\text{negative}} \) is the negative blood flow,
\( t_0 \) is the time of the first phase,
\( t_n \) is the time of the last phase;

- **Cardiac output** \((CO, \text{measured in l/min})\). The value is calculated according to the formula below:

\[
CO = V_{\text{net}} \times HR
\]  
(2.9)

where \( V_{\text{net}} \) is the blood flow volume,
\( HR \) is the heart rate.

2.19.6 Designing a Trajectory for the Pulse Wave

**Functionality is available in the Pro edition**

**This function cannot be used for establishing a diagnosis**

You need to build a trajectory for the pulse wave to calculate the Pulse wave travel distance auxiliary parameter, which is used for Pulse wave velocity parameter evaluation.

**Attention! To build the pulse wave trajectory, the study must contain a sagittal plane series.**

If there is no sagittal plane series in the study, but the pulse wave travel distance is known, it can be entered manually by the user in the PWV settings dialog box (Fig. 2.51). For details see Section 2.19.7.

To design a pulse wave trajectory, proceed as follows:

1. Open the MAG MRI and PC MRI series in the blood flow parameters evaluation mode (for details see Section 2.19.1).

2. Open a sagittal plane study series. To simplify the process of building the trajectory, we advise you to enable the display of scout lines in the selected window (see Section 2.23).

3. Go to the PWV tab. When you first click on the PWV tab the PWV settings dialog box is displayed (Fig. 2.51).

Any two sections of the same vessel placed on the same slice or on different slices may be selected as the input and output vessels. The vessel characterized by a smaller time to peak value of the blood flow graph is selected as the input vessel. If the time to peak values are the same for both vessels, the one placed higher on the Vessels table is selected as the input vessel. The PWV tab will be available after such a pair of vessels has been found.
4. In the **PWV settings** dialog box (Fig. 2.51), you will see the list of the series opened in the current study window, except for those that have been selected as the PC MRI and MAG MRI. Select a sagittal plane study series.

![PWV settings dialog box](image)

*Figure 2.51: The PWV settings dialog box*

To proceed with building the pulse wave trajectory, click the **OK** button, to go back to the **General** tab, click **CANCEL**.

If you have not chosen a series from the **Sagittal MRI** list or entered the pulse wave travel distance value (for details see Section 2.19.7), the **OK** button will be disabled.

5. Activate the **Pulse wave travel path** tool on the panel for blood flow parameters evaluation with the left, right, or middle mouse button. Use the same button to work with the tool. For details on working with tools, see Section 1.14.

![Attention!](image)

**Attention!** The «Pulse wave travel path» tool may only be activated may if the current tab is the «PWV» tab.

6. Press and hold the mouse button to build the trajectory. Release the button to finish the process. The trajectory must connect the two different slices of the vessel (Fig. 2.52). The pulse wave trajectory is smoothed to fend off aliasing which causes lengthening of the curve.
7. To edit a trajectory, mouse over the line to be edited. The trajectory line will be highlighted. Press the mouse button at the point where you want to edit the trajectory and draw a new line towards one of the ends of the trajectory while holding the button. Release the mouse button to finish the editing process. All the parameters for advanced blood flow analysis will be reevaluated. Press Esc on your keyboard while still holding the mouse button to cancel the trajectory building or editing operations.

You can change the Pulse Wave Travel Distance (PWTD) value in three ways:

- by editing the trajectory of the pulse wave;
- by clicking on the PWV settings button and enter a new value in the dialog box. Previously constructed pulse wave trajectory is removed;
- by manually changing the value in the PWTD column of table Pulse wave parameters. Previously constructed pulse wave trajectory is removed.

If after returning to the General tab, you delete one of the vessels considered in the process of advanced blood flow analysis, the pulse wave trajectory and the pulse wave parameters (PWTD, PTT, and PWV) will be deleted.

If you close the sagittal plane window, the pulse wave trajectory designed will be deleted, but the PWTD, PTT, and PWV parameters will be saved.
2.19.7 Getting the Results of Advanced Blood Flow Analysis without Building a Pulse Wave Trajectory

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

If there is no sagittal plane series in the study, but the pulse wave travel distance is known, you may enter this value manually to display the results of advanced blood flow analysis.

To get the results of advanced blood flow analysis without building a pulse wave trajectory, proceed as follows:

1. Open the MAG MRI and PC MRI series in the blood flow parameters evaluation mode (for details see Section 2.19.1).

2. Go to the PWV tab. When you first click on the «PWV» tab the PWV settings dialog box is displayed Fig. 2.53).

   Any two sections of the same vessel placed on the same slice or on different slices may be selected as the input and output vessels. The vessel characterized by a smaller time to peak value of the blood flow graph is selected as the input vessel. If the time to peak values are the same for both vessels, the one placed higher on the Vessels table is selected as the input vessel. The PWV tab will be available after such a pair of vessels has been found.

3. In the PWV settings dialog box (Fig. 2.53), enter the pulse wave travel distance value (in millimeters).

   Figure 2.53: The dialog box for providing the pulse wave travel distance value

To get the results of advanced blood flow analysis, click the OK button. To go back to the General tab, click the CANCEL button.

You can change the Pulse Wave Travel Distance (PWTD) value in two ways:

- by clicking on the PWV settings button and enter a new value in the dialog box;
- by manually changing the value in the PWTD column of table Pulse wave parameters.
2.19.8 Blood Flow Analysis Panel. Displaying the Results of Advanced Blood Flow Analysis

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

The results of advanced blood flow analysis are displayed as graphs and tables. Chart display settings are configured similarly to the settings of charts on the General tab (see Section 2.19.4).

![Graph showing blood flow parameters](image)

*Figure 2.54: The graphs showing the blood flow parameters for the selected pair of vessels*

The Vessels table (Fig. 2.55) is used to customize the display settings for the vessels’ ROI and graphs.

![Vessels table](image)

*Figure 2.55: The Vessels table*

The ROI display and vessels graph settings are described in the Section 2.19.4.

In the Current phase parameters table are displayed the blood flow parameters. Similar to the table on the General tab (see Section 2.19.4).
In the **Integral parameters** table integral blood flow parameters are displayed. Similar to the table on the **General** tab (see Section 2.19.4).

In the **Pulse wave parameters** table (Fig. 2.56) you will see the results of the evaluation of the following parameters:

- **Pulse wave travel distance (PWTD).** There are three ways to specify this parameter:
  - manually, in the **PWV settings** dialog box (see Section 2.19.7);
  - manually, in the **PWTD** column of the **Pulse wave parameters** table;
  - by way of building a pulse wave trajectory (see Section 2.19.6).

- **Pulse transit time (PTT);**

- **Pulse wave velocity (PWV).**

![Pulse wave parameters table](image)

*Figure 2.56: The Pulse wave parameters table*

If the **PWTD** parameter has not been specified, in the respective cell of the table, you will see a *No data* sign instead of the assessment result. The **PTT** and **PWV** parameters will be calculated automatically. If an error occurs during the calculation procedure, you will see a *No data* sign in the cell for the respective parameter.

In the section named **Calculation method of PTT**, you choose the method of calculating the pulse transit time:

- **Foot-to-foot** (the default value);

- **Peak-to-peak**.

The **Use interpolation** check box enables cubic spline interpolation of the data for **PTT** calculation. When you check/uncheck this box, the **PPT** and **PWV** parameters will be reevaluated.
2.19.9 Evaluation of the Parameters for Advanced Blood Flow Analysis

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

In advanced blood flow analysis for the vessel slices pair, the PWV parameter is calculated based on two auxiliary parameters.

Advanced blood flow analysis implies the calculation of additional parameters, such as:

- **Pulse wave travel distance** ($PWTD$, measured in mm). This parameter is calculated as the distance between a pair of vessel slices. The trajectory between the sections may be built with the Pulse wave travel path tool;

- **Pulse transit time** ($PTT$, measured in ms). This parameter is calculated on the basis of the blood flow graphs of vessel slices by two methods:
  
  - **Foot-to-foot**. The value is calculated according to the formula below:

    \[
    PTT = TTF_{OV} - TTF_{IV}
    \]  

    where $TTF_{OV}$ is the time to the foot of the output vessel graph, $TTF_{IV}$ is the time to the foot of the input vessel graph;

![Figure 2.57: Graphical interpretation of the Foot-to-foot method](image)

![Figure 2.57: Graphical interpretation of the Foot-to-foot method](image)
- **Peak-to-peak.** The value is calculated according to the formula below:

\[
PTT = TTP_{OV} - TTP_{IV}
\]  
(2.11)

where \(TTP_{OV}\) is the time to the peak of the output vessel graph, \(TTP_{IV}\) is the time to the peak of the input vessel graph;

**Figure 2.58: Graphical interpretation of the Peak-to-peak method**

- **Pulse wave velocity** \((PWV, \text{measured in m/s})\). The value is calculated according to the formula below:

\[
PWV = \frac{PWTD}{PTT}
\]  
(2.12)

### 2.19.10 Blood Flow Parameters Evaluation for Two Slices

Functionality is available in the **Pro edition**

⚠️ This function cannot be used for establishing a diagnosis

Each pair of series (MAG MRI and PC MRI) that can be used for blood flow analysis represents a separate slice. Besides the PWV parameter evaluation, work with two or more slices
provides an opportunity to compare common blood flow parameters for sections of the vessels placed on different slices.

To perform blood flow parameters evaluation for two slices, proceed as follows:

1. Open several pairs of series (MAG MRI and PC MRI) suitable for blood flow analysis. Each pair of series represents a separate slice. Provide the missing parameters if required (see Section 2.19.1).

Figure 2.59: The mode for blood flow parameters evaluation on the basis of two slices

Figure 2.60: The dialog box for changing PC MRI parameters for each slice

2. To change the configuration parameters for a PC MRI series, click the PC MRI button.
parameters button on the blood flow analysis panel. In the **PC MRI parameters** dialog box (Fig. 2.60) change the current parameter values for each slice. For more information see Section 2.19.2.

3. Build or edit the vessel ROI for each slice (see Section 2.19.3).

   On the **General** tab, general blood flow results are analyzed for each vessel detected. The results of general blood flow analysis are presented as graphs and tables. For more information see Sections 2.19.4 and 2.19.5).

4. To evaluate the **PWV** parameter, build a trajectory for the pulse wave between the selected vessel sections Fig. 2.61, (see Section 2.19.6). If there is no sagittal plane series

---

*Figure 2.61: Trajectory for the pulse wave between the slices*
in the study but the pulse wave travel distance is known, enter the value manually (see Section 2.19.7).

In the PWV tab (Fig. 2.62) of the blood flow analysis panel, the results of advanced blood flow analysis are shown as graphs and tables (see Sections 2.19.8 and 2.19.9).

Figure 2.62: The results of advanced blood flow analysis for two slices

2.20 Visualize Images

2.20.1 Select CLUT

Select the CLUT (colour look-up table) from the drop-down menu on the rendering setup panel (Fig. 2.63).

Figure 2.63: Rendering setup panel

You can choose from the following groups of CLUTs:

- relative [WL];
- absolute CT and XA;
- special, **Palette color**. This type of CLUT is used for adequate display of the images belonging to series where there is at least one image with the Photometric Interpretation (0028,0004) tag value equal to PALETTE COLOR.

If, when a series is opened, the first image displayed has the Photometric Interpretation (0028,0004) tag value equal to PALETTE COLOR, the **Palette color** CLUT will be automatically selected. If the first image displayed has a different Photometric Interpretation (0028,0004) tag value, the relative [WL] CLUT will be selected for the group. In this case, you will have to select the **Palette color** CLUT manually to view the images with the PALETTE COLOR value of the Photometric Interpretation (0028,0004) tag.

When the **Palette color** CLUT is used, the **Custom W/L** button is unavailable.

### 2.20.2 Edit CLUTs List

To edit the list, open the CLUTs setup tab by clicking the **CLUTs** button. The tab is shown in Fig. 2.64.

![Figure 2.64: CLUTs setup tab](image)

CLUTs setup panel is located on the right-hand side of the window (Fig. 2.65).
2.20. VISUALIZE IMAGES

Figure 2.65: CLUTs setup panel

The CLUTs list edit buttons are located at the top of the panel.

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Add a new CLUT as a copy of the current one" /></td>
<td>adds a new CLUT as a copy of the selected one</td>
</tr>
<tr>
<td><img src="image" alt="Add a new group" /></td>
<td>adds a new group of CLUTs</td>
</tr>
<tr>
<td><img src="image" alt="Remove the selected CLUT/group" /></td>
<td>deletes the selected CLUT or group. Predefined groups and some CLUTs cannot be deleted</td>
</tr>
<tr>
<td><img src="image" alt="Reset the selected CLUT to its original state" /></td>
<td>sets up default parameters for the selected CLUT</td>
</tr>
<tr>
<td><img src="image" alt="Edit CLUT/group" /></td>
<td>opens the CLUT or group setup dialog</td>
</tr>
</tbody>
</table>
The groups contain several CLUTs (e.g., WL, CT, XA) and are intended for structuring the list. They are marked by the arrow (Fig. 2.66) on the drop-down menu (Fig. 2.63). For the description of the process of assigning the group type to the user CLUTs, see Section 2.20.4.

To add a new group, set the following parameters in the dialog box (Fig. 2.67):

1. **Name**: any name of group;
2. **Required tags**: labels that must contain CLUTs to be included in the group.
2.20.3 CLUT Parameters

To browse the settings for the selected CLUT, click the Rendering transfer function button. The panel displaying the visualization transfer function graph will appear at the bottom of the study window (see the example in Fig. 2.68).

![Figure 2.68: Rendering transfer function graph](image1)

You cannot change the setup parameters for predefined CLUTs. Intensity will be displayed on the horizontal axis, while the number of points with a particular intensity will be shown on the vertical axis (blue line). The default scale may not allow you to see the intensity distribution graph (blue) at once. To change the horizontal axis scale, move the scroll under the axis or roll the mouse wheel while the cursor is located on the scrollbar. The scale value will be displayed to the right of the scrollbar. To change the vertical axis scale, roll the mouse wheel while the cursor is located on the visualization setup panel, but not on the scrollbar. Fig. 2.69 shows the same graph as in the previous figure, but with a greater intensity distribution scale (on the vertical axis).

![Figure 2.69: Intensity distribution graph with a greater vertical axis scale](image2)

The color/transparency chart (white line) is superimposed on the intensity distribution scale. The horizontal axis shows the intensity, and the vertical axis shows the transparency of the color highlighting the points with this intensity. The color is displayed below the graph. The
horizontal axis scale changes for both graphs simultaneously, while the vertical axis scale for
the color/transparency chart does not change. To move the graph along the horizontal axis,
hold the left mouse button.

![Figure 2.70: Displaying the window level and width edges](image)

To show the current edges of the window level and width (W/L) in the histogram window,
click the **Adjust W/L** button on the rendering transfer function panel. This mode is
switched on by default. The current edges of the window level and width are displayed as
blue vertical lines in the histogram window (Fig. 2.20.3).

The DICOM Viewer provides an opportunity to adjust the edges of the window level and
width in the histogram window. To do it, mouse over one of the edges so that the cursor is
displayed as 🔷. Move the edge while holding the left mouse button. On the flat image
viewer tab, the edges of the window level and width are only displayed for relative CLUTs (the
CLUTs with the [WL] group label). If the CLUT selected on the **Image viewer** tab is absolute
(and has a CT group label), the edges of the window level and width will not be shown in
the histogram. The **Adjust W/L** button on the rendering transfer function panel will
be disabled. On the **MPR reconstruction** and **Volume reconstruction** tabs, the edges of the
window level and width will be shown in the histogram for all the types of CLUTs.

To find out what percentage of tissue has a density in a given range, click on the **Histogram
percentage** button, move the cursor to the beginning of the range and move the cursor
to the end of the range, holding the left mouse button. The percentage of tissue that has a
density within the range is indicated in red (fig. 2.71). To edit a range, move the cursor to its
border and move the border with the left mouse button pressed. To move a range, move the
cursor on it so that the cursor would look as follows 🔷, and move the cursor, holding the
left mouse button. Multiple ranges can be built at the same time. To remove the built ranges,
click the **Histogram percentage** button again.

To export data on the distribution of densities, click on the ➡️ button, in the dialog that
opens, specify the file name and folder, click **Save** to finish or **Cancel** for cancel.

![Figure 2.71: Histogram percentage](image)
2.20.4 Create and Edit CLUT

To create your own CLUT:

1. Click the CLUTs button to open the CLUT setup tab.

2. Copy one of the existing CLUTs by selecting it from the list and clicking on the Add a new CLUT as a copy of the current one button.

3. To rename a CLUT, double-click the left mouse button on it, enter the new name and press the Enter key on the keyboard. In our example, in Figure 2.65, the table is renamed «[WL]Example».

4. Specify the required parameters:
   - **Color.** Select a point on the color/transparency chart. The color settings for this point will become available. To set the color of the current point for all the points of the chart, click the Apply to all chart points button.
   - **Density.** Sets the position of the point on the horizontal axis. The alternative way to set this parameter is to move the point along the horizontal axis using the mouse.
   - **Opacity.** Sets the opacity of the color. 1 — maximum, 0 — minimum. The alternative way to set this parameter is to move the point along the vertical axis using the mouse.

5. To add a point, locate the cursor on the graph so that it looks like , right-click the mouse and select the Add point item.

6. To delete a point, locate the cursor on the point so that it looks like , right-click the mouse and select the Remove point item.

7. To restore the original settings for this CLUT, click the Reset the selected CLUT to its original state button.

8. To assign a group type to the CLUT, click the Edit CLUT/group button at the top of the CLUTs settings panel. In the CLUT dialog box (Fig. 2.72), select the group type to which the table belongs from the drop-down list:
   - **Window,** if the CLUT is relative and has a group label [WL];
   - **Absolute,** if the CLUT is absolute and has a group label CT and XA.

   Click OK to apply the settings or CANCEL to cancel.

9. To add the tags that the CLUT should contain, click the Edit CLUT/group button at the top of the CLUTs panel. In the CLUT dialog box (Fig. 2.72), click the ADD TAG button and enter the tag name in the input area. To rename a tag, double-click on the tag name, enter the new name and press the Enter key on your keyboard. To remove a tag, select it and click the REMOVE TAG button.

   Click OK to apply the settings or CANCEL to cancel.
Figure 2.72: CLUT dialog box

To delete a CLUT, click the Remove the selected CLUT/group button.

The DICOM Viewer allows you to add additional color/transparency charts. To add:

1. Click the Add chart button. A new chart will appear at the bottom part of the window, and its name will be added to the drop-down chart menu. The opened menu is shown in Fig. 2.73.

2. To rename the selected chart, click the Edit chart name button, type new name and press Enter key on the keyboard.

3. To delete the selected chart, click the Remove chart button.

4. To move all the charts along the horizontal axis, locate the cursor so that it would not to be on any chart and move it, holding the left mouse button.

5. To move any chart, select Auto detection from the drop-down chart menu, locate the cursor on the some chart and move it, holding the left mouse button.

6. To move a certain chart, select its name from the drop-down chart menu, locate the cursor on this chart and move it holding the left mouse button. This mode is useful if the charts overlap.

If the charts overlap, the colors are mixed.
2.20.5 User CLUTs Import

User CLUTs may be imported from one of the program versions to another. This function provides an opportunity to use the CLUTs created by another user or in another DICOM Viewer version. For details, see the Import CLUTs section.

2.21 SUV Measurement

Functionality is available in the Pro edition

SUV (Standardized Uptake Value) is a value reflecting the intensity of contrast accumulation in tissues. To measure the SUV:

1. Open a series suitable for SUV measuring.

2. Select the Image main menu, select the SUV item and the Show SUV command. If the selected series is not suitable for SUV measuring, then the Show SUV command is disabled. If SUV measuring is already activated, then the Show SUV command is marked with a flag.

3. If necessary, change the CLUT to [WL]PET by selecting it from the drop-down list or by pressing the Shift+F8 key combination on the keyboard. For details, see Section 2.20.1.

4. If the data contained in the study is insufficient, then the dialog shown in Fig. 2.74 appears. Specify the following data:

- **SUV Type.** Choose one of four ways to measure SUV:
  - by body weight: **SUV Body Weight (SUVbw):**
    
    \[
    SUV_{bw}(g/ml) = pixel(Bq/ml) \times \frac{weight(g)}{dose(Bq)}
    \]  

  - by body surface area: **SUV Body Surface Area (SUVbsa):**
    
    \[
    SUV_{bsa}(cm^2/ml) = \frac{pixel \times kg^{0.425} \times 0.007184 \times 10000(cm^2/m^2)}{dose(Bq)}
    \]
– by the body mass index according to the James method: **SUV Lean Body Mass (SUVlbm James)**; For men:

\[
SUVlbm \left( \frac{g}{ml} \right) = \frac{\text{pixel}(\frac{Bq}{ml})(1.1 \ast \text{weight}(kg) - 120.0(\text{weight}(kg) \ast \text{height}(cm))^2)}{\text{decayedDose}}
\]  
(2.15)

For woman:

\[
SUVlbm \left( \frac{g}{ml} \right) = \frac{\text{pixel}(\frac{Bq}{ml})(1.07 \ast \text{weight}(kg) - 148.0(\text{weight}(kg) \ast \text{height}(cm))^2)}{\text{decayedDose}}
\]  
(2.16)

– by the body mass index according to the Janmahasatian method: **SUV Lean Body Mass (SUVlbm Janmahasatian)**:

\[
SUVlbm \left( \frac{g}{ml} \right) = \frac{\text{pixel}(\frac{kBq}{ml})}{\text{dose}(MBq) \ast \text{lbm}(Kg)}
\]  
(2.17)

\[
bmi(Kg/m^2) = \frac{\text{weight}(kg)}{\text{height}(m)^2}
\]  
(2.18)

For men:

\[
\text{lbm}(Kg) = \frac{9270 \ast \text{weight}(kg)}{6680 + 216 \ast \text{bmi}(Kg/m^2)}
\]  
(2.19)

For woman:

\[
\text{lbm}(Kg) = \frac{9270 \ast \text{weight}(kg)}{8780 + 244 \ast \text{bmi}(Kg/m^2)}
\]  
(2.20)

- **Patient weight (Kg)** (optional for the method of calculating by body surface area);
- **Patient height (cm)**;
- **Injected dose (MBq)**;
- **Injection date time**;
- **Acquisition date time**;
- **Half-life (min)**;

**Sex** (optional for the method of calculating by body weight and by body surface area);

if it is necessary to display the SUV measurement results for ROI tools then check the **Use SUV for ROI tools** box.

To measure the SUV, click **OK**, to cancel the operation, click **CANCEL**. If there is not enough data to calculate (for example, the patient’s weight or height is not specified or is zero), then the **OK** button is disabled.
2.21. SUV MEASUREMENT

5. To change the SUV calculation settings, select the **Image** main menu, select the **SUV** item and the **Settings...** item.

6. When the SUV measurement is activated, the value at the point where the cursor is located appears in the top left-hand corner of the window. For example: 
   \[
   \text{SUVlbm: } -0.092 \text{ g/ml}
   \]
   Move the cursor over the image to measure the SUV. Please note that the **Display information** button must be pressed (see Section 2.24).

7. To calculate the SUV in a particular area or point, use the ROI tools (see Section 2.17.5). Please note that the **Use SUV for ROI** box must be checked in the SUV settings.

If the time and the date of the series creation is greater than the time and the date of the study, then the message **Warning: This series may be post-processed in which date of series creation unrelated to acquisition** appears in the SUV Settings dialog.

To disable the SUV measurement, select the **SUV** in the main menu **Image** and select the **Show SUV** command. The density information will be displayed for the built ROIs.
2.22 Calcium Scoring

Functionality is available in the Pro edition

The DICOM Viewer allows you to measure calcium in the coronary arteries. CT-series with information about the slice thickness are suitable for the measurement. For all other series, the tools are not applicable.

The tool selection button will look different depending on the tool that was used last:

<table>
<thead>
<tr>
<th>Ca</th>
<th>Calcium scoring (ellipse) (selected by default)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ca</td>
<td>Calcium scoring (polygon)</td>
</tr>
</tbody>
</table>

To switch between these tools click the arrow on the right side of the tool selection button and select the desired tool.

2.22.1 Selection of measurement areas

Functionality is available in the Pro edition

To measure calcium:

1. Open a CT series suitable for calcium scoring.

2. Select the image to measure.

3. Activate the Calcium scoring (ellipse) tool or Calcium scoring (polygon). These tools are similar to ROI ellipse and ROI polygon (see Section 2.17.5). If the study does not contain information about the age and/or gender of the patient, the dialog shown in Fig. 2.75 appears. Enter missing information and click OK to continue or CANCEL to cancel the measurement. After clicking OK, this dialog no longer appears until the Flat Image viewer window is closed. To change the gender and/or age of the patient, close the Flat Images View window and return to step 1.

4. When the calcium scoring tool is active, a window shown in Fig. 2.76 is displayed on the screen. Move the window if necessary. To do this, move the cursor over the window title (highlighted in red in the figure) and move it, holding the left mouse button. In the upper part of the window there are vessel selection buttons:

   - LM — Left main coronary artery
   - LAD — Left anterior descending coronary artery
2.22. CALCIUM SCORING

- **LCX** — Left circumflex coronary artery

- **RCA** — Right coronary artery

Select the artery for measurement by clicking the corresponding button. The choice of an artery does not affect the measurement result.

5. Build an ellipse or a polygon around the affected area. For details on how to build one, see Section 2.17.5 (the **ROI ellipse** and **ROI polygon** tools). A block with the following data is displayed near the measurement:

- The name of the artery (corresponds to the button pressed while building);

- Area of calcified lesion. If the measurement area contains several lesions then their total area is displayed;

- Agatston score;

- Volume score.

*Figure 2.75: Patient data entry dialog*
To deactivate the tool click the tool selection button Calcium scoring (ellipse) tool or Calcium scoring (polygon) or close the Calcium scoring window. All the changes made are saved until the Flat images view window is closed.

2.22.2 Actions with measurement areas

Functionality is available in the Pro edition

For details on how to move measurement areas, see Section 2.17.8, for how to move measurement results, see Section 2.17.9.

To edit the drawing parameters:

1. Activate the calcium scoring tool.

2. Locate the cursor on the measurement or the measurement results to highlight them.
3. Right-click the mouse and select the **Tool options...** item from the context menu.

4. In the dialog box that appears, enter the measurement name.

5. Set the color by clicking on the color box.

6. Set the line thickness and the font size.

7. To connect the block with the measurement results with a dotted line, the **Footnote line** box must be checked.

8. To display the block with the measurement results, the **Show labels** box must be checked.

9. To use these parameters by default, check the box **Set as default**.

10. To apply the settings, click **OK**. To cancel, click **CANCEL**.

### 2.22.3 Measurement results

**Functionality is available in the Pro edition**

The measurement results are displayed in the window shown in Fig. 2.76:

1. For each vessel separately and in total:
   - total lesion area (for all lesions);
   - lesion number (N);
   - Agatston score (AS);
   - Volume score (VS).

2. Patient gender

3. Age group

4. Percentile

**Formula for Agatston index scoring:**

\[
I_{cs} = \left( \sum_{i=1}^{n} S_i F_i \right) \frac{T_{slice}}{3.00}
\]

\(I_{cs}\) — Agatston index, \(n\) — lesion number, \(S_i\) — \(i\)-lesion area, \(F_i\) — \(i\)-lesion density factor, \(T_{slice}\) — slice thickness. The \(F_i\) value is determined by the maximum pixel density in the lesion area:

<table>
<thead>
<tr>
<th>Maximum pixel density</th>
<th>(F_i)</th>
</tr>
</thead>
<tbody>
<tr>
<td>130—199 HU</td>
<td>1</td>
</tr>
</tbody>
</table>
Maximum pixel density

| 200—299 HU | 2 |
| 300—399 HU | 3 |
| ≥ 400 HU   | 4 |

Formula for calcium scoring:

\[ V_{cs} = \left( \sum_{i=1}^{n} S_i \right) T_{slice} \]  \hspace{1cm} (2.22)

\( V_{cs} \) — Agatston index, \( n \) — lesion number, \( S_i \) — \( i \)-lesion area, \( T_{slice} \) — slice thickness.

Electron beam tomographic coronary artery calcium score percentiles for men and Women within each age strata

<table>
<thead>
<tr>
<th>Age</th>
<th>&lt;40</th>
<th>40-44</th>
<th>45-49</th>
<th>50-54</th>
<th>55-59</th>
<th>60-64</th>
<th>65-69</th>
<th>70-74</th>
<th>&gt;74</th>
</tr>
</thead>
<tbody>
<tr>
<td>Man (25251)</td>
<td>3504</td>
<td>4238</td>
<td>4940</td>
<td>4825</td>
<td>3472</td>
<td>2288</td>
<td>1209</td>
<td>540</td>
<td>235</td>
</tr>
<tr>
<td>25th percentile</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>4</td>
<td>13</td>
<td>32</td>
<td>64</td>
<td>166</td>
</tr>
<tr>
<td>50th percentile</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>15</td>
<td>48</td>
<td>113</td>
<td>180</td>
<td>310</td>
<td>473</td>
</tr>
<tr>
<td>75th percentile</td>
<td>3</td>
<td>9</td>
<td>36</td>
<td>103</td>
<td>215</td>
<td>410</td>
<td>566</td>
<td>892</td>
<td>1071</td>
</tr>
<tr>
<td>90th percentile</td>
<td>14</td>
<td>59</td>
<td>154</td>
<td>332</td>
<td>554</td>
<td>994</td>
<td>1299</td>
<td>1774</td>
<td>1982</td>
</tr>
<tr>
<td>Woman (9995)</td>
<td>641</td>
<td>1024</td>
<td>1634</td>
<td>2184</td>
<td>1835</td>
<td>1334</td>
<td>731</td>
<td>438</td>
<td>174</td>
</tr>
<tr>
<td>25th percentile</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>3</td>
<td>9</td>
</tr>
<tr>
<td>50th percentile</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>3</td>
<td>24</td>
<td>52</td>
<td>75</td>
</tr>
<tr>
<td>75th percentile</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>23</td>
<td>57</td>
<td>145</td>
<td>210</td>
<td>241</td>
</tr>
<tr>
<td>90th percentile</td>
<td>3</td>
<td>4</td>
<td>2</td>
<td>55</td>
<td>121</td>
<td>193</td>
<td>410</td>
<td>631</td>
<td>709</td>
</tr>
</tbody>
</table>

The measurement results are exported in the html format and can be inserted into text editors that support the html markup, for example, LibreOffice Writer or Microsoft Word. To do
2.23 Scout Lines

The [Show series scout lines] tool is used if two or more series are opened for a particular study. The tool allows you to display the series image scout lines in images from other series if they are synchronized.

By default, the current image scout line is highlighted in green, and the boundary scout lines are highlighted in yellow (Fig. 2.77). If the [Show all scout lines] mode is active, the intermediate scout lines are highlighted by a dotted line, and current and boundary scout lines are highlighted by solid lines.

Figure 2.77: The left-hand image scout line is displayed in the right-hand image

The study series must have the same value of the FrameOfReferenceUID (0020,0052) tag. If study series have different values of FrameOfReferenceUID (0020,0052) tag, then the scout lines for these series are not displayed.

2.23.1 The Tool Menu

The [Show series scout lines] tool menu (fig. 2.78) contains the following items:

1. Mode [Show all scout lines] shows the scout lines of all series images, not just of the current one.
2. The **Show bound scout lines** mode shows boundary scout lines in all the open windows. The mode is set by default.

3. Mode **Scout lines on selected view** shows in the current window scout lines of images opened in other windows.

4. Mode **Selected view scout lines** shows the scout lines of the current image in other windows.

5. **Line settings...** opens the dialog to configure the scout lines settings (Fig. 2.79).

![Figure 2.78: The menu for setting the scout lines display mode](image)

To activate/deactivate the mode of this tool, click on the arrow on the right side of the button and check/uncheck the corresponding item. The modes are activated independently.

By default, the **Show series scout lines** tool is active and the **Selected view scout lines** mode is checked. To activate/deactivate the tool, click the button on the toolbar.

### 2.23.2 Line Settings

To set the color and width of lines:

1. Click on the arrow on the right side of the button and select the **Line settings...** item. A dialog box shown in Fig. 2.79 will be displayed.

2. Set the line color. To do this, click the color change button, select a color in the dialog box and click **OK**.

3. Set the line width.

4. Click **OK** to apply the changes or **CANCEL** to cancel the actions.
2.24 Set Up Viewer Workspace

The **Show labels** tool allows you to display or hide the information about an image in the series windows. The settings are applied to all the series opened in the current tab. By default, the tool is active. To activate/deactivate the tool, click the **Show labels** button on the toolbar.

You can adjust the visibility of:

- **Orientation cube.** Located in the lower right corner of the window (for more information see Section 2.27.1). To show (hide) the Orientation cube, click the arrow on the right side of the **Show labels** and check (uncheck) the **Show orientation cube** box. Orientation cube is active by default;

- **Point coordinates.** The point coordinates are displayed under the cursor. To show (hide) the Point coordinates, click the arrow on the right side of the **Show labels** and check (uncheck) the **Show point coordinates** box. The point coordinates are shown in the viewer window where the cursor is placed. The coordinates are displayed as the first line in the left-hand bottom corner, in «X: px Y: px» format for original images and in «X: vx Y: vx Z: vx» format for reconstructed images;

- **Point value.** To show (hide) the Point value, click the arrow on the right side of the **Show labels** and check (uncheck) the **Show point value** box. The intensity value is displayed...
as the second line in the left-hand bottom corner of the viewer window where the cursor is placed. It is shown in the «Value: k HU» format for CT series and in «Value: k», where k is the intensity value at the point under the cursor. If the value is inaccurate, you will see a «*» symbol next to it. This can happen when you use an MPR reconstruction tab or interpolation filters. For details see Sections 2.4 and 5.3;

- **Visible tags.** To customize the list of displayed tags, click the arrow on the right side of the **Show labels** button, select the **Select visible tags...** command and in the dialog that opens (Fig. 2.80) set the flags for the required tags;

![Set visible tags dialog](image)

*Figure 2.80: Set visible tags dialog*

Click **OK** to apply the changes or **CANCEL** to cancel the actions.

To customize the Annotations text size, click the arrow on the right side of the **Show labels** button, select the **Set annotations text size...** command and in the dialog that opens, enter an integer or fractional value. Click **OK** to apply the changes or **CANCEL** to cancel the actions.

### 2.25 Export Images

#### 2.25.1 Export to DICOM

The export to DICOM allows you to export images to a series that is available while the current study is open. To export:

1. Click on the arrow on the right side of the **Quick export images** button on the toolbar and select the **Export images...** item or press **Ctrl+E**.

2. Select the **Export to DICOM** tab. The export window will look as shown in Fig. 2.81.
3. Select the series to export. If no series has been exported yet, only the Create new series item will be available. If an export has been conducted before, you can export the data to the last created series by selecting the Use exists series option.

4. If you need to load the exported images to the DICOM server immediately, check the option Upload image to the default server. If the default server is not set in the DICOM Viewer this option will be inactive.

5. Select a set of images for export. Three options are available:
   - Current image;
   - Entire series;

Figure 2.81: DICOM export window
6. Select the capture type. Three options are available:

- **View screenshot:** the entire view window workspace is captured, including the image information without conversions performed by the user;
- **Image screenshot:** only the image visible in the workspace (with conversions performed by the user) is captured;
- **Raw image data:** the whole image is captured; of all the user’s conversions, only mirroring is taken into account.

7. Set the image size if necessary.

8. To initiate export, click **OK**. To cancel the export, click **CANCEL**.

To continue exporting images to the DICOM format with the current settings, click on the **Quick export images** button or press **F5**.

This tool is also available from the **Image** main menu item.

### 2.25.2 Export to Image

The export to image allows you to export the current image to a .png or .jpg file. To export data to an image:

1. Click on the arrow on the right side of the **Quick export images** button on the toolbar and select the **Export images** button or press **Ctrl+E**.

2. Select the **Export to image** tab. The export window will look as shown in Fig. 2.82.

3. Set the path to the folder for export by entering it into the **Path to export** field or click the button and select the path in the dialog box.

4. Enter the file name.

5. Select the file extension from the drop-down menu.

6. Select a set of images for export. Three options are available:

   - Current image;
   - Entire series;
   - Current phase images (only for multiphase series).

7. Select the capture type. Three options are available:

   - **capture view area:** the entire view window workspace is captured, including the image information;
   - **capture visible image:** only the image visible in the workspace is captured (scale-sensitive);
   - **all image:** only the image is captured, irrespective of scale.
8. Set the image size if necessary.

9. To initiate export, click **OK**. To cancel the export, click **CANCEL**.

![Export image to file window](image)

**Figure 2.82: Export image to file window**

To continue exporting images to a file with the current settings, click on the **Quick export images** button or press **F5**. The file names will be specified automatically. If you attempt to export the same image twice, the DICOM Viewer will return the «**File with the same name already exists. Do you want to overwrite it?**» warning. To overwrite the image, click **YES**. To cancel, click **NO**.

This tool is also available from the **Image** main menu item.
### 2.26 DSA Mode

Using the DSA mode you can process multiphase and multiframe series with a varying concentration of a contrast agent, subtracting images in such a way that the tissues containing contrast are best seen. Applicable to series with CT, MRI and X-ray modalities.

The following outlines how to view multiframe series. Viewing multiphase series of studies is done in the same way.

**High-density tissue (e.g. bone) images may be subtracted from the images of contrast-enhanced vessels, which will lead to data loss.**

#### 2.26.1 Single-image subtraction view

For studies containing multiframe series with a varying concentration of a contrast agent, one of the frames is subtracted from all frames in the series. To apply the DSA mode:

1. Open the series of study in the View Flat Images window.
2. Click on the **Digital Subtraction Angiography (DSA)** button. The first frame of the series has been subtracted from all the frames of this series.
3. Scroll through the frames by moving the slider or rotating the mouse wheel, hovering the cursor over the scroll bar on the Frame Scroll Bar (Fig. 2.83).
4. If you want to subtract another frame from all the frames, select this image using the scrollbar in the Frame Scroll Bar, click on the arrow on the right side of the button and select the command **Set the current frame as a key frame**.
5. If the series frames are offset relative to each other, then correct it by selecting the command **Auto adjust key image offset** from the **Digital Subtraction Angiography (DSA)** tool menu.
6. To manually correct the offset, select the command **Manual Adjustment** from the **Digital Subtraction Angiography (DSA)** tool menu and change the location of the frames using the buttons that appear in the image view window (Fig. 2.84) or using the keys.
7. If necessary, change the window width and the window level.

![Figure 2.83: Frame Scroll Bar](image)
2.26. DSA MODE

Figure 2.84: The button for manual adjustment is highlighted in red

Figure 2.85: View tissues with a varying concentration of a contrast agent in DSA mode

2.26.2 Series subtraction view

For studies containing at least two related series of frames and images with different concentrations of a contrast agent, the frames and images of one series are subtracted from the corresponding frames and images of the other series. To apply the DSA mode:

1. Open the series of study in the View Flat Images window.
2. Choose a series whose images you want to subtract from the images of the other series.
3. Click on the button.

4. Click on the arrow on the right side of the Digital Subtraction Angiography (DSA) button. If the series contains the necessary data, then the command Set the frame series as key frames is available. Select this command.

5. Select another series of frames by rotating the mouse wheel or moving the slider on the right side of the image view window.

6. Scroll through the images by moving the slider or rotating the mouse wheel, hovering the cursor over the scroll bar on the Frame Scroll Bar (Fig. 2.83).

7. If necessary, change the window width and the window level.

This tool is also available from the Image main menu item.

### 2.26.3 Viewing Several Series of the Same Study Fused in One Multiphase Series with Subtraction

A fused series may be viewed in the digital subtraction angiography (DSA) mode and used for assessment of contrast distribution in tissues at regular time intervals.

1. Open a fused series in the flat image viewer mode (see Section 2.10).

2. Scroll the phases and images of the series by moving the sliders on the phases and images scroll bars.

3. Activate the DSA mode by clicking the Digital Subtraction Angiography (DSA) button.

4. Chose a phase whose images are to be subtracted from the images belonging to other phases. Click the arrow on the right-hand side of the button and select the Set the current frame as a key frame option on the tool menu.

5. Change the window width and level if required.

This tool is also available from the Image main menu item.

### 2.27 Image Information in the Series Window

#### 2.27.1 Orientation Cube

The Orientation Cube is located in the bottom right-hand corner (Fig. 2.86). The markers on the cube show the side the image is viewed from:

- A — Anterior
- R — Right
2.27. IMAGE INFORMATION IN THE SERIES WINDOW

L — Left
P — Posterior
F — Foot
H — Head.

Figure 2.86: Orientation cube

If «F» is written on the cube face, it means that the image is viewed from below; if «R» is written beside a rib, it means that the patient’s right side is on this side of the image.

For details on the display settings for the orientation cube and letters (markers), see Section 2.24.

2.27.2 Scale

A graduated 10-cm scale is displayed on the right side of the window.

2.27.3 Image Information

The image information is displayed in the bottom left-hand corner. It may include the following parameters, depending on the study type:

- **Image No** — current image number in the series/total number of images in the series;
- **Image size** — image size (pixels);
- **FOV (field of vision)** — image size (millimeters);
- **Location** — image location determined by the device;
- **Thickness** — interval between slices.

For details on customizing the data concerning the image, see Section 2.24.
2.27.4 Patient Information

The information about the patient is displayed in the top left-hand corner.

For details on customizing the data concerning the patient (the patient ID, name, age, date of birth etc.), see Section 2.24.

2.28 View DICOM Tags

To view the DICOM tags of the image:

1. Open the image.

2. Open the image context menu by right-clicking on the image.

3. Select the Show image tags item. The DICOM tags will be displayed in a new tab (see Section 16).

2.29 Viewing Structured Reports

Structured reports are used for transferring and storing structured medical documents.

A structured report contains information on the patient and the study. Series of structured reports have SR modality.

To view a structured report, open an SR series (see Section 2.1).

A series is opened in a new flat image viewer tab, in a separate window (Fig. 2.87).

![Figure 2.87: Window for viewing structured reports](image)

In the structured reports viewer window, you can choose the mode for arranging series (see Section 2.8). The automatic mode is selected by default.
At the top of the structured reports viewer window, you can see general information on the patient, the study, and the report status. In the lower part of the window, you can see structured information.

If an SR series comprises more than one document, you will see a horizontal scroll bar at the top of the window. The order of the documents depends on the names of the files containing such documents. There are several ways to switch between documents:

- by moving the slider;
- by hovering over the scroll bar and scrolling the mouse wheel;
- with the help of Switch to previous image \( \leftarrow \) and Switch to next image \( \rightarrow \) buttons on the toolbar.

Structured reports cannot be edited. There are two ways to copy text from the structured reports viewer window to the clipboard:

- select the text, open the context menu by right-clicking on the text, and click Copy;
- select the text and press Ctrl+C on the keyboard.

There are several methods to select text in the structured reports viewer window:

- to select a word, double-click on that word with the left mouse button;
- to select a line, click three times on any word in that line with the left mouse button;
- to select a text fragment, place the cursor before the first word of the fragment, click the left mouse button and drag the cursor to the end of the fragment while holding the button;
- to select the complete text of the document, open the context menu by right-clicking within the window and choose Select all. Alternatively, you can press the Ctrl+A combination on the keyboard.

To maximize the report window and restore its size, proceed as follows:

- double-click with the left mouse button on the title of the series window;
- click on the Expand \( \square \) button in the right-hand upper corner of the series window.

To close the window with structured reports, click the Close \( \times \) button on the right-hand side of the window header.

### 2.30 Graphic Label Tool

#### 2.30.1 General

This tool allows you to create graphic labels (as arrows, ellipses, polygons, freeform lines and text fields) on an image. The labels will be applied during the entire session of working with the series. The labels are attached to specific points on the image and panned, scaled or rotated together with the image.
The button design depends on the selected tool. The default tool is *Arrow*, and the tool selection button looks like this: ➡️.

To activate/deactivate the selected tool, click on the graphic label tool selection button. To select and activate one of the tools, click on the right side of the tool selection button and select the tool (Fig. 2.88).

![Graphic label tool menu](image)

*Figure 2.88: Graphic label tool menu*

This tool is also available from the image context menu and from the *Image* main menu item.

The annotation tools are available on the *MPR reconstruction*, *Vessel analysis*, *Coronary arteries analysis* and *PET Analysis* tabs.

### 2.30.2 Create Labels

To create a label on an image:

1. Activate the *Arrow* tool by clicking the left/right/middle mouse button. The button will look as follows: ➡️. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. You can draw a arrow in two ways:

   - Click the mouse button at the point where the arrow tip is to be placed and, while holding the mouse button, move the cursor to the opposite end of the arrow. To fix the point, release the mouse button.
   - Click the mouse button at the point where the arrow tip is to be placed. Click the mouse button again where the opposite end of the arrow should be placed. The arrow is shown in Fig. 2.89.

3. To cancel an incomplete creation, press **Esc**.
To create a freeform shapes and lines on an image:

1. Activate the **Pencil** tool by clicking the left/right/middle mouse button. The button will look as follows: 🖊️. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Click the mouse button at the point where you want the line to begin and, while holding the mouse button, move the cursor. This displays a line that follows the cursor trajectory. To complete the drawing, release the mouse button.

3. To cancel an incomplete creation, press Esc.

To create a text label on an image:

1. Activate the **Text** tool by clicking the left/right/middle mouse button. The button will look as follows: 📝. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Click the mouse button where the text should be located.

3. Enter text in the **Edit text** dialog box and click OK to add it to the image or CANCEL to cancel the action.

To create a polygon on an image:

1. Activate the **Polygon** tool by clicking the left/right/middle mouse button. The button will look as follows: 🟢. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Click the mouse button where the first point of the polygon should be located.

3. Move the cursor to the location of the next point. The lines connecting the points of the polygon will be displayed on the screen.

4. Click the mouse button to save the point.
5. Repeat Steps 3 and 4 until the last but one point is set.

6. Double-click the mouse to create the last point. The polygon is complete (Fig. 2.90).

7. To cancel an incomplete creation, press Esc.

To create an ellipse on an image:

1. Activate the Ellipse tool by clicking the left/right/middle mouse button. The button will look as follows: . To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. To build an ellipse, just build the rectangle the ellipse is inscribed into. You can draw an ellipse in two ways:

   - Click the mouse button to mark the first end of the ellipse and while holding the mouse button move the cursor to the place where the opposite end should be located. The ellipse will be displayed on the screen. To fix the point, release the mouse button.

   - Click the mouse button to mark the first end of the ellipse. Move the cursor to the place where the opposite end of the ellipse should be located. The ellipse will be displayed on the screen. To fix the second end of the ellipse, click the mouse button. The ellipse is shown in Fig. 2.91.

3. To cancel an incomplete creation, press Esc.
2.30.3 Actions with Labels

The DICOM Viewer allows you to perform the following actions with labels:

- Drag. Locate the cursor on the figure line or text and drag the object, holding down the left mouse button or the button to which this tool is assigned.

- Drag a point (an apex for an arrow or polygon and a rectangle apex for an ellipse). Locate the cursor on a point and drag the point, holding down the left mouse button or the button to which this tool is assigned.

- Delete. Locate the cursor on the label border, right-click the mouse and select the Remove object item from the context menu.

- Set render params. Locate the cursor on the label border, right-click the mouse and select the Tool options... item from the context menu. In the dialog box that appears, set the line color and thickness for a figure or the font color and size for text. If the box Set as default checked, these settings will be applied by default when creating new annotations. Click OK to apply the changes or CANCEL to cancel the actions.

- Edit text label. Locate the cursor on the text, right-click the mouse, and select the Edit text command from the context menu.

To set the default render parameters, click on the right side of the button and select the command Default tool options...

To delete all objects, click the Delete all annotations and measurements button. In the dialog box that appears, Click YES to delete or NO to cancel. If you want the DICOM Viewer to always delete annotations and measurements without this confirmation, check the box Don't show this dialog again and click YES. If you want the DICOM Viewer to show the confirmation dialog, check the box Ask before deleting all annotations and measurements (see Section 15.6.1).

Attention! All measurements and other objects created manually will be deleted.
2.31 Synchronize Images

Synchronization is applied if two or more series are opened for the same study. This function allows you to scroll images in several series synchronously. By default the option is enabled.

To set up the synchronization options you need, proceed as follows:

1. Click on the arrow on the right side of the Sync series button on the toolbar. This tool is also available from the Image main menu item.

2. In the drop-down menu for the button (Fig. 2.31), choose the synchronization types and modes:

![Figure 2.92: Activating the image synchronization types and modes](image)

- **Sync scroll.** Provides an opportunity to scroll images from the series with the same frameOfReferenceUid tag values simultaneously in the By patient coordinates mode. If the frameOfReferenceUid tag values are different for different series, scrolling will not be synchronized in the By patient coordinates mode. To synchronize series with different frameOfReferenceUid tag values, select the Manual mode.

  Synchronization is performed for the sections parallel to the synchronizing section;

- **Sync W/L.** Window width and level (W/L) synchronization is performed for the series with CT modality. For series with other modality types, synchronization will only be performed if the recommended window width and level (W/L) values are the same. The mode chosen does not impact this synchronization type;

- **Sync zoom and position.** Provides an opportunity to synchronize image scaling and moving. This option will work differently depending on the mode chosen.
  
  - In the By patient coordinates mode:
    
    * image scaling and moving is synchronized for the images from the series with the same frameOfReferenceUid tag values. If the frameOfReferenceUid tag values are different, synchronization will not be performed;
    
    * the real size of the image is taken into account. For sections of the same size, objects are displayed in the same way;
2.32 Synchronization by a Point

- the centers of the windows are synchronized. In the window center, you see the projection of the center point of the synchronizing window on the synchronized window section;
- if the Synchronize scale and position of slices in different projections option on the Tools tab of the Image viewer module (for details see Section 15.6.1) is disabled, synchronization will only be performed for the sections parallel to the synchronizing section. If this option is enabled, parallel orientation of the sections will not be taken into account for scaling and position synchronization.

- In the Manual mode:
  - the real size of the image is taken into account. For sections of the same size, objects are displayed in the same way;
  - if the position of the synchronizing window center is changed, the position of the synchronized window center is changed accordingly;
  - if the Synchronize scale and position of slices in different projections option on the Tools tab of the Image viewer module (for details see Section 15.6.1) is disabled, synchronization will only be performed for the sections parallel to the synchronizing section. If this option is enabled, parallel orientation of the sections will not be taken into account for scaling and position synchronization.

- Sync phases. The image phases are synchronized by number. If the phase number for the synchronizing series is greater than the total number of phases in the synchronized series, then the phase with the greatest number will be selected for the synchronized series. The mode chosen does not impact this synchronization type.

If there are several images in the window, then the properties of the first image will be used for scaling and movement evaluation.

Image synchronization is performed automatically. To disable synchronization, click on the Sync series button.

To disable the default synchronization on the DICOM Viewer startup, uncheck the Turn on sync image by default box in the image viewer setup dialog box (see Section 15.6.1).

2.32 Synchronization by a Point

To choose the slices in all the windows that are the closest to the point selected, use the Sync by point tool. To synchronize, choose a reference point in one of the viewer windows. You will see crosshairs at this point. The synchronized windows will show the slices that are the closest to the point chosen; you will see crosshairs at the closest point of the synchronized slice.

If the reference point is not present on the synchronized slice, the crosshairs shown will have a black spot in the centre

The slice thickness is determined by the modality.
2.33 Mirror Image Horizontally/Vertically

This tool allows you to mirror images. The button will look different depending on the mode that was used last (izontal, — vertical). The horizontal mode is used by default.

To activate/deactivate the tool, click on the button. If several series are opened in the view window, the mirroring is activated for each series independently.

To change the mirroring mode, click on the arrow on the right side of the button and check the required mode. Both modes can be activated simultaneously.

This tool is also available from the Image main menu item.

2.34 Calibration sizes

X-ray image sizes are increased as compared with the real size of the tissues (Fig. 2.93).

Figure 2.93: The green arrow shows the actual size of the tissues and red arrow shows the size of the image

Hence, the size determined by X-ray modality may be incorrect. If a picture contains an object whose size is known (e.g., a catheter), it is possible to calibrate the image size. To calibrate the size:

1. Select the Images main menu and the Calibration tool.

2. A calibration segment can be built in two ways:

   • Mark the first point by clicking the left mouse button. Drag the cursor over the screen. The distance from the first point to the current point will be displayed beside the line. To fix the second point, click the left mouse button.

   • Click the mouse button at the first point of the calibration segment and move the cursor to the endpoint while holding the mouse button. The distance from the first point to the current point will be displayed beside the line. To fix the endpoint, release the mouse button.

3. In the dialog box that appears, type the real length of the interval constructed (Fig. 2.94). To calibrate the size, click OK, to cancel, click Cancel.

184
2.35. APPARENT DIFFUSION COEFFICIENT

Functionality is available in the Pro edition

DICOM Viewer allows to show parametric maps for diffusion-weighted images. To activate the ADC mode, click on the Apparent diffusion coefficient (ADC) map button.

The mode is available for MRI study series containing information on the «b» value (Diffusion sensitization factor).

To set values factor, click on the arrow on the right side of the button and select the Set values factor... item.
Chapter 3

Volume Reconstruction

In Volume Reconstruction window, diagnosis can only be established on the basis of CT, MR, MG, and XA series.

The DICOM Viewer supports 16-bit images. If the source data width is significant, data may be partially lost.

It is recommended to use a render device supporting the CUDA technology (preferable) or the OpenCL technology to build a volume model. The settings are described in Section 15.6.3.

On macOS 10.15 and later, it is recommended to use a visualization device that supports Metal polygonal and voxel rendering. The settings are described in Section 15.6.3.

Color tables are needed for displaying voxels representing different density values in different colors for improved perception. The shades on the screen are different from the real shades.

3.1 View Images

To open a study in the volume reconstruction window:

1. Load the studies to the DICOM Viewer.

2. Select the study from the study panel.

3. Click the Volume Reconstruction button on the toolbar. To select the tab location (in the current window, in a separate window, or in the full screen mode), click on the arrow on the right side of the button. To open the volume reconstruction window in a new tab in the current window, click on the button. This process may take some time.
Fig. 3.1 illustrates the volume reconstruction window. The right side of the screen displays the toolbar with the volume edit tools and the windows for viewing the axial, frontal and sagittal sections. You can work with the sections in the 3D cursor mode described in Section 5.4.1.

The right side of the screen displays the toolbar with the volume edit tools and the windows for viewing the axial, frontal and sagittal sections. You can work with the sections in the 3D cursor mode described in Section 5.4.1.

The volume reconstruction of tissues is located on the left side of the screen. To move the cursor in MPR reconstruction windows, to move the cursor to a point on the model, activate the Select model point tool and click the mouse button to select the desired point. To deactivate the tool, click the button again. For details on setting and operating the Select model point tool, see in Section 3.5.

The tool is also available in the Volume section of the main menu.

3.2 Model Projection

The DICOM Viewer creates an opportunity to show the model in the perspective (Fig. 3.3) and parallel (Fig. 3.2) projection. The button will look different depending on the projection selected:
Switch to parallel projection. The perspective projection is now selected (selected by default)

Switch to perspective projection. The parallel projection is now selected

---

**Figure 3.2: Parallel projection of the 3D model**

**Figure 3.3: Perspective projection of the 3D model**

The Clipping Box tool in Fig. 3.2 and Fig. 3.3 is included for clarity and described in detail in Section 3.10.

### 3.3 Actions with Model

The DICOM Viewer allows you to perform the following actions with a model:

- Pan leftward and rightward using the keys.

- Zoom the 3D image by rolling the mouse wheel or using the keys.

- Rotate by moving the mouse holding the wheel or using the Rotate tool (see Section 3.4.2).

On the left-hand side of the window, you can see a standard space orientation panel (Fig. 3.4). To jump to a different space orientation option, click the buttons on the panel. To
open additional options for the «LAO» and «RAO» buttons, click the arrow on the right side of the corresponding button. By clicking the buttons on the panel, you can only work with the window in which the panel is placed.

![Space orientation selection buttons](image)

*Figure 3.4: Space orientation selection buttons*

The panel with space orientation selection buttons (Fig. 3.4) is available in the **Volume reconstruction** and **3D view** windows of the **MPR reconstruction, Vessel analysis** and **Coronary arteries analysis** tabs. You can set the visibility of the standard space orientation panel in the **UI** tab. To do that, go to the **3D reconstruction** and **Vessel analysis** module settings (see Sections 15.6.3 and 15.6.4).

### 3.4 Model Positioning Tools

#### 3.4.1 Model Shift

There are two ways to move the model in the volume reconstruction window:

1. Move the mouse holding the wheel and the **Shift** key on the keyboard. This key combination is set by default. You can disable or change the setting in the **3D controllers** tab of the **3D reconstruction** module (see Section 15.6.3).

2. Activate the **Pan** tool on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. To move a model, move the cursor around the screen while holding down the mouse button.

This tool is also available from the image context menu.
3.4.2 Model Rotation

Activate/deactivate the Rotate tool by clicking the left/right/middle mouse button. By default, the tool is active. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

Note that the initial point of the cursor does not affect the rotation. If the cursor is moved vertically, the image is rotated round the horizontal axis. If the cursor is moved horizontally, the image is rotated round the vertical axis. That is, the image follows the cursor. If the cursor moves along a slanting line, the image slants the same way.

This tool is also available from the image context menu and from the Volume main menu item. Activation is only possible with the left mouse button.

3.4.3 Model Scaling

The tool allows you to zoom the model with the mouse, holding the button. Move the cursor up to zoom in or down to zoom out.

Activate/deactivate the Zoom tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

This tool is also available from the image context menu and from the Volume main menu item.

3.5 «Select Model Point» Tool

The Select model point tool is available on the toolbar in the Volume reconstruction and MPR reconstruction tabs. In the MPR reconstruction tab, the tool becomes available when the 3D view mode is chosen. Besides, the tool is available in the Volume section of the main menu of the Volume reconstruction tab.

Activate the Select model point tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

Mouse over the volume model and choose a point. The point of intersection of the cutting planes in the MPR Reconstruction windows is moved to the specified point on the volume model. The point specified may be used as the initial point for measuring and editing the model volume.

Attention! For more precise choice of the point on the volume model, provide the correct value of the opacity threshold for the «Render settings» tool (see Section 3.14).

3.6 The Play Tool

The DICOM Viewer allows you to automatically rotate a volume model around one of the three orthogonal axes relative to the center, or play phases. The center of the model can be changed using the Centrate tool (see Section 3.9). To configure playback, click the arrow on
3.7. VIDEO RECORDING

the right side of the Play button and specify the necessary parameters in the button context menu.

1. If the series contains several phases, then the DICOM Viewer allows you to switch between the model rotation and the phase playback. To switch between these modes, select the Play phases or the Volume rotation item from the Play button context menu. The selected item is marked with a flag. Only items suitable for this series are available in the context menu.

2. Select the speed (5, 10, 20 or 25 frames per second only for the phase playback). If you want to set a different playback speed, select the User defined... item and in the dialog that opens set the value from 1 to 100. The selected speed will be marked with a flag.

3. If you want to play phases cyclically, select the Loop item. The item will be marked with a flag. To disable the cyclic playback, select this command again. The flag will be removed.

4. To select the rotation axis of the model, select the Settings... command; in the dialog that opens, select the axis from the Axis drop-down list and click OK to apply the setting or CANCEL to cancel.

5. To adjust the rotation speed of the model select the Settings... command; in the dialog that opens, enter a value in the Degrees per second field and click OK to apply the setting or CANCEL to cancel.

   To start playback, click on the Play button on the toolbar. During playback, the button looks like Play . To end playback, click the button.

3.7 Video recording

Functionality is available in the Pro edition

The DICOM Viewer allows you to record video for the volume model view window. The following objects will be recorded:

- base volume and segmented structures tissues;
- measurements;
- annotations;
- markers;
- clipping box;
- tags;
- orientation cube;
- the Select model point tool label.

Other features of the tool are similar to those described in Section 2.13.
3.8 Cutting Tools

There are several cutting tools on the right toolbar.

3.8.1 Polygon Cut

The Polygon Cut tool allows you to build a polygon or an area with smooth borders that the cut area is projected on.

To build a polygon:

1. Activate the Polygon Cut tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Click the mouse button to set the apices of the polygon marking the figure to be cut, except the last point.

3. Fix the last point by double-clicking the mouse.

4. To cancel an incomplete building, press Esc.

To build an area with smooth borders (Lasso mode):

1. Activate the Polygon Cut tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Press and hold the Shift key on the keyboard.

3. Circle the area to be cut, holding down the mouse button.

4. To complete the building, release the mouse button or click another mouse button.

5. To cancel an incomplete building, press Esc.

The part of the model to be projected on the area will be cut.

3.8.2 Inverse Polygon Cut

The tool is similar to the previous one, except that the part of the model not to be projected on the area will be cut. To activate/deactivate the tool, use the button on the toolbar.

3.8.3 Cut object

The tool allows you to delete an area of a 3D model not associated with its other parts.

Activate/deactivate the Cut object tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.
3.8.4 Cut all except object

The tool is similar to the previous one, except that all areas excluding the selected area are deleted. To activate/deactivate the tool, use the \( \text{button} \) on the toolbar.

3.8.5 Cutting Tools Parameters

For the Cut object and Cut all except object tools, the following parameters can be set:

1. Grow from surface (mm). The tissue surrounding the deleted area will be deleted too. This parameter specifies the distance from the surface on which the tissue will be deleted. If this parameter is set to zero, the model surface may look rough, so use a value of zero only if necessary.

2. Min object thickness (mm). If the value is greater than zero, the tissue with a thickness less than the set value will be ignored during deletion.

The parameters for each tool are set separately.
To set these parameters, click on the arrow on the right side of the appropriate tool button and select the Parameters... item and in the dialog box that appears, specify the required values.

3.8.6 Sphere Cut, Sphere Restore and Restore by Mask Tools

The Brush cut, Brush restore and Restore by mask tools allow to remove tissue within a sphere or cylinder and restore the tissue deleted by cutting tools. To select one of these tools (Brush cut, Brush restore, Restore by mask) and modes (Sphere, Cylinder), click the arrow on the right side of the tool buttons. The button will look different depending on the tool that was used last:

The Brush restore and Restore by mask tools are assigned to the same button. To select a tool, click on the arrow on the right side of the tool selection button. The button looks different, depending on the tool selected:

<table>
<thead>
<tr>
<th></th>
<th>Brush restore (is selected by default)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Restore by mask</td>
</tr>
</tbody>
</table>

To select one of modes (Sphere, Cylinder), click the arrow on the right side of the tool buttons. The same mode is chosen for Brush restore and Restore by mask tools.

The cursor will look different depending on the mode that is selected. The cursor for the Sphere mode is shown in Fig. 3.5, and the cursor for the Cylinder mode is shown in Fig. 3.6.

193
To activate/deactivate the tool, click on the tool button. If any tool is activated, the button is highlighted.

To cut tissue:

1. Activate the **Brush cut** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Set the tool diameter, moving the mouse while holding the **Alt** key. The **Brush cut** and **Brush restore** tools are set to the same diameter value.

3. For the **Cylinder** mode, set the height if it is necessary. To do it, click the arrow on the right side of the tool button and select the **Cylinder settings...** item. In the dialog box that appears, set the cut height.

4. Click the mouse button in the place where you want to cut tissue. Part of the tissue will be cut. The green dot indicates where the great circle of the sphere (the base area of the cylinder) touches the surface of the model. The great circle passes through the center of the sphere and is parallel to the plane of the screen.

5. Repeat steps 2 and 4 if necessary.

The **Brush restore** tool allows you to perform the reverse process of brush cutting.

The **Restore by mask** tool allows you to restore tissue by mask (this tool is used for segmentation). If mask is not set, this mode is analogous to the **Brush restore** mode. For details how to set mask, see Section 6.2.4.
3.8.7 Tools for intelligent volume editing

Functionality is available in the Pro edition

The Grow (dilation), Shrink (erosion), Fill and Cut invisible volume tools allow to edit tissue within special algorithms. The Multi-segment growing (Voronoi diagram) tool allows you to edit segmented structures. To select one of these tools, click the arrow on the right side of the tool buttons. The button will look different depending on the tool that was used last:

<table>
<thead>
<tr>
<th>Tool</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grow (dilation)</td>
<td>(set by default)</td>
</tr>
<tr>
<td>Shrink (erosion)</td>
<td></td>
</tr>
<tr>
<td>Remove noise (opening)</td>
<td></td>
</tr>
<tr>
<td>Remove holes (closing)</td>
<td></td>
</tr>
<tr>
<td>Multi-segment growing (Voronoi diagram)</td>
<td></td>
</tr>
<tr>
<td>Fill</td>
<td></td>
</tr>
<tr>
<td>Cut invisible volume</td>
<td></td>
</tr>
</tbody>
</table>

The Grow (dilation) tool allows you to increase the volume by a certain value from the surface in one iteration. This value is specified in the Settings menu of this tool (parameter Growing radius). The increase is possible only within the original volume, for example, after the use of cutting tools. When you use this tool to edit a segmented structure, an increase is possible only within the mask. The tool is used to fine-tune the structure if, initially, the required volume was not obtained.

The Shrink (erosion) tool performs the opposite action. The reduction value is specified by the parameter Growing/Shrinking radius.

The Remove noise (opening) tool allows to remove noise from the volume. This tool is equivalent to the consistently applied tools Shrink (erosion) and Grow (dilation).

The Remove holes (closing) tool allows to remove little holes from the volume. This tool is equivalent to the consistently applied tools Grow (dilation) and Shrink (erosion).

Each time the Grow (dilation), Shrink (erosion), Remove noise (opening), and Remove holes (closing) tools are used, a dialog box (Fig. 3.7), in which the operation radius should be set in millimeters or voxels is displayed.
The **Multi-Segment Growing (Voronoi diagram)** tool allows you to simultaneously build several structures and base volume. It is used to edit segmented structures (see Section 6.8.6). If the tool is applied only to the base volume, then it works like the **Grow (dilation)** tool.

The **Fill** tool allows you to fill the voids in the volume. If you are working with segmented structures, the tool is used to improve structures, built on a «grainy» mask. Such masks are typical, for example, for kidneys.

The **Cut invisible volume** tool sets the mask according to the visible volume.

### 3.8.8 Remove Table

The tool allows you to delete areas resembling the medical equipment table. To delete, click the button on the toolbar.

*Some objects that have been misrecognized as the modality table may be deleted by mistake.*

To undo or redo the last action associated with cutting, use the **Undo** and **Redo** buttons.

### 3.9 Centrate

The tool allows you to set the center point. The model rotates and scales with respect to this point. This may be necessary if the model is altered with cutting tools. The tool has two modes: auto and interactive (manual). To select mode, click on the arrow on the right side of the **Centrate** button on the toolbar and select the mode. The current mode is marked with a flag.

Centering is performed in space. Depth centering can be disabled. To enable/disable depth centering, click on the arrow on the right side of the **Centrate** button and select the **Centrate depth** item. If depth centering is enabled, the item is marked with a flag. Centering in a plane parallel to the screen plane is always performed.

To activate the tool, click on the **Centrate** button. If the auto mode is selected, activate the tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see
Section 1.14. If the auto mode is selected, centering will be performed immediately after the tool is activated. If the interactive mode is selected, the cursor takes the form of a crosshair. Set the center point by clicking on it with the left mouse button.

To center the model without activating the tool, press **Alt + middle mouse button**. To do this, click the middle mouse button while holding the **Alt** key on the keyboard. When you click on a selected point, the visible model will be centered with respect to this point. When you click on the screen beyond the model, the model will be centered with respect to the center of the visible part.

### 3.10 Clipping Box

The clipping box allows you to cut off all tissues outside it. To build a box, click on the **Clipping Box** button on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

To build a minimum box not cutting the model, click on the arrow on the right side of the **Clipping Box** button and select the **Fit to model** command.

To build a box by the image borders, click on the arrow on the right side of the **Clipping Box** button and select the **Reset clipping box** command.

To cut off parts of tissues, move the box face so that it intersects the 3D model. To do this, locate the cursor on the box face so that its borders are highlighted in green (Fig. 3.8).

![Figure 3.8: Editing the Clipping Box. The active face ready for moving is highlighted in green](image)

Next, move the face using the mouse while holding the left button. Only the faces located in the foreground (highlighted in white) can be moved. The faces unavailable for moving are highlighted in grey. To be able to work with the faces that are unavailable for moving, rotate the image. The box is rotated synchronously with the image.
To zoom the box symmetrically, move the mouse, holding the mouse button with which the tool was activated and Ctrl key.

To pan the box, move the mouse, holding the mouse button with which the tool was activated and Shift key.

To rotate the box, move the mouse, holding the mouse button with which the tool was activated and Alt key.

If the Clipping Box tool is deactivated, the sections made using the tool will be saved. To restore the initial look of the model, use one of the following options:

1. Activate the Clipping Box tool and move the faces to make the model visible.

2. Click on the arrow on the right side of the Clipping Box button and select any of the building options. If the Clipping Box tool is inactive, the box will not be visualized, but the section will still be reset.

This tool is also available from the Volume main menu item.

3.11 Measurements

The tool allows you to make linear and polygonal linear measurements of distances in an image.

**The measurement accuracy is up to one screen pixel. As a screen pixel is smaller than a source image pixel, the true linear measurement accuracy is up to one source image pixel. Errors may also occur in density measurements. The most accurate measurements are performed with bilinear interpolation (see Section 2.4).**

3.11.1 Ruler

To make linear measurements:

1. Activate the Ruler tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. You can measure the distance in two ways:
   - Mark the first point by clicking the mouse button. Drag the cursor over the screen. The distance from the first point to the current point will be displayed beside the line. To fix the current point, click the mouse button.
   - Click on the mouse button at the starting point and move the cursor to the endpoint while holding the mouse button. The distance from the first point to the current point will be displayed beside the line. To fix the endpoint, release the mouse button.

3. To cancel an incomplete measurement, press Esc.

To move the ruler border:
3.11. MEASUREMENTS

1. Locate the cursor on the point to be moved.
2. Drag the point, holding the left mouse button.
3. Release the left mouse button.

To delete a ruler:
1. Locate the cursor on the line to be deleted.
2. Right-click the mouse and select the **Delete all Measurement** command.

This tool is also available from the model context menu and from the **Volume** main menu item. Activation is only possible with the left mouse button.

3.11.2 Polygonal Ruler

To perform polygonal linear measurement:

1. Activate the  

   **Polygonal ruler** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.
2. Mark the first point on the toolbar by clicking the mouse button.
3. Drag the cursor over the screen. The distance from the first point to the current point will be displayed beside the line.
4. To fix the current point, click the mouse button.
5. Repeat Steps 3 and 4 until the last but one point is fixed.
6. Fix the last point by double-clicking the mouse.
7. To cancel an incomplete measurement, press **Esc**.

To move the linear measurement point:
1. Locate the cursor on the point to be moved.
2. Drag the point, holding the left mouse button.
3. Release the left mouse button.

To delete a point:
1. Locate the cursor on the point to be deleted.
2. Right-click the mouse and select the **Remove point** command.

To insert a point:
1. Locate the cursor on the ruler where you want to insert a point.
2. Right-click the mouse and select the **Insert point** command.
To resume a completed polygonal linear measurement:

1. Locate the cursor on the point from which you want to continue the measurement, so that it would look as follows: 

2. Right-click the mouse and select the Resume ruler command.

3. Perform the polygonal linear measurement.

This tool is also available from the model context menu and from the Volume main menu item. Activation is only possible with the left mouse button.

### 3.11.3 Surface ruler

Functionality is available in the Pro edition

A distance on the surface of a visible volume may only be measured in the Volume reconstruction tab.

To measure a distance on the surface of a visible volume or a surface, proceed as follows:

1. Activate the Surface ruler tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Mark the first point on the toolbar by clicking the mouse button.

   > **There may be a delay before the first point is displayed as it takes some time to bind the first point to the segmented structure.**

3. Drag the cursor over the screen. The next point number is displayed next to the cursor.

4. To fix the current point, click the mouse button.

5. Repeat Steps 3 and 4 until the last but one point is fixed.

6. Fix the last point by double-clicking the mouse.

The line reflecting the change is built along the shortest path between the points on the surface of only one segmented structure. The distance is measured on the surface of the segmented structure where the first point is placed.

Selecting a segmented structure to place the first point is based on the Point projection setting of the Render settings tool. For details on render setting tool management, see Section 3.14.

If more than one segmented structure is created in the project that satisfies the criterion for placing the first point, the point is placed on the structure located in the foreground. You can measure the distance on the surface of the structure in the background in several ways:

- rotate the volume model so that there are no other structures in front of the selected structure;
3.11. MEASUREMENTS

- turn off the visibility of the structure in the foreground;
- change the opacity value of the foreground structure.

If the path cannot be built, an **Unable to find the path** message pops up, and the last path that was successfully built is restored. The measurement path is highlighted when you hover over it, and the numbers of the points are shown.

> **It is impossible to measure a distance on the surface of a imported or copied surface.**

Imported and copied surfaces are structures without a 3D model. If the user attempts to make a measurement on the surface of an imported/copied surface, a warning message will pop up.

If a measurement path is built on the surface of a segmented structure (base volume, or surface) that is invisible, a warning will pop up if a user attempts to edit the path.

In the merged series opened in the **Volume reconstruction** tab, the distance on the surface of the segmented structure is measured in the same way. The first measurement point along the surface of the structure is placed on the layer that is in the foreground. To measure the distance on the surface of the structure located on the background layer, decrease transparency of the foreground layers.

In addition to commands, the context menu of the **Surface ruler** (Fig. 3.9) contains information concerning the layer and the segmented structure on which the measurement path to be edited was built. To open the context menu for the tool, right-click on a point, the path or the text describing the path length.

![Surface ruler context menu](image)

> **Figure 3.9: The Surface ruler context menu**

To move a point of a measurement path, proceed as follows:

1. Locate the cursor on the point to be moved so that it would look like this.
2. Drag the point, holding the left mouse button or the button, with which the tool is activated.

To add a point in order to proceed with building a measurement path, proceed as follows:

1. Locate the cursor over the first or the end point of the measurement path so that it would look like this.
2. Right-click the mouse and in the context menu select the **Add surface point** command.
3. Proceed with building the measurement path.
To add a new point to a path between two existing points, proceed as follows:

1. Hover the cursor over the place on the path where you want to add a point so that it would look like this.[hand]
2. Right-click the mouse and in the context menu select the *Insert surface point* command.
3. Drag the cursor over the screen. To fix the new point, click the mouse button.

To delete a point:

1. Locate the cursor on the point to be deleted so that it would look like this.[hand]
2. Right-click the mouse and in the context menu select the *Remove surface point* command.

The deletion of a single point does not lead to rebuilding the measurement path completely. Only the segment between the two neighboring points will be rebuilt.

To rebuild the edited measurement path, hover the cursor over the path or the text describing the path length so that it would look like this.[hand]. Right-click and select the *Rebuild the entire ruler* option in the context menu.

There are several ways to delete a measurement:

1. To delete an incomplete measurement, press Esc.
2. To delete a measurement path, hover the cursor over the path, a point, or the text describing the path length so that it would look like this.[hand]. Right-click and select the *Remove surface ruler* option in the context menu.
3. To delete all measurements, click the *Delete all Measurements* button on the toolbar. In the dialog box that appears, Click YES to delete or NO to cancel. If you want the DICOM Viewer to always delete annotations and measurements without this confirmation, check the box *Don't show this dialog again* and click YES. If you want the DICOM Viewer to show the confirmation dialog, check the box *Ask before deleting all annotations and measurements* (see Section 15.6.1).

The *Surface ruler* tool is also available from the model context menu and from the *Volume* main menu item. Activation is only possible with the left mouse button.

### 3.11.4 3D Angle

To measure an angle on the model:

1. Activate the *3D Angle* tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.
2. Make two points on the model clicking the mouse button. The second point is the angle apex.
3. Move the cursor over the screen to set the other side of the angle.

4. Click the mouse button to fix the second side of the angle.

5. To cancel an incomplete measurement, press Esc.

To move the 3D angle point:

1. Locate the cursor on the point to be moved.

2. Drag the point, holding the left mouse button.

To remove the 3D angle:

1. Locate the cursor on the line of the 3D angle to be deleted.

2. Right-click the mouse and select the Remove 3D angle command.

This tool is also available from the model context menu and from the Volume main menu item. Activation is only possible with the left mouse button.

### 3.12 Markers

Working with markers is mostly similar to the procedure described in Section 5.11. The differences are as follows:

- To drag a marker, locate the cursor on the circle in the middle of the marker. If the image scale is relatively small, the circle size may exceed the marker size.

- If the marker is on a surface currently hidden behind other tissues, only the circle in the middle of the marker will be visible, and the marker itself will be hidden. If you drag the marker, it will be moved to the model surface that is currently visible. The line marker in this situation is not visible.

### 3.13 Export Model

Functionality is available in the Pro edition

All the tabs may not fit in the box, in this case, scroll through the tabs, using the left and right arrows.

The export of a model to DICOM or to an image is similar to the image export described in Section 2.25.
3.13.1 Export Rotation to Series

To export a rotation to series:

1. Set the series description.
2. Specify the rotation axis (the default is Y).
3. Set the rotation angle (the default is 90 degrees).
4. Set the rotation step (the default is 5 degrees).
5. If you need to load the exported series to the server at once, check the option Upload exported series to the default server. If the default server is not specified in the DICOM Viewer this option will be inactive.
6. Specify the image size if necessary.
7. To export the rotation, click OK. To cancel, click CANCEL.

3.13.2 Export Rotation to Images

To export a rotation to images:

1. Set the path to the folder for export.
2. Enter the file name.
3. Select the file extension from the drop-down menu. Other parameters are described in the previous section.
4. To export the rotation, click OK. To cancel, click CANCEL.

This tool is also available from the Volume main menu item.

3.14 Render settings

The Render settings tool allows for setting the rendering quality of the 3D model and the opacity threshold. The tool is available on the toolbar of the Volume reconstruction tab, MPR reconstruction tab, Vessel analysis tab, Coronary arteries analysis tab and in the Volume section of the main menu. The tool allows you to set the quality of the model both in dynamic and static state.

The opacity threshold allows to ignore relatively transparent tissue when performing measurements and creating segments. That is, the tissue whose transparency level is below a predetermined value will be visible, but the points of the measuring tools will be projected on the tissue with a higher level of transparency. Such tissue will not be included in the segment.

To set quality:

1. Click on the Render settings button on the toolbar. The dialog shown in Fig. 3.10 will be displayed.
2. Move the sliders to set the quality of the model in dynamic state (Dynamic quality) and in static state (Static quality). Move the slider to the right for maximum quality.

3. Provide the opacity threshold value for measuring tools as percentage (the Point projection parameter). The ability to change the threshold value makes it easier to work with linear and angular measurement tools, markers and Select model point tool (Section 3.5).

The tools for editing the volume (Cut object, Cut all except object and Brush cut) delete the tissues whose opacity is below the threshold value. For details on volume editing tool management, see Section 3.8.

4. Provide the opacity threshold value in the Segmentation field. The value provided in this field affects the voxel opacity level in the Segmentation mode.

5. Click the CLOSE button.

![Render settings dialog box](image)

*Figure 3.10: Render settings dialog box*

If the quality is high, the update image may be delayed because of low computer resources.

### 3.15 Reconstruction by Series with Varying Distances between Slices

If a series contains images made with a varying step, volume reconstruction by the standard algorithm is impossible. There are two solutions to this problem.

1. The missing images are interpolated (recreated). In this case, the reconstruction will not be accurate. The DICOM Viewer will return a warning like Series slice distance varies too much: most unique distance: 7.5 mm; min distance: 7.5 mm; max distance: 22.5 mm. Model may be inaccurate.
2. The reconstruction is made within the part of the series where the distances between slices are the same. In this case the reconstruction will be incomplete. The DICOM Viewer will return a warning like Series slice distance varies too much. Only slices 1-22 of 28 are used.

The first method is used by default. For details on how to specify the preferable reconstruction method, see Section 15.6.3.

3.16 Remove Bone Tissue

3.16.1 Remove Bone Tissue Manually (Interactive)

Interactive bone tissue removal is performed by watershed method. To enable the interactive mode, click on the arrow on the right side of the Remove Bones button on the toolbar and check the Interactive box.

To remove bone tissue:

1. Open the series containing bone tissue in the volume reconstruction window.
2. Activate the Remove bones tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. The tool initiation process may take some time.
3. Set markers on the tissue that should not be deleted. To do that, click the mouse button with which the tool was activated on the tissue while holding the Ctrl button.
4. To delete bone and other tissue, click the mouse button with which the tool was activated on this tissue. The deletion process may take time.
5. To undo this action, click the Undo button; to redo the action, click the Redo button.

To set the tool parameters, click the arrow on the right-hand side of the Remove bones button and select Options....

3.16.2 Removing Bone Tissue Manually (Automatic)

You can remove the bone tissue for any series specifying the required parameters manually. To do that, you need to disable the interactive mode of the tool. Click the arrow on the right side of the Remove bones button on the toolbar and uncheck the Interactive box.

To remove bone tissue manually:

1. Open the series containing bone tissue in the volume reconstruction window.
2. Click the Remove bones button on the toolbar. A dialog box (Fig. 3.11) will pop up.
3. Set the **Min bones density (HU)** value in the dialog box. All tissues whose density exceeds this value will be deleted. If you set the minimum bone density value equal to the surface layer density, some tissues other than bones may be removed as well.

4. Set the **Grow bones (voxels)** value. This value allows you to set the thickness of the soft bone surface layer in voxels.

5. Click the **OK** button to remove bones or **CANCEL** to cancel.

6. As a result of the operation, bone tissues are removed. Other tissues adjacent to bone tissue, such as vessels, are not deleted.

   All these values should be adjusted experimentally. The default values are not optimum. To remove bone tissues with a lesser density, click the **Remove bones** button and reduce the minimum bone density value. If the value turns out to be too small, undo the last removal using the **Undo** button, and increase the minimum bone density value during the next removal.

   Some tissues that are different from bone structures may be deleted by mistake. This function should only be used as an auxiliary. The diagnosis should be established on the basis of the original images.

   This tool is also available from the **Volume** main menu item.

### 3.16.3 Remove Bone Tissue for Fused Series

**Functionality is available in the Pro edition**

This tool is used for angiographic and other studies containing at least one series with contrast and one series without it for the same body area.

To remove the bone tissue:

1. Fuse the series with contrast and without it in the **Series fusion** tab (see Chapter 4). The series fusion is stored in the local storage in the same study.
2. Open the fused series in the **Volume reconstruction** or **MPR reconstruction** tab. To do this click the or button on the toolbar or select the corresponding command in the **View** section of the main menu.

3. In the layer list select the series with contrast. By default, the first series is selected.

4. Click the **Subtract bones (Choose layer to subtract from first)** button on the toolbar.

   In the dialog box (Fig. 3.12) that opens, enter the name of the new series. By default, the new series is named `<Name of the first layer>(Bones subtracted)`. Under the name of the new series, the names of the layers for the created series are displayed. Click **OK** to create a new series or **CANCEL** to cancel. The process may take some time. Upon completion, a series without bones will appear on the series panel for this study.

   

   ![Figure 3.12: Creating a fused series for subtracting bones](image)

5. Go to the **Local storage** tab. Open the new series in the **Volume reconstruction** or **MPR reconstruction** tab. To do this click the or button on the toolbar or select the corresponding command in the **View** section of the main menu.

6. Change the current CLUT to the **CT-Bones** on the visualization setup panel (see Section 2.20).
Figure 3.13: The bone tissue has been removed

If required, edit the image removing bone tissue with editing tools.

Some tissues that are different from bone structures may be deleted by mistake. This function should only be used as an auxiliary. The diagnosis should be established on the basis of the original images.
Chapter 4

Series Fusion

There are certain peculiarities associated with fused series depending on the type of the rendering device:

- On a CPU-based renderer, the display of merged series may not be accurate in the Volume reconstruction tab.
- For the CUDA renderer, no more than four fused series may be displayed in the Volume reconstruction tab.
- For OpenCL and Metal rendering devices, no more than four fused series may be displayed in the Volume reconstruction tab and no more than eight fused series may be displayed in the MPR reconstruction tab.

4.1 Create Series Fusion

Functionality is available in the Pro edition

To create a series fusion:
1. Open the study.
2. Select the series.
3. Click the Series fusion button on the toolbar or select the View menu and the Series fusion item. The selected series can be found on the Slice list panel.
4. Select another series on the Available series panel.
5. Click the Add series as a new fusion layer button. If the series fusion is already open in the Multiplanar reconstruction or Volume reconstruction window, then the series will be also added in these windows.
4.2 Merge Series from Different Studies

Functionality is available in the Pro edition

To merge series from different studies:

1. Select the first study from the study panel.
2. Select one of the series from this study.
3. Click the Series fusion button on the toolbar or select the View menu and the Fusion item. The Series fusion tab will be opened.
4. Switch to the previous tab.
5. Select another study from the study panel.
6. Select the series to be merged with the selected series from the first study.
7. Drag the series to the Series fusion tab. The second series will be added to the slice list (Fig. 4.1).
8. To delete a slice, click the Remove fusion layer button or select the Fusion menu and the Remove layer item.
9. Set the visualization mode for the second slice (see Section 2.20.1).

The order of selecting series is important. The first (basic) series of images is located behind the second series in the flat image view window. The volume model is based on the first series, and even if the second series covers a larger volume of tissue, only those images are used in the reconstruction, the location of which is the same in both series, and the others are ignored.
Merged series can be opened in the Volume Reconstruction, Multiplanar Reconstruction and Virtual Endoscopy windows.

### 4.3 Merge layers

Functionality is available in the **Pro** edition

Fused layers do not always coincide, particularly in cases when two different studies are fused (Fig. 4.2). In this case, you need to merge layers.

To merge layers:

1. Open the fused series in the Multiplanar Reconstruction window by clicking the **MPR reconstruction** button on the toolbar.

2. In the Multiplanar Reconstruction tab, open the segmentation panel by clicking the **Segmented structure panel** button. There is the **Fusion of layers** panel at the bottom of the **Segmentation** panel (Fig. 4.3).

3. Select the layer which must be merged with the base one. If the selected layer has the same «FrameOfReferenceUID» tag value as any other layer, then you will see a **button on the **Fusion of layers**. You will find more information on merging layers with a locked system of coordinates in Section 4.3.1.
4. Merge layers automatically (see Section 4.3.2), manually (see Section 4.3.3) or by points (see Section 4.3.4).

![Figure 4.2: Not merged layers](image)

![Figure 4.3: Fusion of layers panel](image)

To reduce the **Fusion of layers** panel, click the **Hide** button. To expand the reduced panel, click the **Show** button.

To customize the fusion mode settings, click the **Options** button on the **Fusion of layers** panel. The respective dialog box is shown in Fig. 4.4.
4.3.1 Locking the Frame of Reference for a Layer

Functionality is available in the Pro edition

The position of series of the same study is normally specified in the same frame of reference. The identifier of the frame of reference is provided in the «FrameOfReferenceUID» DICOM tag. Series with the same «FrameOfReferenceUID» tag value have the same frame of reference.

If the selected layer has the same frame of reference as any other layer, you will see the button on the fusion of layers panel. This button is not shown for the first (basic) layer. When layers are fused, layers with a locked frame of reference change their position simultaneously with the other layers that have the same frame of reference. If a layer with a locked frame of reference has the same frame of reference as the basic (first) layer, it cannot be merged without unlocking.

To merge layers with a locked system of coordinates, proceed as follows:

1. Select the layer whose coordinate system you want to unlock for merging. You will see a button on the Fusion of layers panel.

2. Click the  button on the Fusion of layers panel. The button for a layer with unlocked coordinate system appears as .

3. Merge layers automatically (see Section 4.3.2), manually (see Section 4.3.3) or by points (see Section 4.3.4).

4. If needed, unlock the coordinate system of the other layers and merge again.
The frame of reference is locked and unlocked for each layer separately. Layers with an unlocked frame of reference can be moved independently. When you customize the position of layers with a locked frame of reference, it has no impact on the layers with an unlocked frame of reference.

To restore the original frame of reference for a layer, click the Lock layer frame of reference button on the fusion of layers panel. After unlocking, the layer restores the position it had before the Lock layer frame of reference button was pressed.

The settings concerning the position of layers and the information on locking are saved in the segmentation project (see Section 6.11.1) and when matrices are exported to DICOM (see Section 4.3.5).

4.3.2 Merge layers automatically

Functionality is available in the Pro edition

To merge layers automatically:

1. Click the Merge layers automatically button on the Fusion of layers panel (Fig. 4.3). This starts the merging process, the Optimizing correlation dialog will open.

2. To cancel the merging process, click the CANCEL button in the Optimizing correlation dialog.

3. When the merging process is completed, click the DONE button.

4. Merging quality can be poor if the tissue density on the merged layers is very different. In this case, check the Gradient correlation box on the Fusion mode settings dialog (see Section 4.3, Fig. 4.4) and repeat steps 1-3.

5. To change the merge accuracy, move the Accuracy of automatic fusion slider on the Fusion mode settings dialog (see Section 4.3, Fig. 4.4). Move the slider to the right for maximum quality. High accuracy requires more time to merge.

To merge layers by part of their volume:

1. Choose a layer you need to merge with the base layer.

2. Create a segmented structure for this layer. The mask of the structure should conform to the volume to be merged. The merge is performed by mask rather than by the created segmented structure volume.

3. Click the Merge layers automatically button.
4.3.3  Merge layers manually

Functionality is available in the Pro edition

To merge layers manually:

1. Activate the Manual layer fusion tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Match the images in three projections. To do this:
   - drag the selected slice, holding the left mouse button or pressing the cursor management keys and ;
   - rotate the selected slice, holding the Alt key and the left mouse button;
   - zoom the selected slice in and out, holding the Ctrl key and the left mouse button.

3. To cancel all transformations, click the Reset layer transformations button.

4. To cancel zoom, click the Reset layer zoom button.

5. To set the displacement step, set the desired value in the Keyboard move step field of the Fusion mode settings dialog box (see Section 4.3, Fig. 4.4).

6. When the slices are matched satisfactorily, close the MPR reconstruction tab. The Series fusion tab will reappear on the screen.

7. Browse the series fusion images to see the result. If the result is unsatisfactory, repeat the merging process.

4.3.4  Merge layers by control points

Functionality is available in the Pro edition

To merge layers by control points:

1. Make all the layers transparent except the base one. To do this, move the transparency slider for the MPR windows of the corresponding layer to the left. The transparency slider is highlighted in red in Fig. 4.5.

2. Select the base layer on the segmentation panel.

3. Activate the Mark the points tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.
4. Put at least three control points on the image. Each point has its own colour and number.

5. Select the layer that you want to fit with the base. Make all the layers transparent except this one.

6. Put on this layer the same number of control points in the same places as on the base layer. Point numbering starts over again. The colours of the corresponding points are the same.

7. If necessary, adjust the position of points on all three orthogonal planes. When you locate the cursor on a point, it is highlighted on all three orthogonal planes.

8. To delete point, locate the cursor on it, right-click the mouse and select the **Remove point** item.

9. To switch to slices containing a point, move the cursor to this point, right-click the mouse and select the **Go to point** item. The point on the current slice is brighter than others.

10. To delete all points, click on the **Remove all points** button on the **Fusion of layers** panel. In the dialog box that opens, click **YES** to confirm the deletion, or click **NO** to cancel.

11. To change the point diameter, open the **Fusion mode settings** dialog (see Section 4.3, Fig. 4.4). Set the diameter of the points.

12. Click on the **Fit layers by points** button on the **Fusion of layers** panel. The second layer will be moved in such a way that the corresponding points are as close to each other as possible.

13. If necessary, adjust the position of the points and repeat the previous step again.

14. If necessary, add the same number of points on all the layers.

![Control layer slider](image)

*Figure 4.5: Control layer slider*

Fig. 4.6 illustrates the example of control points location. Red dots (#1) are located on the tip of the nose, green (#2) on top, blue (#3) on the right eye.
Figure 4.6: Control points

If the points are set correctly, they match with little margin of error. If the points are set inaccurately, the result looks something like in Fig. 4.7.
4.3. MERGE LAYERS

Figure 4.7: Control points are matched with a large margin of error due to location errors

4.3.5 Export and Import Matrices of Merge Layers

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The DICOM Viewer exports and imports matrices of merge of layers into DICOM Spatial Registration IOD (modality REG).

To export merge of series, click the Export series registration to DICOM object button on the Fusion of layers panel (Fig. 4.3).

In the dialog box Export to DICOM Registration (Fig. 4.8) add the description of the exported merged series. By default, the series description is «Registration». Click OK button to export series or CANCEL to cancel.

Figure 4.8: The dialog box «Export to DICOM Registration»

The exported merged series will be saved in the local storage as a new series with REG modality. A thumbnail for the new series will be added to the series panel in the study containing the base layer.
To import a matrix merged layers:

1. Make a series fusion from the series for which the object was exported DICOM Registration. Pay attention to the order of the series selection. Select the first (base) layer.

2. Click the Import series registration from DICOM object button on the Fusion of layers panel (Fig. 4.3).

3. In the dialog box Import from DICOM Registration (Fig. 4.9) select a REG modality series to import. Click OK button to import series or CANCEL to cancel.

![Import from DICOM Registration dialog box](image)

*Figure 4.9: The dialog box «Import from DICOM Registration»*

The layers are merged relative to the first (base) layer.

### 4.4 Image registration

Functionality is available in the **Pro** edition

This function cannot be used for establishing a diagnosis

This tool allows you to deform the images so that their coincidence is maximal. If the inconsistencies of the series are too large (for example, the patient turned), you must first merge the layers manually or automatically (see Section 4.3) and then register the images.

If a study contains images with a varying density over time (for example, due to the introduction of contrast), then registration may not be performed correctly. To do this, exclude the tissue with varying density.

- Set the maximum value of the density for which registration is performed. In this case, the tissues with a density higher than the specified value do not participate in the registration, and their deformation is performed according to another algorithm.

- Check the **Use image gradient** in the Series registration settings dialog. This mode requires a large amount of video card memory. If the registration failed due to a lack of video card memory of the video card, turn off this mode or select a CPU(software) render device (see Section 15.6.3).
If the images contain air outside the patient’s body, then the density of such areas for CT examinations is usually less than or equal to -1024. It makes no sense to register these sections of images. Hence, for CT studies, the default minimum density value is -1023.

If the registration failed due to a lack of video card memory, select a CPU(Software) render device (see Section 15.6.3). In this case, the registration takes more time, but it is performed regardless of the amount of GPU memory.

### 4.4.1 Series registration

**Functionality is available in the Pro edition**

To register two series:

1. Create a fused series of at least two series.

2. Open the fused series in the Multiplanar Reconstruction window.

3. If the inconsistencies between the series are too large (for example, the patient turned over), you must first merge the layers manually or automatically (see Section 4.3). More accurate merging of layers enables faster registration.

4. Open the segmentation panel by clicking the Segmented structure panel button.

5. Select a base layer on the layers panel (fixed layer). Its images will not be changed.

6. Click the Volumes registration button. The dialog shown in Fig. 4.10 appears. If more than two series are fused, then the list from which you must select one series for registration (Choose moving series layer).
7. The **Output series description** field will be automatically filled in based on the name of the series being registered, and it will contain the «registered» mark. If necessary, change the description.

8. Select the desired registration options, checking the **Affine registration**, **Non rigid registration** and **Use image gradient** boxes.

9. Set the minimum size of the parts that will affect registration. The default size is 20 voxels. The smaller the value is, the more minor details are registered, but the risk of incorrect registration increases.
10. Set the percentage of voxels that are used during the registration. The larger the value is, the higher the accuracy is, but the lower the registration rate gets.

11. If it is necessary to perform registration for a specific range of densities, then set the minimum and/or maximum values. To do this, set the appropriate flag and enter a numeric value. If the flag is set, but the value is not set, then the OK button is unavailable. For CT series, the minimum default value is -1023.

12. Click OK to export the series or CANCEL to cancel. Registration may take a long time depending on the amount of RAM and the speed of the computer.

### 4.4.2 Phases registration

Functionality is available in the Pro edition

To register the phases of one series:

1. Open the multiphase series in the Multiplanar or Volume Reconstruction window.

2. Open the segmentation panel by clicking the Segmented structure panel button.

3. Click the Volumes registration button. The dialog shown in Fig. 4.11 appears.

4. The Output series description field will be automatically filled in based on the name of the series being registered, and it will contain the «registered» mark. If necessary, change the description.

5. Select the base phase that should not be changed (fixed phase).

6. Select the desired registration options, checking the Affine registration, Non rigid registration and Use image gradient boxes.

7. Set the minimum size of the parts that will affect registration. The default size is 20 voxels. The smaller the value the more minor details are registered, but the risk of incorrect registration increases.

8. Set the percentage of voxels that are used during the registration. The larger the value is, the higher the accuracy is, but the lower the registration rate gets.

9. If it is necessary to perform registration for a specific range of densities, then set the minimum and/or maximum values. To do this, set the appropriate flag and enter a numeric value. If the flag is set, but the value is not set, then the OK button is unavailable. For CT series, the minimum default value is -1023.

10. Click OK to export the series or CANCEL to cancel. Registration may take a long time depending on the amount of RAM and the speed of the computer.
Figure 4.11: Phases registration settings dialog
4.5 **Actions with the fused series**

Functionality is available in the **Pro edition**

Action buttons on the toolbar:

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="rotate" /></td>
<td>The <strong>Rotate</strong> tool is described in Section 2.14</td>
</tr>
<tr>
<td><img src="image" alt="zoom" /></td>
<td>The <strong>Zoom</strong> tool is described in Section 2.14</td>
</tr>
<tr>
<td><img src="image" alt="pan" /></td>
<td>The <strong>Pan</strong> tool is described in Section 2.14</td>
</tr>
<tr>
<td><img src="image" alt="adjust-wl" /></td>
<td>The <strong>Adjust W/L</strong> tool is described in Section 2.15</td>
</tr>
<tr>
<td><img src="image" alt="ruler" /></td>
<td>The <strong>Ruler</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="angle" /></td>
<td>The <strong>Angle</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="cobb-angle" /></td>
<td>The <strong>Cobb angle</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="point-value" /></td>
<td>The <strong>Point value</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="roi-rectangle" /></td>
<td>The <strong>ROI rectangle</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="roi-ellipse" /></td>
<td>The <strong>ROI ellipse</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="roi-polygon" /></td>
<td>The <strong>ROI polygon</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="delete-all" /></td>
<td>The <strong>Delete all annotations and measurements</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td><img src="image" alt="export" /></td>
<td>The <strong>Quick export images</strong> tool is described in Section 2.25</td>
</tr>
<tr>
<td><img src="image" alt="add-to-print-list" /></td>
<td>The <strong>Add to print list</strong> tool is described in Section 17</td>
</tr>
</tbody>
</table>
4.6 Image stitching mode

Functionality is available in the Pro edition

If a study contains several series that are the results of scanning sections of an extended area, then such series can be fused into one in the «stitching» mode. The mutual arrangement of images from different series is determined automatically according to the scanner data.

To «stitch» images:

1. Open the study containing the series that need to be «stitched» in the series fusion window.

2. Make a series fusion. If the image does not fit in the window, use the image positioning tools Zoom and Pan (see Section 4.5).

3. Click the Image stitching mode button on the toolbar. The image will change as shown in Fig. 4.12 (the right-hand image is the image after «stitching»).

![Image of a spine with an arrow pointing to a change in the stitching mode]

Figure 4.12: Changes in the «stitching» mode (the right-hand image is the image after stitching)

In the «stitching» mode, the Adjust W/L tool applies to the entire series.
4.7 Volume Stitching

Functionality is available in the Pro edition

This function cannot be used for establishing a diagnosis

The DICOM Viewer provides an opportunity to export several fused series to the current study as a new series. The fused series will be stitched as one layer.

To export a fused series to the current study as a new series, proceed as follows:

1. Open the series in the MPR reconstruction tab.

2. Click the Export button on the segmented structure panel and select the Export volume stitching option on the dropdown menu (Fig. 4.14).
3. In the **Volume stitching options** (Fig. 4.15) dialog box that pops up, add a description of the series created. By default, the description is generated automatically according to the following template:

   *stitching of <description of the 1st layer series> and ... <description of the N layer series>*

4. Specify the position and the boundaries of the exported area in the coordinates of the voxel model of the first (basic) layer. The size of the exported area will be calculated automatically and may be changed by the user. The position and the boundaries of the exported area are shown in the windows of the **MPR reconstruction** tab and may be changed when editing the numeric values.

   The acceptable range of values for the coordinates of the exported area position is from -8192 to 8192, for the coordinates of the boundaries — from 1 to 8192.
4.7. VOLUME STITCHING

The boundaries of the exported area along the X and Y axes are determined by the volume of the basic layer.

5. Click OK to stitch the layers of the fused series and export the new series to the current study, or click CANCEL to cancel. The stitching and export procedure may take some time.

Make sure that all the volume required has been exported.

The exported series is saved in the local storage as a new series. A thumbnail for the new series will be added to the series panel.

If one or several original series are multiphase series, the stitching and export procedures are only performed for the current phase.
Chapter 5

Multiplanar Reconstruction (MPR)

In Multiplanar Reconstruction window, diagnosis can only be established on the basis of CT, MR, XA and MG series

5.1 Open Study in Multiplanar Reconstruction window

To open a study in the multiplanar reconstruction window:

1. Load the studies to the DICOM Viewer.

2. Select the target study from the study panel.

3. Click the MPR reconstruction button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open the multiplanar reconstruction window in a new tab in the current window, click on the button. The process may take some time.

Fig. 5.1 illustrates the multiplanar reconstruction window.
5.2 MPR View Elements

The tab will display three image view windows. The top left window displays the axial section, the right window shows the coronal section, the bottom left window contains the sagittal section.

To maximize any cutting plane window from the MPR reconstruction tab and restore its size, proceed as follows:

- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.

To maximize window **3D view** from the MPR reconstruction tab and restore its size, proceed as follows:

- double-click with the left mouse button on the series window;
- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.

If some tool, such as the tool for measurements or render annotations, has been activated with the left mouse button, you can expand a window or restore its size in two ways:

- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.
CHAPTER 5. MULTIPLANAR RECONSTRUCTION (MPR)

The DICOM Viewer allows you to move the borders between the image view windows. To do it, locate the cursor on the border so that it would look like ⬇️ or ⬆️, and drag the border, holding the left mouse button. You can set the priority of the image view window borders (see Section 15.6.1). For details, on how to save the image view window configuration, see Section 15.6.3.

The top part displays the toolbar on the left (Fig. 5.2) and the image setup panel on the right (Fig. 5.3).

![Toolbar](image1)

*Figure 5.2: Toolbar*

![Image setup panel](image2)

*Figure 5.3: Image setup panel*

To open a study in the **3D view** window of the **MPR reconstruction** tab, click the **3D** button on the toolbar. A **3D view** window will pop up, in which you will see a 3D model and a standard space orientation panel (for details see Section 3.3).

5.3 **Resampling filter**

To change the Resampling filter, open the **MPR** main menu, select the **Resampling filter** menu item and in the submenu that opens, select a filter. The active filter is marked with a flag.

The following filters are available:

- Bilinear;
- B-spline;
- Mitchel;
- Catmull-Rom;
- Lanczos3;
- Lanczos5;
- Lanczos7.

By default the Bilinear filter is active.

> **When filters are used (except for the Bilinear filter), distortions may occur. If you see any dubious artifacts, select the Bilinear filter.**

232
5.4 Working with Orthogonal Planes

5.4.1 View Modes

Click the Switch navigation mode button and select one of the three view modes:

1. The 3D cursor mode. It allows you to drag and rotate orthogonal cutting planes using the mouse. The Switch navigation mode button will look as follows:

2. The on click 3D cursor mode. It allows you to move orthogonal cutting planes similarly to the 3D cursor mode, but the plane lines are visible only during the dragging (while the left mouse button is pressed). The Switch navigation mode button will look as follows:

3. The planes cursor mode. The cutting planes are displayed permanently. Their moving is described in the next section. The rotation of planes is similar to the 3D cursor mode and is described in Section 5.4.2. The Switch navigation mode button will look as follows:

In all the view modes the current plane can be moved in several ways:

- Scroll the mouse wheel. If you scroll the wheel forward, the plane will withdraw, if you scroll it backward, the plane will move nearer. One click of the mouse wheel changes the plane position by the distance equal to the thickness of the slice from the initial series.

- By se the scrollbar on the right side of the section view window to move the section.

- Use the Scrolling tool. Activate the tool on the toolbar by clicking the left/right/middle mouse button and move the cursor up to withdraw the plane or down to move it nearer, holding down the button with which the tool was activated. To learn more about tool control, see Section 1.14.

5.4.2 Working with Planes in 3D Cursor Mode

To move orthogonal planes, click the left mouse button at the point you want to move the planes to, or move the mouse, holding the left button. When the button is released, the position of the planes is fixed. To rotate a plane while maintaining orthogonality:

1. Locate the cursor on the radial bidirectional arrow on the plane line (see red arrows in Fig. 5.4). The bidirectional arrow will be highlighted.

2. Move the cursor, holding the left mouse button to rotate the plane by the required angle. The images on the other planes will change.

3. Release the left mouse button to fix the current position of the plane.
To rotate a plane without maintaining orthogonality, follow the steps above, holding the \texttt{Shift} key while performing the step 2.

To undo the rotation of all planes, click the \texttt{Undo rotation} button on the toolbar.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{image.png}
\caption{Rotate an orthogonal plane}
\end{figure}

\textbf{Note that all the other view changes will be undone as well.}

\section*{5.4.3 Working with Planes in the Cutting Plane Mode}

The DICOM Viewer allows you to move planes one by one in the image view modes. To do this:

1. Locate the cursor on the plane line to highlight it.

2. Move the line, holding the left mouse button.

Scroll the images in some window to see how the target plane is moving in the other windows.

For convenience, zoom the image in and out by rolling the mouse wheel, holding the \texttt{Ctrl} key.

There are two ways to move images in the window for viewing cutting planes:

1. Move the mouse holding the wheel and the \texttt{Shift} key on the keyboard. This key combination is set by default. You can disable or change the setting in the Controllers tab of the Image viewer module (see Section 15.6.1).

2. Activate the Pan tool on the toolbar by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn
more about tool control, see Section 1.14. To move an image, move the cursor around the screen while holding down the mouse button.

This tool is also available from the image context menu and from the MPR main menu item.

5.5 Series Synchronization in MPR Reconstruction Tabs

Series synchronization is used for viewing series of one or several studies simultaneously. The opportunity to compare series created at different times allows the user to evaluate the changes and improves diagnostic accuracy. Series can be compared in MPR reconstruction tabs.

To compare series, open them in MPR reconstruction tabs. The tabs may:

- be placed in the main program window or be unattached to it;
- be placed on the same or on different monitor screens. The monitors may be different in size and have different settings (e.g. scaling, resolution, brightness, contrast etc.).

To enable synchronization, click the Sync series button. Synchronization provides the user an opportunity to change window width and level (W/L) settings, move, scale and scroll images from different series in section plane windows. Synchronization is disabled by default. If synchronization is enabled and the user opens a new tab, the new tab will be synchronized with the one that was opened earlier.

To set synchronization types and modes, proceed as follows:

1. Click the arrow on the right-hand side of the Sync series button on the toolbar.
2. Select the synchronization types and modes from the drop-down menu (Fig. 5.5):

   - Sync planes. Planes and rotation angles of orthogonal planes are synchronized in MPR reconstruction tab windows (Axial plane, Coronal plane and Sagittal plane). Other MPR reconstruction tab windows are not synchronized;
CHAPTER 5. MULTIPLANAR RECONSTRUCTION (MPR)

– in the **By patient coordinates** mode, synchronization is only performed for series with the same `frameOfReferenceUid` tag value. If synchronization is enabled, the orthogonal planes of the new tab are synchronized with the planes of the tab that was opened earlier;

– in the **Manual** mode, synchronization is performed for series with different `frameOfReferenceUid` tag values. In this case, the same changes regarding scrolling the synchronized and the synchronizing viewer window will be applied in the patient's coordinate system. Planes in synchronized windows will be turned around the line of intersection of orthogonal planes through the same angle;

**Sync W/L.** Changes in the window width and level (W/L) will be synchronized for series with the CT modality. For series with other modalities, synchronization will only be performed if the modalities of the series and the recommended width and level (W/L) values are the same. Series with different modalities cannot be synchronized. The chosen mode has no impact on this synchronization type.

If synchronization has been enabled, the window width and level (W/L) values of the tab opened will be synchronized with those of the tab that was opened earlier. Merged series are synchronized layer by layer. Layers are synchronized by their respective numbers (the first layer is synchronized with the first one, the second layer is synchronized with the second one etc.);

**Synk zoom and position.** The scaling and position changes are synchronized in **MPR reconstruction** tab windows (Axial plane, Coronal plane, and Sagittal plane). Other **MPR reconstruction** tab windows are not synchronized. Merged series are synchronized on the basis of the data for the first layers of the series. This synchronization type functions differently depending on the mode chosen.

– in the **By patient coordinates** mode:
  * synchronization is only performed for series with the same `frameOfReferenceUid` tag value;
  * the actual image size is taken into account. For sections of the same size, objects are displayed in the same way;
  * window centers are synchronized. In the window center, the user sees the projection of the center point of the synchronizing window on the synchronized window section;
  * if synchronization is enabled, the scale and the position of the image in the new tab will be synchronized with the scale and the position of the image in the tab that was opened earlier;

– in the **Manual** mode:
  * the actual image size is taken into account. For sections of the same size, objects are displayed in the same way;
  * if the position of the synchronizing window center is changed, the position of the synchronized window center is changed accordingly;
  * if synchronization is enabled, the scale of the new tab will be synchronized with the scale of the tab that was opened earlier. The position will be synchronized in compliance with the changes in the synchronizing section position;
• **Sync phases.** The image phases are synchronized by number. If the phase number for the synchronizing series is greater than the total number of phases in the synchronized series, then the phase with the greatest number will be selected for the synchronized series. This synchronization type does not depend on the chosen mode.

## 5.6 Curvilinear Reconstruction

### 5.6.1 Build Surface

**Functionality is available in the Pro edition**

Curvilinear reconstruction is a section of tissues by a curvilinear surface whose configuration is set by the trajectory passing through the middle of this surface. This trajectory is called a **curve**.

To activate the Curvilinear reconstruction mode, click the **Curve mode** . To get back to the **Multiplanar reconstruction** mode, click the **Curve mode** button again. The curve built in the **Curvilinear reconstruction** mode is not shown in the **MPR reconstruction** mode.

To build a surface:

1. Select the plane in which it would be convenient to start building a curve.
2. Roll the mouse wheel to select the slice where the first point will be located.
3. Fix the first point on the image by clicking the left mouse button.
4. If necessary, move to another slice by rolling the mouse wheel.
5. Move the mouse to select the location of the next point. Fix the point by clicking the left mouse button. The point will appear in the current slice.
6. Repeat Steps 4 and 5 until the last but one point is fixed.
7. Fix the last point by left-clicking the mouse twice. While building the curve, the current section will be displayed in the bottom right-hand window. The other windows will display the projections of the curve on the corresponding planes ((Fig. 5.6)).
8. If necessary, correct the projections of the curve on the two other planes. For details on how to correct, see the section **5.6.4.**
To maximize any cutting plane window from the MPR reconstruction tab and restore its size, proceed as follows:

- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.

To maximize window Involute from the MPR reconstruction tab and restore its size, proceed as follows:

- double-click with the left mouse button on the series window;
- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.

If some tool, such as the tool for measurements or render annotations, has been activated with the left mouse button, you can expand a window or restore its size in two ways:

- double-click with the left mouse button on the title of the series window;
- click on the **Expand** button in the right-hand upper corner of the series window.
5.6.2 Choosing a Display Mode for an Involute of a Curve

Functionality is available in the Pro edition

Click the arrow on the right-hand side of the **Curve mode** button and choose the display mode for the involute of the curve from the button menu (Fig. 5.7). The current mode is ticked.

![Figure 5.7: Curve mode button menu](image)

- **Straightened involute.** The mode is set by default. In the straightened involute curve window (Fig. 5.8), the curve built by the user is transformed into a straight line. The distortions of space along the curve are marginal and increase with distance from the curve. We recommend this mode when the region of interest is placed near the curve. This option provides for the highest possible level of detail along the curve.

![Figure 5.8: Straightened Involute curve mode](image)

- **Involute curve in orthogonal planes** (Fig. 5.9). Unlike the **Straightened involute** mode, this mode provides for a lower distortion degree at a distance from the curve, but the
level of detail along the curve is also lower. Unlike the **Involute curve from first to last point**, this mode is less dependent on the position of points on the curve. It is used when you need an involute similar to an orthogonal projection. The orthogonal projection is chosen automatically to provide for the highest possible level of detail along the curve. Still, the level of detail along the curve is lower compared to other curve modes.

![Involute curve in orthogonal planes](image)

*Figure 5.9: Involute curve in orthogonal planes*

- **Involute curve from first to last point** (Fig. 5.10). Compared to the **Straightened involute** mode, the distortion degree at a distance from the curve is lower, but the level of detail along the curve is also lower. The involute is highly dependent on the position of the first and the last point on the curve. The level of detail along the curve is greater than in the **Involute curve in orthogonal planes** mode.

![Involute curve from first to last point](image)

*Figure 5.10: Involute curve from first to last point*

The selected curve mode will be applied the next time the **Curvilinear Reconstruction** mode is activated.
5.6. CURVILINEAR RECONSTRUCTION

In the **Straightened involute** mode, the **Ruler**, **Polygonal Ruler**, **Angle**, and **Kobb angle** tools cannot be used in the window with the involute.

### 5.6.3 Curve settings

**Functionality is available in the Pro edition**

The parameters of the curve can be set in the **Curve options** dialog box (Fig. 5.11). The appearance and the functions of the **Curve options** dialog box depend on the way you call for it. There are two ways to call for the **Curve Options** dialog box:

1. Click the arrow on the right-hand side of the **Curve mode** button on the toolbar and then select **Default curve options...** from the button menu. You will see the dialog box shown in Fig. 5.11a.

2. Right-click on the curve or a point on the curve and select **Curve options...** from the menu that pops up. You will see the dialog box shown in Fig. 5.11b.

![Figure 5.11: Curve options dialog box](image)

You can set up the following parameters:

- **color**;

- **line width** in pixels;
• **point radius** in pixels.

Setting the curve visibility mode:

• **Always.** When the curve is being built, it is shown in all the windows of the tab with plane projections, as well as in the involute window. After the curve has been built, it is always shown in all the windows of the tab with plane projections, as well as in the involute window. This mode is set by default.

• **Do not display on the involute.** When the curve is being built, it is shown in all the windows of the tab with plane projections, except for the involute window. After the curve has been built, it is always shown in all the windows of the tab with plane projections, except for the involute window.

• **Hover.** When the curve is being built, it is shown in all the windows of the tab with plane projections, as well as in the involute window. After the curve has been built, it is shown in all the windows of the tab with plane projections, as well as in the involute window if the cursor is placed on the curve.

• **Never.** When the curve is being built, it is shown in all the windows of the tab with plane projections, as well as in the involute window. After the curve has been built, it is hidden. Choose another visibility mode to see the curve.

If you open the **Curve options** window from the **Curve mode** button menu (Fig. 5.11a), the settings will always be applied to the curve by default.

If you tick the **Set as default** box in the **Curve options** dialog window opened from the curve context menu (Fig. 5.11b), the settings will be applied by default when a curve is built.

To apply the settings, click **OK**. To cancel, click **CANCEL**.

### 5.6.4 Actions with a Curve

*Functionality is available in the Pro edition*

Actions with a curve can be performed only if the curvilinear reconstruction mode is active. The following actions are available:

• Drag a point. Locate the cursor on the point so that it enlarges, and drag the point holding down the left mouse button or the button to which this tool is assigned. Then release the mouse button.

• Add a point. Locate the cursor on the curve where the point should be added. Right-click the mouse and select the **Add point** item.

• Delete a point. Locate the cursor on the point. Right-click the mouse and select the **Remove point** item.

• Continue a curve. Locate the cursor on one of the border points of the curve. Right-click the mouse and select the **Resume curve** item. Then, perform Steps 3 and 4 of the curve building algorithm.

• Delete a curve. Locate the cursor on any position on the curve or on a point. Right-click the mouse and select the **Remove curve** item.
5.6.5 Position of a Curve, Its Nodes and Surface in Space

By the color of the curve, you can determine which part of the curve is located in front of the current image in space. This part of the curve is brighter than the part behind the image.

In Fig. 5.12, the central part and the third point are a brighter color. This means they are located in front of the current section.

![Figure 5.12: Reconstruction by a curve](image)

To make it easier to find a node on the curve on all the projections, locate the cursor on this node. The node will be magnified on all the projections.

To rotate the surface relative to the curve, move the cursor to the bottom right-hand window (Surfase by curve) and roll the mouse wheel.

To move the cutting planes to the selected point of the curve, move the mouse cursor to the selected point on the curve in the selected window. Left-click while holding down the Ctrl key on the keyboard. The point of intersection of the cutting planes is moved to the specified point on the curve in all the windows.
5.6.6 Curved Reconstructions Cross Sections Mode

Functionality is available in the Pro edition

The curved reconstruction cross section mode is aimed for viewing the planes that are perpendicular to the curve and evenly spaced.

You can view curve slices if Curvilinear reconstruction mode is activated and a curve has been built. To activate the Curvilinear reconstruction mode, click the Curve mode button.

To select the window arrangement template, click the arrow on the right-hand side of the button or the Switch layout template button and choose one of the options provided (see Figure 5.13):

![Switch layout template](image)

Figure 5.13: Switch layout template

- **Curve 2x2.** In the MPR reconstruction tab, you see three windows with multiplanar reconstruction cutting planes and a Involute window. This mode is selected by default.

- **Curve slices 1x2.** The tab is divided into two windows. The Involute window is placed at the top, and the Curve slices window is at the bottom.

- **Curve slices 2x1.** The tab is divided into two windows. The Involute window is placed on the left-hand side, and the Curve slices window is on the right-hand side.

- **Curve slices 2x2.** The tab is divided into four windows. The Axial projection and the Volume reconstruction windows are placed on the left-hand side, while the Involute and the Curve slices windows are placed on the right-hand side.

The window arrangement template settings will be applied next time you choose the Curve mode.

To maximize any cutting plane window from the MPR reconstruction tab and restore its size, proceed as follows:

- double-click with the left mouse button on the title of the series window;
- click on the Expand button in the right-hand upper corner of the series window.
5.6. CURVILINEAR RECONSTRUCTION

To maximize windows **Involute, 3D view** and **Curve slices** from the **MPR reconstruction** tab and restore their size, proceed as follows:

- double-click with the left mouse button on the series window;
- double-click with the left mouse button on the title of the series window;
- click on the Expand button in the right-hand upper corner of the series window.

If some tool, such as the tool for measurements or render annotations, has been activated with the left mouse button, you can expand a window or restore its size in two ways:

- double-click with the left mouse button on the title of the series window;
- click on the Expand button in the right-hand upper corner of the series window.

If you see the **Volume reconstruction** window or the segmentation panel in the tab, the volume editing tools are available.

![Figure 5.14: Curve slices 2x2 mode](image)

In the **Involute** window, a straightened curve and perpendicular cutting planes projections are shown. When you mouse over a cutting plane in the **Involute** window, the respective plane and projection will be highlighted. The point in which the cutting plane crosses the curve will be marked with a crosshair in the slices window.

To rotate the surface round the curve, mouse over the **Involute** window and scroll the mouse wheel or move the slider in the slices window.

To move the cutting planes along the curve, mouse over the slices window and scroll the mouse wheel or move the slider in the slices window.

To move the cutting planes automatically, activate the Play tool (see Section 5.9).
To set the curve slices parameters, click the arrow on the right-hand side of the button or the **Switch layout template** button and choose the **Curve slices options...** (Figure 5.15).

*Figure 5.15: Activating the dialog box for curve slices properties*

A dialog box will pop up (Fig. 5.16), in which you can set the following parameters:

- the size of the slices window grid. Choose the suitable number of rows and columns (5x2 or 3x3);
- the distance between slices (in millimeters);
- the scrolling increment. Choose one of the two variants: **Auto** (the increment is equal to one voxel) or specify the increment in millimeters;
- the color of the cutting plane lines;
- the thickness on the cutting plane line and the crosshair in pixels;
- the color of the selected cutting plane line and the frame of the slices window;
- the crosshair space in pixels. Set the distance from the lines forming the crosshair to its virtual center;
- the size of the crosshair in pixels.

If you have checked the **Set as default** box, these settings will be used by default when you switch to the Curve slices mode.
5.6. CURVILINEAR RECONSTRUCTION

There are two ways to activate the Curve slices options dialog box from the right-click menu:

1. Mouse over one of the cutting planes in the Involute window. Right-click and choose Set curve slices options...

2. Mouse over the crosshair of one of the slices in the slices window. Right-click and choose Set curve slices options...

Rotate, Zoom, Pan and Adjust W/L tools are simultaneously activated for all the slices.

DICOM Viewer records videos, exports and prints images from the Involute window or the slices window, whichever is active.

In the slices window, only the image from the top left-hand cell will be printed. To print or export the slice you need, move the cutting planes along the curve, so that the slice you need appears in the top left-hand cell. You can move the cutting planes by scrolling your wheel or moving the slider in the slices window.

In the slices window, video is recorded for the top left-hand cell. To record a video for the slice you need, move the cutting planes along the curve, so that the slice you need appears in the top left-hand cell.

To record a video, activate the Start video record tool (see Section 5.10).

To escape from the curve slices mode, click the Curve mode button.
5.7 Displaying Section Planes on 3D Models

The MPR planes on 3D view tool is used for setting up and displaying section planes on 3D models in the 3D view window.

The tool is available on the toolbar in MPR reconstruction, Vessel analysis and Coronary arteries analysis tabs only when a 3D reconstruction is displayed in the 3D view window. In the Fig. 5.17, you can see an example of section planes displayed on a 3D model in the 3D view window of the MPR reconstruction tab.

![Figure 5.17: Section planes displayed in the 3D view window](image)

To enable the mode for displaying section planes, click the MPR planes on 3D view button on the toolbar.

The tool is only available when a 3D reconstruction is displayed in the 3D view window. To enable the 3D reconstruction display mode, click the 3D button on the toolbar.

To enable the planes display, click the arrow on the right-hand side of the MPR planes on 3D view button and select the display mode on the button menu (see Fig. 5.18):
5.7. DISPLAYING SECTION PLANES ON 3D MODELS

Figure 5.18: MPR Planes on the 3D View button menu

**Planes of open windows.** In the 3D view window, the section planes that are shown in the open windows of the tab are displayed. This mode is enabled by default.

To enable the display of certain cutting plains, disable the **Planes of open windows** mode. You can enable the display of the following planes:

- **Axial plane**;

- **Coronal plane**;

- **Sagittal plane**;

- **Curved surface**[^PRO]. A curvilinear surface may be displayed in the 3D view window after a curve is built (see Section 5.6.1). On the curvilinear surface plane, the centerline is shown in dark red;

- **Curved slice plane**[^PRO]. The curve slices are displayed when the curve slices window is opened for the first time (see Section 5.6.6). In the 3D view window, the plane of the first slice is displayed.

All the planes are displayed by default.

**Borders of the planes.** The mode is used to enable/disable the display of borders of the cutting planes on a 3D model. The display of borders of the planes is enabled by default.

**Transparency settings.** In the dialog box that pops up (Fig. 5.19), move the slider to set up the planes transparency. The extreme right position equals maximum opacity. The maximum opacity level is set by default.
Planes transparency is not supported:

- if the CPU has been chosen as the visualization device;
- if the program is installed on Linux;
- if the program is installed on macOS and any device different from Metal is used as the visualization device.

To make the background visible, uncheck the **Transparent background** box. The box is checked by default. To close the transparency settings dialog box, click the **CLOSE** button.

![Figure 5.19: Dialog box for setting cutting planes transparency](image)

The colors of the plane borders are the same as the colors of the windows of the respective
cutting planes. On the curvilinear surface plane, the centerline is shown in dark red. The borders of the curve slice plane are shown in blue.

5.8 «Render settings» Tool

The Render settings tool allows for setting the rendering quality of the 3D model and the opacity threshold in the 3D view window. The tool is available on the toolbar only when a volume reconstruction is displayed in the 3D view window. The operation of the tool is described in Section 3.14.

To enable the volume reconstruction mode, click the 3D button on the toolbar of the MPR reconstruction tab.

5.9 The Play Tool

The DICOM Viewer allows you to automatically play slices and phases in the MPR View windows and the Volume Reconstruction window. To configure the playback, click the arrow on the right side of the Play button and specify the necessary parameters in the button context menu.

1. If the series contains several phases, then the DICOM Viewer allows you to switch between the slice and phases playback. To switch select the Play phases or the Play slices item from the Play button context menu. The selected item is marked with a flag. Only the items suitable for this series are available in the context menu.

2. Select the speed (5, 10, 20 or 25 frames per second). If you want to set a different playback speed, select the User defined... item and in the dialog that opens set the value from 1 to 100. The selected speed will be marked with a flag.

3. If you want to play phases and slices cyclically, select the Loop item. The item will be marked with a flag. To disable the cyclic playback, select this command again. The flag will be removed.

To start playback, click on the Play button on the toolbar. During playback, the button looks like . To end playback click the button.

5.10 Video recording

Functionality is available in the Pro edition

The DICOM Viewer allows you to record video for the volume model view window. The following objects will be recorded:

- tissues;
• measurements;
• annotations;
• markers;
• tags;
• orientation cube;
• the Select model point tool label.

The other features of the tool in the MPR View windows are similar to those described in Section 2.13 and the features in the Volume Reconstruction window are similar to those described in Section 3.7.

5.11 Markers

5.11.1 General

A marker is a point, line or polygonal line in space, associated with a model. The DICOM Viewer allows you to display the length of the marker line and the polygonal marker line and the angles of the polygonal marker line.

The following tools are used to add markers: Marker, Line marker and Polygonal Line marker. To select one of these tools, click on the arrow on the right side of the tool selection button. The button will look different depending on the selected tool:

<table>
<thead>
<tr>
<th></th>
<th>Marker (selected by default)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Line marker</td>
</tr>
<tr>
<td></td>
<td>Polygonal Line marker</td>
</tr>
</tbody>
</table>

Activate/deactivate the currently selected tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

The added markers are located in the displayed slice.

5.11.2 Add Markers

To add a marker as a point:

1. Activate the Marker tool by clicking the button on the toolbar.

2. Mark a place on an image by clicking the left mouse button. The marker will appear in all three windows.
After adding all the markers, deactivate the **Marker** tool. This tool is also available from the image context menu and from the **MPR** main menu item. Activation is only possible with the left mouse button.

### 5.11.3 Add Line Markers

To add a Line marker:

1. Activate the **Line marker** tool by clicking on the button on the toolbar. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. A marker line can be built in two ways:
   
   - Mark the first point by clicking the mouse button. If required, go to the next section by rotating the mouse wheel. Move the cursor over the screen to the second point of the marker line. To fix the current point, click the mouse button.
   
   - Click the mouse button at the first point of the marker line and move the cursor to the endpoint while holding the mouse button. To go to the next section, rotate the mouse wheel while holding the mouse button. To fix the endpoint, release the mouse button.

3. To cancel an incomplete addition, press **Esc**.

When building a marker line, the start and the end points are chosen on the selected sections. This allows for performance of measurements between the points placed on different sections. You can tell by the color of the marker line which part of it is in front of the current image. This part of the line will be brighter than the part placed behind the image (see Fig 5.21).

After adding all the line markers, deactivate the **Line marker** tool. This tool is also available from the image context menu and from the **MPR** main menu item. Activation is only possible with the left mouse button.

Length measurements made with marker lines are saved in a file project.

### 5.11.4 Polygonal Marker line

To add a Polygonal Marker line:

1. Activate the **Polygonal Line marker** tool by clicking on the button on the toolbar.

2. Roll the mouse wheel to select the slice where the first point will be located.

3. Mark a point by clicking the mouse button.

4. If necessary, move to another slice by rolling the mouse wheel.

5. Move the mouse to select the location of the next point. Fix the point by clicking the mouse button.

6. Repeat steps 4 and 5 until the last but one point is fixed.
7. Fix the last point by double-clicking the mouse.

8. To cancel an incomplete addition, press Esc.

When building a polygonal marker line, the start and the end points, as well as the intermediate points, are chosen on the selected sections. This allows for performance of measurements between the points placed on different sections. You can tell by the color of the marker line which part of it is in front of the current image. This part of the line will be brighter than the part placed behind the image (see Fig 5.21).

After adding all the polygonal line markers, deactivate the Polygonal Line marker tool. To continue the polygonal marker line, move the cursor to the end point of the line, right-click and select the Continue line item. This tool is also available from the image context menu and from the MPR main menu item. Activation is only possible with the left mouse button.

The length and angle measurements made with polygonal marker lines are saved in the project file.

### 5.11.5 Actions with Markers

The following actions are available:

- Drag a point or line and polygonal line marker points. Locate the cursor on the marker or point so that it would look like \[ \text{\text{hand}} \], and drag it, holding down the left mouse button or the button to which this tool is assigned. The location of the marker will change accordingly in all the windows. The marker will be moved parallel to the displayed slice.
- Remove. Locate the cursor on the marker so that it would look like \[ \text{\text{trash can}} \], right-click the mouse and select the Remove marker item.
- Remove all the markers. If you need to delete all the markers, locate the cursor on any marker so that it would look like this: \[ \text{\text{trash can}} \], right-click the mouse and select the Remove all markers item or select the corresponding item from the Marker tool menu.

### 5.11.6 Marker Properties

You can set the following properties:

- **Text**;
- **Diameter** or **Line width**;
- **Color**;
- **Show length** (for Line Markers);
- **Show angle** (for Polygonal Line Markers).

To set properties for previously added marker, locate the cursor over the marker, right-click and select the **Set marker properties...** item.

To set the default marker properties, click the arrow on the right side of the **Marker** button and select one of the **Default marker options...**, **Default marker line options...** or **Default marker polygonal line options...** items.
5.11.7 Position of Markers in Space

If the marker is in or near the current slice, it is displayed as a circle; otherwise, it is displayed as a ring with a dot in the center. The further the marker slice is from the current slice, the darker the marker is.

You can determine how the marker line is located relative to the plane of the current image, judging by the color of the marker line. The line (or its part) located in front of the plane is brighter than the line (or its part) behind the plane. In Fig. 5.21, the bottom part of the line is located behind the image.

![Figure 5.21: Position of Line Marker in Space](image)

5.12 Reconstruction Modes. Slice Thickness

5.12.1 Render Modes

To switch between modes, the **Switch render mode** button on the toolbar is used.

Four render modes are available:

1. The **MPR** mode. Sections are available for viewing. Set by default.

2. The **MIP** mode. A slice of a particular thickness is viewed instead of a section. A point with maximum intensity in the slice is projected on each point in the image. For details on how to set the thickness, see the next section.

3. The **MinIP** mode. Similar to the previous mode, but points with minimum intensity are projected on the image.

4. The **AIP** mode. Similar to the previous mode, but the intensity of each point equals the average intensity of the points projected on this point in the image.

This tool is also available from the **MPR** main menu item.

5.12.2 Slice Thickness

In the **MIP**, **MinIP** and **AIP** render modes, the slice thickness is set using the **Thickness** button on the toolbar. Click the button and select the predefined values from the list, or click
the **User defined** button to specify your own value. In the projection window, the slice borders are marked by lines (the red arrows in Fig. 5.22).

To set the thickness of solely the slice which is projected on a certain plane, move the cursor to any line, marked by the arrows in Fig. 5.22, for the corresponding slice and move it, holding the left mouse button.

![Slice borders](image)

*Figure 5.22: Slice borders*

Setting the thickness is also available from the **MPR main menu item**.

### 5.13 Rotate Image in the Section Plane

To rotate an image by an angle multiple of 90 degrees:

1. Activate the window in which the target image is located. To do this, click the left mouse button on the window area or header (marked by the arrow in Fig. 5.23).

2. Click on the arrow on the right side of the **Rotate** button and select the angle from the drop-down menu.

3. To restore the initial image position, select the **Set image rotation angle 0°** item.

4. To rotate an image by an arbitrary angle, activate the **Rotate** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. Rotate the image by moving the mouse while holding down the button that activated the tool.
To cancel the rotation of all the images, click the **Reset views orientation** button on the toolbar.

*Note that all the other view conversions will be undone as well.*

This tool is also available from the image context menu and from the **MPR** main menu item.

### 5.14 Mirror Image Horizontally/Vertically

The tool is described in Section 2.33.

### 5.15 Show labels tool

The tool is described in Section 2.24.

On the **MPR reconstruction**, tab this tool has 3 menu items, which can be checked independently:

- **Show orientation cube**;
- **Show orientation letters**;
- **Show render annotations**.

This tool is also available from the image context menu and from the **MPR** main menu item.
5.16 Export Images

The export of a model to DICOM or to an image is similar to the image export described in Section 2.25.

5.17 Reslice

Functionality is available in the Pro edition

The reslice functionality allows you to export the series generated in the multiplanar reconstruction window, setting the area, size, step images and other parameters.

The MPR window doesn’t show the source data, it shows 3D structure slices. That is why tweening errors may occur. To avoid tweening errors, when creating a series, you should use the MPR reconstruction based on the series obtained from the modality, rather than the series that was created before.

To reslice:

1. Select the plane whose sections should be exported to the series. To do this, click the left mouse button on the corresponding window.

2. Open the image export window by clicking on the Reslice button. The window will look as shown in Fig. 5.24.

Figure 5.24: Reslice
3. Enter the series description in the dialog shown in Fig. 5.25.

![Reslice dialog box](image)

*Figure 5.25: Reslice dialog box*

4. Set the step to generate images in the series.

5. Set the images number.

6. If you need to load the exported images to the DICOM server at once, check the option **Upload image to the default server**. If the default server is not specified in the DICOM Viewer this option will be inactive.

7. Set the image size if necessary.

8. The image area that is to be exported is highlighted by a white frame positioned symmetrically with respect to the intersection point of the cutting planes. To resize the area, drag the white frame, holding the left mouse button.

9. To rotate the reslice area, rotate the cutting planes. The cutting planes are described in Section 5.4.2.

10. The other two planes display projections of the exported slices. If necessary, move or rotate them in the same way.
11. Click **OK** to export the series or **CANCEL** to cancel.

This tool is also available from the **MPR** main menu item.

The **Reslice** button is not available for the **Involute** and **Curve slices** windows in the **MPR reconstruction** tab.

### 5.18 Measurements

The **MPR window doesn’t show the source data, it shows 3D structure slices. That is why tweening errors may occur**

As the images in MinIP, MIP, and AIP modes are the results of original images processing, tweening errors may occur. The measurements performed in these modes may be erroneous

The measurement accuracy is up to one screen pixel. As a screen pixel is smaller than a source image pixel, the true linear measurement accuracy is up to one source image pixel. Errors may also occur in density measurements. The most accurate measurements are performed with bilinear interpolation (see Section 5.3)

The **MPR mode is not meant to be used for PET studies, use the specialized module (see Section 8).**

Errors may occur when intensity is measured in a certain point. In this case, the intensity value will be marked by an asterisk. For accurate measurements, use the bilinear interpolation filter (see Section 5.3).

The measurements are conducted in the same way as for flat images (Section 2.17).
5.19 Annotations

Annotations are described in Section 2.30.

5.20 Volume Reconstruction window

In the Multiplanar Reconstruction window, you can view and edit a 3D model. To open it, click the 3D button on the toolbar. The model will be displayed in the bottom right-hand window. The following tools are available for working with the model:

- Clipping box;
- MPR planes on 3D view;
- Centrate;
- Select model point;
- Ruler and Polygonal ruler;
- all the tools for editing the model and creating segmented structures\textsuperscript{PRO}.

The Volume Reconstruction window is described in Chapter 3.

5.21 Diffusion Tensor Imaging (DTI) Mode

Functionality is available in the Pro edition

Tractography results cannot be used for establishing a diagnosis

The DICOM Viewer allows you to show the result of the fiber tractography for the series of Diffusion MRI. Fig. 5.26 shows tracks which are the result of brain tractography.
CHAPTER 5. MULTIPLANAR RECONSTRUCTION (MPR)

5.21.1 Open series in DTI Mode

Functionality is available in the Pro edition

The tracks which are the result of tractography are referred to as fibers in the DICOM Viewer interface and in the User Manual.

Figure 5.26: Result of brain tractography

The tractography will be performed automatically for the series made in the DTI mode.
when you open it in the Multiplanar Reconstruction Mode. To display fibers over the images not made in the DTI mode (for the same study):

1. Open the series not made in the DTI mode.
2. Click the **DTI** button on the toolbar.
3. In the dialog that appears, select the series made in the DTI mode.
4. Click **SELECT** to display fibers over the images or **CANCEL** to cancel.

### 5.21.2 Select Visible Fibers

**Functionality is available in the Pro edition**

If you want to make only some fibers visible, specify the areas through which the fibers pass as visible or invisible. Use the ROI tools from the **Fibers** panel. The operation of these tools is similar to using ROI from the toolbar at the top of the window (see Section 2.17.5). Note that you cannot use the ROI tools from the top toolbar to adjust the visibility of the fibers.

To make some fibers visible:

1. Open the series made in the DTI mode or display fibers over the series not made in the DTI mode.
2. Select the plane and the image in which you want to specify the area through which the target fibers pass.
3. Open the Segmented Structure panel by clicking the **Segmented structure panel** button. The **Fibers** panel will be located at the bottom.
4. Specify the desired area using the ROI tools (**Rectangle**, **Ellipse**, **Polygon**) on the **Fibers** panel. The similar tools from the toolbar at the top of the window cannot be used to adjust the visibility of the fibers. After making the ROI, only the fibers passing through the region specified by the ROI will be visible. A new group appears on the **Fibers** panel. This group includes the new ROI.
5. To delete ROI select it and click the **Remove ROI** button on the **Fibers** panel.
6. To make fibers which pass through the area invisible, check the **Inverse** box for this ROI on the **Fibers** panel.
7. To hide ROI, check the **Hide ROI** box for this ROI (marked with number «1» in Fig. 5.28). To hide all the ROIs in the group, check the **Hide ROIs** box for this group (marked with number «2» in Fig. 5.28). To hide all the ROIs, check the **Hide ROIs** box in the header of the table (marked with number «3» in Fig. 5.28). The visibility of the ROI does not affect the visibility of the fibers.
8. Make new ROIs until you see only the target fibers. Only the fibers which pass through all the ROIs are visible (or invisible if you check the Inverse box).

![Image](image1.png)

*Figure 5.27: The Fibers Panel*

![Image](image2.png)

*Figure 5.28: ROIs visibility*

When you create the first ROI, a group is automatically created for it. New ROIs are added to the same group.

The flag to the left of the name of the ROI group and the Base fibers group allows you to display or hide the relevant fibers. If the box is checked, then the fibers are displayed. This flag does not affect the visibility of fibers, it only allows you to temporarily hide them, for example, to adjust the visibility of other fiber groups.

To make other fibers visible without changing the visibility of the fibers previously made visible:

1. If necessary, hide the previously displayed fibers by unchecking the box to the left of the fiber group name.

2. Show the base fibers by checking the box on the left of the Base fibers group.

3. Add a new group by clicking the Add ROI group on the Fibers panel.

4. Add a new ROI to make only the target fibers visible. To ensure that the ROI is in the right group, this group must be selected before making a ROI.

5. If necessary, show some other fibers by checking the boxes to the left of the other group names.
To show the image containing a certain ROI, select this ROI in the table and click the **Find ROI** button on the **Fibers** panel.

### 5.21.3 Fiber Color

**Functionality is available in the Pro edition**

By default, fibers are colored in accordance with the DEC (Direction Encoded Color) scheme. It means that the color of a fiber depends on its direction. You can set color for each group manually. Color is indicated by the pictogram in the DEC mode and by the single-colored pictogram if the color is set manually.

To set color manually, uncheck the **DEC** box for the group, double-click the left mouse button on the color pictogram and in the dialog button that appears, select the color or leave the default color.

To switch to the DEC scheme, check the **DEC** box.

### 5.21.4 Scalar Maps

**Functionality is available in the Pro edition**

The DICOM Viewer allows to display scalar maps for series made in the DTI mode. The following types of maps are available:

- Fractional Anisotropy (FA);
- Mean Diffusivity (MD);
- Axial Diffusivity (AD);
- Radial Diffusivity (RD).

By default, the maps are not displayed. To display the map, select the target map on the drop-down list **Scalar map type** (Fig. 5.29). To hide the map, select an empty value from the list.

![Figure 5.29: Select scalar map](image-url)
5.21.5 Building a Surface

Functionality is available in the Pro edition

DICOM Viewer allows for building fiber surfaces in the Multiplanar reconstruction window. Select a group of fibers or a ROI for the selected group of fibers. A polygon surface is built for a group of fibers. If you change the ROI visibility for the group of fibers, it won’t have any impact on the surface to be built.

Each fiber is represented by a solid cylinder-shaped figure. The polygonal surface is built on the basis of such parameters as the cylinder diameter and the number of points on the cylinder circumference.

To set the parameters for the surface model surface, click the button Convert tracks to polygonal mesh on the Fibers panel. In the dialog box for the surface model parameters (Figure 5.30), provide the following parameters:

1. **Fiber contour points**, from 3 to 360. In most cases, six points are enough to ensure decent accuracy. The accuracy of the model, the time required for estimation and the memory space required increases with the number of points on the contour.

2. **Fiber diameter**, from 0.01 to 10 mm.

![Figure 5.30: The dialog box for surface model options](image)

Click **OK** to apply the settings or **CANCEL** to cancel.

A surface is created for the chosen group of fibers and added to the list on the Segmented structure panel. The name of the surface, as well as the name of any structure without a volume model, is shown in italics. The name of the surface is copied from the name of the group on the Fibers panel.

You can view the built surface in the MPR reconstruction tab. To open a volume reconstruction, click the 3D button on the toolbar. The volume reconstruction will be displayed in the right-hand bottom window.

The work with the structures from the segmented structure list is described in Section 6.4. The surfaces created can be exported or imported. For details on surface and structure export and import, see Section 6.7. The procedures of saving and opening segmentation projects and DTI projects are described in Section 6.11.
5.21.6 Creating a Voxel Model of Fibers

Functionality is available in the Pro edition

DICOM Viewer allows for building voxel models of fibers in the Multiplanar reconstruction window.

Select a group of fibers or a ROI for the selected group of fibers. A voxel model is built for a group of fibers. If you change the ROI visibility for the group of fibers, it won’t have any impact on the model to be built.

To build a voxel model, click the Voxelize tracks button on the Fibers panel.

A voxel model is created for the chosen group of fibers and added to the list on the Segmented structure panel. The name of the structure is copied from the name of the group on the Fibers panel.

To create a voxel model based on all the fibers, select the Base fibers group and click the Voxelize tracks button on the Fibers panel.

The voxel model is created for the chosen group of fibers (Base fibers) and added to the list on the Segmented structure panel under the name DTI tracktography.

You can view the model built in the MPR reconstruction tab. To open a volume reconstruction, click the 3D button on the toolbar. The volume reconstruction will be displayed in the right-hand bottom window.

The work with the structures from the segmented structure list is described in Section 6.4. The surfaces created can be exported or imported. For details on structure export and import, see Section 6.7. The procedures of saving and opening segmentation projects and DTI projects are described in Section 6.11.

5.21.7 Saving data in a file

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The DICOM Viewer provides an opportunity to save ROI and groups in files with .spj extension. The procedure for saving and opening files is described in Section 6.11. When a file is opened, the data contained in it is added to the data from the Fibers panel.
Segmentation

Segmentation is the division of an object into its component parts to facilitate research and modelling.

The tasks that segmentation solves:

- researching separate tissue parts with a certain density range. Usually, such parts have a complicated form and are hidden inside other tissues, hence it is impossible or difficult to highlight them with the cutting tools, e.g.: teeth and their roots, tumors, bones, vessels;
- calculating the volume of tissue, such as tumors;
- studying mutual disposition of tissues that can not be visible simultaneously;
- fusing a segment and a whole model to see its location within the tissue;
- exporting the structure surface for further use, such as 3D-printing;
- importing the objects used in the treatment to simulate their location in the tissues;
- dividing tissues into separate fragments for better visualization.
- cutting tissue by a mask created from a segmented structure.

To solve these problems, the DICOM Viewer allows you to build segmented structures both automatically and manually.

The segmentation of tissues is possible in the Volume Reconstruction window and the Multiplanar Reconstructions window. In both modes you work with the same segmented structure (structures), thereby for its/their construction you can use the benefits of both modes, switching between them.

Fig. 6.1 illustrates the segmented root of a tooth highlighted in yellow. Fig. 6.2 illustrates segmented kidneys highlighted in red and blue. The base volume is highlighted with the CLUT so that the bones can be seen best and the other organs are not visible.
Figure 6.1: Segmented root of tooth
Figure 6.2: Segmented kidneys
## 6.1 The Segmented Structures Panel

**Functionality is available in the Pro edition**

The segmented structures panel for the **MPR reconstruction** tab is shown in Fig. 6.3. This panel is identical in the **Volume reconstruction** tab, except that the MPR MPR nested element is not displayed for the base volume.

The panel contains the Control buttons:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1" alt="" /></td>
<td><strong>Parameters</strong> button is used to call up the popup menu for surface creation parameters setup and export/import parameter setup (see Section 6.7).</td>
</tr>
<tr>
<td><img src="image2" alt="" /></td>
<td><strong>Save segmentation project to file</strong> button is used to call up the dialog box for saving a segmentation project in a file (see Section 6.11).</td>
</tr>
<tr>
<td><img src="image3" alt="" /></td>
<td><strong>Open segmentation project from file</strong> button is used to call up the dialog box for opening a segmentation project saved in a file (see Section 6.11).</td>
</tr>
<tr>
<td><img src="image4" alt="" /></td>
<td><strong>Add a new structure</strong> button creates a new structure with an empty mask.</td>
</tr>
<tr>
<td><img src="image5" alt="" /></td>
<td><strong>Create surface for current segment</strong> button creates a surface for a selected structure or for the base volume.</td>
</tr>
<tr>
<td><img src="image6" alt="" /></td>
<td><strong>Import masks from DICOM RT mask set...</strong> button imports a mask of segmented structure from DICOM RT (see Section 6.7.5).</td>
</tr>
<tr>
<td><img src="image7" alt="" /></td>
<td><strong>Import surface(s)</strong> button imports a segmented structure from ply, obj or stl file formats.</td>
</tr>
<tr>
<td><img src="image8" alt="" /></td>
<td><strong>Duplicate structure/Duplicate mask/Duplicate surface</strong> button, depending on the element selected on the segmentation panel, makes a copy of the whole structure, the mask of structure, or the surface in a separate structure (see Section 6.3.1). If the <strong>Structure</strong> or <strong>Base volume</strong> option has been selected, the structure <strong>Mask</strong> and the <strong>Surface</strong> (when built) are copied to the new structure. If the <strong>MPR</strong>, <strong>Base volume</strong>, or structure <strong>Mask</strong> option has been selected, only the structure mask is copied to the new structure. If the <strong>Surface</strong> option has been selected, only the surface is copied to the new structure.</td>
</tr>
<tr>
<td><img src="image9" alt="" /></td>
<td><strong>Restore base volume by mask</strong> makes the main volume the same as the selected segmented structure. For the <strong>MPR reconstruction</strong> tab, the <strong>3D view</strong> window must be activated.</td>
</tr>
<tr>
<td><img src="image10" alt="" /></td>
<td><strong>Remove structure/Remove surface</strong> button deletes either the whole structure or the surface depending on the option selected on the hierarchical list. When a structure is deleted, a confirmation dialog box pops up.</td>
</tr>
</tbody>
</table>
### The Export button

The Export button opens export menu for surfaces and masks.

### The Hide all masks/Show all masks button

The Hide all masks/Show all masks button is used to hide/display the masks for the base volume and the structures on the segmentation panel. When all the masks are hidden, the icon is replaced by a crossed out version.

### The Hide all surfaces/Show all surfaces button

The Hide all surfaces/Show all surfaces button is used to hide/display all the surfaces for the base volume and the structures on the segmentation panel. When all the surfaces are hidden, the icon is replaced by a crossed out version.

### The Optimal view button

The Optimal view button is used to display all the elements of the list up to the third nesting level and hide all the elements from the third nesting level.

### The Collapse all button

The Collapse all button collapses all the elements of the list on the segmentation panel.

### The Expand all button

The Expand all button shows all the elements of the list on the segmentation panel.

### The Surface positioning button

The Surface positioning button moves the imported surface within the screen (only for the 3D reconstruction window). The tool may be activated with the left, right, or middle mouse button. To continue work with the tool, use the button with which the tool was activated. For details on tool control, see Section 1.14.
The hierarchical list of items on the segmented structures panel consists of the list of layers and the list of segmented structures for each layer.

By default, the optimal view of the list is presented (the items up to the third nesting level are shown). To see all the items, click the **Expand all** button on the segmented structures panel. To see some particular items, press the arrow on the left-hand side of the name of the item.

In the line referring to the layer, you can see a description of the layer, a thumbnail for the layer series, and a button for customizing visibility of all the child items for this layer. The layer comprises the following items:

- **Base volume.** In this line, the visibility button for all the child items is shown. If a surface has been created for the base volume, then the symbol is shown in the line. The color of the surface is the same as the color of the initial model. Alternatively, the user...
may select the color (see Section 6.4).
The **Base volume** item comprises the following elements:

- **MPR** (shown only in the **MPR reconstruction** tab). It comprises a visibility button for the child items, as well as a field showing the current opacity value for MPR windows. When you mouse over the respective line, a slider is shown. To change the opacity value, move the slider or enter the required numeric value in a percentage.

  The **MPR** comprises the following items:
  
  * a CLUT settings control element for the **MPR reconstruction** tab;
  * **Statistics**. This item provides for the results of base volume measurements. Besides the visible voxel volume, the minimum, maximum, and average intensity values are shown, as well as the standard intensity value deviation.

- **Volume model**. It comprises a visibility button for the base volume, as well as a field showing the current opacity value for the **3D view** window and the **Volume reconstruction** tab. When you mouse over the respective line, a slider is shown. To change the opacity value, move the slider or enter the required numeric value in a percentage.

  The **Volume model** comprises the following items:
  
  * a CLUT settings control element for the **3D view** window and the **Volume reconstruction** tab;
  * **Statistics**. This item provides for the results of base volume measurements. Besides the visible voxel volume, the minimum, maximum, and average intensity values are shown, as well as the standard intensity value deviation;

- **Surface** (if created). It comprises a visibility button for the surface, as well as a field showing the current opacity value. When you mouse over the respective line, a slider is shown. To change the opacity value, move the slider or enter the required numeric value in a percentage.

  The **Surface** comprises the following items:
  
  * a field for changing the number of triangles forming the surface;
  * the **Change surface creation parameters** button used to call up the dialog box for customizing the surface parameters;
  * **Details**. This item provides the information about the volume of voxels around which the surface was built, the number of vertices and the surface area.

In the **Structure** line for the segmented structure, you see the name of the structure, color control elements, and a visibility button for the structure and its child items. The **Structure** comprises the following items:

- **Mask**. This element is used for control of the segmented structure voxel model, and its structure is similar to the **Volume model** element. It comprises a visibility button for the structure mask. When you mouse over the respective line, you see the current structure mask opacity value. To change the opacity value, move the slider or enter the required numeric value in a percentage.

- **Surface**. This element is used for customizing the surface settings, and its structure is similar to the **Surface** element for the layer.
6.2 The Mask

6.2.1 Creating a new structure and mask

Functionality is available in the Pro edition

1. Click the Add a new structure button. The dialog shown in Fig. 6.4 appears.

![Figure 6.4: Set mask for a new structure](image)

2. Enter the name of the new structure in the Name field. By default, the name of the structure is automatically generated by the <Structure X> template, where X is the counter with the increment of one point. The first value is 1.

3. Set the tissue density values for the mask. You can do it in one of the three ways:
   - using the Threshold mode. In this mode the mask is set for the tissue whose density is greater or less than the specified threshold value. To set the mask for the tissue with a density less than the threshold, select the Low intensity setting, and vice versa. Set the threshold;
   - using the Interval mode. In this mode the mask is set for the tissue whose density is in the range from minimum to maximum;
• using color tables. In this mode the mask is set for the tissue displayed for the selected color table.

4. Click **OK** to create a new structure and mask or **CANCEL** to cancel.

### 6.2.2 Changing the structure mask using CLUTs

*Functionality is available in the Pro edition*

You can change the mask of the current structure in several ways:

1. Using the **Adjust W/L** tool:
   (a) Select the target structure on the panel of segmented structures.
   (b) Click the **Adjust W/L** button on the toolbar.
   (c) Change the window width and level for the editing mask (see Section 2.15). The green editing mask changes in real time in the MPR window.

2. Selecting the color table from the dropdown list (see Section 2.20.1) or with the **Custom W/L** tool (see Section 2.15).

3. For the properties tree on the Segmented structure panel (Figure 6.5):
   (a) Unfold the list of the segmented structure properties.
   (b) In the drop-down list, select the editing mask mode or the color table you need:
      - The **High intensity** and **Low intensity** mode provides the editing mask for tissues whose density is above or below the threshold value.
      - The **Interval** mode provides the editing mask for tissues whose density is within the set value range.
      - The **CLUT** mode provides the editing mask for the tissues displayed for the chosen color table.
   (c) To change the interval or the density threshold, click with the left mouse button on the values (see the red box in Figure 6.5). Provide the values you need and press **Enter** key on the keyboard.
6.2. THE MASK

The editing mask parameters (the color table, the intensity threshold value and the interval) are changed for each segmented structure separately. The color table type and the editing mask mode for the segmented structure selected is shown on the visualization setup panel.

4. For the Volume Reconstruction window only: using the Set mask tool (see Section 6.2.4).

You can change the editing mask visibility for the current structure using the editing mask setup panel (see Section 6.2.3).

6.2.3 The Editing mask

Functionality is available in the Pro edition

The editing mask is a pattern beyond which the structure mask is not visible.

The editing mask is not visible in the volume reconstruction window, and it is displayed in green in the MPR window. If necessary, the editing mask can be inverted. In this case, the tissues not under the editing mask are displayed in green. To invert the editing mask, set the flag Invert edit mask on MPR (see Section 15.6.3).

The editing mask can be changed at any time (see Section 6.2.2). If the editing mask is reduced and the structure goes beyond the editing mask, then this part of the structure becomes invisible and is not taken into account in the calculations. However, it is not removed and when the editing mask is increased, it becomes visible again.

You can change the editing mask visibility for the current structure using the editing mask setup panel (Fig. 6.6). The panel is placed at the bottom of the segmented structures panel and is only available in the MPR reconstruction tab.
There are two ways to change the visibility of the editing mask:

- move the slider or roll the mouse wheel while the cursor is placed on the slider;
- enter the opacity value in the field on the right-hand side of the slider.

The editing mask opacity value is expressed as a percentage.

To see the outline of the editing mask, check the Outline box.

To conceal the editing mask, click the Hide mask button on the editing mask setup panel. To display the editing mask, click the Show mask button. The Hide mask button is unavailable if at least one tool for segmentation or volume editing has been activated.

To minimize the editing mask setup panel, click the Hide button. To display the hidden panel, click the Show button.

### 6.2.4 Set Mask Tool

Functionality is available in the Pro edition

The tool is only available for the Volume reconstruction tab. To set a structure as a mask for another structure or base volume, proceed as follows:

1. On the list of structures, select the structure (base volume) for which you want to change the mask.

2. Click on the Set Mask button. The dialog shown in Fig. 6.7 will be displayed.

3. On the list of structures, select the structure (base volume) you want to set as the mask.

4. Click OK to confirm or CANCEL to cancel the action.
6.3 Creating segmented structure

6.3.1 Creating a structure by copying

Functionality is available in the Pro edition

When you create a structure by copying, a new structure is created. Depending on the selected element, the current structure is copied to the new structure as a whole (the mask of the current structure and the surface, if it was built), only the mask of the structure or only the surface. To create a structure:

1. Open the segmentation panel by clicking the Segmented structure panel button.

2. Choose the base volume or the structure created earlier as the initial volume.

3. Click the Duplicate structure button on the segmented structure panel or place the cursor over the structure, click the right mouse button and choose the Duplicate structure point in the right-click menu. Depending on the option selected, the whole structure or just the surface is copied to a separate structure.
If the Structure or Base volume option has been selected, the structure mask and the surface (when built) are copied to the new structure. If the MPR, Volume model, or Mask option has been selected, only the structure mask is copied to the new structure. If the Surface option has been selected, only the surface is copied to the new structure.

### 6.3.2 Creating a Structure with a Empty Mask

**Functionality is available in the Pro edition**

To create a structure with a empty mask, proceed as follows:

1. Open the segmentation panel by clicking the *Segmented structure panel* button.

2. Click the *Add a new segmentation structure* button. Set the mask in the dialog that opens (see Section 6.2.1). A structure is created with an empty structure mask and an editing mask with the specified parameters.

3. Fill out the structure using volume editing tools (see Section 6.8).

### 6.4 Actions with structure

**Functionality is available in the Pro edition**

The DICOM Viewer allows you to perform the following actions with structures:

- **Renaming.** Can be done in two ways:
  - double left-click the structure name. Enter a new name and press the *Enter* key on the keyboard;
  - place the cursor over the structure, click the right mouse button and choose the *Rename structure* point in the right-click menu. Enter a new name and press the *Enter* key on the keyboard.

- **Disabling visibility.** The visibility button (Fig. 6.8) turn off visibility of structure mask and surface for this structure. This action is also available for the base volume.
6.4. ACTIONS WITH STRUCTURE

Figure 6.8: Button to change the visibility of mask and structure surface

- Color change. To do this:

  1. To set the user’s color, check the box in the line representing the structure (see the red arrow in Fig. 6.9). To change the color, click the colored rectangle in the line representing the structure and choose the color you need.

  2. To use the color of the initial model, uncheck the box. The color of the mask and the surface of the structure takes on the color of the initial model.

- Deletion. Can be accomplished in two ways:

  - on the segmented structure panel, select the surface you want to delete. Click the **Remove structure/Remove surface** button on the segmented structure panel;

  - place the cursor over the structure, click the right mouse button and choose the **Remove structure/Remove surface** point in the right-click menu. In the dialog box that pops up, click **REMOVE** to delete the structure or **CANCEL** to cancel.

Figure 6.9: Custom color check box

If you want the DICOM Viewer to always delete structure without this confirmation, check the box **Don't show this dialog again**. If you want the DICOM Viewer to show the confirmation dialog, check the box **Confirm on the structure removing** (see Section 15.6.3).
6.5 Building surface

Functionality is available in the Pro edition

The DICOM Viewer allows you to create a surface for segmented structures and base volume in the Volume Reconstruction window and in the Multiplanar Reconstruction window. In multiphase series, you can build a surface for base volume of the each phase.

Attention! Polygon model transparency is not supported if:

- a CPU has been chosen as the render device;
- the software was installed on macOS lower operating system than 10.15.

On macOS 10.15 and later, it is recommended to use a visualization device that supports Metal polygonal and voxel rendering. The settings are described in Section 15.6.3.

On the segmented structures list, select the base volume or the structure for which you want to build a surface.

To customize the parameters used by default when building a surface, click the Parameters button on the segmented structures panel and select the Default surface parameters... option. In the dialog box that pops up (Fig. 6.11), provide the required default parameters for building surfaces.

![Segmentation panel](image)

*Figure 6.10: Surface parameters*

To build a surface, click on the Create surface for current structure button on the
segmented structures list. The surface is built according to the current settings.

To customize the parameters for each of the surfaces built, unfold the surface properties tree on the segmented structure panel (see Fig. 6.10). Click the **Change surface creation parameters** button.

Set the surface parameters in the dialog box that pops up (see Fig. 6.11).

![Surface creation parameters](image)

Figure 6.11: Surface creation parameters

- The smoothness of the surface is defined by the **Smoothing pass count** parameter. With this parameter set at zero value, the form of the surface is as close as possible to the structure. With an increase in the value, the surface roughness disappears.

- If the **Interpolate vertex positions** box is checked (checked by default), the surface is smoothed at the border of the volume.

- To create the surface only for the largest structure, check the **Remove secondary volumes** box.

- To fill the cavities and hollows, check the **Fill cavities** box. As an alternative, you can use the **Fill** tool (see Section 3.8.7).

- To fill small cavities, check the **Perform morphological closing** box. As an alternative, you can use the **Remove holes (closing)** tool (see Section 3.8.7). The volume of
the model is first increased and then decreased by the operation radius provided (in millimeters or voxels). The shape of the surface and the external dimensions are not changed.

- To eliminate visual surface defects, check the Perform morphological opening box. As an alternative, you can use the Remove noise (opening) tool (see Section 3.8.7). The volume of the model is first decreased and then increased by the operation radius provided (in millimeters or voxels). The shape of the surface and the external dimensions are not changed.

- If the Apply current clipping box box is checked, then the surface is built only for that part of the structure which is inside the cube.

To apply the settings, click OK. To cancel, click CANCEL.

When the segmentation project is saved, all the surface building parameters are saved in the file. For details on saving projects, see Section 6.11.

The surface is represented by a polygon model made of triangles. The program automatically determines the maximum possible number of triangles required for creating a surface imitating the volume surface. The number of the triangles making up the surface may be changed on the Segmented structure panel.

To change the number of the triangles making up the surface, unfold the surface properties tree on the Segmented structure panel (Figure 6.10). Double-click with the left mouse button on the value in the field with a triangle icon. Change the value showing the number of triangles and press Enter key on the keyboard.

If the number of triangles entered is too small or too large to build a surface, the DICOM Viewer will use the value from the permitted range which is the closest to the value provided by the user.

If the entered value equals 0, the program will build a surface using the maximum possible number of triangles which will be shown in the field with a triangle icon.

If visibility for this structure or surface is disabled, you cannot use the cutting tools, as well as the Segmentation from point by mask, Region growing and Vessel tree segmentation tools.

You can only edit hidden structures with intelligent volume editing tools, such as Grow (dilation), Shrink (erosion), Remove noise (opening), Remove holes (closing) (for details see Section 3.8.7), as well as with the Union, Subtract, Subtract dilated, and Intersect tools (for details see Section 6.9). In this case, the following message pops up: «The target structure is hidden. Are you sure you want to apply the operation to it?» Click Yes to proceed or No to cancel.

6.6 Copying a Surface

Functionality is available in the Pro edition

The DICOM Viewer provides for copying segmented structure surfaces in the MPR Reconstruction and Volume Reconstruction windows. You can copy a segmented structure surface:
6.6. COPYING A SURFACE

- in one study series;
- in a merged study series.

To make a copy of a segmented structure surface in a single study series, proceed as follows:

1. On the segmented structure panel, select the surface you want to copy.

2. Click the **Duplicate surface** button on the segmented structure panel or place the cursor over the structure, click the right mouse button and choose the **Duplicate surface** point in the right-click menu.

On the segmented structure list, you will see a copy of the surface with a «**surface copy**» note. The name of the surface copy, as well as the name of any structure without a structure mask, is shown in italics.

![Segmentation Panel](image)

*Figure 6.12: Surface copy*

To make a copy of a segmented structure surface in a merged series, proceed as follows:

1. On the segmented structure panel, select the surface you want to copy.

2. Click the **Duplicate surface** button on the segmented structure panel or place the cursor over the structure, click the right mouse button and choose the **Duplicate surface** point in the right-click menu.

3. In the **Layer selection** (see Fig. 6.13), select from the drop-down list the layer where you want to place the surface copy.
CHAPTER 6. SEGMENTATION

Figure 6.13: Layer selection dialog box

4. Click OK to copy the surface to the selected layer or CANCEL to cancel.

On the segmented structure panel for the layer selected, you will see a copy of the surface with a «surface copy» note. The name of the surface copy, as well as the name of any structure without a structure mask, is shown in italics.

To move the copied surface manually, activate the tool Surface positioning by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. Move the surface on the plane of the screen, holding the mouse button with which the tool was activated.

To create a segmented structure for a surface, place the cursor over the copy of the surface, click the right mouse button and choose the Create mask by surface point in the right-click menu.

The things you can do with the surfaces and structures on the segmented structure list are described in Section 6.4. The surfaces you have built or copied may be exported or imported. For details on export and import of surfaces and structures, see Section 6.7. The procedures of saving and opening segmentation and DTI projects are described in Section 6.11.

6.7 Import and Export

6.7.1 Export surface

Functionality is available in the Pro edition

To customize the parameters used by default when exporting a surface, click the Parameters button on the segmented structures panel and select the Export/Import parameters... option. In the dialog box that pops up (Fig. 6.14), provide the required default parameters for exporting surfaces.

- to move the reference point (the point relative to which the model can be deformed in the Vector graphics editors) to the geometrical center of the surface, in the dialog box check the Center surface box. The option is disabled by default;

- to use the patient’s coordinates when exporting, check the Import and export surfaces using patient coordinates box. Check box is set by default;
6.7. IMPORT AND EXPORT

Figure 6.14: Surface export and import parameters

To apply the settings, click OK. To cancel, click CANCEL.
To export a segmented structure surface, proceed as follows:

1. On the segmented structures panel, select the surface to be exported.

2. Call up the popup menu with the export options in one of the following ways:
   
   - click the Export button on the segmented structures panel and choose the type of export from the popup menu;
   - mouse over the structure on the list, right-click and choose the Export option from the right-click menu. Then select the type of export.

There are three options for exporting a surface:

- **Export selected surface.** Only the surface that is currently chosen is exported. It may be exported in .ply, .obj, .stl or .glb format. In the dialog box that appears, select the file type and save the surface;

- **Export all visible surfaces.** All the visible surfaces for which visibility in the segmented structures panel is enabled are exported. They may only be exported in .glb format;

- **Export all surfaces.** All the surfaces on the segmented structure panel are exported. They may only be exported in .glb format.
If export is performed for several layers, the hierarchy is retained: layers (with the name of the respective series) occupy the first level, while the second level is occupied by surfaces. When surfaces are exported from the same layer, only one hierarchy level (surfaces) is retained.

The name, the color of the apices and the transparency are retained for each surface. When several surfaces are exported, their relative position which is the same as the relative position in the DICOM Viewer at the time of export is retained.

You need to be aware that when the surface is printed by a 3D printer, errors may occur for the following reasons:

1. The surface accuracy depends on the voxel size; the margin of error cannot be smaller than the voxel size.

2. The boundaries of the structure mask for which the surface is created depend on the color palette for the initial volume. If a wrong palette is chosen, some tissues that are needed may become invisible, while some negligible tissues may become visible.

3. The boundaries between tissues characterized by different density values may be blurred because of the physical principles behind the tissue scanning technology. The margin of error may be up to several voxels.

4. The surface accuracy is subject to antialiasing and depends on the polygon count.
6.7.2 Import surface

Functionality is available in the Pro edition

To customize the parameters used by default when importing a surface, click the Parameters button on the segmented structures panel and select the Export/Import parameters... option. In the dialog box that pops up (Fig. 6.16), check the following boxes:

- to use the patient’s coordinates, check the Import and export surfaces using patient coordinates box;
- to align the centers of the imported surface and the model when importing, check the Add to the center box;
- to merge the vertices of the triangles when importing a surface in (stl) format, check the Merge imported STL vertices box. This box is checked by default.

Click OK to apply the settings or CANCEL to cancel.

Figure 6.16: Surface export and import parameters

There are two ways to import surfaces:

- click the Import surface(s) button. In the dialog box that pops up, select the files and click Open;
• mouse over the structure on the list, right-click and choose the Import->Import surface(s)... option from the right-click menu. In the dialog box that pops up, select the files and click Open.

The name of the imported surface, as well as the name of any structure without a structure mask, is shown in italics. In Figure 6.17 you see an imported surface Surface_example-1. You cannot change the number of triangles for the imported surface.

To move the imported surface manually, activate the tool Surface positioning by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. Move the surface on the plane of the screen, holding the mouse button with which the tool was activated.

To create a segmented structure for a surface, place the cursor over the copy of the surface, click the right mouse button and choose the Create mask by surface point in the right-click menu.

6.7.3 Export a structure to the current study

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

DICOM Viewer allows for exporting masks of segmented structures to the current study as a new series or as DICOM RT Structure Set IOD.

To export a structure mask to the current study as a new series, proceed as follows:
6.7. IMPORT AND EXPORT

1. Select the structure mask you need on the Segmented structure panel.

2. Export the structure mask to the current study in one of the following ways:

   • click the Export button on the segmented structures panel and choose the Export mask as new series option from the popup menu;

   • mouse over the structure on the list, whose mask you want to export right-click and choose the Export option from the right-click menu. Then select the Export mask as new series option.

The exported structure mask will be saved in the local storage as a new series of the current study. A thumbnail for the new series will be added to the series panel.

The exported structure mask can be opened in the flat image viewer, volume reconstruction, or MPR reconstruction tab.

The position of slices in a new series is in compliance with the window that was selected when the Export mask as new series command was given. If a 3D view window is selected, then the position of the planes will be in compliance with the position of the slices in the Axial plane window.

6.7.4 Export a structure to DICOM RT

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

To export a structure mask of the segmented structure to DICOM RT, proceed as follows:

1. On the segmented structures panel, select the structure whose mask to be exported to DICOM RT.

2. Call up the popup menu with the export options (Fig. 6.18) in one of the following ways:

   • click the Export button on the segmented structures panel and choose the type of export to DICOM RT from the popup menu;

   • mouse over the structure on the list whose mask you want to export, right-click and choose the Export option from the right-click menu. Then select the type of export to DICOM RT.
There are three ways to export a mask of structure to DICOM RT:

- **Export selected mask to DICOM RT...** Only the mask of the currently selected structure is exported;

- **Export visible masks to DICOM RT...** All the visible masks of structures from the segmented structures panel (for which the visibility button has been activated) are exported;

- **Export all masks to DICOM RT...** All the masks of structures from the segmented structures panel are exported.

In the **Export to DICOM RT** (Fig. 6.19) dialog box that pops up, add a description of the exported RTSTRUCT series. The default series description is «Segmentation».

Click **OK** button to export mask of structure or **CANCEL** to cancel.

The exported mask of structure will be saved in the local storage as a new series with RTSTRUCT modality. A thumbnail for the new series will be added to the series panel.

If a series has several phases, the mask of structure will only be exported for the current phase. If no mask was exported during the export procedure (e.g. no voxels are visible under the editing mask), an error message will pop up.
6.7.5 Importing a Structure from DICOM RT

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

There are two ways to import a mask of segmented structure from DICOM RT:

- click the **Import masks from DICOM RT...** button on the segmented structures panel;

- mouse over the structure on the list, whose mask you want to import right-click and choose the **Import** option from the right-click menu. Then select the **Import masks from DICOM RT...** option.

In the **Import from DICOM RT** dialog box (Figure 6.20), select an RTSTRUCT modality series to import.

![Image of Import from DICOM RT dialog box]

*Figure 6.20: Import from DICOM RT*

Click **OK** button to import structure mask or **CANCEL** to cancel.

In the **Structures to import** section of the dialog box (Figure 6.21), check the box next to the structure whose mask you want to import. To import all the masks of the structures from the list, check the upper box. By default, the boxes are not checked.
Figure 6.21: Structure selection dialog

Click **OK** to import structure mask or **CANCEL** to cancel.

### 6.8 Changing the structure mask with segmentation tools

**Functionality is available in the Pro edition**

When working with segmented structures, pay attention to which structure or volume is selected. All the editing operations are performed with a selected visible structure mask or volume. If the visibility button (Fig. 6.22) hides the visibility of mask and surface for this structure editing is not possible because the cutting tools (Segmentation from point by mask, Region growing and Vessel tree segmentation) are deactivated.

Figure 6.22: Button to change the visibility of all masks and structure surfaces

294
Invisible structures can be edited with smart volume editing tools, such as Grow (dilation), Shrink (erosion), Remove noise (opening), Remove holes (closing) (for details see Section 3.8.7), as well as Union, Subtract, Subtract dilated, and Intersect tools see Section 6.9.

In this case, the dialog box is displayed: The target structure is hidden. Are you sure you want to apply the operation to it? Click Yes to proceed or No to cancel.

If the volume model is open (see Section 5.20), then the created structure appears simultaneously on the model. This causes additional load on the processor. If you want to reduce the load, click the arrow on the right side of the Growing Region button and uncheck the Interactive 3D Update item. After this, the structure on the volume model will be updated after the next structure creation phase is completed.

If a base volume or mask of segmented structure is edited, the respective surfaces are automatically rebuilt.

To edit a structure mask, use specialized tools (described below) and volume editing tools:

- Polygon Cut (see Section 3.8.1);
- Inverse Polygon Cut (see Section 3.8.2);
- Delete Area (see Section 3.8.3);
- Delete All Areas except Selected Area (see Section 3.8.4);
- Brush Cut (see Section 3.8.6);
- Brush Restore (see Section 3.8.6). The use of the tool is possible only if a part of the structure is already created;
- Contour segmentation (see Section 6.10);
- Grow (dilation) (see Section 3.8.7);
- Shrink (erosion) (see Section 3.8.7);
- Remove noise (opening) (see Section 3.8.7);
- Remove holes (closing) (see Section 3.8.7);
- Multi-segment growing (see Section 3.8.7);
- Fill (see Section 3.8.7).
- Cut Invisible Volume (see Section 6.9);
- Vessels Tree Segmentation (see Section 6.8.4);
- Segmented structures regions growing (see Section 6.8.7);
- Union (see Section 6.9);
- Subtract (see Section 6.9);
- Subtract dilated (see Section 6.9);
- Intersect (see Section 6.9).
6.8.1 Tools for automatic segmented structure mask filling

Functionality is available in the Pro edition

The **Segmentation from point by mask** tool allows you to create a structure mask for a bound area. It is necessary that the structure mask for this area does not touch the structure masks of the neighboring areas. To create a structure mask:

1. Activate the **Segmentation from point by mask** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Click on the bound area.

3. If the structure mask was created for a larger area than required, undo the action by clicking the **Undo** button. Change the window width and level so that the editing mask for this area is not in contact with the masks of the neighboring areas and create the mask again.

If it is impossible to get a bound area completely separated from other tissues, then if you use the tool **Segmentation from point by mask**, there will be leaks (segmentation beyond the required area). To create a segment quickly and with minimal leaks, use the **Region growing** tool:

1. Activate the **Region growing** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14. The tool modes are described in Section 6.8.3.

2. Select the point on the editing mask roughly in the center of the region you want to segment.

3. Move the cursor in any direction, holding the mouse button. The structure mask will grow. The growth occurs faster in those directions in which the curvature of the surface is less (in thin sections the growth is slower to avoid leaks). The direction of the cursor movement does not matter, the distance from the starting point of the movement is important. When the cursor moves in the opposite direction, the structure mask does not decrease.

4. If the structure is completely created or if any further growth leads to leaks, stop the growing process by releasing the left mouse button.

5. If necessary, repeat the growing process for the tissue not yet segmented.

6. To undo an action, click the **Undo** button, to redo the canceled action click the **Redo**. However, keep in mind that the tool will operate at regular intervals, so with a single click on the **Undo** button, you can only delete that part of the structure mask that was added as part of the previous execution or a series thereof, but not along.
6.8.2 Brush restore tool

Functionality is available in the Pro edition

To fill out the structure mask using the Brush restore tool:

1. Activate the Brush restore tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Set the tool diameter. To do this, move the mouse cursor up and down, holding the Alt key on the keyboard.

3. Move the mouse cursor to the area for which you want to create a structure mask.

4. Click the mouse button. The tissues that are under the editing mask and inside the sphere will be added to the mask. The tissue color changes to the one set for the structure.

5. To undo the action, click the Undo button, to repeat the canceled action, click the Redo button.

6. To add a large area to the structure, move the Brush restore tool, holding the mouse button. However, keep in mind that the tool will operate at regular intervals, so with a single click on the Undo button you can only delete that part of the structure mask that was added as part of the previous execution or a series thereof, but not along.

7. To remove a part of the tissue from the structure, activate the Brush cut tool. The tool works in the same way as to the Brush restore tool, but unlike the Brush restore tool, it removes the tissue from the structure.

8. To disable or enable the editing mask, click the visibility button on the Editing mask panel.

In the Volume Reconstruction window, the tool is used for structure mask growth regardless of the editing mask. To grow a structure mask, use Restore by mask tool. Note that to fill the structure mask, you need some volume (base volume or the structure) to be visible. The visibility button (see the red arrow in Fig. 6.23) turn on visibility of all masks and surfaces for this structure. Otherwise, you won’t be able to grow another mask.
6.8.3 Region growing tool

Functionality is available in the Pro edition

When using the Brush restore tool, there may be leaks (structure mask beyond the required area). The Region growing tool takes into account the shape and density of the segmented areas and allows users to minimize leaks. The tool has two modes: EDT Method and Level Set Method. To switch the mode, click the arrow on the right of the button and select the desired mode. The current mode is marked by the flag.

The EDT Method mode allows you to create a structure mask in the editing mask space. To create a structure mask:

1. Activate the Region growing tool in the EDT Method mode by clicking the left-/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Select the point on the editing mask roughly in the center of the region you want to segment.

3. Move the cursor in any direction, holding the mouse button. The structure mask will grow. The growth occurs faster in those directions in which the curvature of the surface is less (in thin sections the growth is slower to avoid leaks). The direction of the cursor movement does not matter, the distance from the starting point of the movement is important. When the cursor moves in the opposite direction, the structure does not decrease.

4. If the structure mask is completely created or if any further growth leads to leaks, stop the growing process by releasing the left mouse button.

5. If necessary, repeat the growing process for the tissue not yet segmented.
6.8. CHANGING THE STRUCTURE MASK WITH SEGMENTATION TOOLS

6. To undo an action, click the **Undo** button, to redo the canceled action, click the **Redo** button. However, keep in mind that the tool will operate at regular intervals, so with a single click on the **Undo** button you can only delete that part of the structure mask that was added as part of the previous execution or a series thereof, but not along.

If the **Level Set Method** is selected, the tool uses its own editing mask created according to a special algorithm. Hence, the created structure mask can go beyond the standard editing mask, and when you change the mask boundaries, it will be visible. To create a structure mask:

1. Activate the **Region growing** tool in the **Level Set Method** mode by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

2. Select the point on the mask roughly in the center of the region you want to segment.

3. Press and hold the mouse button. A separate blue tool editing mask appears in the window in which you are working. If the mask is poorly visible against the background of the standard editing mask, reduce the opacity of the editing mask. To do this, reduce the opacity value in the **Editing Mask** panel (see Section 6.2.2).

4. Access the coverage of the tissues by the blue editing mask. The density of the tissues that are under the blue editing mask depends on the density under the cursor. If the blue editing mask is not built correctly, then release the left button, cancel the mask creation by clicking the **Undo** button or deleting the mask; move the cursor to the tissue section with the desired density, and repeat this step.

5. The red circle around the cursor shows the curvature of the areas that will be segmented (the smaller the diameter of the circle is, the greater curvature is allowable, that is, the thinner tissues will be segmented). To change the diameter of the circle, move the cursor up or down, pressing the **Alt** key on the keyboard.

6. Move the cursor in any direction, holding the mouse button. The structure mask will grow under the blue editing mask. If the blue editing mask goes beyond the standard editing mask, the mask can be built beyond the standard editing mask, but it will be visible only within the standard editing mask.

7. If the structure mask is completely created or if any further growth leads to leaks, stop the growing process by releasing the mouse button.

8. If necessary, repeat the growing process for the tissue not yet segmented.

9. To undo an action, click the **Undo** button, to redo the canceled action click the **Redo** button. However, keep in mind that the tool will operate at regular intervals, so with a single click on the **Undo** button you can only delete that part of the structure mask that was added as part of the previous execution or a series thereof, but not along.
CHAPTER 6. SEGMENTATION

If the volume model is open (see Section 5.20), then the created structure appears simultaneously on the model. This causes additional load on the processor. If you want to reduce the load, click the arrow on the right side of the Growing Region button and uncheck the Interactive 3D Update item. After this the structure on the volume model will be updated after the next structure creation phase is completed. The visibility of the surface does not affects the ability to edit the structure mask. The segmentation tools work if visibility for the structure and/or surface mask is enabled.

6.8.4 Vessel tree segmentation tool

Functionality is available in the Pro edition

The tool is used for blood vessels segmentation.

Segmentation is performed only for the visible part of the structure (base volume). Before using the tool, delete the parts of the image you don’t need with the help of cutting tools. For lung vessels you can use the lung vessels area selection tool. To do that, click on the arrow in the right-hand part of the Vessel tree segmentation button and choose Extract lung vessels area. It may take time. After the lung vessels area has been selected, a colour lookup table «[WL] High Intensity» is assigned. For details on CLUTs see Section 2.20.

The Extract lung vessels area tool works correctly only on studies with contrast.

To perform segmentation:

1. Select the target structure (the base volume). The visibility button turn on visibility of structure mask.

2. Activate the Vessel tree segmentation tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

3. Specify the following parameters in the dialog box:

   • **Max vessel diameter (cm)**. The higher is the value of this parameter, the larger vessels are detected. At the same time, the risk of misrecognition of other tissues and mistaking a group of vessels for one vessel increases. If a smaller value is provided, the vascular tree is divided into several trees, as large vessels connecting smaller trees are excluded.

   • **Vessel tree structures count**. The parameter limits the maximum number of vessel tree structures. The structures are only created for the largest trees.

    After segmentation has been completed, the tool remains active for work with the trees. The segmentation panel shows the structures created. To select a vessel, move the cursor to the vessel. To select a vessel and its subtrees, move the cursor while holding the Shift button. Figure 6.24 shows a vessel that has been selected.
6.8. CHANGING THE STRUCTURE MASK WITH SEGMENTATION TOOLS

To join a vessel to another tree, select the respective tree structure on the segmentation panel, choose the vessel with the cursor, so that it is highlighted, and click on it. The vessel and the structure will be the same colour.

The vessels that are not related to any trees are considered invalid. To disconnect a vessel from one tree without connecting it to any other trees, you just need to mark it as invalid. To do that, select the vessel with the cursor and double-click it or click holding down the Ctrl key on the keyboard. Use the button with which the tool was activated. You can choose an incorrect vessel on the base volume holding down the Alt key on the keyboard and join it to any tree.

Attention! Undu and Redo functions are not supported when joining vessels to trees.
The action history for the selected structure will also be lost after joining vessels. It is strongly recommended that advanced editing procedures be performed after the vessel trees have been formed.

After the tool has been deactivated, you can no longer select vessels, join them or mark as invalid. To proceed with the trees created, click the Vessel tree segmentation button. A warning will appear on the screen: The vessels are already computed for that volume. Do you want to recompute them using current structure mask? click No in the dialog box.

To perform vessels segmentation without deleting the results of the previous segmentation, choose the structure (base volume), for which you need to perform segmentation, click the Vessel tree segmentation button and click Yes in the dialog box. The vessels that have been created after you used the tool for the last time will be selected.

### 6.8.5 Watershed segmentation tool

Functionality is available in the Pro edition

The tool is used for segment volume using the watershed method and allows you to split the volume into several non-overlapping parts.

The tool has two modes (directions for basin filling):

1. **low dencity** for the separation of soft tissues surrounded by more dense tissues: organs containing air, as well as the brain. In this case, the filling of the basins progresses from a lower tissue density to a greater one. The minimum density of tissues (Min dencity) is the point from which the filling of the basins begins, and the Max dencity value limits the density of the tissues to be segmented from above.

2. **high dencity** for separation of dense tissues surrounded by less dense tissues: bones and contrasted organs. In this case, the filling of the basins begins with the maximum density (Max dencity) and progresses in the direction of its reduction. The minimum density of the tissues to be segmented is limited from below by the Min dencity value.

To speed up the segmentation process and avoid the creation of unnecessary segments, exclude unnecessary tissues from the segmented volume, using the cutting tools.

To perform the Watershed segmentation:

1. Select the volume to be segmented.
2. If necessary, cut off the tissues that do not need to be segmented.
3. Activate the Watershed segmentation tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.
4. In the dialog that opens, set the following parameters:
   - Min dencity;
   - Max dencity;
6.8. CHANGING THE STRUCTURE MASK WITH SEGMENTATION TOOLS

- **Min depth**: the minimum depth of basins which can be combined;
- **Max basins**: the maximum number of created structures (no more than 31);
- Select the mode (Low density High density);
- Select the source structure for segmentation from the Source drop-down list.
- To set this structure as default, check the Remember selected structure box.
- To hide the source structure, check the Hide source structure box.
- To hide the structures which will not be changed after segmentation, check the Hide other structures box.

5. Click **OK** to perform segmentation or **Cancel** to cancel action. The process takes some time.

After the segmentation is complete, you can manually distribute the tissue into the basins, using the markers of the segmented structures. If the tissues do not fall into the required structure, it is necessary to install the markers corresponding to the structure on this tissue.

**Warning! The structure changes made using markers cannot be undone!**

To perform the watershed segmentation using markers:

1. Select a structure on the list.
2. Activate the **Segment marker** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.
3. Add one or more markers in the required places by clicking the mouse.
4. If necessary repeat steps 1-3 for the other structures.
5. Click the **Watershed segmentation** button.
6. Make sure the **Use structure markers** box is checked.
7. Select the source structure for segmentation from the Source drop-down list.
8. To set this structure as default, check the Remember selected structure box.
9. To hide the source structure check, the Hide source structure box.
10. To hide the structures which will not be changed after segmentation, check the Hide other structures box.
11. Click **OK** to perform segmentation or **Cancel** to cancel action. The process takes some time.

If the markers of different structures are put in one basin then the segmentation fails. The source structure is not modified. The structures without markers are not modified.
To show/hide markers for the selected structure, click on the right side of the Segment marker button and check/uncheck the **Show current structure markers** box in the button menu (Fig. 6.25). The selected item is marked with a flag.

To show/hide marker numbers for the selected structure check/uncheck the **Show current structure marker numbers** box. The option is disabled by default. This function simplifies work with structures having many markers. E.g., if a watershed segmentation attempt results in an error, this function helps you find out the number of the marker that caused this error. The selected item is marked with a flag.

![Segment marker button menu](image)

*Figure 6.25: «Segment marker» button menu*

To show/hide markers for all segmented structures, click on the right side of the Segment marker button and select the **Show all structure markers** or **Hide all structure markers** respectively.

To remove markers from the current segmented structure select the **Remove current structure markers**.

To change marker parameters of the selected structure, select the command **Current structure markers options**....

The other features of the segment markers are similar to those described in Section 5.11.

If segmentation is performed for a fused series, then only markers for the selected layer are displayed. Markers are editable regardless of which structure is selected.

### 6.8.6 Multi-segment growing tool

*Functionality is available in the Pro edition*

This tool is used when it is necessary to increase masks of several structures so that they do not intersect. It is similar to **Grow (dilation)** (see Section 3.8.7), but can be applied simultaneously to an arbitrary number of structures and to the base volume. To use the tool:

1. Build the required number of structures whose masks you want to increase without intersection.
2. Activate the **Multi-segment growing** tool (see Section 3.8.7). The dialog shown in Fig. 6.26 will be displayed.

3. The currently selected structure (base volume) is marked with a flag in the dialog. Check all the structures (base volume) whose masks you need to simultaneously increase with flags. If only one structure (volume) is checked, then the tool works similarly to the **Grow (dilation)** tool.

4. Set the maximum growing radius in the **Growing radius (mm)** field.

5. Click **OK** to apply the tool or **Cancel** to cancel action. The process takes some time. If the building is incomplete, repeat steps 2-4.

6. To undo or redo the action, use the **Undo** and **Redo** buttons for each structure you have built up.

*Figure 6.26: Multi-segment growing settings dialog*
6.8.7 Segmented structures regions growing Tool

Functionality is available in the **Pro** edition

This tool is used when several masks of segmented structures are to be grown in one iteration (including within editing mask) so that they do not meet. To use this tool, you need at least one structure that is not empty.

Proceed as follows:

1. Click the **Segmented structures regions growing** button. The dialog box shown in Fig. 6.27 will pop up.

2. In this dialog box, choose the structures whose masks to be grown.

3. If required, choose a structure or the main volume as the editing mask. You cannot choose the same structure for growing and as the editing mask.

4. Click **OK** to grow the structure or **Cancel** to cancel the operation. The process may take some time.

To undo this action, click the **Undo** button, to redo the action, click the **Redo** button.

![Figure 6.27: Dialog box for setting segmented structures regions growing](image)

In the tab for viewing the volume reconstruction, the mask is grown within the color table assigned to this structure; in the tab for viewing the multiplanar reconstruction — within the green editing mask.

The growth speed has exponential relationship with the distance to the boundaries of the editing mask within which the structure is grown. It allows for effective division of the areas linked by narrow connectors.
6.9 Union, subtraction and intersection of structures

Functionality is available in the Pro edition

This tool allows you to create the unions, intersections and subtractions structures masks. The button will look different depending on which instrument was last used:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>![Button]</td>
<td>Union (selected by default)</td>
</tr>
<tr>
<td>![Button]</td>
<td>Subtract</td>
</tr>
<tr>
<td>![Button]</td>
<td>Subtract dilated</td>
</tr>
<tr>
<td>![Button]</td>
<td>Intersect</td>
</tr>
</tbody>
</table>

To use a tool that is already selected, simply click on the tool buttons. To select another tool, click on the arrow on the right of the button and select an appropriate item from the list.

6.9.1 Union

Functionality is available in the Pro edition

The unification structures masks is the addition of one structure mask to another. The structure mask added structure remains unchanged. To unite structures masks of structures:

1. Select the current structure on the Segmented Structure Panel (e.g., the left lung).
2. Click on the **Union** button. The dialog box shown in Fig. 6.28 will be displayed.
3. Select the structure with the mask of which you want to merge the mask of the current structure. (e.g., the right lung). If you want to make the right lung invisible after the merging process, check the **Hide selected structure** box. To make it visible later, enable its visibility with the change structure visibility button on the segmented structure panel.
   If you want to hide the base volume, check the **Hide selected layer base volume** box. If you want the base volume to be displayed, enable its visibility with the change structure visibility button on the segmented structure panel.
4. If the **Place the result in a new structure** box is checked, a new structure is created, in which mask the procedure result is placed. The current structure is not changed.
5. To merge masks of structures, click **OK**, to cancel, click **CANCEL**.
After the merging process, the original structure tissue will consist of the tissues contained in both structures.

![Image of segmentation interface]

**Figure 6.28: Union**

### 6.9.2 Subtraction

*Functionality is available in the Pro edition*

The subtraction structures masks is the removal of voxels present in the mask of another structure from the original structure mask. To subtract structure masks:

1. Select the current structure on the Segmented Structure Panel (e.g., the lungs).

2. Click on the **Subtract** button. The dialog box, similar to the one shown in Fig. 6.28, will be displayed.
3. Select the structure whose mask you want to subtract from the current one (e.g., the right lung). If you want to make the right lung invisible after subtraction, check the **Hide selected structure** box. To make it visible later, enable its visibility with the change structure visibility button on the segmented structure panel.

If you want to hide the base volume, check the **Hide selected layer base volume** box. If you want the base volume to be displayed, enable its visibility with the change structure visibility button on the segmented structure panel.

4. If the **Place the result in a new structure** box is checked, a new structure is created, in which mask the procedure result is placed. The mask of current structure is not changed.

5. To subtract, click **OK**, to cancel, click **CANCEL**.

After subtraction, the right lung tissue will be removed from the original structure (Lungs).

### 6.9.3 Intersection

*Functionality is available in the Pro edition*

The intersection structures masks is the removal of all voxels from the one structure mask except those present in the masks of both structures. To intersect structures masks:

1. Select the current structure on the Segmented Structure Panel.

2. Click on the **Intersect** button. The dialog box, similar to the one shown in Fig. 6.28, will be displayed.

3. Select the structure whose mask you want to intersect with the current one. If you want to make the second structure invisible after intersection, check the **Hide selected structure** box. To make it visible later, enable its visibility with the change structure visibility button on the segmented structure panel.

If you want to hide the base volume, check the **Hide selected layer base volume** box. If you want the base volume to be displayed, enable its visibility with the change structure visibility button on the segmented structure panel.

4. If the **Place the result in a new structure** box is checked, a new structure is created, in which mask the procedure result is placed. The mask of current structure is not changed.

5. To intersect, click **OK**, to cancel, click **CANCEL**.

After intersection, the current structure will consist of the tissues contained in both structures.
6.9.4 «Subtract dilated» Tool

Functionality is available in the Pro edition

The Subtract dilated tool performs the morphological opening operation for the radius provided after subtraction. The morphological opening procedure is performed for the voxels corresponding to the voxels obtained as a result of dilation of the structure mask with the same radius. The radius is provided by the user in millimeters or voxels.

To subtract structure mask:

1. Select the current structure on the Segmented Structure Panel (e.g., «Structure 1»).
2. Click on the Subtract dilated button. The dialog box shown in Fig. 6.29.

![Editing structures dialog](image)

Figure 6.29: Editing structures dialog
3. Select the structure whose mask you want to subtract from the current one (e.g., the «Structure 2»). If you want to make the Structure 2 invisible after subtraction, check the Hide selected structure box. To make it visible later, enable its visibility with the change structure visibility button on the segmented structure panel.

If you want to hide the base volume, check the Hide selected layer base volume box. If you want the base volume to be displayed, enable its visibility with the change structure visibility button on the segmented structure panel.

4. In the Place the result in a new structure box is checked, a new structure is created, in which mask the procedure result is placed. The mask of current structure is not changed.

5. Click the OK button to apply the settings or CANCEL to cancel.

6. In the dialog box (Fig. 6.30), set the operation radius in millimeters or voxels.

```
Figure 6.30: Operation radius dialog box
```

7. To subtract, click OK, to cancel, click CANCEL.

### 6.10 Building Mask with Contours

Functionality is available in the Pro edition

#### 6.10.1 General Information

Contours are used for segmentation of the organs whose density is comparable with the density of the surrounding tissue, e.g., the heart, the liver, and joints. In such cases, it is hard to see the boundaries of the region. Hence, the automatic segmentation procedure cannot be applied.

Contours are built on sections in the MPR reconstruction tab. If the 3D view window is opened in the tab, the structure mask created is simultaneously shown on the volume model.

To customize the contours display, click the arrow on the right-hand side of the Contour segmentation button and provide the required parameters in the menu.
CHAPTER 6. SEGMENTATION

• To enable/disable the contours display on the volume model, check/uncheck the box next to the **Show contours in 3D** option. By default, the option is enabled.

• To enable/disable the synchronization point display when the user hovers over the contour, check/uncheck the box next to the **Show syncpoint** option. By default, the option is disabled.

• to enable/disable automatic rebuilding of a structure mask in alignment with the contours, check/uncheck the **Interactive voxelization** box. By default, this option is enabled. If the interactive voxelization option is disabled, use the **Voxelize** function on the tool context menu to rebuild the mask manually. For details, see Section 6.10.3.

6.10.2 Building a Structure Mask with Contours

To build a structure mask with contours, proceed as follows:

1. Open the study in the **MPR Reconstruction** tab. Create a structure with an empty mask and configure the editing mask by setting the tissue density. For the details on editing mask creation, see Section 6.2.1.

2. Activate the **Contour segmentation** tool by clicking the left/right/middle mouse button. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

   Build the contour in one of the following ways:

   • **Building contours manually.** Build a contour around the chosen area while holding the mouse button with which the tool was activated. To finish the procedure, release the mouse button. To cancel the contour that has not been closed, press **Esc** on the keyboard while holding the button.

   • **Building contours with an isoline.** Move the cursor around the selected area while holding the **Shift** button on the keyboard. Under the cursor, you will see an isoline characterized by even points density. You can only see an isoline on the surfaces where a contour can be built. To build a contour with an isoline, click the left mouse button or the mouse button with which the tool was activated.

3. Go to the next slice and draw a contour around the selected area. Contours are only built on parallel planes. Contours are used to create a mask with regard for the editing mask. You need at least two contours to build a structure mask.

   Structure mask may not be shown on the sections with the first and the last contour.

   **Building contours automatically with segmented structure sections.** Contours are built on the current section of the structure mask. The structure mask on which contours are built may be built with any tools. The following conditions must be met in order to build a contour on a structure mask:

   • the current section must be placed in parallel with other contours;

   • there must be no other contours of the same structure mask on the current section;

   • the structure mask must be visible on the current section.

312
6.10. BUILDING MASK WITH CONTOURS

Mouse over a section parallel to the structure mask contours. The mask should be visible in the current slice. Click the right mouse button and select the Create contour option from the menu, or press X on the keyboard. The contour will be built on the current section (indicated by the red arrow in the fig. 6.31) around the perimeter of the visible part of the current structure mask (indicated by the black arrow in the fig. 6.31). If a contour (or several contours) already exists on the current section, no other contour will be built.

To undo an action, click the Undo button, to repeat the canceled action, click the Redo button. You can use the Undo and Redo buttons to delete or restore the contours that were built in one click.

Contours projections are shown on perpendicular sections of the MPR reconstruction tab, in the 3D view window and on the sections where they were built. If a slice is not perpendicular to the contour plane, the projection of this contour is not shown.

When you hover over the contour line, it is highlighted in all the windows of the tab.

Figure 6.31: Building contours automatically with segmented structure sections

If the Show syncpoint option is enabled and the user hovers over the contour in any of the cutting plane windows or in the 3D view window, the crosshair under the cursor and the synchronized crosshairs on the contours in other windows of the tab are displayed.

If you click the mouse button while the cursor is on the contour line in the 3D view window, you will go to the section with this contour in the MPR reconstruction window.
6.10.3 Work with Contours

DICOM Viewer provides for the following actions with contours:

- **Editing.** To edit a contour, place the cursor over it. When you hover over the contour line, it is highlighted in all the windows of the tab. Place the cursor over the area that needs editing and click the mouse button. Draw a new contour while holding the button. To finish the editing procedure, release the mouse button.
  
  To undo an action, click the **Undo** button, to repeat the canceled action, click the **Redo** button. You can use the **Undo** and **Redo** buttons to delete or restore the parts of the contour that were built in one click (from the moment you press the mouse button to the moment the button is released);

- **Rebuilding a mask manually.** This function is used when the automatic structure mask rebuilding function is disabled in the **Contour segmentation** button menu. To do it, you need to mouse over the contour line, click the right mouse button and choose the **Voxelize** option on the context menu. If the contour is built for a structure mask created with the help of other tools, you will not be able to undo an action after voxelization. Before voxelization is performed, a dialog box pops up informing you that the change history will be lost (Fig. 6.32);

To accept the changes, click the **CONTINUE** button. To cancel voxelization, click the **CANCEL** button.

- **Deleting.** Place the cursor over the contour line, click the right mouse button and choose the **Remove contour** option in the right-click menu.
  
  To undo an action, click the **Undo** button, to repeat the canceled action, click the **Redo** button. You can use the **Undo** and **Redo** buttons to delete or restore the parts of the contour that were built in one click (from the moment you press the mouse button to the moment the button is released).

6.10.4 Setting the Contour Display Parameters

You can customize the contour display parameters in the **Tool options** dialog box (Fig. 6.33). The appearance and the functions of the **Tool options** dialog box depend on the way you call for it. There are two ways to call for the **Tool Options** dialog box:
6.10. BUILDING MASK WITH CONTOURS

1. Place the cursor over the contour line, click the right mouse button and choose the Tool options... point in the right-click menu. The dialog shown in Fig. 6.33a appears.

2. On the volume editing panel, click the arrow on the right-hand side of the Contour segmentation button and select Default options... from the button menu. The dialog shown in Fig. 6.33b appears.

![Figure 6.33: Contour parameter settings dialog box](image)

In the dialog box that pops up (see Fig. 6.33), in the Display section select the color and the contour line thickness in pixels. From the Interpolation drop-down list in the Voxelization section, select the interpolation type for the segmented structure built with contours. The interpolation types available are:

- **Linear**;
- **Hermitian spline** (set by default).

The interpolation type chosen will be displayed next time you open the structure selection dialog box.

The parameters selected in the dialog box Fig. 6.33a will be applied to the contours of the current structure mask. If you check the Set as default box, the settings will be used by default when building the contours of a new structure mask.

The parameters set in the dialog box shown in Fig. 6.33b are applied by default to the Contour segmentation tool. The changes are not applied to the built contours of masks. To restore the initial tool parameters, click the DEFAULT button.

Click OK to apply the settings or CANCEL to cancel.
6.11 Saving and Opening Segmentation Projects and DTI Projects

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The DICOM Viewer allows for saving segmentation projects and DTI projects in a file. One project may contain structures and DTI data from different series, as well as source DICOM data. If a project was saved without source DICOM data, it cannot be opened without downloading the corresponding series first.

Save segmentation project to file and Open segmentation project from file buttons (shown with the red frame in Fig. 6.34) are located on the segmented structures panel.

![Project management buttons](image)

*Figure 6.34: Project management buttons*

6.11.1 Saving a Project

To enable/disable the saving of source DICOM data, in the main menu, select Options->Settings...->Modules->3D reconstruction, then choose the Project tab and check/uncheck the Save DICOM data of series box. This option is activated by default.
The **DEFAULTS** button restores the checkbox **Save DICOM data of series**. Click **OK** to apply the settings or **CANCEL** to cancel.

To save a project, click the **Save segmentation project to file** button on the segmented structures panel. In the dialog box that pops up, provide the path to the file and the file name. Click **OK** to save or **Cancel** to cancel. The project file has (spj) extension.

Orientation and projection data on the model are saved in the project. The orientation and projection of the model is restored when the project is opened.

If the project is opened in the **MPR reconstruction** tab, the following characteristics are restored:

- cutting planes turn and arrangement;
- model position;
- model scale.

The turn of the model slice in the **MPR reconstruction** tab is not restored. If the project is opened in the **Volume reconstruction** tab or in the **3D view** window of the **MPR reconstruction** tab, the following characteristics are restored:

- model turn;
- model position;
• model scale;
• projection type.

If the project was saved in the MPR reconstruction tab and opened in the Volume reconstruction tab, the parameters that can be applied only to the 3D view window are restored.

The markers — Marker, Line marker, or Polygonal line marker — are saved in the project for each layer. The length and angle measurements performed with polygonal marker lines are saved in the project file. The work with markers is described in Section 5.11.

### 6.11.2  Saving Projects Automatically

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

Segmentation projects are saved automatically to prevent loss of data as a result of a program crash caused by a technical failure or the user’s actions. Autosave and data recovery are available in MPR reconstruction and Volume reconstruction tabs.

If the license for the extended segmentation module is active and it is the first time the user adds, deletes or edits

• a segmented structure or base volume;
• a surface for a segmented structure or base volume;
• a group of ROI DTI, or individual ROI DTI;
• a marker (except for segmented structure markers),

in the MPR reconstruction or Volume reconstruction tab, then a dialog box for segmentation projects autosave activation (Fig. 6.36) will pop up.

![Figure 6.36: Dialog box for segmentation projects autosave activation](image)

Click YES to enable segmentation projects autosave or NO to cancel.
To enable/disable segmentation projects autosave, on the main menu, select **Options**->**Settings...**->**Modules**->**3D reconstruction**, then choose the **Project** tab (Fig. 6.35) and check/uncheck the **Enable autosaving** box. By default, segmentation projects autosave is disabled. On the **Timeout** dropdown list, select autosave frequency. The default value is five minutes.

**Autosave option is available only when the extended segmentation module is activated. If the extended segmentation module is not activated, the Enable autosaving option is automatically disabled.**

Segmentation projects are automatically saved in the background mode without blocking the interface. Autosave frequency may be selected on the **Timeout** dropdown list.

When a segmentation project is saved automatically, a file with `.autospj` extension is created in a temporary system folder. This file contains:

- segmentation results;
- DICOM data source information.

The DICOM data source may be:

- a local storage;
- a folder with DCM files;
- a DICOMDIR file;
- an XML file;
- a third-party SPJ file;
- an archive with DCM files.

The data concerning the changes in the base volume in different tabs working with the current segmentation project are saved as separate segmented structures. If the user works with the same segmentation project in several **MPR reconstruction** or **Volume reconstruction** tabs, the data are automatically saved in the same file.

If a segmentation project is saved manually with the help of the **Save segmentation project to file** button on the segmented structures panel (see Section 6.11.1), the `.autospj` file is deleted automatically.

When the user closes the last tab of a segmentation project with unsaved changes, a dialog box for saving the project changes (Fig. 6.37) will pop up.

![Figure 6.37: Dialog box for saving the changes in a segmentation project](image-url)
Click **SAVE** to save the changes in the project or **DISCARD** to close the tab without saving the changes. To resume work on the project, click **CANCEL**. After the project has been saved or the changes have been discarded, the `.autospj` file is deleted automatically.

### 6.11.3 Resuming Work with Segmentation Projects

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

If the segmentation projects autosave option is enabled, an `.autospj` file is created and saved in a temporary folder.

The name of the `.autospj` file is generated as follows:

```
<patient name>_<description of the 1st layer series>…_<description of the n layer series>_<project #>_<time and date>.autospj,
```

where `<project #>` — is the unique number that is automatically assigned to a segmentation project for a series or a fused series, and `<time and date>` — is the time and date of the file creation in `hhmssddMMyyyy` format, where «hh» stands for hours, «mm» — for minutes, «ss» — for seconds, «dd» — for the day, «MM» — for the month, and «yyyy» — for the year.

The maximum length of the `.autospj` file name is 100 characters. If this limit is exceeded, the name will be cropped and a «~» symbol will be placed before `<project #>_<time and date>`.

![Disaster recovery settings](image)

*Figure 6.38: Dialog box with crash recovery settings*

In case of the program crash, the project file is restored automatically when the DICOM
6.11. Saving and Opening Segmentation Projects and DTI Projects

If there is an .autospj file in the temporary folder, it is decided that the project must be restored, and a dialog box for resuming work with the last autosaved version of the segmentation project pops up (Fig. 6.38).

In the Disaster recovery settings dialog box, check the autosaved files for the projects that have to be restored. If none of the files has been selected, the OK button is inactive. You can choose the mode in which the restored project will be opened: 3D, MPR or Both. Click OK to open the selected segmentation project in the mode specified or CANCEL to cancel.

If there are several projects, work with them will be resumed in the order in which .autospj files are listed in the Disaster recovery settings dialog box. If any of the projects cannot be restored, it does not affect the other projects.

If you click CANCEL, .autospj files are deleted from the temporary folder.

An .autospj file contains only the information on the third-party DICOM data source. If this source cannot be accessed, the segmentation project cannot be restored.

If the user cannot resume work with any of the segmentation projects as the DICOM data for the series are unavailable, a dialog box will pop up advising to save the data from the autosave file to a separate .spj file on the disk. After the user confirms that the data must be saved, a standard Save As dialog box pops up. The name of the file and its location are to be specified by the user.

After the file is saved or the user chooses not to save it, the .autospj file is deleted from the temporary folder.

6.11.4 Opening a Project with Source DICOM Data

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

When a project is opened, the DICOM Viewer shows it in the Volume Reconstruction or Multiplanar Reconstruction tab. To choose a default tab, in the main menu, select Options->Settings...->Modules->3D reconstruction, then choose the Project tab (Fig. 6.35), and choose the 3D, MPR or Both opening mode. The 3D mode is chosen by default.

The DEFAULTS button restores the checkbox Save DICOM data of series. Click OK to apply the settings or CANCEL to cancel.

Orientation and projection data on the model are saved in the project. The orientation and projection of the model is restored when the project is opened. For more information, see Section 6.11.1.

There are three ways to open a project containing source DICOM data in the default tab:

1. Choose the Open project... option in the File menu. Select the project file in the window that pops up. Click Open to open the project or Cancel to cancel.

2. Double-click with the left mouse button on the project file in the Explorer window. This function is available by default only on Windows OS. On macOS and Linux, you have to use the system functions to create a link between (spj) format and the DICOM Viewer software.
3. Drag and drop the project file to the DICOM Viewer shortcut (this option is only available on Windows and macOS). If you drag and drop several project files to the DICOM Viewer shortcut, each file will be opened in a separate tab.

To open a part of the project and specify the tab in which it is to be opened, proceed as follows:

1. In the main menu, select File->Open project as.... A window will pop up, in which you will have to choose the file containing the project for this series. Click Open to open the project or Cancel to cancel the action. The dialog box shown in Fig. 6.39 will pop up.

2. Choose the tab in which you want to open the project (3D, MPR or Both). The selected mode will be set by default.

3. Select the series in the Series list box that need to be opened. By default, all series of the project are selected. Uncheck the box against the series if you don’t want it to be opened in the project.

4. The order in which the series are displayed is important for working with the project. By default, the series are displayed in the Series list in the same order as when the segmentation project was saved. To change the series order, highlight a series in the Series list box. Use Move up and Move down buttons (indicated by the red frame in Fig. 6.39) to move the selected series up or down.

5. Click OK to open the project or CANCEL to cancel the operation.

6. The first series on the Series list is considered to be the basic series.

   - The basic series on the MPR tab is displayed as the background layer behind the other layers. The background layer is fixed. The center of the background layer coincides with the center of the window. You can move the layers about the background layer or each other with the help of the tools you see on the Fusion of layers panel. The procedure of merging layers is described in Section 4.3.

   - The project opened in the volume reconstruction window is displayed as 3D models created independently of each other. The basic series of the project is displayed as a 3D model fixed at the point of origin which is at the same time the center of the model. The models from other series are located in space with respect to the first layer model. The change of the order of the layers at the time of opening the project does not affect the mutual arrangement of the models.

If the project does not contain any source DICOM data, when you attempt to open it, an error notification will pop up: Cannot find DICOM data in the project file. The procedure of opening projects without DICOM data is described in Section 6.11.5.
6.11.5 Opening a Project without Source DICOM Data

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To open a project without source DICOM data, you first need to open the source data in the Volume Reconstruction or Multiplanar Reconstruction tab.

To open a project that does not contain any source data:

1. Open the initial series for which the project was saved in the Volume Reconstruction or Multiplanar Reconstruction tab.

2. Open the segmented structure panel by clicking the  button.

3. Click the Open segmentation project from file button on the segmented structure panel. A window will pop up, in which you will have to choose the file containing the project for this series. Click Open to open the project or Cancel to cancel the operation.

Orientation and projection data on the model are saved in the project. The orientation and projection of the model is restored when the project is opened. For more information see Section 6.11.1.
The segmented structures and DTI data for this series contained in the project are added to the segmented structure panel. When the project is opened for the second time, the data are added again without replacing the old data. When the structures are edited on the segmentation panel, the file contents are not changed. If a project file contains data for several series, only the data referred to the series that is currently open on the volume or multiplanar reconstruction tab will be added.

### 6.12 Histograms

Functionality is available in the Pro edition

The sections with color tables described in Section 2.20.3 are available for segmented structures. The difference is that in the Flat images view mode a histogram is built for the entire density range, and for the structure it is built only for the range of the density that corresponds to the structure mask.

### 6.12.1 Rendering a Histogram for a Structure

Functionality is available in the Pro edition

The DICOM Viewer provides for rendering histograms for the base volume and selected segmented structures.

To view a histogram for a selected segmented structure in the MPR Reconstruction window, click the Rendering transfer function button on the toolbar.

At the bottom of the tab, you will see the panel of the rendering transfer function with the histogram for the selected segmented structure. The color of the histogram for the selected segmented structure will be the same as the user color of the segmented structure. The name of the segmented structure is provided in the histogram legend.

If you have chosen the base volume on the segmentation panel, then only the base volume histogram will be displayed on the panel of the rendering transfer function. The changes in the visibility and transparency of the selected segmented structure or the base volume do not affect the histogram rendering.
When you hover over a point of the base volume or the selected segmented structure histogram, a tip pops up.

The pop-up tip provides the following parameters:

- **Chart** — the name of the histogram;
- **Density (HU)** — the Hounsfield density value;
- **Value** — the number of points characterized by the density value provided;
- **Normalized value** — is calculated by the following formula:

$$\frac{y - y_{\min}}{y_{\max} - y_{\min}}$$  \hspace{1cm} (6.1)

where:
- $y$ — the present histogram value;
- $y_{\min}$ — the minimum histogram value;
- $y_{\max}$ — the maximum histogram value.

The base volume and the name of the segmented structure is stated in the histogram legend.

If the **3D view** window is active in the **MPR Reconstruction** tab, then the histogram for the base volume and the transfer function for the current color table will be displayed on the panel of the rendering transfer function.

When you hover over a point of the rendering transfer function graph, a tip pops up.

The pop-up tip provides the following parameters:
• **Density (%)** — the density measured as percentage of the window width/level (W/L). The parameter is calculated by the following formula:

\[
D_\% = \left( D - \frac{\text{Min}_{W/L}}{\text{Max}_{W/L} - \text{Min}_{W/L}} \right) \times 100
\]

(6.2)

where:
- \( D \) — the density value;
- \( \text{Min}_{W/L} \) — the minimum window dimensions;
- \( \text{Max}_{W/L} \) — the maximum window dimensions;

• **Opacity** — the opacity value from 0.0 to 1.0.

The opacity value shown in the pop-up tip is rounded off to 0.001.

### 6.12.2 Histogram for a ROI

Functionality is available in the Pro edition

A histogram for a ROI is a graph for the density range of the points within the ROI. The DICOM Viewer displays histograms for ROI in the **Image Viewer** tab, **MPR Reconstruction** tab, and **PET Analysis** tab.

To view a histogram for a ROI in the selected window, click the **Rendering transfer function** button on the toolbar. At the bottom of the study tab, you will see the rendering transfer function panel with the histogram for the ROI and the rendering transfer function over it.

In the **Flat Image Viewer** tab, the histogram is built for all the ROI displayed in the selected tab window. When you add a new ROI, scroll or switch windows, the histogram for the ROI is changed accordingly.

If you have chosen a mode where several images of the same series are displayed simultaneously, e.g. 2x2, 2x3 etc., then the histogram for the ROI is built in the top left-hand corner.

In the **MPR Reconstruction** tab, histograms for ROI are shown in the **Axial plane**, **Sagittal plane**, **Coronal plane**, and **Involute** windows. If the **MPR Reconstruction** tab is open for merged series, then, when you switch layers, the ROI histogram is changed in accordance with the density values for the current section of the layer selected.

In the **PET Analysis** tab, the histogram is built for all the ROI of the current image in the selected window: **PT**, **CT**, or **Fusion (PET+CT)**. In the **Fusion (PET+CT)** window, the histogram is built for the PET layer.
Chapter 7

Vessel analysis module

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

In Vessel Analysis window, diagnosis can only be established on the basis of CT and MR series. The anomalies detected should be studied using the original images in the Image Viewer window.

Errors may occur when intensity is measured in a certain point. In this case, the intensity value will be marked by an asterisk. For accurate measurements, use the bilinear interpolation filter (see Section 5.3).

The DICOM Viewer allows you to open CT, MR and XA modality series in the Vessels analysis module.

The DICOM Viewer contains the Vessel analysis module (universal) and the Coronary artery analysis module (adapted for the analysis of the coronary arteries). Both of these modules are licensed separately. Their functionality basically coincides, and the differences are based on the location of the coronary arteries.

This chapter describes the Vessel analysis module. Differences related to the Coronary artery module are described in Section 7.7.

7.1 Open Studies in Vessel Analysis Module

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To open a study:

1. Load studies to the DICOM Viewer.
2. Select the angiographic study and the series with contrast.
3. Click the **Vessel analysis** button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open the virtual endoscopy window in a new tab in the current window, click on the button. The process may take some time.

If you open a CT study, then the DICOM Viewer promt you to select a series without contrast to remove bones.

**The dialog box for selecting a non-contrast-enhanced series pops up automatically only if the series is opened for the first time. When the same series is opened again, the dialog box does not pop up, but you can open it manually in the menu of the «New vessel» button.**

The following series are not shown in the dialog box for selecting non-contrast-enhanced series (Fig. 7.1):

- Series with a modality other than CT;
- Series incompatible with 3D;
- The current series (opened in the **Vessel analysis** tab).

![Choose non-enhanced series to remove bones](image)

*Figure 7.1: The dialog box providing an opportunity to select a non-contrast-enhanced series for deleting bones*

In the dialog that opens, select the series without contrast and click **OK** to remove bones or **CANCEL** to cancel deletion.
7.1. OPEN STUDIES IN VESSEL ANALYSIS MODULE

If the study does not contain any series with an opportunity to delete bones, the dialog box does not pop up.

To open the bone removal dialog (Fig. 7.1) manually, click the arrow on the right side of the New vessel button and select the Subtract bones item. The command is only available for series with CT modality. If there are no suitable series, a notification will pop up when the user selects the Subtract bones command.

This process takes some time.

To enable/disable the function of displaying a dialog box requesting a non-contrast-enhanced series for bones deletion when opening a study, in the main menu select the Options->Settings...->Modules->Vessel analysis, UI tab and check/uncheck the Request a non-enhanced series to remove bones on window opening box. The dialog box is displayed by default.

The vessel analysis window is shown in Fig. 7.2.

![The Vessel analysis window](image)

Figure 7.2: The Vessel analysis window

The windows display the axial, coronal, sagittal sections and a 3D view. In the 3D view window, you see a 3D model and a standard space orientation panel (for details see Section 3.3). These windows are used to build the centerline. Vessel sweep is displayed in the Involute curve window.

To cancel rotation of all the images and the involute curve, click the Reset views orientation button on the toolbar.
7.1.1 Vessels list

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The built centerlines can be saved on the list of vessels until the window is closed. To save the built line select the vessel category from the drop-down list **Categories** in the panel shown in Fig. 7.3; next, select the vessel below and click the **BIND** button. The pictogram appears to the right of the selected vessel on the list. To switch to the previously saved centerline, select the vessel on the list and click the **SWITCH TO** button. To remove the centerline from the list, click the **UNBIND** button. The pictogram disappears.

**Attention! If the current centerline is not bound to any of the vessels on the list, then when you build another line, it will be lost.**
7.2  «Render settings» Tool

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The Render settings tool allows for setting the rendering quality of the 3D model and the opacity threshold in the 3D view window. The tool is available on the toolbar of the Vessel analysis tab and Coronary arteries analysis tab. The operation of the tool is described in Section 3.14.

7.3 The Play Tool

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The tool in the MPR View windows is similar to that described in Section 2.13 and the tool in the Volume Reconstruction window is similar to that described in Section 3.7.

7.4 Video recording

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The DICOM Viewer allows you to record video for the MPR view, the surfaces view and the volume reconstruction view windows. The following objects will be recorded:

- tissues;
- measurements;
- annotations;
- markers;
- tags;
- orientation cube;
- the center line.

The other features of the tool in the MPR View windows are similar to those described in Section 2.13 and the features in the Volume Reconstruction window are similar to those described in Section 3.7.
7.5 Centerline building mode

For analysis, it is necessary to build a centerline which is automatically located in the notional center of the vessel. Only one centerline can be built at a time. To save the built line and build a new one, bind it to a specific vessel from the list in the left part of the window (see Section 7.1.1).

You need to control the process of building the centerline and make corrections, if needed.

7.5.1 Building the centerline

You can build the centerline in two methods. To select a method click the arrow on the right side of the **New Vessel** button and select the appropriate method (Fig 7.4). The current method is marked with a flag.

![Select a method to build the centerline](image)

**Figure 7.4: Select a method to build the centerline**

1. Building by one point. In this mode the line is built in both directions from the starting point for a maximum distance. If the vessel splits along the construction line, then the line is built in an arbitrary branch. To build the line, click the left mouse button at the starting point. To extend a vessel line, left-click in the right spot. The line will be built from the closest existing point and will pass through the new point.

2. Building by two points. In this mode, the line is built from the starting point to the end point. To build the line, click at the starting and end points. The DICOM Viewer adds the
required number of intermediate points to set the centerline. If the line is not completely built, then select the point up to which you want to extend the line and click in at it. The line will be built from the nearest existing point.

If the centerline for the selected points cannot be built, then the message **Unable to trace vessel centerline from this point(s)** appears.

If the line is not built correctly, then start building it again by clicking on the **New vessel** button or edit the line.

- **Drag a point.** Locate the cursor on the center line of the vessel. The points are displayed when you hover the cursor over the center line of the vessel. Select a point on the curve you need to move. The selected point is centered in the cutting planes windows. While holding the left mouse button, move the point in the cutting planes windows. To escape from the **Drag a point** mode, left-click near the curve.

- **Add a point.** Locate the cursor on the center line of the vessel. The points are displayed when you hover the cursor over the center line of the vessel. To add a point, move the cursor to the place where you want to add a point, right-click and in the context menu and select the **Add point** command. The centerline will change so as to pass through a new point. A new point may be added to extend the centerline of a vessel.

- **Continue curve to the end of the vessel.** Locate the cursor on the center line of the vessel. The points are displayed when you hover the cursor over the center line of the vessel. To extend a curve, select the end point on the curve, right-click and select the **Trace from this tip** command in the context menu. The curve will be extended to the end of the vessel.

- **Delete part of a curve (segment).** To delete part of the line, delete a segment. The segment is deleted along with the shorter part of the line adjacent to the point. To delete a segment, right-click on the first point of the segment and select the **Remove segment** item. The shorter part of the centerline is removed from one side of the point and the section between this and the next point from the other side.

- **Delete a point.** Locate the cursor on the center line of the vessel. The points are displayed when you hover the cursor over the center line of the vessel. To delete a point, move the cursor over this point so that all the points are highlighted, right-click and in the context menu and select the **Remove point** command.

The initial research data or the volume reconstruction data can be used for building. To select the data source, click the arrow on the right side of the **New vessel** button and select the appropriate source.

The centerline is shown in Fig. 7.5.
To choose the vessel centerline visibility mode, click the arrow on the right-hand side of the **New vessel** button and choose the **Centerline visibility mode** option (see Figure 7.6). The same command is available in the right-click menu. The current centerline visibility mode is ticked.

- **Always.** The vessel centerline is always displayed in the **Cutting planes** windows, as well as in the **Volume reconstruction**, **Involute curve**, and **Straightened vessel** windows. If you mouse over the centerline, you will see the points.

- **Hover.** The vessel centerline is always displayed only in the **Volume reconstruction** window. The vessel centerline is displayed in the **Cutting planes** windows, as well as in
the **Straightened vessel** and **Involute curve** windows if you mouse over it or select one
of the points.

- **Never.** The vessel centerline is always displayed only in the **Volume reconstruction**
  window. It is not displayed in any other windows.

The vessel centerline visibility settings will be applied next time you open the Vessel anal-
ysis window.

### 7.6 Vessel Analysis Mode

Functionality is available in a separate module which is activated in the Pro edition for an extra
fee

After building the necessary centerlines, switch to the Vessel analysis mode by clicking on
the **Analysis mode** button. The window in the Vessel analysis mode is shown in Fig. 7.7.

![Figure 7.7: The vessel analysis mode](image)

The volume reconstruction is shown in the **3D view** window, the curved surface is shown
in the **Involute curve** window. The vessel sweep following the straightening of its centerline
and the marking of its borders is shown in the **Straightened vessel** window. The sections by
the planes that are perpendicular to the centerline are shown in the **Section** window.

You cannot edit the centerline in the Vessel analysis mode. To do it switch to Centerline
building mode by clicking the **Analysis mode** button.
CHAPTER 7. VESSEL ANALYSIS MODULE

7.6.1 Vessel borders

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The DICOM Viewer calculates the inner and outer borders of a vessel and the border of calcifications inside a vessel (Fig. 7.9). If no calcifications are found, then the corresponding value remains empty.

If the Adaptive box is checked, threshold density values will be evaluated for each vessel section individually. This ensures more accurate display of contours of vessels and calcifications. The box is checked by default.

To see the tissues that correspond to the density ranges, click the Show vessel tissue button. In the Section views window the tissues with an intensity between the inner border and the calcium border (vessel lumen) are highlighted in green, the tissues with an intensity between the outer and inner border (vessel wall) are highlighted in brown, and the tissues with an intensity higher than the calcium border (calcifications) are highlighted in white. The borders of the vessel are built in accordance with the threshold values, but due to certain smoothing they do not exactly correspond to the threshold values. In the Straightened vessel window, the green line indicates the inner border of the vessel, the red line indicates the outer border (fig. 7.10).

If the Adaptive box is checked on the threshold value panel, then threshold density values are only highlighted in the Section views window as in this case threshold density values are evaluated for each vessel section individually. If the Adaptive box is unchecked, threshold density values are also highlighted in the Straightened vessel window.

The central line is shown as a straight line.

To edit borders, activate the Edit vessel contours tool, click the left mouse button at an arbitrary place near the border, the border will pass through the selected point. When you move the mouse while holding the left button, the border repeats the path of the cursor.

You need to control the process of boundaries creation, as well as the threshold boundary and calcification values. If needed, change the boundaries and the threshold values manually.

To choose a visibility mode for vessel contours, press the arrow on the right-hand side of the Analysis mode button and select the Contours visibility mode command (Fig. 7.8). The same command is available in the right-click menu if the vessel analysis mode is active. The current contours visibility mode is ticked.
7.6. VESSEL ANALYSIS MODE

Figure 7.8: Select the contours visibility mode

- **Always.** Vessel contours are constantly displayed in Section views and Straightened Vessel windows. The mode is selected by default.

- **Hover.** Vessel contours are displayed in Section views and Straightened Vessel windows when the user hovers over the contours.

- **Never.** Vessel contours are not displayed in any windows of the tab.

To change the threshold values, uncheck the Adaptive box and enter new values in the appropriate fields and click the APPLY button. The border will be rebuilt in accordance with the new values. To return to the threshold values calculated automatically, click the RESTORE button.

Figure 7.9: Threshold value panel

To undo the all changes and return to the initial borders, click on the arrow on the right side of the Analysis mode button button and select the Rebuild edges command.

At the bottom of the Straightened Vessel window, there is a graph showing changes in the vessel lumen. The areas in which stenosis is possible are highlighted in red on the graph, the remaining sections are highlighted in green.
7.6.2 Section analysis

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To add a section, move the cursor to the centerline in the Involute curve, Straightened vessel or 3D view window, right-click and select the Add section command or Add reference to add a reference section.

To delete a section, select the Remove section command in the context menu of the section or click on the cross in the upper right-hand corner of the current section window (Fig. 7.11).

The position of the cross on the section corresponds to the position of the centerline. The borders are outlined by the green and red lines. When editing borders in the current section window (Fig. 7.11), the Edit vessel contours tool can be deactivated.

The yellow line in the current section window shows the cutting plane for the current section shown in the Straightened vessel window. To rotate the cutting plane, move the cursor over it so that a bidirectional arrow appears, hold the left mouse button and move the mouse.

The following parameters are calculated in the section view windows:

- Lumen
- Short diameter
- Long diameter

with the percentage of stenosis.

If you set one section as a reference, then the diameter and lumen values for the other sections are relative to the corresponding values for the reference section. If you set two sections as a reference, then the values for the other sections are relative to the average values for the reference sections. It is recommended to locate the reference sections on both sides of the section of interest if the vessel narrows. To set the type of the section, select it from the drop-down list in the upper left-hand corner of the section view window (Fig. 7.11).
7.6.3 Curved surface analysis

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

A vessel sweep is displayed in the **Involute curve** and **Straightened vessel** windows.

The **Straightened vessel** window displays the distance from the beginning of the vessel to the cross section.

To analyze the vessel interval, select this interval in the **Straightened vessel** window. To do this, move the cursor to the beginning of the interval and move the mouse to the end of the interval, holding down the left mouse button, then release the button. The built interval is shown in Fig. 7.12. The borders of the interval are displayed as white sections.
The following parameters are calculated for the interval:

- Length;
- Avg lumen;
- Min lumen;
- Avg SD;
- Min SD.

To move the interval border, move the cursor to the corresponding white section in any of the **3D view**, **Involute curve** or **Straightened vessel** windows and move it with the mouse while holding down the left button. To delete an interval, click the left mouse button at an arbitrary place in the **Straightened vessel** window. To build multiple intervals, build them holding down the **Ctrl** button on the keyboard.

**7.6.4 Export vessel surface mesh**

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To export the vessel surface to a file, click on the **Export vessel surface mesh** button, in the dialog that opens, select the file type (ply, obj or stl) and save the surface.
To close the ends of the vessel, click on the arrow on the right side of the Export vessel surface mesh button, select the Export parameters... item and in the dialog that opens, check the Close sides box.

## 7.7 Coronary Artery Analysis

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

In Coronary Artery Analysis window, diagnosis can only be established on the basis of CT series. The anomalies detected should be studied using the original images in the Image Viewer window.

The DICOM Viewer contains the Coronary Artery Analysis Module to analyze the coronary vessels. Its functionality is basically the same as that of the Vessel Analysis module.

An advantage of the Coronary Artery Analysis module is the automatic detection of the aorta. The central line of the coronary artery is cut off at the entrance to the aorta.

The features of the Coronary Artery Analysis module are:

1. Only the CT series are suitable for analysis.
2. The module does not contain the bone subtraction functionality.
3. Only coronary arteries are available on the vessel list.

To open a series in the Coronary Artery Analysis window, click the Coronary Artery Analysis button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open the Coronary Artery Analysis window in a new tab in the current window, click on the button. The process may take some time.

The Coronary arteries analysis tab comprises the windows with Axial, Coronal, and Sagittal plane sections, as well as the 3D view window. In the 3D view window, you see a 3D model and a standard space orientation panel (for details see Section 3.3). In the Involute curve window, the vessel involute is displayed.
Chapter 8

PET analysis

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

8.1 Open Studies in PET Analysis tab

To open a study:

1. Load studies to the DICOM Viewer.
2. Select a study containing at least one CT and one PET series.
3. Select one CT and one PET series by clicking the left mouse button while holding down the Ctrl key on the keyboard.
4. Click the PET analysis button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open the study in a new tab in the current window, click on the button PET analysis. The process may take some time.
5. Choose a windows arrangement template for the required number of series (see Sections 8.2.1 and 8.2.2).

The DICOM Viewer displays data in the following modes:

- 3D MIP (Maximum Intensity Projection) for the PET series (3D MIP mode);
8.1. OPEN STUDIES IN PET ANALYSIS TAB

- Original CT series (CT mode);
- Original PET series (PET mode);
- Fused CT + PET series (Fusion (PET+CT) mode). The image displayed in the window is the same as in the fused series window (see Chapter 4).

The PET analysis window is shown in Fig. 8.1.

![PET analysis window](image)

**Figure 8.1: PET analysis window**

### 8.1.1 Fuse series from the same study in the PET analysis tab

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To fuse series of one study, proceed as follows:

1. Open the study in the PET analysis tab (see Section 8.1).
2. On the series panel of current study select the series required by left-clicking on them while holding down the **Ctrl** key.
3. Drag the series to the window you need. If the series may be dragged to this window, the cursor will have the shape of ![image](image). If it is impossible to drag the series to this window, the cursor will have the shape of ![image](image). In this case, choose another window or change the display mode in this window (Section 8.2.1). Release the mouse button. The series (fused series) will be opened in this window.
4. If needed, repeat the actions described in points 2-3 for other series.

8.1.2 Fuse series from different studies in the PET analysis tab

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The DICOM Viewer allows you to fuse series from different studies in the PET analysis tab, e.g. to monitor the changes. If the studies differ in the following parameters:

- the patient's name (not case sensitive) (tag (0010,0010));
- the patient's ID (tag (0010,0020));
- the patient's sex (tag (0010,0040));
- the date of birth (tag (0010,0030))

such studies are considered to be carried out for different patients. If you attempt to open them in the same tab, the following notification will pop up: **Maybe you are trying to add study from different patients. Would you like to continue?** To add the study, click **YES**, to cancel click **NO**.

To fuse several series from different studies, proceed as follows:

1. Open the series of the first study in the PET analysis tab.
2. Go to the second tab with the list of studies and choose the second study.
3. Select the studies required by left-clicking on them while holding down the **Ctrl** key.
4. Holding down the left mouse button, drag the series to the PET analysis tab (surrounded by the red frame in Fig. 8.2). Do not release the button. The PET analysis tab is displayed above other tabs.
5. Drag the series to the window you need. If the studies may be dragged to this window, the cursor will have the shape of 🔄. If it is impossible to drag the studies to this window, the cursor will have the shape of 🚫. In this case, choose another window or change the display mode in this window (Section 8.2.1). Release the mouse button. The series (fused series) will be opened in this window.
6. If needed, repeat the actions described in points 2-5 for other series.

![Figure 8.2: PET analysis tab button](image)
8.2. PET ANALYSIS TAB ELEMENTS

8.1.3 Viewing Images of a Series in the PET Analysis Tab

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The procedure of viewing images of a series in the PET analysis tab is similar to viewing series in the flat image viewer tab, which is described in Section 2.5.

8.2 PET Analysis Tab Elements

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

8.2.1 PET Analysis tab Windows

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The PET analysis tab may contain 1-6 image viewing windows:

- One window;
- Two windows side by side;
- 2X2 grid;
- 2X3 grid.

The mode may be changed by pressing the respective button on the toolbar. The button will look different depending on the current mode:

<table>
<thead>
<tr>
<th>3D MIP</th>
<th>3D MIP mode. The mode may be switched to Mono PET</th>
</tr>
</thead>
<tbody>
<tr>
<td>PT</td>
<td>Mono-PET mode. The mode may be switched to 3D MIP</td>
</tr>
<tr>
<td>CT</td>
<td>Mono-KT mode</td>
</tr>
<tr>
<td>PT+CT</td>
<td>Fusion PET+KT mode. The mode may be switched to Mono CT</td>
</tr>
</tbody>
</table>
To switch the mode, activate the respective window by left-clicking on it, click the mode button and choose the mode you need from the menu. The current mode is highlighted in blue. The procedure of setting the template for each mode is described in Section 8.2.2.

On the left, you can see the Series List panel showing all the series for the study. To open the required series in the PET Analysis window, drag it into the window. The MIP window may only be used for PET series, but you can drag PET, CT or fused series to other windows.

Double-click any of the four windows with the left mouse button to unfold it. Please, note that you shouldn’t activate any of the measuring tools, annotation tools or the magnifier with the left mouse button.

### 8.2.2 Setting the templates for windows arrangement in the PET analysis tab

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To set the windows arrangement templates, click the mode selection button ( depending on the mode) and select Settings... A dialog box shown in Fig. 8.3 will pop up.

![Figure 8.3: Dialog box for setting window arrangement templates](image)

Choose a template from the drop-down menu (One, Two near, 2x2, 2x3). To use this template as default, tick the Use current template as default box.
To set a template window, select this window with the mouse. It will be highlighted (in Fig. 8.3 the upper left window is selected). Then proceed as follows:

1. Choose the modality from the drop-down menu (Unspecified, CT, PT or PT+CT). If the Unspecified modality has been chosen, the cell will be empty.

2. The DICOM Viewer allows you to open either only the corrected PET series or only those that haven’t been corrected. To choose the series to be opened, check either Corrected or Uncorrected in the Data box. The default value is Uncorrected. If a series does not comply with this parameter, it will not be shown.

3. Check the MIP box for the PET series to display the maximum intensity projection.

To restore the default settings for the current template, click the DEFAULT button. In the dialog box that pops up, click YES to restore the settings or NO to cancel. By default, the following template settings are provided:

1. One Template: PET+CT combination is shown.

2. Two near Template: 3D MIP for the corrected PET series in the left window, Fusion (PET+CT) — in the right window.

3. 2x2 Template: from left to right, downwards: 3D MIP for the corrected PET series, corrected PET series, CT series, Fusion (PET+CT).

4. 2x3 Template: from left to right, downwards: 3D MIP for the corrected PET series, corrected PET series, CT series, Fusion (PET+CT), two empty windows.

Click OK to apply the settings or CANCEL to cancel the operation. The changes in the template do not affect the tabs that had been opened before such changes were introduced.

### 8.3 MIP mode

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The DICOM Viewer allows you to change the section thickness for flat images, i.e. the image is actually shown in MIP (Maximum Intensity Projection) mode. To change the section thickness, you need to sort the images by phases and frames (the default setting for the sorting procedure; for details see Section 2.1). The changes are possible within 0-50 mm range. You cannot make the section thinner than the source image.

To change the thickness, use the tool shown in Figure 8.4, which you will find on the right-hand side of the window in Mono-CT, Mono-PET and Fusion PET+CT modes (see Section 8.2). In the centre you can see the current section thickness. The sliders adjusting the thickness are marked with arrows. To change the thickness, you need to move either of the sliders by pressing the left, right or middle mouse button. To make the section thicker, move the slider outwards, to make it thinner — inward.
The thickness set with the help of the tool is used when exporting and adding to the print list.

![Figure 8.4: The section thickness tool for MIP](image)

When you are working with such tools as **Point value**, **ROI rectangle**, **ROI ellipse** and **ROI polygon**, the data shown are for MIP mode images. When the thickness is changed, the value is automatically scaled. All the other measurements are performed for the source data.

### 8.4 The Play Tool

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The tool is similar to that described in Section 5.9.

### 8.5 Video recording

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The tool is similar to that described in Section 2.13.
8.6 PET Window settings

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

For details see Section 15.6.8.

8.7 Image Positioning

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

Use the following tools for image positioning:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reset views</strong></td>
<td>The tool cancels all the actions made with the <strong>Rotate</strong>, <strong>Zoom</strong>, <strong>Pan</strong> tools.</td>
</tr>
<tr>
<td><strong>Rotate</strong></td>
<td>The tool is described in Section 2.14. It allows to rotate images.</td>
</tr>
<tr>
<td><strong>Zoom</strong></td>
<td>The tool is described in Section 2.14. It allows to zoom images. If the other windows displays images in the same projection, they are scaled synchronously.</td>
</tr>
<tr>
<td><strong>Pan</strong></td>
<td>The tool is described in Section 2.14. It allows to pan images. If the other windows displays images in the same projection, they are moved synchronously.</td>
</tr>
<tr>
<td><strong>Axial projection</strong></td>
<td>The tool displays images in the axial plane.</td>
</tr>
<tr>
<td><strong>Coronal projection</strong></td>
<td>The tool displays images in the coronal plane.</td>
</tr>
<tr>
<td><strong>Sagittal projection</strong></td>
<td>The tool displays images in the sagittal plane.</td>
</tr>
<tr>
<td><strong>Sync series scroll</strong></td>
<td>The tool allows you to simultaneously scroll the images in the PET, CT and PET+CT windows.</td>
</tr>
<tr>
<td><strong>Select model point</strong></td>
<td>The tool displays in the PET, CT and PET+CT windows the images corresponding to the point selected in the MIP window.</td>
</tr>
</tbody>
</table>

The MIP projection rotates around a vertical axis. To rotate move the cursor right and left holding the left button, or move the scroll slider.
8.8 Visualize Images

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

Color tables are needed for displaying pixels and voxels representing different density values in different colors for improved perception. The shades on the screen are different from the real shades.

Image visualization is described in Section 2.20. To change the CLUT for a specific window, first select this window with a mouse click. In the PET+CT window you can change the CLUT for the PET layer only.

To change the PET layer opacity in the PET+CT window, move the slider at the top of the PET+CT window (marked with number «1» in Fig. 8.5).

The PET+CT window contains the scale of the CLUT for the PET layer (marked with number «2» in Fig. 8.5). If the SUV mode is disabled, the scale borders coincide with the minimum and maximum window values for the PET layer. If the SUV mode is enabled, then the scale borders coincide with the minimum and maximum values of the SUV in the current image of the PET layer.

![Figure 8.5: The PET+CT window](image)

Changing the window width and the window level using the Adjust W/L tool is described in 2.15. To change the window width and the window level for CT images in the CT and PET+CT windows, select the CT window with the mouse. To change the values for all PET images, select any window with the mouse, except for the CT window.
Attention! You can change only the upper window limit in the PET+CT and PET windows for the PET layer, using the «Adjust W/L» tool.

The default upper window level value is determined by the Window upper limit setting. There are two ways to adjust the upper limit:

1. **Max SUV value.** In this case, the default window upper limit is set equal to the corresponding value in the SUV mode.

2. **Max window percent.** In this case, the default window upper limit is set equal to the specified percentage of the recommended window width. Since the default lower limit for PET is zero, the window width is numerically equal to the upper limit, and the percentage is actually calculated from its value. If different recommended upper limits are set for different images of the series, then the percentage is calculated from the maximum of these values.

### 8.9 Measurements and Annotations

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

Use the following tools to measure:

<table>
<thead>
<tr>
<th>Tool</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ruler</td>
<td>The <strong>Ruler</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>Polygonal ruler</td>
<td>The <strong>Polygonal ruler</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>Angle</td>
<td>The <strong>Angle</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>Point value</td>
<td>The <strong>Point value</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>ROI rectangle</td>
<td>The <strong>ROI rectangle</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>ROI ellipse</td>
<td>The <strong>ROI ellipse</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>ROI polygon</td>
<td>The <strong>ROI polygon</strong> tool is described in Section 2.17</td>
</tr>
<tr>
<td>VOI Sphere</td>
<td>The <strong>VOI Sphere</strong> tool is described in Section 8.10</td>
</tr>
<tr>
<td>Delete all annotations and measurements</td>
<td>The <strong>Delete all annotations and measurements</strong> tool is described in Section 2.17</td>
</tr>
</tbody>
</table>
To open the SUV settings dialog click the arrow on the right side of the Show SUV button and select the Settings... item.

To display the SUV value after opening a study in the PET analysis window, set the Enable SUV mode automatically (see Section 15.6.8). If there is not enough data to calculate SUV, then a dialog for entering parameters is displayed. For details, see Section 2.21.

8.10 Measure the Intensity Average and Standard Deviation in Space

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The VOI Sphere tool is similar to the ROI tools described in section 2.17, but the measurements are performed in the space bounded by a sphere.

8.10.1 Create sphere

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

To create a sphere:

1. Select a series to measure, go to the image in which the center of the sphere should be located.
2. Activate the **VOI sphere** tool by clicking the button on the toolbar. To continue work with this tool, use the button with which the tool was activated. To learn more about tool control, see Section 1.14.

3. The VOI sphere can be built in two ways:

   - Move the cursor to the point where the center of the sphere should be located. Click mouse button. Choose the desired sphere diameter by moving the mouse. To complete the drawing, click the mouse button.
   - Click the mouse button at the point where the center of the sphere should be located and set the desired sphere diameter while holding the mouse button. Release the mouse button to fix the sphere diameter.

4. To cancel creation, press the **Esc** button on the keyboard.

The following parameters are displayed near the sphere (Fig. 8.5):

- minimum intensity value;
- maximum intensity value;
- average intensity value;
- standard deviation;

The results only for the corresponding series are displayed in the CT and PET windows, the results for both series are displayed in the PET+CT window.

### 8.10.2 Sphere location in space

---

**Functionality is available in a separate module which is activated in the Pro edition for an extra fee**

---

All spheres are always displayed in the MIP window. The line of the intersection of the sphere with the image plane and the measurement results are displayed in the other windows. As the distance from the center of the sphere increases, the diameter of this circle decreases. If the sphere does not intersect with the image plane, the measurement results for the sphere are not displayed in this window.

If the center of the sphere is in the current image and the **VOI Sphere** tool is activated, crosses are displayed in the center of the sphere and on its border.
CHAPTER 8. PET ANALYSIS

8.10.3 Actions with the sphere

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

To edit a sphere:

1. Go to the image that contains the center of the sphere. To do this, slide the images until the crosses appear in the center and on the border of the sphere.

2. To move the sphere, move the cursor over the cross in its center and move the mouse holding down any mouse button. When you locate the cursor over the cross it increases.

3. To change the radius, move the cursor over the cross on the sphere border and move the mouse, holding down any mouse button. When you locate the cursor over the cross it increases.

To move the block with the measurement results, locate the cursor over it and move the mouse, holding down the left mouse button or the button to which this tool is assigned. For this, it is not necessary that the center of the sphere be on the current image.

To remove a sphere right-click on the corresponding block with the measurement results or on the cross in the center or on the border of the sphere and select the Remove object command.

8.10.4 Drawing Parameters

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

To change the drawing parameters:

1. Locate the cursor over the block with the measurement results or on the cross.

2. Right-click.

3. Select the item Tool options... in the context menu.

4. In the dialog box that appears, set the color by clicking on the color box.

5. Set the object name, the line thickness and the font size.

6. To connect the block with the measurement results and the sphere of the dotted line, check the Footnote line box.

7. To use these settings by default, check the Set as default box.

8. To apply the settings, click OK. To cancel, click CANCEL.
8.11 Synchronization in the PET analysis tab

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

Synchronization will be applied if several images from the same study are opened in the PET Analysis tab. This function provides an opportunity to scroll images from different series simultaneously. By default, image scrolling is synchronized for the same study.

All the series are panned and zoomed simultaneously, including the series from different studies.

To enable synchronization:

1. Click on the arrow on the right side of the Sync series scroll button on the toolbar.

2. Check one of the following items:
   - **Sync series (Same study)**. This option provides an opportunity to scroll images from the series with the same values of the `frameOfReferenceUid` tag simultaneously. If the values of the `frameOfReferenceUid` tag are different for different series, synchronization will not be performed;
   - **Sync from current position**. This option provides an opportunity to scroll images simultaneously from the current position.

3. If this button is not pressed, press it.

Synchronization is performed for the sections parallel to the synchronizing section.

To disable synchronization, click on the Sync series scroll button.
Chapter 9

Virtual Endoscopy

9.1 Open Studies in Virtual Endoscopy window

Functionality is available in the Pro edition

To open a study in the virtual endoscopy window:

1. Load studies to the DICOM Viewer.

2. Select the target study from the study panel.

3. Click the Virtual endoscopy button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open the virtual endoscopy window in a new tab in the current window, click on the button. The process may take some time.

The virtual endoscopy window is shown in Fig. 9.1.
9.2. VIEW ELEMENTS. CUSTOMIZE MPR PANEL

9.2 View Elements. Customize MPR Panel

9.2.1 View Elements

Functionality is available in the Pro edition

The toolbar is displayed in the top left part of the tab (Fig. 9.2).

![Toolbar](image1)

Figure 9.2: Toolbar

The MPR navigation panel is on the right side of the tab. The view setup panel is in the top right part of the tab (Fig. 9.3).

If the camera is in dense body tissues, there will be no image on the left side of the screen. In this case, you need to move the camera to a body cavity manually. For details on how to move the camera, see Section 9.3.
Once you start auto-moving (see Section 9.3.1), the cavity surface sweep will appear at the bottom of the window (Fig. 9.4).

Cavity surface sweep should only be used for navigation purposes. You cannot make a diagnosis on its basis. To establish a diagnosis, open the respective series in the Image Viewer window.

9.2.2 Customize MPR Navigation Panel

Functionality is available in the Pro edition

The MPR (multiplanar reconstruction) panel consists of three parts, each displaying a body section by one of the three orthogonal planes.

To hide/display the MPR navigation panel, click the MPR navigation button on the toolbar.

To change the panel size, move its border. To do this, move the cursor to the panel border so that it would look like this: ⬤, and drag the border holding the left mouse button.

To change the size of the panel parts displaying the sections by various planes, move the borders dividing the panel parts.
9.3 Move Camera

9.3.1 Move Camera Automatically

Functionality is available in the Pro edition

If the camera is moved automatically, there is a danger to overlook important areas. Use this option only in combination with manual control.

To move the camera automatically:

1. Drag the camera to a body cavity, using the MPR navigation panel. If the left side of the screen displays the red cavity surface, it means that the camera is in the cavity. If not, the camera is located in dense tissues. In this case, correct its position.

2. Start auto-moving by clicking the Space key or the Fly-through camera button on the toolbar.

The camera can be stopped in a similar way.
After you activate automatic movement, the central line appears. The camera moves along the central line. The color of this line is green. The vertical line on the sweep panel corresponds to the camera position.

If the image quality is poor, the central line may be drawn incorrectly. You need to make sure that it is drawn correctly.

To increase the movement speed, press + on the keyboard, to decrease the speed, press -.

9.3.2 Manage Camera Manually

Functionality is available in the Pro edition

You can manage the camera manually, using the cursor management keys. Key functions:

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>move the camera forward</td>
<td>move the camera back</td>
</tr>
<tr>
<td>rotate the camera anticlockwise</td>
<td></td>
</tr>
</tbody>
</table>
CHAPTER 9. VIRTUAL ENDOSCOPY

To manage the camera, using the mouse and the keyboard:

1. To change the camera rotation angle, move the mouse, holding the wheel. The camera turns in the same direction as the cursor. The camera direction vector will be displayed on the MPR navigation panel.

2. To move the camera over the image plane, move the mouse, holding the wheel and the **Shift** key. The camera turns in the same direction as the cursor.

3. To move the camera at random, use the MPR navigation panel. Click the left mouse button at the target place in any projection window or move the mouse, holding the left button. The camera will move in the same direction as the cursor.

4. To move the camera along the central line, move the surface sweep, holding the left button. The vertical line on the sweep panel corresponds to the camera position.

5. To point the camera at the point on the surface, click the right mouse button on this point on the sweep panel.

9.4 Video recording

*Functionality is available in the Pro edition*

The DICOM Viewer allows you to record video for the surface view window. The following objects will be recorded:

- tissues;
- the center line;
- measurements;
- markers;
- tags;
- orientation cube;

The other features of the tool in the MPR View windows are similar to those described in Section 2.13.
9.5 Customize Image

Functionality is available in the Pro edition

To increase or decrease the camera angle, turn the mouse wheel backward or forward respectively. To change the view configuration, use the visualization setup panel in the top right part of the tab. For details on how to work with the panel, see Section 5.4.

9.6 Measurements and Markers

Functionality is available in the Pro edition

The DICOM Viewer allows you to place markers on an image and conduct linear measurements. For details on working with the Marker tool, see Section 3.12. The use of the Ruler and Polygonal ruler tools is described in Section 2.17 and Section 3.11.2. However, in the virtual endoscopy window you should switch between the Polygonal ruler and Ruler tools, using the menu that opens by clicking on the arrow on the right side of the button (or in the polygonal ruler mode).

9.7 Multiplanar Reconstruction

Functionality is available in the Pro edition

To switch to multiplanar reconstruction, click the MPR reconstruction button. Reconstruction will open in a new tab. Multiplanar reconstruction is described in Chapter 5.

The camera position is synchronized with the cursor position in MPR, and navigation is performed synchronously. For convenience, you can open MPR in a separate window and position it next to the virtual endoscopy window.
CHAPTER 9. VIRTUAL ENDOSCOPY

9.8 Surface Reconstruction

9.8.1 Create Surface

Functionality is available in the Pro edition

For reconstruction, click the Surface reconstruction button on the toolbar. The process may take some time. A sample reconstruction is shown in Fig. 9.5.

![Surface reconstruction](image)

*Figure 9.5: Surface reconstruction*

To display/hide the camera orientation in the surface window, click the Show camera orientation button. The camera orientation on the surface is synchronized with the virtual endoscopy tab. For convenience, you can open surface reconstruction in a separate window and position it next to the virtual endoscopy window. The camera position is highlighted by the blue marker. The yellow vector shows the view direction, and the green one points upward from the camera (Fig. 9.6).

![Camera orientation view elements](image)

*Figure 9.6: Camera orientation view elements*
9.8.2 Surface Orientation and Navigation

Functionality is available in the Pro edition

- To rotate the surface, move the mouse, holding the wheel. To select one of the predefined orientations, use the buttons on the orientation panel. (Fig. 9.7).

  **Figure 9.7: Surface orientation panel**

- To move the camera, activate the camera orientation view and click the left mouse button on the 3D surface reconstruction. The camera will move to the selected place in the center of the cavity. If there are overlapping body cavities, the camera will be located in the cavity nearest to the user.

- To change the camera vector, right-click the mouse at any point on the surface. The vector will be directed to this point.

- To change the model transparency, move the **Model transparency** scroll.

- To drag the surface, move the mouse, holding the wheel and the **Shift** key.

- To zoom the surface, move the mouse, holding the wheel and the **Ctrl** key.
Functionality is available in the Pro edition

The export of images is similar to the image export described in Section 2.25, but you cannot export an entire series.
Chapter 10

ECG Viewer

The diagnosis can only be established for body-surface ECG.

10.1 Select Data Source

Select the data source. The source selection algorithm is described in Section 1.5.

10.2 Open Series in ECG View window

Load studies to the DICOM Viewer and select the target study. There are five ways to open a series:

1. Click the ECG Viewer button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open an ECG in a new tab in the current window, click on the button.

2. Double-click the left mouse button on the study title on the study bar.

3. Double-click the left mouse button on the series icon on the series panel.

4. Drag the series icon to the study panel, holding the left mouse button.

5. Right-click the mouse to call the context menu for the series icon and select one of the items in the ECG Viewer section. The ECG will open in a new tab in the current window (Fig. 10.1).
10.3 View Graphs

If the graphs do not fit on the screen, then:

- pan them horizontally with the mouse, holding the left button;
- pan them vertically by rolling the mouse wheel.

If a series contains several pages, the View pages panel appears in the upper right-hand part of the window (fig. 10.2).

Figure 10.2: View pages panel

To view the pages move the cursor over the scroll bar and rotate the mouse wheel or click the ← → buttons. The panel displays the current page number and the total number of pages.
10.4 Toolbar

The toolbar is at the top of the tab (Fig. 10.3).

![Figure 10.3: Toolbar](image)

10.4.1 Select Lead

To select the ECG leads to be displayed:

1. Click the **Set visible leads** button on the toolbar. The window shown in Fig. 10.4 will be displayed.

2. Check the leads to be displayed. By default, all the leads are displayed.

3. Click **OK** to apply the settings or **CANCEL** to cancel the actions.

![Figure 10.4: Lead selection window](image)

10.4.2 ECG Speed

Two speed values are available: 25 and 50 millimeters per second. The default speed is 50 millimeters per second. The required value is set using a switch (Fig. 10.5).
10.4.3 Scale

Two scale values are available: 10 and 20 millimeters per millivolt. The default scale is 10 millimeters per millivolt. The required value is set using a switch (Fig. 10.6).

10.4.4 Length Interval

To select a length interval:

1. Activate the **Interval** tool on the toolbar.

2. Move the mouse along the graph to find the point to start with (it does not matter if the point is located on the left or on the right).

3. Click any mouse button to fix the point.

4. Move the mouse along the graph to locate the second point. The interval length value will be displayed against the interval background.

5. Click any mouse button to fix the point.

To move the interval, locate the cursor on it and drag it holding down the left mouse button or the button to which this tool is assigned.

Only one interval can be built at a time.

To delete the interval, deactivate the **Interval** tool.

10.4.5 Value Interval

To select a value interval:

1. Activate the **Values Interval** tool on the toolbar.

2. Move the mouse over the graph to locate the point to start with (it does not matter if the point is located at the top or at the bottom).

3. Click any mouse button to fix the point.
4. Move the mouse over the graph to locate the second point. The value matching the interval will be displayed against the interval background.

5. Click any mouse button to fix the point.

The units of measure of a value interval for an ECG series are determined automatically on the basis of the DICOM tags for the series. If the required data are missing, the value of the selected interval is not displayed.

To move the interval, locate the cursor on it and drag it, holding down the left mouse button or the button to which this tool is assigned.

Only one interval can be built at a time.

To delete the interval, deactivate the Values Interval tool.

10.4.6 Move to a Time Point on the Graph

To move to a particular time point on the graph, enter the values (minutes, seconds and milliseconds) into the corresponding areas on the toolbar (Fig. 10.7) and click the GO TO button. The graph will move to display its part starting from the specified time. You can drag the graph with the mouse at any time.

If the entered time value exceeds the study duration, the graph will be out of vision. Enter a new value or move the graph manually.

If some parameter has a zero value, it does not need to be entered. For instance, to move to the time point 1 minute 110 milliseconds, enter the values as shown in Fig. 10.7.

![Figure 10.7: Go to the time point 1 minute 0 seconds 110 milliseconds](image)

10.4.7 Set Up Coordinate Plane

To display the scale on the coordinate plane, activate the Scale ECG tool on the toolbar (by default it is inactive). To hide the scale line, click the button again.

The ECG scale is determined automatically on the basis of the DICOM tags for the series. If the required data are missing, the scale line is not displayed.

To change the color scheme, click the Choose color scheme button on the toolbar. Two color scheme options are available: classic (set by default) and green (Fig. 10.8).
10.5 Frequency Filters

Functionality is available in the Pro edition

If an ECG is recorded with distortions, use filters to correct the graphs.

When filters are used, graphs are changed. To establish a diagnosis, you need to use original data.

These filters remove the components whose frequency is higher than 35 Hz (the \text{Low pass filter 35 Hz} button) or 75 Hz (the \text{Low pass filter 75 Hz} button). To apply the filter, click the corresponding button. To cancel filtering, click the corresponding button again. Only one filter can be applied at a time.

To remove power line interference from the ECG signal, use the Notch filter. The tool has 2 predefined values (50 Hz and 60 Hz). To select a filter value, click on the arrow on the right side of the \text{Notch filter} button. The current value is marked with a flag. If you need to set a different value, select the Custom... item in the button menu and set the value in the dialog that opens. To use the filter with the current value, click the \text{Notch filter} button. To cancel filtering, click the button again.

To remove the walks of the baseline of the graph, use a High pass filter 1Hz. To apply the filter, click the \text{High pass filter 1Hz} button. To cancel filtering, click the button again.
10.6 Export series

Functionality is available in the Pro edition

When exporting, a series is saved in the filtered form. The series is stored in the local storage in the same study. To open the export dialog, click on the arrow on the right side of the Quick export ECG button.

If necessary, change the description of the series.

To upload the series to the default PACS server when exporting, check the Upload ECG to the default server box in the export dialog.

To export the series with the default settings, click the Quick Export ECG button.
Chapter 11

Image annotation

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The module described in this chapter is aimed for marking various objects on DICOM images manually with the help of contours and exporting them in JSON format. The results of image annotation may be used for training neural networks created for recognition of image components.

The following terms will be used in the description of the image annotation module:

- **Object** — A selected part of an image.
- **Annotation** — Marking objects.
- **Class (of objects)** — Objects united by a quality specified by the user. A class is characterized by a unique name and properties.

The image annotation module is available in the flat image viewer tab and provides for the following functions:

- create / edit a list of object classes and unite classes in groups;
- select objects belonging to different classes with contours;
- export and import the tree of object classes and groups;
- save image annotation results and open them to continue work;
- export annotation results with DICOM data.
11.1 Licensing the Image Annotation Module

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The image annotation module provides for dual-level access to the function. The users with extended rights have an additional opportunity to create and edit classes and groups. The other users may use the standard functions of the module, while the functions of creating, editing and exporting the tree of object classes and groups is not available for them.

When a user launches the module and attempts to open the image annotation results, the annotation panel with the standard functions of the module appears on the screen. If the user does not have an active license for the image annotation module, a dialog box (see Fig. 11.1) pops up suggesting that a free trial period should be activated.

![License Dialog Box](Image)

*Figure 11.1: The dialog box for the trial period activation*

Additional functions of the image annotation module are available upon the user’s request. No free trial period will be available in this case. If the license or the free trial period has expired, the annotation panel will not be opened. A dialog box notifying the user that a license must be purchased will pop up instead.
11.2 Opening a Series in the Image Annotation Mode

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To open a series in the image annotation mode, proceed as follows:

1. Open the series in the flat image viewer tab.
2. Choose Image annotation on the main Image menu.

The image annotation panel will be opened on the right-hand side of the window (see Fig. 11.2). This panel contains function buttons (in the red box) and the tree of groups and classes (in the green box).

Figure 11.2: The flat image viewer tab in the image annotation mode
### 11.3 Creating a Tree of Object Groups and Classes

**Functionality is available in a separate module which is activated in the Pro edition for an extra fee**

A tree of groups and classes is a hierarchical list of items. The items of the superior level are object groups and/or classes. The classes of objects that do not belong to any group are shown at the top of the list.

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Add class" /></td>
<td>The Add class button is available when no elements or just one element has been selected on the tree of groups and classes. If a group is selected, the new class will be added to this group. If a class is selected, the new class will be added to the group where the selected class belongs. If the selected class does not belong to any group, the new class will be added to the superior level. The button is only available for users who have extended rights.</td>
</tr>
<tr>
<td><img src="image" alt="Remove group/class" /></td>
<td>The Remove group/class button deletes the selected groups and classes. The button is only available for users with extended rights.</td>
</tr>
<tr>
<td><img src="image" alt="Add group" /></td>
<td>The Add group button creates a new empty group if there are no classes among the selected list items. If one or more classes have been selected in the list, the selected classes are combined into a new group.</td>
</tr>
<tr>
<td><img src="image" alt="Import the tree of groups and classes" /></td>
<td>The Import the tree of groups and classes button opens a dialog box for selection of a JSON file in order to import a tree of groups and classes.</td>
</tr>
<tr>
<td><img src="image" alt="Export the tree of groups and classes" /></td>
<td>The Export the tree of groups and classes button opens a dialog box for selection of a JSON file in order to save the results. When the user presses the Save button, a new JSON file is created or the existing JSON file with the data on the current tree of groups and classes is overwritten. The button is only available for users with extended rights.</td>
</tr>
<tr>
<td><img src="image" alt="Save results" /></td>
<td>The Save results button allows for saving the current annotation results in order to resume work with them after the program is relaunched. When the user presses the button, a dialog box pops up for saving the data on all the objects that have been marked for all the study series in the current tab. DICOM data are not saved.</td>
</tr>
<tr>
<td><img src="image" alt="Export results with DICOM" /></td>
<td>The Export results with DICOM button exports the image annotation results together with the DICOM data. The data are exported into a separate folder or archive.</td>
</tr>
</tbody>
</table>
11.3.1 Creating a New Class of Objects

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

Attention! This function is only available for users with extended rights.

There are two ways to add a new object class:

- click the Add class button on the image annotation panel;
- through the context menu: right-click on the annotation panel and select the Add class... option.

In the New class dialog box (Fig. 11.3), print the name of the object class. By default, an object class is assigned a name in Class <unique number> format.

![New class dialog box](image)

*Figure 11.3: The dialog box for adding a new object class*

In order to avoid intersection of object contours, uncheck the Enable intersections of objects box. The box is checked by default. Customize the color of the contours for this class of object by pressing the color icon and selecting a suitable color in the respective dialog box.

Click OK to create a new object class or CANCEL to cancel.

If a group is selected when the user presses the Add class button, the new object class will be added to the selected group. If a class is selected, the new object class will be added to the group to which the selected class belongs. If the selected class does not belong to any group, the new object class will be added to the superior level of the tree.
11.3.2 Creating a Group of Object Classes

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

**Attention! This function is only available for users with extended rights.**

There are two ways to add a new group:

- click the **Add group** button on the image annotation panel;
- through the context menu: right-click on the annotation panel and select the **Add group...** option.

In the **New group** dialog box (Fig. 11.4), print the name of the group. By default, a group is assigned a name in **Group <unique number>** format.

![New group dialog box](image)

**Figure 11.4:** A dialog box for adding a new group

Click **OK** to create a new group or **CANCEL** to cancel.

If one or several classes are selected on the list when the user presses the **Add group** button, these classes are automatically transferred to the new group. Otherwise, a new empty group will be added.

11.3.3 Operations with Object Classes and Groups

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

**Attention! This function is only available for users with extended rights.**

If the current tree of object classes and groups is changed, it may result in incompatibility with the trees that were created earlier (see Section 11.3.4).
The following actions may be performed with groups and classes:

- **moving.** To change the structure of a tree of groups and classes, mouse over a group or class and drag the selected group or class to another place on the tree while holding the left mouse button;

- **renaming.** Double-click on the name of a group or class, type the new name and press Enter on the keyboard;

- **editing class parameters.** Click the Settings button for the selected object class and change the parameters in the Class settings dialog box. The interface of the Class settings dialog box is identical with the interface of the dialog box for creating a new class (see Fig. 11.3);

- **deleting.** Select a group or class. Click the right mouse button and select the Remove group/class option from the context menu or click the Remove group/class button on the image annotation panel.

When the user terminates work with the program, the current state of the tree of groups and classes is saved in a JSON file if it contains at least one group and/or class. Otherwise, the JSON file will be deleted. The file named ia_classes.json is placed in the <Path to the storage>/ImageAnnotation directory where the <Path to the storage> is the path specified in the Workspace section of the general settings window (see Section 15.1).

When the program is launched, the current tree of groups and classes is automatically opened from the Specified JSON file. If such a file does not exist, an empty image annotation panel will pop up when the program is launched.

### 11.3.4 Compatibility of Trees of Groups and Classes

Each tree of groups and classes is assigned a unique identifier (uid) and a number of the version which is changed when the structure of the tree is altered.

If the user, after importing/exporting the classes and groups tree, saving results or exporting results with DICOM data, performs one of the following actions with the tree of groups and classes:

- adds a new class;
- changes the parent group for the class (by dragging);
- adds a new group;
- deletes a group;
- changes the name of a group,
then the version of the tree of groups and classes will be changed (increased by 1). The unique identifier (uid) of the tree will stay the same.

If the user, after importing/exporting the classes and groups tree, saving results or exporting results with DICOM data, performs one of the following actions with the tree of groups and classes:

- deletes a class;
- changes the name of a class;
- changes the color of objects for a class;
- changes the intersection option for objects belonging to a certain class,

then a new uid will be generated for the tree of groups and classes, and the tree version will be reset to 1.

Trees with the same uid are compatible and may be upgraded (see Section 11.4.2). Trees with different uids are incompatible, but one tree may be replaced by another (see Section 11.6.2).

The uid value and the tree version number are saved in a JSON file when the tree is exported, or when the annotation results are exported or saved.

### 11.4 Export and Import of the Tree of Groups and Classes

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The export and import option provides an opportunity to save and transfer a tree of groups and classes as a JSON file from one computer to another. A tree of groups and classes created by a user with extended rights may be shared by common users.

#### 11.4.1 Export of the Tree of Groups and Classes

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

**Attention! This function is only available for users with extended rights.**

The function of exporting the current state of the tree of groups and classes provides an opportunity to save the data on the tree of groups and classes specified on the image annotation panel in a JSON file.

To export the current state of the tree of groups and classes, click the **Export the tree of groups and classes** button on the image annotation panel. In the dialog box that pops
CHAPTER 11. IMAGE ANNOTATION

up, choose a place where you want to save the file with the data and enter the name of the file. Click **Save** to save the file or **Cancel** to cancel.

In case of an error, a respective dialog box will pop up.

### 11.4.2 Import of a Tree of Groups and Classes

**Functionality is available in a separate module which is activated in the Pro edition for an extra fee.**

The function of importing a tree of groups and classes provides an opportunity to open a tree of groups and classes from a JSON file on the image annotation panel.

To import a tree of groups and classes, click the **Import the tree of groups and classes** button on the image annotation panel. In the dialog box that pops up, choose an exported JSON file with data on groups and classes.

To upgrade a tree of groups and classes, import a superior version of the tree.

The imported JSON file with data on the tree of groups and classes from the image annotation panel must be created by exporting the tree of groups and classes (see Section **11.4.1**).

Click **Open** to import the tree of groups and classes or **Cancel** to cancel.

### 11.5 Marking Objects with Contours

**Functionality is available in a separate module which is activated in the Pro edition for an extra fee.**

You can use contours to mark objects in DICOM images. Contours are drawn separately for each image (slice, phase, or frame) with the **ROI object (contour)** tool in the **Image viewer** tab in the image annotation mode.

To mark an object with a contour, proceed as follows:

1. Open a series in the **Image viewer** tab. Enable the image annotation mode (see Section **11.2**).

2. If there is no tree of groups and classes on the image annotation panel, it must be imported or created.

3. In the line for the respective class on the image annotation panel, activate the **ROI object (contour)** tool with the left, right, or middle mouse button. Use the same button to work with the tool. For details on the use of tools, see Section **1.14**.

4. Build a contour in one of the following ways:
   - **building contours manually.** Build a contour around the chosen area while holding the mouse button with which the tool was activated. To finish the procedure,
release the mouse button. To cancel the contour that has not been closed, press Esc on the keyboard while holding the button;

- **building contours with an isoline.** Move the cursor around the selected area while holding the Shift button on the keyboard. Under the cursor, you will see an isoline characterized by even points density. You can only see an isoline on the surfaces where a contour can be built. To build a contour with an isoline, click the left mouse button or the mouse button with which the tool was activated.

The color of the contour is the same as the color selected for the class of objects.

Contours may intersect if the Enable intersections of objects box in the object class parameters is checked for at least one of them. This box is checked by default.

To disable intersection of contours, uncheck the Enable intersections of objects box in the object class parameters. If intersection of contours is disabled, corrections will be made after a contour is built or edited: the shared areas will be deleted.

When a contour is built or edited, intersection of the current contour with those that have already been built may be prohibited. To prohibit intersection for the current contour, press and hold the Ctrl key on the keyboard when finishing the building or editing procedure. The shared areas will be deleted.

If one of the contours is inscribed in the other, they are not considered intersecting.

### 11.5.1 Actions with Object Contours

Functionality is available in a separate module which is activated in the Pro edition for an extra fee

The DICOM Viewer provides for the following actions with object contours:

- **editing.** To edit a contour, place the cursor over it. When you hover over the contour line, it is highlighted. Place the cursor over the area that needs editing and click the mouse button. Draw a new contour while holding the button. To finish the editing procedure, release the mouse button;

- **deleting.** Place the cursor over the contour line, click the right mouse button and choose the Remove object option from the right-click menu;

- **deleting all the Contours.** To delete all the contours of the objects for the current series, choose the Remove all objects option from the right-click menu. In the dialog box that pops up, click YES to delete or NO to cancel.
11.5.2 Changing the Class of Object Contour

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

If the current tree of object classes and groups is changed, it may result in incompatibility with the trees that were created earlier (see Section 11.3.4).

To change the class of the object contour, proceed as follows:

1. Place the cursor over the contour. When you hover over the contour line, it is highlighted.
2. Click the right mouse button and select the Classes option from the right-click menu (Fig. 11.5). The group and the class of the selected object contour are ticked on the dropdown list.
3. Change the class of the object contour by selecting a suitable option from the list.

![Right-click menu for object contours](image)

Figure 11.5: Right-click menu for object contours

The characteristics of the selected class are applied to the contour.
11.6 Saving and Opening Annotation Results

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

The DICOM Viewer provides for an opportunity to save the annotation results in a JSON file, as well as to open files with annotation results in order to resume work. When a file is opened, the data contained in it are added to the data that already exist.

11.6.1 Saving Annotation Results

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To save the image annotation results, click the Save results button on the image annotation panel. In the dialog box that pops up, choose the directory where the file with the annotation results is to be saved and print the name of the file. Click Save to save the file or Cancel to cancel.

The results are saved in a JSON file containing the following information:

- data on groups and classes;
- data on images (study ID, series ID, image ID);
- data on objects of the contours.

The saved file contains information on all the objects annotated for all the study series in the current tab (for all series from the series panel of the current tab). The file is saved without DICOM data.

11.6.2 Opening Annotation Results

Functionality is available in a separate module which is activated in the Pro edition for an extra fee.

To open the image annotation results that were saved earlier, select the Open image annotation results... option on the File menu. In the dialog box that pops up, select a saved JSON file with annotation results.

The following conditions must be met in order to open the annotation results successfully:

- the uid of the tree of groups and classes in the JSON file must be the same as the uid of the tree of groups and classes opened in the program;
- the version of the tree of groups and classes in the JSON file must be inferior to or the same as the version of the tree of groups and classes opened in the program;
- in the local DICOM Viewer storage, there must be at least one series specified in the JSON file.

If at least one of these conditions is not met, a dialog box notifying of the error will pop up and the annotation results will not be opened.

If the version of the tree of groups and classes in the JSON file is superior to the version of the tree opened in the program, a respective tree replacement notification will pop up when the user attempts to open the annotation results.

If some of the series specified in the JSON file are missing from the local storage, a respective notification will pop up when the user attempts to open the annotation results.

### 11.7 Export of Annotation Results

**Functionality is available in a separate module which is activated in the Pro edition for an extra fee**

The DICOM Viewer provides an opportunity to export image annotation results with DICOM data. The data are exported in a separate folder or archive.

Exported data includes:
- a JSON file named `ia_results.json` that contains data about the tree of groups and classes and about the marked outline objects;
- `DICOM` folder with dcm files of the series, on the images of which the objects were marked and the DICOMDIR file.

To export annotation results:

1. Click the **Export results with DICOM** button on the image annotation panel.

2. In the **Export image annotation results with DICOM** dialog box (Fig. 11.6), enter the name of the destination folder in the **Folder name** field.

*Figure 11.6: A dialog box for export of image annotation results with DICOM*
3. Specify the path to the destination folder in the Create in field or click on the folder button to select a folder in the folder selection dialog box. If the path specified does not exist, an error notification will pop up when the OK button is clicked.

4. To compress the exported data, check the Compress files box. The name of the Folder name field will be changed to File name. The data will be exported to a ZIP file, the name of which will be specified in the File name field. By default, the Compress files box is not checked.

Click OK to export the annotation results or CANCEL to cancel.
To avoid personal data disclosure, secure channels should be used for data transfer via the network.

12.1 Services

12.1.1 DICOM Service (PACS Server functionality)

The DICOM Viewer can take on the role of a PACS server. The data in the Local Storage will be available for clients. To do this, enable and set up the DICOM Service and add clients to the PACS Servers list (section 12.2).

Select the Services... item from the Network menu. In the drop-down menu, choose the DICOM Listener... option. The dialog box shown in Fig. 12.1 will pop up.

![DICOM Listener](image)

*Figure 12.1: Service DICOM Listener*

To set up the DICOM Listener Service:

1. Check the Enable box.
2. In the **AE Title** field, enter a user-defined title for the computer that is installed on to identify it on the server. The length of AE Title value shall not exceed 16 characters. Cyrillic letters and «» symbols in AE titles are not allowed.

3. In the **Port** field, specify any free port of the computer the DICOM Viewer is installed on. If you are not sure which value to specify, use the default value. This information can be obtained from your system administrator.

4. To restore the service default settings, click **DEFAULTS**.

5. To save the current settings for all the users of this PC, check the **Shared settings (for all users)** box. It can only be done if the DICOM Viewer was launched by a user with administrator privileges. The users who do not have administrator privileges cannot check or uncheck this box. In such a case an error message will pop up.

6. Click **OK** to apply the settings or **CANCEL** to cancel. If the port is busy, the message **Dicom Listener cannot be run. Error message: The address is protected** will pop up. In this case, select another port and repeat the previous action.

### 12.1.2 HIS/HTTP Service

This service is used to manage the DICOM Viewer using the http protocol. Select the **Services...** item from the **Network** menu. In the drop-down menu, choose the **HIS/HTTP Service...** option. The dialog box shown in Fig. 12.2 will pop up.

![HIS/HTTP Service dialog box](image)

**Figure 12.2: HIS/HTTP Service dialog box**

To set up the HIS/HTTP Service:

1. Check the **Enable** box.

2. In the **Port** field under the **Enable** checkbox, specify any free port of the computer the DICOM Viewer is installed on. If you are not sure which value to specify, use the default value. The default port number is 8080. This information can be obtained from your system administrator.

3. To restore the default settings, click **DEFAULTS**. By default, the **Enable** box is unchecked, and port 8080 is used.

4. Click **OK** to apply the settings or **CANCEL** to cancel. If the port is busy, the message will pop up. In this case, select another port and repeat the previous action.
12.3 Web Access

Functionality is available in the Pro edition

Select the Services... item from the Network menu. In the drop-down menu, choose the Web Service... option. The dialog box shown in Fig. 12.3 will pop up.

![Web service dialog box](image)

*Figure 12.3: Web service dialog box*

To set up the Web access:

1. Check the Enable box.

2. In the Port field under the Enable web Access checkbox, specify any free port of the computer the DICOM Viewer is installed on. If you are not sure which value to specify, use the default value. The default port number is 8090. For access from other computers, add the web access port to your firewall exceptions. If necessary, contact your system administrator.

3. In the User name field, enter the user name.

4. In the Password field, enter the user password.

5. In the Session timeout (sec.) field, enter a timeout after which the session is terminated if the connection is lost. When the connection is restored, you need to enter your user-name and password again.

6. To restore the default settings, click DEFAULTS. By default, the Enable box is unchecked, and port 8090 is used.

7. Click OK to apply the settings or CANCEL to cancel.
At the bottom of the dialog, there is a link that must be entered into the browser for web access to the DICOM Viewer http://youraddress:<port>, where instead of youraddress you need to type in the ip address or the computer name on which the DICOM Viewer is installed.

### 12.1.4 Secure DICOM Listener Service

The secure DICOM listener service provides for secure data transfer over the net using the TLS protocol.

The secure DICOM listener service and the open DICOM listener service may be used simultaneously by different ports.

Select the Services... item from the Network menu. In the drop-down menu, choose the Secure DICOM Listner... option. The dialog box shown in Fig. 12.4 will pop up.

![Secure DICOM Listner dialog box](image)

*Figure 12.4: Secure DICOM Listner dialog box*

To set up the Secure DICOM Listner Service:

1. To enable the secure DICOM listener service, check the Enable box.

2. In the AE Title field, print an arbitrary name of the computer with the DICOM Viewer installed for identification on the server. The length of AE Title value shall not exceed 16 characters. Cyrillic letters and «:» symbols in AE titles are not allowed.

3. In the Port field, specify any unoccupied port of the computer with the DICOM Viewer installed. The port number must be different from the values stated for other services.
(such as Web Service, HIS/HTTP Service, DICOM Listener Service). The default port number is 3100.

4. In the **Trusted peer certificates**, a list of trusted (root) certificates for the DICOM service is created. By default, the list is empty.

A trusted certificate (root certificate) is a public key certificate which is used to sign the peer certificate. It is used to confirm the identity of the peer (the unit on the other end of the line).

To create a list of trusted certificates, click the **CHOOSE** button. In the **Trusted peer certificates** dialog box (Figure 12.5), the list of trusted certificates is provided.

To add a certificate, click **ADD**. In the dialog box that pops up, choose the certificate file. Certificate files must have (pem), (crt), or (cer) extension.

In Figure 12.5, you see that the file «root_Example.crt» is added to the trusted certificates list. It is the server root certificate.

If the certificate you are trying to add has already been added to the list, an error message will pop up.
To delete a certificate from the list, highlight the respective line and click REMOVE. To delete all the trusted certificates, click REMOVE ALL.

Click OK to apply the settings or CANCEL to cancel.

The trusted certificates added to the list are saved in the OS registry or in the configuration file as binary data. After the settings are saved, there is no need to keep the certificate files on the disk.

To enable verification of the certificates of the clients connected, check the Verify peer certificate box. In this case, when a secure connection to the DICOM service is established, authentication of the client is performed. For successful authentication, the client’s certificate has to be signed by one of the trusted DICOM Service certificates. If the Verify peer certificate box is not checked, the secure DICOM Service accepts any client connections.

5. In the Certificate box, the paths to the public key certificate files and DICOM listener service private key files are to be provided. By default, these paths are not provided.

A public key certificate is an electronic document containing the public key, the information about the key owner and its intended use. The certificate is signed by the certification authority having issued the key and proves that the public key belongs to its owner.

The public key is available to anyone. It is used to encrypt data when the client establishes a connection with the server.

The private key is kept at the server. It is used to decrypt data received from the client.

To provide the paths to the public key certificate file and the private key file, click CHOOSE.

To provide the paths to the public key certificate file and the private key file, click BROWSE in the Certificate and private key dialog box (see Figure 12.6). In the box that pops up, choose the files you need. The public key certificate file must have (pem), (crt), or (cer) extension. The private key file must have (key) extension.

Figure 12.6: Certificate and private key dialog box

In our example shown in Figure 12.6, we have added the paths to the client’s private key file «INOBITEC.key» and the public key certificate file «INOBITEC.crt».
In the lower part of the Certificate and private key dialog box, you see the verification status of the public key certificate and the private key. Here are the possible variants of the verification status:

- **No certificate** — the path to the public key certificate file has not been provided.
- **No private key** — the path to the private key file has not been provided.
- **Incorrect certificate** — the path provided is invalid / the file for which the path has been provided does not exist / the file for which the path has been provided is damaged or does not contain a valid public key certificate.
- **Incorrect private key** — the path provided is invalid / the file for which the path has been provided does not exist / the file for which the path has been provided is damaged.
- **Data in the following format:** `<Certificate name>, <Company name>, <Country abbreviation>` — the public key certificate and the private key provided is valid.

**Attention! You cannot check the compatibility of the public key certificate file with the private key in the Certificate and private key dialog box.**

The OK button will be activated after you provide the valid paths to the public key certificate file and the private key file. Click **OK** to apply the settings or **CANCEL** to cancel.

6. To save the current settings for all the users of this PC, check the **Shared settings (for all users)** box. It can only be done if the DICOM Viewer was launched by a user with administrator privileges. The users who do not have administrator privileges cannot check or uncheck this box. In such a case an error message will pop up.

7. To restore the default settings, click **DEFAULTS**.

8. Click **OK** to apply the settings or **CANCEL** to cancel.

### 12.2 Set Up PACS Server Connection

In this window, you can set up the connections with the applications which can exchange data with the DICOM Viewer, using the DICOM protocol. In this case, the DICOM Viewer can take on the role of a PACS server and the other applications will be clients, and vice versa. Since most of the applications with which a connection can be established can take on the role of a PACS server, the connections with them are set up in this window, regardless of whether they will be servers or clients in relation to the DICOM Viewer.

To open the window to connect to PACS servers, select the **Network** menu and the **Server list** item or press **Ctrl+S**. The dialog box shown in Fig. 12.7 will pop up.
The DICOM Viewer allows you to download several series from the PACS server at the same time, making several parallel connections to the PACS Server. However, not all PACS Servers support a large number of simultaneous connections, and this leads to errors when downloading data. Setting the maximum number of connections is described in 15.6.5. This setting applies to all PACS Servers.

### 12.2.1 Add PACS Server

To add a new PACS server:

1. Click the button.
2. Enter the server name in the **Server nickname** field.
3. Enter a comment in the **Server description** field. This field may be left blank.
4. Select **DICOM** from the **Server type** dropdown menu.
5. Select the target mode from the **Server mode** dropdown menu.

6. Select the server character set from the **Character set** dropdown menu.

7. In the **Client name (SCU)** field, enter the value specified in Section 12.1.1 in the **AE Title** field.

8. In the **Service name (SCP)** field, enter the name of the server that the PACS server is installed on.

9. In the **Server host name or IP** field, enter the server name or IP address.

10. In the **Server port** field, enter the server port to accept connections by the DICOM protocol.

11. To establish a secure connection, check the **Use secure mode (TLS)** box. For details see Section 12.2.2.

12. To save the information without closing the window, click **OK**.

13. To save the information and close the window, click **SAVE**.

14. To close the window without saving the changes, click **CANCEL**.

The required information can be obtained from your system administrator. Other PACS servers are added in a similar way.

If you have several servers on your list, you can assign a server that will be active by default when starting the DICOM Viewer. To do this, check the **Default server** box in the server connection settings.

If another default server is already assigned, its box will be unchecked when you assign a new server.

If this server is also a client in relation to the DICOM Viewer, it is necessary to allow it to exchange data. To do this, check the box **Allow C-FIND and C-MOVE**. Configure the client application in accordance with the User Manual of this application. The connection configuration of two «Inobitec DICOM Viewer» applications is described in section 12.2.4.

To make the server available to all the users, you need to check the **Shared server (multi-user support)** box for this server. To do that, you need to run the DICOM Viewer as an administrator. Otherwise the box will be inactive. The users that do not have the administrator privileges cannot change the public server settings or delete it.

To delete a server from the list, click the button.

**Attention! After you click this button, the deletion cannot be undone.**

### 12.2.2 Secure PACS Server connection via the TLS protocol

**Attention! If you launch the DICOM Viewer 2.4 or an inferior version of the program on your PC, all the TLS parameters will be reset.**

By default, the AE Title of the secure connection via the TLS protocol is the same as the AE Title of the non-secure connection. Hence, it is recommended to change the name in the
settings window. The secure TLS connection service and the non-secure connection may be used simultaneously by different ports.

To enable the secure connection mode, check the **Use secure mode (TLS)** box in the server parameters dialog box (see Figure 12.7). By doing this, you will activate the **TLS SETTINGS** button for secure mode setup.

The **TLS SETTINGS** dialog box is shown in Figure 12.8.

![TLS Settings dialog box](image)

Figure 12.8: TLS Settings dialog box

To add a trusted peer certificate, click **CHOOSE**. In the dialog box that pops up, choose the trusted (root) PACS Server certificate file. The trusted (root) PACS Server certificate file must have (pem), (crt), or (cer) extension.

In our example, the root certificate file «root_Example.crt» is being added.

To enable verification of the trusted (root) certificate at the time of establishing a connection with the PACS Server, check the **Verify peer certificate** box. In this case, when a connection is being established, the client's authentication is performed. For successful authentication, the PACS Server certificate has to be signed by a trusted certificate.

The program automatically checks the presence of a valid certificate in the file. If the file is damaged or does not contain a certificate, a message will pop up.

If you have chosen the file containing the valid certificate, you will see the following information in the **Trusted peer certificate** box: `<Certificate name>,<Company name>, <Country abbreviation>.

If the peer certificate verification mode has been enabled on the PACS Server, the client’s authentication must be performed to establish a connection. Check the **Authentication of the client** box and click **CHOOSE**.

In the **Certificate and private key** dialog box (Figure 12.9), the paths to the public key certificate file and the private key file are provided.
To provide the paths to the public key certificate file and the private key file, click BROWSE. In the box that pops up, choose the files you need. The public key certificate file must have (pem), (crt), or (cer) extension. The private key file must have (key) extension.

In our example shown in Figure 12.9, we have added the paths to the client’s private key file «INOBITEC.key» and the public key certificate file «INOBITEC.crt».

In the lower part of the Certificate and private key dialog box, you see the verification status of the public key certificate and the private key. Here are the possible variants of the verification status:

- **No certificate** — the path to the public key certificate file has not been provided.
- **No private key** — the path to the private key file has not been provided.
- **Incorrect certificate** — the path provided is invalid / the file for which the path has been provided does not exist / the file for which the path has been provided is damaged or does not contain a valid public key certificate.
- **Incorrect private key** — the path provided is invalid / the file for which the path has been provided does not exist / the file for which the path has been provided is damaged.
- **Data in the following format:** `<Certificate name>, <Company name>, <Country abbreviation>` — the public key certificate and the private key provided is valid.

**Attention! You cannot check the compatibility of the public key certificate file with the private key in the Certificate and private key dialog box.**

The OK button will be activated after you provide the valid paths to the public key certificate file and the private key file. Click OK to apply the settings or CANCEL to cancel.

### 12.2.3 Check PACS Server Availability

To check if the server is available, click the button in the PACS server connection window. If the server is available, the system will return the following message: **Server network status: Online.**
Otherwise the following message will be returned: **Server network status: Offline.** The error details will be displayed below.

- Server is unavailable.
- Connection request failed.
- Failed to establish association
- 0006:0317 Peer aborted Association (or never connected)
- 0006:031c TCP Initialization Error: No error

If a message similar to the one shown below appears, it, most likely, means that the **Server host name or IP** or **Server port** fields are filled in incorrectly, or the target PACS server is not running.

### 12.2.4 Configuring the connection of two applications Inobitec DICOM Viewer

Let's assume that DICOM Viewer #1 takes on the role of a PACS-server and DICOM Viewer #2 takes on the role of a client.

**Parameters of DICOM Viewer #1:**

- **AE Title:** VIEWER-SERVER;
- **IP:** 192.168.1.101;
- **Port:** 3001.

**Parameters of the DICOM Viewer #2:**

- **AE Title:** VIEWER-CLIENT;
- **IP:** 192.168.1.102;
- **Port:** 3002.

To configure the server:

1. Enable and set up the DICOM service (section 12.1.1), set **AE Title** as VIEWER-SERVER, set **Port** as 3001.

2. Add a client in the **Set Up PACS Server Connection** window (section 12.2.1). Set the following parameters for the fields:

   - for field **Server type** — DICOM;
   - for field **Server mode** — C-MOVE;
   - for field **Client name (SCU)** — VIEWER-SERVER;
   - for field **Service name (SCP)** — VIEWER-CLIENT;
   - for field **Server host name or IP** — 192.168.1.102;
   - for field **Server port** — 3002;
   - check the box **Allow C-FIND and C-MOVE**.

Now, DICOM Viewer #1 is ready to accept incoming connections from the client with the AE Title = VIEWER-CLIENT, IP = 192.168.1.102 and port = 3002.
To set up a client:

Add the server in the Set Up PACS Server Connection window (section 12.2.1). Set the following parameters for the fields:

- for field **Server type** — DICOM;

- for field **Server mode** — C-MOVE;

- for field **Client name (SCU)** — VIEWER-CLIENT;

- for field **Service name (SCP)** — VIEWER-SERVER;

- for field **Server host name or IP** — 192.168.1.101;

- for field **Server port** — 3001;

Now DICOM Viewer #2 is ready to connect to the server with AE Title = VIEWER-SERVER, IP = 192.168.0.101 and port = 3001.

If you enable and set up the DICOM-service and check the box **Allow C-FIND and C-MOVE** for the VIEWER-SERVER server in the DICOM Viewer #2 settings, then DICOM Viewer #2 will be able to take on the role of a server and DICOM Viewer #1 will be able to take on the role of a client. Thus, the DICOM Viewer can take on the role of a client and a server simultaneously.

### 12.3 Network Operation Status

Network operations refer to information transfer and reception between the DICOM Viewer and the PACS servers.

To view the network operation status, select the **Network** menu and the **Network status** item.

The window contains three tabs: **Downloading**, **Uploading** and **History**. The **Downloading** and **Uploading** tabs display the queues of studies loaded from the PACS server or sent to the PACS server respectively.

If some data is being transferred at the moment, the study queue will be displayed in the corresponding tab (Fig. 12.10). The studies positioned at the top of the list are the first to be processed.
12.3. NETWORK OPERATION STATUS

Figure 12.10: Queue of studies sent to the PACS server

When using the **Downloading** and **Uploading** tabs, the same actions are used. The following actions with a study can be performed (select a study first):

- change the position in the queue, using the ↑ and ↓ buttons respectively;

- cancel the study processing, using the button. In this case, only the information that is already loaded will remain on the server.

To clear the queue, click the button. In this case, the studies, including the one currently processed, are deleted from the list, and their processing is interrupted. If a study is already being processed (in **progress** status), you cannot change its position in the queue.

The top of the **History** tab displays the list of studies loaded, sent or canceled. At the bottom of the tab, there is a list of studies whose transfer failed.
Chapter 13

The Local Storage

The storage is a folder on the computer disk where the DICOM data is stored.

The data kept in the local storage may be lost through the hard drive damage, improper users' activities, or third-party software impact. To avoid data loss, back up the data.

13.1 View Storage Status

To view the storage status, select the Storage menu and the Storage status... item. The window shown in Fig. 13.1 will pop up.

![Figure 13.1: Storage info](image)

The following information is displayed in the window: the number of studies in the storage; the total number of images in all studies; the size of data stored in the storage (gigabytes and bytes).
13.2 Verify Storage

To check the storage, select the Storage menu and the Verify storage... item. The checking process shows whether all images related to the studies are located in the storage. The checking progress (percentage of work performed) is displayed on the screen.

If all the files are found in the storage, the All files in storage are valid message will be displayed.

If any of the files are not found in the storage, the message like Found 10 missed files in the local storage. Please, try again to download studies. will be returned. In this case, you need to reload all the studies to the storage to display all the images properly. To clear the storage, perform the actions described in the next section.

13.3 Clear Storage

To clear the storage, select the Storage menu and the Clear storage... item. In this case, the All local studies will be deleted. Do you really want to clean up the local storage? message will be displayed. Click YES to clear the storage or NO to cancel. After the storage is cleared, click OK in the clearing progress window.

13.4 Automatic Local Storage cleaning

Automatic cleaning is performed at the following intervals:

- every time;
- once a day;
- once a week;
- once a month.

To activate/deactivate automatic cleaning, check/uncheck the Automatic local storage cleaning box and select the cleaning interval (see section 15.6.6).
Chapter 14

Disk Creator

14.1 General information

The disk creator allows you to write information to CDs, DVDs and Memory Cards. To open the disk creator, click the DICOM CD/DVD Creator button on the toolbar. To select the tab location (in the current window, in a separate window or in the full screen mode), click on the arrow on the right side of the button. To open the creator window in a new tab in the current window, click on the button.

The disk creator window is shown in Fig. 14.1.

![Figure 14.1: Disk creator](image-url)
To work with the creator, the Work Folder should be set up, i.e. the folder to store the disk image to be written. By default, the Work Folder is located in the temporary folder of the operating system. To change it, click on the **Select the work folder where DICOM CD/DVD image will be created** button and select the directory in the dialog that opens. If, when opening the creator, the Work Folder already contains data, then the dialog with the question **Do you want to clear work folder before inserting new data?** is displayed. Click **YES** to clear or **NO** to leave the data.

If the disk image is damaged, it may become impossible to work with it. If errors occur when adding or removing data, manually clean the Work Folder.

After being written, the data in the Work Folder can be saved for later use or it can be automatically deleted. Automatic cleaning of the Work Folder can be enabled before burning the image (see Section 14.3).

The top part of the creator contains the control buttons:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Select a work folder where DICOM CD/DVD image will be created" /></td>
<td>is used to change the Work Folder.</td>
</tr>
<tr>
<td><img src="image" alt="Remove series from the DICOM CD/DVD image" /></td>
<td>to delete the selected series, click on the button. To delete the selected study, click on the arrow on the right side of the button and select the <strong>Remove studies</strong> command.</td>
</tr>
<tr>
<td><img src="image" alt="Clear DICOM CD/DVD image" /></td>
<td>deletes all studies from the image.</td>
</tr>
<tr>
<td><img src="image" alt="Include DiskViewer to the DICOM CD/DVD image" /></td>
<td>button described in Section 14.2.3.</td>
</tr>
<tr>
<td><img src="image" alt="Burn created DICOM CD/DVD image to the optical disk" /></td>
<td>writes information from the creator to the disk.</td>
</tr>
<tr>
<td><img src="image" alt="Write created DICOM CD/DVD image to the flash card or folder" /></td>
<td>writes information from the creator to the memory card (flash card) or folder.</td>
</tr>
</tbody>
</table>

The **Size** parameter displays the size of the disk image. The same information is duplicated by the green bar on the graph (Fig. 14.2).

![Figure 14.2: Disk Image size](image)
14.2 Add Data to Disk Creator

14.2.1 Automatically Add Data to a Disk Image

Since version 1.14.0, it is possible to automatically add data to a disk image.

To set up automatic adding of studies select the main menu Options->Settings...-> Modules->DICOM CD/DVD Creator and click the Settings button. In the window that opens check the Add selected studies at opening DICOM CD/DVD Creator box. By default the box is checked. Click OK to apply the settings or CANCEL to cancel.

To add studies to the disk image automatically:

1. Load studies to the DICOM Viewer.
2. Select the required study (several studies, holding down the Shift or Ctrl keys. For more information, see Section 1.9).
3. Click the DICOM CD/DVD Creator button on the toolbar. If the creator is closed, it opens, and the selected studies are added to the image.

If the Work Folder is not set. Choose Work Folder and try again error occurs, then set the Work Folder for the creator (see Section 14.1), or it will be automatically created in the temporary folder of the operating system the next time you start the Disk Creator.

14.2.2 Manually Add Data to a Disk Image

To add studies or series to the disk image manually:

1. Load studies to the DICOM Viewer.
2. Select the required study (or several studies, holding down the Shift or Ctrl key. For more information on how to select several studies, see Section 1.9).
3. To add an entire study to the disk image, click the Add selected studies to DICOM CD/DVD image button on the Studies Import/Export Panels.
4. To add a series, select it on the series panel and click on the left part of the Add selected series to DICOM CD/DVD image button on the Series Import/Export Panels. The information will be added to the creator. To select several series, hold down the Shift or Ctrl keys. For more information, see Section 1.9).

If the Work Folder is not set. Choose Work Folder and try again error occurs then set the Work Folder for the creator (see Section 14.1) or it will be automatically created in the temporary folder of the operating system the next time you start the Disk Creator.

14.2.3 Adding the DICOM Viewer to the Disk Image

To be able to view the images recorded on the disk without having to install special software, add the Compact Disk DICOM Viewer Edition to the disk image. It requires no installation and runs directly from the disk on Windows and macOS.
To add the Compact Disk DICOM Viewer Edition to the disk image, click the Include DiskViewer to the DICOM CD/DVD image button. When cleaning the disk image the Compact Disk DICOM Viewer Edition is stored in the disk image.

To remove the Compact Disk DICOM Viewer Edition from the disk image, click the button. In the dialog box that opens, click YES to confirm the deletion or click NO to cancel.

14.3 Burn image

If you need to write a DICOMDIR file to a disk (memory card), enable the corresponding option in the Disk Creator settings dialog (see Section 15.6.7).

Data burning may fail for some models of CD/DVD-ROMs. To increase the reliability of recording enable image buffering (see Section 15.6.7). In this case, the buffer file for writing is created entirely in the temporary folder of the current user just before writing to disk. Buffer files are created before each recording and are deleted from the hard disk only when the DICOM Viewer is closed. Hence, the amount of free space on the hard disk should be taken into account when writing to the disk multiple times within one session of the program.

14.3.1 Write to Disk

Attention! In Linux and macOS you can write data to a memory card or burn a disk image created in the Work Folder to a disk, using the operating system tools.

More detailed information in the Section 14.3.3.

To write information to a disk:

1. Click the Burn created DICOM CD/DVD image to the optical disk button on the Disk Creator toolbar. The window shown in Fig. 14.3 will pop up.

2. If necessary, select the recorder device from the dropdown menu.

3. Edit the disk name if necessary.

4. If necessary, check/uncheck the Set minimal write speed box.

5. If necessary, check/uncheck the Automatically clean up the DICOM CD/DVD image after burning disk box.

6. Click OK to write or CANCEL to cancel.
14.3.2 Write to Memory Card or Folder

To write information to a memory card (flash card) or folder:

1. Click the Write created DICOM CD/DVD image to the flash card or folder button on the Disk Creator toolbar. Dialog box is shown in Figure 14.4.

2. Select a memory card or folder on your hard disk. To do this, enter the path in the Path to write field or click the button and select the path in the dialog that opens.

3. If necessary, check/uncheck the box Automatically clean up the DICOM CD/DVD image after writing data.

4. Click OK to write or CANCEL to cancel.
14.3.3 Burn an image to CD / DVD in Linux and macOS operating systems

To write information to a disk:

1. The Work Folder should be created, i.e. the folder to store the disk image to be written.
2. Save the information to the created directory, in accordance with the Section 14.3.2.
3. Burn a disk image created in the Work Folder to a CD/DVD using the operating system tools or special applications.

14.4 View studies written on disk

Insert a disk or memory card with DICOM data and the Compact Disk DICOM Viewer Edition into the computer. If autorun of disks and cards is enabled on the computer, the Compact Disk DICOM Viewer Edition will start automatically. Otherwise, on Windows run the Start_Win file, on macOS run the DICOMViewer file. Both files are located in the root directory of the disk or card.

The written studies are automatically displayed on the Study Panel.
Chapter 15

DICOM Viewer Settings

To change the settings, select the **Options** menu and the **Settings...** item. The window shown in Fig. 15.1 will pop up.

![DICOM Viewer setup window](image)

*Figure 15.1: DICOM Viewer setup window. General settings*

The setup menu will be displayed on the left side of the window. The **DEFAULTS** button allows you to restore the settings for the current window which are set upon the very first launch of the DICOM Viewer on the computer.
15.1 General

The following parameters are set up in this section:

- Working directory path. This is the local storage location. The path can be entered manually or selected from the dialog box. To open the dialog box, click the button to the right of the path input string.

- Log file path. The information about the DICOM Viewer operation is saved in the log. The path can be entered manually or selected from the dialog box. To open the dialog box, click the button to the right of the path input string. If the parameter is not specified, the log file will be located in the directory where the DICOM Viewer is installed.

- Log file name.

- DICOM Viewer log specification. The following specification levels are available:
  - Failure: registering information about errors that led to the DICOM Viewer failure;
  - Error: registering information about all errors that may lead to the incorrect operation of the DICOM Viewer;
  - Warning: registering all errors, whether or not they might lead to the incorrect operation of the DICOM Viewer;
  - Info: registering all errors as well as standard actions of the DICOM Viewer;
  - Debug: registering all errors and standard DICOM Viewer actions with detailed information.

After changing the logging level, you do not need to restart the program.

- Use License Proxy Server (the Use License Proxy Server box) and its parameters. To check the availability of the server, click the button after you have filled in the Host and Port fields. The information will be displayed on the right.

- Use a shared folder to store service information (the Use shared settings (multi-user support) box) and path to a shared folder.

- Customize the cache memory limits. You may provide for a soft and a hard limit.
  - In the Soft field, specify the maximum volume of cache to be used by the program before it makes an attempt to clear the memory by deleting the data that are not used. The default value is determined automatically on the basis of the amount of RAM on the device with the DICOM Viewer installed.
  - In the Hard field, specify the maximum volume of cache that can be allocated for cached data. The default value is equal to the amount of RAM on the device with the DICOM Viewer installed.

The cache memory limit is specified in Gibibytes (GiB), accurate to a thousandth, from 0.125 to 999999999999.999. Its value must not exceed the memory size. If you attempt to set a limit exceeding the memory size, a warning message will pop up. The value provided in the Hard field must be greater than the value in the Soft field. If the limit values fail to meet these requirements, a warning message will pop up.
The fields for setting cache memory limits are provided with a restore recommended value button \( \textcircled{\text{C}} \). The restore recommended value button is displayed when the limit value provided is different from the recommended value. To restore the recommended value of a cache memory limit, click the \( \textcircled{\text{C}} \) button in the respective field.

After the cache memory limits have been changed, the program must be relaunched. A dialog box will pop up notifying the user of this necessity.

- Anonymous statistics collection (telemetry) function can be activated/deactivated. Telemetry function provides an opportunity to collect anonymous statistics in order to improve the product.

### 15.2 User interface

The following parameters are set up in this section:

- **Interface language.** Can be chosen from the drop-down list. The respective changes will be applied after the program is restarted.

- **Help language.** Can be chosen from the drop-down list of the help system languages. By default, the **Auto** option is selected, and the interface language is used as the help language.

  If the selected interface language is not used for the help system, English will be used as the help language. If the user didn’t install the help system when installing the software, the choice of the help language will not be available.

  The selected help language will be applied after the program is restarted.

- **Using native OS open/save file dialogs.** For Windows XP, you can use dialogs only in the DICOM Viewer style.

- **Request for confirmation before closing the DICOM Viewer.**

- **Display Tooltips (the **ToolTips** box), Shortcuts and play Slideshows on the Tooltips.** If the **ToolTips** box is unchecked, the tooltips are not displayed at all.

- **Close to tray (the **Show system tray icon** box) and minimize to tray (the **Minimize to tray** box).**

### 15.3 DICOM

The following DICOM files processing parameters are set up in this section:

- **Reading character set (character set of DICOM data);**

- **The **Ignore parse errors** option can be checked/unchecked;**

- **The **Ignore file meta header length** option can be checked/unchecked;**

- **The **Allow reading broken files** option can be checked/unchecked;**
15.4. SCREEN

- The **Perform color space conversion from YCbCr to RGB** option can be checked/unchecked. The option is disabled by default. The option is used when the color model provided for in the *PhotometricInterpretation (0028,0004)* tag is invalid. When the option is enabled, the color space is transformed from YCbCr to RGB. When the setting is changed and saved, the program must be relaunched. A dialog box will pop up notifying that the new setting will be applied the next time the program is launched. When the program is restarted automatically, the option is not applied.

### 15.4 Screen

This section is meant for customizing the DICOM Viewer windows display on the monitors available for the OS.

#### 15.4.1 Setting an Additional Monitor

The DICOM Viewer provides an opportunity to display information on several monitors, and the user does not have to move the windows manually.

To use an additional monitor, proceed as follows:

1. Select the **Options** menu and the **Settings...** item.

2. Open the **Screen** section. The window similar to the one shown in Fig. 15.2 will pop up.

3. On the **Special parameters of screen** list, select the screen(s) to be used for the DICOM Viewer. The screen status will be changed to **Used**.

4. Click **OK** or **APPLY** to apply the changes or **CANCEL** to cancel the actions. To restore default settings, click the **DEFAULTS** button.

5. The DICOM Viewer needs to restart to apply the changes. The DICOM Viewer will request confirmation before restarting: **The changes you are made requires restarting the program to take effect. Do you want to restart the application?**

If you are still working with the opened studies, or if the information needs to be saved, click **NO** to cancel the restart and set up the displays later. To restart the DICOM Viewer click **YES**.
CHAPTER 15. DICOM VIEWER SETTINGS

Figure 15.2: Monitor settings

If only one screen is selected, the DICOM Viewer will be opened on this screen. If more than one screens are checked, the DICOM Viewer windows are opened on the marked screens. To close the DICOM Viewer just close any of the windows.

15.4.2 Customizing the Screen Parameters

The DICOM Viewer provides an opportunity to divide the screen into two parts and place two windows side by side at launch.

To change special parameters of the screen, proceed as follows:

1. Select the Options menu and the Settings... item.

2. Open the Screen section. The window similar to the one shown in Fig. 15.2 will pop up.

3. Select the screen you want to split in the Special parameters of screen list. A Not used screen cannot be selected.

4. Check the Split the screen for the selected screen (see Fig. 15.3).
5. Select the left or the right window as the primary by choosing the respective option in the **Set as primary** line. When the DICOM Viewer launched, the tab with the study list appears automatically in the primary window. Only one window may be selected as the primary. In other windows, the tab with the study list may be opened manually from the main menu **File->Study list**.

6. In the **Open the series by default** line, check the boxes for the windows in which you want to open series in the respective tabs (**Image viewer**, **Volume reconstruction**, **MPR reconstruction** etc.) by double-clicking on the thumbnail or by pressing the respective button on the toolbar. The order of opening series in the windows for which the **Open the series by default** box has been checked is determined by the arrangement of the windows (left-to-right or top-down).

7. Click **OK** or **APPLY** to apply the changes or **CANCEL** to cancel the actions. To restore default settings, click the **DEFAULTS** button.

8. In the restart confirmation window, click **YES** to restart or **NO** to cancel restart and continue working.

When the user chooses the **Show as detached window** series arrangement (see Section 1.4), the window is opened in the center of the screen. To fix a detached window, click...
the **Fix window** button in the window header. The window will be added as a tab to the left window of the respective screen.

When the user chooses the **Show fullscreen** series arrangement (see Section 1.4), the window is expanded to full screen. Open series windows may overlap. When the user exits full screen mode, the series window is added as a tab to the respective program window.

### 15.4.3 High resolution monitor support

To automatically scale the interface for high-resolution monitors according to the scale of the operating system, check the **Enable High-DPI scaling** box. The change will take effect the next time you launch DICOM Viewer.

### 15.5 Skins

The following parameters are set up in this section:

- the DICOM Viewer layout (skin):
  - light;
  - dark (used by default).
- use the Viewer layout for the Help System.
15.6 Modules

In this section you can specify the settings for particular modules (Fig. 15.4).

To browse the detailed information about each module, select the module and click the Module info button. For some modules, special parameters are set. To do this, select the module from the Installed modules list and click the SETTINGS button.

15.6.1 Set Up Image Viewer Module

Select the Image Viewer module from the Installed modules and click the SETTINGS button. The Image viewer settings window contains four tabs with the following parameters:

1. Image arrangement tab. The following parameters are set up:
   - Confirm series closure on the arrangement changing option. The option is enabled by default. Switches off/on the display of the dialog box for series deletion confirmation when the user selects a grid with fewer view windows than there are open series in the study. The option is exported to the file saving the current DICOM Viewer settings (see Section 15.8.1);
   - default series arrangement;
• splitter priority;
• default image arrangement;
• the number of images scrolled per click;
• image sorting method.

These parameters can be set for a specific modality. To add a modality, click the ADD button and enter the name of the modality in the dialog that appears. To change the settings for a previously added modality, select it in the Settings for modality drop-down list. To delete the selected modality click the REMOVE button.

2. **Tools** tab. The following parameters are set up:

   • default tool (the one that activates when opening an image). Options:
     - no tool;
     - Adjust W/L;
     - Ruler;
     - Angle;
     - ROI rectangle tool;
     - ROI ellipse tool;
     - ROI polygon tool;
     - Sync by point;
   • default mode. Options:
     - no mode selected;
     - DSA mode;
   • request for confirmation before deleting all annotations and measurements;
   • enable/disable the warnings of non-bilinear interpolation;
   • show TSE values in annotations;
   • enable/disable default synchronization of series image scrolling;
   • enable/disable slices scaling and position synchronization for various projections.

3. **Controllers** tab. Sets up the actions associated with mouse actions.

4. **W/L settings** tab. Sets up the default W/L values. If a value is not specified, the default is 0.

5. **W/L settings** tab. The following parameters are set up:

   • option Use recommended W/L for Series can be checked/unchecked;
   • default W/L for DSA mode can be activated/deactivated;
15.6.2 Set Up Study List Module

Select the StudyList module from Installed modules and click the Settings button. The following parameters are set up in the Study list config window:

- option Load local storage automatically can be checked/unchecked;
- option Ask to keep in storage autodownloaded series can be checked/unchecked;
- the period for which the data is loaded can be checked/unchecked;
- font options can be set up;
- option Allow to edit patient name and description can be checked/unchecked;
- option Warn about editing patient name and description can be checked/unchecked;
- option Download whole study by double click can be checked/unchecked;
- option Fixed thumbnail height can be checked/unchecked.

15.6.3 Set Up 3D Reconstruction Module

Select the 3D Reconstruction module from Installed modules and click the Settings button. The window contains two tabs with the following parameters:

1. Render tab.

- Sets up the render device. Options:
  - Auto;
  - CPU (using the software facilities);
  - OpenCL support;
  - CUDA support.
  - Metal support. Supported on macOS version 10.15 and greater.

  The options available may vary depending on the configuration and equipment settings.

- Customize the cache memory limits for the selected imaging device.

By default, the imaging device is selected by the program automatically and is shown on the drop-down list as the Auto option. The cache memory limits that can be changed are displayed for this device. For each device on the drop-down list, the amount of memory available for caching is displayed.

The fields for setting cache memory limits are provided with a restore recommended value button 🔄. The restore recommended value button is displayed when the limit value provided is different from the recommended value. To restore the recommended value of a cache memory limit, click the 🔄 button in the respective field.

You cannot customize the cache memory limits for the CPU (software). The cache memory limits for this device are calculated on the basis of the values provided in the General tab (see Section 15.1).
2. **Segmentation** tab. The following parameters are set up:

- sets the default structure opacity;
- option **Invert edit mask on MPR** can be checked/unchecked;
- option **Confirm on the structure removing** activates the confirmation dialog box when deleting a structure. The option is enabled by default.

3. **Project** tab.

- Sets up the function of saving projects:
  - Enables/disables the **Save DICOM data of series** option;
  - Enables/disables the **Enable autosaving** option;
  - Sets the autosave frequency on the **Timeout** dropdown list.

- Selects the mode in which the saved project is to be opened: **3D, MPR or Both**.

4. **Reconstruction** tab.

- option **Warn about varied slices distance** can be checked/unchecked;
- option **Warn about reducing quality because of reslicing** can be checked/unchecked;
- sets up reconstruction by series with varying distances between slices. Options:
  - Non uniform slice interpolation;
  - Max uniform distance slice range.

5. **UI** tab. The following parameters are set up:

- Saving MPR view sizes. To change this parameter, checks/uncchecks option **Save MPR view sizes**. By default, it is unchecked;
- MPR plane line thickness;
- MPR plane line colors;
- Disabling the display of the standard space orientation panel in the **Volume reconstruction** and **3D view** windows of the **MPR reconstruction** tab. By default, it is enabled. To disable the display of the panel, untick the **Show a panel of standard projections in a 3D view** box. The changed panel display settings are not applied to the tabs and windows that had been opened before the changes were introduced;
- selects in the list the action to be performed after CLUT is change if W/L is changed;
- Request for confirmation before deleting all measurements;
- Split brush cut and brash restore tools.

6. **3D controllers** tab. Sets up the actions associated with mouse actions in the Volume Reconstruction window.

7. **MPR controllers** tab. Sets up the actions associated with mouse actions in the MPR, Planning of Pedicle Screw Installation and Vessel Analysis windows.
15.6.4 Set Up Vessel Analysis Module

Select the Vessel analysis module from Modules and click the Settings button. The window contains tab with the following parameters:

1. UI tab. The following parameters are set up:

   - Enabling saving the window size in the Vessel analysis tab. By default, it is disabled.
   - Disabling the display of the standard space orientation panel in the 3D view window of the Vessel analysis and Coronary arteries analysis tab. By default, it is enabled. To disable the display of the panel, untick the Show a panel of standard projections in a 3D view box. The changed panel display settings are not applied to the tabs and windows that had been opened before the changes were introduced.
   - Disabling the option Request a non-enhanced series to remove bones on window opening. By default, it is enabled.

15.6.5 Set Up Network Support Module

Select the Network support module from Installed modules and click the SETTINGS button. You can specify the maximum count of connections to a PACS Server.

15.6.6 Set Up Local Storage Module

Select the Data storage module from Installed modules and click the SETTINGS button. The window contains the following parameters:

1. the Automatic local storage cleaning option can be checked/unchecked;

2. cleaning interval can be set.

15.6.7 Set Up «DICOM CD/DVD Creator»

Select the DICOM CD/DVD creator module from the Installed modules and click the SETTINGS button. You can specify the following parameters:

   - the «Add selected studies at opening DICOM CD/DVD creator» option can be checked/unchecked;
   - the «Add DICOMDIR file to created DICOM CD/DVD image before writing data» option can be checked/unchecked;
   - the «Enable image buffering» option can be checked/unchecked.
15.6.8 Set Up PET Analysis Module

Select the PET Analysis module from Installed modules and click the SETTINGS button. You can specify the following parameters:

The Common tab:

- Enable SUV mode automatically;
- MIP layer CLUT by default;
- window upper limit. The Max SUV value and Max window percent items are available;
- First layer modality by default for the PET+CT window;
- PET layer CLUT by default for the PET+CT window;
- CT layer opacity (%) by default for the PET+CT window;
- PET layer opacity (%) by default for the PET+CT window;
- option Ask before deleting all annotations and measurements can be checked/unchecked.

In the Controllers MIP tab you can associate tools with the mouse wheel and move operations for the MIP window, in the Controllers 2D tab you can do it for the CT and PET windows. The settings are applied the next time you open the PET Analysis window. To restore default values, click the DEFAULTS button.

15.7 Set Up Hotkeys Module

In this section, you can specify hotkeys to perform different actions. To set up hotkeys:

1. Select the Options menu and the Settings... item.
2. Open the Hotkeys section. The window similar to the one shown in Fig. 15.5 will pop up.
3. Select the target action in the table. If necessary, enter action name or hotkey in the Filter field to filter the action list. The hotkeys specified for the selected action are displayed in the Key sequence column.
4. To modify or set hotkeys:
   - change the value in the Key sequence field or
   - click the RECORD button; next, press the key sequence you wish to assign on the keyboard and to finish, click the Stop recording button.

The entered value will be immediately displayed in the Key sequence column of the table.

5. To delete hotkeys, erase the value in the Key sequence field.
6. If the entered hotkeys are already used, a warning similar to the one shown in Fig. 15.6 will be displayed, and the value in the **Key sequence** column will be written in red. To see which action corresponds to this hotkeys, click **Show**. Do not set the same hotkeys for the actions performed in one window. If the entered value cannot be set, a warning similar to the one shown in Fig. 15.7 will be displayed.

7. To restore the original value of the hotkeys for the selected action, click the **RESET** button.

8. To restore the original values of the hotkeys for all actions, click the **RESET ALL** button.

9. Click **OK** or **APPLY** to apply the changes or **CANCEL** to cancel the actions.

10. In the restart confirmation window, click **YES** to restart or **NO** to cancel the restart and continue working.

![Image of Hotkeys module setup window]

*Figure 15.5: Hotkeys*
CHAPTER 15. DICOM VIEWER SETTINGS

Figure 15.6: Warning about key sequence potential conflict

Figure 15.7: Warning about invalid key sequence

The types of hotkeys are described in the following table:

<table>
<thead>
<tr>
<th>Hotkey type</th>
<th>Designation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single key: any key of the alphanumeric keyboard or a functional key</td>
<td>Single key, e.g.: &lt;A&gt; or &lt;F5&gt;</td>
</tr>
<tr>
<td>Group of keys: two keys should be pressed simultaneously. The first key is Ctrl, Alt or Shift, the second one is any key of the alphanumeric keyboard or a functional key</td>
<td>Two single keys coupled by &lt;+&gt;, e.g.: &lt;Ctrl+S&gt; or &lt;Shift+F5&gt;</td>
</tr>
<tr>
<td>A sequence of several keys of the alphanumeric keyboard or functional keys: keys should be pressed one by one</td>
<td>Single keys or groups of keys, separated by comma, e.g.: &lt;A,B,C&gt; or &lt;Ctrl+F1,Ctrl+F2&gt;</td>
</tr>
</tbody>
</table>

15.8 Import and Export Settings

15.8.1 Export Settings

The export functionality allows you to save the current DICOM Viewer settings in a file. To export settings:

1. Select the **Options** menu and the **Export settings** item. The save file dialog box will pop up.

2. Select the location to save the settings file to and enter the file name.

3. Click **Save** to save the settings file or **Cancel** to cancel the actions.
15.8.2 Import Settings

The import functionality allows you to apply the settings specified earlier and saved in a file. To import settings:

1. Select the **Options** menu and the **Import settings** item. The DICOM Viewer will request confirmation for this action because all the current settings will be lost after the import. Click **Yes** to continue or **No** to cancel the import.

2. If you click **Yes**, the settings file selection dialog box will pop up. Select the needed file.

3. To import the settings, click **Open**. The DICOM Viewer will be restarted, and the settings will be applied. To cancel the import, click **Cancel**.
Chapter 16

DICOM Tag Viewing

16.1 DICOM Tags. General Information

A DICOM file presents data as a sequence of elements containing information about the image (graph etc.), where the last element has the image (graph etc.) itself. Each element comprises several parts, including:

- **Tag** — a unique element identifier comprised of a pair of values represented in the hexadecimal number system and determining the group number and the element number

- **Data type** — a line showing the data type abbreviation (two symbols)

- **Data field length**;

- **Data** — the information comprised in the element, including the image (graph etc.) itself

If the Data field contains information that cannot be represented in the form of a text (e.g. an image or graph), then the respective column will read: **Binary content. Hidden.**

If the tag is standard, its name will be shown. If the tag is reserved by a certain modality manufacturer or there is an error in its name, then the field will read: **Unknown Tag & Data.**

To learn about the data contained in this tag, you will need to study the documents for the modality used in the study. The **7fe0,0010 (PixelData)** tag contains an image, a graph or some other visual data.

Examples of elements:

<table>
<thead>
<tr>
<th>Element name</th>
<th>Tag</th>
<th>Type</th>
<th>Length</th>
<th>Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>StudyDate</td>
<td>0008,0020</td>
<td>DA</td>
<td>8</td>
<td>20130107</td>
</tr>
<tr>
<td>StudyInstanceUID</td>
<td>0020,000d</td>
<td>UI</td>
<td>56</td>
<td>1.3.12.2.1107.5.2.6.24186.30000013011710501018700000060</td>
</tr>
<tr>
<td>Modality</td>
<td>0008,0060</td>
<td>CS</td>
<td>2</td>
<td>MR</td>
</tr>
</tbody>
</table>
### 16.2. DICOM Tag Viewer Window

You can open the DICOM Tag Viewer window from the Study List (see Section 1.4) and Image Viewer (see Section 2.28) windows. The DICOM Tag Viewer window is shown in Fig. 16.1.

#### 16.2.1 Toolbar

The toolbar is placed in the upper part of the window (Fig. 16.2).

![Figure 16.2: Toolbar](image)

**Tools:**

<table>
<thead>
<tr>
<th>Element name</th>
<th>Tag</th>
<th>Type</th>
<th>Length</th>
<th>Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unknown Tag &amp; Data</td>
<td>0051,1009</td>
<td>LO</td>
<td>4</td>
<td>1.0</td>
</tr>
<tr>
<td>PixelData</td>
<td>7fe0,0010</td>
<td>OW</td>
<td>2</td>
<td>Binary content. Hidden.</td>
</tr>
</tbody>
</table>
16.2.2 Tag Tree

The tag tree is placed under the toolbar. If several tags belong to the same group, the group is unfolded and the tags are shown. Groups can be nested, one inside another. To unfold a group, click + on its left; to collapse a group, click -. To unfold all the groups, click the Show All button on the toolbar; to collapse all the groups, click Collapse All; to unfold only second level groups, click the Best View button. To copy the value from the element field, select it with the left mouse button and click Copy on the toolbar, or else choose Copy in the context menu.
16.3. ANONYMIZE STUDIES AND SERIES

16.2.3 Search

To open the search bar, click the Search button on the toolbar. The search bar will be displayed at the bottom of the window. To close the search bar, click the cross on the right or the Search button.

You can perform search by any data contained in the element. To perform search, enter the text you need to find in the Search field. The elements with fully or partially matching values will be highlighted in green; the first element found will be highlighted in orange. If no matches are found, the text entered will turn red. The number of the element chosen and the total quantity of the elements found is displayed on the right. To go to the next element found, click the Next button; to go to the previous element, click the Previous button. To perform case sensitive search, check the Match Case box. To highlight all the values found, check the Highlight All box (it is checked by default).

16.3 Anonymize studies and series

Anonymization is possible only for the studies in the Local Storage or for those that are opened from a folder or from a CD.

The data stored in the following tags will be replaced with Anonymous value:

- PatientName;
- PatientBirthDate;
- PatientSex;
- InstitutionName (institution or organization to which the identified individual is responsible or accountable);
- InstitutionAddress (mailing address of the institution or organization to which the identified individual is responsible or accountable);
- OperatorsName (name(s) of the operator(s) supporting the Series);
- PerformingPhysicianName (name of the physician(s) administering the Series);
- ReferringPhysicianName (name of the patient’s referring physician).

The PatientID (patient’s identifier) tag value will be replaced with a random alphanumeric value.

To anonymize values stored in other tags, you must add these tags to the list (see below). To anonymize studies:

1. Select one or more studies in the Local Storage, a local folder or a CD.
2. Select the Studies menu and Create anonymized copies of the selected studies...
3. To add a tag to anonymize, type the group number to the Group field and type the element number to the Element field and click the button (Fig. 16.3).
4. To delete a tag to anonymize, click the button.
5. By default, the data stored in tags is replaced by «Anonymous». To change the text value of the tag, left-click on the respective field and enter the new value.

   **Warning! The format of the input data must comply with the DICOM standard.**

6. To disable tag anonymization without deleting the tag from the list, uncheck the box against the chosen tag. By default, the boxes for all the tags added to the anonymization list are checked.

7. To restore the default tag list, click the **DEFAULTS** button.

8. To Anonymize, click **OK**, to cancel click **CANCEL**.

   ![Anonymization Dialogue](image)

   *Figure 16.3: Dialogue of anonymization*

   If other tags contain data that matches the data contained in anonymized tags, the warning appears (Fig. 16.4).
16.3. ANONYMIZE STUDIES AND SERIES

To view the tags containing the same data as the anonymized tags, click SHOW DETAILS.... To save the study without changing the tag data, click YES. To change the tag values, click NO and add the selected tags to the anonymization list.

The tags with the data that matches the data contained in the anonymized tags are automatically added to the Anonymization box (Figure 16.3). By default, the added tags are ticked. To anonymize the tags, click OK; to cancel, click CANCEL.

The selected studies will be anonymized and saved to the Local Storage with the patient's name Anonymous.

To anonymize the selected series:
1. Select study in the Local Storage, a local folder or a CD.
2. Select the series that you want to Anonymize. For details on how to work with series, see Section 1.10.
3. Select the Studies menu and Create anonymized copy of series...
4. To add a tag to anonymize, type the group number to the Group field and type the element number to the Element field and click the button (Fig. 16.3).
5. To delete a tag to anonymize, click the button.
6. By default, the data stored in tags is replaced by «Anonymous». To change the text value of the tag, left-click on the respective field and enter the new value.

**Warning! The format of the input data must comply with the DICOM standard.**

7. To disable tag anonymization without deleting the tag from the list, uncheck the box against the chosen tag. By default, the boxes for all the tags added to the anonymization list are checked.
8. To restore the default tag list, click the DEFAULTS button.
9. To Anonymize, click OK, to cancel click CANCEL.

The selected series will be anonymized, saved to the Local Storage and marked anonymized.

**Make sure that no personal data are retained in customized tags and that standard tags only have anonymized data.**
Chapter 17

Print Images

The DICOM Viewer allows you to print images on paper or film using DICOM printers. You must add images to the print list, then open the list in the preview window and print the images.

17.1 Working with Print List

To print images, you should add them to the print list first. You can do this in the following windows:

- View Flat Images window;
- Multiplanar Reconstruction window;
- Volume Reconstruction window;
- Planning of Pedicle Screw Installation window;
- Coronary Artery analysis window;
- PET Analysis window;
- Series Fusion window.

Depending on the way the image is captured, you can change the window level and width in the print preview window (in this case, the labels on the screen are not captured) or cannot change the window level and width (in this case the image is captured with all the labels and annotations). For details, see the next Sections.

If the Add to print list button is inactive, click the left button on the header of the window with the image to be printed or removed.

The print list is saved until the program is closed.
17.1 Add/Delete Images in View Flat Images and Fusion windows

To add the current image to the print list, click on the Add to print list button. The button will look as follows: . When browsing images, the button will look like this if the current image is not on the print list, and like this if it is. If there are several image views opened in the tab, note which view window is active (highlighted by a red frame).

To remove the current image from the print list, click on the Add to print list button that should look like this: . The image will be removed, and the button will change to.

Also, you can remove images in the Preview window (see Section 17.2).

In the View Flat Images and Fusion windows, there are two image capturing modes for printing:

- **View screenshot**: the entire image, including the labels and annotations, is captured. There is no capability to change the window width and level in the Preview window.

- **Image capture**: only the image of tissues is captured. There is a capability to change the window width and level in the Preview window.

When you click on the Add to print list button, the previously selected capture mode is used. To switch the capture mode, click the arrow on the right of the Add to Print List button and select the target mode. The selected mode is marked with a flag and saved as the default capture mode for the View Flat Images and Series Fusion windows.

If the image was captured in the Series Fusion window, then changing the window width and level in the Preview Window is possible only for the first layer.

17.1.2 Add Images in Multiplanar Reconstruction and Volume Reconstruction windows

To add the current image to the print list, click on the Add to print list button.

In the Multiplanar Reconstruction and Volume Reconstruction windows, there are three image capturing modes for printing:

- **View screenshot**: the entire image, including the labels and annotations, is captured. There is no capability to change the window width and level in the Preview window.

- **Image screenshot**: only the image of tissues is captured. There is no capability to change the window width and level in the Preview window.

- **Entire image**: only the image of tissues is captured. There is a capability to change the window width and level in the Preview window (except the images captured in the Volume Reconstruction window).

When you click on the Add to print list button, the previously selected capture mode is used. To switch the capture mode, click the arrow on the right of the Add to Print List button and select the target mode. The selected mode is marked with a flag and saved as the default capture mode for the Multiplanar Reconstruction, Volume Reconstruction windows.
If the fused image was captured in the **Entire image** Mode in the Multiplanar Reconstruction Window, then changing the window width and level in the Preview Window is possible only for the first layer.

Deletion of the images captured in these modes is available in the Preview window (see Section 17.2.3).

### 17.1.3 Add Series and Clear Print List

To add an entire series to the print list, click on the arrow on the right side of the **Add to print list** button and select the **Add entire series**. **Images will be added with default mode** menu item. This functionality is available only for the View Flat Images and Fusion windows.

To clear the print list, click on the arrow on the right side of the **Add to print list** button and select the **Clear print list** item.

### 17.1.4 Add Images from Different Studies

If the print list is not empty, and you are trying to add an image from another study, the DICOM Viewer will return a warning **You are trying to add image from different study**.

To add the image, click **YES**. To clear the print list and add the current image, click **REWRITE**. To cancel the addition and leave the current print list as it is, click **NO**.

### 17.2 Edit print list in Preview window

#### 17.2.1 Preview

The Preview windows are intended to control the printing and final editing of the print list. The **Preview** window is used to view printing on paper and save images to a pdf file, the **DICOM Preview** is used for printing on film. To open the target window, select the **File** menu and the **Preview** item or the **DICOM Preview** item. The settings made in one window do not affect the settings in the other one except deleting images. The print list is common for both windows, hence, the images deleted in one of the windows are deleted from the print list, and they disappear in the other window.

The **DICOM Preview** tab is shown in Fig. 17.1.
Figure 17.1: DICOM preview window

The toolbar is located at the top (Fig. 17.2), and the bottom part shows what the printed images will look like (preview page).

Figure 17.2: Toolbar

The toolbar contains the following elements:

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="icon-update.png" alt="Update" /></td>
<td>The <strong>Update</strong> button refreshes the preview page after the print list has been changed</td>
</tr>
<tr>
<td><img src="icon-fit-width.png" alt="Fit width" /></td>
<td>The <strong>Fit width</strong> button adjusts the preview page size to the screen width</td>
</tr>
<tr>
<td><img src="icon-fit-page.png" alt="Fit page" /></td>
<td>The <strong>Fit page</strong> button adjusts the preview page size to the tab size</td>
</tr>
<tr>
<td><img src="icon-page-scale.png" alt="Page scale" /></td>
<td>The <strong>Page scale</strong> field. The scale is entered from the keyboard manually or selected from the dropdown menu. To open the dropdown menu, click on the arrow on the right side of the panel</td>
</tr>
<tr>
<td><img src="icon-zoom-in.png" alt="Zoom in" /></td>
<td>The <strong>Zoom in</strong> button zooms in the page. The current scale is displayed in the <strong>Page scale</strong> field</td>
</tr>
</tbody>
</table>
### CHAPTER 17. PRINT IMAGES

<table>
<thead>
<tr>
<th>Icon</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Zoom out" /></td>
<td><strong>Zoom out</strong> button zooms out the page. The current scale is displayed in the <strong>Page scale</strong> field</td>
</tr>
<tr>
<td><img src="image" alt="Portrait" /></td>
<td><strong>Portrait</strong> button sets the portrait layout for the page</td>
</tr>
<tr>
<td><img src="image" alt="Landscape" /></td>
<td><strong>Landscape</strong> button sets the landscape layout for the page</td>
</tr>
<tr>
<td><img src="image" alt="First page" /></td>
<td><strong>First page</strong> button is used to jump to the first page if the images do not fit into a single page</td>
</tr>
<tr>
<td><img src="image" alt="Previous page" /></td>
<td><strong>Previous page</strong> button is used to jump to the previous page if the images do not fit into a single page</td>
</tr>
<tr>
<td><img src="image" alt="Next page" /></td>
<td><strong>Next page</strong> button is used to jump to the next page if the images do not fit into a single page</td>
</tr>
<tr>
<td><img src="image" alt="Last page" /></td>
<td><strong>Last page</strong> button is used to jump to the Last page if the images do not fit into a single page</td>
</tr>
<tr>
<td><img src="image" alt="Page template" /></td>
<td><strong>Page template</strong> drop-down list. It allows to select a predefined page template (see Section 17.2.2)</td>
</tr>
<tr>
<td><img src="image" alt="Edit page template" /></td>
<td><strong>Edit page template</strong> button opens the Page Template Settings dialog (see Section 17.2.2)</td>
</tr>
<tr>
<td><img src="image" alt="Resolution (DPI)" /></td>
<td><strong>Resolution (DPI)</strong> drop-down list (only for the <em>Preview</em> window). The list allows to set print resolution (clarity)</td>
</tr>
<tr>
<td><img src="image" alt="Printer" /></td>
<td><strong>Printer</strong> dropdown menu (only for the <em>DICOM Preview</em> window). It specifies the DICOM printer</td>
</tr>
<tr>
<td><img src="image" alt="Zoom" /></td>
<td><strong>Zoom</strong> tool allows to zoom selected images</td>
</tr>
<tr>
<td><img src="image" alt="Pan" /></td>
<td><strong>Pan</strong> tool allows to shift selected images inside cells</td>
</tr>
<tr>
<td><img src="image" alt="Reset transformation" /></td>
<td><strong>Reset transformation</strong> tool allows to reset all the transformations made using the <strong>Zoom</strong> and <strong>Pan</strong> tools</td>
</tr>
<tr>
<td><img src="image" alt="Adjust W/L" /></td>
<td><strong>Adjust W/L</strong> tool allows to change the window width and level</td>
</tr>
<tr>
<td><img src="image" alt="Arrow" /></td>
<td><strong>Arrow tool</strong> allows to make graphic labels such as arrows. For details on how to do it see Section 2.30</td>
</tr>
<tr>
<td><img src="image" alt="Pencil" /></td>
<td><strong>Pencil tool</strong> allows to build freeform contours. For details on how to do, it see Section 2.30</td>
</tr>
</tbody>
</table>
17.2. EDIT PRINT LIST IN PREVIEW WINDOW

The **Text tool** allows to make text labels. For details on how to do, it see Section 2.30

The **Ellipse** tool allows to make graphic labels such as an ellipse. For details, on how to do it see Section 2.30

The **Rectangle** tool allows to make graphic labels such as a rectangle. For details, on how to do it see Section 2.30

The **Polygon** tool allows to make graphic labels such as a polygon. For details, on how to do it see Section 2.30

The **Show labels** tool allows to show the information about an image. For details, on how to do it see Section 17.2.4

The **Show reference image** tool allows to display a reference image. For details, on how to do it see Section 17.2.5

The **Remove selected images** button allows to remove selected images from the print list (see Section 17.2.3)

The **Page setup** (only for the **Preview** window) opens the print settings dialog

The **Print** button opens the print dialog

The **Clear print list** command removes all the images from the print list. To use it, click the arrow on the right side of the **Print** button and select the **Clear print list** item

The **Export to PDF** tool (only for the **Preview** window) saves images to a pdf file

### 17.2.2 Set Up Page Templates

The Page templates tool allows you to arrange images in arbitrary order. After the program has been installed, the following templates will be available:

- one image on the screen;
- two images, one on top of the other;
- 2x2 grid;
- 3x2 grid.

To open the page template editing dialog, click the **Edit page template** button. The dialog box for the print preview window is shown in Fig. 17.3. For the DICOM preview tab, in the dialog box, instead of the **Spacing** parameter you will see a drop-down menu for choosing the film size.
Select the desired template from the drop-down list. To add a new template, click the CREATE TEMPLATE button, to delete a template, click the DELETE button.

**Attention! Deleting a template cannot be undone.**

To change a template name, enter a new name in the Template Name field. For the Preview tab set the space between images in the Spacing (mm) field.

For the DICOM preview tab, choose the film size from the “Film size” drop-down menu. The default value is Chosen film size for printer. If this value is chosen, the size of the film will be as set for your printer. The DICOM printer settings are described in Section 17.3.2. If you choose a different value for the printing template, the size provided for by the printer settings will be ignored.

On the left-hand side of the window you see the arrangement of images on the page. To divide any cell into any number of lines and columns, left-click on that cell to select it and enter the required number of lines and columns in the left and the right fields indicated by the arrows in Fig. 17.3. Then click SPLIT.

If the column and/or row count is greater than 1, you can merge an arbitrary number of cells. The merged cells must form a rectangle. For example, set the Row count to 3 and the Column count to 4. Next, select cells 7, 8, 11, 12. To do it, move the cursor from cell 7 to cell 12, holding the left mouse button. Next, click MERGE. The four selected cells will be merged.
To split any cell into an arbitrary number of rows and columns, select this cell, enter values in the **rows** and **columns** fields and click the **SPLIT** button. The cells made by splitting can only be merged with each other.

The cells created in such a way can only be merged with other cells from the same group.

To add the header and/or the footer, proceed as follows:

1. Check the **Header** box to add the header and the **Footer** box to add the footer. The header and the footer will be shown in the scheme representing the cell arrangement.

2. Specify the header/footer height in points.

3. Choose an image for the header/footer. To do that, click the **BROWSE** button and choose a file with **jpg, jpeg, jpe** or **png** extension in the dialog box that pops up.

4. To use this header/footer for all the templates without a header/footer (including the new templates by default), click the **Set this header as default** or **Set this footer as default** button in the dialog box. Then click **YES** to apply or **NO** to cancel.

To save the changes, click **OK** or **APPLY**, to cancel, click **CANCEL**.

### 17.2.3 Cells

If the page template contains several cells, then to apply the **Zoom**, **Pan**, **Adjust W/L** tools to several images on one page or to delete an image (images), you need to select the corresponding cells. To select, click the left mouse button on the cell. To remove a selection, click on the image again. To select multiple cells:

- To select multiple cells that are contiguous (next to each other): click on the first cell and click on the last one, holding the **Shift** key on the keyboard.

- To select multiple cells that are anywhere on the page: click the left mouse button on each one, holding the **Ctrl** key on the keyboard.

- To remove a selection, click on the any selected cell again.

**Warning! If any of the graphic label tools or one of the «Zoom», «Pan», «Adjust W/L» tools is active, selection and removing of the selection are not available.**

To remove the images in the selected cells click the **Remove selected images** button.

To swap images in cells, drag an image to the target cell, holding the left mouse button. The images will be swapped.

### 17.2.4 Print Labels

If an image is captured without labels, you can add them in the Preview Window. To do it, click the **Show labels** button. The tags that should be displayed are marked with flags. To display or hide a label, click the arrow on the right side on the **Show labels** button and select the target item.
To set the font size, select the **Show annotation text size**... item in the button menu.

To select the DICOM tags that should be displayed in the left-hand bottom corner, select the **Set visible tags**... item in the button menu and in the dialog that appears mark the target tags with flags.

If one or more cells are selected, the settings will be applied only to these cells.

### 17.2.5 Reference image

The DICOM Viewer provides an opportunity to add reference images to the print list. You can ascribe the same reference image to all the images on the list, or a different image to each of the images on the list. To ascribe several reference images to each study added to the print list, you can create a separate list of reference images.

To add a reference image:

1. Choose an image from the same study that has been added to the print list. Click the arrow on the right side of the **Add to print list** button and select the **Add as reference image** item. This image will by default be ascribed to all the images from the same study included in the print list.

2. If you need to add a new reference image to the list or replace it with a different one, repeat the previous step. You will see a notification that a reference image has already been added. To add another reference image to the list, click the **YES** button; to replace the previous reference image, click the **REWRITE** button, to cancel, click the **NO** button.

3. Open the Preview or DICOM Preview window. If the **Show reference image** tool is inactive, activate it with the left mouse button. A reduced reference image is displayed in the corner of each image. If there is more than one image on the list of reference images, the first image added to the list will be displayed.

4. To adjust the display of the reference image, click the arrow on the right side of the **Show reference image** button and select the **Reference image settings**... item. You can set up the following properties:
   - image alignment;
   - dimension ratio;
   - project line width (mm).

5. To replace the reference image attributed to a separate image, highlight it and click the arrow on the right side of the **Show Reference Image** button, then click the **Select Reference Image**... button. Choose the image you need in the dialog box and click **CHOOSE**. If no image has been selected, the reference image will be changed for all the images on the print list. If there are images from different studies on the print list, the reference image can be changed only for the images selected. The **Select Reference Image**... function is also available in the right-click menu.

6. To delete a reference image from the list, click the arrow on the right side of the **Show Reference Image** button, then click **Select Reference Image**... item. Choose the image you need in the dialog box and click the **DELETE** button.
7. To hide/show a reference image, click the **Show Reference Image** button. If there are some images selected, the action will be performed only for them.

If there are images from different studies on the print list, reference images will be ascribed to them separately.
17.3 Print Images on Film

17.3.1 Set Up DICOM Printers

To set up the DICOM printing parameters, select the **Network** menu and the **DICOM printer setup...** item. The window shown in Fig. 17.4 will be displayed.

![DICOM printing settings window](image)

*Figure 17.4: DICOM printing settings window*

To add a DICOM printer to the list:

1. Click the **Add printer** button on the toolbar. The printer setup dialog box (Fig. 17.5) will be displayed.

2. Enter a user-defined printer name into the **Name** field.
3. In the **SCU AE Title** field, enter the name of the client allowed to access the printer (this parameter is defined in the printer settings).

4. In the **SCP AE Title** field, enter the printer name (this parameter is defined in the printer settings).

5. Enter the printer network address in the **Host** field.

6. Enter the printer port in the **Port** field.

7. Check the **Default** box if the printer should be used by default.

8. Click **OK** to apply the changes or **CANCEL** to cancel them. To save the information without closing the window, click **APPLY**.

![DICOM printer setup dialog box](image.png)

*Figure 17.5: DICOM printer setup dialog box*

All the added printers will appear on the printer list. The default printer can be assigned directly from the list by checking the box next to the printer.

To delete a printer from the list, select it and click the **Remove printer** button. Click **YES** in the confirmation dialog to delete the printer or **NO** to cancel the deletion.

To edit the printer settings, select the printer and click the **Edit printer** button.

To check whether a printer is available, select it and click the **Info printer** button. If the printer is available, the printer list will display the **Online** status for the printer. If not, the **Offline** status will be displayed. If the status has not been checked, its value will be **Unknown**.

### 17.3.2 Set Up DICOM Printing Parameters

To set up the DICOM printing parameters, select the **Network** menu and the **DICOM Printer setup** item. The window shown in Fig. 17.4 will pop up.
CHAPTER 17. PRINT IMAGES

The settings must be in strict compliance with the specification for the DICOM printer.

Set the required parameters on the printing setup panel:

1. Set the film source (Unit or Processor).

2. Set the film cutting.

3. Set the magnification type. If you need to print the images with the original resolution, select None. If you need to fit the images to the film size, select one of the magnification types (Bilinear, Cubic or Replicated). In this case, the printer will change the image resolution according to the selected algorithm to maximize the image size on the page and retain its proportions.

4. Select the resolution to print the images (Standard or High). Set the print quality in DPI (dots per inch) for the options Standard and High.

5. Choose the film size from the Film size drop-down menu.

6. Choose the media type from the Medium drop-down menu.

7. Since version 1.11, you can not deactivate the Print as one image option.

8. If necessary, enable the printing of labels.

9. For color printing check the Color print box.

You can also specify the film size in the tab for setting the page templates. If the Chosen film size for printer parameter has been chosen, the size of the film will be as set for your printer. Otherwise, the size of the page template will be used (see Section 17.2.2).

17.3.3 Setting Up the Default DICOM Print Parameters

Certain makes of DICOM printers may not support some print parameters described in the DICOM standard. If a parameter passed to the printer is not supported, an attempt to print may fail. To prevent such errors, the DICOM Viewer provides for an opportunity not to specify certain parameters and not to pass them to the DICOM printer.

To set up the default DICOM printing parameters, select the Network menu and the DICOM Printer setup... item.

In the DICOM Print dialog box (Fig. 17.6), the user may choose Default values for the following parameters:

- Film Destination;
- Trim;
- Magnification type;
- Medium.
17.3. PRINT IMAGES ON FILM

A Default value means that the value has not been specified and is to be determined by the DICOM printer.

The values for the Film size and Resolution (dpi) parameters must be chosen from the drop-down lists.

---

**Figure 17.6:** DICOM printing settings by default

---

17.3.4 Print

You can print images on a DICOM printer from the DICOM preview window (see Section 17.2). To open it select the File menu and the DICOM Preview item. To print images on a DICOM printer, click the DICOM print button on the toolbar. The window shown in Fig. 17.7 will
be displayed.

![Print settings window](image)

*Figure 17.7: DICOM print*

The parameters in the window correspond to the default parameters specified during the printing setup. Change these parameters if necessary and click the PRINT button to initiate the printing or CANCEL to cancel.

If the printer is not available the message like *Printer «PrinterName» is not available* will be displayed.

### 17.4 Print Images on Paper

For this purpose, a printer for printing on paper should be connected to your computer and set up. The DICOM Viewer does not have the functionality to set up such a printer.

Printing on paper is possible from the preview window (see Section 17.2). To open it, select the File menu and the Preview item. The Preview tab will be displayed.

The preview window is similar to the DICOM printer preview window, except the Print setup button on the toolbar opening the printing system settings. Printing is carried out by the OS facilities. If necessary, consult the printer manual and the OS help reference.

To enable/disable printing annotations, click the Show labels button on the toolbar. To set the displayed annotation parameters, press the arrow on the right-hand side of the Show labels button (for details see Section 2.24).

### 17.5 Printing Pages Export

The DICOM Viewer provides an opportunity to export pages for printing to the default DICOM server or to the local storage. The default DICOM server settings have been described in Section 12.2. The image is exported in compliance with the current print settings.

> **Attention! The red frame shows the images to be exported**

Export to the local storage is performed regardless of whether or not the images have been successfully uploaded to the DICOM server. Each time the same set of pages is exported, a new series is created in the local storage.
To export the current page, click the ![Export page to default server](image) button. To export all the pages containing images for printing, click the arrow on the right side of the *Export page to default server* button and choose the *Export all pages* item.
Chapter 18

Integration

18.1 Launch from the Command Line

**Attention! On macOS, command line parameters are not supported.**

The command line parameters may be sent to the launched DICOM Viewer (see [Launch multiple instances of the program](#)).

Launching the program from the command line allows you to set specific parameters for the current session of the program, change the settings and get help information about the command line options. To launch the DICOM Viewer use the following syntax on the command line:

```
```

**--help:** display the help information about the command line options, exit the program.

**--study-folder <path>:** display the study (studies) contained in the specified folder. If there are several studies, then the following options are applied to the first study in the list:

- **--open-series-images:** display the first series in the flat image view window
- **--open-series-mpr:** display the first series in the multiplanar reconstruction window
- **--open-series-volume:** display the first series in the volume reconstruction window
- **--open-series-endoscopy** **PRO:** display the first series in the virtual endoscopy window

Any of these parameters can be used with the following parameters:

- **--series-uid <seriesUID>:** show the series with the specified seriesUID
18.1. LAUNCH FROM THE COMMAND LINE

--series-index <seriesIndex>: show the series with the specified seriesIndex

--pacs-aetitle <aetitle>: attempt to open study list from PACS Server which AE Title matches the specified AE Title. The following options can be used with this option in different combinations:

  --patient-id <patientID>: show the study with the specified patientID. Parameter has higher priority than --study-uid

  --study-uid <studyUID>: show the series with the specified studyUID

--series-uid <seriesUID>: select the series with the specified seriesUID. If several studies are found, the first one on the list is used

--series-index <seriesIndex>: select the series with the specified seriesIndex. If several studies are found, the first one on the list is used

--open-series-images: display the selected series in the flat image view window. If a series is not selected, the first one of the first study is used

Example: C:\Users\user\DICOMViewerPro1.9.1\viewer.exe --study-folder D:\dicom_data --open-series-images --series-index 1 shows series with seriesIndex 1 of the first study from the D:\dicom_data folder in the Flat images view window.

If the option is wrong, then the help information about the command line options is displayed, and the program exits. If the option value is wrong (e.g. there are not DICOM data in the specified folder, there is no series with the specified seriesUID or seriesIndex), then this and all subsequent options are ignored.

Attention! If some AE Titles of several PACS Servers match, then data will be searched on the first PACS Server on the list. PACS Servers are sorted by the «Server nickname» field.

For details on how to set up connection to PACS Server, see Section 12.2.

The length of AE Title value shall not exceed 16 characters. Cyrillic letters and «\» symbols in AE titles are not allowed.

The following options are used to change the settings. After executing any of these commands, the program exits. In case of a successful execution, the word Done appears on the command line.

--aet <aetitle>: parameter AE Title for DICOM Listener is set to <aetitle>

--import-settings <file>: imports settings from <file>

  --use-imported-listener-aetitle: parameter AE Title for DICOM Listener is set to value from <file>

  if the option --aet <aetitle> is used at the same time then AE Title for DICOM Listener is set to <aetitle>

  --update-scu-aetitle: Client name (SCU) for PACS Servers of the DICOM Listener will remain the current

  if the option --aet <aetitle> is used at the same time then Client name (SCU) for PACS Servers is set to <aetitle>

--export-settings <file>: exports settings to <file>.

447
18.2 Launching the DICOM Viewer with a URL Command

The DICOM Viewer may be launched by clicking the link on the web browser page. The URL parameters from the command line may be sent to the launched DICOM Viewer (see Launch multiple instances of the program).

18.2.1 Enabling the DICOM Viewer Launch with a URL Command on Windows

To enable the DICOM Viewer launch with a URL Command on Windows, the DICOM Viewer must be registered in the URI system as inobitec.

The DICOM Viewer is automatically registered in the URI system when the software is installed. To enable the support of the DICOM Viewer launch with a URL Command, check the Register the schema «inobitec» to launch a viewer with parameters from browser box in the Launch by browser window (Fig. 7). By default, the box is not checked. If this option has been activated, administrator privileges will be required in the process of software installation. When the DICOM Viewer is deleted, it remains registered in the URI system.

18.2.2 Enabling the DICOM Viewer Launch with a URL Command on Linux

In order to enable the DICOM Viewer launch from a browser on Linux, when the ApplImage file is run for the first time, it must be integrated with the system. A support program, such as AppImageLauncher may be required for the OS to make an integration request.

When the application is integrated, the scheme is registered for the current user (the desktop file from Applimage is installed in ~/.local/share/applications).

The Firefox browser installed with Snap or Flatpack deployment utilities will not follow any third-party URI schemes due to the security policy.

18.2.3 Enabling the DICOM Viewer Launch with a URL Command on MacOS

The support of the DICOM Viewer launch from a browser on MacOS is enabled automatically when the DMG file with the application is opened.

To reset the scheme provided, use the following command:
/System/Library/Frameworks/CoreServices.framework/Frameworks/LaunchServices.framework/Support/lsregister -u <Path to the installed app file>

18.2.4 Launching the DICOM Viewer with the help of a URL Command

To test the DICOM Viewer launch, enter the inobitec:// command in the address bar of the browser.

The DICOM Viewer window will be opened after confirmation of the request.

The following parameters (in the key=<value> or key format) are available for URL requests:
study-folder=<path> — the path to the directory with the study files

study-uid=<study_uid> — the unique identifier (UID) of the study containing a series to be opened by the image viewer

series-uid=<series_uid> — the unique identifier (UID) of the series to be opened

series-index=<series_index> — the index of the series to be opened

patient-id=<patient_id> — the identifier of the patient, for whom the study list is to be opened

pacs-aetitle=<pacs_aetitle> — provide the AE Title for the PACS server

open-series-images — open the images of the series

open-series-mpr — open the series in the multiplanar reconstruction tab

open-series-volume — open the series in the volume reconstruction tab

open-series-endoscopy — open the series in the virtual endoscopy tab

The following format of the URL command is used for launching the DICOM Viewer inobitec://?param_1="value_1"&...&param_m=&...&param_n="value_n"

In this format, the param_m parameter has no value. Quote symbols must be replaced by the respective code designations. It is also recommended to replace any symbols different from letters and numbers by code designations in the names of parameters and values.

Below you can see some examples of console commands and respective URL commands.

Example 1.
viewer.exe --study-folder “D:/DicomData/001” --series-index “0” --open-series-mpr console command corresponds to
inobitec://?study%2Dfolder=%22D%3A%2FDicomData%2F001%22&series%2Dindex=%220%22&open%2Dseries%2Dmpr= URL command.

In the multiplanar reconstruction window, the command opens a series with 0 index of the first study contained in the D:/DicomData/001.

Example 2.
viewer.exe --pacs-aetitle “PACS_Inobitec” --patient-id “9Htqj5c” --open-series-images console command corresponds to
inobitec://?pacs%2Daetitle=%22PACS%5FInobitec%22&patient%2Did=%229Htqj5c%22&series%2Dindex=10&open%2Dseries%2Dimages= URL command.

In the flat image viewer window, the command opens the first series of the first study with 9Htqj5c patient id, which is placed on the PACS Server with AE Title PACS_Inobitec.

If there is a mistake in the URL request, the DICOM Viewer window is opened, and an error notification is added to the log file. If there is a mistake in one of the request parameters, the other parameters are processed all the same.
CHAPTER 18. INTEGRATION

18.3 HTTP RPC service

The Inobitec DICOM Viewer provides an HTTP RPC Service that allows you to execute commands. Now two commands are supported:

- **DownloadAndOpenStudy**;
- **DisplayStudy**.

18.3.1 Command «DownloadAndOpenStudy»

- **DownloadAndOpenStudy** — command allows you to download the study from the PACS Server to the Local Storage and then open it. When this command is received, the DICOM Viewer searches the required study in the Local Storage. If the study is in the Local Storage, then the DICOM Viewer opens its first series in flat images view mode. If the required study is not found in the Local Storage, the DICOM Viewer will send a download request to the PACS Server and after the start of the downloading files will open study in the flat images view mode.

To execute the **DownloadAndOpenStudy** command:

1. In the DICOM Viewer, switch on the DICOM and HIS/HTTP services by selecting the **Services** option on the **Network** menu (for details, see Sections 12.1.1 and 12.1.2).
2. Send HTTP RPC request to open study by sendind POST request containing xml file in the special format (e.g. **downloadAndOpenStudy.xml** in the demo folder).

Specify the following parameters in the **downloadAndOpenStudy.xml** file:

- **PatientID** (optional) — ID of the patient whose study should be opened;
- **StudyInstanceUID** — UID of the study to be opened;
- **AccessionNumber** — Accession Number of the study to be opened;
- **AET** — AE Title of the PACS Server;
- **IP** — network address of the PACS Server;
- **port** — DICOM port of the PACS Server;
- **CommandType** (optional) — method to download images from the PACS Server to the DICOM Viewer. The values C-GET (by default) and C-MOVE can be used. If you use the C-MOVE method then the PACS Server must be configured appropriately.

The values of the **StudyInstanceUID** and **AccessionNumber**, parameters provided in the xml file must belong to the same study. If the **StudyInstanceUID** and **AccessionNumber** parameters do not belong to the same study, you will not be able to download the study.

You may search for and download a study using only the value of the **AccessionNumber** parameter. To do that, delete the values of the **PatientID** and **StudyInstanceUID** parameters from the **downloadAndOpenStudy.xml** file leaving only the **AccessionNumber** and the PACS Server parameters (**AET**, **IP**, and **port**).
If the **AET**, **IP**, and **port** values have not been provided, the study will be downloaded from the DICOM Server (PACS) set by default. If only one or two parameters out of three (**AET**, **IP**, and **port**) have been provided, the command is considered invalid.

Also you can use the test page (**testpage.html** in the **demo** folder):

1. In the DICOM Viewer, switch on the DICOM and HIS/HTTP services by selecting the **Services** option on the **Network** menu (for details, see Sections 12.1.1 and 12.1.2).
2. Open the testpage.html file.
3. Fill in the following fields:
   - **AET** — AE Title of the PACS Server;
   - **IP** — network address of the PACS Server;
   - **Port** — DICOM port of the PACS Server;
   - **StudyUID** — UID of the study to be opened;
   - **Destination IP** — network address of the DICOM Viewer;
   - **Destination port** — HTTP port of the DICOM Viewer.
4. Click the «Send command» button.


### 18.3.2 Command «DisplayStudy»

- **DisplayStudy** — command allows you to open study from the Local Storage. When this command is received, the DICOM Viewer searches the required study in the Local Storage. If the study is in the Local Storage, then the DICOM Viewer opens its first series in the flat images view mode. At the moment to obtain this command the study should already be stored in the Local Storage.

To execute **DisplayStudy** command:

1. In the DICOM Viewer, switch on the DICOM and HIS/HTTP services by selecting the **Services** option on the **Network** menu (for details, see Sections 12.1.1 and 12.1.2).
2. Send HTTP RPC request to open study by sendind POST request containing xml file in the special format (e.g. **displayStudy.xml** in the **demo** folder).

Specify the following parameters in the **displayStudy.xml** file:

- **PatientID** (optional) — ID of the patient whose study should be opened;
- **StudyInstanceUID** — UID of the study to be opened.

Also you can use the **display.bat** test script from the **demo** folder:

1. In the DICOM Viewer, switch on the DICOM and HIS/HTTP services by selecting the **Services** option on the **Network** menu (for details, see Sections 12.1.1 and 12.1.2).
2. Specify the following parameters in `displayStudy.xml` file:

- **PatientID** (optional) — ID of the patient whose study should be opened;
- **StudyInstanceUID** — UID of the study to be opened.

3. Execute the script in the command line with the following parameters:

   `display.bat [ip] [port]`

   where:

   - **ip** — network address of the DICOM Viewer;
   - **port** — HTTP port of the DICOM Viewer.


### 18.3.3 Configuration Files of HTTP RPC service

The templates for configuration files of HTTP RPC remote procedure call service are provided below.

```xml
<?xml version="1.0" encoding="utf-8"?>
<methodCall>
  <methodName>DownloadAndOpenStudy</methodName>
  <params>
    <param>
      <value>
        <struct>
          <member>
            <name>PatientID</name>
            <value>
              <string>9Htqj5c</string>
            </value>
          </member>
          <member>
            <name>StudyInstanceUID</name>
            <value>
              <string>1.2.840.113704.1.111.5600.1107858801.1</string>
            </value>
          </member>
          <member>
            <name>AccessionNumber</name>
            <value>
              <string>value</string>
            </value>
          </member>
          <member>
            <name>AET</name>
            <value>
            </value>
          </member>
        </struct>
      </value>
    </param>
  </params>
</methodCall>
```


<string>PACS_Inobitec</string>
</value>
</member>

<member>
  <name>IP</name>
  <value>
    <string>192.168.0.235</string>
  </value>
</member>

<member>
  <name>port</name>
  <value>
    <string>3000</string>
  </value>
</member>

<member>
  <name>CommandType</name>
  <value>
    <string>C-MOVE</string>
  </value>
</member>

</struct>
</value>
</param>
</params>
</methodCall>

«displayStudy.xml»

<?xml version="1.0" encoding="utf-8"?>
<methodCall>
  <methodName>DisplayStudy</methodName>
  <params>
    <param>
      <value>
        <struct>
          <member>
            <name>PatientID</name>
            <value>
              <string>9Htqj5c</string>
            </value>
          </member>
          <member>
            <name>StudyInstanceUID</name>
            <value>
              <string>1.2.840.113704.1.111.5600.1107858801.1</string>
            </value>
          </member>
        </struct>
      </value>
    </param>
  </params>
</methodCall>
Chapter 19

Licensing

19.1 Trial period

The demo mode allows users to try out the DICOM Viewer using it without any functionality limitations for 14 days. The only requirement is connecting your computer to the Internet. After the 14 day trial period, the DICOM Viewer will go inactive. To continue working with it, you must purchase a license. The trial period for each edition is set separately.

A license key enables you to activate the DICOM Viewer versions released within a year of the key purchase. The versions released after the one-year period are not activated, but the trial period is available for them. To extend the activation period of the new versions for another year, purchase a subscription to updates.

Starting from version 1.11.0, specialized modules can additionally be connected to the Pro edition. Such modules are licensed and paid for separately. The main functionality remains available in the Pro edition.

19.2 The First Launch and Licensing

19.2.1 Registration on the License Server Using Internet

When you first start the DICOM Viewer after installing, it will attempt to register itself on the license server. During its registration, the DICOM Viewer does not transmit any personal data.

If you have a license key, select License... from the Help section of the main menu. In the dialog box that opens (Fig. 19.1), enter the license key and click OK to confirm or CANCEL to cancel the input. If the license key is not valid, the activation fails.
To close the DICOM Viewer, select Exit from the File section of the main menu. The Lite and Pro editions are registered separately.

If the license key does not support the activation of Additional Modules, and you need to replace it with a new one, click on the ENTER NEW KEY button and enter the new key.

19.2.2 License Proxy Server for automated corporate licensing

To automatize the licensing of a large number of copies of the program in a company, a License Proxy Server is used. The License Proxy Server must have a permanent connection to the License Server. It is installed on the computer located in the local network of the company, and it loads the set of keys necessary for licensing all the copies of the program. At the first start, the program accesses the License Proxy Server and asks for the key. It saves users the need to enter the license keys. If necessary, additional keys can be loaded into the License Proxy Server.

19.3 Purchase of a License

14 days after the activation date of the trial version, a dialog box similar to the one shown in Fig. 19.1 will be displayed upon starting the DICOM Viewer. Further work without the license key input will be impossible.

To purchase a license, follow the https://inobitec.com/eng/buy/ link. Instructions for purchasing INOBITEC, LLC products are available at the (https://help.inobitec.com/kb/faq.php?id=43) link. Call +7 (920) 405-67-43 or send a request for further information to the market@inobitec.com address.
Chapter 20

Help System and User Assistance

20.1 Help System

The Help System is available from the DICOM Viewer interface. To use the Help System, you need to check the box Help->Assistant for the required languages during the installation of the program.

The Help System language is the same as the one previously set in the DICOM Viewer. If the help files for selected language are missing, or the Help System is not installed, a dialog with a relevant message appears at the Help System startup. In this case, reinstall the DICOM Viewer and check the box Help->Assistant for the required languages during the installation of the program.

The Help System interface language coincides with the language set in the operating system.

20.1.1 Launch the Help System

The Help System is context-sensitive, it allows to open the sections describing the interface elements, the features that are currently in use. There are three ways to launch the Help System:

1. From the main menu. Open the Help menu and select the Contents... item. The Help System will open on the page containing information about the active tab.

2. From a tooltip. Place your cursor on a button to display a tooltip. If this button corresponds to a page of the help system, then there will be a Help link in the tooltip. Click this link to open the Help System page. The tooltips are described in section 20.2.

3. Using the hotkey. Place your cursor on the required interface object (button, panel, dialog window, etc) and press the hotkey to open the Help System. If this object corresponds to the interface page, the Help System will be opened on this page.

If the Help System is already running, then it opens the required page.

If the selected interface object does not correspond to any page, the Help System will be opened on the last viewed page.
20.1.2 Help System Settings

The default Help System skin coincides with the DICOM Viewer skin. To disable the use of the DICOM Viewer skin, uncheck the *Use the selected style for Help System* box (see Section 15.5).

20.2 Tooltips

Tooltips appear while hovering the cursor over a button or another interface element. It contains information about this item.

The tooltip for a button contains the following information:

- button name;
- hotkey (if specified);
- a link to a page in the Help System (if specified);
- a slideshow with a brief demonstration of the instrument capabilities or a view mode (if specified).

A slideshow appears 3 seconds after the appearance of the tooltip and is played back cyclically. After that, to close a tooltip, click a mouse button or rotate the mouse wheel. If there is a slideshow for this button, a countdown appears in the form of points in the lower right part of the tooltip. To display a slideshow, check the box *Slideshow Tips* during the installation of the DICOM Viewer.

The DICOM Viewer allows you to disable the display of hotkey, slideshow or completely disable the tooltips (see Section 15.1).
“Hotkeys”

Most part of the hotkeys can be changed (Chapter 15.7).

Note that we only use Latin characters for default key combinations. To use a default key combination, switch to the Latin keyboard layout.

Accepted Abbreviations

LMB — left mouse button;
RMB — right mouse button;
MMB — middle mouse button;
MW — mouse wheel;
Left — left arrow;
Right — right arrow;
Forward — forward arrow;
Back — back arrow.

Key Combinations Used in All Windows

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctrl+S</td>
<td>Command+S</td>
<td>DICOM server list management window</td>
</tr>
<tr>
<td>Ctrl+N</td>
<td>Command+N</td>
<td>Network message queue management window</td>
</tr>
<tr>
<td>Ctrl+E</td>
<td>Command+E</td>
<td>Call the image export setup dialog</td>
</tr>
<tr>
<td>Ctrl+Q</td>
<td>Command+Q</td>
<td>Quit the program</td>
</tr>
<tr>
<td>Ctrl+Z</td>
<td>Command+Z</td>
<td>Undo</td>
</tr>
</tbody>
</table>
F1 — open the help System;
F11 — switch to the full screen mode and exit from it;
Esc — exit from the full screen mode.

## Key Combinations Used in Image View Window

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctrl+Y</td>
<td>Command+Y</td>
<td>Redo</td>
</tr>
<tr>
<td>Delete</td>
<td>fn+Backspace</td>
<td>Delete markers and measurements</td>
</tr>
<tr>
<td>MW</td>
<td>Scrolling</td>
<td>Switch from slice to slice</td>
</tr>
<tr>
<td>Shift+LMB</td>
<td>Shift+LMB</td>
<td>Browse images (forward)</td>
</tr>
<tr>
<td>Ctrl+LMB</td>
<td>Command+LMB</td>
<td>Browse images (back)</td>
</tr>
<tr>
<td>move the mouse holding RMB</td>
<td>move the mouse holding RMB</td>
<td>Edit W/L</td>
</tr>
<tr>
<td>Ctrl+MW</td>
<td>Command+Scrolling</td>
<td>Zoom</td>
</tr>
<tr>
<td>Shift+MMB</td>
<td>RMB</td>
<td>Drag the image</td>
</tr>
<tr>
<td>RMB</td>
<td>RMB</td>
<td>Call the context menu</td>
</tr>
<tr>
<td>Ctrl+E</td>
<td>Command+E</td>
<td>Call the image export setup dialog</td>
</tr>
</tbody>
</table>

[ — switch to previous image;
] — switch to next image;
H — mirror image horizontally;
V — mirror image vertically;
K — activate the tool Marker;
N — activate the tool Line marker;
I — activate the tool Rotate;
Z — activate the tool Image scaling;
M — activate the tool Image shift;
W — activate the tool Adjust W/L;
A — activate the tool Arrow tool;
T — activate the tool Text tool;
O — activate the tool Polygon tool;
E — activate the tool Ellipse tool;
R — activate the tool Ruler;
C — activate the tool Angle;
B — activate the tool Kobb angle;
P — activate the tool Point value;
L — activate the tool ROI rectangle;
Q — activate the tool ROI ellipse;
G — activate the tool ROI polygon;
Y — activate the tool DSA;
F5 — export the image with the latest settings.

Key Combinations Used in 3D Reconstruction Window

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>MW, Ctrl+MMB</td>
<td>Scrolling</td>
<td>Zoom</td>
</tr>
<tr>
<td>Shift+MMB</td>
<td></td>
<td>Drag the model</td>
</tr>
<tr>
<td>Alt+MMB</td>
<td>Alt+MMB</td>
<td>Centrate the model</td>
</tr>
<tr>
<td>MMB</td>
<td>Option+LMB</td>
<td>Rotate the model</td>
</tr>
</tbody>
</table>

**Key combinations for Clipping Box tool**

<p>| Ctrl+holding the mouse button with which the tool was activated | Command+holding the mouse button with which the tool was activated | Zoom the Clipping Box symmetrically |</p>
<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shift+holding the mouse button with which the tool was activated</td>
<td>Shift+holding the mouse button with which the tool was activated</td>
<td>Pan the Clipping Box</td>
</tr>
<tr>
<td>Alt+holding the mouse button with which the tool was activated</td>
<td>Option+holding the mouse button with which the tool was activated</td>
<td>Rotate the Clipping Box</td>
</tr>
</tbody>
</table>

I — activate the tool Model rotation;
Z — activate the tool Model scaling;
M — activate the tool Model shift;
C — activate the tool Polygon cut;
T — activate the tool Remove table;
W — activate the tool Adjust W/L;
B — activate the tool Clipping box;
J — activate the tool Ruler;
K — activate the tool Marker;
N — activate the tool Line marker;
P — activate the tool Select model point;
F5 — export the image with the latest settings.
Key Combinations Used in DICOM Tag View Window

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctrl+F</td>
<td>Command+F</td>
<td>Open the search panel</td>
</tr>
<tr>
<td>Esc</td>
<td>Esc</td>
<td>Close the search panel</td>
</tr>
<tr>
<td>Ctrl+C</td>
<td>Command+C</td>
<td>Copy the selected cell</td>
</tr>
</tbody>
</table>

Key Combinations Used in Curvilinear Reconstruction Mode

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctrl+LMB on a curve</td>
<td>Command+LMB on a</td>
<td>Jump to the surface the point is located on</td>
</tr>
<tr>
<td></td>
<td>curve</td>
<td></td>
</tr>
<tr>
<td>Shift+drag the mouse</td>
<td>Shift+drag the mouse holding LMB</td>
<td>Drag the curve</td>
</tr>
<tr>
<td>holding LMB</td>
<td>holding LMB</td>
<td></td>
</tr>
<tr>
<td>RMB on a curve</td>
<td>RMB on a curve</td>
<td>Context menu</td>
</tr>
</tbody>
</table>

Key Combinations Used in Multiplanar Reconstruction Window

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctrl+MW</td>
<td>Command+Scrolling</td>
<td>Zoom</td>
</tr>
<tr>
<td>Shift+MMB</td>
<td>Scrolling</td>
<td>Drag the image</td>
</tr>
<tr>
<td>MW</td>
<td>Scrolling</td>
<td>Switch from slice to slice</td>
</tr>
</tbody>
</table>

Left, Right, Forward, Back — move planes;

F5 — export the image with the latest settings;
HOTKEYS

Z — activate the tool Model scaling;
M — activate the tool Model shift;
K — activate the tool Marker;
N — activate the tool Line marker;
J — activate the tool Ruler;
O — activate the tool Polygonal ruler;
C — activate the tool Angle;
B — activate the tool Kobb angle;
P — activate the tool Point value;
L — activate the tool ROI rectangle;
Q — activate the tool ROI ellipse;
G — activate the tool ROI polygon.

Key Combinations Used in Virtual Endoscopy Window

<table>
<thead>
<tr>
<th>For Windows and Linux</th>
<th>For macOS</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>LMB in the navigation menu</td>
<td>LMB in the navigation menu</td>
<td>Set the camera position</td>
</tr>
<tr>
<td>MMB</td>
<td></td>
<td>Rotate the camera</td>
</tr>
<tr>
<td>Shift+MMB</td>
<td></td>
<td>Drag the camera</td>
</tr>
<tr>
<td>MW</td>
<td>Scrolling</td>
<td>Zoom</td>
</tr>
<tr>
<td>RMB</td>
<td>RMB</td>
<td>Context menu</td>
</tr>
</tbody>
</table>

Left, Right — rotate the object relative to the camera axis;
Forward, Back — move the object along the camera axis;
R — activate the tool Ruler;
K — activate the tool Marker;
N — activate the tool Line marker.
Index

3D Reconstruction .......... see Volume Reconstruction

A
AIP ...................................... 255
Anonymize .............................. 427
Arrangement
  of Images ............................ 415
Axial section ......................... 187, 231

B
Brightness .................................. 96

C
Camera Orientation ..................... 362
Clipping Box .............................. 197
Closing .................................. 195
CLUTs .................................... 150
Command Line Keys ..................... 25
Command Line Options ............... 446
Contrast ................................ 96
Coronal section ......................... 231
Curved MPR .............................. 237
Cut invisible volume ................... 195

D
DICOM Printer ......................... 440
DICOM Service ........................... 386
DICOM Tags ................................ 176
DICOM tags ................................ 424
Diffusion Tensor Imaging .............. 261
Digital Subtraction Angiography ....... 172
Dilation .................................. 195
Disk Creator ............................. 56, 72, 402
  Adding viewer to image .............. 404
  Write to Disc in Linux and macOS 407
  Write to Disk .......................... 405
  Write to Memoky card ............... 406
Display mode
  of images
    custom ................................ 88
grid ...................................... 88
stacked ................................... 88
of series
  auto ................................... 84
custom ................................... 86, 87
grid ....................................... 85
stacked ................................... 85
DSA ....................................... 172
DTI ....................................... 261

E
ECG ....................................... 56
ECG Viewer .............................. 56, 365
Edit
  Patient Name ......................... 67
  Study Description ................... 67
Erosion .................................. 195
Export surface ......................... 286

F
Fill ....................................... 195
Frequency Filters ..................... 370
Frontal section ...................... 187
Full Screen Mode ...................... 49, 53, 54, 460
Fusion .................................. 56, 210

G
glb ....................................... 286
Grow ..................................... 195
Grow bones ............................. 207

H
Help System ............................. 457
Hotkeys ................................ 420, 459

I
Image annotation ...................... 372
Image registration ..................... 220
Import surface ......................... 289
Importing a Structure from DICOM RT .... 293
Installing .............................. 25
INDEX

J
jpg........................................170

L
Label......................................181
Launching....................................25
Launching the Program....................41
Launching the Web Viewer...............46
Leads........................................367
License.............................455, 456
Local Storage..................55, 59, 72, 400, 409, 417

M
Maximum Intensity Projection........255
Merge layers.............................212
automatically..........................215
by point................................216
manually................................216
Minimum Intensity Projection.......255
MinIP......................................255
MIP..........................................255
MPR.....................see Multiplanar Reconstruction
Multi-monitor Window Design........411
Multi-segment Growing..............195, 304
Multiplanar Reconstruction.........211, 212, 230, 361, 463
3D Cursor Mode..........................233
Build Surface............................237
Curvilinear Reconstruction........237
Cutting Plane Mode..................234
Export......................................258
Line Markers............................253
Markers....................................252
Mirror Image Horizontally and Vertically
257
Orthogonal Planes.....................233
Polygonal Line Markers.............253
Reslice..................................258
Rotate Image............................256
Rotate Planes...........................233
Slice Thickness........................255
Multiplanar reconstruction........55

N
NETWORK..........................450–452
Network.................................386, 398

O
obj..............................286, 340
Opening........................................195
Opening DICOM studies by dragging and
dropping.................................58
Opening Segmentation Projects.......58
Opening Zipped DICOM Studies......57
Orientation Cube......................174

P
PACS Server........................65, 392
pdf..........................................56
Perfusion Scoring......................111
PET.........................................56
PET analysis.............................342
ply..........................................286, 340
png..........................................170
Print Images.............................430
by default.............................442
Export......................................444
on Films.................................443
on Paper.................................444
Page template..........................435
Print images
Reference Image......................438
Product Registration................455
Projection..............................187

R
Region Growing......................298
Remove holes............................195
Remove noise............................195
Rendering transfer function.........153
ROI
ellipse.................................108
polygon.................................108

S
Sagittal section......................187, 231
Saving Segmentation Projects.......316
Scout lines..............................165
Search......................................56, 63
Segmentation..........................268
Intersection of structures...........309
Mask........................................275
Subtraction structures.............308
Unification of structures..........307
Setting
CLUTs.................................150
Render settings......................204
Scout lines.............................166
<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Visualization</td>
<td>149</td>
</tr>
<tr>
<td>Workspace</td>
<td>167</td>
</tr>
<tr>
<td>Settings</td>
<td>408</td>
</tr>
<tr>
<td>Export</td>
<td>422</td>
</tr>
<tr>
<td>Import</td>
<td>422</td>
</tr>
<tr>
<td>Modules</td>
<td>415</td>
</tr>
<tr>
<td>Monitor</td>
<td>411</td>
</tr>
<tr>
<td>Shortcuts</td>
<td>39</td>
</tr>
<tr>
<td>Shrink</td>
<td>195</td>
</tr>
<tr>
<td>Skins</td>
<td>414</td>
</tr>
<tr>
<td>Sort studies</td>
<td>67</td>
</tr>
<tr>
<td>Splited Screen</td>
<td>77</td>
</tr>
<tr>
<td>Stitching Mode</td>
<td>226</td>
</tr>
<tr>
<td>stl</td>
<td>286, 340</td>
</tr>
<tr>
<td>Storage</td>
<td>55, 59, 72, 400, 409, 417</td>
</tr>
<tr>
<td>Structure Export</td>
<td>290, 291</td>
</tr>
<tr>
<td>Structure Export to DICOM RT</td>
<td>291</td>
</tr>
<tr>
<td>Study List Export</td>
<td>69</td>
</tr>
<tr>
<td>Surface</td>
<td>282, 284</td>
</tr>
<tr>
<td>SUV</td>
<td>157</td>
</tr>
<tr>
<td>Switch between Series</td>
<td>81</td>
</tr>
<tr>
<td>Synchronize Images</td>
<td>182</td>
</tr>
<tr>
<td>System Requirements</td>
<td>25</td>
</tr>
<tr>
<td><strong>T</strong></td>
<td></td>
</tr>
<tr>
<td>Tab</td>
<td>52</td>
</tr>
<tr>
<td>Tab display mode</td>
<td>49, 53, 56</td>
</tr>
<tr>
<td>Technical Support</td>
<td>16</td>
</tr>
<tr>
<td>Tooltips</td>
<td>458</td>
</tr>
<tr>
<td><strong>U</strong></td>
<td></td>
</tr>
<tr>
<td>Uncompress series</td>
<td>73</td>
</tr>
<tr>
<td>Uninstalling</td>
<td>25</td>
</tr>
<tr>
<td><strong>V</strong></td>
<td></td>
</tr>
<tr>
<td>Vessel analysis</td>
<td>327</td>
</tr>
<tr>
<td>Vessel Tree Segmentation</td>
<td>300</td>
</tr>
<tr>
<td>Vessles</td>
<td>55</td>
</tr>
<tr>
<td>View Flat Images</td>
<td>75, 460</td>
</tr>
<tr>
<td>ADC</td>
<td>185</td>
</tr>
<tr>
<td>Calibration Sizes</td>
<td>184</td>
</tr>
<tr>
<td>Export</td>
<td>168</td>
</tr>
<tr>
<td>Graphic Label Tool</td>
<td>177</td>
</tr>
<tr>
<td>Mirror Image Horizontally and Vertically</td>
<td>184</td>
</tr>
<tr>
<td>View flat images</td>
<td></td>
</tr>
<tr>
<td>Angle</td>
<td>105</td>
</tr>
<tr>
<td>Cobb angle meter</td>
<td>106</td>
</tr>
<tr>
<td>Delete Measurements</td>
<td>110</td>
</tr>
<tr>
<td>Distance measurement on US studies</td>
<td>111</td>
</tr>
<tr>
<td>Drawing Parameters</td>
<td>109</td>
</tr>
<tr>
<td>Intensity at a Point</td>
<td>107</td>
</tr>
<tr>
<td>Intensity Average</td>
<td>108</td>
</tr>
<tr>
<td>Magnifier</td>
<td>103</td>
</tr>
<tr>
<td>Measurement of blood flow velocity on US studies</td>
<td>111</td>
</tr>
<tr>
<td>Move Measurements</td>
<td>109</td>
</tr>
<tr>
<td>Move Measurements Results</td>
<td>110</td>
</tr>
<tr>
<td>Pan</td>
<td>95</td>
</tr>
<tr>
<td>Play</td>
<td>92</td>
</tr>
<tr>
<td>Polygonal Ruler</td>
<td>105</td>
</tr>
<tr>
<td>Rotate</td>
<td>96</td>
</tr>
<tr>
<td>Ruler</td>
<td>104</td>
</tr>
<tr>
<td>Standard Deviation in an Area</td>
<td>108</td>
</tr>
<tr>
<td>Time lapse measurement on US studies</td>
<td>111</td>
</tr>
<tr>
<td>Video recording</td>
<td>93</td>
</tr>
<tr>
<td>Zoom</td>
<td>95</td>
</tr>
<tr>
<td>View Several</td>
<td></td>
</tr>
<tr>
<td>Images at a Time</td>
<td>88</td>
</tr>
<tr>
<td>Series at a Time</td>
<td>83</td>
</tr>
<tr>
<td>Studies at a Time</td>
<td>81</td>
</tr>
<tr>
<td>Virtual Endoscopy</td>
<td>211, 356, 464</td>
</tr>
<tr>
<td>Camera Fly</td>
<td>359</td>
</tr>
<tr>
<td>Customize MPR Navigation Panel</td>
<td>358</td>
</tr>
<tr>
<td>Export</td>
<td>364</td>
</tr>
<tr>
<td>Measurements and Markers</td>
<td>361</td>
</tr>
<tr>
<td>Move Camera</td>
<td></td>
</tr>
<tr>
<td>Automatically</td>
<td>359</td>
</tr>
<tr>
<td>Manually</td>
<td>359</td>
</tr>
<tr>
<td>Surface Reconstruction</td>
<td>362</td>
</tr>
<tr>
<td>Virtual endoscopy</td>
<td>56</td>
</tr>
<tr>
<td>Visualization</td>
<td></td>
</tr>
<tr>
<td>CPU</td>
<td>417</td>
</tr>
<tr>
<td>CUDA</td>
<td>186, 417</td>
</tr>
<tr>
<td>Metal</td>
<td>186, 282, 417</td>
</tr>
<tr>
<td>OpenCL</td>
<td>186, 417</td>
</tr>
<tr>
<td>Volume Reconstruction</td>
<td>186, 211, 461</td>
</tr>
<tr>
<td>3D Angle</td>
<td>202</td>
</tr>
<tr>
<td>Centrate</td>
<td>196</td>
</tr>
<tr>
<td>Delete All Areas except Selected Area</td>
<td>192</td>
</tr>
<tr>
<td>Delete Area</td>
<td>192</td>
</tr>
<tr>
<td>Delete Table</td>
<td>196</td>
</tr>
<tr>
<td>Export Rotation to Series</td>
<td>203</td>
</tr>
<tr>
<td>Inverse Polygon Cut</td>
<td>192</td>
</tr>
<tr>
<td>Markers</td>
<td>203</td>
</tr>
</tbody>
</table>
INDEX

play........................................... 190
Polygon Cut................................. 192
Polygonal Ruler.......................... 199
Remove Bone Tissue...................... 206
Rotation.................................. 189
Ruler....................................... 198
Scaling.................................... 190
Shift......................................... 189
Sphere Cut.................................. 193
Sphere Restore........................... 193
Surface ruler................................ 200
Volume reconstruction.................... 55
Volume stitching........................... 227

W
Window Level................................ 96
Window Width.............................. 96
Glossary

**editing mask** — a template that restricts the structure mask. The editing mask is defined by the CLUTs. 277

**multiphase series** — series contained more then one phase. 170, 223

**phase** — image group with different location. If the study contains images of the same body part taken at intervals (for example, contrast studies), then images with different locations are grouped into phases and sorted according to the time taken to create the image. 170, 223

**structure** — part of the volume defined by the mask or surface. 268

**structure mask** — voxel volume obtained as a result of segmentation. 276

**voxel** — element of a 3D image containing the value of a raster element in 3D space. 207
Thanks for selecting our product! The Inobitec, LLC team is constantly working to improve it. We will be grateful for any feedback, comments and suggestions how to enhance the product functionality, user-friendliness and visualization quality.

We wish you success in your work!