QyScore Documentation

Release 1.8.0, rev 2

Qynapse

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Contents

Legal notices

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1.2 Indications for use

QyScore is an advanced processing and visualization software for automatic labeling and volumetric quantification of segmented central nervous system structures for patients older than 18 years of age. The software is intended to be used by medical personnel or neuroimaging trained personnel to support diagnosis of central nervous system diseases.

1.3 Description and intended use

QyScore is an advanced processing and visualization software for automatic labeling and volumetric quantification of segmented central nervous system structures for patients older than 18 years of age.

The software:

- retrieves imaging data from a DICOM server,
- sends said data to Qynapse's analysis server,
- enables the user to view the results (segmentations and numerical results) in a dedicated interface,
- enables the user to edit a summary report of the results (segmentations and numerical results) from the same interface.

The software is designed to be user-friendly and intuitive.

It is intended to be used by medical personnel or neuroimaging trained personnel to support diagnosis of central nervous system diseases.

Caution: Federal law restricts this device to sale by or on the order of a physician.

1.4 Global presentation

QyScore contains 3 user interfaces:

- a connection interface,
- a data management interface,
- a visualization interface.

QyScore interfaces and features are detailed in this user manual.

To start using QyScore, two modes of operation are available:

- sending data directly from the DICOM server (PACS) (see chapter 4.2),
- connecting via the **QyScore front-end** icon on your desktop (see chapter 3.1).

1.5 Technical description

1.5.1 Installation

QyScore is installed by the QYNAPSE team, on a computer with the following minimal requirements:

- RAM: 8Go
- CPU: Intel Core i5
- Screen resolution 1600*900

The operating system must be the following: Ubuntu 14.04 LTS. To ensure proper function of the software, this operating system must not be modified.

The computer must be connected to a DICOM server to enable data sending to the analysis server.

1.5.2 Performances

QyScore automatically analyses MRI images and provides results on the following brain structures:

- Grey matter

- White matter

- Hippocampus

- Amygdala

- White matter hyperintensities

In the conditions described in chapter 1.6, the performances of the volumetric quantification methods can be obtain by simple request to support@qynapse.com.

The volumes are provided in absolute values (mL) and in relative values (% of intracranial volume)

1.5.3 Maintenance

Le computer containing the analysis server must be turned on for the software to function properly. In case of a planned power cut, it shall therefore be turned back on. The database with the analysis results is automatically purged when a given storage capacity is reached.

1.5.4 Safety

If a safety breach is detected, the analysis server will be shut down by Qynapse to avoid potential fraudulent use. In that case, new data analyses won't be possible, but the analyses previsouly performed will remain available on the DICOM server.

1.6 Required imaging parameters

QyScore is designed to analyze non-injected 3DT1 (1.5T or 3T), as well as T2FLAIR (3T). The required acquisition parameters are the following:

	T1	
	Required	Tolerated
Voxel size in plane (mm)	[1, 1]	Min: [0.74, 0.74] Max: [1.5, 1.5]
Field of view (mm)	[192, 256, 256]	Min: [145, 220, 132] Max: [320, 320, 320]
Slice thickness (mm)	1	Min: 0.75 Max: 1.5
Interpolation	No	Yes
Acquisition direction	Sagittal	Axial, Coronal
Acquisition type	3D	3D
Field strength	1.5T, 3T	1.5T, 3T

	T2FLAIR2D		T2FLAIR3D	
	Required	Tolerated	Required	Tolerated
Voxel size in plane (mm)	[1, 1]	Min: [0.65, 0.65] Max: [1.1, 1.1]	[1, 1]	Min: [0.46, 0.46] Max: [1.1, 1.1]
Field of view (mm)	[192, 256, 192]	Min: [148, 220, 148] Max: [320, 320, 320]	[192, 256, 192]	Min: [152, 220, 152] Max: [320, 320, 320]
Slice thickness (mm)	3.3	Min: 2.5 Max: 5	1	Min: 0.8 Max: 1.4
Interpolation	No	Yes	No	Yes
Acquisition direction	Axial	Coronal, Sagittal	Sagittal	Axial, Coronal
Acquisition type	2D	2D	3D	3D
Field strength	3T	3T	3T	3T

> ⚠ In case of non-compliance with the parameters given above, the obtained results won't be optimal, in terms of processing time as well as reliability. If the acquisition parameters are outside of the tolerated range, the analysis won't be launched. See chapter 4.3.3 for more details.

1.7 Normative data

The statistics generated by QyScore are computed by comparison to results obtained on a normative database of healthy subjects.

The database is a concatenation of the following databases:

Name	Age (years)	Sex	# healthy subjects	Description
ADNI	74.0 +/- 6.3 (56 - 90)	48% M	441	The Alzheimer's Disease Neuroimaging Initiative (ADNI) is a longitudinal multicenter study designed to develop clinical, imaging, genetic, and biochemical biomarkers for the early detection and tracking of Alzheimer's disease (AD). See http://adni.loni.usc.edu for details.
HCP	27.5 +/- 4.8 (23 - 38)	49% M	172	The HCP 1200 Subjects Release (S1200) includes behavioral and 3T MR imaging data from 1206 healthy young adult participants (1113 with structural MR scans) collected in 2012-2015. See https://www.humanconnectome.org/study/hcp-young-adult for details.
IXI	50.6 +/- 15.8 (56 - 86)	45% M	363	The IXI Dataset is a collection of nearly 600 MR images from normal, healthy subjects. The data was collected at three different hospitals in London using 1.5T and 3T scanners. See https://brain-development.org/ixi-dataset for details
OASIS	48.0 +/- 23.5 (20 - 90)	35% M	225	Cross-sectional MRI data in young, middle-aged, non-demented and demented older adults, including individuals with early-stage Alzheimer's Disease (AD). See http://www.oasis-brains.org for details.
PPMI	59.1 +/- 10.4 (31 - 82)	63% M	91	The mission of the Parkinson's Progression Markers Initiative (PPMI) is to identify one or more biomarkers of Parkinson's disease progression. See http://www.ppmi-info.org for details.

1.8 Warnings

Users must make sure to read this manual to become familiar with the software and be able to obtain reliable analysis results.

⚠️ QyScore is intended to be used by medical personnel or neuroimaging trained personnel. The software should not be used for purposes other than those indicated in the section 1.2.

⚠️ Staying in front of a computer for too long may make your muscles, joints or eyes hurt. If your muscles, joints or eyes become tired or sore, take a break in the use of the software.

⚠️ QyScore does not include accessibility modes.

⚠ The segmentations computed by QyScore may be incorrect and shall be taken with care.

⚠ Considering the lack of measure precision for the input DICOM data, QYNAPSE cannot guarantee the precision of volumes that are expressed in mL. Said volumes are given as indications only. Please refer to relative volumes (in % of intracranial volume) for reliable results.

⚠ The patients for whom QyScore analyzes the data must be older than 18 years of age.

⚠ Corrupted data sent from the DICOM server won't be analyzed. You will be informed in that case.

⚠ QYNAPSE is not responsible for the management of third-parties tools such as the DICOM server, nor for the quality of the infrastructure (except for the offered material).

1.9 European regulations

CE 2797	QyScore is qualified as a class IIa medical device. It complies with the requirements of the Europen Medical Device Directive 93/42/CEE and the medical device software - software life cycle processes standard IEC 62304.

1.10 Electronic instructions for use

Please note that QyScore software is supplied with electronic instructions for use.

These instructions may be accessed in the following ways:

- Through the graphical user interface of QyScore software by clicking the "Help" and then "User manual" buttons.

- From the online Qynapse document library: http://qynapse.com/pdf/manuals.

Please note that the instructions for use on PC are provided in **PDF** format. A suitable reader, such as Adobe Acrobat Reader is required to view them. Adobe Reader may be obtained from https://get.adobe.com/reader.

A hard-copy of the instructions for use may be obtained within 7 calendar days at no additional charge by contacting Qynapse at the following address: 130 rue de Lourmel, 75015 Paris, France.

CHAPTER 2

Conventions

The following conventions are used throughout this manual.

2.1 Mouse

Click Press and release the primary mouse button. If you are lefthanded, you may have set the right mouse button as your primary mouse button.

Long click Press the primary mouse button and move the mouse. If you are lefthanded, you may have set the right mouse button as your primary mouse button.

Right-click Press and release the secondary mouse button. If you are lefthanded, you may have set the left mouse button as your secondary mouse button.

Middle-click Press and release the wheel button or the middle mouse button.

Long middle-click Press the wheel button or the middle mouse button and move the mouse.

2.2 Typography

OK Buttons, fields and clickable menus names in the user interface are capitalized and in bold.

Login Non-clickable labels in the user interface are indicated in italic.

Settings > Configuration A sequence of menu options that you select to perform a specific task is indicated by angular brackets and in bold.

2.3 Symbols

⚠ Warns you to pay extra care to a specific point while using QyScore.

2.4 Glossary

Standard visualization window (or standard window) In the visualization interface, simple volume visualization window.

False colors Color applied to a zone or an object in a grey-scaled image, with the only purpose to highlight it. This color is chosen arbitrarily and any resemblance with the actual color of the zone or object is purely coincidental.

Special window In the visualization interface, visualization window which content depends on the view mode.

LUT Colors look-up table. For modes other than the "Atrophy" mode, it indicates the correspondance between the color of a pixel and its real intensity, or in other words the colored intensity range of the entire volume.

Z-score Standard deviation to mean value.

Percentile Value that divide the population in 100 equally-sized groups (each percentile corresponds to 1 % of the population).

Connect to QyScore

3.1 Global presentation

You can connect to the QyScore software by using its connection interface.

Fig. 3.1: Connection interface

3.2 Login

Enter your login and password in the corresponding fields. The password is initially given by QYNAPSE upon installation.

Click on **Ok**.

If the login and password are correct, depending on the configuration mode, either the data management interface or the visualization interface is launched.

3.3 Change password

We recommend that you change your password when first connecting to the service.

Follow the steps:

- Click on **Change password**
- *Login*: type your login
- *Current password* : type your current password
- *New password* : type your new password
- *Comfirm password* : confirm your new password
- Click on **OK** to save the new password
- Click on **Cancel** to cancel the procedure and close the window

⚠ The password must contain at least an upper letter, a lower letter, a digit, and between 6 and 12 characters.

3.4 Forgotten password

If you forget your password, please contact QYNAPSE at support@qynapse.com.

CHAPTER 4

Send data

4.1 Global presentation

Data can be sent to QYNAPSE's analysis server via the data management interface or directly via your DICOM server (e.g. PACS). In both cases, the received data are automatically analyzed.

4.2 Via the DICOM server (e.g. PACS)

If properly configured, you can send data directly from your DICOM server, by selecting the sequences to analyze and exporting them to QyScore. Please refer to the user manual of your DICOM server for further information.

You can also export the whole exam for a given patient, but the processing time will be longer.

The export of all the exams for a given subject is currently not handled.

Once the analysis is finished, the results are sent directly in DICOM format to your server.

You can also view them using the visualization interface:

- Connect to the service (see chapter 3.1),

- The visualization interface is launched. Select the patient and exam for which you wish to view the results (for further information and description of features, see chapter 5.1).

⚠ The database is regularly cleaned to save disk space. As a consequence, if the exam you wish to view is no longer available, please relaunch the analysis.

4.3 Data management interface

The data management interface enables you to send data and open the visualization interface.

Fig. 4.1: Data management interface

4.3.1 Configure connection parameters

To configure the network settings of QYNAPSE's analysis server and your DICOM server:

- Click on **Settings > Configuration**,
- Modify the IP adresses, the ports and the AETitle of the DICOM server.

4.3.2 Choose data to send

In the interface:

- Click on a patient's name to select him/her,
- Click on an acquisition date to select the corresponding study,
- Click on the checkbox on the left-hand side of a sequence to select it.

> ⚠ The analysis that will be performed depends on the type of sent data and on the license that you subscribed with QYNAPSE.

4.3.3 Send data

Once the data selected, click on **Send**.

The chosen data are copied and sent to QYNAPSE's analysis server. The results are sent back to the data management interface when the analysis is finished, and transferred directly to the DICOM server.

The processing time depends on the sequences' modalities and on the images resolutions. For your information, when following the recommendations, the processing times are 10min and 20min for a 3DT1 sequence and for a (3DT1, T2FLAIR) group respectively.

Analysis progression status

A status bar indicates the progression of the current analysis, along with the results of the quality control of the acquisition parameters. Those parameters are compared to those indicated at the chapter 1.6. The color of the status bar indicates their compliance to the recommended protocol:

 Exactly compliant with QYNAPSE's recommendations.

 Non compliant with QYNAPSE's recommendations but tolerated.

 Non compliant with QYNAPSE's recommendations and not tolerated.

In case of an **orange** color bar, the results won't be optimal, in terms of processing time as well as reliability. Extra care will be needed when viewing the results.

In case of an **red** color bar, the data cannot be processed since the acquisition parameters are not handled by QyScore.

Note: More generally, a red color bar indicates an error that prevents the analysis from being completed. Such error can be due to the non respect of the acquisition parameters, a communication issue with the analysis server, or linked to the type of sent data. You will be informed of the error type in all cases. Please refer to chapter 6 for the corresponding procedure.

4.3.4 View results

Once the analysis are finished, you can view the results for a given exam.

In the interface:

- If not already selected:
    - Click on a patient's name to select him/her,
    - Click on an acquisition date to select the corresponding study,
- Click on **View**.

The visualization interface is launched for the selected study.

4.3.5 Refresh the displayed content of the DICOM server

It may be necessary to refresh the data management interface's content if new MR exam have been acquired while it was opened. This is done by clicking on **Refresh**.

Results visualization interface

5.1 Global presentation

QyScore's visualization interface is dedicated to view the results computed for the patient and exam chosen in the data management interface.

It consists of two tabs:

- **View**: interacting tools to navigate in the MR volumes, segmented structures and corresponding statistics.
- **Report**: tools to view and edit the summary report that contains the analysis results.

5.1.1 *View* tab

To display the *View* tab:

- Click on **View**

Fig. 5.1: *View* tab

The control panel on the left-hand side consists of several sub-parts:

- *Patient information*: informations on the selected patient

- *View mode*: to switch between view modes (default is "Table")

- *Modalities*: to choose the displayed modalities

- *Segmentations*: to choose the displayed segmented structures

- *Window options*: to modify visualization options, to ensure a better visual confort

- *Cursor position*: cursor position and volumes' values at said position

The viewing part on the right-hand side consists of three standard visualization windows that display the volume in the standard orthogonal orientations (coronal, sagittal, axial). The fourth window is called "special window" and its content depends on the chosen view mode.

5.1.2 *Report* tab

To display the *Report* tab:

- Click on **Report**

Fig. 5.2: *Report* tab

The displayed report is a summary of the analysis results. It can be edited by adding comments and screenshots.

5.2 Navigating across the volumes

5.2.1 Standard visualization windows

Fig. 5.3: Standard visualization window

The window consists in:

1. a non-interactive LUT that indicates the intensity range applied to the displayed volume,

2. the volume,

3. a 3D cursor to navigate in the volume, by choosing the slice to display,

4. a screenshot icon,

5. a zooming icon (Fig. 5.4)

Fig. 5.4: Zoomed window

5.2.2 Mouse controls

On the displayed volume:

- Click on any point of the volume: adjusts the other standard viewing windows to the same point. Also works with a long clic.

- Scroll: zooms on the volume

- Long middle-click: moves the volume in the window

- Right-click: displays the context menu

5.3 View modalities, segmentations and numerical results

The following instructions can be used regardless of the chosen view mode. The control panel is located on the left-hand side of the *View* tab.

5.3.1 View imaging modalities

Imaging modalities that can be displayed are given in the *Modalities* part of the control panel. These modalities were sent by the user and selected by QyScore for analysis.

To display or hide a modality:

- Clic on the modality name or on the ⊚ / ⊘ icon on its left-hand side.

- : modality displayed

- : modality masqued

Fig. 5.5: Choice of modalities

5.3.2 View segmented structures

Fig. 5.6: Choice of segmented structures

The list of segmented structures that can be displayed is given in the *Segmentations* section of the control panel. These structures were segmented by QyScore from the imaging data sent for the selected patient and exam.

They are grouped in the following way:

- Group of structures (eg: "Brain substructures")
  - Whole structure (eg: "Hippocampus")
    * Lateral structure (eg: "Left Hippocampus")

To display / hide a whole structure in the table:

- Click on the ▸ / ▾ icon on the left-hand side of the group of structures containing the whole structure.

To display / hide a lateral structure in the table (if applicable) :

- Click on the ▶ / ▼ icon on the left-hand side of the whole structure.

View the segmentations

Displayed structures can be viewed in "false colors" in the standard windows.

Note: See chapter 5.5.3 to modify the false color assigned to a given structure.

To display / hide a group of structures:

- Click on the group name or the 👁 / 👁 icon on its left-hand side: every structure of the group is either displayed or hidden.

- 👁: indicates that at least one structure of the group is displayed.

- 👁: indicates that no structure of the group is displayed.

To display / hide a whole structure:

- If it does not appear in the table: see previous section

- Click on the structure name or the 👁 / 👁 icon on its left-hand side: the structure in its whole (both sides, if applicable) is either displayed or hidden.

- 👁: indicates that at least one side of the structure is displayed.

- 👁: indicates that the structure is hidden.

To display / hide a whole structure (if applicable):

- If it does not appear in the table: see previous section

- Click on the structure name or the 👁 / 👁 icon on its left-hand side.

- 👁 : indicates that the structure is displayed.

- 👁: indicates that the structure is hidden.

View the numerical results

Numerical results can be viewed in the *Segmentations* table by using the horizontal scrollbar:

- the absolute volume in mL,

- the relative volume in % of intracranial volume,

- the z-score computed by comparison with normative data (described in chapter 1.7),

- the percentile computed by comparison with normative data (described in chapter 1.7),

- an asymetrie index, defined as the ratio between a structure's left volume and its right volume,

- the number of lesions, for the white matter hyperintensities (*WMH*) only.

Note: Z-scores and percentiles are computed only for certain structures.

5.4 Switch view mode

Fig. 5.7: Switch view mode

Switching between view modes has an effect on the content of the special window, along as the content of the standard window in certain cases. Only one mode can be chosen at a time.

Available modes are described hereafter.

5.4.1 *Table* mode

Fig. 5.8: *Table* mode

This is QyScore's default mode.

It displays the standard visualization of segmented structures and associated statistics, as described in chapter 5.3.

To enter the mode:

- Click on the **Table** button

The special window displays a copy of the table contained in the *Segmentations* section of the control panel.

5.4.2 *Graphs* mode

Fig. 5.9: *Graphs* mode

This modes enables you to view, in addition of the standard view, graphs of comparison with normative data (described in chapter 1.7).

To enter the mode:

- Click on the **Graphs** button

The special window displays graphs of comparison with normative data for the latest selected structure (see chapter 5.3.2).

Note: Such graphs are only available for the structures in the *Whole brain* and *Brain substructures* groups.

The graphs are the following:

- a global graph for the whole structure,
- a graph for each side of the structure (if applicable).

Each graph displays the volume of the structure in comparison with the volumes computed on a normative dataset of subjects with similar age, described in chapter 1.7. If several exams have been processed by QyScore for the selected patient, the volume of the structure at each timepoint is also displayed to enable a longitudinal follow-up.

5.4.3 *Atrophy* mode

Fig. 5.10: *Atrophy* mode

In this mode, the color assigned to each structure indicates its z-score by comparison with normative data (described in chapter 1.7), instead of being a "false color" (as described in the chapter 5.3.2).

To enter the mode:

- Click on the **Atrophy** button

The LUT on the left-hand side of the standard windows indicated the correspondences between the colors and the z-scores.

The segmented structures can be chosen similarly as in chapter 5.3.2.

The special window displays a copy of the table contained in the *Segmentations* part of the control panel (similarly as in chapter 5.4.1).

5.4.4 *Thumbnails* mode

Fig. 5.11: *Thumbnails* mode

This mode enables a slice-by-slice visualization of the volume.

To enter the mode:

- Click on the **Thumbnails** button

The special window displays thumbnails that are by default axial slices with a step-size of 2 (slices 1, 3, 5. . .), with the same modalities and structures displayed in the standard windows. It can be parametred using the instructions given in 5.5.3.

Interactively select the slices to display

You can also select directly the slices that you wish to display, by:

- Click on the first selected slice,
- Long click until the last slice that you wish to display.

5.4.5 *3D* mode

Fig. 5.12: *3D* mode

This mode enables you to view 3D meshes of the selected structures.

To enter the mode :

- Click on the **3D** button
- In the pop-up window:
    - Click on **Ok** to enter the mode
    - Click on **Cancel** otherwise

⚠️ The meshes computation can take up to 2 minutes.

The segmented structures can be chosen similarly as in chapter 5.3.2.

The special window displays a mesh of all selected structures, cut with a 2D axial view of the patient.

Note: If a structure A contains a structure B (eg, A being the white matter and B the hippocampus), only the mesh of A will be visible.

5.5 Change visualization options

Visualization options are available via the *Window options* section of the control panel. They are hidden by default and can be displayed by clicking the ▲ icon.

Fig. 5.13: Visualization options

Changing the options has a direct consequence on the displayed volume in standard windows (and on the special window for the modes "Atrophy", "Thumbnails" or "3D"). Available options are described hereafter.

5.5.1 *LUT* tab

Fig. 5.14: Visualization options - LUT

This tab enables you to modify the intensity range and color palette of the displayed modalities.

The *Volume*, *Palette*, *Start* and *End* sections, along with the interactive LUT and cursors mentionned in the following instructions are highlighted in Fig. 5.14.

To choose the modality on which the changes will apply:

- Click on the list of the *Volume* section
- Click on the chosen modality

To change the color palette:

- Click on the list of the *Palette* section
- Click on the chosen palette

To change the intensity range:

- To change the minimum value:
    - Long click on the left cursor of the interactive LUT
    - OR click on the arrows of the *Start* section
    - OR directly replace the value in the *Start* section

- To change the maximum value:
    - Long click on the right cursor of the interactive LUT
    - OR click on the arrows of the *End* section
    - OR directly replace the value in the *End* section
- To change both values:
    - Long click on the interactive LUT located between the cursors

Following those steps, the LUT is updated in each standard visualization window.

To restore default settings:

- Click on the **Reset** button

5.5.2 *Fusion* tab

Fig. 5.15: Visualization options - Fusion

The tab enables you to modify the fusion rate between displayed modalities, along with the transparency ratio of displayed segmented structures.

To restore default settings:

- Click on the **Reset** button

Change fusion rate

- Long click on the *Modalities fusion* cursor

This option is available only when exactly two modalities are displayed at the same time.

Changing its position changes the visibility of the modalities indicated on both of its sides: the more it is positionned close to a modality, the more said modality will be visible in the standard windows (and on the special window for the modes "Atrophy", "Thumbnails" or "3D").

Change transparency ratio

- Long click on the *ROIs transparency* cursor

This option is available only when at least a structure is displayed.

Changing the cursor position changes the visibility of structures: the more it is positionned toward the right, the more they are visible.

5.5.3 *Colors* tab

Fig. 5.16: Visualization options - Colors

This tab enables you to modify the "false colors" assigned to the displayed segmented structures. It is not available when the "Atrophy" mode is enabled.

Similarly to the *Segmentations* table, the tab is organized in the following way:

- Group of structures (eg: "Brain substructures")
  - Whole structure (eg: "Hippocampus")
    * Lateral structure (eg: "Left Hippocampus")

The navigation in the tab is the same as in chapter 5.3.2.

Color manipulation can be done via the color table (Fig. 5.17).

Fig. 5.17: Visualization options - Color table

To restore default settings:

- Click on the **Reset** button

Note: the colors are reinitialized to default values every time the interface is closed.

Change a color

The colors can be changed only for whole structures and their sides, in the following way:

- Display in the tab the structure which color needs to be changed

- Click on the colored icon on the left-hand side of the structure

- In the pop-up window (Fig. 5.17), change the color:

   - Click on one of the colors from the *Basic colors* section

   - OR click on one of the colors from the *Custom colors*

   - OR long clic on the color and saturation palettes until the desired color is obtained in the preview window

   - OR replace the *Hue / Sat / Val* values until the desired color is obtained in the preview window

      * Click on the arrow of the *Hue / Sat / Val* sections

      * OR directly replace the *Hue / Sat / Val* values

   - OR replace the *Red / Green / Blue* values until the desired color is obtained in the preview window

      * Click on the arrow of the *Red / Green / Blue* sections

      * OR directly replace the *Red / Green / Blue* values

- Click on **OK** to assign the new color and close the window

- Click on **Cancel** to close the window without changing the color

Save and assign a personalized color

To save a custom color for this session:

- Display in the tab the structure which color needs to be changed

- Click on the colored icon on the left-hand side of the structure

- In the pop-up window (Fig. 5.17), create a new color :

  - Long click on the color and saturation palettes until the desired color is obtained in the preview window

  - OR replace the *Hue / Sat / Val* values until the desired color is obtained in the preview window

    * Click on the arrow of the *Hue / Sat / Val* sections

    * OR directly replace the *Hue / Sat / Val* values

  - OR replace the *Red / Green / Blue* values until the desired color is obtained in the preview window

    * Click on the arrow of the *Red / Green / Blue* sections

    * OR directly replace the *Red / Green / Blue* values

  - Click on **Add to Custom Colors**

  - Close the window:

    * Click on **OK** to assign the new color and close the window

    * Click on **Cancel** to close the window without changing the color

5.5.4 *Thumbnails* tab

Fig. 5.18: Visualization options - Thumbnails

This tab enables you to customize the special view of the *Thumbnails* mode. It is available only when the *Thumbnails* mode is enabled (see chapter 5.4.4).

To change the slices orientations in the special window (one choice at a time):

- Click on [icon]: displays axial slices

- Click on [icon]: displays coronal slices

- Click on [icon]: displays sagittal slices

To change the step size between slices:
- Click on the arrows of the *Step* section
- OR directly replace the *Step* value

To change the first displayed slice:
- Click on the arrows of the *Start* section
- OR directly replace the *Start* value

To change the last displayed slice:
- Click on the arrows of the *End* section
- OR directly replace the *End* value

To automatically compute the range of non-background slices and display them:

- Click on [icon]

To restore default settings:
- Click on the **Reset** button

5.6 Display and edit the summary report

Fig. 5.19: Report tab

To display the report:

- Click on **Report** to switch to the report tab

5.6.1 Global presentation

The report contains a summary of QyScore analysis results.

A number of fields are automatically generated by QyScore:

- *Patient information*: patient-related information (name, age, sex), acquisition date and imaging system information.

- *Quality control summary*: summary of automated quality control performed by QyScore.

- *Results*: numerical results automatically computed and graphs of comparison with normative data (described in chapter 1.7).

The *Additions* field is not visible by default since it is designed to contain users' additional contents, as described hereafter. These additions are saved even after the current session is closed.

5.6.2 Edit the report

Add / delete / modify comments

To display the comments edition section:

- Display the report
- Click on **Edit**

Each comment is displayed on a new line, with the date and time of comment on the right-hand side.

To add a comment:

- Click on the last visible line (should be empty)
- Type your comment
- Click on **Save report** to save the comment
- Click on **Cancel** otherwise

To delete a comment:

- Click on the **Delete** button of the selected comment
- In the pop-up window:
    - Click on **Ok** to delete the comment
    - Click on **Cancel** otherwise

Add / delete screenshots

Screenshots can be added from the standard visualization windows, as well as from the special window of the modes « Atrophy », « Thumbnails » or « 3D ».

To do so:

- Click on the *View* tab to get back to the volumes visualization
- On the selected window, click on the screenshot icon (see Fig. 5.3)

To delete all the screenshots from the report:

- Display the report

- Click on **Reset snapshots**

- In the pop-up window:
    - Click on **Ok** to delete the screenshots
    - Click on **Cancel** otherwise

⚠ All the screenshots will be deleted.

5.6.3 Print the report

To print the report:

- Display the report

- Click on **Print**

Troubleshooting

Please refer to this section before requesting any further assistance.

6.1 The connection interface does not open up

- Try again by double-clicking faster on the icon.
- If this does not solve the problem, open a terminal and type the commandline "qyfront".

6.2 I can't send data from my DICOM server

- If the analysis server is installed locally, make sure that it is turned on.
- Make sure that you have sent an exam or sequences.
- Make sure that you have chosen to send at least a 3DT1.
- Make sure that the chosen sequences are handled by QyScore.
- Make sure that the acquisition parameters are compliant with QYNAPSE's recommendations.
- If this does not solve the problem, please refer to the user manual of your DICOM server.

6.3 I can't connect to the data management interface

- Make sure that the login and password that you entered are correct.
- Make sure that the caps lock is disabled.
- Make sure that the num lock is enabled.

6.4 I can't find the exams from my DICOM server in the data management interface

- Click on Refresh.
- If this does not solve the problem, make sure that the configuration settings are correct (IP adress, port...).

6.5 The data management interface displays "Server is not reachable" when I click on "Send"

- This error indicates a connection issue with the analysis server. The server is relaunched every minute in case of errors; wait a minute and try again.
- If the analysis server is installed locally, make sure that it is turned on, then open a terminal and type the commandline "qyrunserver".
- If this does not solve the problem, make sure that the configuration settings are correct (IP adress, port...).

6.6 I can't send data from the data management interface

- Make sure that you have selected sequences by checking the corresponding boxes.
- Make sure that you have chosen to send at least a 3DT1.
- Make sure that the chosen sequences are handled by QyScore.
- Make sure that the acquisition parameters are compliant with QYNAPSE's recommendations.

6.7 I do not receive the results of my analysis after the indicated time

Via your DICOM server:

- Wait a couple of minutes more: depending on the image resolution, the processing time can be longer than expected.
- If this does not solve the problem, try sending the data again, after making sure that there is at least a 3DT1, that those types of sequences are handled and that the acquisition parameters are compliant with Qynapse's recommendations.

Via the data management interface:

- Make sure that you have clicked on the "Send" button: the status bar must display a value higher than 1%.
- Make sure that no error message has been displayed.
- If the analysis is still running (QYNAPSE logo rotating at the bottom right of the interface), wait a couple of minutes more: depending on the image resolution, the processing time can be longer than expected.
- If this does not solve the problem, it may be due to a connection issue with the analysis server. Please refer to section 6.5.

- If this does not solve the problem, try sending the data again, after making sure that there is at least a 3DT1, that those types of sequences are handled and that the acquisition parameters are compliant with Qynapse's recommendations.

6.8 The visualization interface does not open up

If you have sent data using your DICOM server:

- Try again by double-clicking faster on the icon.
- If this does not solve the problem, open a terminal and type the commandline "qyviewer".

Via the data management interface:

- Wait a minute more: the results are retrieved from the DICOM server and converted, and if many results are available, the conversion time can be longer than expected.
- If this does not solve the problem, close the data management interface and try again.

6.9 I can't find the exam that I wish to visualize

If you have sent data using your DICOM server:

- Make sure that the filters applied in the searching tool are correct.
- The database is regularly cleaned to save disk space. As a consequence, if the exam you wish to view is no longer available, please relaunch the analysis.

Via the data management interface:

- Make sure that the filters applied in the searching tool are correct.

F
False colors, **8**

L
LUT, **8**

P
Percentile, **8**

S
Special window, **8**
Standard visualization window (or standard window), **8**

Z
Z-score, **8**