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# QyScore Documentation

*Release 1.9.0, rev 4*

Qynapse

Jun 17, 2020



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<b>QYNAPSE</b>	<b>QyScore</b>
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## 1.1 Copyright notice and trademark acknowledgements

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DICOM is the registered trademark of the National Electrical Manufacturers Association for its standards publications relating to digital communications of medical information. All other brand, product, and company names mentioned in this document are trademarks or registered trademarks of their respective owners.

## 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 or folder,
- sends said data to Qynapse's analysis server,
- enables the user to view the results (segmentations and numerical results) in dedicated interfaces,
- enables the user to edit a summary report of the results (segmentations and numerical results).

The visualization graphical interfaces allow the user to:

- Browse the segmentations and the measures,
- Compare the results of segmented brain structures to a reference healthy population,
- View and download the summary report.

One of the visualization interfaces is available as a web application that must be used with a web browser.

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 three user interfaces:

- a data management interface on the computer installed by QYNAPSE,
- a visualization interface on the computer installed by QYNAPSE (referred to as “local visualization interface”),
- a visualization interface available on web browsers (referred to as “web-based visualization interface”).

QyScore interfaces and features are detailed in this user manual.

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

- sending data directly from the DICOM server (PACS) (direct connection - see chapter 4.2),
- using the local user interfaces on the computer installed by QYNAPSE (see chapters 4.3 and 6).
- using the web-based interfaces from your computer (see chapters 4.4 and 7)

## 1.5 Technical description

### 1.5.1 Installation

#### QyScore

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
- Mouse
- Keyboard

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.

For the direct connection mode, the computer must be connected to a DICOM server to enable data sending to the analysis server.

Several configurations for the installation of QyScore are possible:

- Distant server: QyScore is located on a cloud server, with the data being stored outside the client organization, on a personal health data hosting system
- Local server: it is located on a computer of the client organization

### Web-based user interface

The minimal requirements for the computer running the web-based user interface are:

- RAM: 4Go
- CPU: Intel Core i5
- Screen resolution 1280\*1024
- Mouse
- Keyboard

Several browser can be used:

- Mozilla Firefox, version 68.0.2 (64-bit) or higher
- Google Chrome, version 76.0.3809.100 (64-bit) or higher

If QyScore is installed remotely, the computer running the interface must be connected to the Internet to enable communication between client and server sides.

## 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](mailto:support@qynapse.com).

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

### 1.5.3 Maintenance

The 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 the maximum 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 previously 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:

	<b>T1</b>	
	Required	Tolerated
Voxel size in plane (mm)	[1, 1]	Min: [0.74, 0.74] Max: [1.5, 1.5]
Field of view (mm)	x: [152, 340] y: [220, 340] z: [152, 340]	x: [145, 340] y: [192, 340] z: [132, 340]
Slice thickness (mm)	1	Min: 0.74 Max: 1.5
Interpolation	No	Yes
Acquisition direction	Sagittal	Axial, Coronal
Acquisition type	3D	2D with isotropic voxel
Field strength	1.5T, 3T	1.5T, 3T

	<b>T2FLAIR2D</b>		<b>T2FLAIR3D</b>	
	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)	x: [152, 340] y: [220, 340] z: [152, 340]	x: [148, 340] y: [220, 340] z: [148, 340]	x: [152, 340] y: [220, 340] z: [152, 340]	x: [152, 340] y: [220, 340] z: [152, 340]
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.

## 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 <a href="http://adni.loni.usc.edu">http://adni.loni.usc.edu</a> 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 <a href="https://www.humanconnectome.org/study/hcp-young-adult">https://www.humanconnectome.org/study/hcp-young-adult</a> 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 <a href="https://brain-development.org/ixi-dataset">https://brain-development.org/ixi-dataset</a> 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 <a href="http://www.oasis-brains.org">http://www.oasis-brains.org</a> 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 <a href="http://www.ppmi-info.org">http://www.ppmi-info.org</a> 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). If QyScore is installed locally, the customer is responsible for the control of physical access to the server.

## 1.9 European regulations




QyScore is qualified as a class IIa medical device. It complies with the requirements of the European 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 local user interfaces of QyScore software by clicking the “Help” and then “User manual” buttons.
- Through the web-based user interface, by clicking the  icon and then **User Manual**
- 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.



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.

**Scroll** Roll the wheel 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).



## 3.1 Global presentation

You can connect to the local interfaces by using the desktop icons available on the computer installed by QYNAPSE.

To connect to the web-based interfaces from your computer, you need to open a web browser and enter the URL provided by QYNAPSE.

## 3.2 Local interfaces

### 3.2.1 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 desktop icon on which on you clicked, either the data management interface or the visualization interface is launched.

### 3.2.2 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
- *Confirm 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.

## 3.3 Web-based interfaces

### 3.3.1 Login

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

Click on **Sign in**.

If the username and password are correct, the interface is launched.

#### Case of first login

If you log in for the first time, you will be asked to change your password.

Choose a new password

Username  
admin

Current password

New password

Confirm new password

CHANGE PASSWORD AND SIGN IN

Fig. 3.1: Change your password

To do so:

- *Current password*: type the current password
- *New password*: type your new password
- *Confirm new password*: confirm your new password
- Click on **Change password and sign in**


---

**Note:** This new password will be required for your next login.

---

### 3.3.2 Change password

Follow the steps:

- Click on the  icon
- Click on **Change password**
- *Current password*: type your current password
- *New password*: type your new password
- *Confirm new password*: confirm your new password
- Click on **Change password** to save the new password
- Click on **Cancel** to cancel the procedure and close the window

### 3.3.3 Logout

To logout:

- Click on the  icon
- Click on **Sign out**

## 3.4 Forgotten password

If you forget your password, please contact QYNAPSE at [support@qynapse.com](mailto:support@qynapse.com).



## 4.1 Global presentation

Data can be sent to QYNAPSE's analysis server:

- directly via your DICOM server (e.g. PACS)
- via the local data management interface
- via the web-based data management interface

In all cases, the received data are automatically analyzed.



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

## 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 view them using the visualization interfaces. For further information and description of features, see chapters 6 and 7.



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 Local data management interface

The local data management interface enables you to send data.

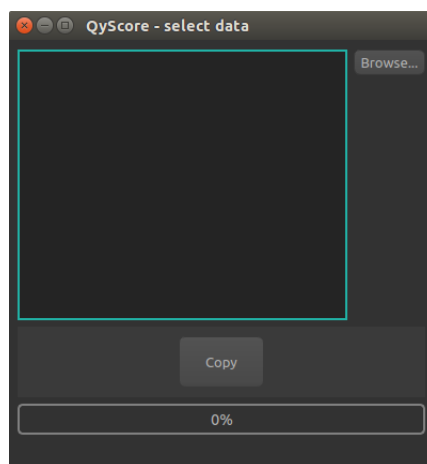


Fig. 4.1: Data management interface

To choose data to send, in the interface:

- Click on **Browse**
- Choose the folder that contains the DICOM data you want to send,
- Click on **Choose**.

---

**Note:** The folder can contain DICOM data for several patients/acquisitions. They will be automatically sorted and the analysis will be launched for each patient and acquisition.

---

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

The chosen data are copied and sent to QYNAPSE's analysis server.

## 4.4 Web-based data management interface

### 4.4.1 Uploading data

Data can be sent using the *Launch new analyses* interface. To open this interface:

- Click on the  icon
- Click on **Launch new analyses**

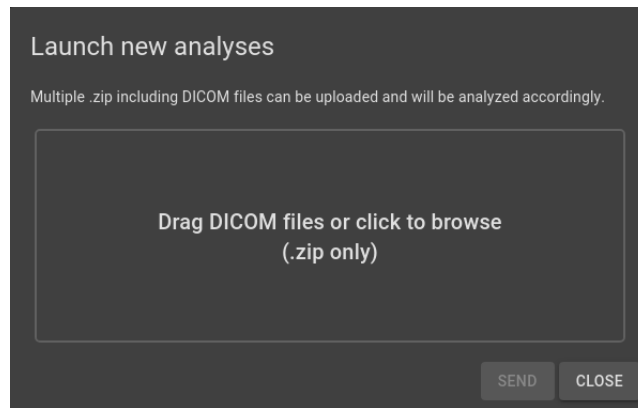


Fig. 4.2: Launch new analyses

In the *Launch new analyses* interface:

- Drag and drop the files in the upload zone or click on the upload zone to browse
- Wait for the uploading to finish. The *Ready* message should be displayed.

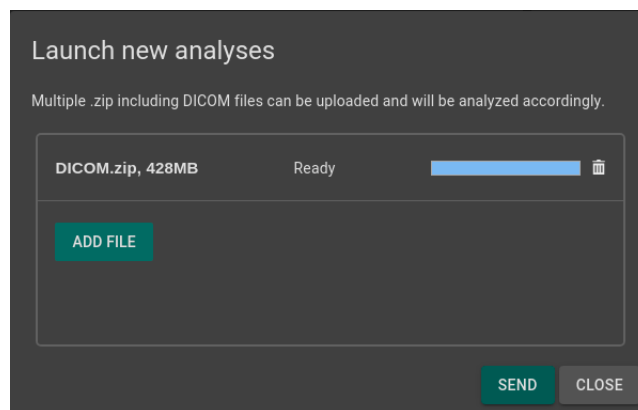


Fig. 4.3: Launch new analyses - Uploaded file

---

**Note:** You must compress your DICOM folders (.zip format) before uploading them via the interface.

---

**Note:** The .zip file can contain DICOM data for several patients/acquisitions. They will be automatically sorted and the analysis will be launched for each patient and acquisition.

---

### Remove an uploaded file

To remove a file from the upload zone, click on the  icon.

### Send data

Once the files are uploaded, click on **Send**.

A confirmation pop-up is displayed.

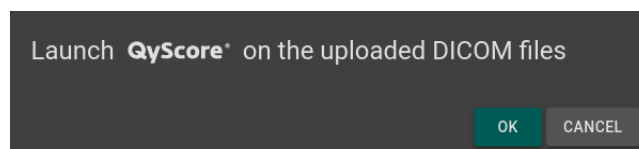


Fig. 4.4: Confirmation for sending data for analyses

- Click on **Ok** to send the uploaded data for analyses
- Click on **Cancel** to cancel the procedure and close the window

The chosen data are copied and sent to QYNAPSE's analysis server. You can follow the progress and monitor the launched analyses in the *Analyses monitoring* interface.

#### 4.4.2 Analyses monitoring

Launched analyses can be monitored in the *Analyses monitoring* interface. To open this interface:

- Click on the  icon
- Click on **Analyses monitoring**

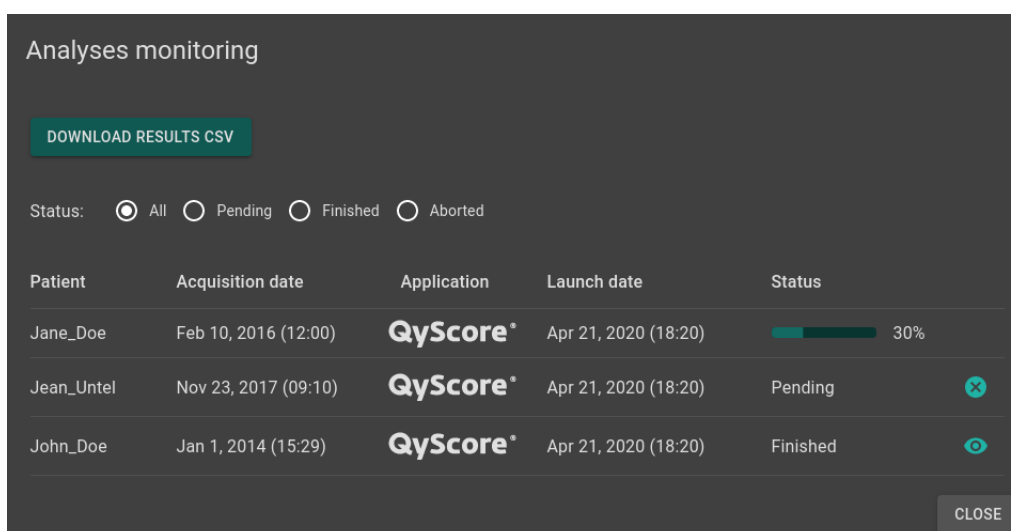


Fig. 4.5: Analyses monitoring

The table displays information about the analyses:

- *Patient*: the patient's name or identifier
- *Acquisition date*: the study date of the patient's exam
- *Application*: the name of the software that runs the analysis
- *Launch date*: the launch date of the analysis
- *Status*: the status of the analysis. It can be:
  - *Pending*: the analysis is waiting to be processed
  - *Running*: the analysis is running (a progress bar is displayed)
  - *Finished*: the analysis is completed
  - *Aborted*: the analysis was cancelled by the user or encountered an unexpected error



### Cancel a *Pending* analysis

*Pending* analyses can be cancelled before they start to run.

To cancel a *Pending* analysis:

- Click on the  icon of the corresponding analysis row

A confirmation pop-up is displayed.

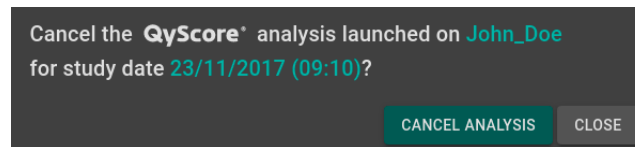


Fig. 4.6: Confirmation for analysis cancellation

- Click on **Cancel analysis** to cancel the *Pending* analysis. It sets its status to *Aborted*.
- Click on **Close** to cancel the procedure and close the window



If the analysis changes from *Pending* to *Running* while the confirmation pop-up is opened, the analysis is not cancelled and the message *Your analysis cannot be cancelled, it has already started* is displayed.


### Filter analyses

To filter the analyses according to their status:

- Click on one of the following:
  - *All*: displays all the analyses
  - *Pending*: displays *Running* and *Pending* analyses
  - *Finished*: displays *Running* and *Finished* analyses
  - *Aborted*: displays *Running* and *Aborted* analyses

### Load the results of a *Finished* analysis

Results of *Finished* analyses can be loaded for visualization. To do so:

- Click on the  icon of the analysis row, for the selected patient/acquisition

A confirmation pop-up is displayed.

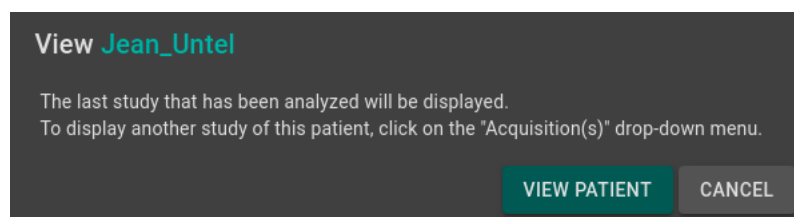



Fig. 4.7: Confirmation for loading a *Finished* analysis

- Click on **View patient** to load the patient onto the interface

- Click on **Cancel** to cancel the procedure and close the window

---

**Note:** Once the patient is loaded onto the interface, the last study that has been analyzed is displayed. To display another study of the loaded patient, click on the  icon of the *Acquisition(s)* drop-down menu and select the corresponding study date.

---

### Download the results

To obtain a file with the results of completed analyses:


- Click on *Download CSV results*

The results are presented in a CSV file, each line referring to a patient/acquisition, and each column referring to a MRI marker.

Results summary report

5.1 Global presentation

The report contains a summary of QyScore analysis results.



Powered by  
**QyScore**<sup>®</sup>

**PATIENT INFORMATION**

NAME	SEX	AGE
Jean_Untel	M	28
ACQUISITION DATE	MANUFACTURER	
20130514_120944	Philips Medical Systems	

COMMENTS

**QUALITY CONTROL SUMMARY**

Control	T1	T2FLAIR
Acquisition parameters	⚠	⚠

See "Advanced Quality Control" for more details

**RESULTS**

Generated with QyScore version 3.6.0.

Structure	Volume (mL / %CV*)	Percentiles	Since last acquisition** (mL / %CV*)	95% 75% 50% 25% 5%	Z-score
Whole Brain	1188.6 / 86.1%	50 - 75	-		0.79
Grey Matter	696.6 / 50.5%	5 - 25	-		-0.06
White Matter	492.0 / 35.7%	> 95	-		1.63
Amygdala	Left: 1.6 / 0.1%	75 - 95	-		0.88
	Right: 2.1 / 0.2%	> 95	-		3.79
Hippocampus	Left: 3.5 / 0.3%	> 95	-		2.84
	Right: 3.7 / 0.3%	> 95	-		2.32
WMH	2.5 / 0.2%	-	-		N/A

\* Brain structures: CV = IntraCranial Volume      \*\* Relative difference between current and previous acquisitions

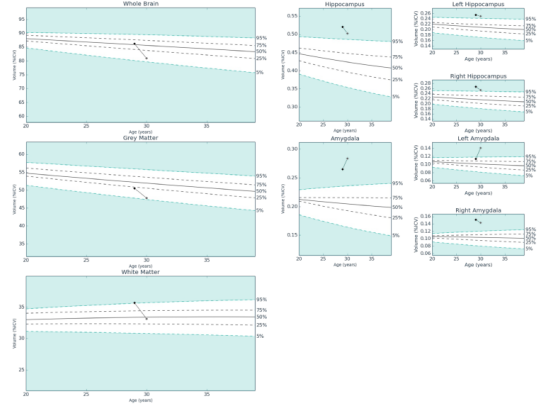
**ADVANCED QUALITY CONTROL**

**ACQUISITION PARAMETERS**

⚠ **T1:** WARNING: The analysis was performed but some acquisition parameters (Field of view) do not follow Qynapse recommendations (see guidelines). Results may be less reliable.

⚠ **T2FLAIR2D:** WARNING: The analysis was performed but some acquisition parameters (Voxel size in plane, Field of view, Is interpolated, Slice thickness31) do not follow Qynapse recommendations (see guidelines). Results may be less reliable.

**ADVANCED RESULTS**



The normative dataset used in these graphs was generated from healthy subjects.

**BRAIN STRUCTURES**

Structure	Volume (mL)	Volume (%CV)	Z-score	Percentiles	Asymetry index (ratio L/R)	
Whole Brain	Total	Both: 1188.572	86.147	0.79	50 - 75	-
	Total	Both: 696.571	50.487	-0.06	5 - 25	-
Cerebellum	Both: 29.342	2.127	1.97	> 95	-	

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© 2019 Qynapse SAS, QyScore\_v\_1.7.0 2/5

Fig. 5.1: Report

A number of fields are automatically generated:

- *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*: summary of results obtained on a the segmented structures (list of structures pre-determined at software installation), including automated numerical results, graph of comparison to normative data and a z-score graph.
- *Advanced quality control*: detailed results of the automated quality control performed by QyScore.
- *Longitudinal analysis*: longitudinal results computed automatically on anatomical structures and brain lesions.
- *Advanced results*: detailed automated results, including numerical results and graph of comparison to normative data (described in chapter 1.7).
- *Voxel-based analysis*: contains images resulting from the voxel-to-voxel analysis of the 3DT1 MRI, shown in different views.

---

**Note:** The *Longitudinal analysis* field is not visible if only one timepoint is available for the selected subject.

---

## 5.2 Display the report

The report can be displayed and printed using either the local (see 6.6) or the web-based (see 7.6) visualization interface.

---

## Local results visualization interface

---

### 6.1 Global presentation

This local visualization interface is designed to view the results computed by the analysis server. It contains 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.

#### 6.1.1 Data selection menu

This menu is available above the tabs *View* and *Report*.



Fig. 6.1: Data selection menu

Four choose data:

- Click on the *Patient name* section and select a patient in the drop-down menu
- Click on the *Study date* section and select a study date in the drop-down menu

---

**Note:** If the selected patient only has one study date available, it will be selected automatically.

---

#### Filter patients and study dates

Filtering tools are available to ease the selection of patients and study dates.

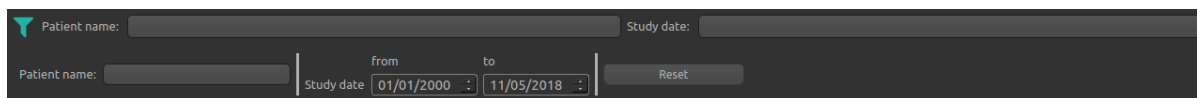



Fig. 6.2: Filtering tools

To filter the available results:

- Click on the icon  to display the filtering options
- Use the *Patient name* text section to filter by patients names
- Use the *Study date* date section to filter by study dates

To reset the filters:

- Click on **Reset**

### 6.1.2 View tab

To display the *View* tab:

- Click on **View**

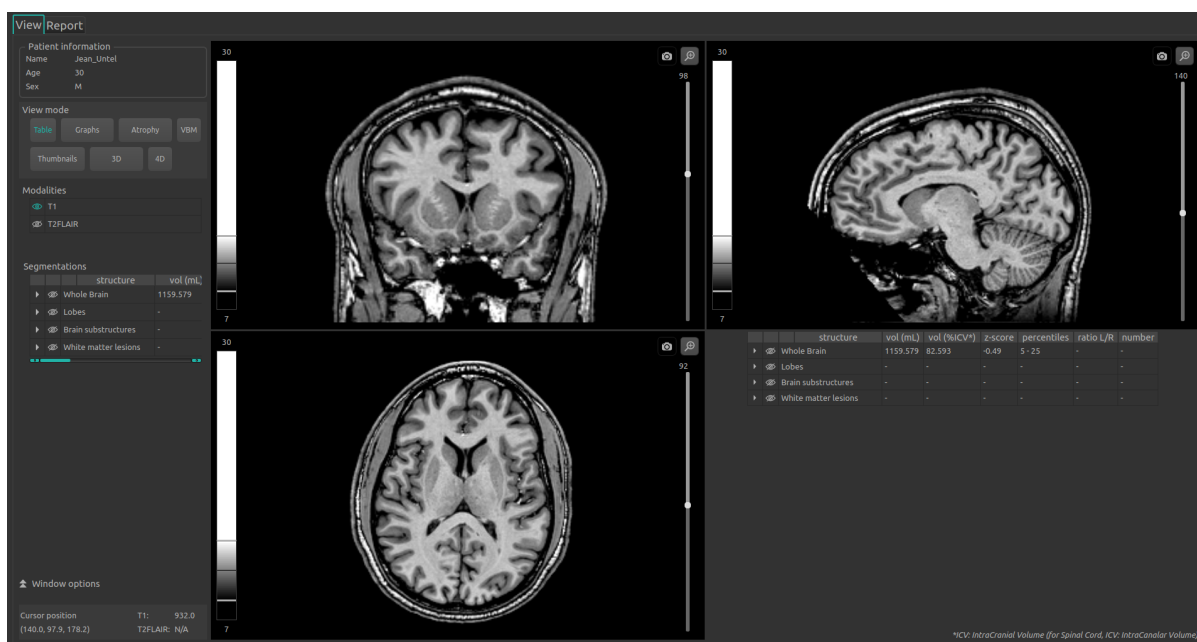


Fig. 6.3: View tab

The control panel on the left-hand side is divided into several sub-parts:

- *Patient information*: information on the selected patient
- *View mode*: to switch between view modes (default is *Table*)
- *Modalities*: to choose the displayed imaging modality
- *Segmentations*: to choose the displayed segmented structures
- *Window options*: to modify visualization options for better visual confort
- *Cursor position*: cursor position and volumes' values at said position

The viewing part on the right-hand side contains 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.

### 6.1.3 Report tab

To display the *Report* tab:

- Click on **Report**

**PATIENT INFORMATION**

NAME	John_Doe	SEX	M	AGE	73
ACQUISITION DATE	01/01/2014	MANUFACTURER	SIEMENS		

**QUALITY CONTROL SUMMARY**

Control	T1
Acquisition parameters	⚠
Image quality	✅

See "Advanced Quality Control" for more details

**RESULTS**

Structure	Volume (ml / %CV*)	Percentiles	Since last acquisition** (mL / %CV*)	95% 75% 50% 25% 5%	Z-score
Whole Brain	999.5 / 58.3%	<5	-		-2.51

To automatically add a snapshot in this report, go back to the "View" tab and click on the "Camera" icon of the view you wish to add (top-right corner of the window).

Fig. 6.4: *Report* tab

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

## 6.2 Navigating across the volumes

### 6.2.1 Standard visualization windows

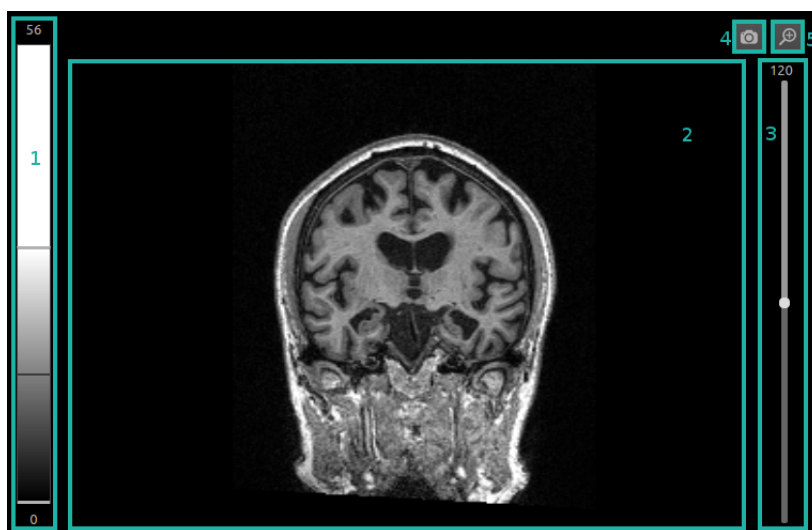


Fig. 6.5: Standard visualization window

The window contains:

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 to display the window in the entire viewing section of the “View” tab

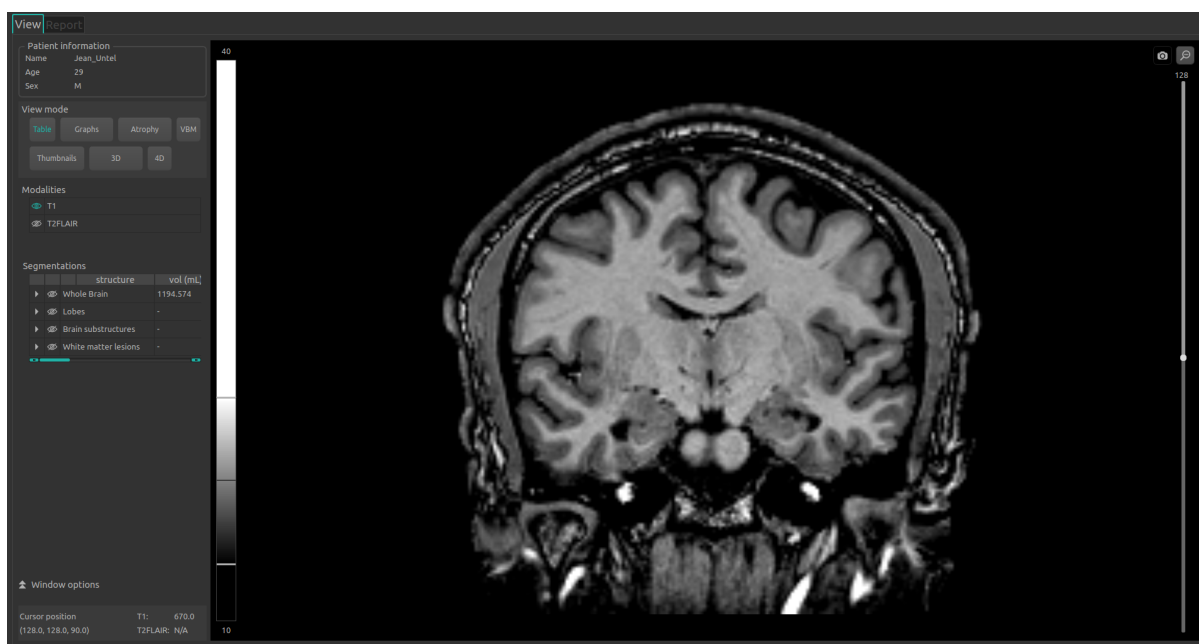


Fig. 6.6: Zoomed window



## 6.2.2 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





## 6.3 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.

### 6.3.1 View imaging modalities

Imaging modalities that can be displayed are indicated 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:

- Click on the modality name or on the  /  icon on its left.
- : modality displayed
- : modality masqued

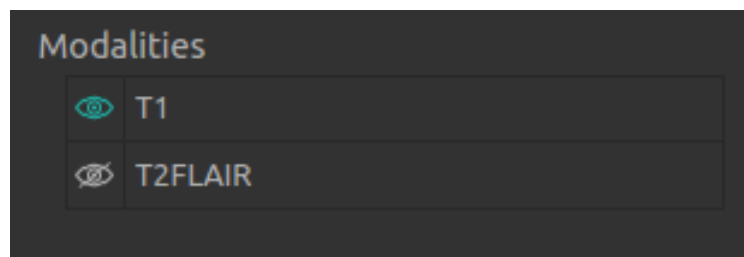
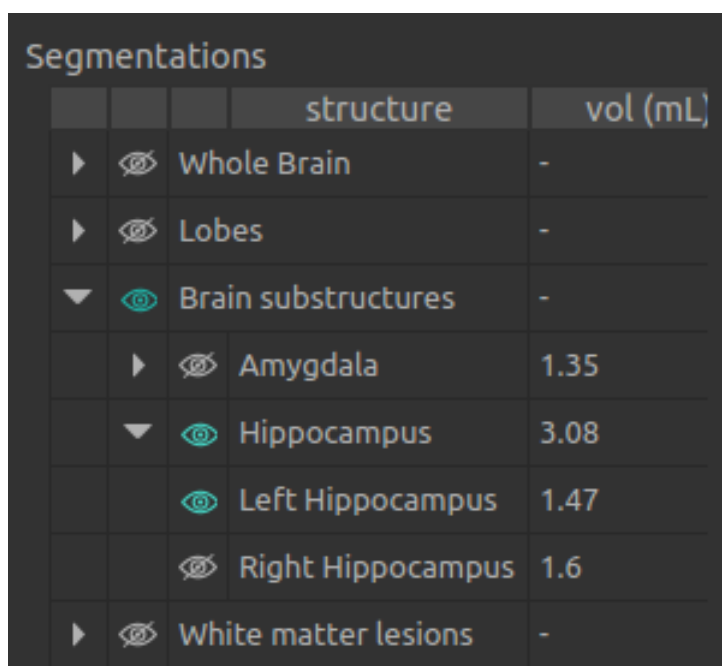


Fig. 6.7: Choice of modalities

### 6.3.2 View segmented structures



		structure	vol (mL)
▶		Whole Brain	-
▶		Lobes	-
▼		Brain substructures	-
▶		Amygdala	1.35
▼		Hippocampus	3.08
		Left Hippocampus	1.47
		Right Hippocampus	1.6
▶		White matter lesions	-

Fig. 6.8: Choice of segmented structures

The list of segmented structures that can be displayed is indicated 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 of the whole structure.

#### View the segmentations

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



---

**Note:** See chapter 6.5.3 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: 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 structure:

- If it does not appear in the table: see previous section
- Click on the structure name or the  /  icon on its left: the structure is either displayed or hidden (both sides, if applicable).
- : indicates that at least one side of the structure is displayed.
- : indicates that the structure is hidden.

To display / hide a lateral 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.
- : indicates that the side is displayed.
- : indicates that the side 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 asymetry index, defined as the ratio between a structure's left volume and its right volume.

---

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

---

## 6.4 Switch view mode

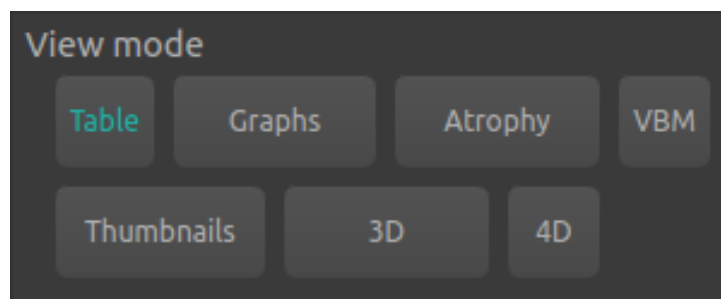


Fig. 6.9: Switch view mode

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

Available modes are described hereafter.

### 6.4.1 Table mode

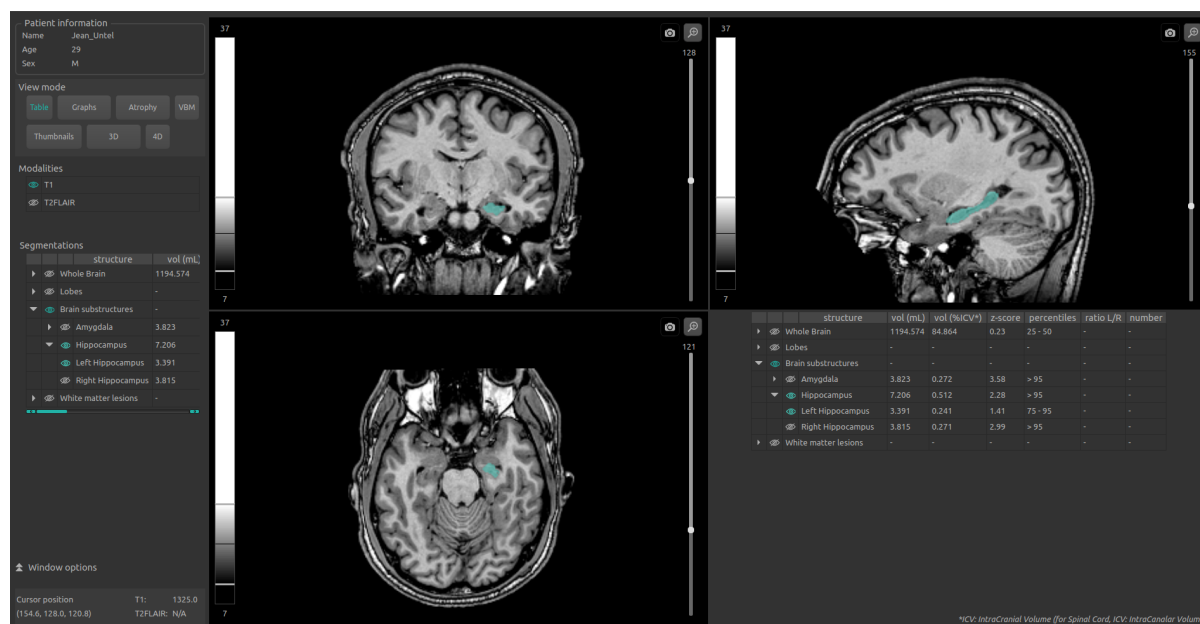


Fig. 6.10: Table mode

This is the default mode.

It displays the standard visualization of segmented structures and associated statistics, as described in chapter 6.3.

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.

## 6.4.2 Graphs mode

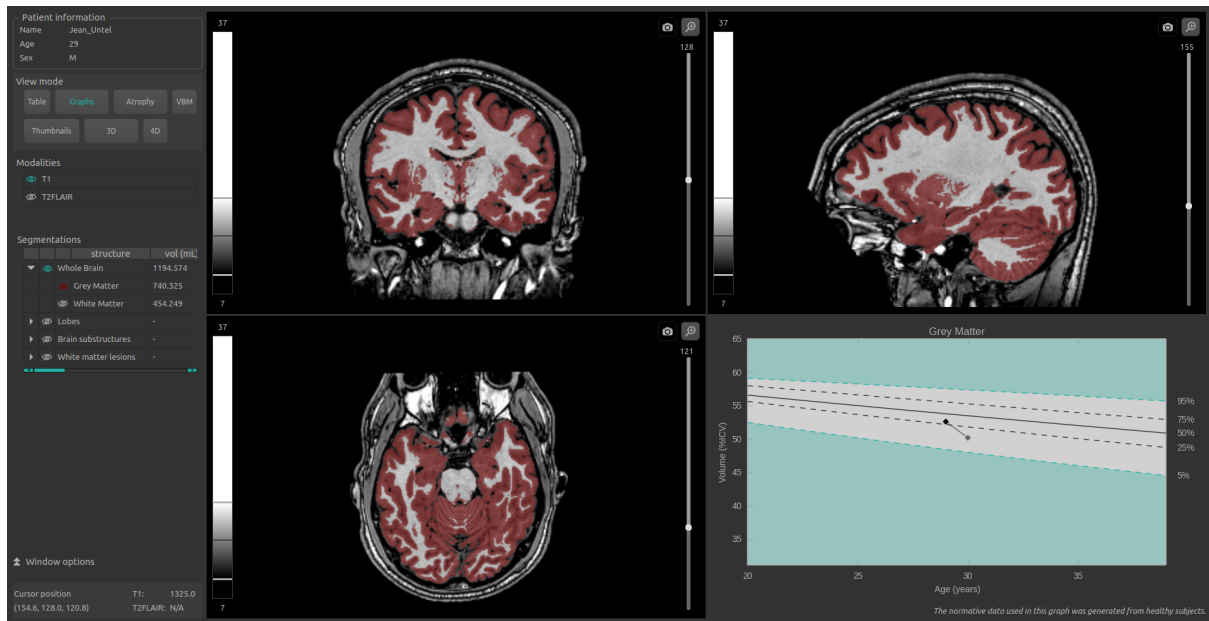


Fig. 6.11: *Graphs mode*

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

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 6.3.2).

---

**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.

### 6.4.3 Atrophy mode

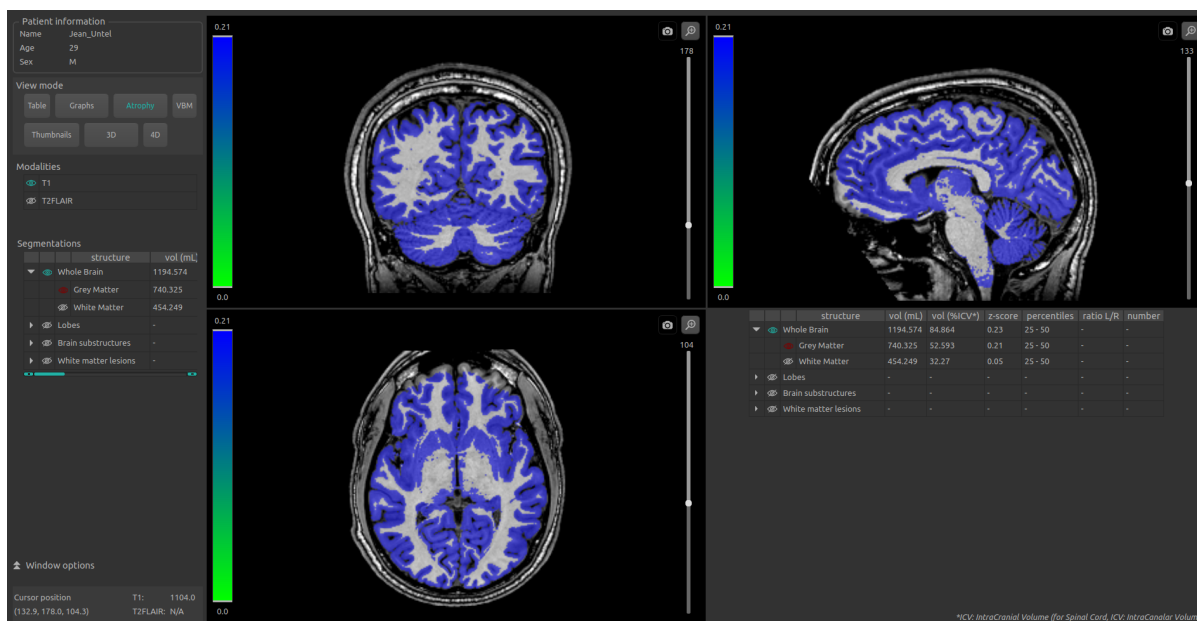


Fig. 6.12: *Atrophy* mode

In this mode, the color assigned to each structure indicates its  $z$ -score in comparison with normative data (described in chapter 1.7), instead of being a “false color” (as described in the chapter 6.3.2).

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 6.3.2.

The special window displays a copy of the table contained in the *Segmentations* part of the control panel (similarly as in chapter 6.4.1).

### 6.4.4 VBM mode

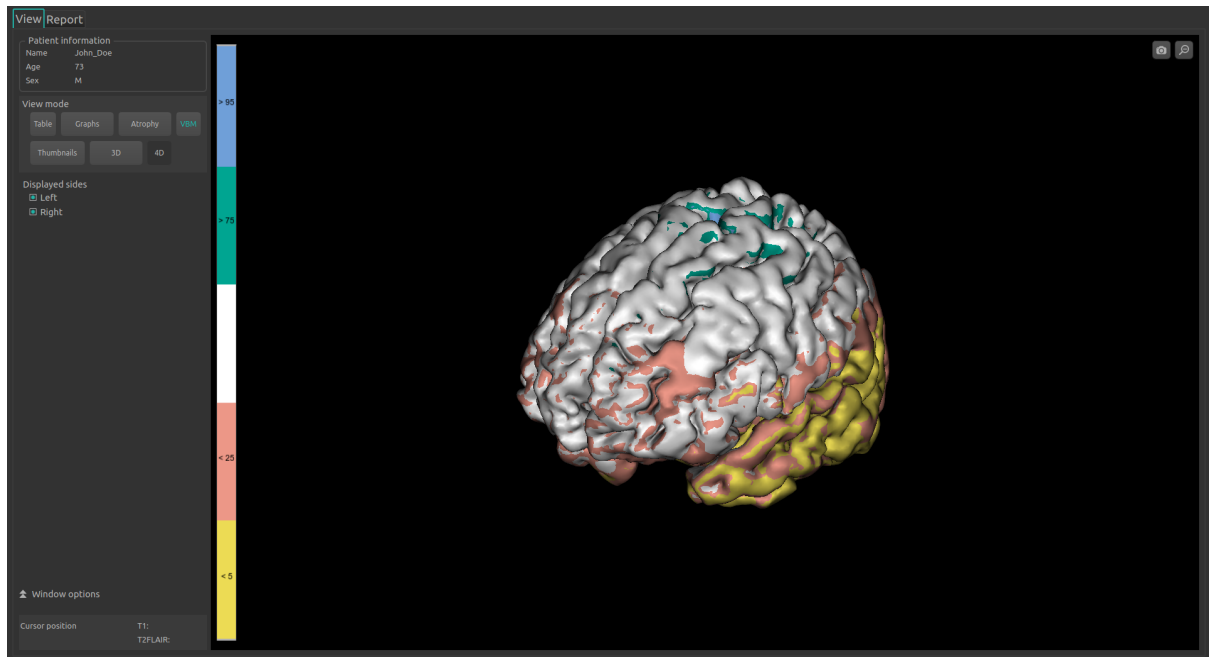


Fig. 6.13: VBM mode

This mode enables the visualization of the z-score map resulting from the voxel-by-voxel analysis of the 3D T1 MRI sequence.

To enter the mode:

- Click on the **VBM** button

The LUT indicates the relationship between the colors of the z-score map and the percentiles.

To display / hide an hemisphere:

- Click on **Right** or **Left** in the *Displayed sides* of the control panel

---

**Note:** In this mode, only the special window is displayed.

---

## 6.4.5 Thumbnails mode

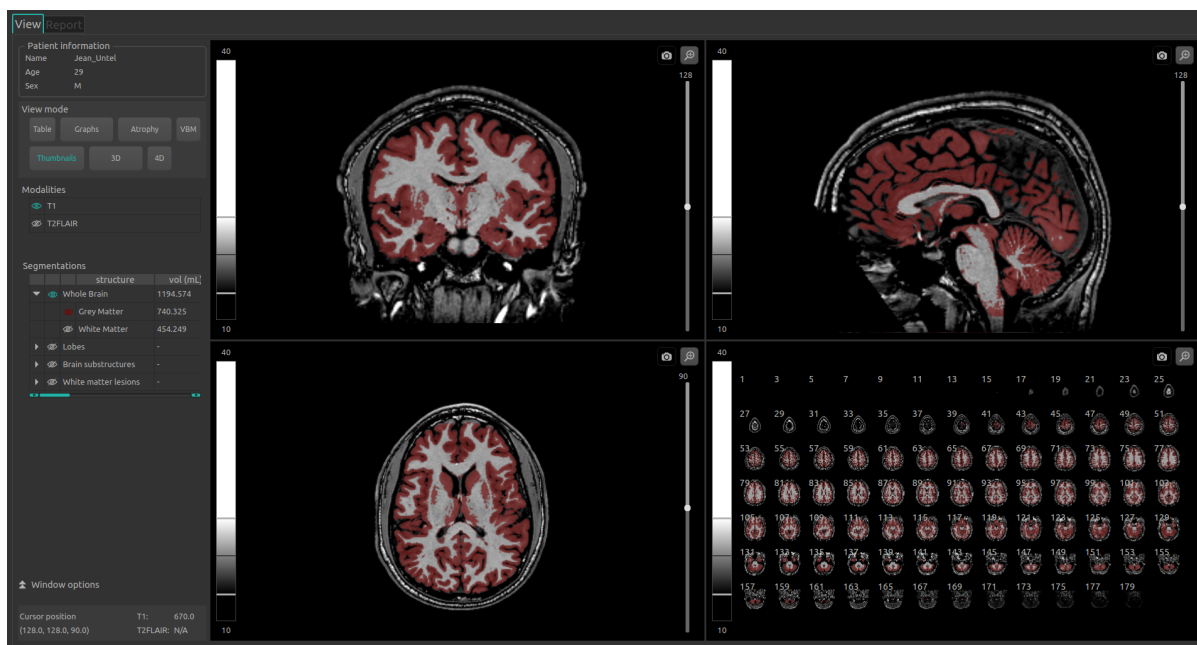


Fig. 6.14: *Thumbnails* mode

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. These parameters can be modified using the instructions given in 6.5.4.

### Interactively select the slices to display

You can 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.



### 6.4.6 3D mode

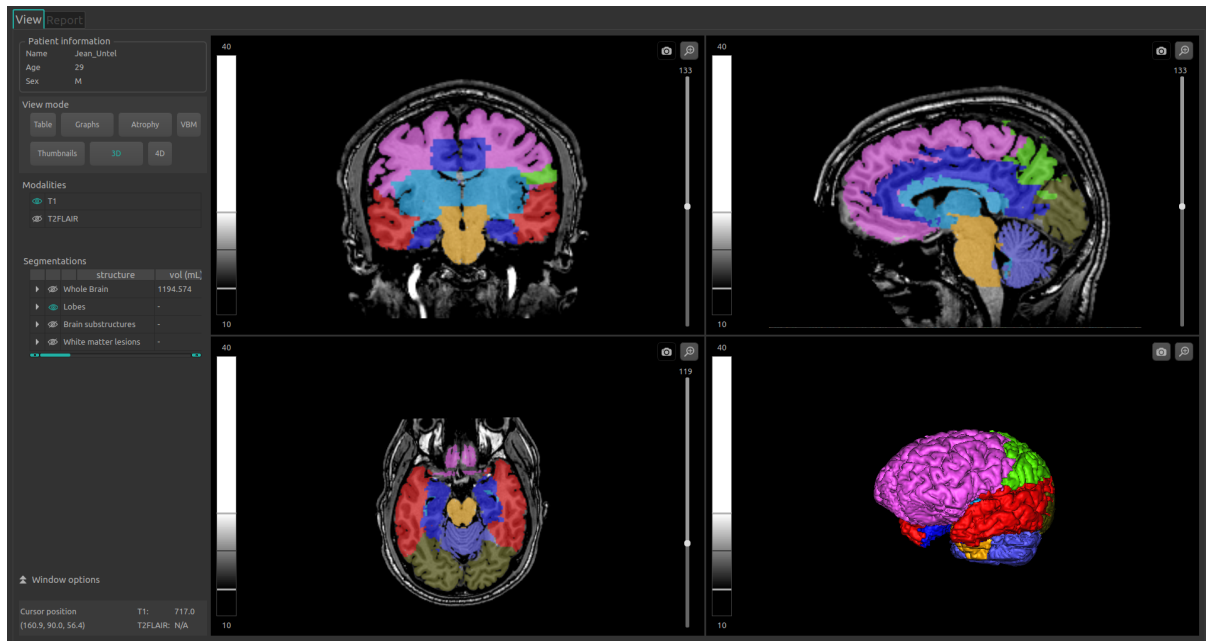


Fig. 6.15: 3D mode

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 6.3.2.

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.

### 6.4.7 4D mode

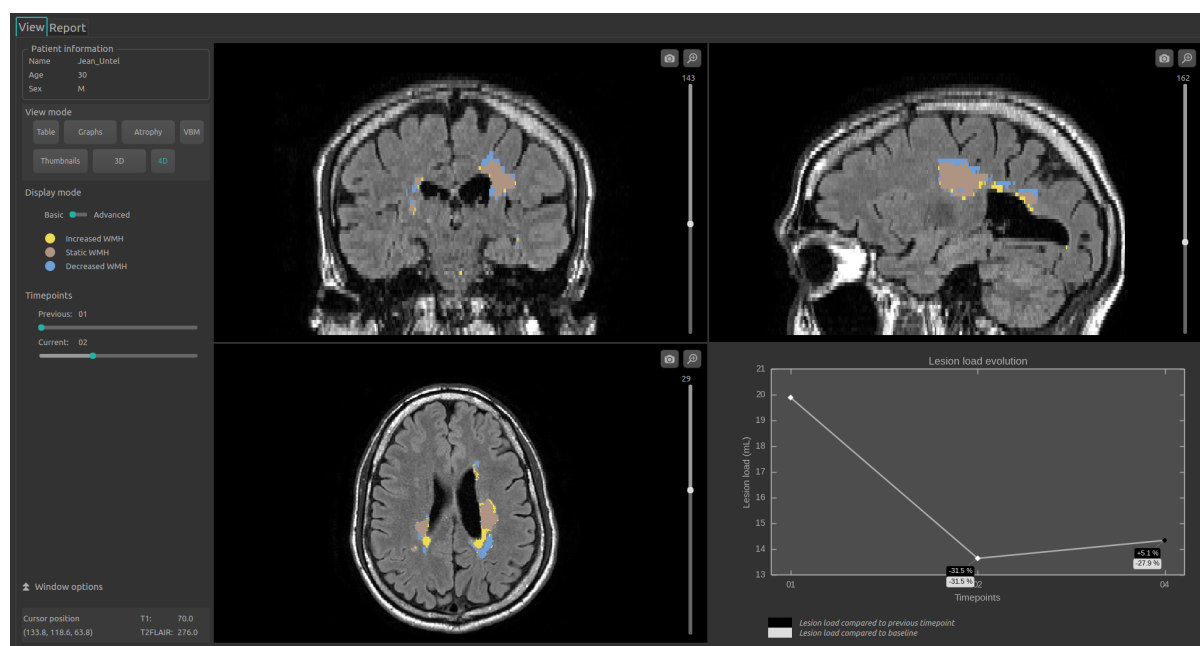


Fig. 6.16: 4D mode - Basic display

In this mode, several tools are available to visualize the evolution of the white matter hyperintensities volume over time.

To enter the mode:

- Click on the **4D** button

---

**Note:** This mode is not available if there is only one study date available for the patient.

---

The special window displays a graph depicting the overall evolution of the lesion load.

The standard visualization windows display the evolution of the lesion load between two study dates. The study dates can be selected by:

- Long clic on the *Previous* and *Current* cursors of the *Timepoints* section

---

**Note:** These cursors are locked when only two study dataes are available.

---

The standard visualization windows are updated accordingly.

Two display modes are available for the standard visualization windows:

- In the *Basic* mode (by default), each type of lesion evolution evolution (increased, decreased, static) is displayed in “false colors”.
- In the *Advanced* mode (see Fig. 6.17, the colors of each lesion is indicative of the intensity difference between the study dates. The range of colors and corresponding intensities are indicated in the LUT.

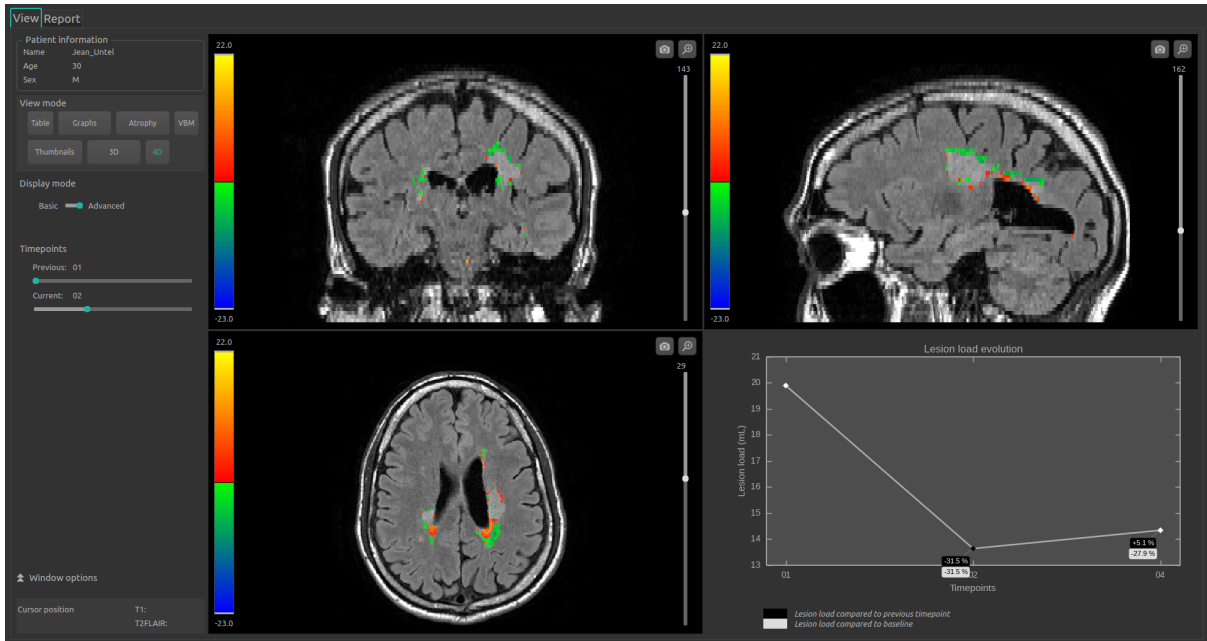



Fig. 6.17: 4D mode - Advanced display

You can switch between display modes by:

- Long click on the *Display mode* cursor

## 6.5 Change visualization settings

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

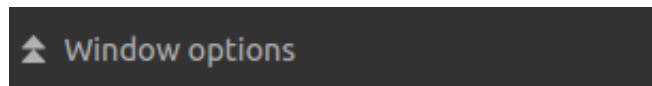


Fig. 6.18: Visualization options

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.

### 6.5.1 LUT tab

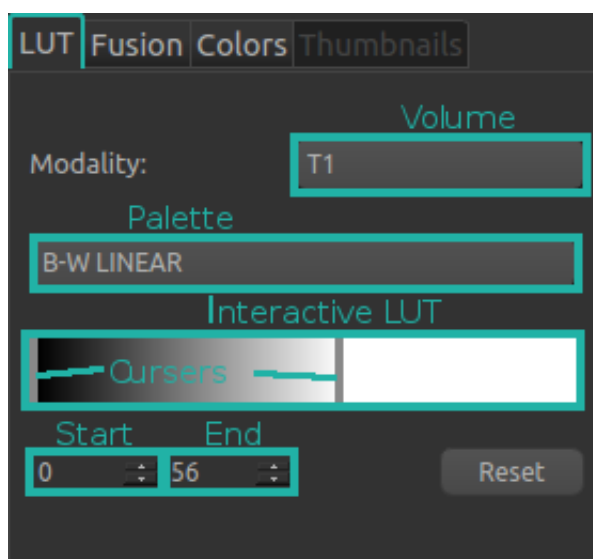


Fig. 6.19: Visualization options - LUT

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 mentioned in the following instructions are highlighted in Fig. 6.19.

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

### 6.5.2 Fusion tab

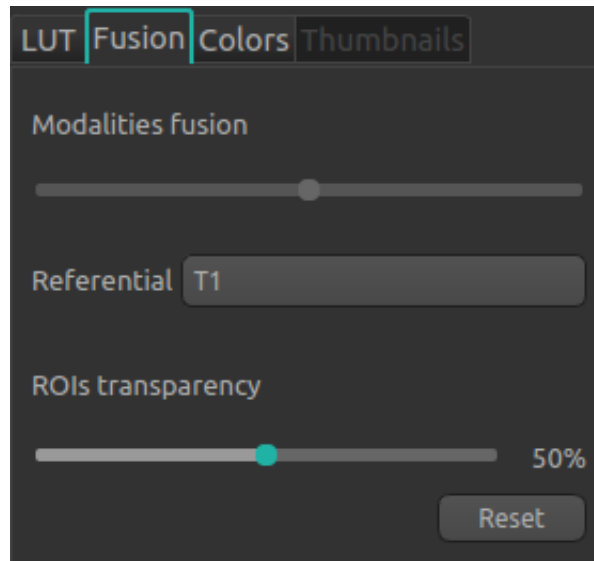


Fig. 6.20: Visualization options - Fusion

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 the position of the cursor changes the visibility of the modalities indicated on both of its sides: the more it is positioned towards 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”).

---

**Note:** In the *4D* mode (see chapter 6.4.7, the modalities are the T2FLAIR of the two study dates displayed).

---

#### Change transparency ratio

- Long click on the *ROIs transparency* cursor

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

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

### 6.5.3 Colors tab

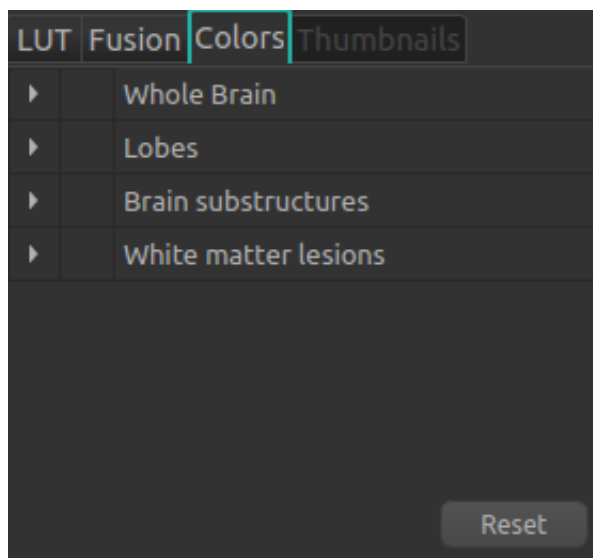


Fig. 6.21: Visualization options - Colors

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 6.3.2.

Color manipulation can be done via the color table (Fig. 6.22).

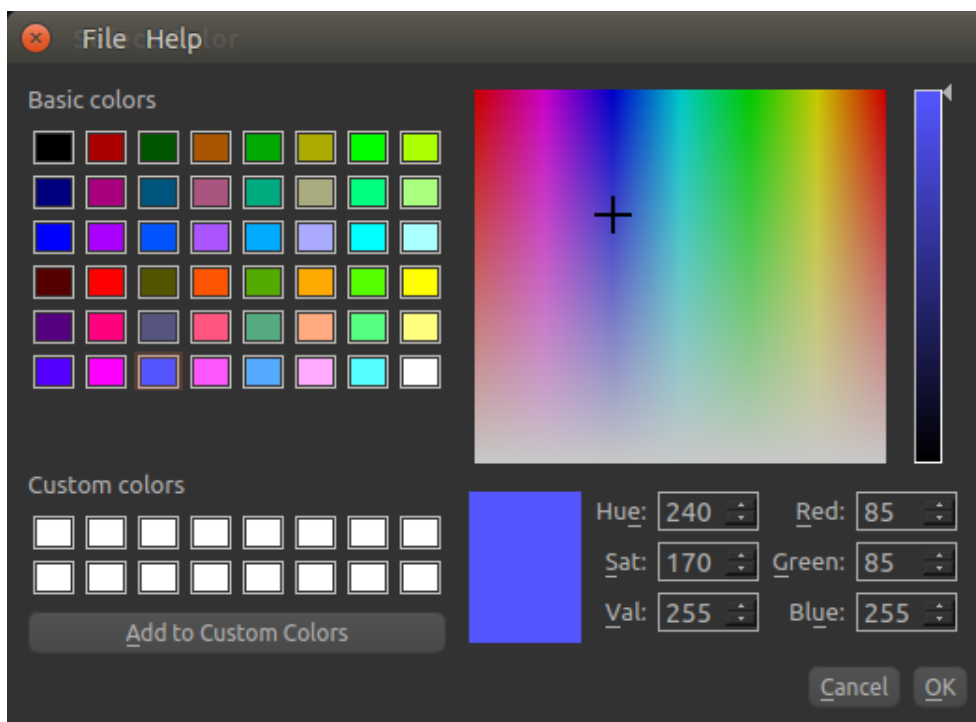


Fig. 6.22: Visualization options - Color table

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. 6.22), 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. 6.22), 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

### 6.5.4 Thumbnails tab

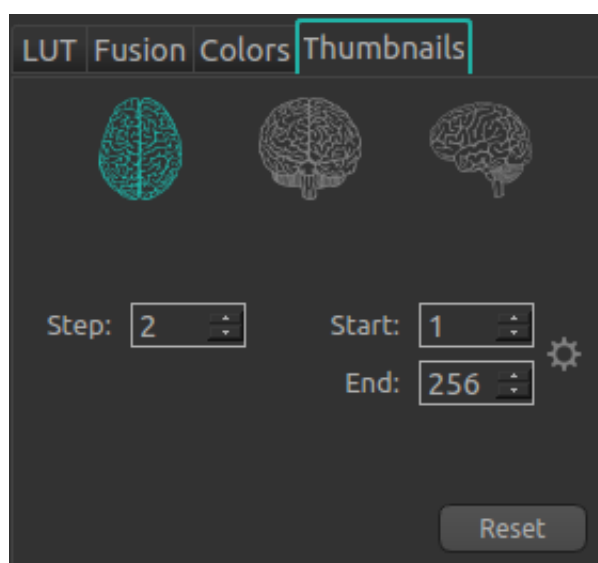





Fig. 6.23: Visualization options - Thumbnails

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 6.4.5).



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

- Click on : displays axial slices
- Click on : displays coronal slices
- Click on : 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

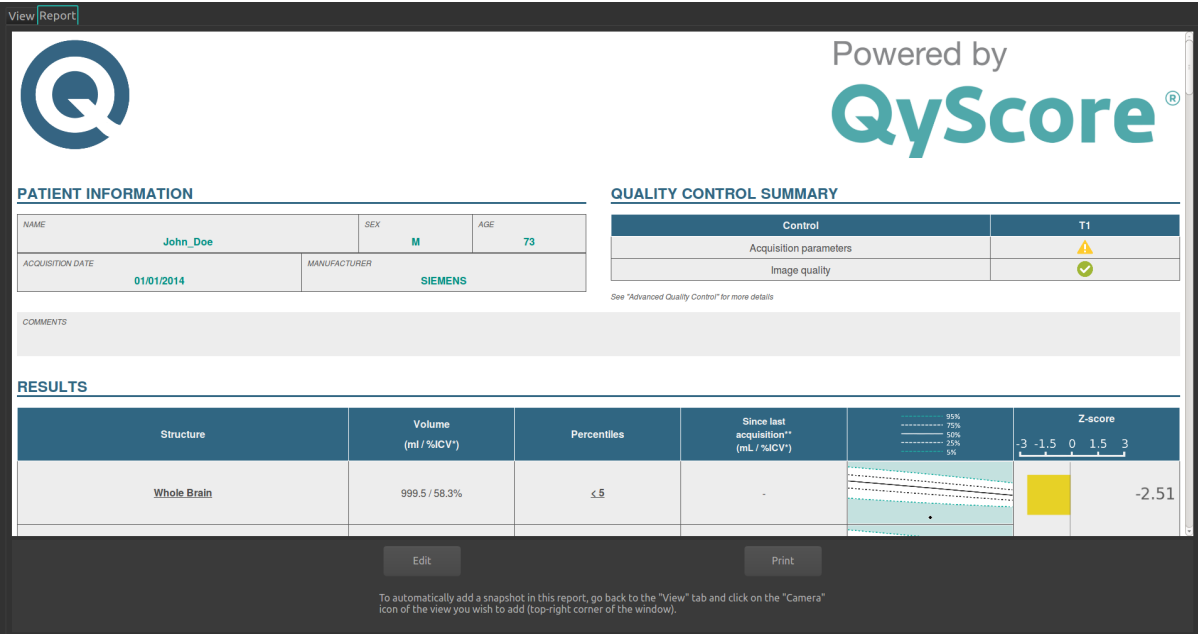
To automatically compute the range of non-background slices and display them:

- Click on 

To restore default settings:

- Click on the **Reset** button

## 6.6 Display and edit the summary report



The screenshot shows the 'View Report' tab in the QyScore software. The interface is divided into several sections:

- PATIENT INFORMATION:** A table with fields for NAME (John\_Doe), SEX (M), AGE (73), ACQUISITION DATE (01/01/2014), and MANUFACTURER (SIEMENS).
- QUALITY CONTROL SUMMARY:** A table comparing 'Control' and 'T1' parameters. 'Acquisition parameters' has a warning icon (yellow triangle), and 'Image quality' has a success icon (green checkmark).
- RESULTS:** A table with columns for Structure, Volume (ml / %CV\*), Percentiles, Since last acquisition\*\*, and Z-score. The 'Whole Brain' structure is highlighted with a yellow background, showing a volume of 999.5 / 58.3%, a percentile of <math>\leq 5</math>, and a Z-score of -2.51. A Z-score scale from -3 to 3 is shown above the Z-score column.

At the bottom of the report, there are 'Edit' and 'Print' buttons, and a note: 'To automatically add a snapshot in this report, go back to the "View" tab and click on the "Camera" icon of the view you wish to add (top-right corner of the window).'

Fig. 6.24: Report tab

To display the report:

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

### 6.6.1 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. 6.5)

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.

## 6.6.2 Print the report

To print the report:

- Display the report
- Click on **Print**



---

## Web-based results visualization interface

---

### 7.1 Global presentation

This web-based visualization interface is designed to view the results computed by the analysis server. It contains three pages:

- A login page
- A general page for:
  - The management of analyses:
    - \* Launch new analyses
    - \* Monitor launched analyses
  - The visualization of the results:
    - \* Interacting tools to navigate in the MR volumes, segmented structures and corresponding statistics
    - \* Tools to view and download the summary report that contains the analysis results
- An account management page for users administration

#### 7.1.1 Login page

You can connect to the interface through the login page. See [3.3](#) for more information.

#### 7.1.2 Visualization page

Once logged onto the interface, the visualization page is displayed.

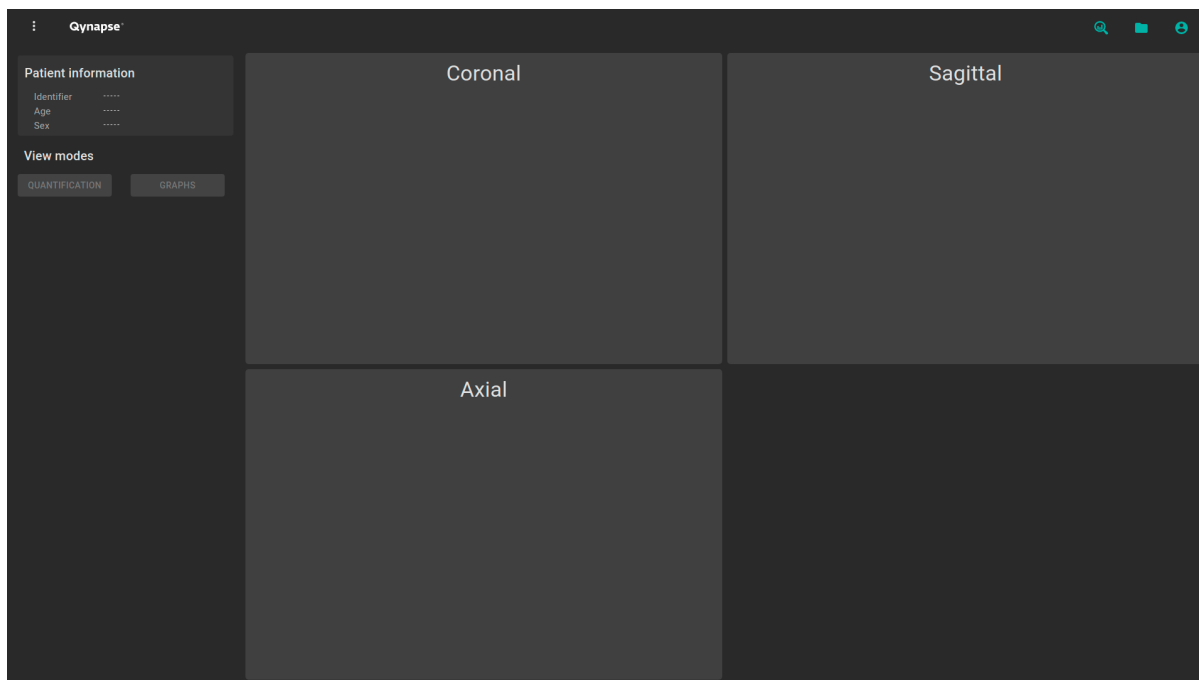


Fig. 7.1: Web-based interface visualization page

After loading patient data (as described in chapter 7.2):

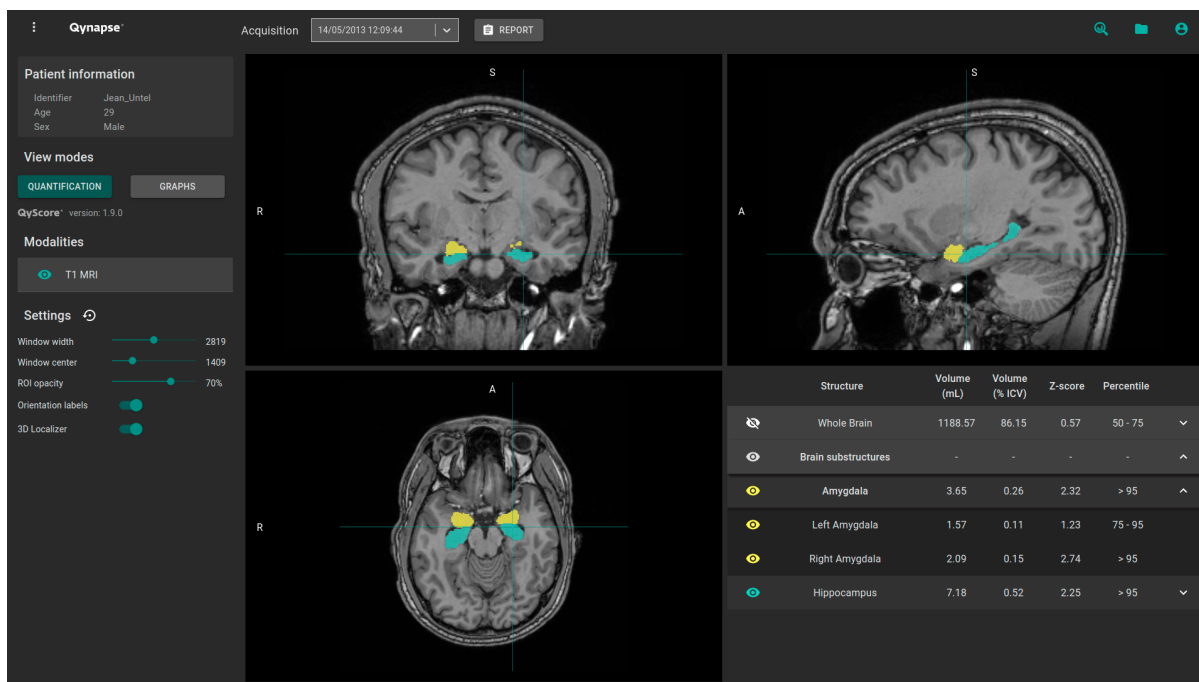






Fig. 7.2: Web-based interface visualization page - Patient loaded

The top bar is divided into several sub-parts:

- *More information* menu: accessible by clicking on the  icon, it provides information about the interface
- *Acquisition(s)* menu: to choose the study exam to display for the selected patient

- *Report* menu: accessible by clicking on the **Report** icon, it allows you to display and download the summary of analysis results
- *Analyses* menu: accessible by clicking on the  icon, it allows you to launch or monitor analyses
- *Load patient* menu: accessible by clicking on the  icon, it allows you to load patient data for visualization
- *Account management* menu: accessible by clicking on the  icon, it allows you to manage the users' accounts


The control panel on the left-hand side is divided into several sub-parts:

- *Patient information*: information on the selected patient
- *View modes*: to switch between view modes (default is *Quantification*)
- *Modalities*: to choose the displayed imaging modality
- *Settings*: to modify visualization options for better visual confort

The viewing part on the right-hand side contains 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.

### 7.1.3 Account management page


Administrators can access this page by clicking on the  icon, then on **Manage account**.

They can create new users or delete existing users of their organization.

## 7.2 Select patient data

### 7.2.1 Choose a patient to load


Follow the steps:

- Click on the  icon
- Click on **Select a database...** to select the relevant database
- Click on **Select a center...** to select the relevant center
- Click on **Type a patient ID...** to filter the patients according to their IDs
- Click on a patient's name to select them
- Click on **Download** to load the selected patient onto the interface
- Click on **Cancel** to cancel the procedure and close the window



It may be necessary to re-open the window if new analyses have been performed while it was opened.

## 7.2.2 Change the acquisition to display

Once a patient is loaded onto the interface, the last study that has been analyzed is displayed. To display another study of the selected patient, click on the  icon of the *Acquisition(s)* drop-down menu and select the corresponding study date.

## 7.3 General visualization

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

### 7.3.1 Browsing the volumes

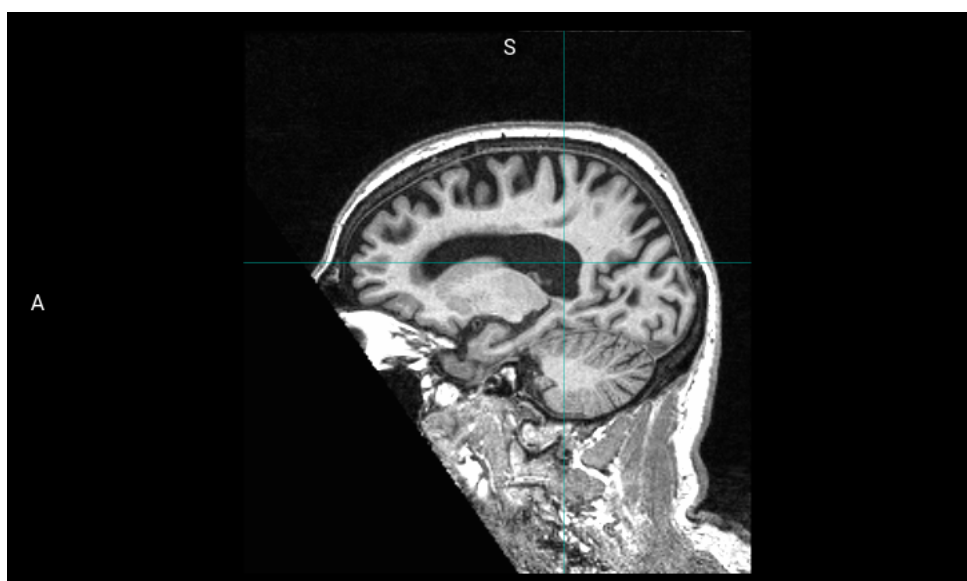


Fig. 7.3: Standard visualization window

The window contains:

- the volume,
- orientation labels: R for Right, S for Superior, A for Anterior,
- a 3D cursor that indicates the point on which the windows are adjusted.

#### 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 click.
- Scroll: changes the slice to display
- Long middle-click: moves the volume in the window
- Right-click: zoom in/out the volume. Also work with a long click.



### 7.3.2 View imaging modalities

Imaging modalities that can be displayed are indicated 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:

- Click on the modality name or on the  /  icon on its left-hand side.
- : modality displayed
- : modality masked

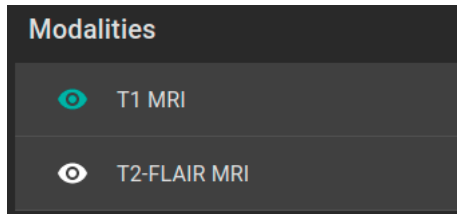


Fig. 7.4: Choice of modalities

### 7.3.3 View segmented structures







	Structure	Volume (mL)	Volume (% ICV)	Z-score	Percentile	
	Whole Brain	1188.57	86.15	0.57	50 - 75	▼
	Brain substructures	-	-	-	-	▲
	Amygdala	3.65	0.26	2.32	> 95	▲
	Left Amygdala	1.57	0.11	1.23	75 - 95	
	Right Amygdala	2.09	0.15	2.74	> 95	
	Hippocampus	7.18	0.52	2.25	> 95	▼



Fig. 7.5: Choice of segmented structures

The list of segmented structures that can be displayed is indicated in the special window. 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 (e.g.: *Brain substructures*)
  - Whole structure (e.g.: *Amygdala*)
    - \* Lateral structure (e.g.: *Left Amygdala*)

To display/hide a whole structure in the table:

- Click on the group name or the  /  icon on the right-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 structure name or the  /  icon on the right-hand side of the whole structure.





### View the segmentations

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





To display/hide a group of structures:

- Click on 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  /  icon on its left-hand side: the structure is either displayed or hidden (both sides, if applicable).
- : indicates that at least one side of the structure is displayed.
- : indicates that the structure is hidden.

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

- If it does not appear in the table: see previous section
- Click on the  /  icon on its left-hand side.
- : indicates that the side is displayed.
- : indicates that the side is hidden.

### View the numerical results

Numerical results can be viewed in the special window when the *Quantification* mode is selected :

- 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).

---

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

---

## 7.4 Switch view modes

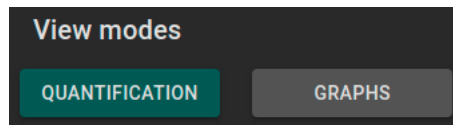


Fig. 7.6: View modes

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

Available modes are described hereafter.

### 7.4.1 Quantification mode



Fig. 7.7: Quantification mode

This is the default mode.

It displays the standard visualization of segmented structures and associated statistics, as described in chapter 7.3.

To enter the mode:

- Click on the **Quantification** button

The special window displays a table that contains:

- the list of the segmented structures that can be displayed,
- the numerical results related to these structures.

## 7.4.2 Graphs mode



Fig. 7.8: *Graphs mode*

This mode enables you to 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 a graph of comparison with normative data for the selected structure.

---

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

---

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.

## Select a graph to display

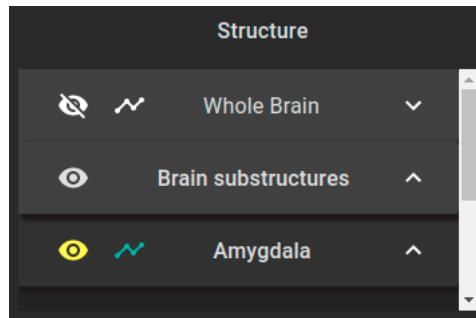



Fig. 7.9: Choice of displayed graph

The list of structures which graphs can be displayed is indicated in a table of the control panel. They are grouped in the same way as described in chapter 7.3.3.

To select the graph of a whole structure in the table (if applicable):

- Click on the  icon on the right-hand side of the whole structure.

To select the graph of a lateral structure in the table (if applicable):

- Click on the  icon on the right-hand side of the lateral structure.

## 7.5 Change visualization settings

Visualization settings are available via the *Settings* section of the control panel.

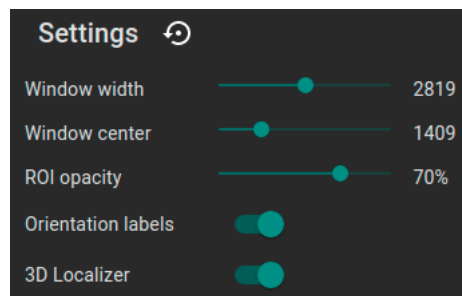


Fig. 7.10: Visualization settings

Changing the settings has a direct consequence on the displayed volume in standard windows. Available settings are described hereafter.

### 7.5.1 *Window width and Window center*

These settings enable you to modify the intensity range of the displayed modality.

To change the intensity range:

- Long click on *Window width* or *Window center* sliders

### 7.5.2 *ROI opacity*

To change the ROI opacity:

- Long click on the *ROI opacity* cursor

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

### 7.5.3 *Orientation labels*

To enable/disable the display of orientation labels:

- Click on the *Orientation labels* switch button


### 7.5.4 *3D Localizer*

To enable/disable the 3D localizer:

- Click on the *3D Localizer* switch button

### 7.5.5 **Reset settings**

To restore default settings:

- Click on the  icon

## 7.6 Display the report

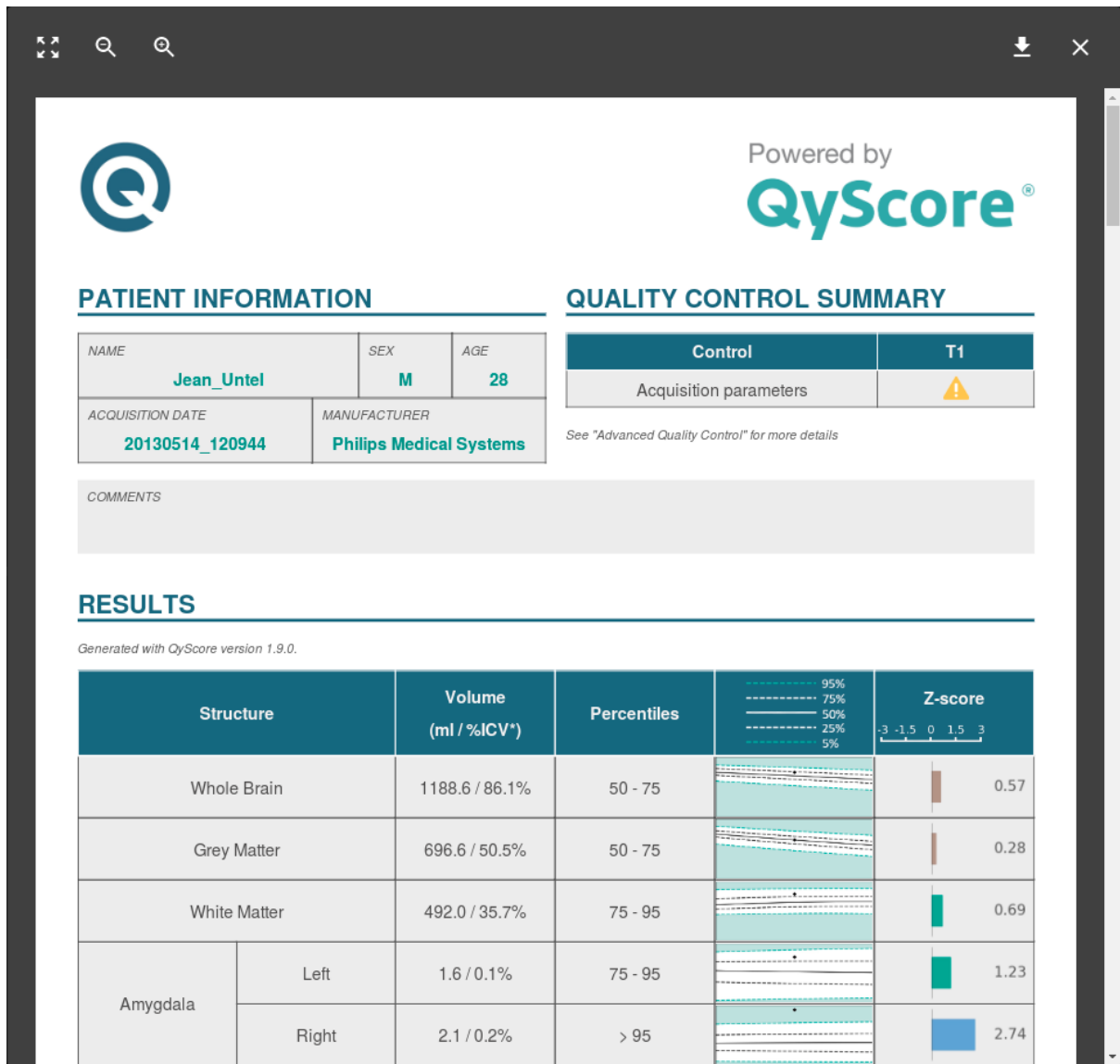




Fig. 7.11: Report visualization

To display the report:

- Click on the **Report** button
- Click on **View report**

### 7.6.1 Navigating the report


To navigate:

- Browse through the pages: scroll
- Zoom in the report: click on the  icon
- Zoom out the report: click on the  icon

- Reset the size of the report: click on the  icon


### Close the report

To close the report window, either:

- Click outside the report pop-up
- Click on the  icon

### 7.6.2 Download the report

To download the report, either:

- Click on the **Report** icon then click on **Download report**
- Click on the **Report** icon, then click on **View report**, then click on the  icon

The report will be saved in the “Downloads” folder of your computer.



Please refer to this section before requesting any further assistance.

## 8.1 I can't connect to the local data management interface

- Try again by double-clicking faster on the icon.
- If this does not solve the problem, open a terminal and type the commandline “select\_data\_to\_scan”.
- 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.

## 8.2 I can't connect to the local visualization interface

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

## 8.3 I can't access the web-based interface

- Make sure that the URL you entered is correct.
- If Qynapse's server is installed locally, make sure that it is turned on.
- If Qynapse's server is installed remotely, make sure your computer is connected to the Internet.

## 8.4 I can't send data from my DICOM server

- If Qynapse's 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.
- Make sure that the configuration settings are correct (IP address, port...).
- If this does not solve the problem, please refer to the user manual of your DICOM server.

## 8.5 I can't send data from the local data management interface

- Make sure that you are sending DICOM data.
- 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.

## 8.6 I can't send data from the web-based interface

- If Qynapse's server is installed locally, make sure that it is turned on.
- If Qynapse's server is installed remotely, make sure your computer is connected to the Internet.
- Make sure that you have uploaded a .zip (compressed format) of your DICOM files
- 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.

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

In any cases:

- Wait a couple of minutes more: depending on the image resolution, the processing time can be longer than expected.

Via your DICOM server or the local data management interface:

- 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.
- If this does not solve the problem, it may be due to a connection issue with the analysis server. The server is relaunched every minute in case of errors; wait a minute and try again.


Via the web-based interface, in the *Analyses monitoring* section:

- Wait a couple of minutes more: depending on the size of the uploaded files, the analyses can take more time to be displayed in the monitoring interface.

## 8.8 I can't find the exam that I wish to visualize

- Make sure that the filters applied in the searching tool are correct.
- In the web-based interface: if this analysis has been performed while the data loading window was opened, close and re-open the window.
- 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.

## 8.9 I can't access the account management page

- Make sure the session you are connected to is yours, by clicking on the  icon. Your username should be displayed on the top of the menu.
- If the message “Your are not authorized to see this page” is displayed, it is because only administrators can access to this page.



F

False colors, **10**

L

LUT, **10**

P

Percentile, **10**

S

Special window, **10**

Standard visualization window (or standard window), **10**

Z

Z-score, **10**