
QyScore User Manual

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Qynapse

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LEGAL NOTICES



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1.1 Copyright notice and trademark acknowledgements

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1.2 Indications for use

QyScore is intended for automated labeling, visualization and volumetric quantification of segmentable brain structures and lesions from a set of MR images. Volumetric data may be compared to reference percentile data.

1.3 Description and intended use

QyScore is intended for automated labeling, visualization and volumetric quantification of segmentable brain structures from a set of MR images. It is intended to automate the manual process of identifying, labeling and quantifying the volume of segmentable brain structures identified on MR images.

The software automatically provides segmentations and measures of brain structures and lesions from a set of MR images.

The software:

- retrieves DICOM MRI data (3DT1 and T2FLAIR series) from a DICOM server or folder,
- sends said data to Qynapse's analysis server for automated segmentation,
- enables the user to view the results (segmentations and numerical results) in a dedicated interface,
- enables the user to download a summary report of the results (segmentations and numerical results).

The outputs of the software include an electronic report and color overlays of the segmentation on the input images.

The visualization graphical interface allows the user to:

- Send imaging data to the QYNAPSE analysis server,
- Browse the segmentations and the measures,
- Compare the results of segmented brain structures to a reference healthy population,
- View and download the summary report.

This interface is a web application that must be used with a web browser.

QyScore integrates with leading RIS/PACS systems, and can be operated with any MRI scan from 1.5T and 3T scanners for T1 MRI processing, and 3T scanners for T2FLAIR MRI processing.

It is intended to be used by medical personnel or neuroimaging trained personnel, and is designed to be user-friendly and intuitive.

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

1.4 Global presentation

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

- Sending data directly from the DICOM server (PACS) (direct connection - see chapter 4.2),
- Using the web-based interface from your computer (see chapters 4.3 and 6)

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

To ensure proper function of the software, this operating system must not be modified.

The computers used to run QyScore components must be equipped with appropriate firewall and antivirus systems. If the hardware is not provided by QYNAPSE, it is the customer's responsibility to ensure that these items are installed.

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 size 1024*768 and resolution 132 PPI
- 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.

The computer running the interface must be equipped with appropriate firewall and antivirus systems. If they are not provided by QYNAPSE, it is the customer's responsibility to ensure that these items are installed.

Performances

QyScore automatically provides segmentations and measures of brain structures and lesions from a set of MR images.

Features include the computation of:

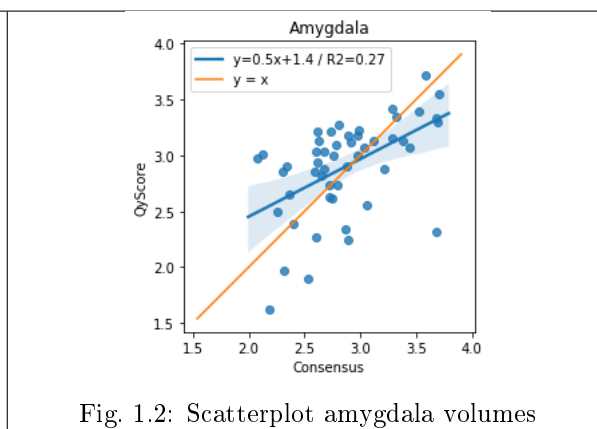
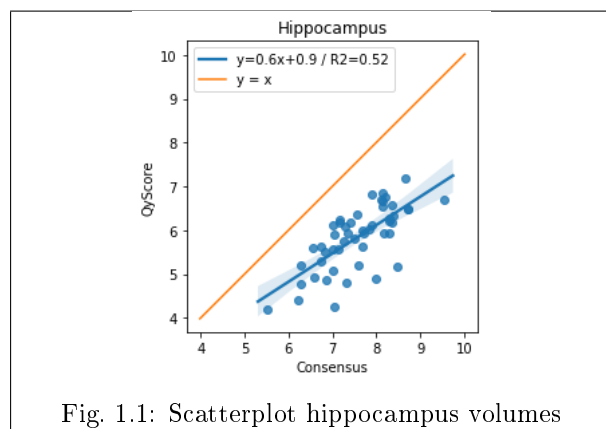
- Total brain volume (Grey and white matter)
- Hippocampal volume
- Amygdala volume
- White matter lesion load

The performances of QyScore were evaluated by comparing the segmentation accuracy with expert manual segmentations, using relevant metrics and thresholds that are widely used and accepted in the literature.

In the conditions detailed in section 1.6, the performances of the quantification methods on 3DT1 scans are the following:

Structure	# subjects	Age range	Sex (M - F)	Field strength (1.5T - 3T)	Dice (mean +/- std)	Relative volume error (% , mean +/- std)
Grey matter	30	20 - 90	16 - 14	15 - 15	0.86 +/- 0.02	7.02 +/- 3.86
White matter	30	20 - 90	16 - 14	15 - 15	0.90 +/- 0.02	4.71 +/- 4.61
Hippocampus	50	20 - 90	27 - 23	24 - 26	0.81 +/- 0.03	22.77 +/- 6.62
Amygdala	50	20 - 90	27 - 23	24 - 26	0.78 +/- 0.04	12.11 +/- 10.24

Note: QyScore tends to always overestimate grey matter volume. QyScore tends to underestimate white matter, especially when the volume is high.



Note: QyScore always underestimates the hippocampal volume.

The white matter lesion load is computed on T2FLAIR scans, paired with the corresponding 3DT1 scans. Only 3T scans are accepted for this measure. The performances were assessed per lesion load subgroups. Results are:

Subgroup	# subjects	Age range	Sex (M - F)	Type (2D - 3D)	Dice (mean +/- std)	Absolute volume error (mL, mean +/- std)
< 5mL	30	26 - 90	13 - 17	19 - 11	0.35 +/- 0.17	0.50 +/- 0.45
5 - 15 mL	26	29 - 84	14 - 12	17 - 9	0.68 +/- 0.08	1.84 +/- 1.69
15 - 30 mL	45	26 - 91	21 - 24	19 - 26	0.75 +/- 0.07	3.38 +/- 2.45
> 30 mL	29	25 - 91	12 - 17	15 - 14	0.79 +/- 0.07	7.58 +/- 4.87

In addition, for white matter lesion load quantification, the lesion-wise true and false positive rates are respectively 0.43 ± 0.21 and 0.46 ± 0.27 .

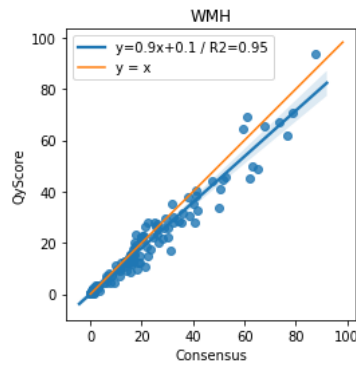


Fig. 1.3: Scatterplot WMH volumes

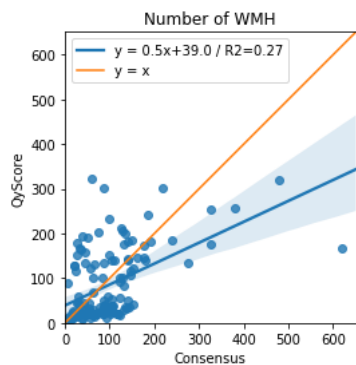


Fig. 1.4: Scatterplot WMH number

Note: QyScore is not intended for use in clinical scenarios that require evaluation of the number of the WMH.

The volumes provided by the software are indicated as absolute and relative (in % of intracranial volume) values.

1.5.2 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.

1.5.3 Safety

If a security breach is detected, the analysis server will be switched off by QYNAPSE to avoid potential fraudulent use. In that case, new data analysis won't be available, but prior results will remain available on the DICOM server.

1.6 Required imaging parameters

QyScore is designed to analyze several kinds of MRI data: non-injected T1 (1.5T or 3T), T2FLAIR 2D (3T), T2FLAIR 3D (3T). The required acquisition parameters are the following:

For T1 sequences:

	T1	
	Required	Tolerated
Voxel size in plane (mm)	[1, 1]	Min: [0.49, 0.49] 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

For T2FLAIR sequences:

	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)	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. See section `parameters` for more details.

In addition, a quick review of the MR data to be sent for analysis is recommended to avoid sending data with obvious imaging artifacts, such as:

- brain not fully covered
- severe aliasing
- bad grey/white contrast
- severe head motion
- severe dental and/or other metallic artifact

These artifacts could cause failure or incorrect segmentation of brain tissues.

1.7 Normative data

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

The normative database is composed of patients aged 18 to 88, except for white matter hyperintensities where patients are aged 53 to 83.

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 Contraindications

Data with gross imaging artifacts and/or motion should not be sent for analysis as they could cause failure or incorrect segmentation of brain tissues.

QyScore shouldn't be used in case of gross anatomical abnormalities, resections or tumors, as these conditions could cause failure or incorrect segmentation of brain tissues.

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

QyScore is not intended for use in clinical scenarios that require evaluation of the number of the WMH.

1.9 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.

When a brain structure volume is below the 5th percentile, it does not automatically indicate a diagnosis.

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 between 20 years old and 90 years old.

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.

1.10 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.

1.11 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 web-based user interface, by clicking the  icon and then **User Manual**

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.

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.

Double-click Press and release the primary mouse button twice. 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 “Comparison” mode, it indicates the correspondence 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 divides the population in 100 equally-sized groups (each percentile corresponds to 1 % of the population).

CONNECT TO QYSCORE

3.1 Global presentation

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

3.2 Login

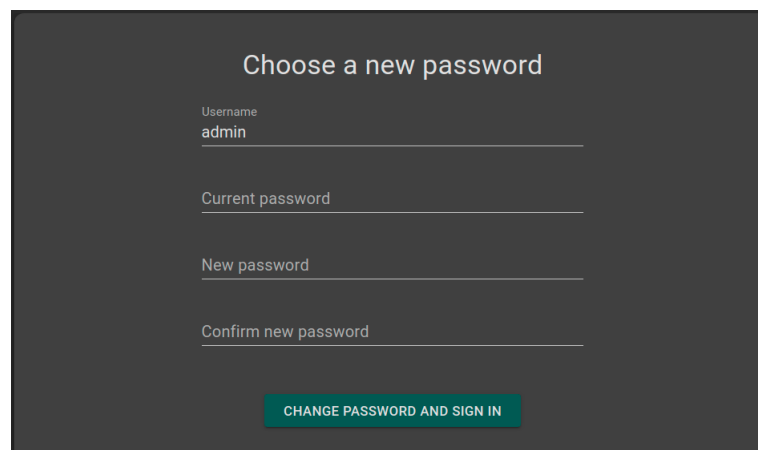
Enter your username and password in the corresponding fields. The password is initially given by your administrator or by QYNAPSE upon installation.

Click on **Sign in**.

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

3.2.1 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 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

3.4 Logout

To logout:

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

3.5 Forgotten password

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

SEND DATA

4.1 Global presentation

Data can be sent to QYNAPSE's analysis server:

- directly via your DICOM server (e.g. PACS)
- 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.

Note: 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.

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 chapter 6.

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 Web-based data management interface

4.3.1 Uploading data

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

- Click on the  icon

Or:

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

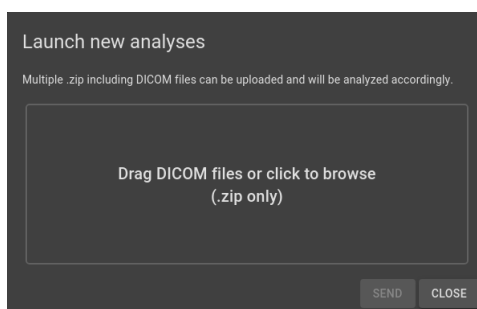


Fig. 4.1: Launch new analyses

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.

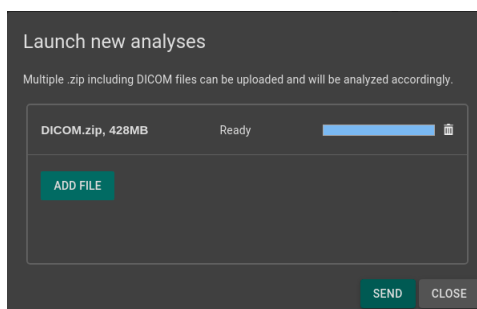


Fig. 4.2: Launch new analyses - Uploaded file

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.

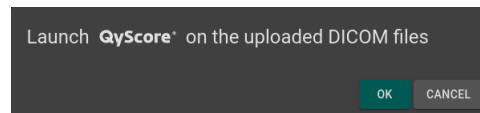


Fig. 4.3: Confirmation for sending data for analyses

- 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.

4.3.2 Analyses monitoring

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

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

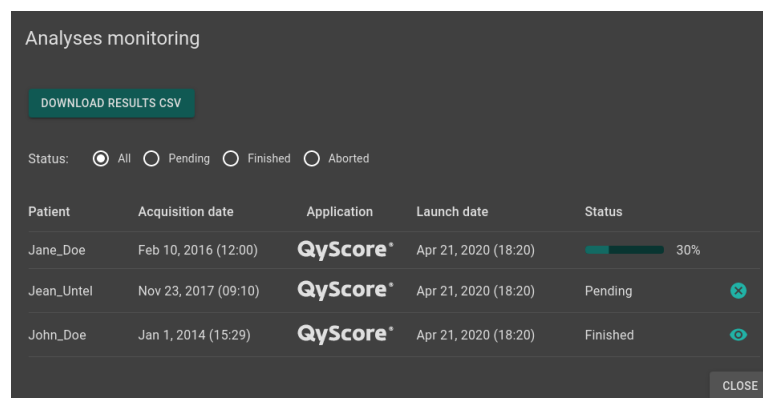


Fig. 4.4: Analyses monitoring

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.

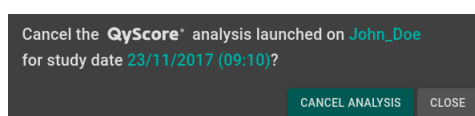


Fig. 4.5: Confirmation for analysis cancellation

- 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.

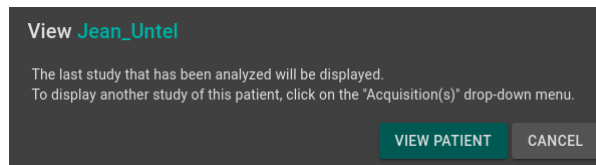



Fig. 4.6: Confirmation for loading a *Finished* analysis

- 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.

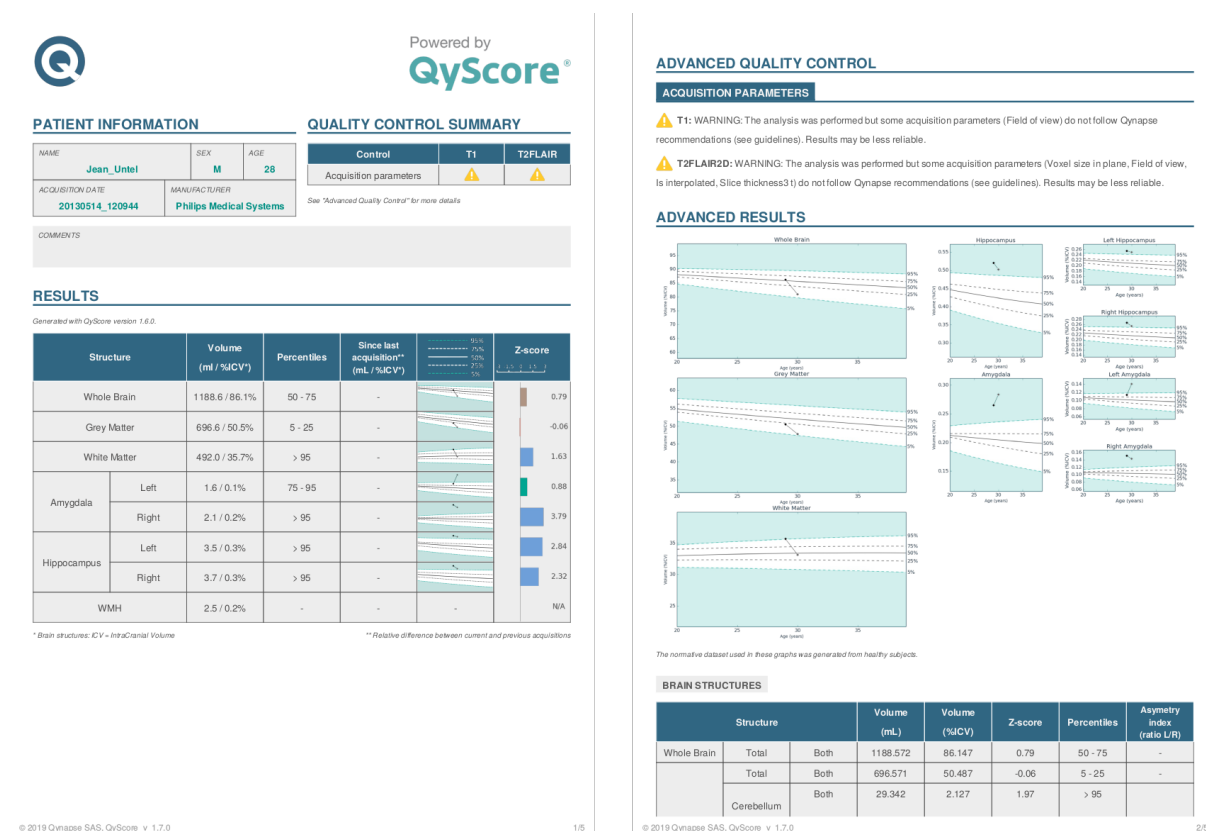


Fig. 5.1: Report

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).

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 the web-based visualization interface (see 6.6).

WEB-BASED RESULTS VISUALIZATION INTERFACE

6.1 Global presentation

This web-based visualization interface is designed to view the results computed by the analysis server. It contains four 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
- A user feedback page to review QyScore analyses

6.1.1 Login page

You can connect to the interface through the login page. See 3 for more information.

6.1.2 Visualization page

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

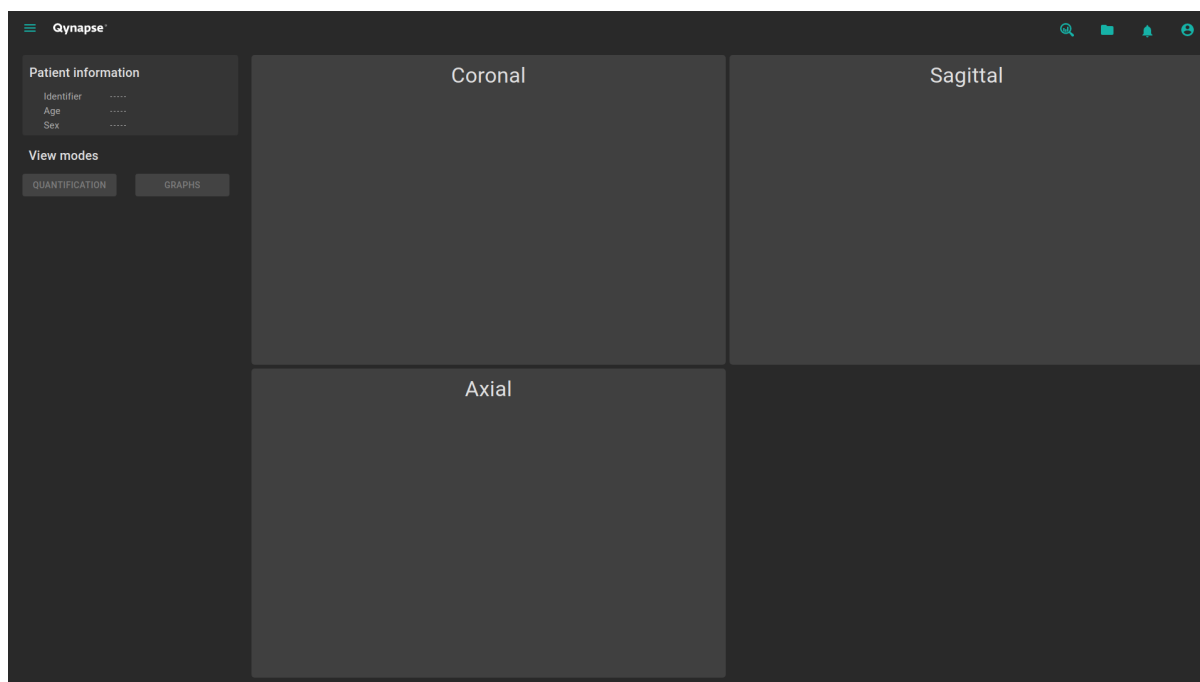


Fig. 6.1: Web-based interface visualization page

After loading patient data (as described in chapter 6.2):

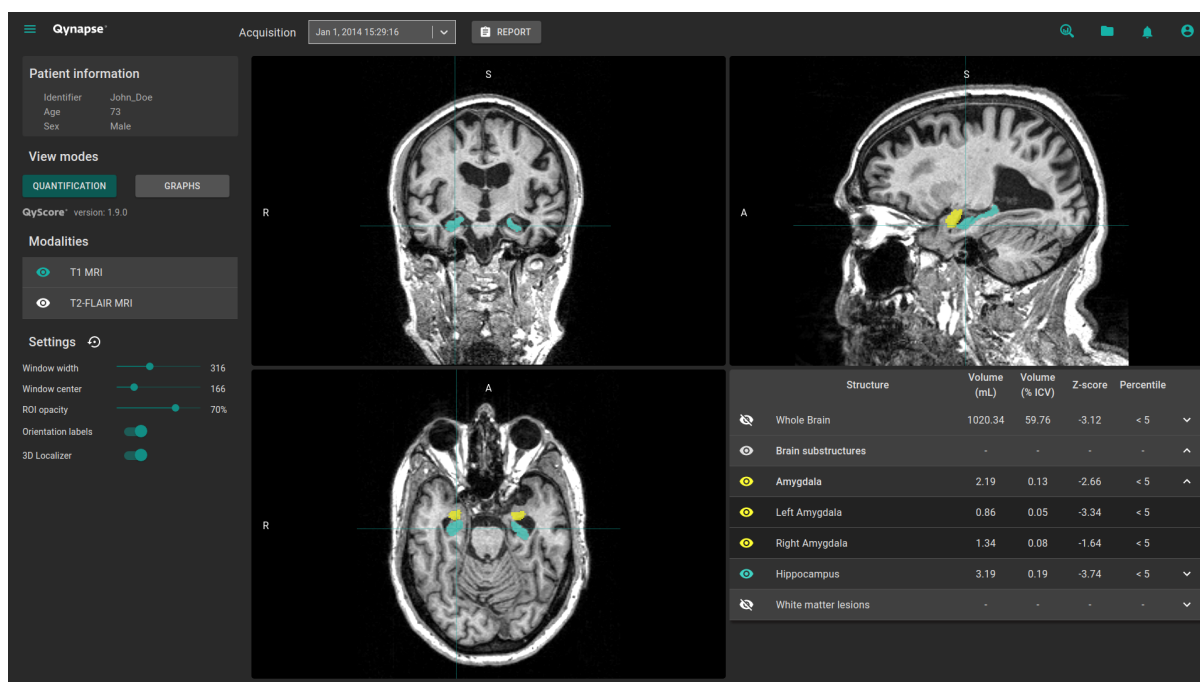







Fig. 6.2: Web-based interface visualization page - Patient loaded

The top bar is divided into several sub-parts:

- Side menu: accessible by clicking on the  icon, it provides access to different features:
 - In the *Analyses* section:
 - * **Launch new analyses** enables to start a new analysis by loading DICOM files

- * **Analyses monitoring** opens the analysis monitoring tool
- * **Analyses feedback** allows access to the page dedicated to user feedback on analyses
- In the *MRI visualization* section:
 - * **Viewer** allows you to go back to the visualization page
 - * **Load patient files** allows you to load analyzed patient data onto the interface
- **User manual** displays QyScore user manual
- **Shortcuts** displays keyboard and mouse shortcuts
- **About** displays information about QyScore

- *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
- *Launch analysis* window: accessible by clicking on the  icon, it allows you to launch a new analysis by loading DICOM files
- *Load patient files* window: accessible by clicking on the  icon, it allows you to load analyzed patient data onto the interface
- *Notifications* menu: accessible by clicking on the  icon, it allows you to consult the list of analyses for which feedback has not been provided
- *My account* menu: accessible by clicking on the  icon, it allows you to manage 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 comfort

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 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.

6.2 Select patient data


6.2.1 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.

6.2.2 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.

6.3 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.

6.3.1 Browsing the volumes



Fig. 6.3: 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.
- Double-click: set/unset the view to full size
- 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.

6.3.2 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

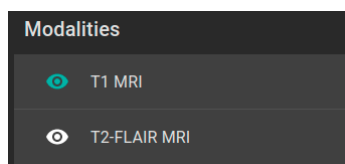


Fig. 6.4: Choice of modalities

6.3.3 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. 6.5: 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.

6.4 Switch view modes

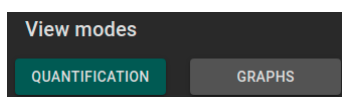


Fig. 6.6: View modes

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.

6.4.1 Quantification mode

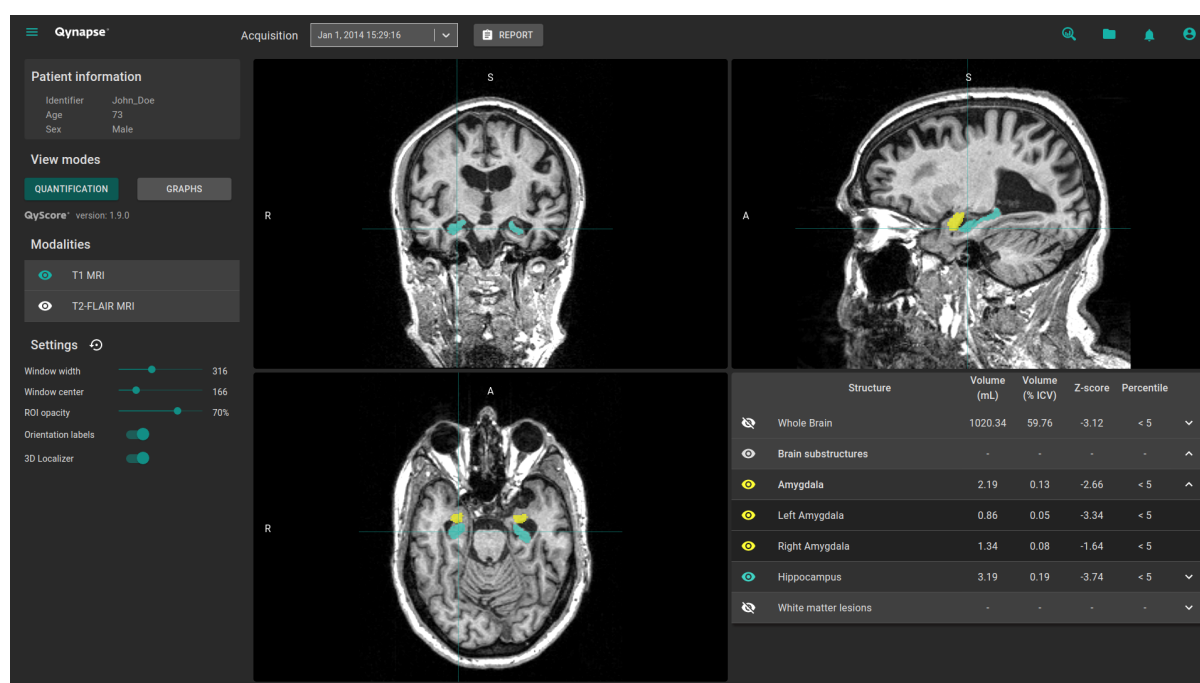


Fig. 6.7: Quantification mode

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 **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.

6.4.2 Graphs mode

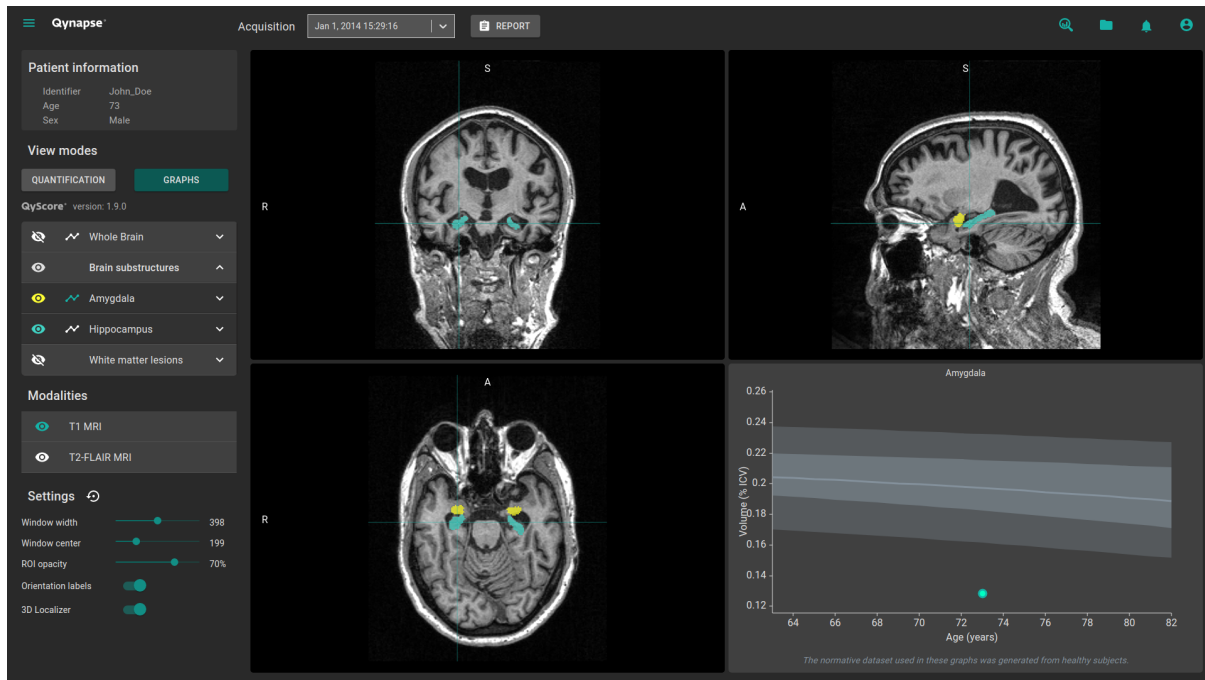


Fig. 6.8: *Graphs* mode

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

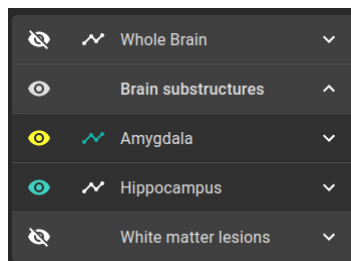




Fig. 6.9: Choice of displayed graph

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 6.3.3.

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.

6.5 Change visualization settings

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

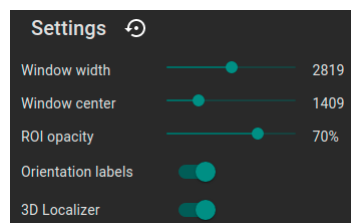


Fig. 6.10: Visualization settings

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

6.5.1 *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

6.5.2 *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.

6.5.3 *Orientation labels*

To enable/disable the display of orientation labels:

- Click on the *Orientation labels* switch button


6.5.4 *3D Localizer*

To enable/disable the 3D localizer:

- Click on the *3D Localizer* switch button

6.5.5 **Reset settings**

To restore default settings:

- Click on the  icon

6.6 Display the report

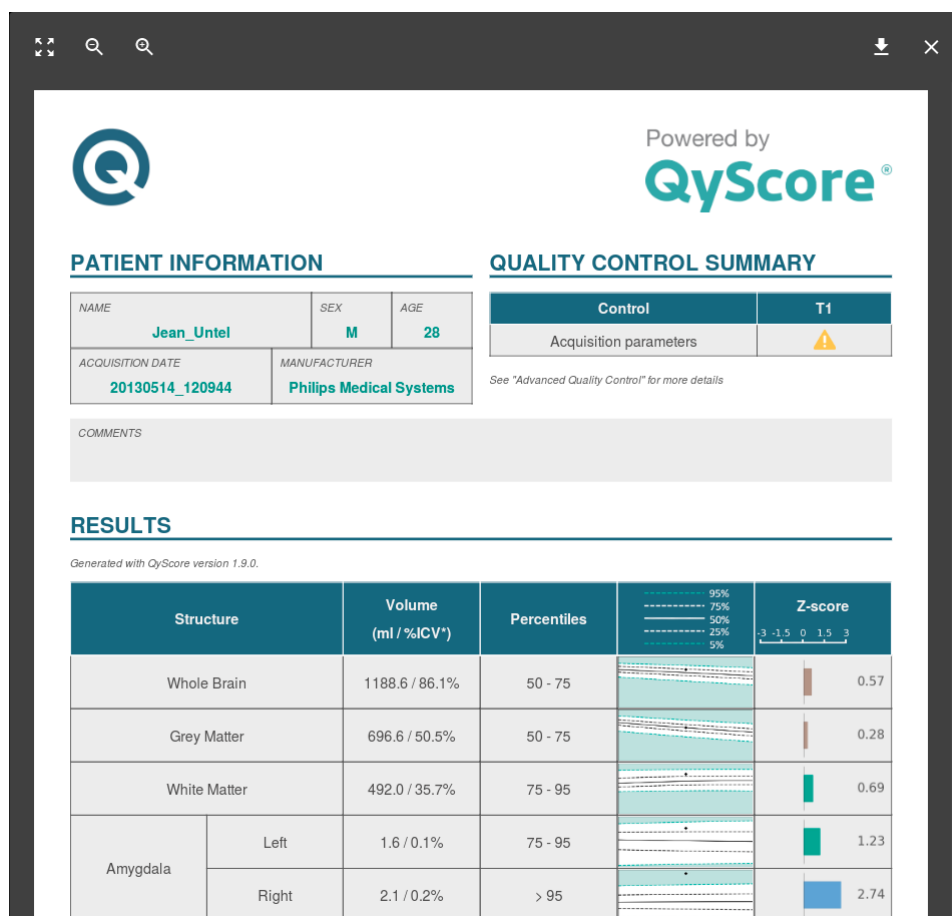





Fig. 6.11: Report visualization

To display the report:

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


6.6.1 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

6.6.2 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.


USER FEEDBACK ON ANALYSES

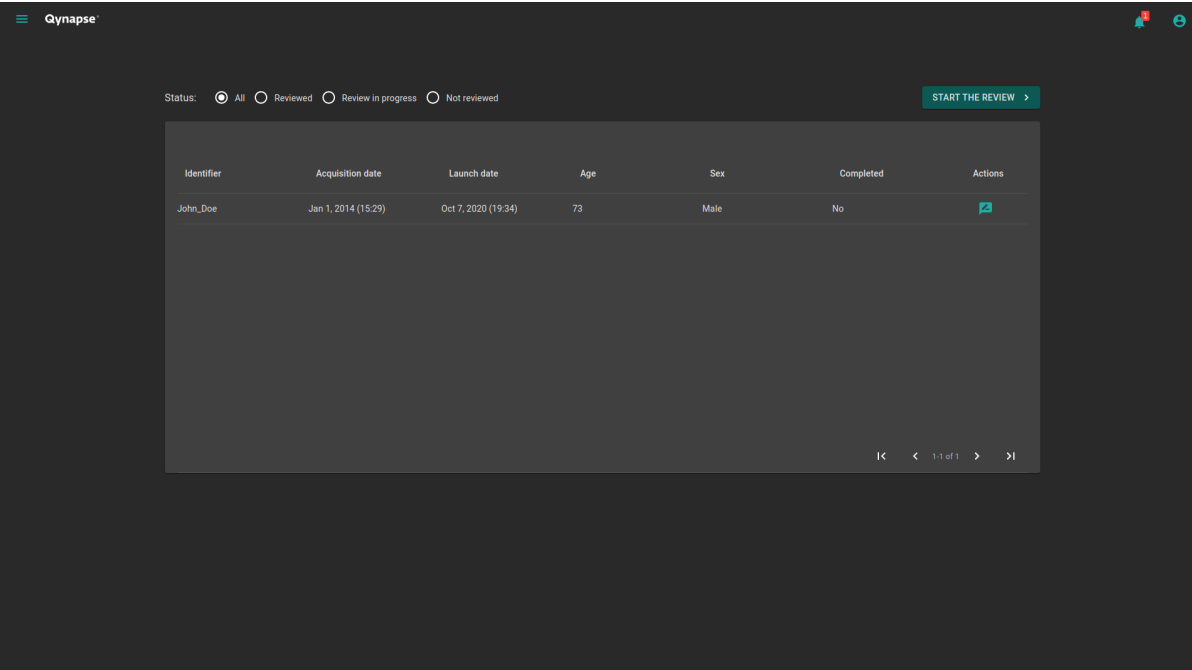
This page allows you to manage your feedback on QyScore analyses.

To access the user feedback tool :

- Click on the  icon
- Click on **Analyses feedback**

Or:

- Click on the  icon
- Click on **View all**



The screenshot shows the Qynapse user feedback list interface. At the top left, there is a hamburger menu icon and the text 'Qynapse'. At the top right, there are notification and user profile icons. Below the header, there is a status filter section with radio buttons for 'All' (selected), 'Reviewed', 'Review in progress', and 'Not reviewed'. To the right of the filter is a 'START THE REVIEW' button. The main content is a table with the following columns: Identifier, Acquisition date, Launch date, Age, Sex, Completed, and Actions. A single row is visible for 'John_Doe' with acquisition date 'Jan 1, 2014 (15:29)', launch date 'Oct 7, 2020 (19:34)', age '73', sex 'Male', and 'No' completed. The Actions column contains a feedback icon. At the bottom right of the table, there are navigation icons and the text '1 of 1'.


Identifier	Acquisition date	Launch date	Age	Sex	Completed	Actions
John_Doe	Jan 1, 2014 (15:29)	Oct 7, 2020 (19:34)	73	Male	No	

Fig. 7.1: Your feedback list

User feedback are listed by analyses:

- *Identifier*: the patient identifier
- *Acquisition date*: the MRI date of acquisition
- *Launch date*: the date of QyScore analysis

- *Age*: the patient age at the acquisition date
- *Sex*: the patient sex
- *Completed*: the feedback status


7.1 Filter user feedback

To filter user feedback depending on the status:

- Click on the relevant option:
 - **All**: display all analyses
 - **Reviewed**: display analyses on which a feedback has been provided
 - **Review in progress**: display analyses on which a feedback is still in progress
 - **Not reviewed**: display analyses on which no feedback has been provided yet

7.2 Give a feedback on an analysis

To give a feedback on a given analysis:

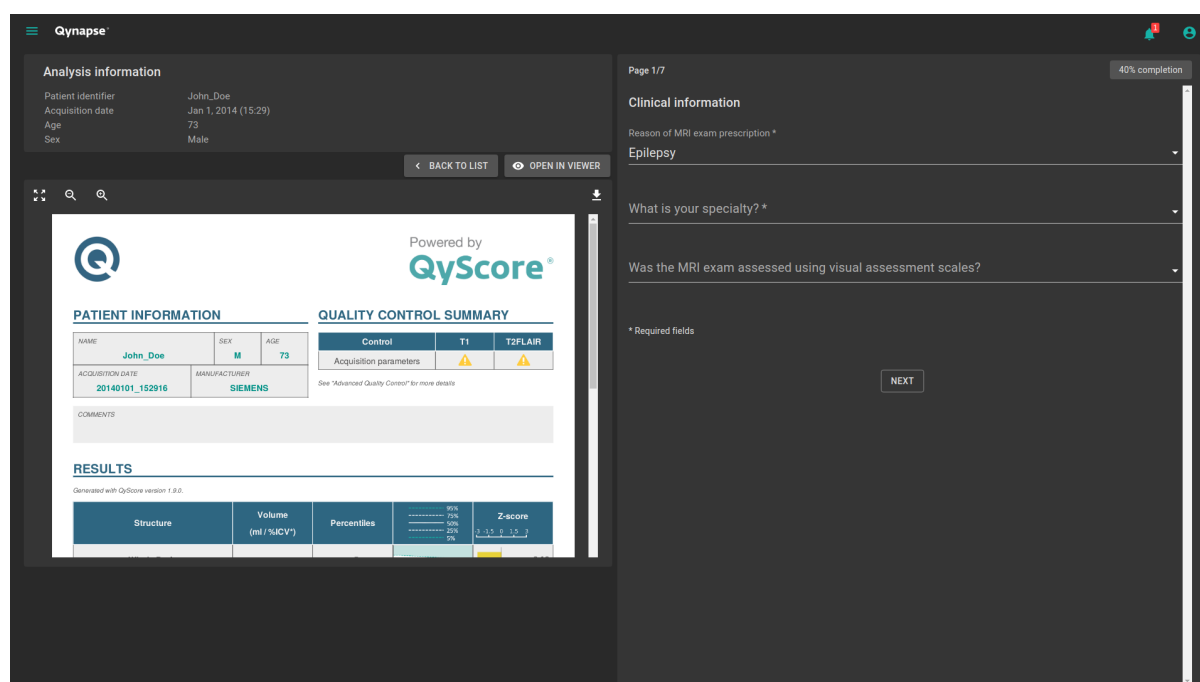
- Click on the  icon of the corresponding row

Or:

- Click on **Start the review**

Note: If **Start the review** has been clicked, the review will start on the oldest analysis.

The user feedback form is displayed.



The screenshot shows the Qynapse user feedback form. It is divided into two main panels. The left panel, titled 'Analysis information', contains patient details: Patient identifier (John_Doe), Acquisition date (Jan 1, 2014 (15:29)), Age (73), and Sex (Male). Below this is a 'QUALITY CONTROL SUMMARY' table with columns for Control, T1, and T2FLAIR. The 'Control' column shows 'Acquisition parameters' with a yellow warning icon. The 'T1' and 'T2FLAIR' columns also show yellow warning icons. The right panel, titled 'Clinical information', shows 'Page 1/7' and '40% completion'. It contains a dropdown menu for 'Reason of MRI exam prescription *' with 'Epilepsy' selected. Below it is another dropdown menu for 'What is your specialty? *'. A 'NEXT' button is located at the bottom right of the form.

Fig. 7.2: User feedback form

This page is divided into two parts:

- On the left, information about QyScore analysis
 - An information section about the analysis
 - A toolbar:
 - * **Back to list** allows you to go back to the list of feedback
 - * **Open in viewer** allows you to browse analysis results in the visualization page in a new tab of the web browser
 - An analysis report
- On the right, the user feedback form

7.2.1 Fill the form

To fill the form, select or fill fields on each page.

To go to the next page:

- Click on **Next**

To go back to the previous page:

- Click on **Previous**


Note: To go to the next page, all required fields must be filled. If you missed some of them and click on **Next**, they will be displayed in red.

Note: For more information about how to fill the form, you can contact support@qynapse.com.


7.3 Download the CSV of user feedback

Depending on your contract with QYNAPSE, you may be asked to provide the CSV of user feedback, at a defined frequency.

To do this:

- Click on the  icon in the list of user feedback
- Click on **Export as CSV**

Then send the CSV to support@qynapse.com.

Note: The  icon does not appear if you have not given a feedback yet, or if your feedback is incomplete.

TROUBLESHOOTING

Please refer to this section before requesting any further assistance.

8.1 I can't access the visualization 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.

8.2 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.

8.3 I can't send data from the visualization 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.

8.4 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.

8.5 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.

8.6 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.

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