QyScore Documentation

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Qynapse

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Contents

Legal notices

QYNAPSE	QyScore
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1.1 Copyright notice and trademark acknowledgements

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

1.3 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 should not be used in case of gross anatomical abnormalities, resections or tumors, as these conditions could cause failure or incorrect segmentation of brain tissues.

1.4 Target patient population

QyScore provides reliable and reproducible segmentations and measures of brain structures for patients older than 18 years old. There are no specific diseases. QyScore can analyse any structural MRI of the brain compatible with the recommended protocol.

1.5 Intended users

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

These users are radiologists, neuroradiologists, neurologists, geriatricians, psychiatrists.

These users need to be able to visualize information displayed with the color codes in a dark or light room with multiple screen environment. Before using the software, the user must have completed a initial training program. This program ensures the training of other users.

1.6 Description

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.

The software:

- retrieves imaging data from a DICOM server or folder,

- sends these data to Qynapse's analysis server,

- enables the user to view the results (segmentations and numerical results) in a dedicated interface,

- enables the user to download a summary report of the results (segmentations and numerical results),

- enables the user to get the results in a structured manner into a DICOM SR that can be use into other informations systems.

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.

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.

1.7 Clinical Benefits

When used as intended and in accordance with this user manual, no direct or immediate clinical benefit is claimed for QyScore. The software does not provide diagnostic or therapeutic recommendations. The clinical benefit is indirect: QyScore provides accurate, standardised, and quantitative MRI information that supports clinical decision-making by qualified healthcare professionals. The final patient outcome depends on further diagnostic and/or therapeutic steps.

Operational benefits for users include:

- Accuracy of quantitative measures comparable to expert manual methods

- Reproducibility consistent with or superior to state-of-the-art automated tools

- Objective and reliable longitudinal quantification for follow-up assessments

- Efficiency and standardisation gains in reporting workflows

Final clinical decisions remain under the sole responsibility of the clinician.

1.8 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)

1.9 Technical description

1.9.1 Installation

QyScore

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

For less than 100 analyses/month:

Greater or equal to:

- RAM: 12 GB

- CPU: architecture x86_64, 6 vCPU minimum

- 500 GB disk capacity

For more than 100 analyses/month:

Greater or equal to:

- RAM: 24 GB

- CPU: architecture x86_64, 12 vCPU minimum

- 3 TB disk capacity

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: 4

- 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.

1.9.2 Compatibility with other devices

QyScore retrieves DICOM MRI data from a DICOM server or the computer and delivers DICOM data (images and statistics).

1.9.3 Performances

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

- Grey matter

- White matter

- Lobes

- Hippocampus

- Amygdala

- White matter hyperintensities

In the conditions described in chapter 1.10, the performances of the volumetric quantification methods can be obtain by simple request to support@qynapse.com.

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

1.9.4 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.

This device is designed for an operating lifetime of up to 3 years, during which Qynapse provides maintenance and support to ensure optimal performance and compliance. The exact duration is defined as the shorter period between installation date + 3 years and the timeframe specified in the signed Commercial Contract, whichever applies.

1.9.5 Deactivation, Uninstallation and Data Disposal

Deactivation/uninstallation of QyScore is performed by QYNAPSE upon request to support@qynapse.com.

For deactivation, QYNAPSE disables the access to the viewer and the mechanism that sends results back to PACS are disabled.

For uninstallation, QyScore is uninstalled and user data are deleted.

The customer remains responsible for any data stored outside the device, such as PACS or institutional archives/backups. Upon completion, the customer receives a confirmation that the software has been deactivated or uninstalled and that user data deletion has been performed.

1.9.6 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.

1.10 Required imaging parameters

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

	T1	
	Required	Tolerated
Voxel size in plane (mm)	[1, 1]	Min: [0.43, 0.43] Max: [1.5, 1.5]
Field of view (mm)	x: [152, 340] y: [220, 340] z: [152, 340]	x: [144, 340] y: [170, 340] z: [132, 340]
Slice thickness (mm)	1	Min: 0.68 Max: 2
Gap between slices (mm)	0	Min : -1 Max : 0
Interpolation	No	Yes
Acquisition direction	Sagittal	Axial, Coronal
Acquisition type	3D	2D with isotropic voxel
Field strength	1.5T, 3T	1.5T, 3T

	T2FLAIR2D		T2FLAIR3D	
	Required	Tolerated	Required	Tolerated
Voxel size in plane (mm)	[1, 1]	Min: [0.43, 0.43] Max: [1.1, 1.1]	[1, 1]	Min: [0.43, 0.43] Max: [1.1, 1.1]
Field of view (mm)	x: [152, 340] y: [220, 340] z: [152, 340]	x: [144, 500] y: [170, 340] z: [132, 340]	x: [152, 340] y: [220, 340] z: [152, 340]	x: [144, 340] y: [170, 340] z: [132, 340]
Slice thickness (mm)	3.3	Min: 2 Max: 5	1	Min: 0.8 Max: 2.0
Gap between slices (mm)	0	Min : 0 Max: 1	0	Min: -1 Max : 0
Interpolation	No	Yes	No	Yes
Acquisition direction	Axial	Coronal, Sagittal	Sagittal	Axial, Coronal
Acquisition type	2D	2D	3D	3D
Field strength	1.5T, 3T	1.5T, 3T	1.5T, 3T	1.5T, 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.

1.11 Normative data

The statistics generated by QyScore (Z-scores and percentiles) are computed by comparison to results obtained on a normative database of healthy subjects.

The database is a concatenation of the following databases:

Database	Mean age	Std age	Minimum age	Maximum age	Healthy subjects	Females	Males	% males
1	59.5	14.7	20	89	805	436	369	46
2	67.1	9.5	43	97	720	397	323	45
3	48.7	16.5	20	86	563	313	250	44
4	38.5	18.3	18	84	468	238	230	49
5	52.2	23.5	20	94	306	191	115	38
6	27.5	4.8	23	38	172	87	85	49
7	34	12.8	18	72	155	102	53	34
8	31.3	8.7	21	50	122	57	65	53
9	78.2	6.8	60	93	57	35	22	39
10	67.1	8.5	46	85	47	26	21	45

1.12 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 fully automated segmentations computed by QyScore can be negatively impacted by image quality (such as motion artefact) and significant neuromorphological abnormalities (such as emerging tumors) as highlighted in section 1.3 above. Therefore, in the presence of such issues, there may be some mis-segmentation and it is recommended the expert clinician visually assess the accuracy of these segmentation overlays to confirm the accuracy of the volume outputs reported.

⚠ 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 and maintenance 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.

⚠ The installation should be supervised by QYNAPSE personnel.

1.13 Reporting of Serious Incidents

In the event of a serious incident related to the use of QyScore, users must notify without any delay:

- the manufacturer (Qynapse, via support@qynapse.com), and
- the Competent Authority of the EU member state where the user or patient is located.

A serious incident refers to any event that has resulted, or could result, in serious public health threat, death or unanticipated serious deterioration in state of health of the patient or user.

1.14 Electronic instructions for use

Please note that QyScore software is supplied with electronic instructions for use. The 🔲 icon signals that additional information or essential instructions are available in the user manual.

These instructions may be accessed in the following ways:

- **Through the web-based user interface, by clicking the ≡ icon**
    - by clicking on **About** and then on the 🔲 icon.
    - by clicking **User Manual**.
- From the online Qynapse document library: https://manuals.qynapse.com.

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: 2-10 rue d'Oradour-sur-Glane, 75015 Paris, France.

1.14.1 EUDAMED

The European database on medical devices (EUDAMED) public website can be found on the following link: https://ec.europa.eu/tools/eudamed.

Conventions

The following conventions are used throughout this manual.

2.1 Mouse

Click
> Press and release the primary mouse button. If you are left-handed, 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 left-handed, 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 left-handed, 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 left-handed, 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.

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'll have to use the forget password procedure.
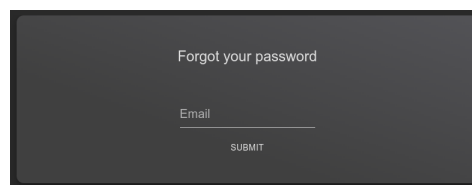
Fig. 3.1: Forgot your password

To do so:

- *Email*: type your email
- Click on **Submit**
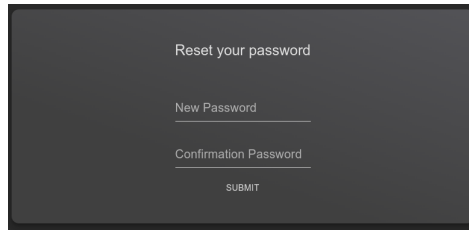
Fig. 3.2: Reset your password

To do so:

- *New password*: type your new password
- *Confirm new password*: confirm your new password
- Click on **Submit**

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.

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.

> 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**
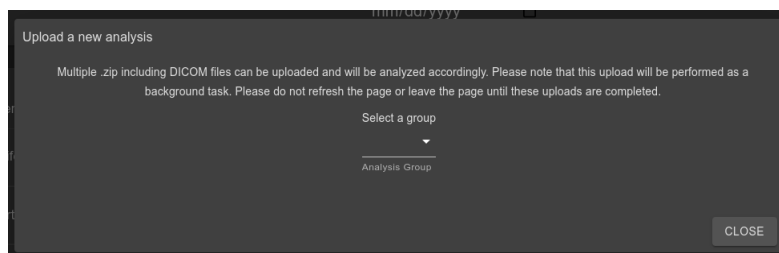
Fig. 4.1: Launch new analyses

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.
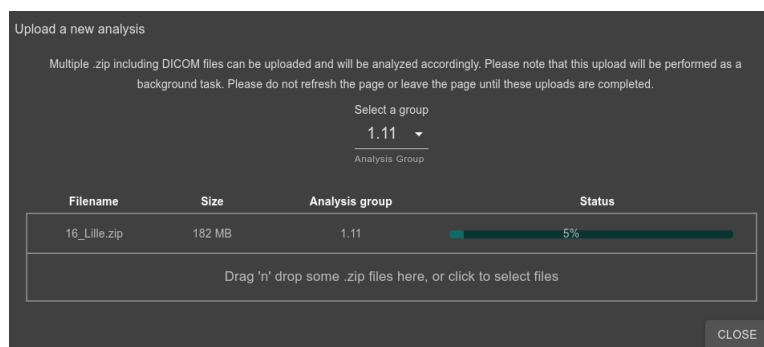
Fig. 4.2: Launch new analyses - Uploaded file

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.
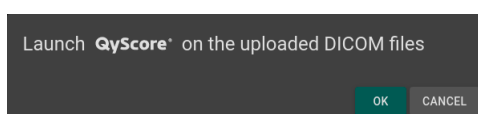
Fig. 4.3: Confirmation for sending data for analyses
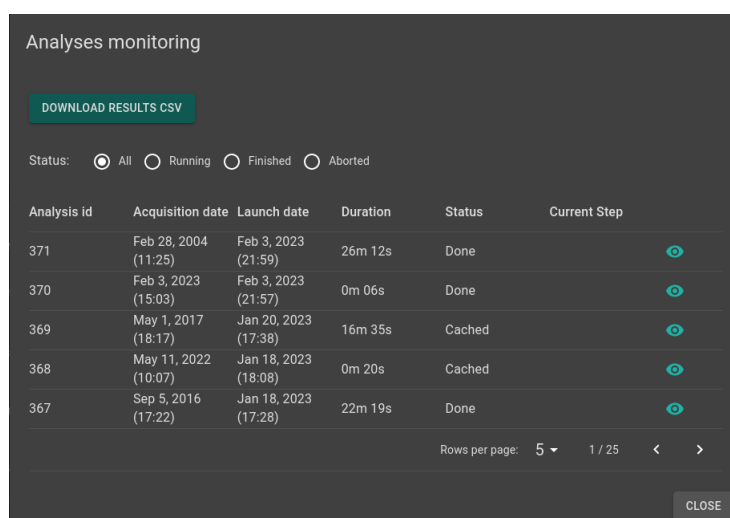
- Click on **Ok** to send the uploaded data for analyses
- Click on **Cancel** to cancel the procedure and close the window

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 last study date of the patient's exams

- *Launch date*: the launch date of the analysis

- *Duration*: the duration of the analysis

- *Status*: the status of the analysis. It can be:
    - *Pending*: the analysis is waiting to be processed (process is in queue)
    - *Scheduled*: the analysis is scheduled for execution (process is about to start)
    - *Running*: the analysis is running (a progress bar is displayed)
    - *Done*: the analysis is completed successfully
    - *Error*: the analysis encountered an unexpected error
    - *Aborted*: the analysis was cancelled by a user
    - *Cached*: the analysis is completed successfully but some steps were skipped because already computed in a previous analysis

- *Current Step*: the analysis evolution in real time

Cancel a *Scheduled* analysis

Scheduled analyses can be cancelled before they start to run.

To cancel a *Scheduled* analysis:

- Click on the icon of the corresponding analysis row

A confirmation pop-up is displayed.
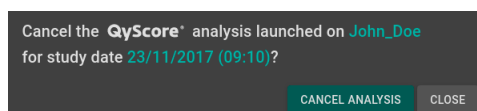
Fig. 4.5: Confirmation for analysis cancellation

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

---

Note: If the analysis changes from *Scheduled* 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
  - *Running*: displays *Running* analyses
  - *Finished*: displays *Finished* analyses
  - *Aborted*: displays *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.
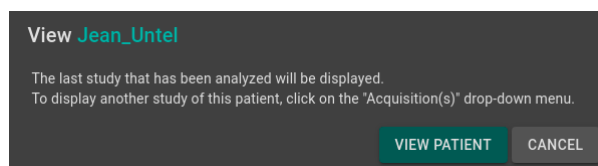
Fig. 4.6: Confirmation for loading a *Finished* analysis

- 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.

CHAPTER 5

Results summary report

5.1 Global presentation

Three templates of reports are available :

- *Generic*: with all QyScore brain quantifications and graphs.
- *Dementia*: with QyScore brain quantifications and graphs specific to follow-up of patients with dementia.
- *Multiple Sclerosis*: with QySCore brain quantifications and graphs specific to follow-up of patients with multiple sclerosis.

Each report contains a summary of QyScore analysis results.
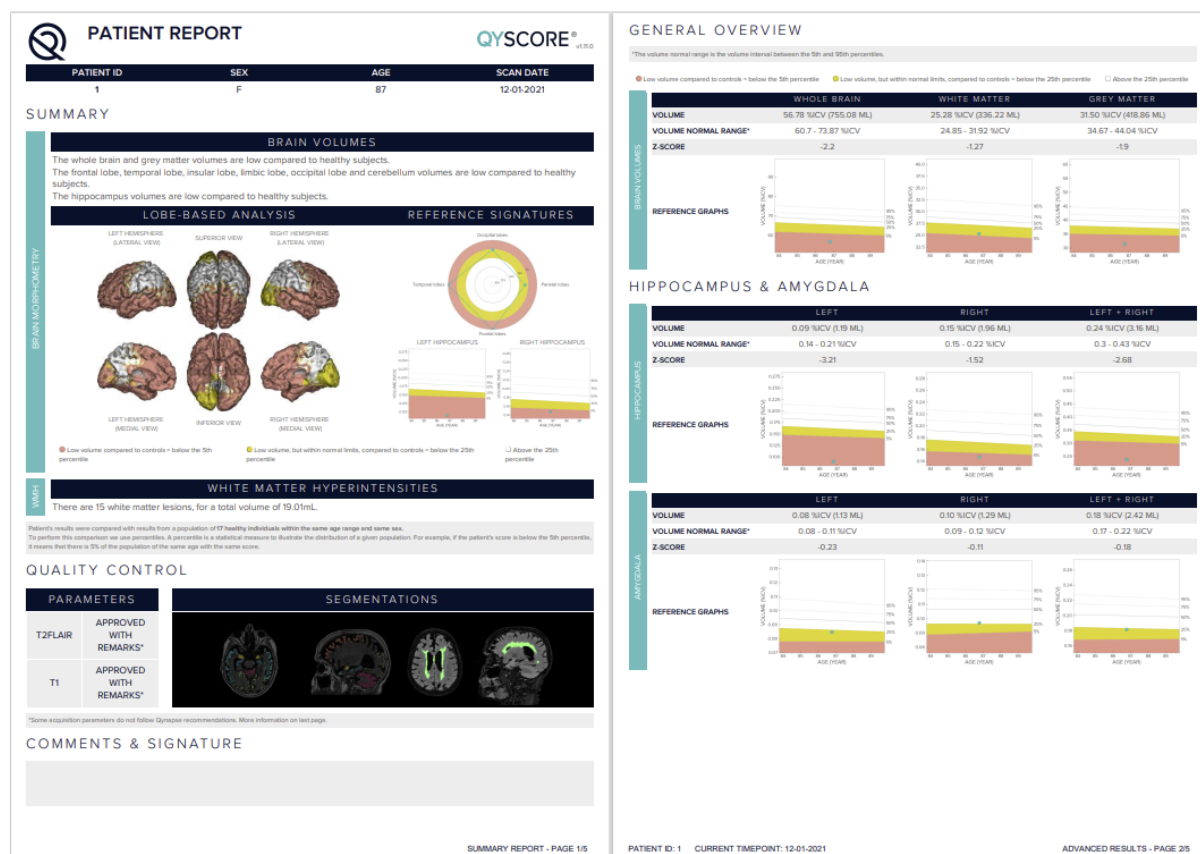
Fig. 5.1: Report

The sections that are available for all reports are the following ones:

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

- *Summary*: summary of results obtained on the segmented structures.

- *Overview*: detailed automated results, including numerical results and graph of comparison to normative data (described in chapter 1.11).

- *Quality control*: detailed results of the automated quality control performed by QyScore.

- *Comments & Signature*: free space to edit comments and to sign.

The section that is specific to a patient with 2 timepoints is the following one:

- *Longitudinal analysis*: longitudinal results computed automatically on anatomical structures and brain lesions.

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

The section that is specific to the Dementia report is the following one:

- *Lobe-based analysis*: contains images resulting from the lobes analysis of the 3DT1 MRI, shown in different views.

5.2 Display the report

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

CHAPTER 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 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

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.
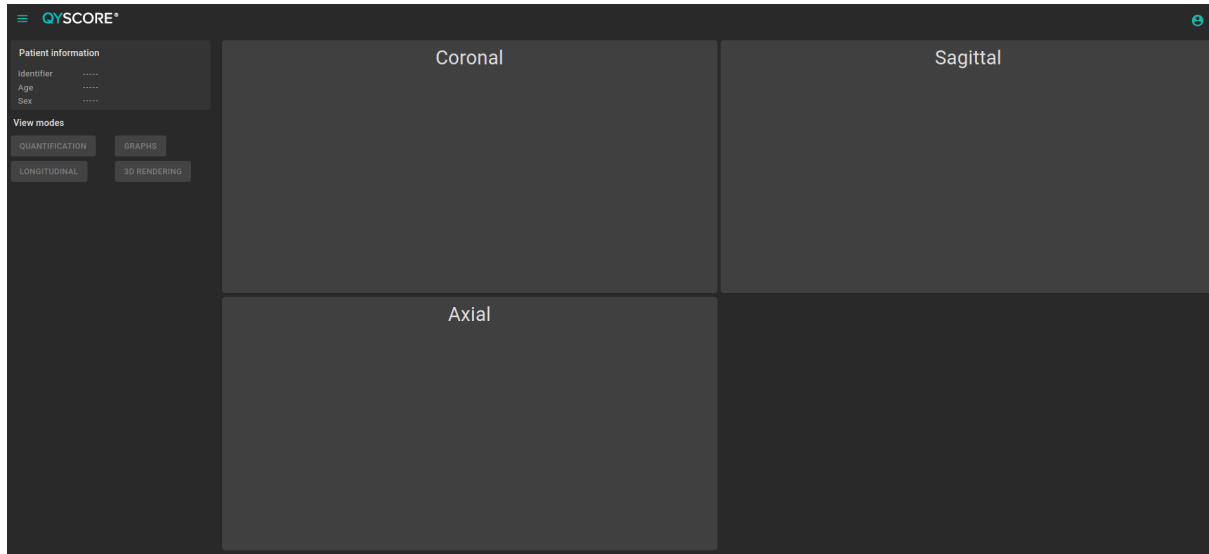
Fig. 6.1: Web-based interface visualization page

After loading patient data (as described in chapter 6.2):
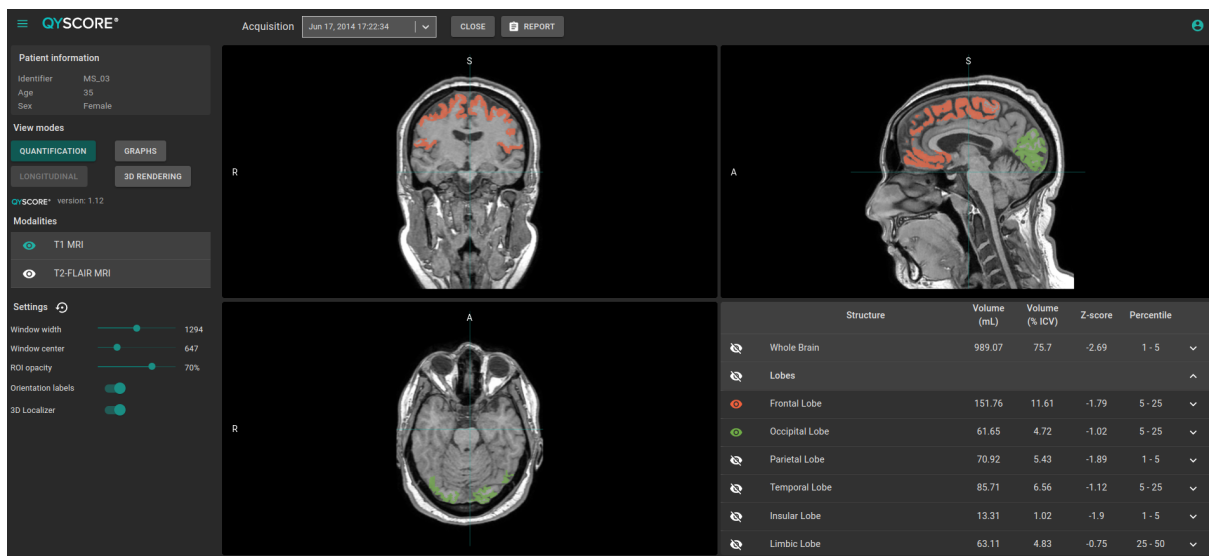
Fig. 6.2: Web-based interface visualization page - Patient loaded

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
    - 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 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.

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

Note: 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
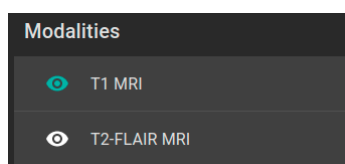
Fig. 6.4: Choice of modalities

6.3.3 View segmented structures

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 1.11),
- the percentile computed by comparison with normative data (described in chapter 1.11).

Note: Z-scores and percentiles are computed only for some structures.
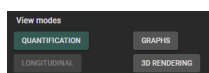
6.4 Switch view modes

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.
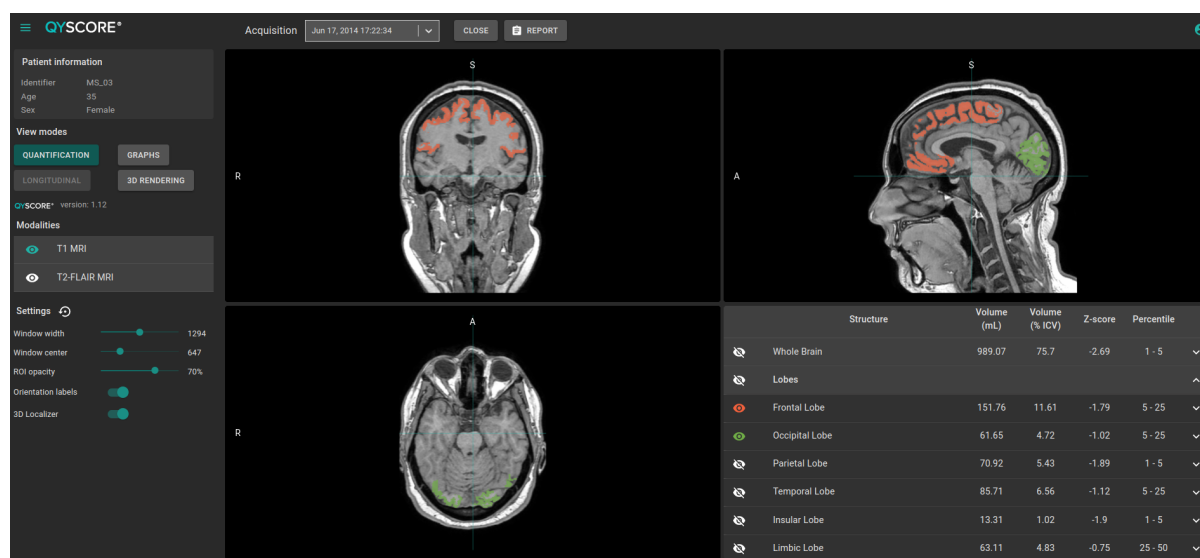
6.4.1 *Quantification* mode

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.
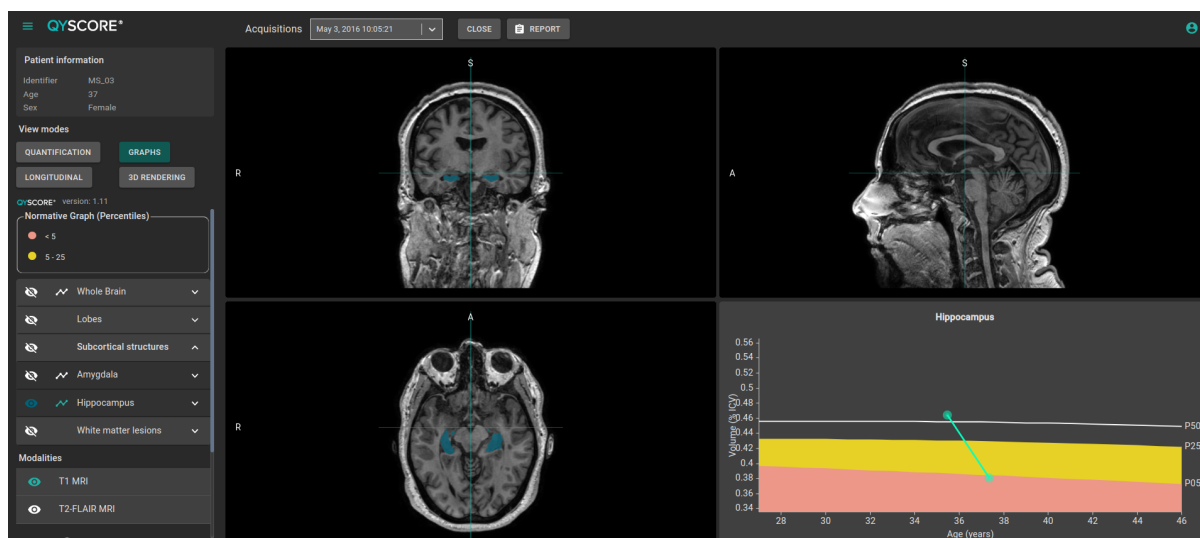
6.4.2 *Graphs* mode

Fig. 6.8: *Graphs* mode

This mode enables you to view graphs of comparison with normative data (described in chapter 1.11).

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 1.11.

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.
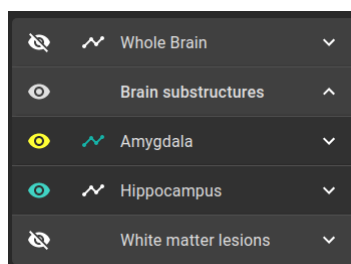
Select a graph to display

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.
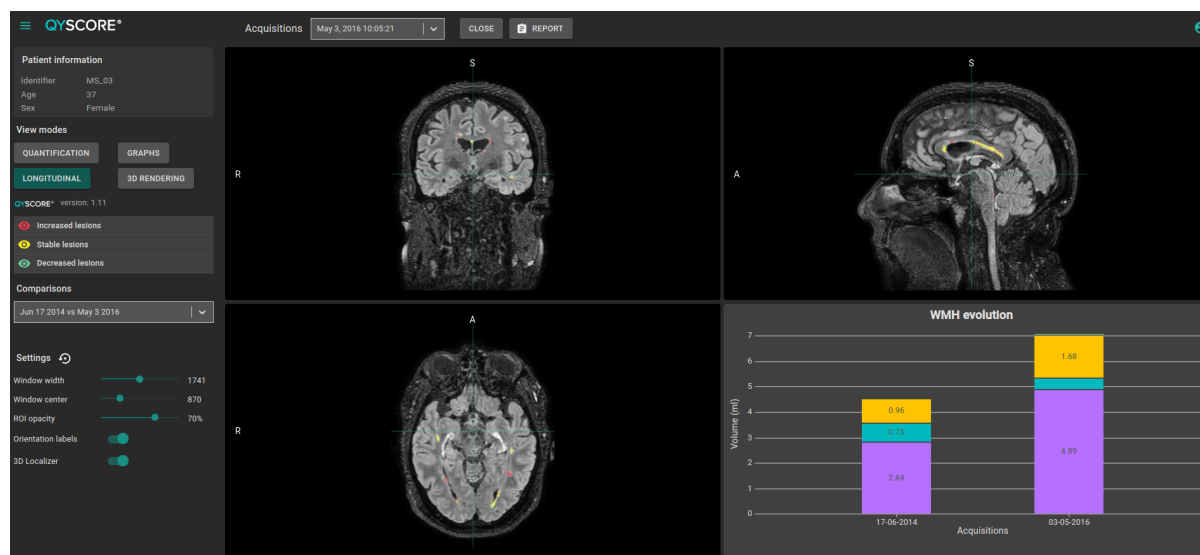
6.4.3 *Longitudinal* mode

Fig. 6.10: *Longitudinal* mode

This mode enables you to view a graph of the lesion load evolution in time.

To enter the mode:

- Click on the **Longitudinal** button

This mode enables to visualize for a same patient the overlay of segmentations performed at several timepoints and to identify the increased, decreased and static lesions with the longitudinal scale.
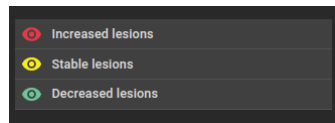

Fig. 6.11: *Longitudinal* scale

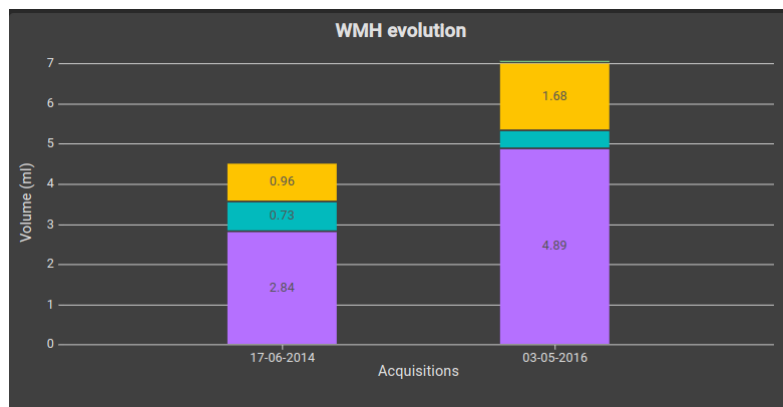The special window displays a graph of the lesion load evolution in time.

Fig. 6.12: *Longitudinal* chart

Note: To ensure accurate longitudinal analysis, it is recommended to use the same acquisition parameters at each time point.

6.4.4 *3D rendering* mode

Fig. 6.13: *3D rendering* mode

This mode enables to visualize the atrophy in 3D and compare to the normative database according to the percentile scale.
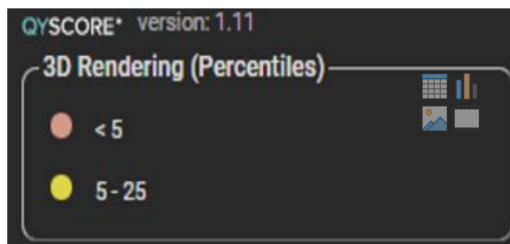

Fig. 6.14: *3D rendering* scale

The 3D brain can be moved and zoomed with the mouse.

Note: The 3D brain rendering is displaying the projection of the patient percentiles on a standard 3D brain render.

Note: The 3D brain rendering is an anatomical view of the brain.

To enter the mode:

- Click on the **3D rendering** button

6.5 Change visualization settings

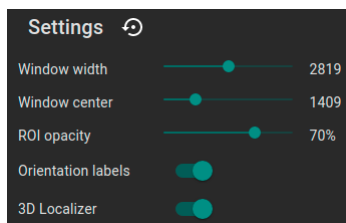Visualization settings are available via the *Settings* section of the control panel.

Fig. 6.15: 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
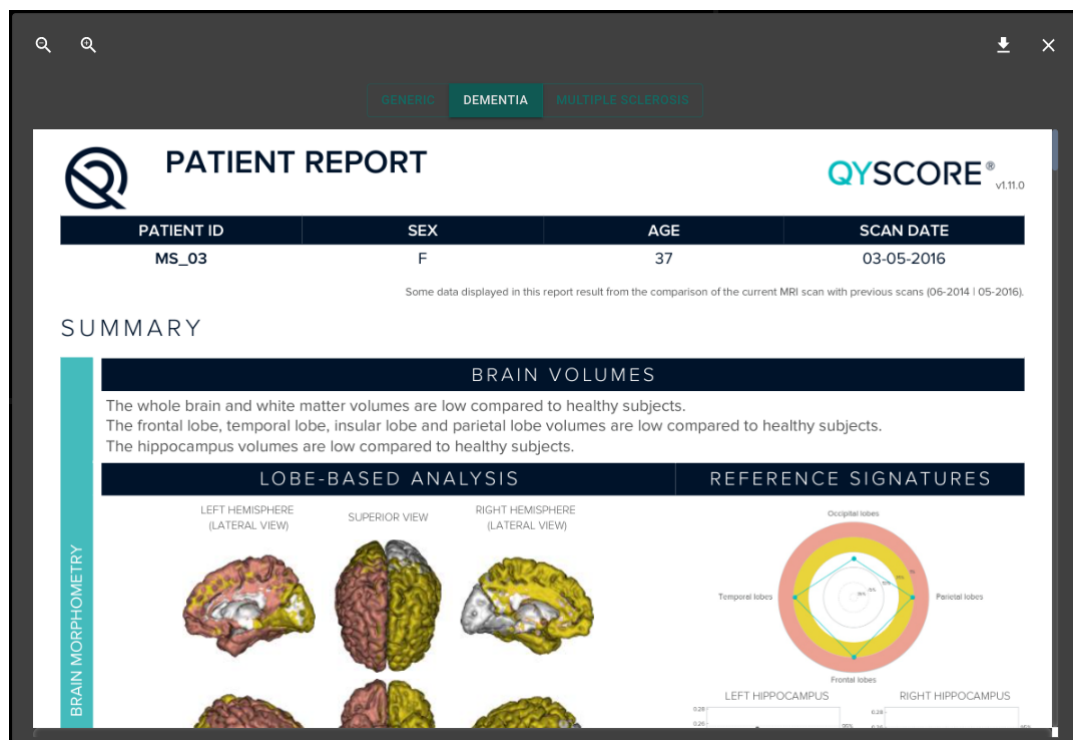
6.6 Display the report

Fig. 6.16: Report visualization

To display the report:

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

Note: Volume changes are always computed by comparing with the first acquisition timepoint.

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.

CHAPTER 7

Troubleshooting

Please refer to this section before requesting any further assistance.

7.1 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.

7.2 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.

7.3 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.

7.4 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.

7.5 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.

7.6 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.

F
False colors, **11**

P
Percentile, **11**

S
Special window, **11**
Standard visualization window (*or standard window*), **11**

Z
Z-score, **11**