LABS
USER
MANUAL

ENGLISH

o&t Labs

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1. LEGAL DISCLAIMER

Products shown in this user guide have not been approved as medical devices or to support clinical decisions. Safety and effectiveness have not been reviewed by any regulatory agencies. o8t Labs is designed for research purposes.

2. VERSION

Market: Global excluding China

Product: o8t™ Labs

Document version: 2

3. ACRONYMS

LAN: Local Area Network

TCP/UCP: Transmission Control Protocol / User Datagram Protocol

fMRI: Functional Magnetic Resonance Imaging

DWI: Diffusion-Weighted Imaging

CSD: Constrained Spherical Deconvolution

CEN: Central Executive Network

DMN: Default Mode Network

DICOM: Digital Imaging & Communications in Medicine

NIFTI: Neuroimaging Informatics Technology Initiative

PACS: Picture Archive and Communication System

4. MINIMUM SYSTEM REQUIREMENTS

4.1 NETWORK

ITEM	REQUIREMENT / STANDARD
Existing LAN	Internet connection with min. 25 Mb/s downstream bandwidth per client & less than 100 ms latency
Ethernet	Provided by the hospital Client must have access to internet through ports 80 & 443
Email	An existing email address is required to use Labs

4.2 HARDWARE/SOFTWARE

ITEM	REQUIREMENT / STANDARD
Computer	CPU: Intel i5 6th generation (or equivalent) Ram: min 8GB required, 16GB or more highly recommended Hard drive: 20GB free space or more
Display Resolution	1280 x 720 (minimum)
Operating System	Windows: Windows 7, 8, 8.1, 10 or later Mac: OS X Yosemite 10.10 or later Linux: 64-bit Ubuntu 14.04+, Debian 8+, openSUSE 13.3+, or Fedora Linux 24+
Internet Brower	Chrome
Internet Browser Version	Min v.85
Tablet	Labs is compatible with tablet devices with Google chrome installed as a browser

5. ACCOUNT LOGIN & PASSWORD RESET

Please use Google Chrome to access to the system. Google Chrome can be downloaded from the link: **https://www.google.com/chrome**

This software is fully cloud based and is accessed by going to the link below: **https://labs.o8t.com/login**

Users will receive an email on sign up providing login details, which are entered into the "**Facility**", "**Email**" and "**Password**" boxes in the login page shown in figure 1.
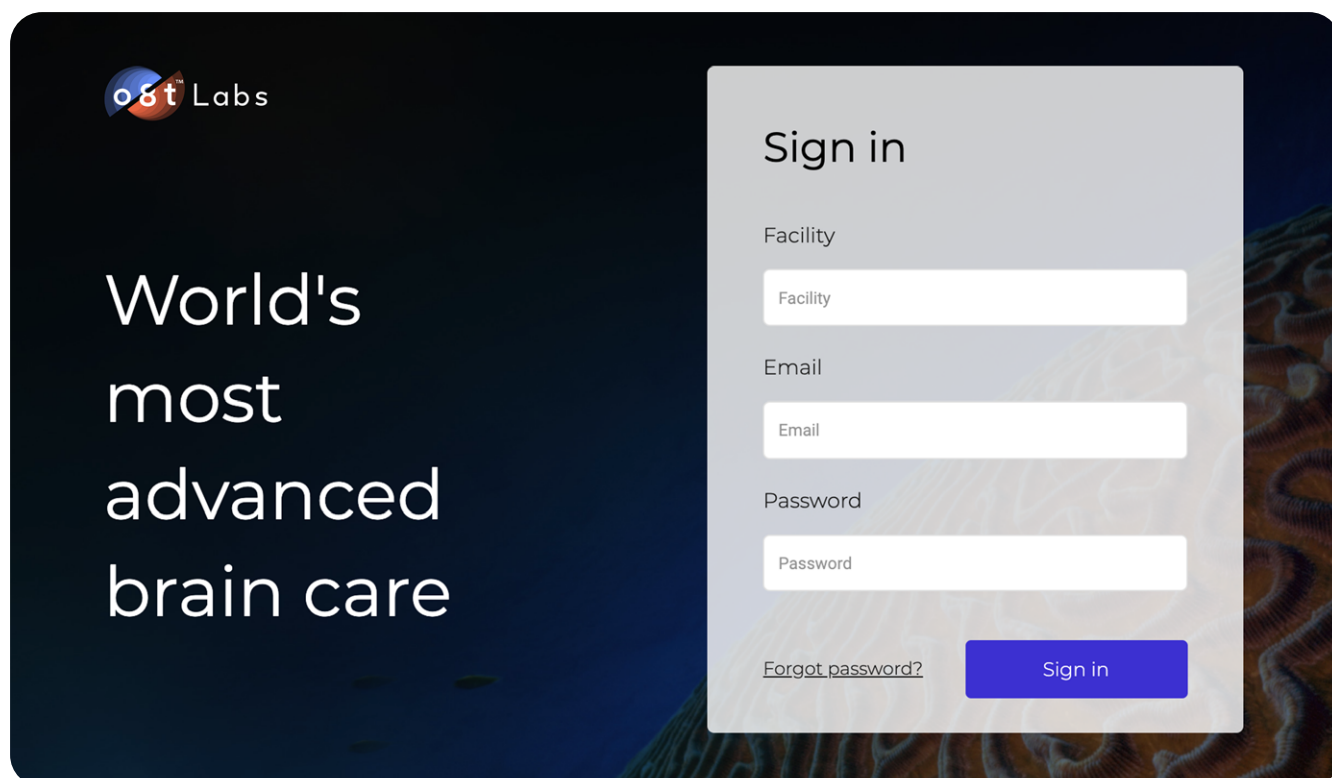

Figure 1 Login Screen

PASSWORD RESET:

To reset your password, click on "**Forgot password?**". An email will be sent to you to reset the password. The new password requires a minimum of 8 characters that contains at least 1 uppercase letter, 1 lowercase letter, 1 number and 1 special character (e.g. !@#$%^&*). Your facility administrator requires your password to be updated every 30 days.

6. HOME PAGE

Figure 2 displays the home page, which consists of all active and completed cases. Clicking on the logo in the top left of screen at any time when using Labs returns you to this home page.
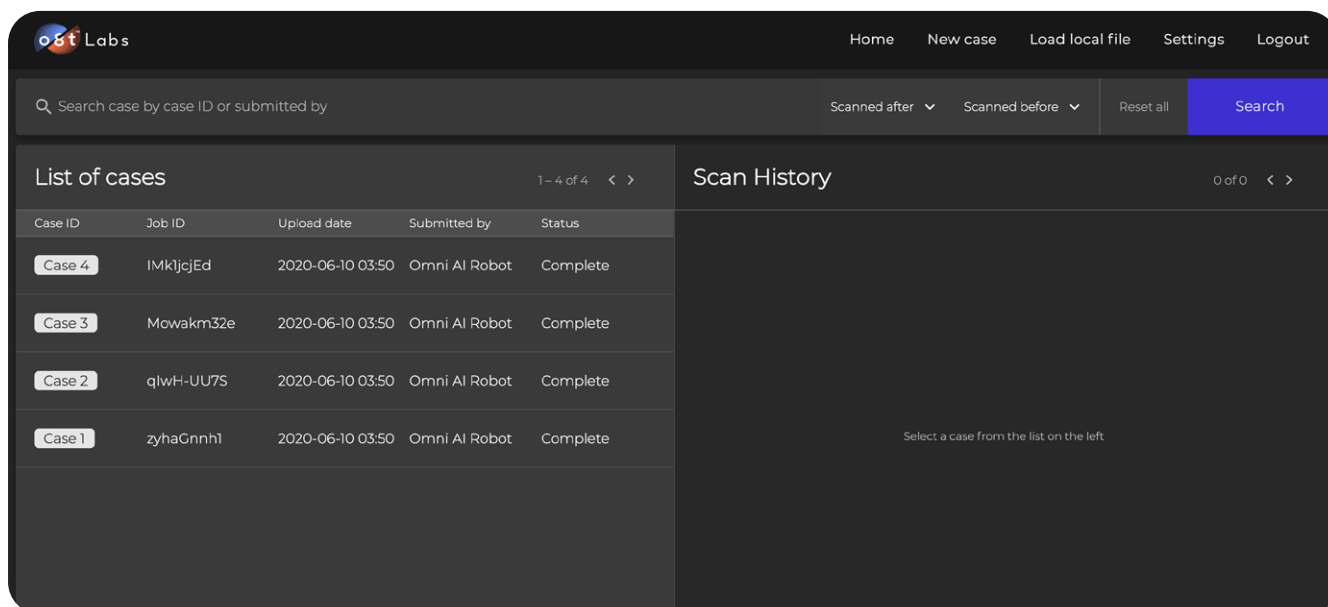

Figure 2 Home Page With Case ID

6.1 LOADING AN ACTIVE CASE

To help users familiarize themselves with the software, four cases have been pre-loaded for exploration. We will use "Case 3 Post Resection" to guide you through the rest of the Labs software:

1. Select "**Case 3**". This will display the active list of studies for that patient.

2. Click on "**View**" on the right panel. The images will then load from the cloud. This comes in several packets. In order to allow you to navigate more quickly, the Diffusion tractography comes in a small packet of 10,000 tracts, and a larger packet later of all the other tracts. The loading process should take under a minute with an Internet download speed of 25 Mbps.

3. Once it is complete, you will see the selected subject's brain co-registered with the machine learning based Glasser Atlas[1].

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[1] Glasser, M. F., Coalson, T. S., Robinson, E. C., Hacker, C. D., Harwell, J., Yacoub, E., Ugurbil, K., Andersson, J., Beckmann, C. F., Jenkinson, M., Smith, S. M., & Van Essen, D. C. (2016). A multi-modal parcellation of human cerebral cortex. Nature, 536(7615), 171–178. https://doi.org/10.1038/nature18933

6.2 NAVIGATING THE MAIN PAGE

Figure 3 highlights the Labs main page and consists of four basic panels (Refer to the below with numbers):

1. **Navigation Panel**
   This panel contains a menu of series and choices designed to help users subset the subject's connectome. Users can locate specific data, such as networks, regions, parcellations, and tracts. Here you can select individual networks and display them individually by clicking "Export selection"

2. **Imaging Panel**
   This panel allows users to view data through the Atlas tool (i.e. brain mapping) and the Connectomic tool (i.e. connectivity matrices). Tools for fMRI and Graphs will be made available in future updates. Users can find a connectomic library in the guide section of the imaging panel.

3. **Control Panel**
   This panel allows users to modify and manipulate the images.

4. **Case Information**
   This panel displays the subject case details, clicking the "download case" button exports selected networks and connectivity analyses.
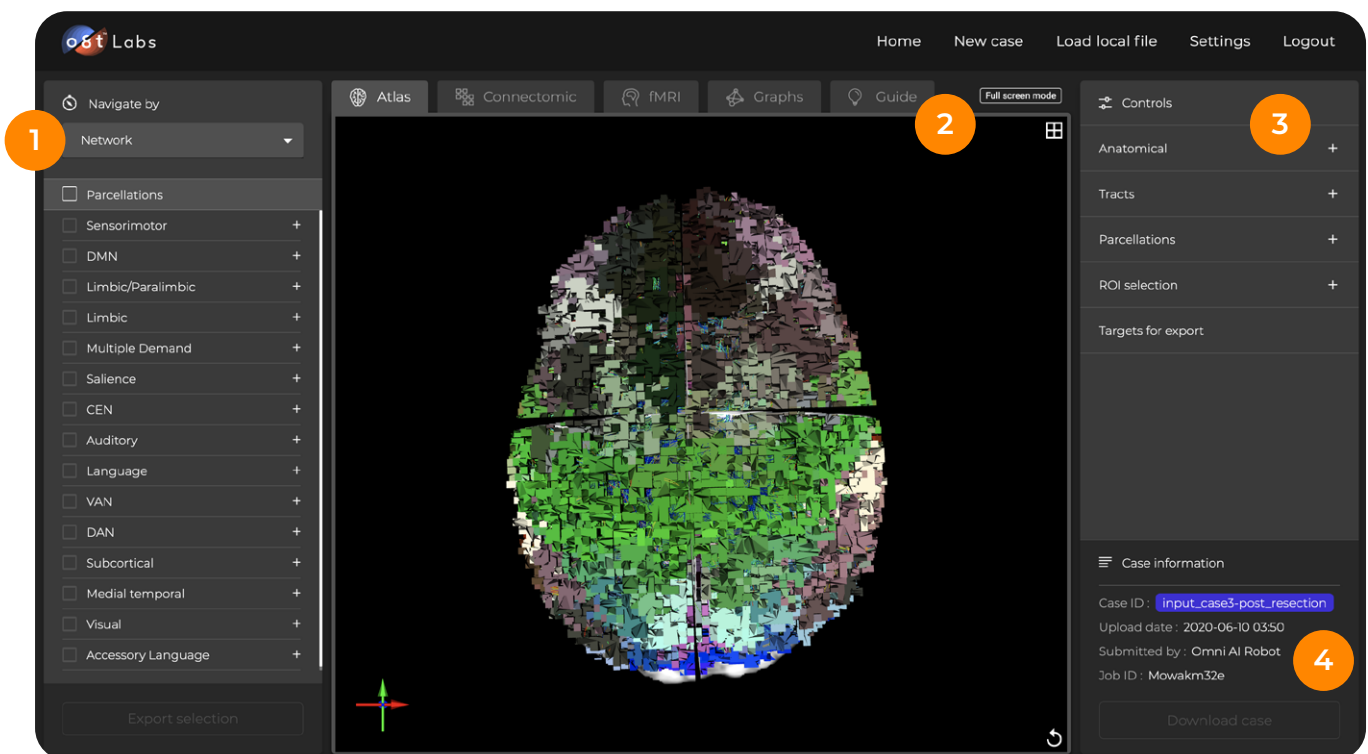

Figure 3 Main Page

7. NAVIGATION PANEL

In the "**Navigation**" panel, users can navigate the scan in 7 different ways. Disease Model, Network, Extended Network, Parcellation, Region, Tract and Function.
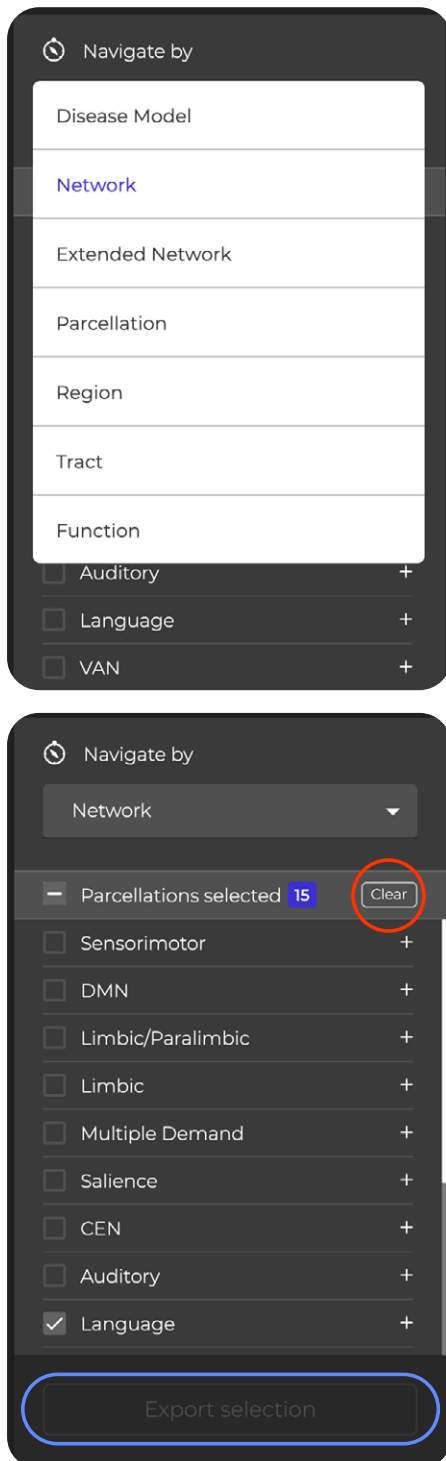

Figure 4 Navigation Panel

1. The "**Disease Model**" are parcellations relevant to the disease state, and includes both negative and protective factors associated with the disease.

2. The "**Network**" is the default setting. The "Network" setting groups parcellations by function into known neural networks.

3. The "**Extended Network**" adds parcellations that are peripheral to the main network of interest.

4. The "**Parcellation**" setting displays single brain areas. Parcellations for the left and right hemisphere, as well as the brainstem are individually selectable. There is a summary of each parcellation under the guide in the imaging panel.

5. The "**Region**" setting groups areas based on their anatomical location within the brain.

6. The "**Tract**" setting groups areas based on which white matter bundle you want to see.

7. The "**Function**" are parcellations known to be involved in specific cognitive processing.

8. Users can subset the network by clicking the tick box.

9. Clear the selection by clicking "Clear" (circle in red) before selecting the next network.

10. After subsetting the network, click on "Export Selection" (circled in blue) to export the selected network. All exports will be added to the queue in the Control Panel. The export is in DICOM format which may be loaded onto 3rd party systems such as image guidance platforms.

8. IMAGING PANEL

8.1 SELECTION BY NETWORK

Select "**Navigate by Network**" in the navigation panel on the left. Selecting "**Language**" will subset the language system in the imaging panel, including only parcellations and tracts involved in this network. Ensure you have selected the atlas setting in the imaging panel (circled in blue), to view the subset network.

In the view panel (shown in figure 5A), click on ⊞ (circled in red) to switch between 2D and 3D. This allows you to toggle between one 3D and three 2D anatomical projections.
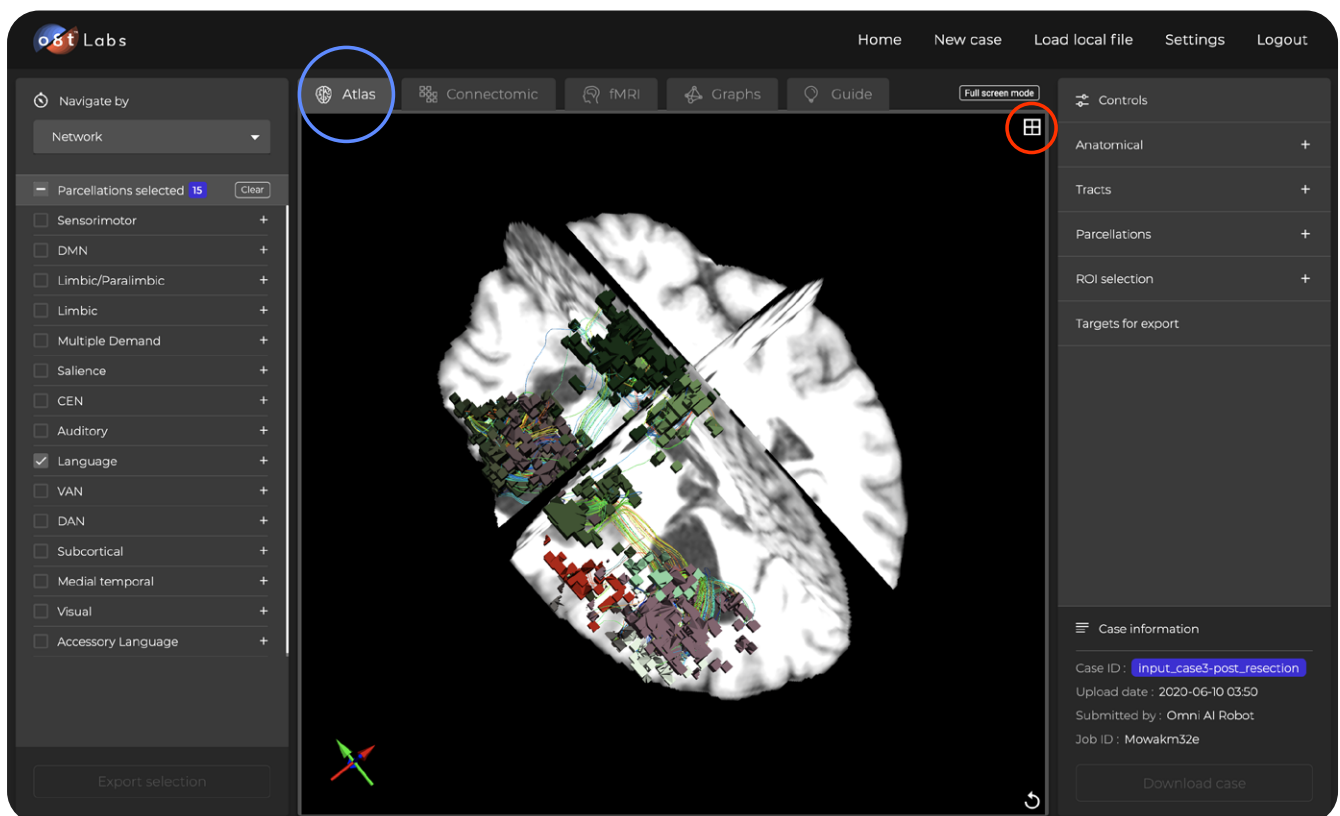
Figure 5A 3D Atlas View On Main Screen

Figure 5B displays all four available views. Clicking on the expand option in the top right corner (circled in red) of the four views will allow you to view a single projection in the imaging panel.
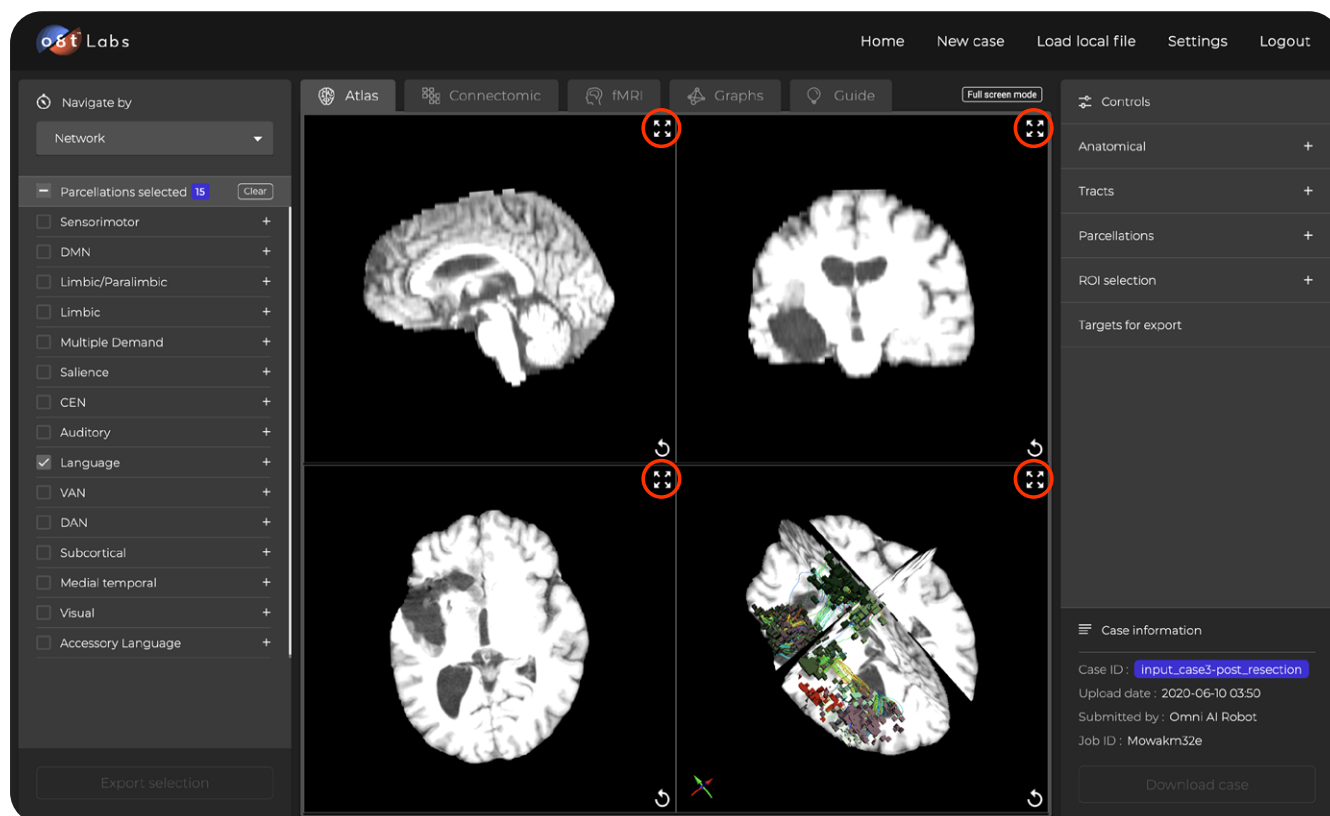

Figure 5B 2D and 3D Atlas View On Main Screen

8.2 AN EXAMPLE FOR LOADING NETWORK CONNECTOMICS

Set the selection panel to "**Network**" and click "**CEN (Central Executive Network)**" in the navigation panel, subsetting areas of the CEN. Selecting "**Connectomic**" in the imaging panel displays the degree of correlation between regions of the CEN. Hover over the data to explore it. Figure 6 displays the expected connectomic output from selecting the CEN. Note that red areas correlate with each other and blue ones are anti-correlated. In general, correlated areas are firing together and are usually part of large-scale brain networks. The x and y axes are the same set of areas; thus the matrix is symmetric and the diagonal (each area with itself) achieves a perfect correlation.
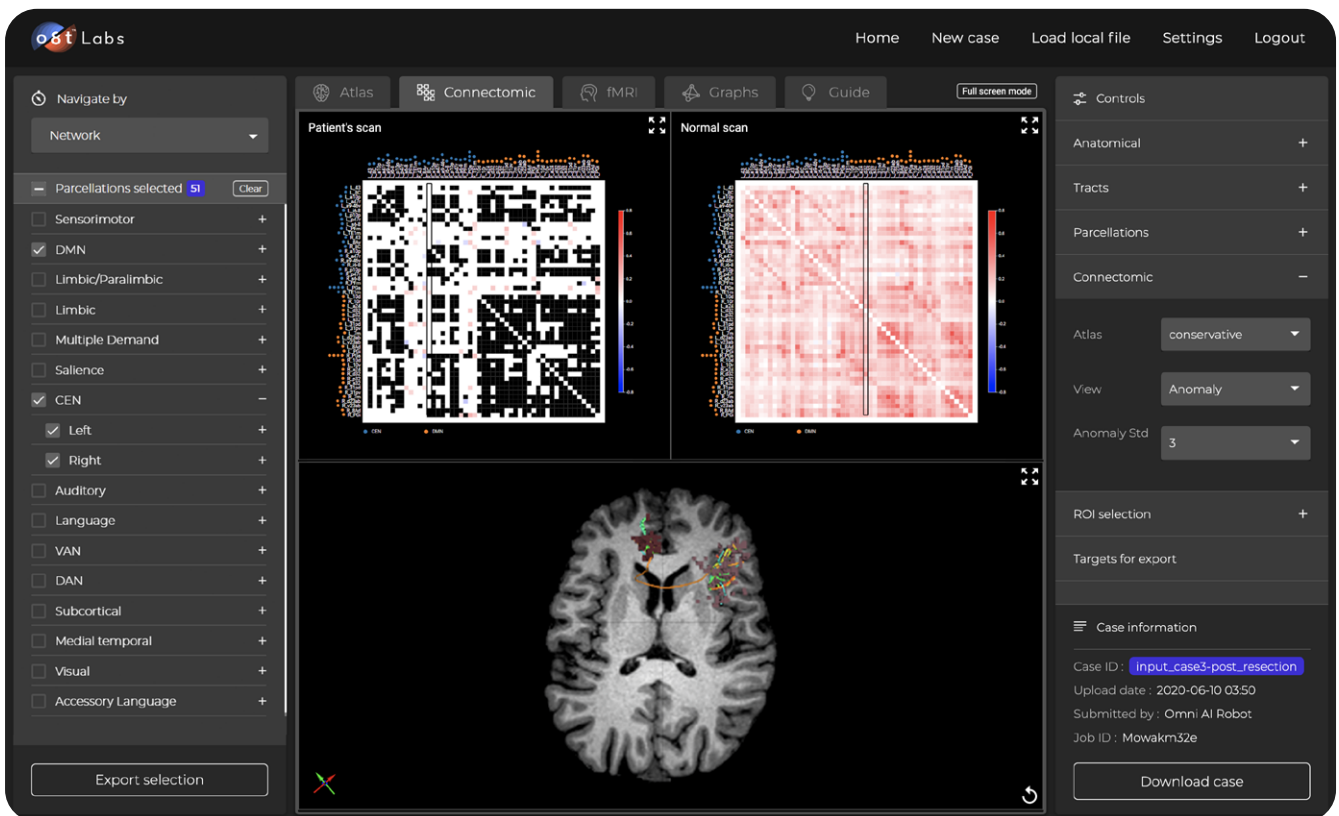
Figure 6 Connectomic View

Figure 6A Connectomic View of DMN and CEN

Click "**DMN (Default Mode Network)**" in the navigation panel. This will add the DMN to the matrix, and now the two networks (DMN and CEN) are compared to each other as well as themselves. Colored dots on the bottom indicate the network origin or each parcellation to aid interpretation. Users can add as many network correlations as desired and can also include single regions or tracts. The proper way to read these diagrams is in columns.

Selecting a single entry in the matrix will display the chosen parcellations in the main screen below the correlation matrix.

Black: connections which are too variable and are excluded

White: areas which communicate normally

Red: areas with more correlation than normal

Blue: areas with less correlation than normal

9. CONNECTOMIC GUIDE

Select "**Guide**" in the imaging panel displays a guide containing a library of what different parcellations are and what is known about them. Users can explore each selected parcellation in detail. When a network or a tract is subset in the navigation panel, the guide will open to the selected relevant section. With the imaging panel's guide button circled in blue, figure 7 displays the auditory section of the connectomic guide.
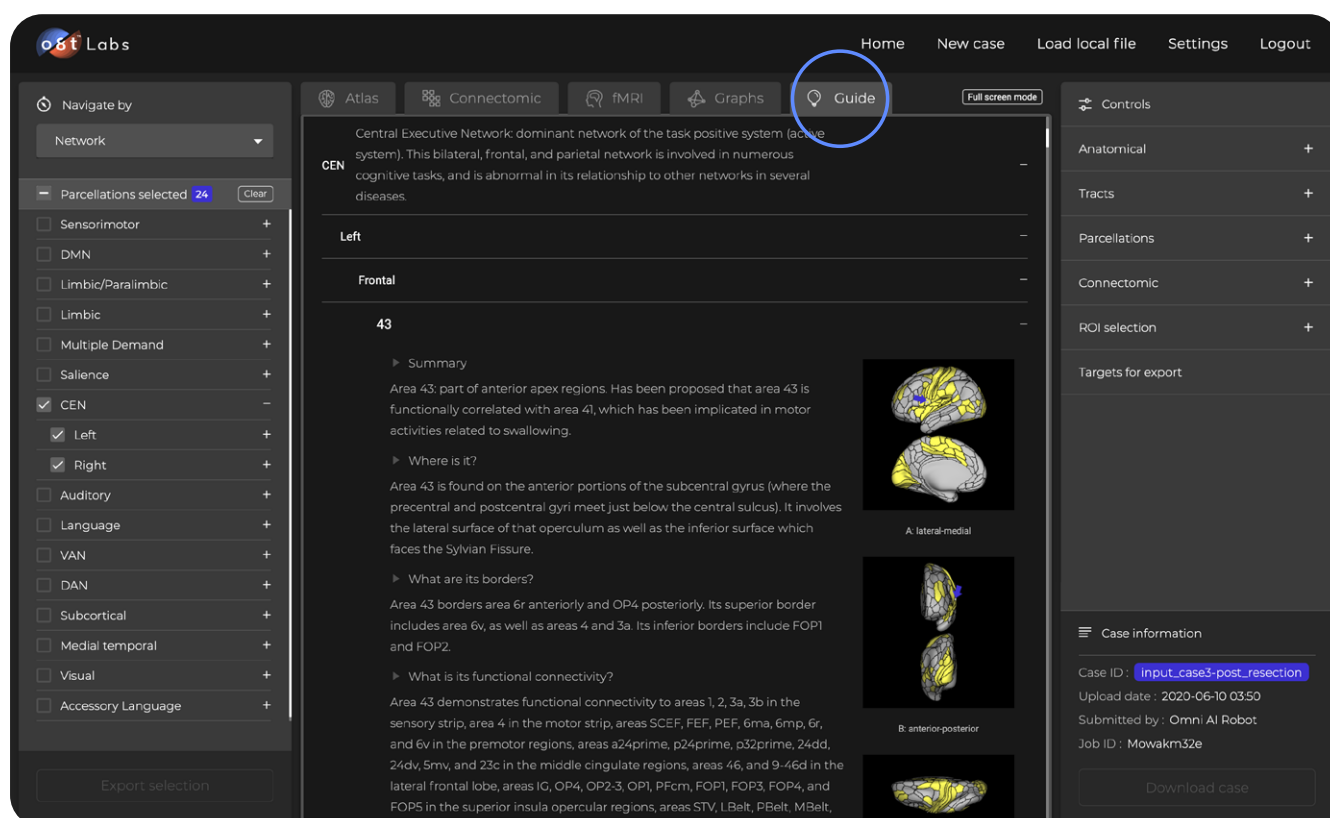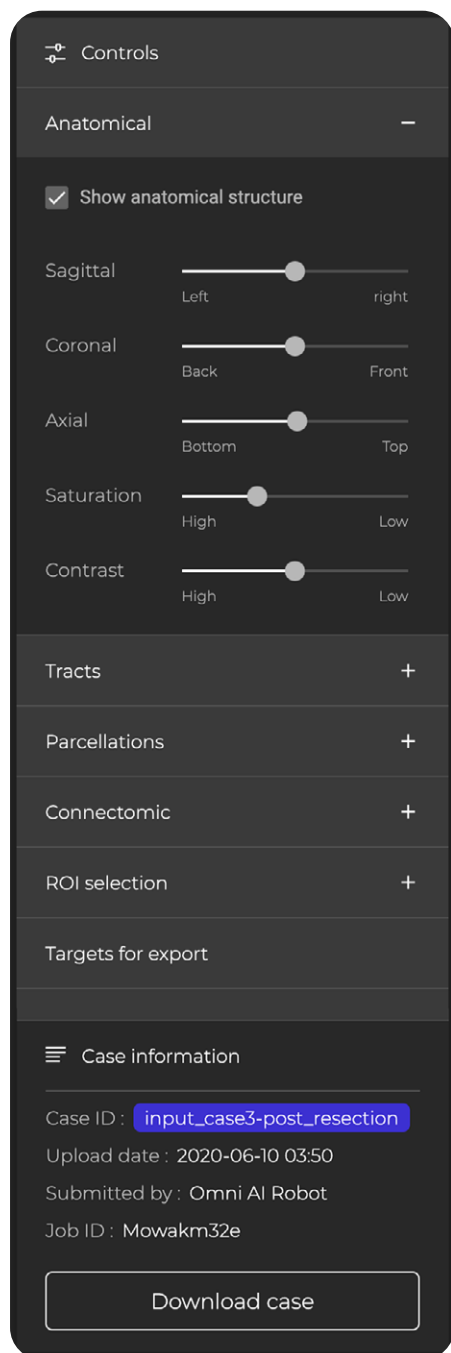

Figure 7 Connectomic Guide

10. CONTROL PANEL

In the control panel, users can control and modify the viewing.

Figure 8 Control Panel

1. **Anatomical**: Basic viewing functions like a PACS operation, including scrolling through axial sagittal and coronal as well adjusting contrast.

2. **Tracts**: This panel allows manipulation of the tractography. This tractography is generated through Constrained Spherical Deconvolution (CSD) with edema correction. Users can adjust the tract length rendered, which can be useful for reducing noise.

3. **Parcellation**: These parcellations are derived from the Human Connectome Project "Glasser Atlas" based on machine learning. The default is the conservative atlas, which is fitted using a machine learning based approach. The "Fitted" model is the atlas which is coregistered to the brain using algorithms not based on machine learning. The conservative atlas is called conservative based on the threshold setting in the machine learning algorithm.

4. **Connectomic**: This section is used for anomaly detector. See diagram below on how to use this function.

5. **Download Case**: For researchers, hit download case to download the full case in a zip file.

10.1 THRESHOLDING CONNECTOMIC ANOMALY DETECTION THROUGH THE CONTROL PANEL

Select the "**Language Network**" in the navigation panel and click the "**Connectomic**" tab in the control panel. One menu option says "**Raw**", click this and switch it to "**Anomaly (Detector)**". The anomaly detector compares the subject's correlation data with a dataset of normal patient scans using our machine learning algorithm and can be thresholded to either two or three standard deviations of difference.

The raw correlation values without comparison to controls can be viewed by toggling between "**Anomaly (Detector)**" and "**Raw**".
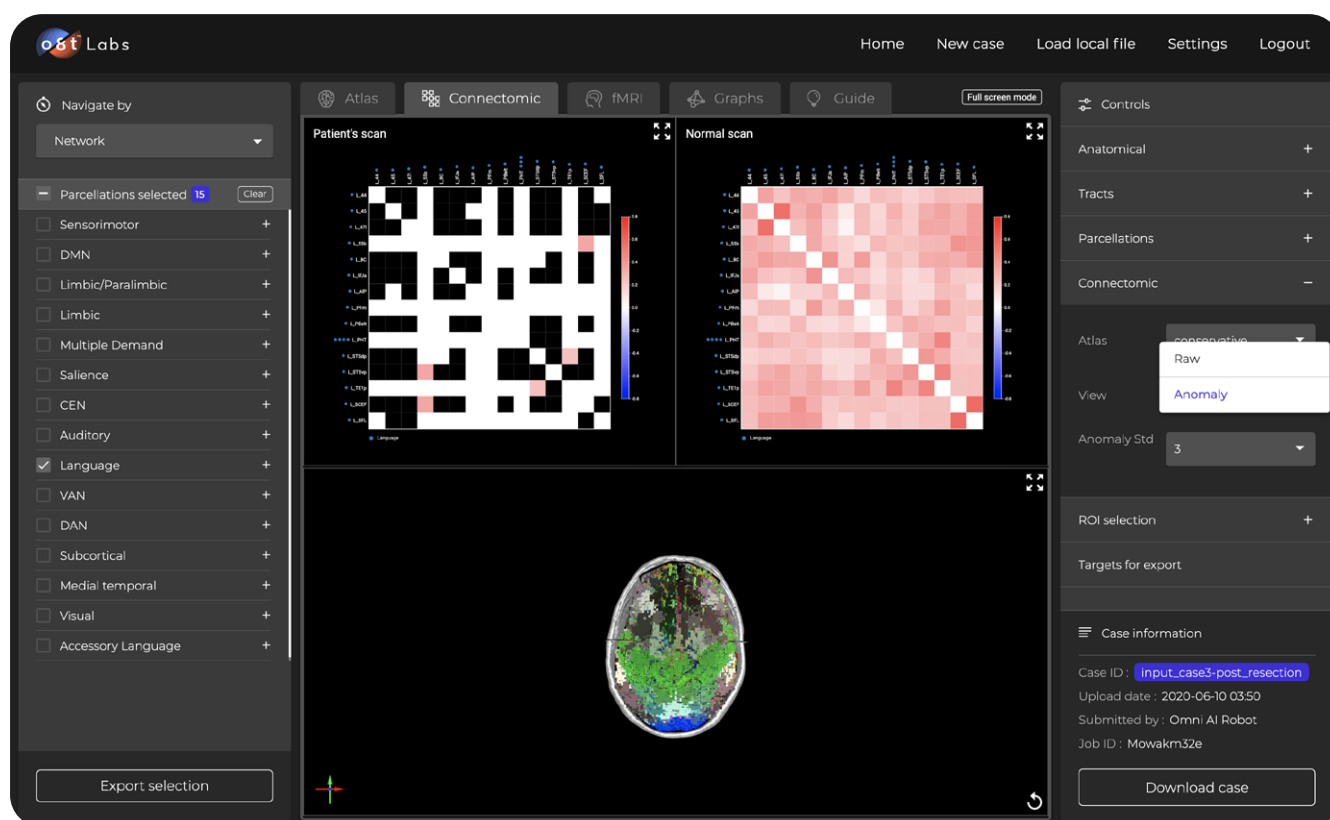
Figure 9A Anomaly Detection

The best approach is to look for columns with multiple colored boxes, as these indicate brain regions which correlate abnormally with multiple brain regions. If you find a column with one or more abnormal squares, in this case **55b**, click it. Maximising the atlas image on the lower half of the screen will display the isolated abnormal parcellation selected (55b) in the matrix.
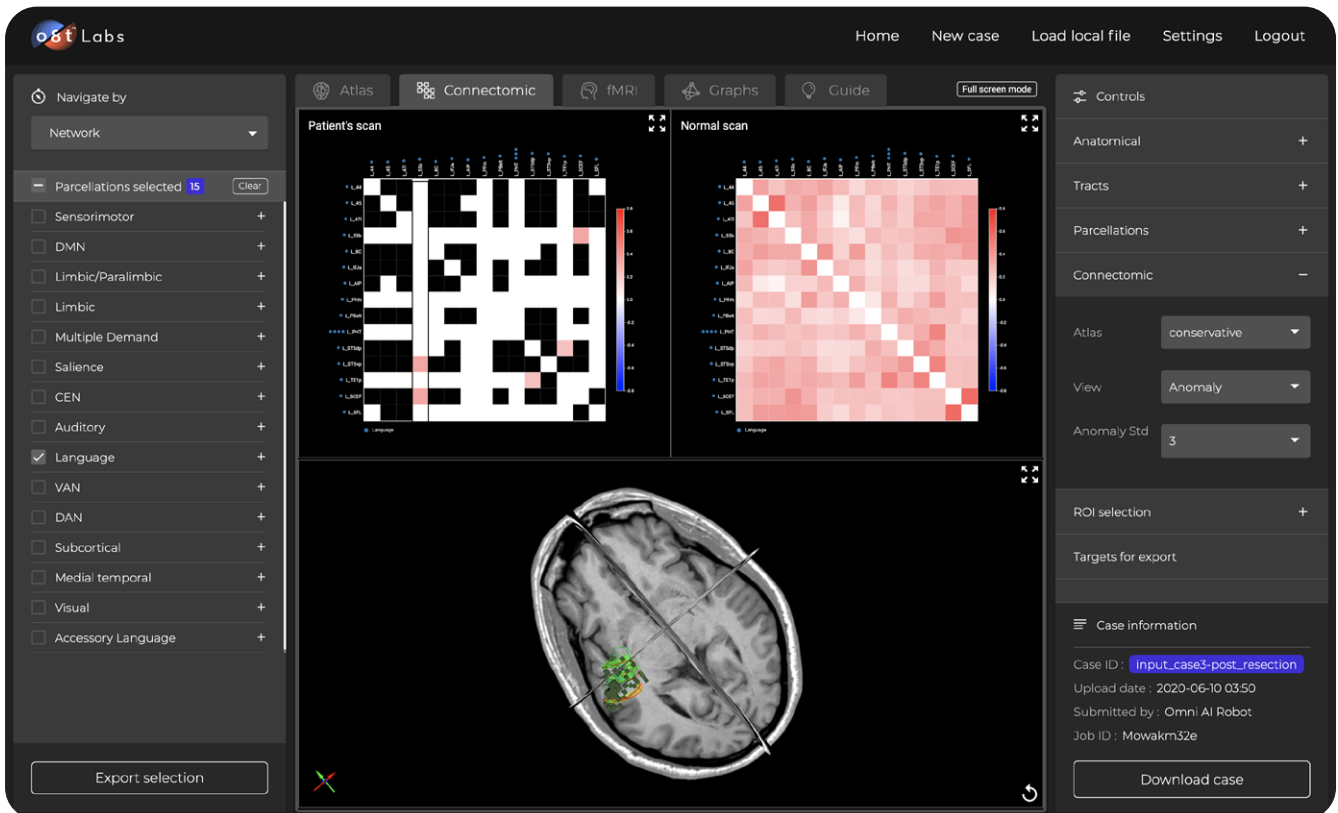

Figure 9B Anomaly Detection - Isolated Abnormal Parcellation (55b)

11. NEW CASE UPLOAD

Click on "**New Case**" on the top right-hand side on the home page which is circled in blue on figure 10.
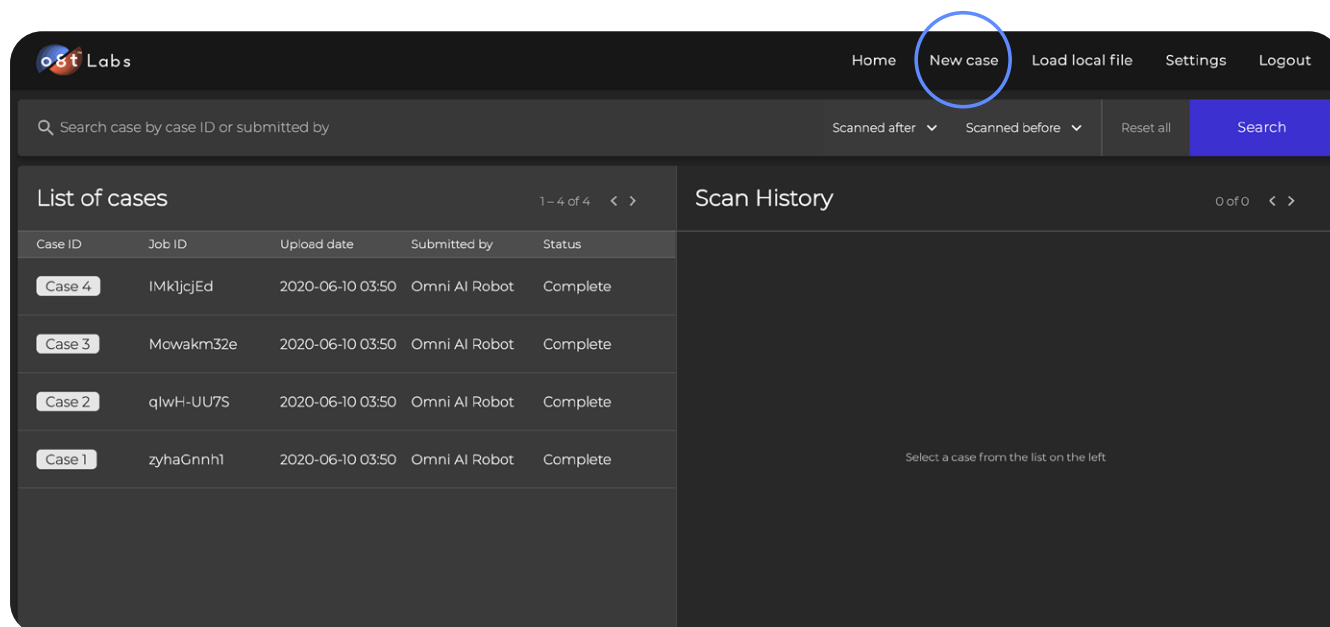
Figure 10 New Case Upload Screen

11.1 UPLOAD PAGE

o8t Labs supports both DICOM and NIFTI file types for upload. To enable PACS integration, please visit **https://infinitome.o8t.com** for information about our Infinitome platform which supports larger clinical research projects. Note that all data uploads are stored, processed, and protected in accordance with our **Privacy Policy**.

11.2 UPLOAD DICOM FILES

Figure 11 displays the upload page with the DICOM upload button highlighted in blue. To upload a DICOM series, first complete the required demographic information, then click on "**Choose a DICOM folder for upload**" or drag the entire folder for the subject to the area. Select the entire folder and click on upload. Note that all DICOM files must be uncompressed before uploading them. NIFTI files need to be compressed (using gzip) except for bval and bvec.
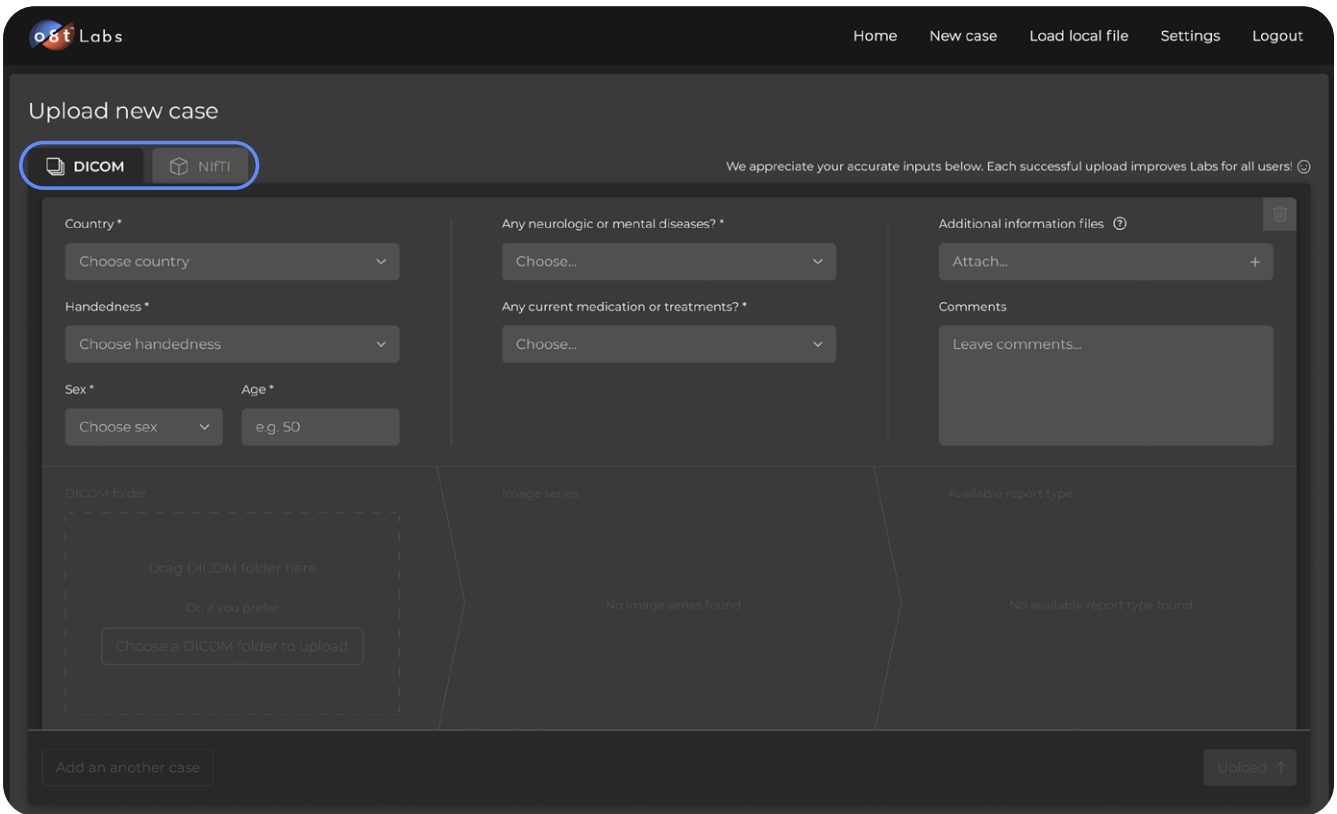
Figure 11 DICOM Upload Screen

A window displaying the number of files loaded will appear before they are uploaded to Labs (shown in figure 12). Click on "**Upload**". Diffusion images suitable for the software typically have around 3000 files or more (30+ directions).
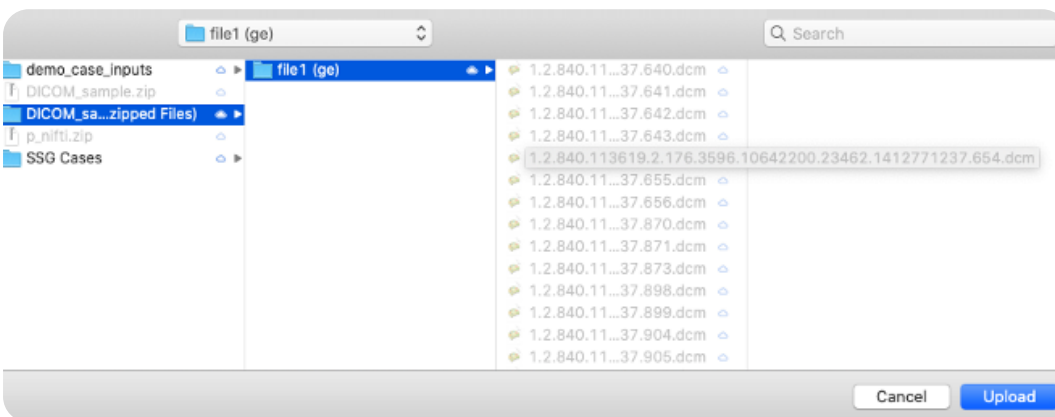

Figure 12 DICOM File Structure

It is critical the correct files are selected for each image series. There might be multiple files for DTI(DWI) and BOLD image series. If this is the case, select the folder that has the most files for each series. The "Connectomic" function will only be available if a BOLD image series (resting state fMRI) is uploaded. Users can create multiple cases for different subjects before starting the uploading process. Figure 13 shows the completed DICOM upload screen – in this case both Rs-fMRI and DTI series have been correctly uploaded, and the connectomic function is made available (circled in blue).
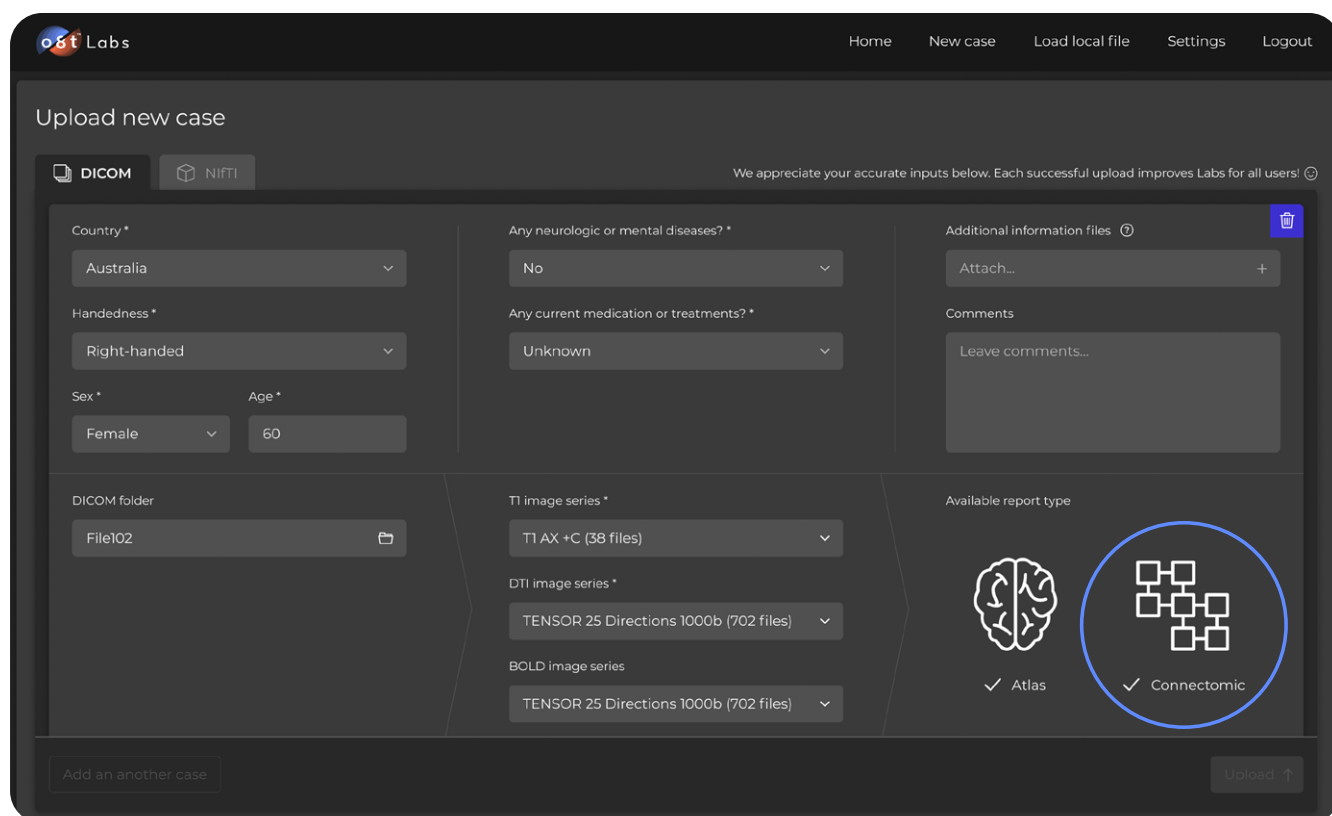
Figure 13 DICOM Upload Screen With Rs fMRI Available.

Under "Available report type", the software predicts the possible outputs based on the files being uploaded. Note, that the software can only confirm if these files are valid once they are fully uploaded and have commenced processing.

11.3 UPLOAD NIFTI FILES

Figure 14 displays the NIFTI upload screen. From the main page, click on "**New Case**" and select "**NIFTI**". Name the case and select the relevant NIFTI files. There may be more than one set of DWI images which have bval / bvec files. It is important to load the correct bval / bvec files for tractography. If in doubt, each DWI image set will have an associated text file. Typically, the image set with more non-zero numbers in the text file name will be correct.
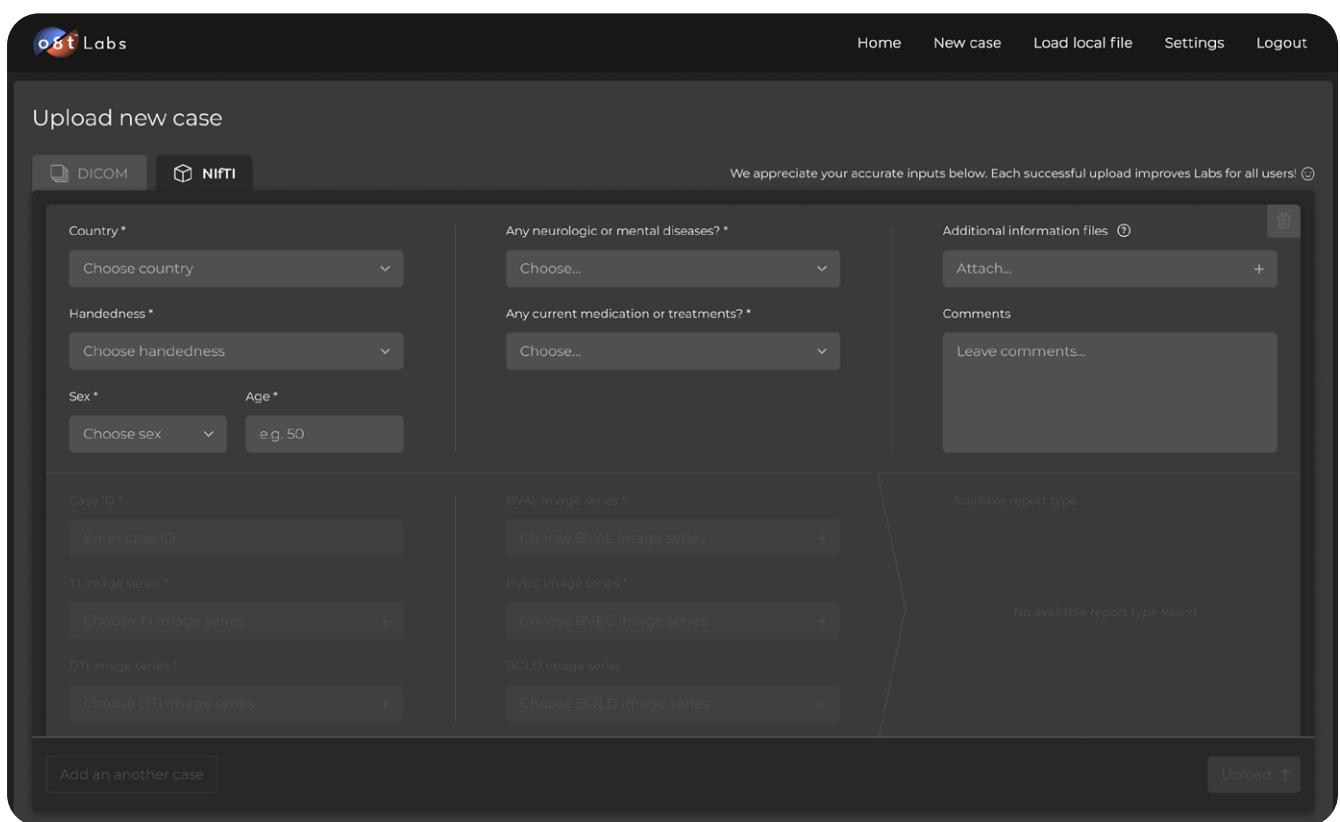

Figure 14 NIFTI Upload Screen With Segregated T1, DTI, Bval, Bvec & BOLD (rs-fMRI) Entries

Figure 15 NIFTI File Structure

Once all the files are correctly selected, available functions (Atlas & Connectomic) will appear. Users can now upload the case or add more cases before uploading them together. Figure 16 displays the completed NIFTI upload screen.

Figure 16 NIFTI Upload Screen With All Files Selected

11.4 UPLOADING PROCESS

All cases selected will run in the background. Do not turn off the computer or close Chrome before this step is done. A job status window will open initially displaying "**STARTED**". It will take approximately 3 minutes for each case to upload to the computer terminal; when complete, you can close the browser. If the message "**Job status: Stopped**" appears, refresh the page and the job should appear in the "**List of Cases**" panel on the home screen and can be restarted. Figure 17 highlights the progression of a successful case upload – with the "**Job Status: STARTED**" message displayed it is imperative that the browser remains open with Labs running.
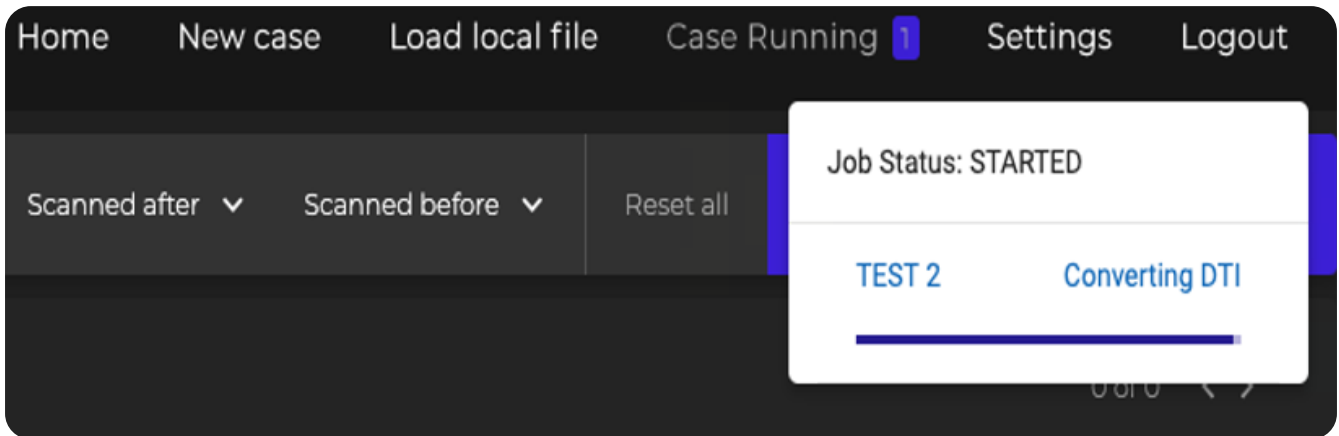
Figure 17 Uploading Process Screen

Once the upload is done on the computer terminal, the job will be uploaded to the cloud. Image processing will take approximately 1 hour. Afterwards, the case will be available for viewing on the Labs home page as displayed in figure 18.

Figure 18 Uploading Process Screen

12. COPYRIGHT & TRADEMARK

The entire contents of this user guide, including but not limited to the graphic design and text, is copyrighted by Omniscient Neurotechnology Pty Ltd. All rights reserved.

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13. SUPPORT

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