LABS USER MANUAL



ENGLISH

V2 2020.10



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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	REQUIREM	REQUIREMENT / STANDARD					
Computer	CPU: Ram: Hard drive:	Intel i5 6th generation (or equivalent) min 8GB required, 16GB or more highly recommended 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: <u>https://www.google.com/chrome</u>

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.

ost Labs						Home	New case	Load loca	l file Se	ettings	Logout
Q Search case	by case ID or subm	nitted by				Scanned after	✓ Scannec	before 🗸		Se	earch
List of cas	ses				Scan Histor	У					
Case ID	Job ID	Upload date	Submitted by	Status							
Case 4	IMkìjcjEd	2020-06-10 03:50	Omni Al Robot	Complete							
Case 3	Mowakm32e	2020-06-10 03:50	Omni Al Robot	Complete							
Case 2	qlwH-UU7S	2020-06-10 03:50	Omni Al Robot	Complete							
Case 1	zyhaGnnh1	2020-06-10 03:50	Omni Al Robot	Complete							

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 preloaded 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 Atlas¹.

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.

Navigate by	
Disease Model	
Network	
Extended Network	
Parcellation	
Region	
Tract	
Function	
Auditory	+
Language	+
VAN	+

Network Parcellations selected 15 Clear Sensorimotor + DMN ++	
Parcellations selected 15 Clear Sensorimotor + DMN +	
Parcellations selected 15 Clear Sensorimotor + DMN +	
Sensorimotor +	
DMN +	
Limbic/Paralimbic +	
Limbic +	
Multiple Demand +	
Salience +	
CEN +	
Auditory +	
✓ Language +	
Export selection	

Figure 4 Navigation Panel

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



ogt Labs				Hoi	me New case	Load local file Settings	Logout
Navigate by		🛞 Atlas 🛛 🎇 Connector	nic 🧟 (MRI	🖨 Graphs 🛛 🛇 Guide	Full screen mode	Controls	
Network		Patient's scan		Normal scan	×	Anatomical	
 Parcellations selected 24 	Clear	• Line • Chi • Chi	1,111 1,1111 1,1111 1,1111 1,1111 1,1111 1,1111 1,1111 1,11111 1,111111	• LNA • LNA	1, 10 %	Tracts	
Sensorimotor	+ +	•U49 •U49 •U49		۰ (رایه ۰ (رایه ۰ (رایه ۰ (رایه		Parcellations	
Limbic/Paralimbic	+	• (, y, %) • (, y, t) • (, y, t) • (, y, t)		• U3% • U40 • U44		Connectomic	
Limbic	+	• 1.65 • 1.66 • 1.67 • 1.670 • 1.670		• LA • LA • LA • RATE		ROI selection	
Salience	+	• R.090 • R.01 • R.02		• RJ140 • RJ50 • RJ50 • RJ40	- 44	Targets for export	
✓ CEN	-	• R,594 • R,976 • 4,756		* 8,040 * 8,070 ***** LPS * 8,710			
✓ Left	+	* A, TEIA © 501		• R_TEIN • CON			

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.

Controls						
Anatomical		-				
Show anate	Show anatomical structure					
Sagittal	Left	right				
Coronal	Back	Front				
Axial	Bottom	Тор				
Saturation		Low				
Contrast		Low				
Tracts		+				
Parcellations		+				
Connectomic		+				
ROI selection						
Targets for ex	port					
Case ID : inp	Case ID : input_case3-post_resection					
Upload date :	2020-06-10 0	3:50				
Submitted by Job ID : Mowa	: Omni Al Ro akm32e	bot				
D	ownload cas	se				

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.
- 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.

							\frown				
ost Labs						Home	New case	Load loca	l file So	ettings	Logout
Q Search case	by case ID or subn	nitted by				Scanned after	 Scanned 	l before 🗸		S	earch
List of cas	ses				Scan Histor	У					
Case ID	Job ID	Upload date	Submitted by	Status							
Case 4	IMk1jcjEd	2020-06-10 03:50	Omni Al Robot	Complete							
Case 3	Mowakm32e	2020-06-10 03:50	Omni Al Robot	Complete							
Case 2	qlwH-UU7S	2020-06-10 03:50	Omni Al Robot	Complete							
Case 1	zyhaGnnhl	2020-06-10 03:50	Omni Al Robot	Complete							

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.



ost Labs		Home New case Load local file Settings Logout
Upload new case	We appreciate your a	eccurate inputs below. Each successful upload improves Labs for all users! ③
Country* Choose country	Any neurologic or mental diseases? * Choose	Additional information files ①
Handedness * Choose handedness	Any current medication or treatments?* Choose	Comments Leave comments
Sex * Age * Choose sex ∨ e.g. 50		

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).

demo_case_inputs	🗅 🕨 🚞 file1 (ge)	🔺 Þ 🧖 1.2.840.1137.640.dcm 🗠
DICOM_sample.zip		
DICOM_sazipped File	s) 🛥 🕨	🧭 1.2.840.1137.642.dcm 🗠
p_nifti.zip	۵.	🗭 1.2.840.1137.643.dcm 🗠
SSG Cases	۵ ۲	1.2.840.113619.2.176.3596.10642200.23462.1412771237.654.dcm
		🧭 1.2.840.1137.655.dcm 🗠
		🗭 1.2.840.1137.656.dcm 🗠
		1.2.840.1137.870.dcm
		1.2.840.1137.871.dcm
		🗭 1.2.840.1137.873.dcm 🛆
		1.2.840.1137.899.dcm
		🗭 1.2.840.1137.904.dcm 🗠

Figure 12 DICOM File Structure

Upload 5,223 files to this site?

This will upload all files from '2nd Scan'. Only do this if you trust the site.





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).

oð t Labs		Home	New case	Load local file	Settings	Logout
Upload new case						
	We appreciate y	your accurate i	nputs below. Eac	h successful upload ir	nproves Labs for	all users! 😳
Country*	Any neurologic or mental diseases? *		Additional i	nformation files ⑦		Ū
Australia 🗸						
Handedness *	Any current medication or treatments?*		Comments			
Right-handed Y						
Sex * Age *						
Female v 60						
DICOM folder	TI image series *		Available re	port type		
File102	TI AX +C (38 files)			_ /	\frown	
	DTI image series *		নি	RA / [と日二	
	TENSOR 25 Directions 1000b (702 files) 🔷		ر م	γ (^L		
	BOLD image series					
	TENSOR 25 Directions 1000b (702 files) 🗸 🗸		\checkmark	Atlas	Connectomic	

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.

oft Labs		Home	New case	Load local file	Settings	Logout
Upload new case						
DICOM 😚 NIFTI	We appreciate	your accurate ir	nputs below. Eacł	n successful upload in	nproves Labs fo	r all users! 😳
Country*	Any neurologic or mental diseases? *		Additional ir	formation files ⑦		
Handedness*	Any current medication or treatments? *		Comments			
Sex* Age*						

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

				Q Search
Cases	△ ▶ [] ir	nput_bold.nii.gz	۵	
NIFITI sample	○ ► □ II	nput_bvec.bvec	0	
🕑 p_nifti.zip	○ I [†] ir	nput_dwi.nii.gz	0	
zipped files	≏ ⊧ [f) ir	nput_t1.nii.gz	۵	
				Cancel Open

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.

ogt Labs			Home	New case	Load local file	Settings	Logout
Upload new case							
DICOM 😚 NIFTI		We appreciat	e your accurate in	outs below. Each	successful upload in	nproves Labs for a	all users! 🔾
Country*		Any neurologic or mental diseases? *		Additional inf	ormation files ③		Ŵ
Handedness *		What are the current medication or treatments? *		Comments			
Right-handed							
Sex * Age *							
Female v 60							
Case ID *		BVAL image series *		Available repo	ort types		
ABC1234567		Input_BVAL.nii.gz	面				
TI image series *		BVEC image series *		لآج کا	,্স 🖸	22_	
Input_Tl.nii.gz	Ŵ	Input_BVEC.nii.gz		$\langle \chi \rangle$	ξ L		
DTI image series *		BOLD image series			, , , , , , , , , , , , , , , , , , ,		
Input_DTI.nii.gz	Û	Input_BOLD.nii.gz	ŵ	✓ At	ias 🗸	Connectomic	

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.



Home	New case Load local file		e Case Ru	inning 1	Settings	Logout
Scanned after 🗸 Scanned before 🗸		Reset all	Job Status: STARTED			
				TEST 2	Conver	ting DTI
					0.01	

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.

List of cas	ses			1-5 of 5 < >
Case ID	Job ID	Upload date	Submitted by	Status
TEST 2	MDSdwq826	2020-06-11 08:20	Jerry	Step 12 of 23
Case 4	IMk1jcjEd	2020-06-10 03:50	Omni Al Robot	Complete
Case 3	Mowakm32e	2020-06-10 03:50	Omni Al Robot	Complete
Case 2	qlwH-UU7S	2020-06-10 03:50	Omni Al Robot	Complete
Case 1	zyhaGnnhl	2020-06-10 03:50	Omni Al Robot	Complete

Figure 18 Uploading Process Screen



12. COPYRIGHT & TRADEMARK

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13. SUPPORT

If you have further queries please get in touch with us via <u>https://labs.o8t.com/contactus</u>.