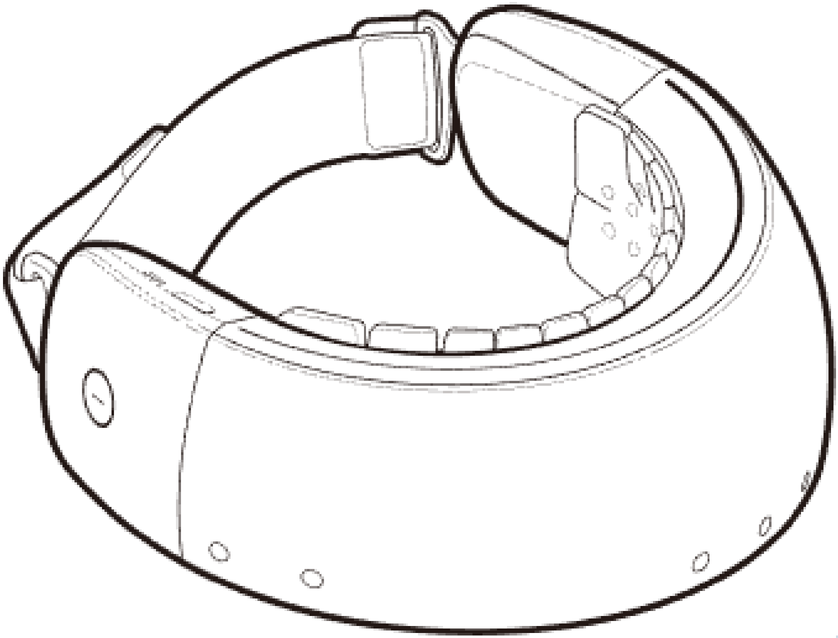
OBELAB



NIRSIT

Analysis Tool Manual

Amendments

Version	Date	Details	Remarks
2.1	18.01.11	Compatible with Version 2.1	
2.2	18.08.17	Compatible with Version 2.2	
2.5	19.05.17	Connectivity function added	
3.0+	19.11.07	GLM function added	
3.5	20.06.14	Bug fix, manual updated	
3.6	20.11.13	GLM function modified	
3.6.1	21.03.26	GLM and Connectivity nidufued	

Notation

Notation is a series of special symbols or conventions used in this manual to denote different items.

This manual uses the following notation for users’ better understanding of the device:

Notation	Description
“ ”	Used to denote a reference. Example: See "Chapter 1. Overview."
Bold	Used to denote GUI elements such as menus and buttons. Example: Click the **STOP** button.
>	Used to list several menus or buttons in sequence. Example: Click the **STOP** > **OPEN** buttons.
▪ ABC ▪ ABC ▪ ABC	Used to divide or list items of the same level in an organized way.
1 ABC **2** ABC **3** ABC	Used to describe a work procedure in order.
❶ ❷ ❸	Used to name or describe components of an image.

Table of Contents

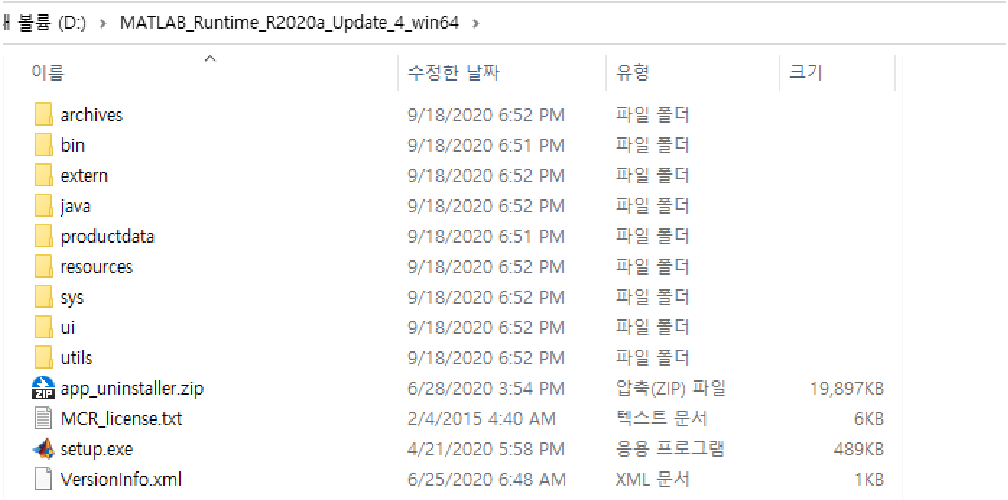
1. Starting NIRSIT Analysis Tool

1.1 Getting started with the .exe file

1.1.1 Install Matlab Compiler Runtime v9.8

You can download MATLAB Compiler Runtime v.9.8, which is shown as R2020a(9.8), directly from https://kr.mathworks.com/products/compiler/matlab-runtime.html.

If MATLAB Compiler Runtime v.9.8 is already installed on your PC under C:\Program Files\MATLAB\MATLAB Runtime\v98, please skip this step.

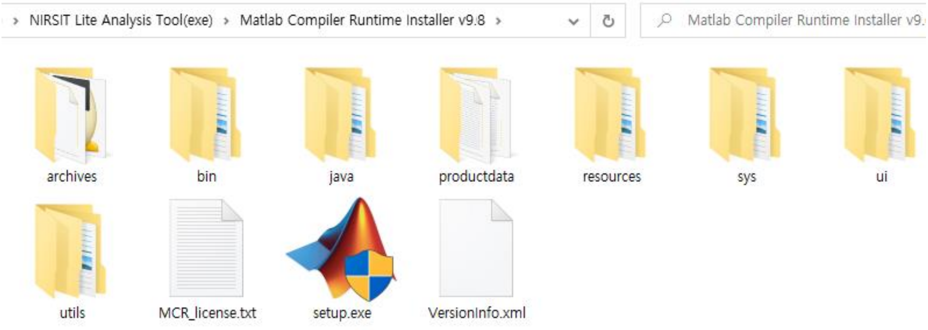


볼륨 (D:) › MATLAB_Runtime_R2020a_Update_4_win64 ›

이름	수정한 날짜	유형	크기
archives	9/18/2020 6:52 PM	파일 폴더	
bin	9/18/2020 6:51 PM	파일 폴더	
extern	9/18/2020 6:52 PM	파일 폴더	
java	9/18/2020 6:52 PM	파일 폴더	
productdata	9/18/2020 6:51 PM	파일 폴더	
resources	9/18/2020 6:52 PM	파일 폴더	
sys	9/18/2020 6:52 PM	파일 폴더	
ui	9/18/2020 6:52 PM	파일 폴더	
utils	9/18/2020 6:52 PM	파일 폴더	
app_uninstaller.zip	6/28/2020 3:54 PM	압축(ZIP) 파일	19,897KB
MCR_license.txt	2/4/2015 4:40 AM	텍스트 문서	6KB
setup.exe	4/21/2020 5:58 PM	응용 프로그램	489KB
VersionInfo.xml	6/25/2020 6:48 AM	XML 문서	1KB

1.1.2 Double-click 'setup.exe' icon shown below

Unpack and execute 'setup.exe' file in the folder as shown below.



› NIRSIT Lite Analysis Tool(exe) › Matlab Compiler Runtime Installer v9.8 ›

Matlab Compiler Runtime Installer v9.

1.1.3 Installation Process

1. After the main screen appears on the PC, please wait for a few seconds.

2. Click **Next** button shown on screen.

This application will install MATLAB Runtime.

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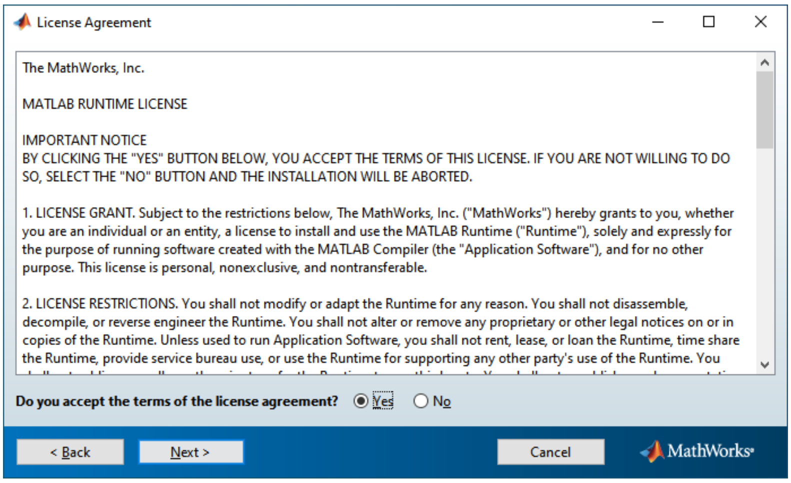
WARNING: This program is protected by copyright law and international treaties. Copyright 1984-2020, The MathWorks, Inc. Protected by U.S. and other patents. See MathWorks.com/patents

1

3. Click **Yes** button to agree to the terms and conditions of the license



The MathWorks, Inc.

MATLAB RUNTIME LICENSE

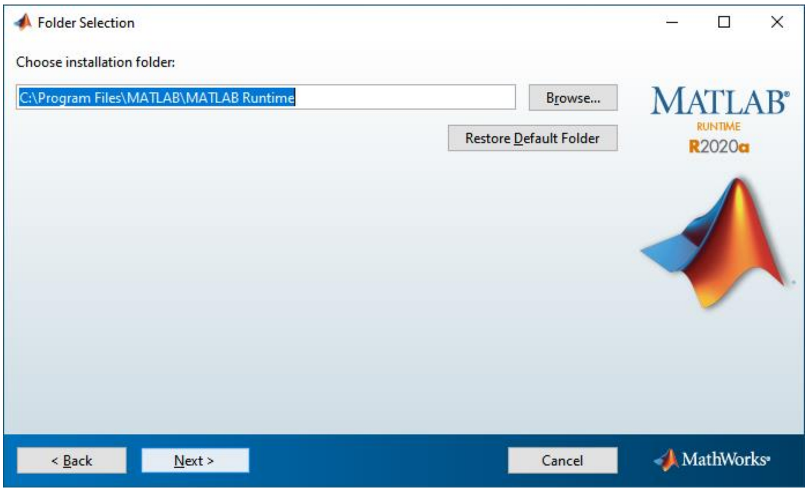
IMPORTANT NOTICE
BY CLICKING THE "YES" BUTTON BELOW, YOU ACCEPT THE TERMS OF THIS LICENSE. IF YOU ARE NOT WILLING TO DO SO, SELECT THE "NO" BUTTON AND THE INSTALLATION WILL BE ABORTED.

1. LICENSE GRANT. Subject to the restrictions below, The MathWorks, Inc. ("MathWorks") hereby grants to you, whether you are an individual or an entity, a license to install and use the MATLAB Runtime ("Runtime"), solely and expressly for the purpose of running software created with the MATLAB Compiler (the "Application Software"), and for no other purpose. This license is personal, nonexclusive, and nontransferable.

2. LICENSE RESTRICTIONS. You shall not modify or adapt the Runtime for any reason. You shall not disassemble, decompile, or reverse engineer the Runtime. You shall not alter or remove any proprietary or other legal notices on or in copies of the Runtime. Unless used to run Application Software, you shall not rent, lease, or loan the Runtime, time share the Runtime, provide service bureau use, or use the Runtime for supporting any other party's use of the Runtime. You

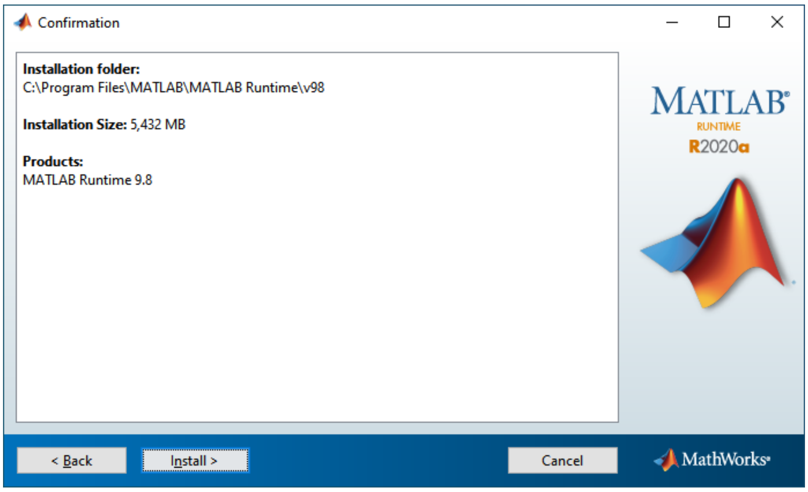
Do you accept the terms of the license agreement? ● Yes ○ No

4. If you already have a Matlab Runtime installed, please skip this step. If you need to re-install Matlab Runtime, click **Install** button for installation.



Choose installation folder: C:\Program Files\MATLAB\MATLAB Runtime

5. Proceed with the installation.

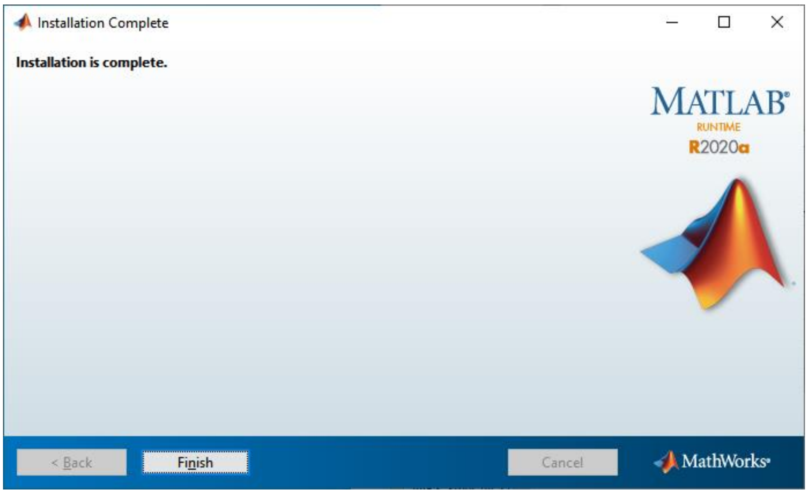

Confirmation

Installation folder:
C:\Program Files\MATLAB\MATLAB Runtime\v98

Installation Size: 5,432 MB

Products:
MATLAB Runtime 9.8

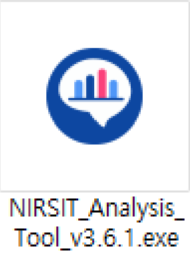
6. Please wait until the installation is completed and 'Installation is complete' shows up on the screen. Click **Finish** button.


Installation Complete

Installation is complete.

1.1.4 Run 'NIRSIT Analysis'

1 Double click 'NIRSIT_Analysis_Toolk_v3.6.1.exe' icon as shown below



2 Splash screen

Please wait for a few minutes after the Loading Screen is turned off. Start Screen will show up momentarily.

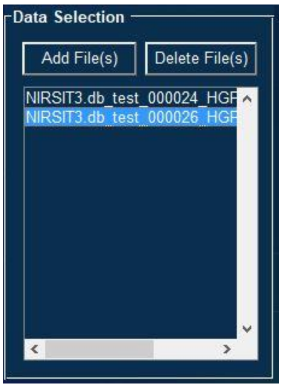
2. Analysis Tool Outline

NIRSIT Analysis Tool is comprised of six panels, as shown below. This tool provides a variety of functions that allow you to easily analyze and process measured data in real time. Chapter 2 describes the specific functions provided in each panel of the analysis tool and how to use them.

No.	Description
1	Data Selection Panel
2	Time Series Graph Panel
3	Time Series Selection Panel
4	Channel Selection Panel
5	Analysis Tool Panel
6	Gyro Graph & Error History

2.1 Data Selection Panel

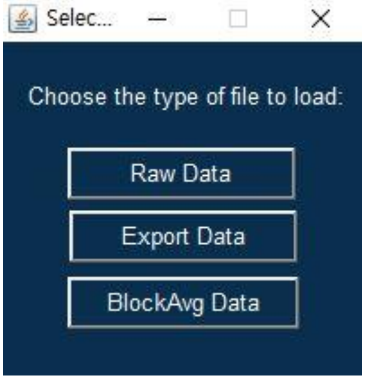
Use this panel to add, select, and delete data files.



2.1.1 Adding files

Load one or more raw data files measured using NIRSIT. You can also load exported data files and Block average concentration data files.

Refer to “3.1.1 Loading data” for details.

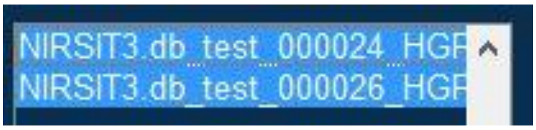


Choose the type of file to load:

2.1.2 Selecting files

Once data files are loaded, the panel displays a list of the files.

To select multiple files, drag the files or click the files while holding down the Shift or Ctrl key.

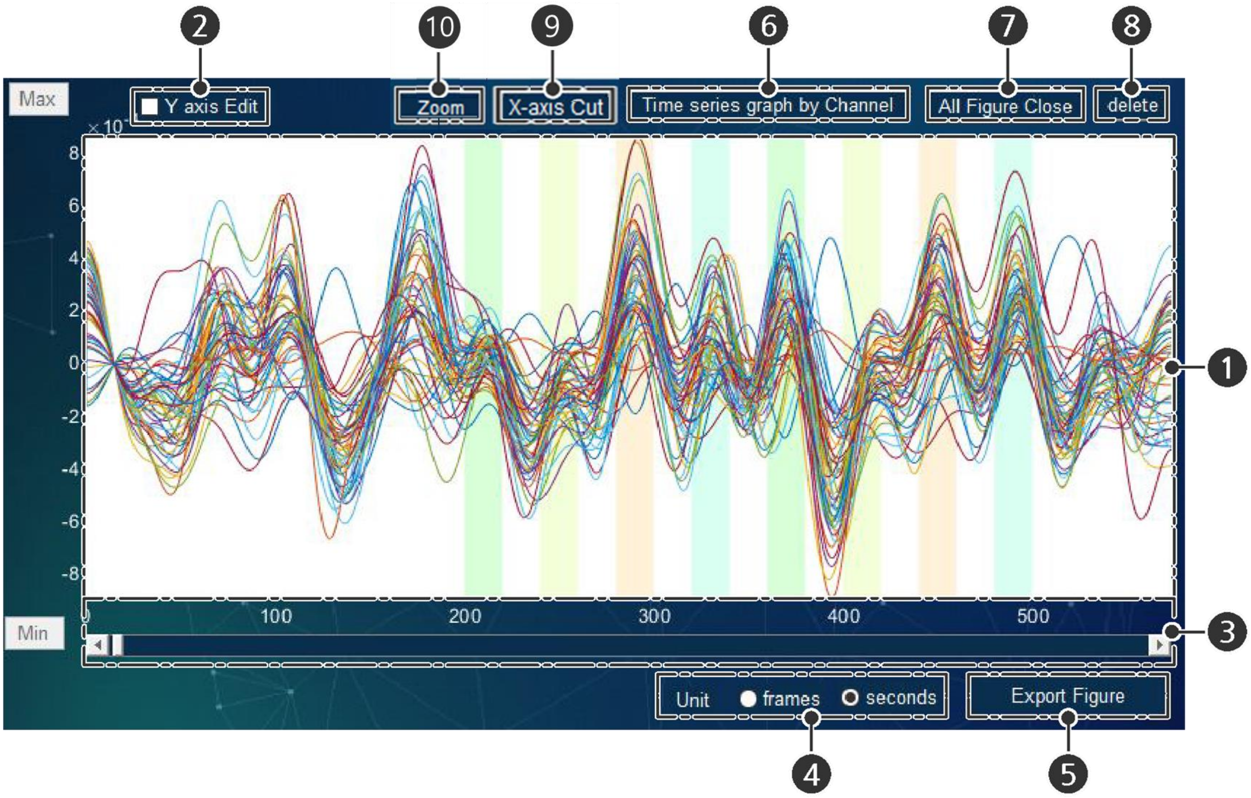


2.1.3 Deleting files

Select and delete one or more files.

2.2 Time Series graph panel

This panel shows data signals, using a time series graph.



No.	Description
1	Time Series graph update
2	Y-axis edit function
3	X-axis slide bar functions
4	Selecting a unit
5	Export Figure
6	Exporting a time series graph by channel
7	Closing displayed graphs—All Figure Close
8	Deleting selected channels from a time series graph
9	Cutting data with typing X-axis range
10	Zoom in/out to the selected area

2.2.1 Time Series graph update

If data or options change, the graph is updated accordingly.

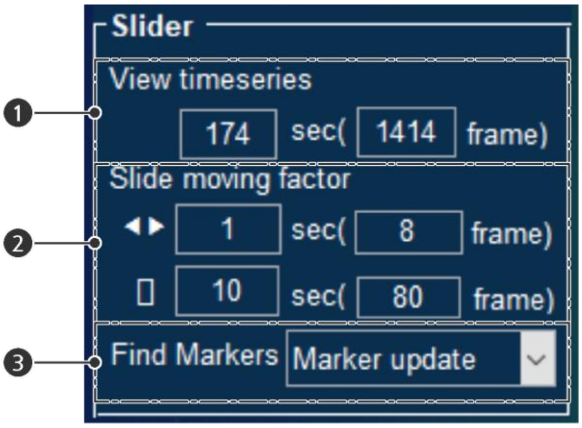
Clicking a curve displays the channel that corresponds to the curve. The channel display will disappear if you click on an area that is not a curve.

2.2.2 Y-axis edit function

If the Y axis Edit checkbox is selected, the Max and Min icons are enabled and minimum or maximum values can be edited.

If the checkbox is deselected, default values are restored.

2.2.3 X-axis slide bar functions



Slider

View timeseries

174 sec(1414 frame)

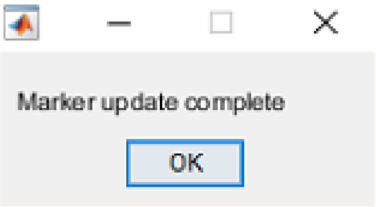
Slide moving factor

◄► 1 sec(8 frame)

▯ 10 sec(80 frame)

Find Markers Marker update

No.	Description
1	**View Time Series** Specify how much time (or frames) to display on a single screen. You can move the slide bar forward for faster display.
2	**Slide bar moving factor** Specify how far the slide bar will move.  (◄► = Both end arrows / [] = Slide bar) The value of ◄► cannot be greater than the value of [].
3	**Find Markers** Click Marker update and select the marker number you want to analyze.

No.	Description
	 Marker update complete If a marker number is selected, you can adjust the total duration for the time series graph to sync with the selected marker period. You can move the slide bar within the period of time. 

2.2.4 Selecting a unit

Set the unit for X axis to either frames or seconds.

The unit can be used for other options, such as Edit Marker and Block Average.

The unit is set to seconds by default. As existing data is measured in frames, some differences can occur (Fs = 8.138 Hz).

2.2.5 Export Figure

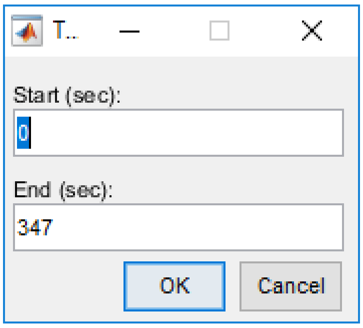
Export a graph in the time series graph panel as an image.

Available options for exporting a graph include Raw (780nm/850nm), Optical Density (780nm/850nm), Hb Concentration (HbO2/HbR/HbT), 3cm, 1.5cm, 2.12cm, and 3.35cm.

2.2.6 T Exporting a time series graph by channel

Available options for exporting a graph include Raw, Optical Density, Hb Concentration, 3cm, 1.5cm, 2.12cm, and 3.35cm.

Click **Time series graph by Channel** button to specify the time range to export a graph.

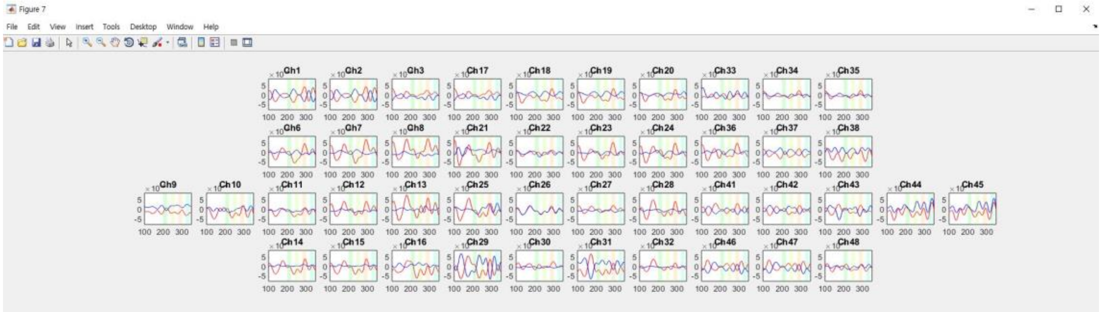


Start (sec): 0

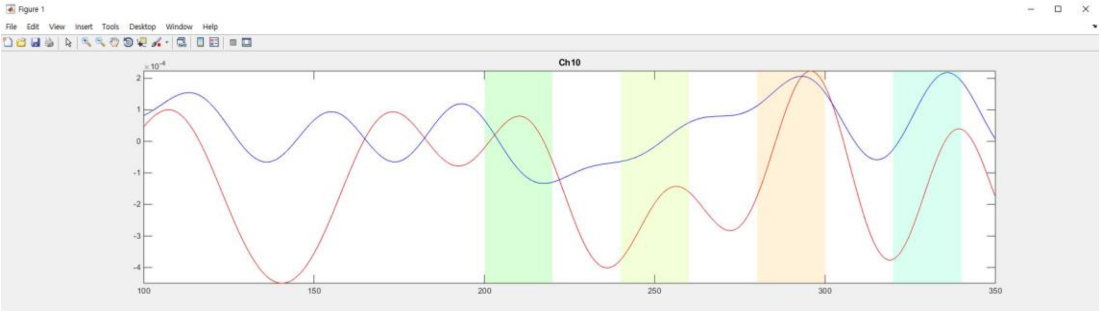
End (sec): 347

- Red line indicates data on 780 nm or HbO2.
- Blue line indicates data on 850 nm or HbR.

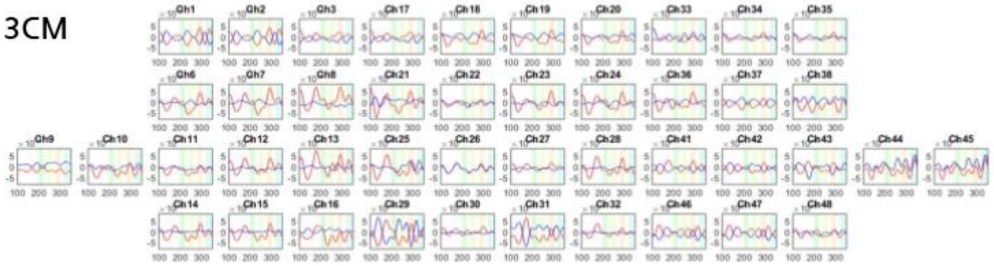
Explanation on graph / Selected graph

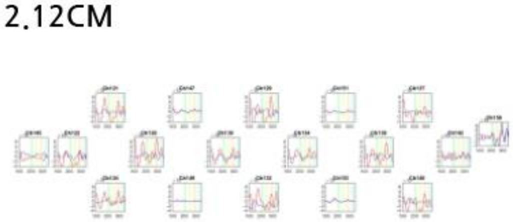


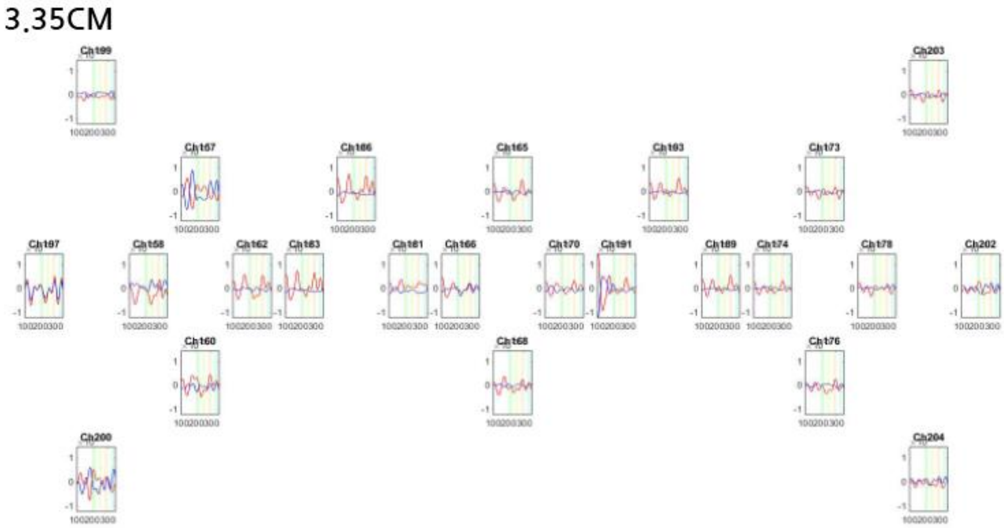
- If channels overlap, the upper channel is displayed by default.
- If the upper channel is rejected, the lower channel is displayed instead. Rejected channels (e.g.: Ch5) are not displayed on the time series graph panel.
- If you click a channel, you can enlarge the graph view of the selected channel (e.g.: click Ch10).



Time series graph by distance-between-sensors







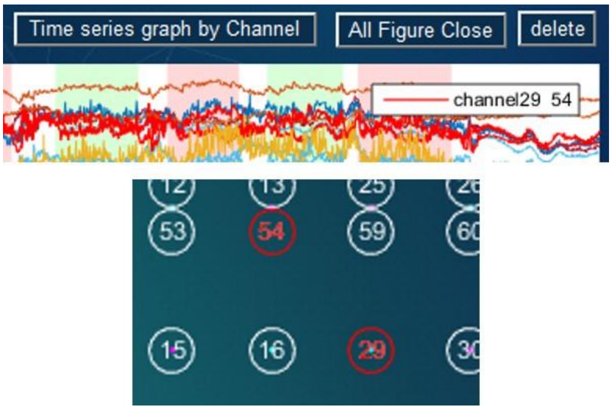
2.2.7 Closing displayed graphs—All Figure Close

You can close multiple windows simultaneously by clicking All Figure Close.

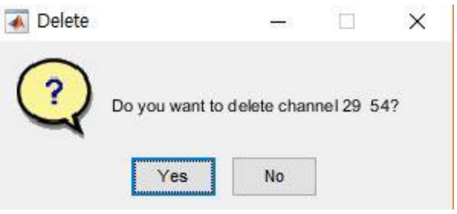
2.2.8 Deleting selected channels from a time series graph

If you click a specific curve in a time series graph, the curve color will change to red and the corresponding channel number will appear. Also, the color of the selected channel number in the channel selection panel will change to red.

- Multiple selection is possible.



- If clicking the **delete** button, a confirmation window appears asking if you want to delete the selected channels. If you click **Yes**, the selected channels will be considered as rejected channels during the rest of the analysis process. If you click **No**, the channels will not be deleted.

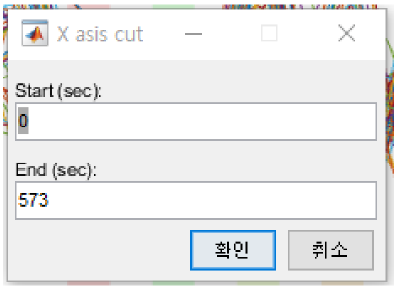


Do you want to delete channel 29 54?

- Deleted channels will be considered as rejected channels for the rest of the analysis process.
- To restore the deleted channels, load raw data or perform signal processing again.

2.2.9 X-axis Cut

You can trim your data with **X-axis Cut** button. If you click this button, you can type start and end time (second) as shown below.



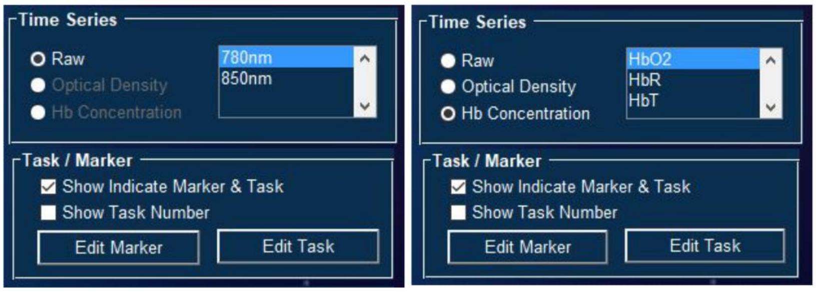
Start (sec): 0

End (sec): 573

2.2.10 Zoom

Once you push the **Zoom** button, mouse cursor turns into '+' shape. And you can enlarge your data figure by dragging with mouse left click. If you want to go back to the original figure, double click the figure anywhere. And when you push **Zoom** button again, then 'Zoom' mode will be disabled.

2.3 Time Series selection panel



Time Series
○ Raw
● Optical Density
● Hb Concentration
780nm
850nm

Task / Marker
☑ Show Indicate Marker & Task
☐ Show Task Number

Time Series
● Raw
● Optical Density
○ Hb Concentration
HbO2
HbR
HbT

Task / Marker
☑ Show Indicate Marker & Task
☐ Show Task Number

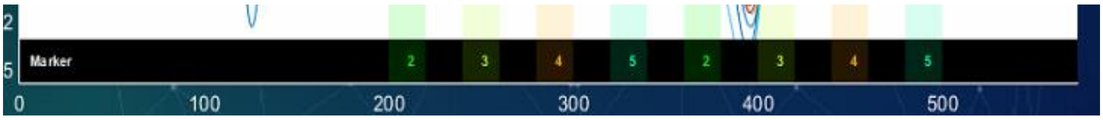
2.3.1 Time Series type

- Raw: Raw data from sensors
  - 780 nm WL
  - 850 nm WL
- Optical Density: Optical density data converted from raw data
  - 780 nm WL
  - 850 nm WL
- Hb Concentration: Hemoglobin concentration data obtained through MBLL calculation process
  - HbO2: Oxyhemoglobin

- HbR: Deoxyhemoglobin
- HbT: Total hemoglobin (HbO2 + HbR)

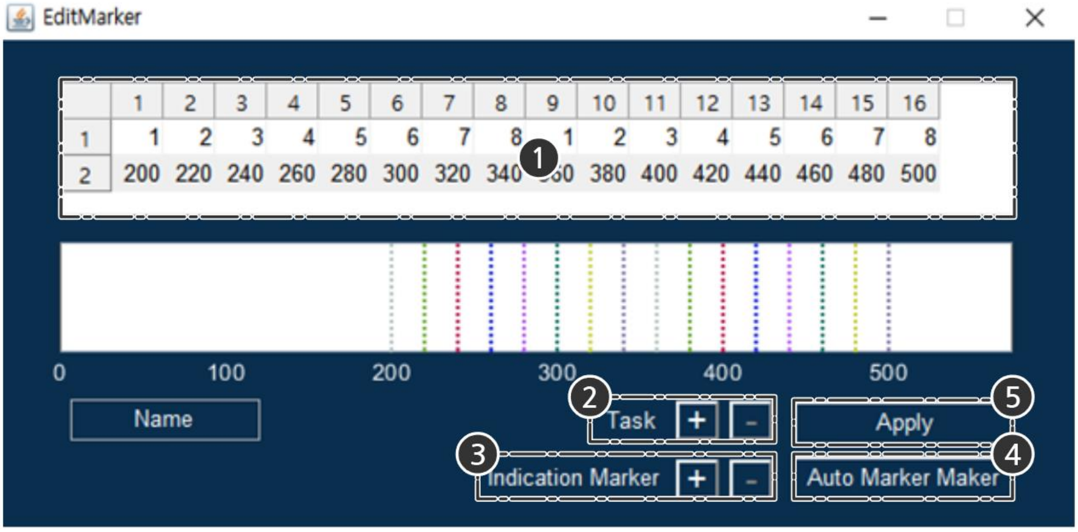
2.3.2 Show Indicate Marker & Task / Show Task Number

- Time series graph does not display marker information if the Show Markers checkbox is deselected.
- The time series graph displays marker names if the Show Marker Name checkbox is selected.



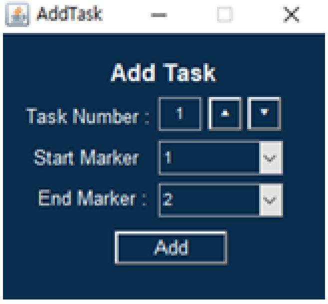
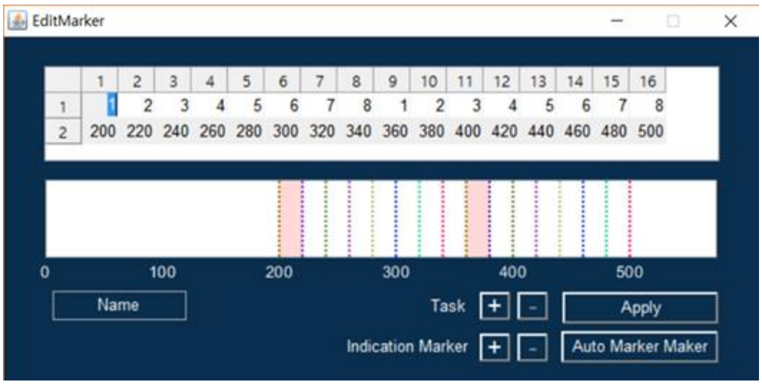
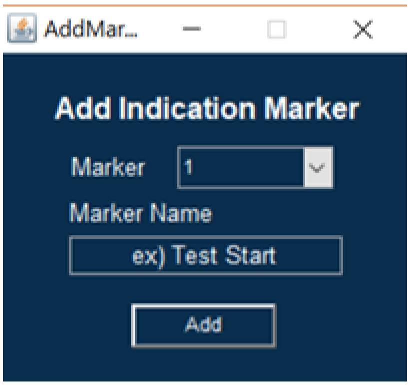
2.3.3 Edit Marker

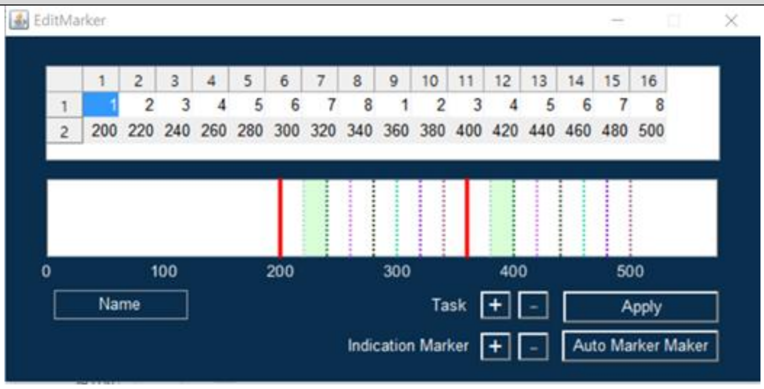
Create a task section by using the displayer markers when a file is loaded in Excel.



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
2	200	220	240	260	280	300	320	340	[illegible]	380	400	420	440	460	480	500

No.	Description
1	▪ **Edit Marker** Edit a marker number and time directly from the table. • If you press **Enter** after editing a marker number and time, the "marker line graph" below the table is updated.
2	▪ **Adding/deleting a task** Add a task by specifying a task number, start marker, and end marker.

No.	Description
	 Add Task Task Number : 1 ▲ ▼ Start Marker 1 End Marker : 2 - **Task Number** can be set in the range 1–9, using the ▲ and ▼ buttons. - If you click **Add**, the "marker line graph" is updated and blocks are created according to the configured number of sections, as shown below.  1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 1: 1 2 3 4 5 6 7 8 1 2 3 4 5 6 7 8 2: 200 220 240 260 280 300 320 340 360 380 400 420 440 460 480 500 - If you select a created block from the "marker line graph," the "**Name**" box shows the task number. - To delete a task, select the block to delete and click **Task –** button. A confirmation message will appear, the "marker line graph" will be updated, and the task will be deleted.
3	▪ **Adding/deleting an indication marker** Add only an indication marker instead of a block, if necessary.  Add Indication Marker Marker 1 Marker Name ex) Test Start - Select the marker numbers to which to add an indication marker, and set the marker names. (e.g., Task Start, Task End, Rest Start, Rest End) - If you click **Add**, the "marker line graph" is updated and thick lines are added to the positions of the configured marker numbers (Marker 1 = indication marker, Markers 2–3 = tasks).

<table>
<tr><th>No.</th><th>Description</th></tr>
<tr><td></td><td>


<table>
<tr><th></th><th>1</th><th>2</th><th>3</th><th>4</th><th>5</th><th>6</th><th>7</th><th>8</th><th>9</th><th>10</th><th>11</th><th>12</th><th>13</th><th>14</th><th>15</th><th>16</th></tr>
<tr><td>1</td><td>1</td><td>2</td><td>3</td><td>4</td><td>5</td><td>6</td><td>7</td><td>8</td><td>1</td><td>2</td><td>3</td><td>4</td><td>5</td><td>6</td><td>7</td><td>8</td></tr>
<tr><td>2</td><td>200</td><td>220</td><td>240</td><td>260</td><td>280</td><td>300</td><td>320</td><td>340</td><td>360</td><td>380</td><td>400</td><td>420</td><td>440</td><td>460</td><td>480</td><td>500</td></tr>
</table>

If you select a created line from the “marker line graph,” the “Name” box shows the marker name.
To delete an indication marker, select the indication marker to delete and click Indication Marker “–” button. A confirmation message will appear, the “marker line graph” will be updated, and the selected indication marker will be deleted.

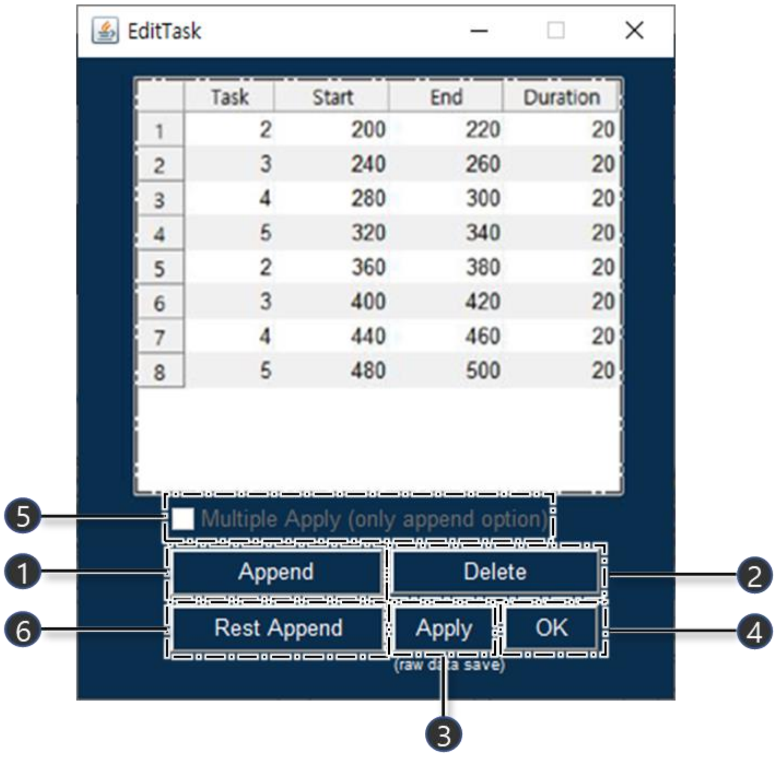
</td></tr>
<tr><td>4</td><td>
Auto Marker Maker
This function is enabled when each pair of all marker numbers is composed of an even number and an odd number with 18 or below. (e.g., A valid set of marker numbers is as follows: (1,2), (3,4) or (3,4), (9,10), (13,14).)

This function creates a task by taking a pair of numbers as a default block.
The button is enabled only when the function is available.

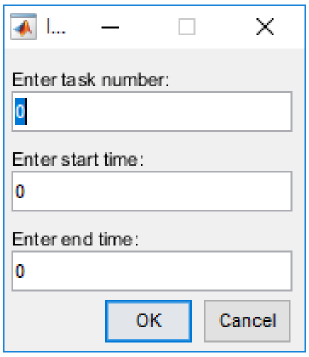
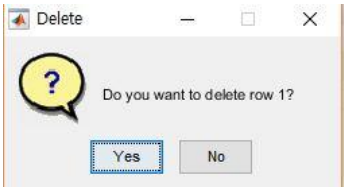
</td></tr>
<tr><td>5</td><td>
Apply
Apply and save added tasks and indication markers as raw data.
Update task and indication marker information to the Time Series graph.
</td></tr>
</table>

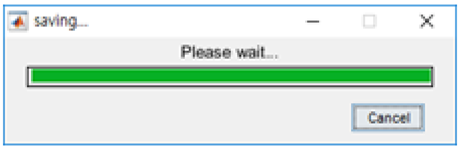
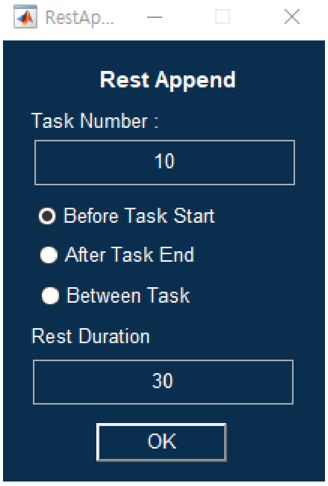
2.3.4 Edit Task

Use **Edit Task** button to add, edit, or delete task information.



	Task	Start	End	Duration
1	2	200	220	20
2	3	240	260	20
3	4	280	300	20
4	5	320	340	20
5	2	360	380	20
6	3	400	420	20
7	4	440	460	20
8	5	480	500	20

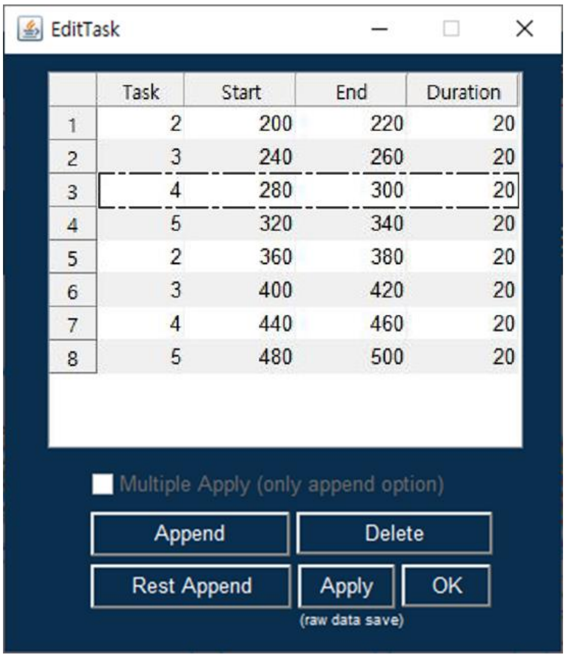
No.	Description
1	▪ **Adding Task** (**Append** button) Add a task by specifying task number, start time, and end time.  Enter task number: 0 Enter start time: 0 Enter end time: 0
2	▪ **Deleting Task** (**Delete** button) Delete task information by selecting marker rows and clicking **Delete** button.  Do you want to delete row 1?

No.	Description
3	▪ **Saving Task** (**Apply** button) To apply and save edited task information, click **Apply**. Task information is applied only within the current analysis tool. 
4	▪ **Applying Task** (**OK** button) To apply edited task information, click **OK.** Task information is applied only within the current analysis tool.
5	▪ **Multiple Apply (only append option)** Selecting multiple data activates this button. You can add the same task into selected data at once by checking this option.
6	▪ **Rest Append**  Task Number : 10 ● Before Task Start ○ After Task End ○ Between Task Rest Duration 30 You can add a 'Rest' block into existing task condition with the above option. This option automatically adds 'Rest' block **Before Task**, **After Task** or **Between Task** with entered **Rest Duration**. Also, it can be used with **Multiple Apply** (only the **Append** option).

To edit task information

Select and click the task in EditTask window you want to edit.

Then edit the information by manually entering a task number, start time, and end time.



	Task	Start	End	Duration
1	2	200	220	20
2	3	240	260	20
3	4	280	300	20
4	5	320	340	20
5	2	360	380	20
6	3	400	420	20
7	4	440	460	20
8	5	480	500	20

- To apply edited task information, click **OK.**
- To apply and save edited task information, click **Apply**.

2.4 Channel Selection panel

Channel Selection

○ 3cm ● 1.5cm ● 2.12cm ● 3.35cm

Delete Multiple Channels Select Select Done Delete

R C L All

☐ Allow toggling rejected channels

2.4.1 Channel group

If a distance between the laser and detector is selected, the channel select panel and time series graph panel are updated.

Channel Selection

○ 3cm ● 1.5cm ● 2.12cm ● 3.35cm

Delete Multiple Channels Select Select Done Delete

R C L All

☐ Allow toggling rejected channels

- 3cm (1ch to 68ch) / 1.5cm (69ch to 120ch) / 2.12cm (121ch to 156ch) / 3.35cm (157ch to 204ch)

2.4.2 Channel and Optodes

- Red dot indicates the laser and blue dot indicates the detector.
- Overlapping channels are displayed stacked together.

  (e.g.: Ch6 and Ch49 are overlapping)

3CM

1.5CM

2.12CM

3.35CM

2.4.3 Deleting multiple channels

3 Click **Select** button on the **Channel Selection** panel.

Wait until multiple channels appear on the screen.

(Note: If you select a channel before the configuration process is completed, some channels may not be displayed.)

4 Select channels to be deleted.

- Selected channels will become red.
- To deselect channels, click them once again. Their original color will be restored.

5 After selecting all required channels, click **Select Done** button.

The **Delete** button will be enabled.

6 Click **Delete** button. The selected channels will be grayed out and deleted.

- Deleted channels will be considered as rejected channels during the rest of the analysis process.
- To restore the deleted channels, load raw data or perform signal processing again.

2.4.4 Selecting left, right, center, or all channels

If you click **R** button, the time series graph for the channels on the right is updated.

- To view all channels except for the left channels, click **R** and **C** buttons.
- This function does not delete (reject) the raw data corresponding to the selected channels.

L is clicked

C is clicked

L and **C** are clicked

R is clicked

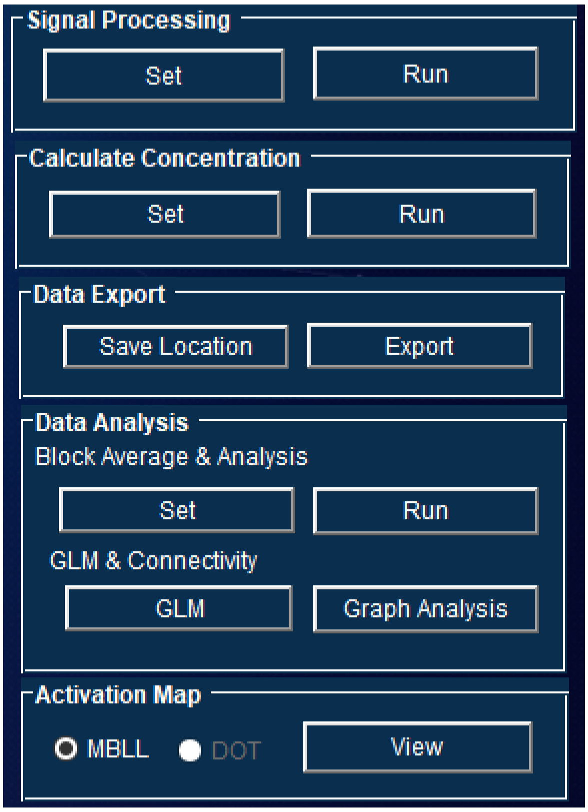
2.4.5 Toggling rejected channels

If the "Allow toggling rejected channels" checkbox is selected, disabled rejected channels are enabled and can be displayed in the time series graph.

- Channels rejected due to poor signal-to-noise ratio are shown in gray and are disabled in the channel selection panel.
- Toggling rejected channels is for display purposes only. It does not affect signal processing or data analysis process.

2.5 Analysis tool panel

This panel processes and analyzes raw data.

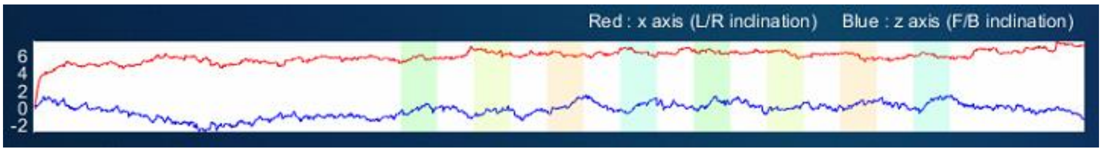


Refer to "3 Data Analysis Process" for details on how to use these buttons.

2.6 Gyro Graph and Error History

2.6.1 Gyro Graph

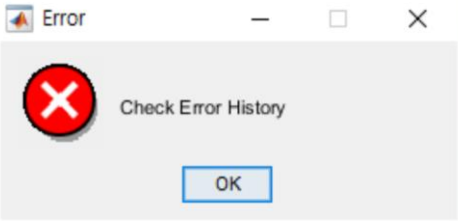
View a gyro graph for data.



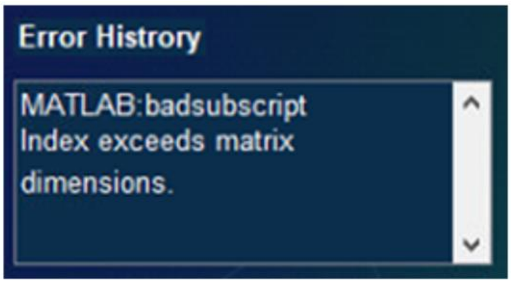
- Red line: x axis (L/R inclination) / Blue line: z axis (F/B inclination)
- The red line indicates x axis movement (head turning), and the blue line indicates z axis movement (head lowering).

2.6.2 Error History

You can check the error history.



Check Error History



MATLAB:badsubscript
Index exceeds matrix dimensions.

If an error occurs, an error message appears.

3. Data Analysis Process

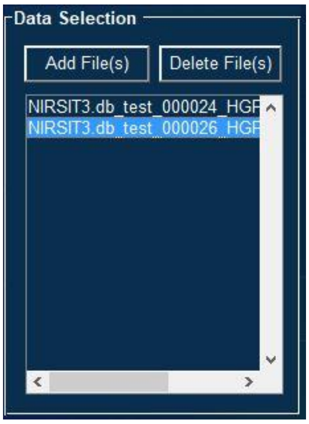
3.1 Signal processing

3.1.1 Loading data (adding files)

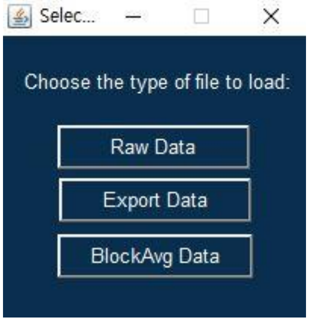
Multiple files can be loaded simultaneously.

A maximum of 100 data files can be loaded. However, the actual number of data files that can be loaded can be smaller than 100, depending on your machine's computing power and processed data size.

7 Click **Add File(s)** in the **Data Selection** panel.



8 Select a file type when a selection window appears as shown below.



- **Raw Data**

  Data without any filter processing.

  - Data received from the DB extractor of the PC tool is saved as a .csv file.
  - Once .csv file is loaded, a mat file is created automatically.
  - The data can be opened as a mat file, which is easier to use than .csv file.

- **Export Data**

  Extracted data through data export function.

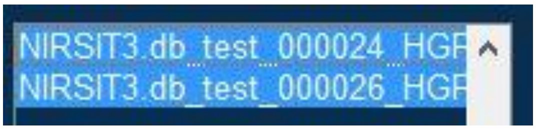
- **BlockAvg Data**

Data containing changes in hemoglobin level. This data is obtained through analysis process.

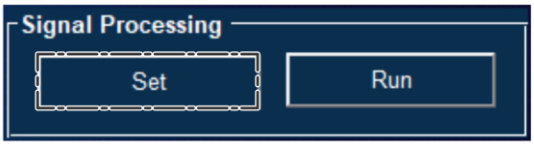
Block Average data, saved as a mat file, can only be loaded by clicking **BlockAvg Data**.

3.1.2 Data Selection

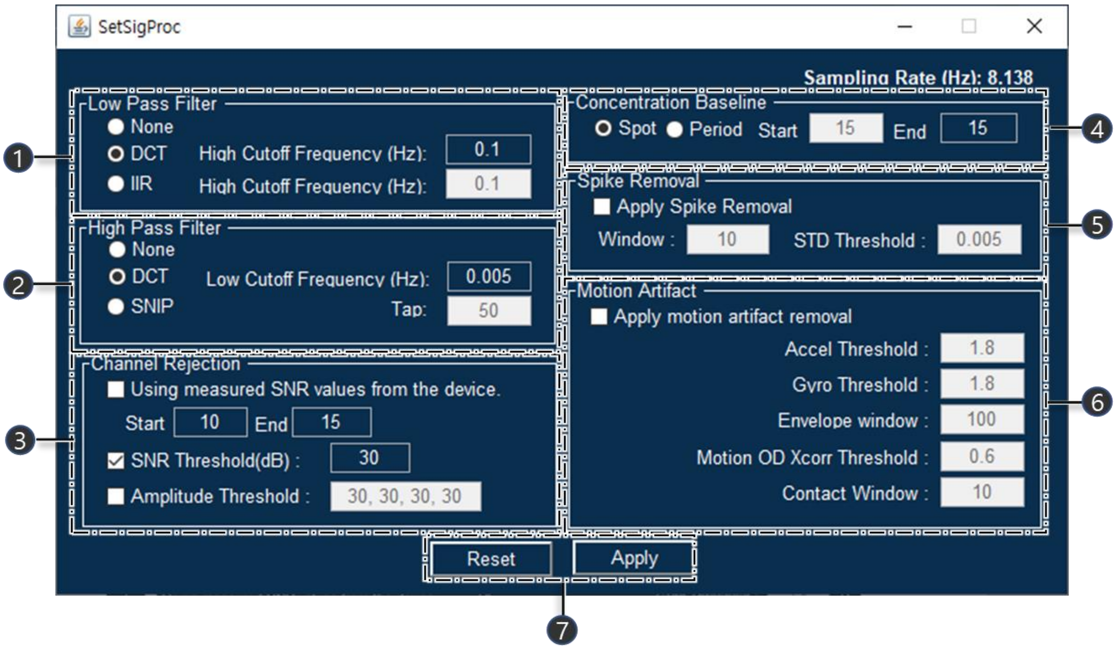
1 Select one or more data files in the **Data Selection** panel for signal processing and click **Set** button in the **Signal Processing** panel.



NIRSIT3.db_test_000024_HGF
NIRSIT3.db_test_000026_HGF



2 The following window appears. Use the window to configure signal processing settings.



Sampling Rate (Hz): 8.138

Low Pass Filter
● None
○ DCT High Cutoff Frequency (Hz): 0.1
● IIR High Cutoff Frequency (Hz): 0.1

High Pass Filter
● None
○ DCT Low Cutoff Frequency (Hz): 0.005
● SNIP Tap: 50

Channel Rejection
☐ Using measured SNR values from the device.
Start 10 End 15
☑ SNR Threshold(dB) : 30
☐ Amplitude Threshold : 30, 30, 30, 30

Concentration Baseline
○ Spot ● Period Start 15 End 15

Spike Removal
☐ Apply Spike Removal
Window : 10 STD Threshold : 0.005

Motion Artifact
☐ Apply motion artifact removal
Accel Threshold : 1.8
Gyro Threshold : 1.8
Envelope window : 100
Motion OD Xcorr Threshold : 0.6
Contact Window : 10

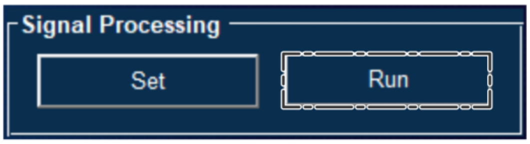
No.	Description
1	**Low Pass Filter** To remove high frequency noises, select a low pass filter type. ▪ None: No low pass filter ▪ DCT: Discrete Cosine Transform ▪ IIR: Infinite Impulse Response
2	**High Pass Filter** To remove low frequency noises, select a high pass filter type. ▪ None: No high pass filter

No.	Description
	▪ DCT: Discrete Cosine Transform SNIP: Sensitive Nonlinear Iterative Peak Clipping Algorithm
3	**Channel Rejection** Set baseline interval and threshold values to be used to reject channels. ▪ Channels with SNR (signal to noise ratio) that do not reach the threshold value during the baseline interval are rejected. ▪ Default baseline interval is around 10 to 15 seconds and default threshold value is 30 dB. ▪ These settings can be customized by the user. ▪ Selecting "Using measured SNR values from the device checkbox" imports the SNR values measured by the system. ▪ Amplitude Threshold: Amplitude variance threshold values of 3cm, 1.5cm, 2.12cm and 3.35cm channels. Channels will be rejected if their variances are lower than the corresponding threshold value.
4	**Concentration Baseline** Set the baseline to be used to calculate concentration. ▪ Baseline can be set for either Spot or Period. ▪ Default baseline is 15 seconds and the value can be customized.
5	**Spike Removal** Apply Spike Removal ▪ If there is a spike in the signal you can remove the noise with this option. You can control Window and Threshold of standard deviation.
6	**Motion Artifact** For data that went through motion calibration, select the Apply motion artifact removal checkbox to remove artifacts caused by motions. ▪ Please note that this algorithm may not work if measured data includes a negative SNR value. ▪ Accel, Gyro Threshold: These values are values to detect abrupt movement using normalized raw Accel and Gyro values. When measuring in a common environment (e.g., sitting in a chair doing cognitive tasks), 1.8 value can detect most of the motion artifacts (such as frowning, displacement of the device). If you want to detect smaller motion artifacts, then you should use smaller values such as 1~1.5. However, you have to be careful that if the detected motion artifact window gets larger, it uses spline interpolation [Scholkmann, F., Spichtig, S., Muehlemann, T., & Wolf, M. (2010). How to detect and reduce movement artifacts in near-infrared imaging using moving standard deviation and spline interpolation. Physiological measurement, 31(5), 649–662.] within the motion artifact window, that will eliminate all the hemodynamic response. We recommend users to visually check and select the threshold by looking at the signal change to match the real artifacts and detected window. ▪ Envelope window is to determine the window size to extract the linear regression features from the angle change of the participant. When the participant swings their head in 20 second period, to extract the exact 20 second oscillation for the linear regression

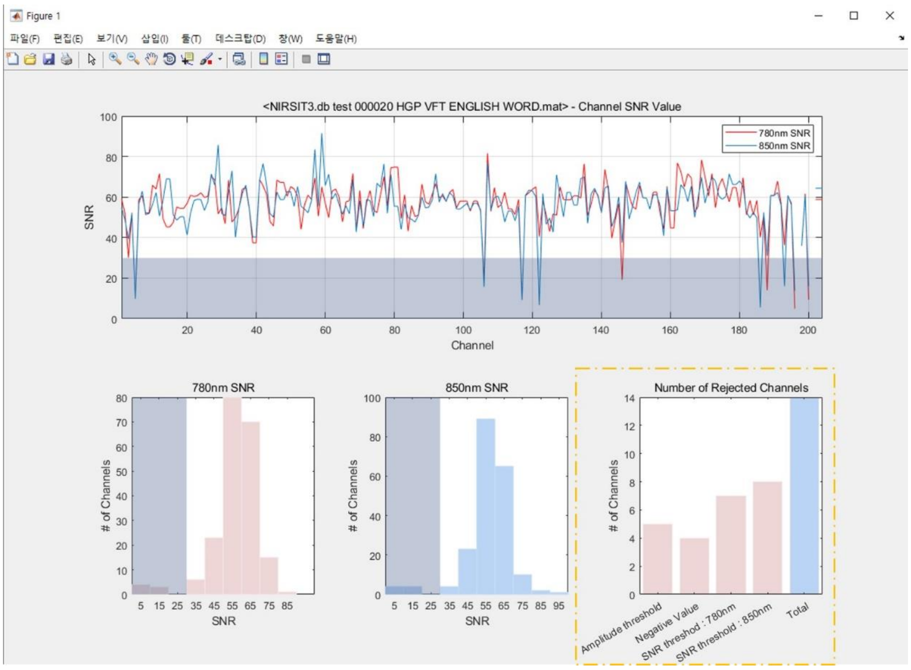
No.	Description
	feature of the head angle, the window size should be smaller than 20 second (in this is the case Envelope window value should be larger than 160 (20 second x 8.138 samples / second), the unit of the envelope window is samples) ▪ Motion OD Xcorr value is to determine whether to subtract out linear regressed result of the head angle and the OD signal for each channel. If you select 0.6, it measures correlation between the fitted head angle feature and the OD signal and if the correlation is higher than 0.6, it subtracts the fitted head angle signal from the OD signal. [Jae-Myoung Kim, et al. "Real-time motion sensor-based algorithm for the removal of motion artifacts for functional near-infrared spectroscopy" 45th Annual Meeting of the International Society on OxygenTransport to Tissue (ISOTT) (2017)] ▪ Contact window (unit sample) is to determine the extrapolation length of spline interpolation window selected from 1. (ex, when the value is 10, (10 sample /8.138Hz = 1.23 second) spline interpolation window will be (-1.23 second) + selected spline interpolation window size + (1.23 second).
7	**Apply and Reset**  ▪ Apply: Apply settings configured for the selected file. ▪ Reset: Reset settings to restore default values.

3.1.3 Apply and Run

If you click **Apply** in the SetSigProc panel and then click **Run** in the Signal Processing panel, the Signal Processing panel starts signal processing.



- After the **Run**, **Optical Density** check box can be selected in the **Time Series Selection** panel.
- 780 nm and 850 nm wavelength SNR graph can be displayed. Signals below threshold are indicated with a gray box.

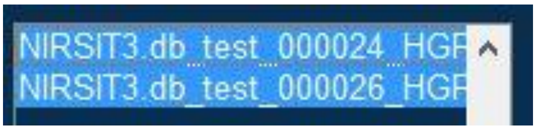


- Time series graph and channel number array are displayed.
- Rejected channels are grayed out.

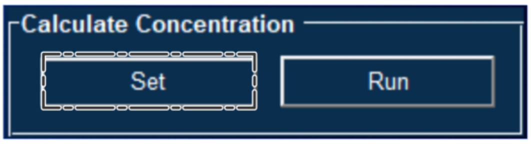
3.2 Calculating concentration

3.2.1 Selecting and configuring data

In the data selection panel, select one or more data files to calculate concentration for, and then click **Set** button.



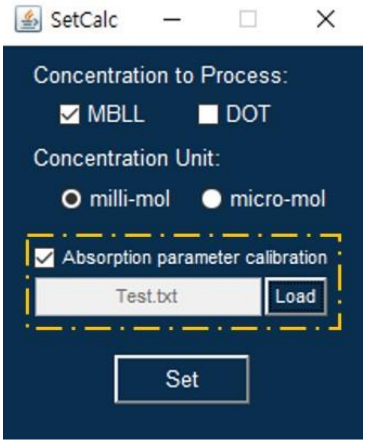
NIRSIT3.db_test_000024_HGF
NIRSIT3.db_test_000026_HGF



A pop-up window appears as shown below "3.2.2". Use the window to configure concentration calculation settings.

3.2.2 Concentration to Process and Concentration Unit settings

- Use the pop-up window to configure settings for **Concentration to Process** and **Concentration Unit**.
- Next, click **Set** button.



SetCalc

Concentration to Process:
☑ MBLL ☐ DOT

Concentration Unit:
○ milli-mol ● micro-mol

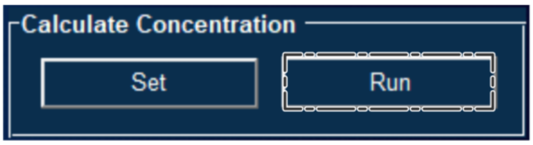
☑ Absorption parameter calibration
Test.txt

No.	Description
1	**Concentration to Process** Select a method to calculate hemoglobin concentration. Both options can be selected at the same time. ▪ MBLL: Modified Beer-Lambert Law ▪ DOT: Diffuse Optical Tomography (To be updated)

No.	Description
2	**Concentration Unit** Select a concentration unit. Default unit is milli-mol and the unit can be changed to micro-mol if necessary.
3	**Absorption parameter calibration** You can manually modify wavelength of your data. Please load wavelength written by notepad(.txt).

3.2.3 Run

Click **Run** in the Calculate Concentration panel.



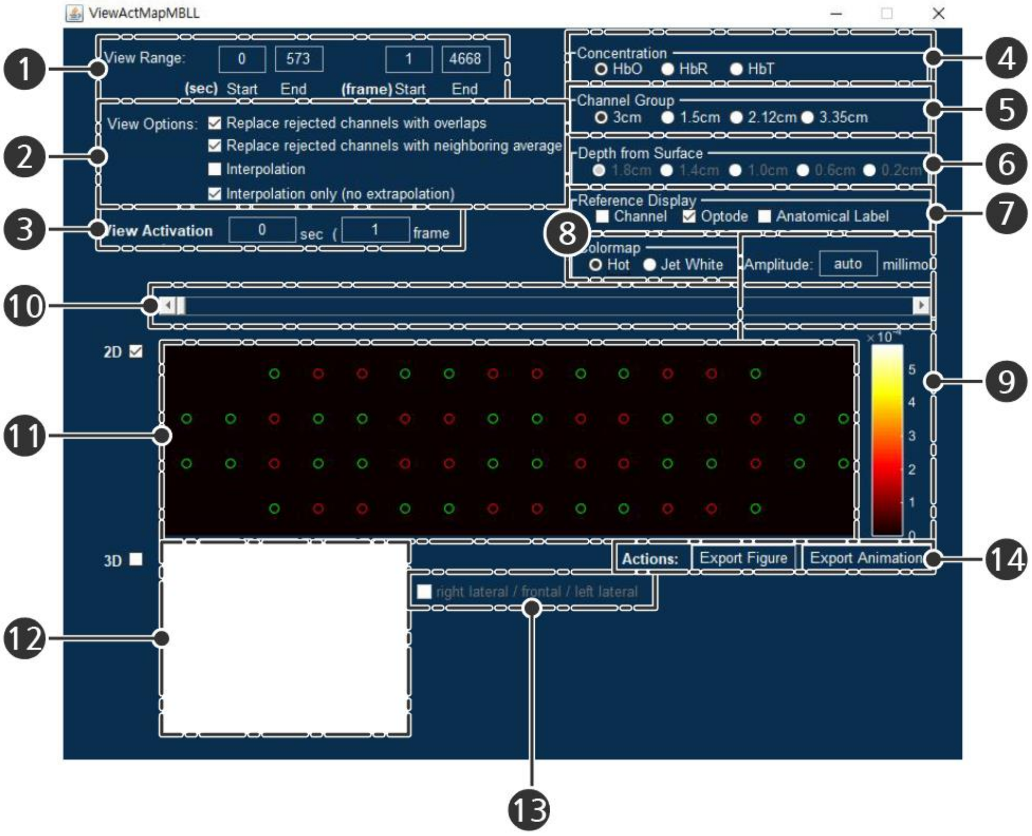
The **Hb Concentration** check box can be selected in the **Time Series Selection** panel. A time series graph can be displayed when calculating with MBLL selected. (* Refer to "2.3 Time Series Selection panel.")

3.3 Activation Map

For data that went through concentration calculation process, activation changes over time can be displayed as shown in the pictures below. For data that did not go through concentration calculation process, this function is not enabled.

3 Select either **MBLL** or **DOT** as view mode and click **View**.

Activation Map options appear in a pop-up window. (DOT is not available for now)

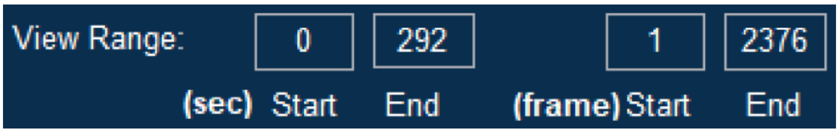


No.	Description
1	View Range
2	View Options (when **MBLL** is selected)
3	View Activation
4	Concentration
5	Channel Group (when **MBLL** is selected)

No.	Description
6	Depth from Surface (when **DOT** is selected)
7	Reference Display
8	Color map
9	Amplitude
10	Slide bar
11	2D Map
12	3D Map
13	3D Map; **right lateral / frontal / left lateral**
14	Export Figure and Export Animation

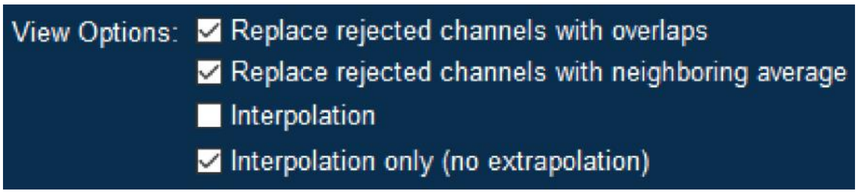
3.3.1 View Range

View the start and end times for measured data in seconds or frames.



If you are viewing Block Average data, the duration of the block average is displayed.

3.3.2 View Option (when MBLL is selected)


View Options:
☑ Replace rejected channels with overlaps
☑ Replace rejected channels with neighboring average
☐ Interpolation
☑ Interpolation only (no extrapolation)

- **Replace rejected channel with overlaps**: If there is a rejected channel with an overlapping channel, the rejected channel can be replaced with the overlapping channel.
- **Replace rejected channels with neighboring average**: If there are rejected channels without overlapping channels, the rejected channels can be replaced with an average of neighboring channels.
- **Interpolation**: Display the whole area with interpolation.
- **Interpolation only (no extrapolation)**: Display only the specific channel location with interpolation.
- By default, the **Replace rejected channels with overlaps and Replace rejected channels with neighboring average** options are selected. These options can be deselected if necessary.
- Only one of either **Interpolation** or **Interpolation only (no extrapolation)** can be selected.

3.3.3 View Activation

View the time or frame for data being displayed in the activation map.

View Activation 0 sec (1 frame

You can enter the time you want to view activation. The corresponding data will be displayed.

3.3.4 Concentration

You can select a hemoglobin concentration type.

Concentration
◉ HbO ○ HbR ○ HbT

HbO (Oxyhemoglobin) / HbR (Deoxyhemoglobin) / HbT (Total hemoglobin)

3.3.5 Channel Group (when MBLL is selected)

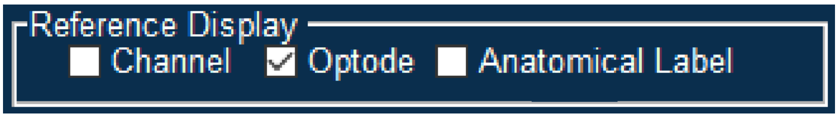
You can select channels by sensor distance for display.

Channel Group
◉ 3cm ○ 1.5cm ○ 2.12cm ○ 3.35cm

- 3cm: 1channel to 68channel
- 1.5cm: 69channel to 120channel
- 2.12cm: 121channel to 156channel
- 3.35cm: 157channel to 204channel

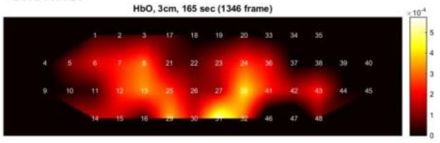
3.3.6 Reference Display

Select options you want to display. Multiple options can be selected at the same time.

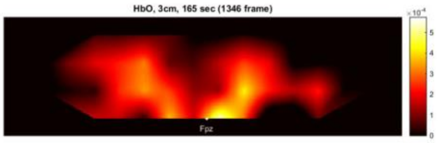


Reference Display
☐ Channel ☑ Optode ☐ Anatomical Label

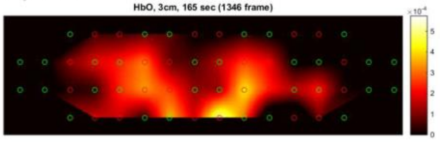
Channel



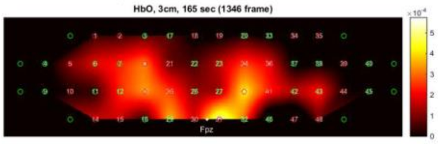
Anatomical Label



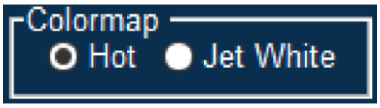
Optode



Channel & Optode & Anatomical Label



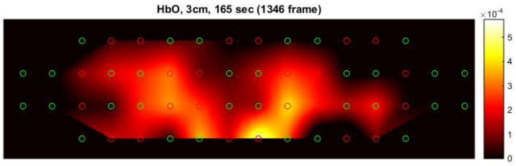
3.3.7 Color map



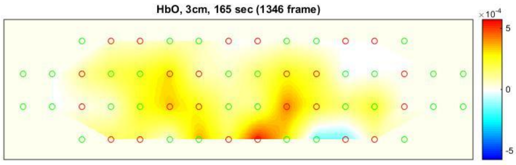
Colormap

○ Hot ● Jet White

- Hot: Displays positive values only.



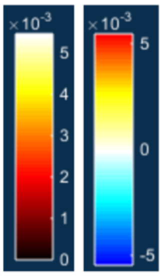
- Jet White: Displays both negative and positive values.



3.3.8 Amplitude

Amplitude is displayed based on the maximum hemoglobin concentration values.

Amplitude: auto millimol



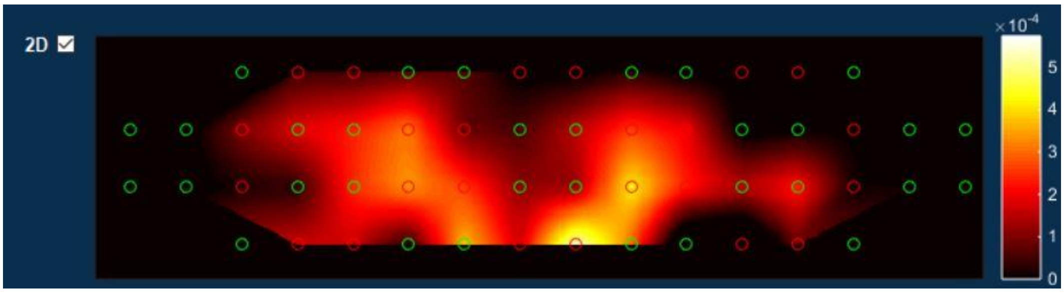
- If Hot is selected under ‘Colormap’, a value between 0 and maximum value is displayed.
- If Jet White is selected under ‘Colormap’, a value between –max and +max is displayed.
- The amplitude value can be customized.

3.3.9 Slide bar

Use the slide bar to view the result at a certain point in time.

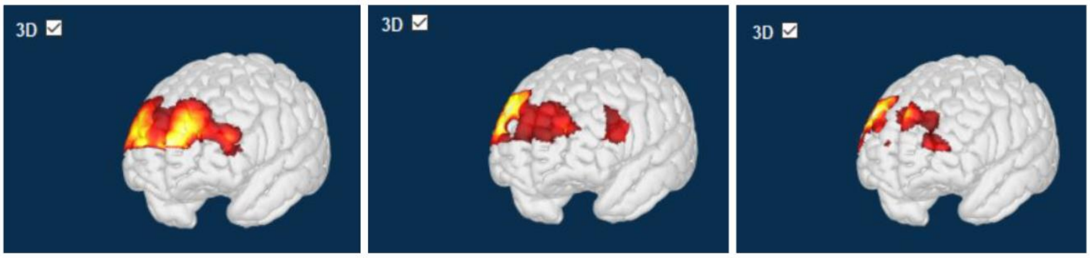
3.3.10 2D Map

2D map is updated according to option settings.



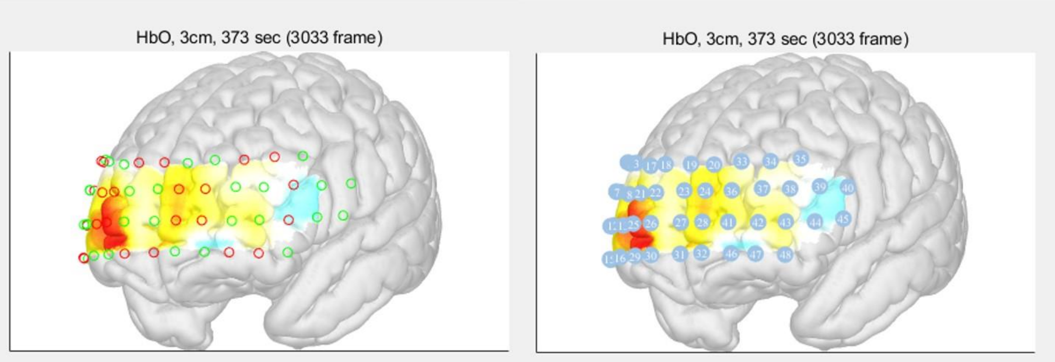
3.3.11 3D Map

If the **3D** checkbox is selected, brain images with activation areas are displayed.



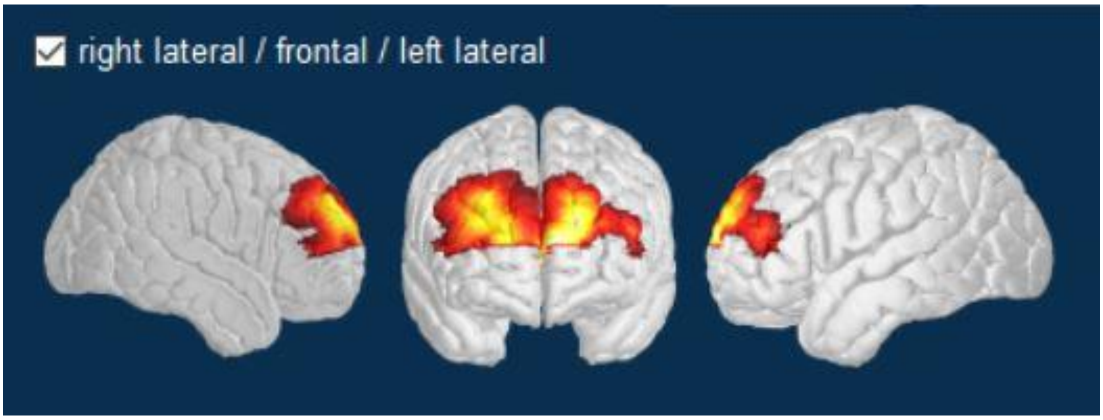
The activation areas will be updated according to the time change in the slide bar.

When you extract 3D brain image, it shows channel and optode positions based on Reference Display option.



3.3.12 3D Map: right lateral / frontal / left lateral

These functions are enabled when the 3D checkbox is selected.

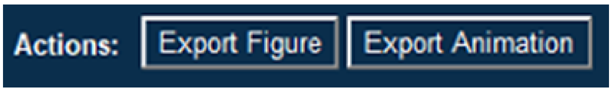


Select the right lateral/ frontal/ left lateral checkbox to display the right, front, and left images of a 3D map.

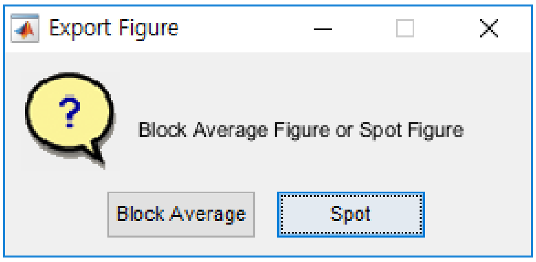
- If you use the slide bar to move to another point in time to view data, the 3D map view will turn off automatically.

3.3.13 Export Figure and Export Animation

2D, 3D, right lateral/frontal/left lateral activation map can be exported as a figure.

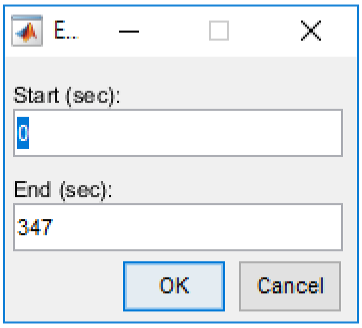


- You can select to extract either block average figure or spot figure.



Block Average Figure or Spot Figure

- Once the animation name and the directory to save the animation are saved, a pop-up window appears where you can set the start and end times for extraction. During the specified duration, 2D animation video can be exported.

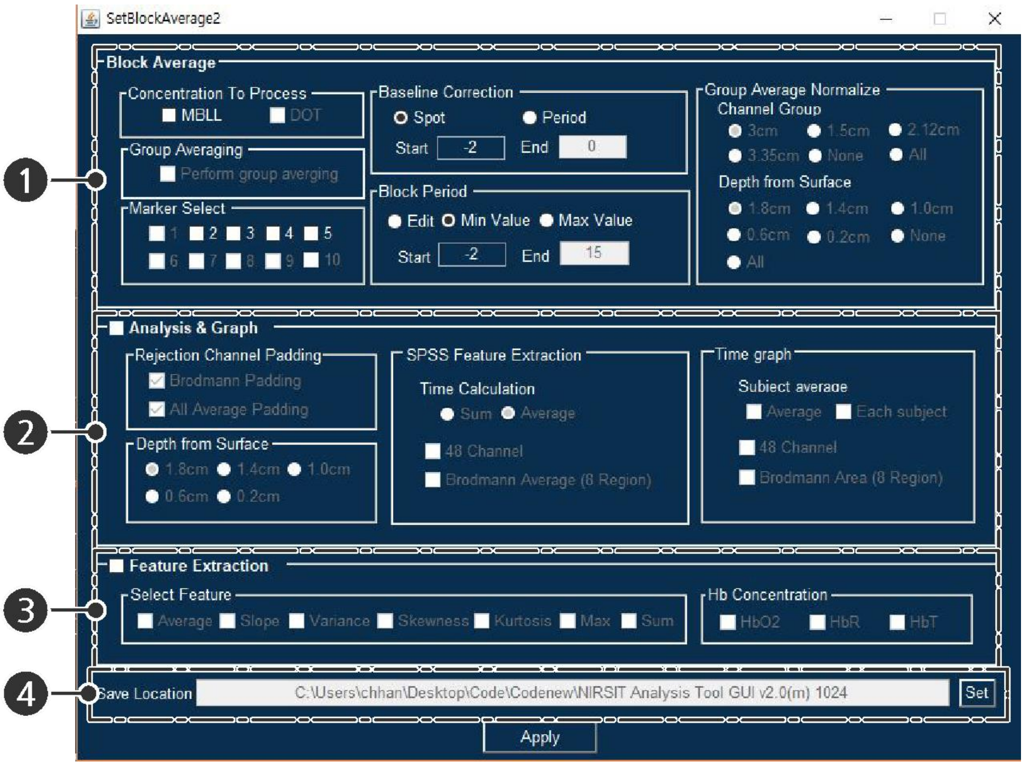


Start (sec): 0

End (sec): 347

- Do not close the window during playback of a video. The video may not be saved properly.

3.4 Data Analysis



Baseline Correction: Start -2 End 0

Block Period: Start -2 End 15

Save Location: C:\Users\chhan\Desktop\Code\Codenew\NIRSIT Analysis Tool GUI v2.0(m) 1024

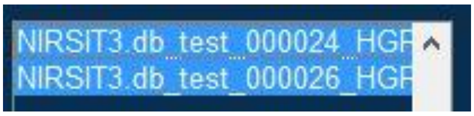
No.	Description
1	**Block Average**
2	**Analysis & Graph**
3	**Feature Extraction**
4	**Save Location**

3.4.1 Block Average

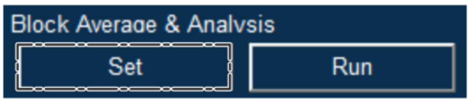
For data that went through concentration calculation process, the Block Average function can be performed based on the marker information.

Block Average is a useful function to determine the activation pattern.

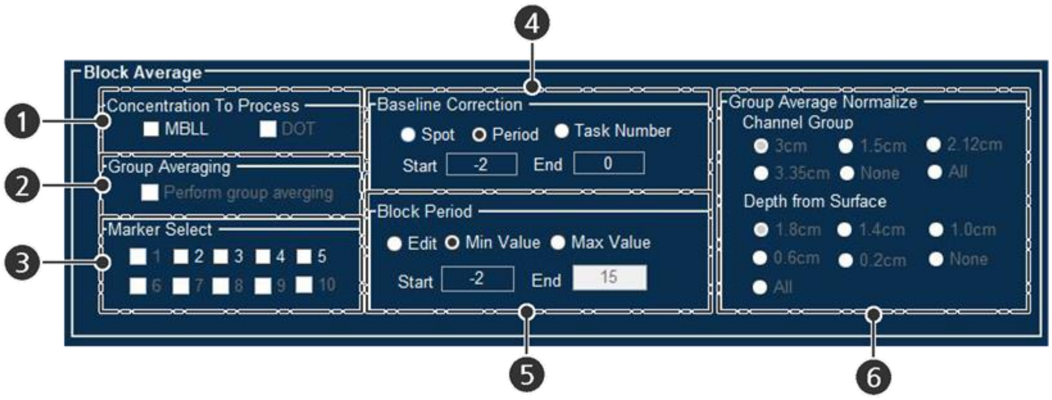
1. Use block average data to create a time series graph. Convert block average data into an Excel table so that the data can be used in the SPSS Statistics program
2. The Feature Extraction function comes with an average HBO2 data option, as well as sub-functions such as Maximum, SUM, Skewness, and Slope.
3. Select one or more data files from the Data Selection panel for signal processing. Click **Set** button in the **Block Average & Analysis** panel.



NIRSIT3.db_test_000024_HGF
NIRSIT3.db_test_000026_HGF



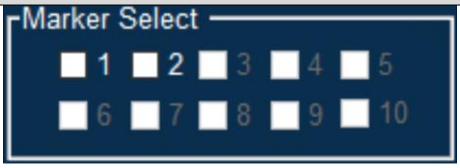
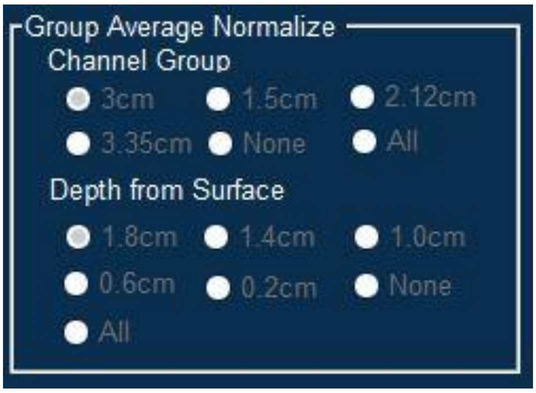
4. A pop-up window appears. Use the window to the block average function settings.



Baseline Correction: Start -2 End 0

Block Period: Start -2 End 15

No.	Description
1	**Concentration To Process** You can select only **MBLL** for now. (DOT will be updated) ▪ Enabled checkboxes vary, depending on the used method of concentration calculation.
2	**Group Averaging** ▪ **The Perform group averaging** checkbox is enabled if two or more data files are selected. ▪ Select the checkbox when you want to calculate the average of multiple blocks of data files for the same task.
3	**Marker Select** Enabled checkboxes vary according to the marker numbers saved in data.

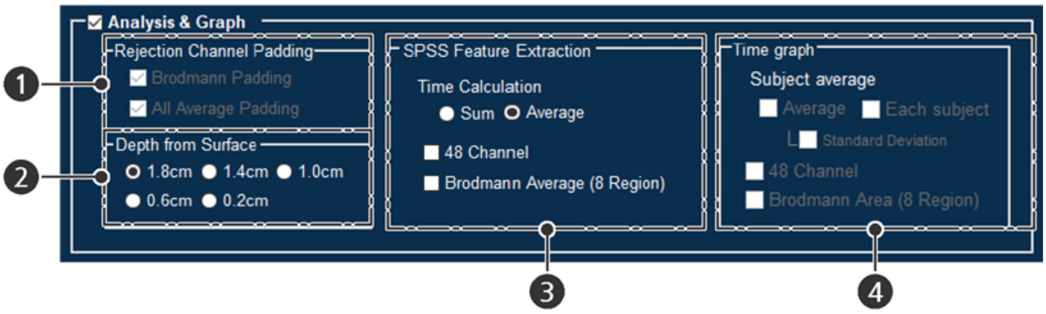
No.	Description
	 ▪ You can select multiple markers for block averaging.
4	**Baseline** Set the baseline of Block Average. ▪ Baseline can be set for either Spot or Period. ▪ Default baseline is -2 second and the value can be customized. ▪ You can use Task number as a baseline. Selected task section will be averaged and it is used as a baseline.
5	**Block Period** Set the Block Period.  Start -2 End 15 ▪ The period can be set up from the start point 0 of set marker. To block prior to the start point of marker, enter a negative value (e.g., if start time value is set at -2 second, this means that the block period starts from 2 seconds prior to the actual marker start time). • Edit: Customize the block period based on the start point of each marker. • Min Value: Set block period using the minimum value of each marker. • Max Value Interpolation: Interpolate data using the maximum value of each marker. ▪ It is recommended that you select Min Value Interpolation if the marker period is almost consistent. ▪ If block average period for multiple markers varies, it is recommended that you use the Max Value Interpolation function.
6	**Group Average Normalize** To activate the group average function, select the Group Average checkbox. 

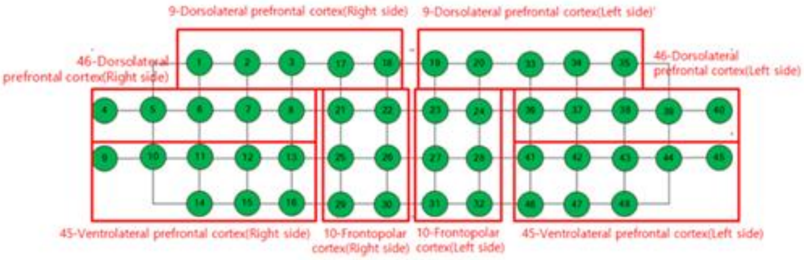
No.	Description
	▪ Block average of each subject data can be normalized with maximum value. ▪ Select Channel Group (for MBLL) or Depth from Surface (for DOT) for display.

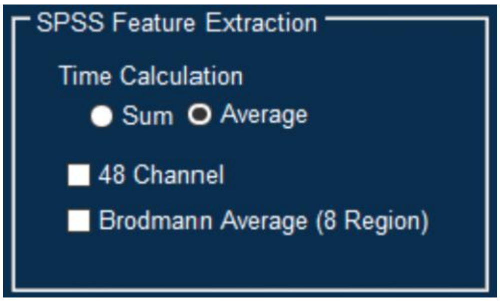
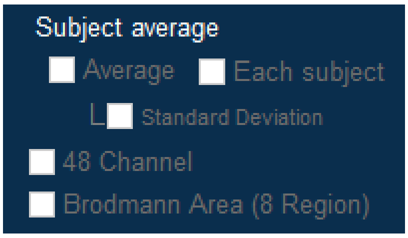
3.4.2 Analysis & Graph

The Analysis & Graph functions are enabled when the **Analysis & Graph** checkbox is selected.

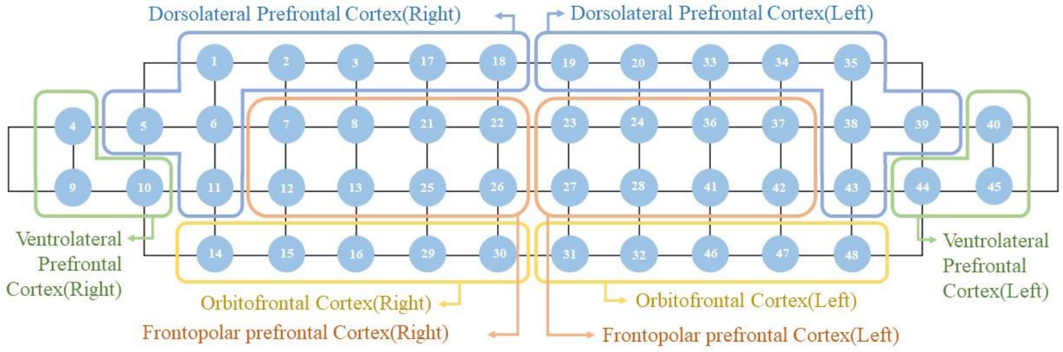
- SPSS feature and time series graph can be made on 48 channels in the case of MBLL.
- SPSS feature and time series graph can be made on 60 areas in the case of DOT.

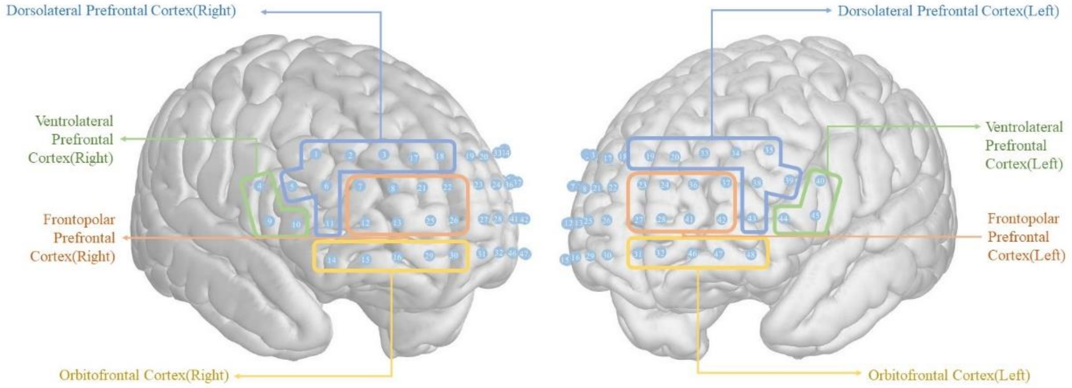


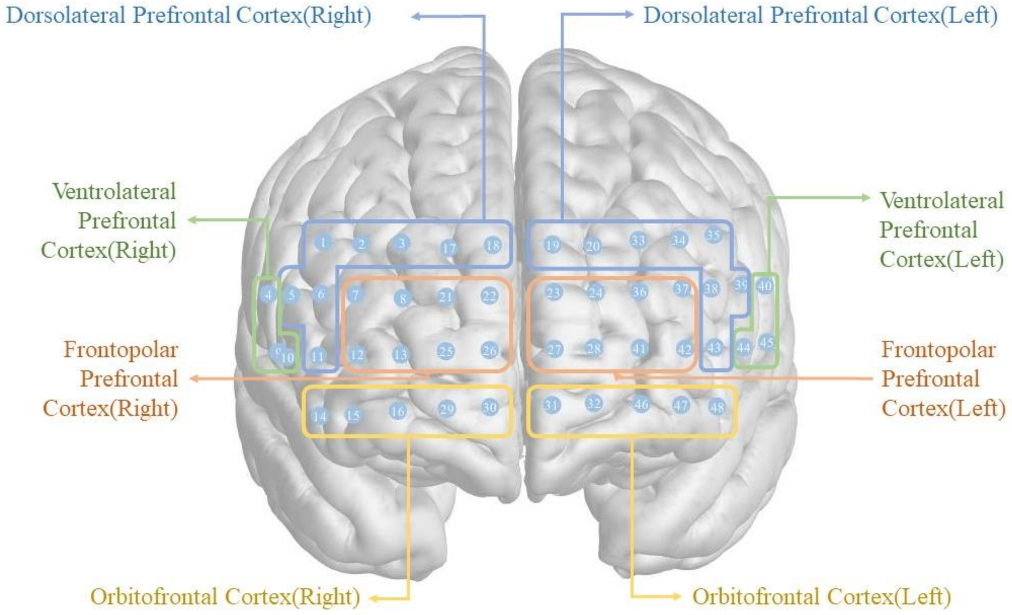
No.	Description
1	**Rejection Channel Padding** The Rejection Channel Padding functions are enabled when the **MBLL** checkbox is selected in the **Block Average** panel. ▪ You can select a Rejection Channel Padding method to cover rejected channels. • Brodmann Padding: Pad the average value of the Brodmann region with rejected channels. • All Average Padding: Pad the average value of all regions with rejected channels. ▪ The All-Average Padding option can be used to pad the average value of all regions. 
2	**Depth from Surface** The **Depth from Surface** functions are enabled when the **DOT** checkbox is selected. Select a depth you want to view.

No.	Description
	 1.8cm (±0.2 cm) / 1.4cm (±0.2 cm) / 1.0cm (±0.2 cm) / 0.6cm (±0.2 cm) / 0.2cm (±0.2 cm)
3	**SPSS Feature Extraction** Extract data that can be used in SPSS. Select whether to do the sum or calculate the average of time intervals.  ▪ Extract HbO2, **HbR** average of 48 channels. ▪ Extract HbO2, **HbR** average of 8 regions. ▪ Both options can be selected at the same time.
4	**Time Graph** ▪ Extract HbO2 and HbR of a task block as a time graph.  • **Average**: Extract an average time graph for subjects. • **Standard deviation**: Extract data with its SD • **Each subject**: Extract a time graph for each subject. • **48 channels**: Extract a time graph for 48 channels. • **Bodmann Area (8 Region)**: Extract a time graph for 8 regions. ▪ The four options can be selected at the same time. ▪ HbO and HbR are separatly extracted and written by csv.

Brodmann Area

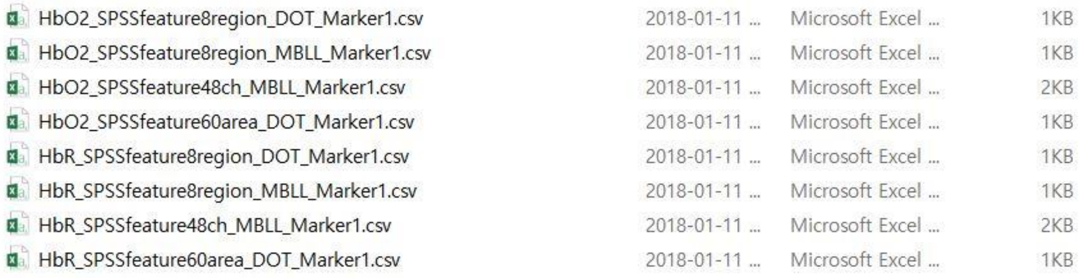




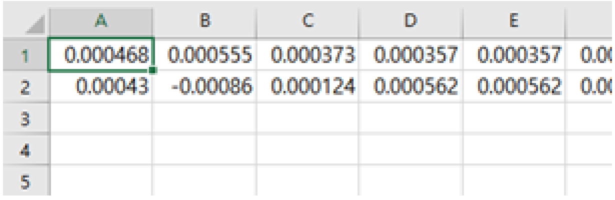


Result

- A .csv file is created based on the selected options.
- The number of rows refers to the number of selected subjects. The number of columns refers to the number of channels (regions).
- Each value is an average or sum of HbO2 and HbR values.

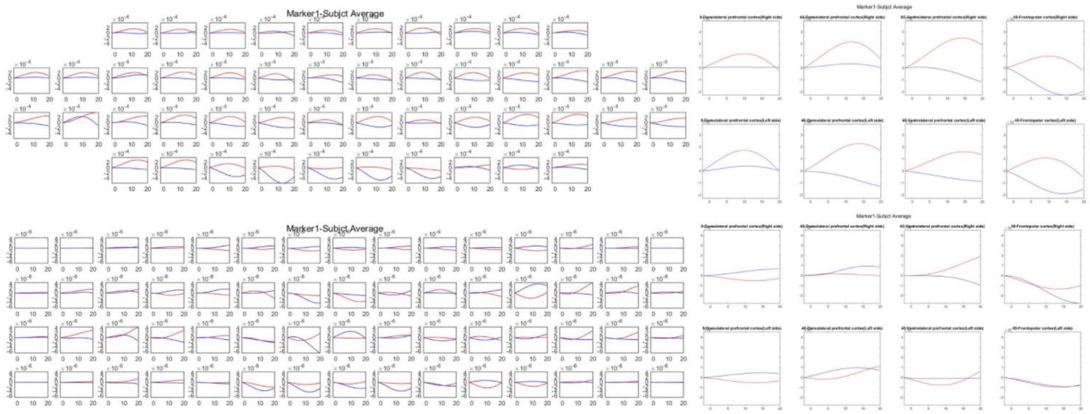


HbO2_SPSSfeature8region_DOT_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	1KB
HbO2_SPSSfeature8region_MBLL_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	1KB
HbO2_SPSSfeature48ch_MBLL_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	2KB
HbO2_SPSSfeature60area_DOT_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	1KB
HbR_SPSSfeature8region_DOT_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	1KB
HbR_SPSSfeature8region_MBLL_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	1KB
HbR_SPSSfeature48ch_MBLL_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	2KB
HbR_SPSSfeature60area_DOT_Marker1.csv	2018-01-11 ...	Microsoft Excel ...	1KB



	A	B	C	D	E	
1	0.000468	0.000555	0.000373	0.000357	0.000357	0.0
2	0.00043	-0.00086	0.000124	0.000562	0.000562	0.0
3						
4						
5						

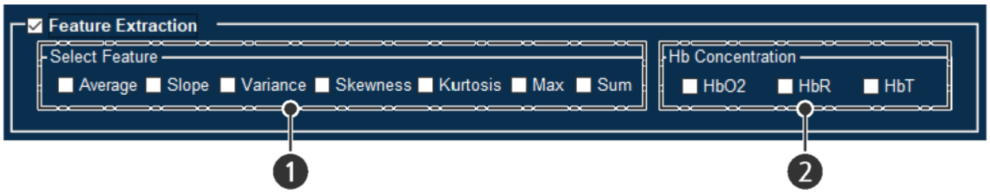
- You can copy saved results to SPSS for use.
- Time graphs are created based on the selected options.



The red line indicates HbO2, and the blue line indicates HbR.

3.4.3 Feature Extraction

Select the checkbox to enable the **Feature Extraction** functions. Extract features, such as average value and maximum value, as a .csv file.



☑ Feature Extraction

Select Feature: ☐ Average ☐ Slope ☐ Variance ☐ Skewness ☐ Kurtosis ☐ Max ☐ Sum

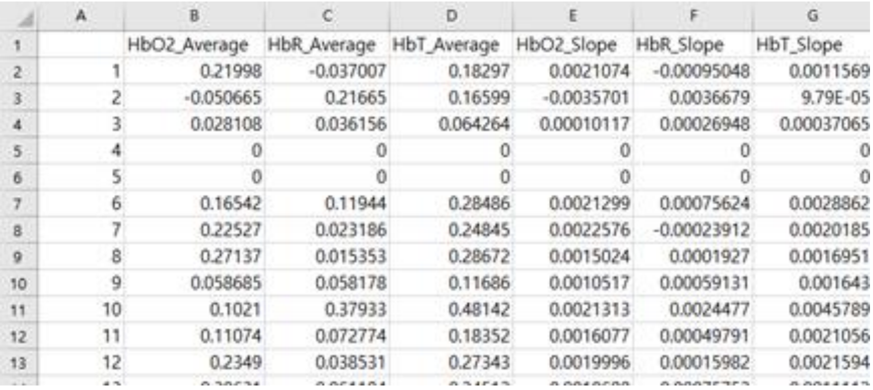
Hb Concentration: ☐ HbO2 ☐ HbR ☐ HbT

No.	Description
1	**Select Feature** Select features you want to extract.
2	**Hb Concentration** Select Hemoglobin concentration type.

Result

- A .csv file is created based on the selected options.
- The first row displays the index of channels while the first column displays the index of selected features.

Feature extraction_DOT_Marker1_Group.csv	2017-10-12 ...	Microsoft Excel ...	983KB
Feature extraction_DOT_Marker1_NIRSIT3.db_test_000024_HGP_ARITHMETIC.csv	2017-10-12 ...	Microsoft Excel ...	968KB
Feature extraction_DOT_Marker1_NIRSIT3.db_test_000026_HGP_ARITHMETIC_2.csv	2017-10-12 ...	Microsoft Excel ...	997KB
Feature extraction_MBLL_Marker1_Group.csv	2017-10-12 ...	Microsoft Excel ...	39KB
Feature extraction_MBLL_Marker1_NIRSIT3.db_test_000024_HGP_ARITHMETIC.csv	2017-10-12 ...	Microsoft Excel ...	37KB
Feature extraction_MBLL_Marker1_NIRSIT3.db_test_000026_HGP_ARITHMETIC_2.csv	2017-10-12 ...	Microsoft Excel ...	38KB



	A	B	C	D	E	F	G
1		HbO2_Average	HbR_Average	HbT_Average	HbO2_Slope	HbR_Slope	HbT_Slope
2	1	0.21998	-0.037007	0.18297	0.0021074	-0.00095048	0.0011569
3	2	-0.050665	0.21665	0.16599	-0.0035701	0.0036679	9.79E-05
4	3	0.028108	0.036156	0.064264	0.00010117	0.00026948	0.00037065
5	4	0	0	0	0	0	0
6	5	0	0	0	0	0	0
7	6	0.16542	0.11944	0.28486	0.0021299	0.00075624	0.0028862
8	7	0.22527	0.023186	0.24845	0.0022576	-0.00023912	0.0020185
9	8	0.27137	0.015353	0.28672	0.0015024	0.0001927	0.0016951
10	9	0.058685	0.058178	0.11686	0.0010517	0.00059131	0.001643
11	10	0.1021	0.37933	0.48142	0.0021313	0.0024477	0.0045789
12	11	0.11074	0.072774	0.18352	0.0016077	0.00049791	0.0021056
13	12	0.2349	0.038531	0.27343	0.0019996	0.00015982	0.0021594

3.4.4 Save Location

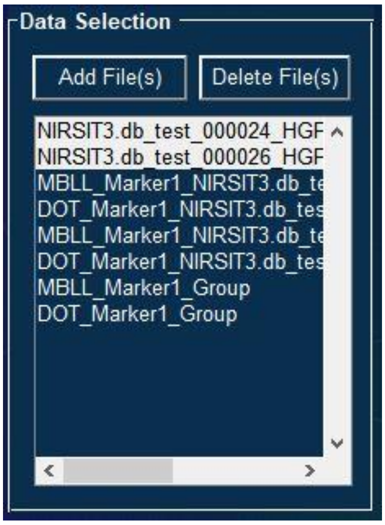
Set the destination folder to save data with Block Average complete. Next, click **Apply** button.

Save Location: C:\WINDOWS\system32

Result

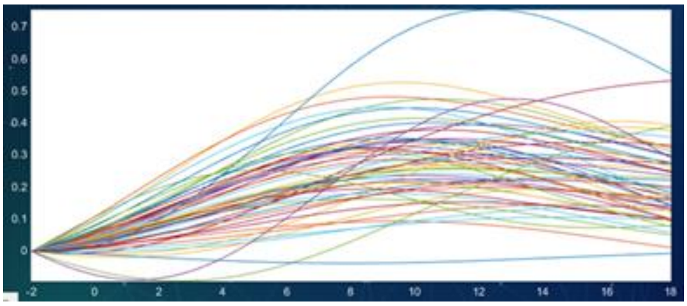
The Block Average function is applied by clicking **Run** in the **Block Average & Analysis** panel.

The result of block average appears in the Data Selection panel.

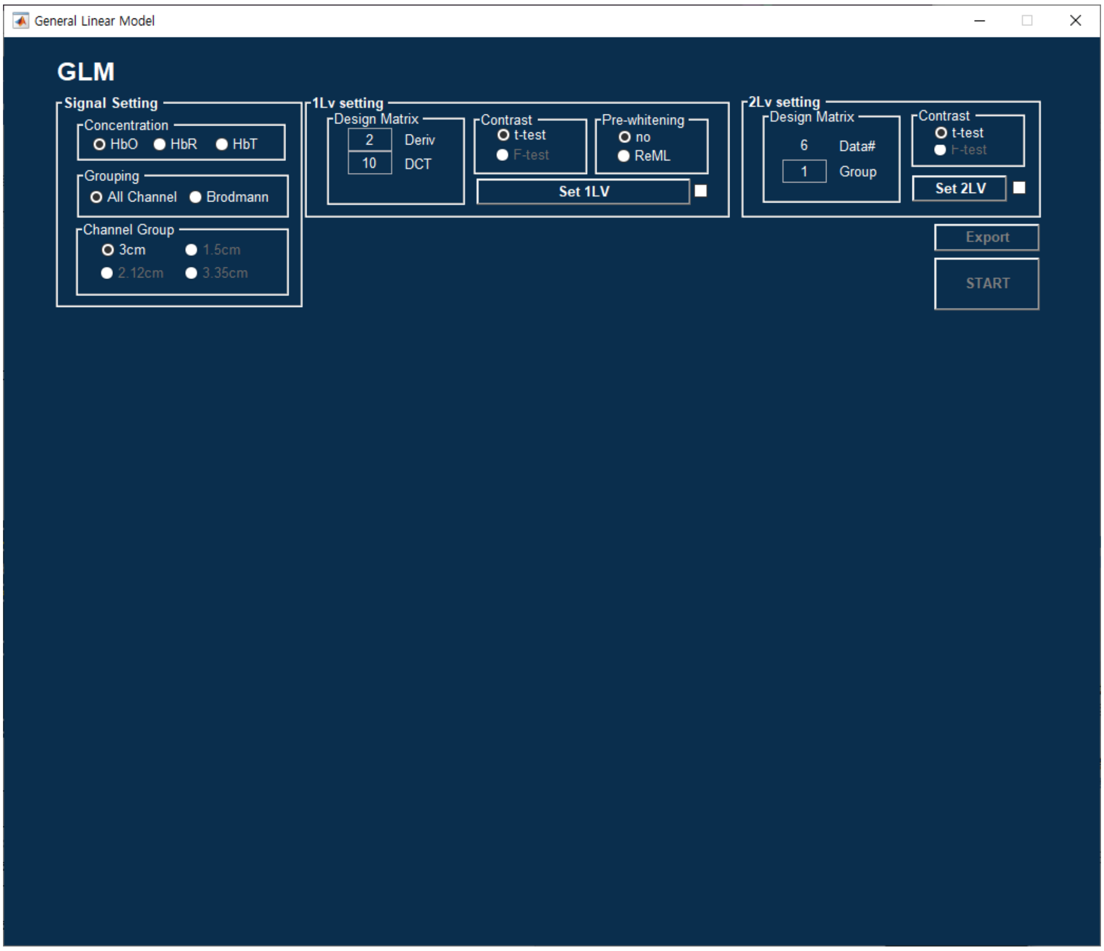


NIRSIT3.db_test_000024_HGF
NIRSIT3.db_test_000026_HGF
MBLL_Marker1_NIRSIT3.db_te
DOT_Marker1_NIRSIT3.db_tes
MBLL_Marker1_NIRSIT3.db_te
DOT_Marker1_NIRSIT3.db_tes
MBLL_Marker1_Group
DOT_Marker1_Group

- Based on the configuration, each subject data and Group Average result will be created, titled with either ‘MBLL’ or ‘DOT’.
- Block average data, saved in the specified destination folder, can be accessed via concentration data.
- Block average data can be shown in the activation map.
- For MBLL data, it is possible to view a time series graph.



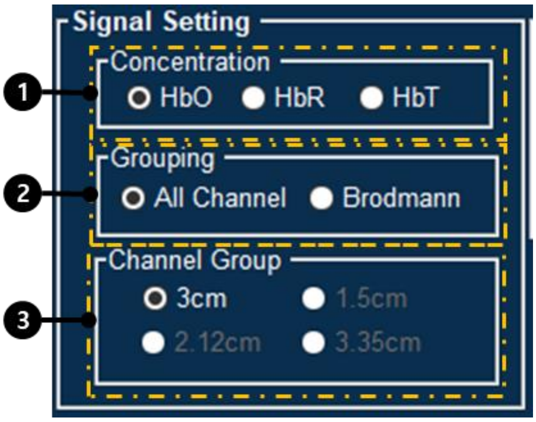
3.5 GLM (Genral Linear Model)



GLM process needs presetting step for 1st level and 2nd level GLM. For more details about GLM, please refer to the online resource "Human Brain Function" with a link below.

(https://www.fil.ion.ucl.ac.uk/spm/doc/books/hbf2/)

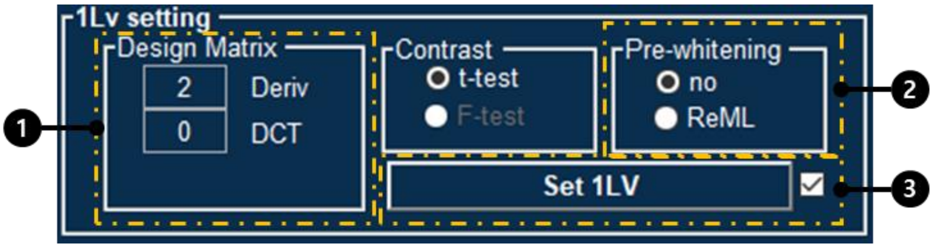
3.5.1 Signal Setting



Select the data type that you analyze.

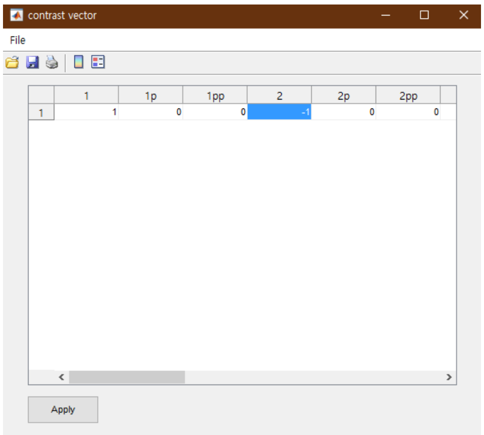
No.	Description
1	**Concentration** Select hemoglobin concentration type.
2	**Grouping** Set the channels. ▪ All Channel: Use all the channels you selected. ▪ Brodmann: Get the average value of Brodmann 8 area.
3	**Channel Group** Get the channels according to distance.

3.5.2 1Lv Setting



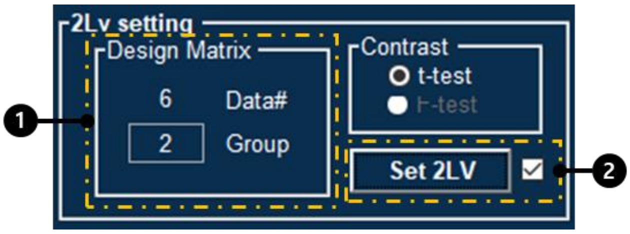
Set the First Level GLM for Single subject analysis.

No.	Description
1	**Design matrix** Make the regressors using HRF for design matrix. ▪ Deriv: additional HRF derivative regressor - 0: None - 1: First derivative (Temporal derivative) - 2: Second derivative (Dispersion derivative) with 1st deriv ▪ DCT (Descrete Cosine Transform): additional DCT regressor

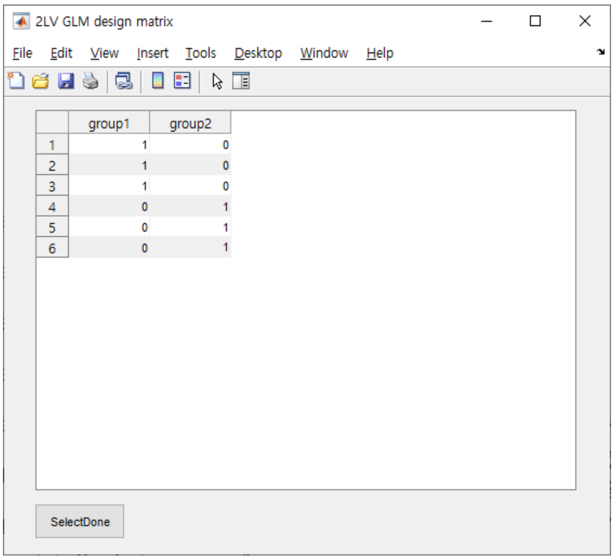
<table>
<tr><th>No.</th><th>Description</th></tr>
<tr><td>2</td><td>**Pre-whitening**
Set the temporal correlation correction.</td></tr>
<tr><td>3</td><td>**Set 1LV**
Set the contrast vector for your tasks.

<table>
<tr><th></th><th>1</th><th>1p</th><th>1pp</th><th>2</th><th>2p</th><th>2pp</th></tr>
<tr><td>1</td><td>1</td><td>0</td><td>0</td><td>-1</td><td>0</td><td>0</td></tr>
</table></td></tr>
</table>

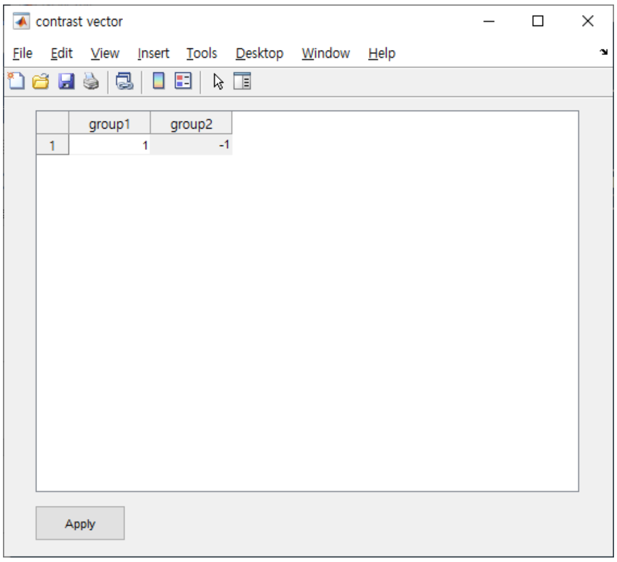
When you complete the setting, checkbox will be checked.

3.5.3 2Lv Setting



Set Second Level GLM for group analysis.

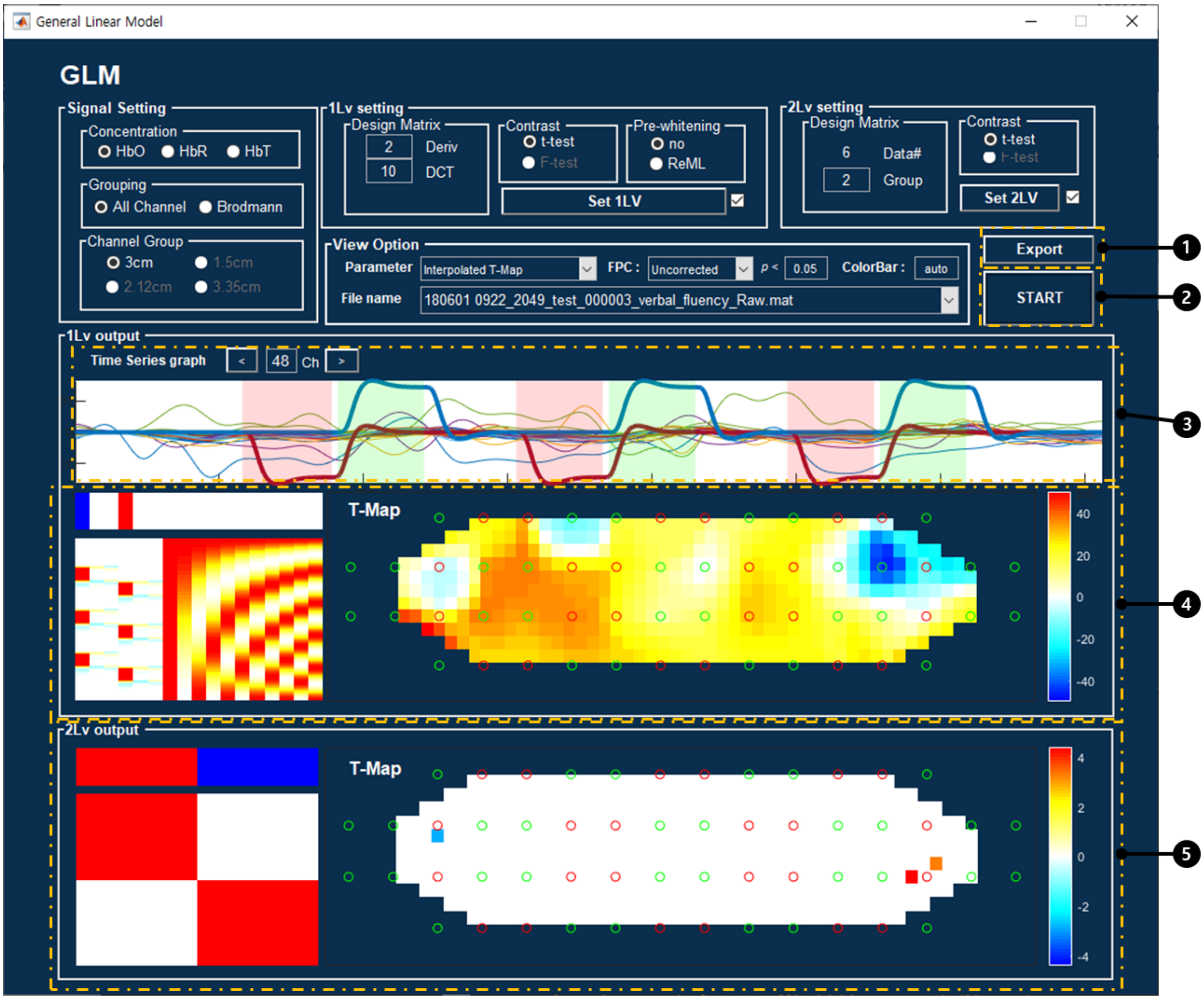
<table>
<tr><th>No.</th><th>Description</th></tr>
<tr><td>1</td><td>Design matrix
▪ Design Matrix: Type the number of groups.</td></tr>
<tr><td>2</td><td>Set 2LV


<table>
<tr><th></th><th>group1</th><th>group2</th></tr>
<tr><td>1</td><td>1</td><td>0</td></tr>
<tr><td>2</td><td>1</td><td>0</td></tr>
<tr><td>3</td><td>1</td><td>0</td></tr>
<tr><td>4</td><td>0</td><td>1</td></tr>
<tr><td>5</td><td>0</td><td>1</td></tr>
<tr><td>6</td><td>0</td><td>1</td></tr>
</table>
You can set the groups with typing 0, 1.


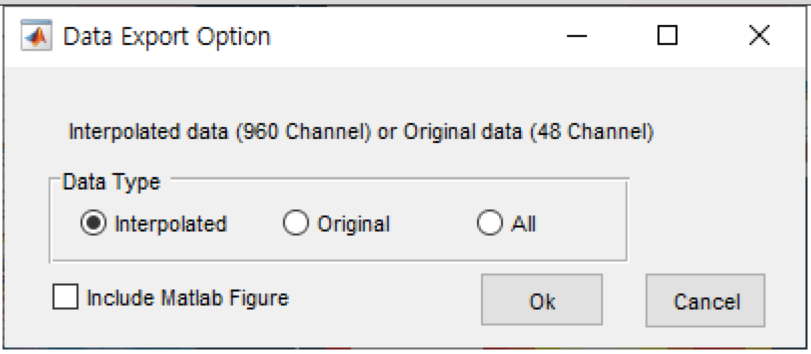
<table>
<tr><th></th><th>group1</th><th>group2</th></tr>
<tr><td>1</td><td>1</td><td>-1</td></tr>
</table>
Next, set the contrast vector for your groups.</td></tr>
</table>

<table>
<tr><th>No.</th><th>Description</th></tr>
<tr><td></td><td>Ex) Two sample T test
<table>
<tr><th>Contrasts</th><th></th></tr>
<tr><td>(1 0)</td><td>Mean group 1</td></tr>
<tr><td>(0 1)</td><td>Mean group 2</td></tr>
<tr><td>(1 -1)</td><td>Mean group1 – Mean group2</td></tr>
<tr><td>(0.5 0.5)</td><td>Mean (group 1, group 2)</td></tr>
</table>
</td></tr>
</table>

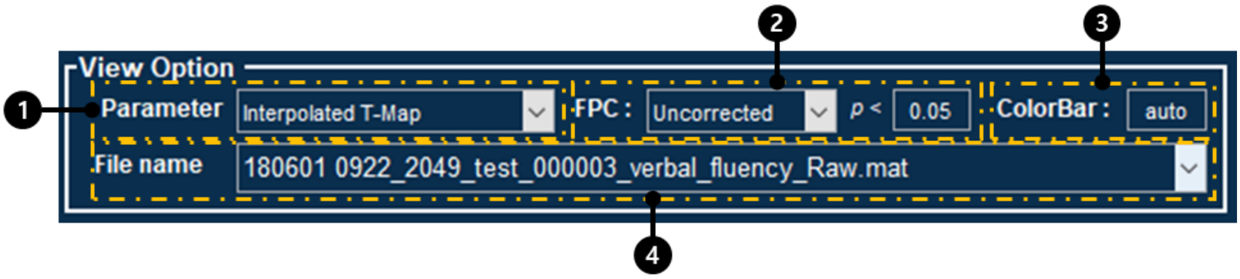
3.5.4 Export / Start



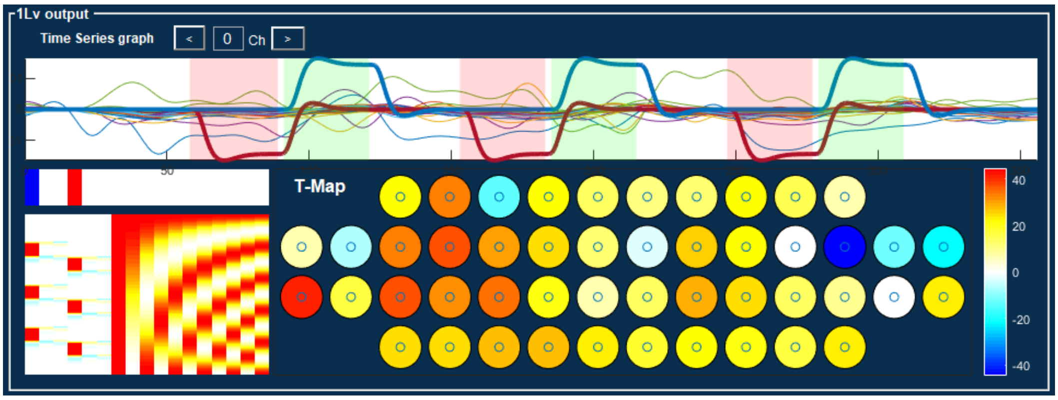
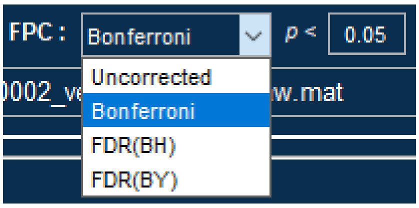
No.	Description
1	**Export** Export contrast beta, t-value and p-value of the 1LV, 2LV data as csv file. Also, 2D and 3D images for all data are exported.

No.	Description
	 Data Export Option Interpolated data (960 Channel) or Original data (48 Channel) Data Type: ● Interpolated ○ Original ○ All ☐ Include Matlab Figure When the image is exported, it is named in order of following : data type, 2D/3D, data name, grouping information, 1Lv/2Lv and p-value. Ex) 48Channel T-Map_3D_verbal_fluency_Raw_48ch_1st_GLM(p 0.05).png And csv file is named in order of following: value type, data name, data type and 1Lv/2Lv. Ex) cB-Value_180529_test_verbalfluency_Raw_48ch__1st_GLM.csv
2	**Start** When Setting is completed, GLM will be calculated with **Start** button.
3	**Time Series graph** It shows data and regressor that you made in time series. And you can choose individual channel result with arrows.
4	**1Lv Output** Display first level GLM for single subject you selected in **File name**.
5	**2Lv Output** Display second level GLM for group analysis.

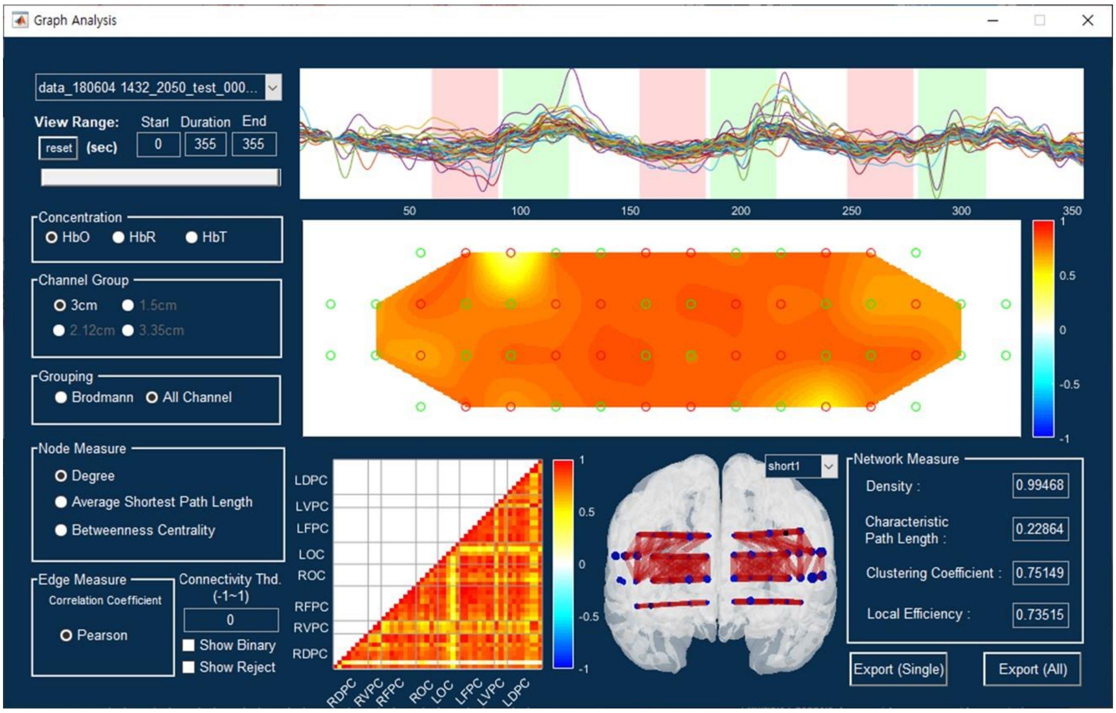
3.5.5 View Option



Parameter: Interpolated T-Map
FPC : Uncorrected
p < 0.05
ColorBar : auto
File name: 180601 0922_2049_test_000003_verbal_fluency_Raw.mat

No.	Description
1	**Parameter** Select channel type. ▪ Interpolated T-Map: Interpolated 960 channels. ▪ 48Channel T-Map: Origianal 48 channels. 
2	**FPC (False Positive Correction)** You can correct type 1 error with FPC option. It provides Bonferroni and FDR (False discovery rate) options.  FPC : Bonferroni p < 0.05 FDR(BH): Benjamini–Hochberg procedure FDR(BY): Benjamini– Yekutieli procedure
3	**ColorBar** Set color scale of 1Lv Output and 2Lv Output. (Default: auto)
4	**File name** It shows 1st level GLM figure according to File name section you selected.

3.6 Graph Analysis



Graph Analysis

data_180604 1432_2050_test_000...

View Range: Start 0 Duration 355 End 355 (sec)

Concentration: ◉ HbO ○ HbR ○ HbT

Channel Group: ◉ 3cm ○ 1.5cm ○ 2.12cm ○ 3.35cm

Grouping: ○ Brodmann ◉ All Channel

Node Measure: ◉ Degree ○ Average Shortest Path Length ○ Betweenness Centrality

Edge Measure: Correlation Coefficient ◉ Pearson

Connectivity Thd. (-1~1): 0

☐ Show Binary

☐ Show Reject

short1

Network Measure

Density : 0.99468

Characteristic Path Length : 0.22864

Clustering Coefficient : 0.75149

Local Efficiency : 0.73515

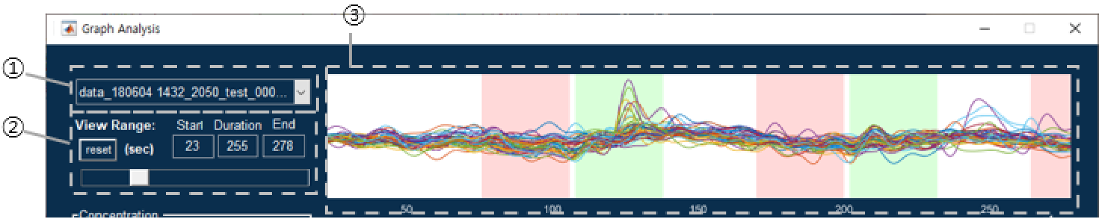
It shows entire signal result for HbO2 in selected data. you can analyze features with controling the various options.

No.	Description
Node	Measured channel
Edge	Connection between channels
Network	Group of node and Edge (Graph)

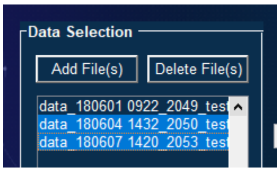
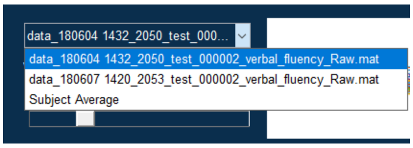
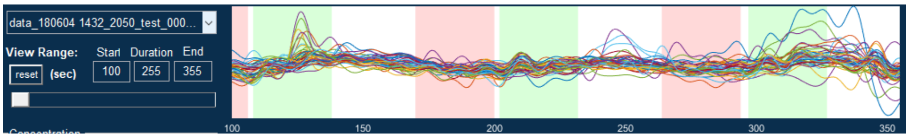
You can find more details of Graph Theory analysis below paper.

Ref: Rubinov M, Sporns O. Complex network measures of brain connectivity: uses and interpretations. Neuroimage. 2010 Sep;52(3):1059-1069

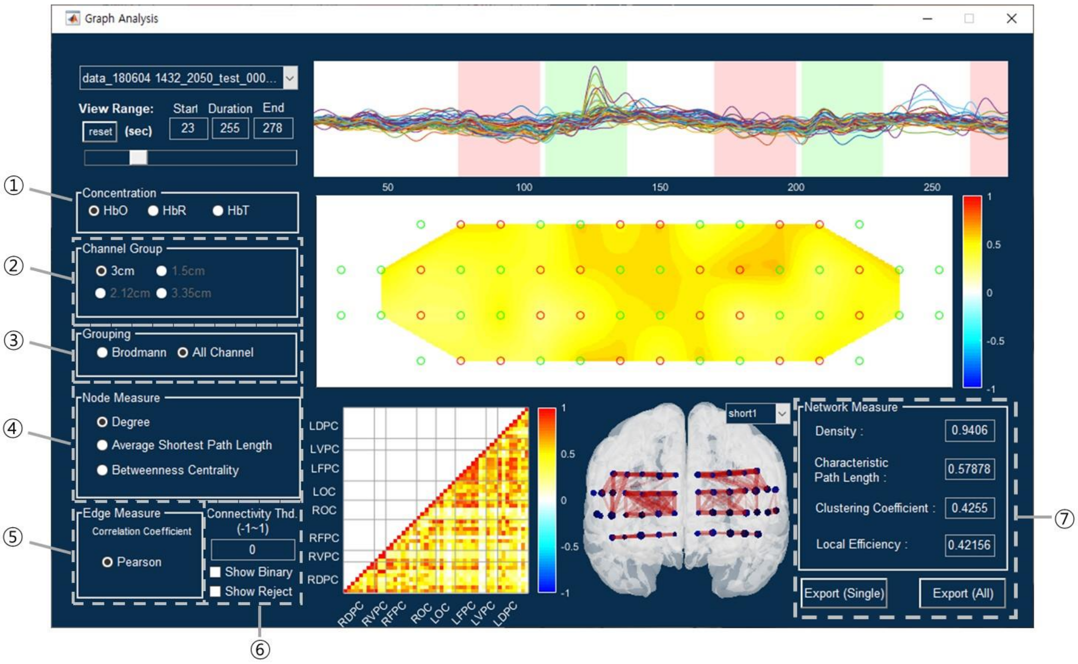
3.6.1 File selection and control view range



data_180604 1432_2050_test_000...
View Range: Start 23 Duration 255 End 278

No.	Description
1	**Data Selection:** If you click the right arrow as in the example below, you can check the data list that will be selected in the analysis tool main window and used for graph analysis. Also, at the very end, you can check the average result of the data loaded at the same time.  data_180601 0922_2049_test data_180604 1432_2050_test data_180607 1420_2053_test  data_180604 1432_2050_test_000... data_180604 1432_2050_test_000002_verbal_fluency_Raw.mat data_180607 1420_2053_test_000002_verbal_fluency_Raw.mat Subject Average (Main Analysis Window) (Graph Analysis Window)
2	Set the signal length with using View range or typing Start, duration, and End value. You can retore original time series using **Reset** button.
3	It shows time series data with using above options. (Conectration selection referes to "3.6.2")  data_180604 1432_2050_test_000... View Range: Start 100 Duration 255 End 355

3.6.2 Variable selection and view output


Graph Analysis

data_180604 1432_2050_test_000...

View Range: Start 23 Duration 255 End 278 (sec)

Concentration: ○ HbO ● HbR ● HbT

Channel Group: ○ 3cm ● 1.5cm ● 2.12cm ● 3.35cm

Grouping: ● Brodmann ○ All Channel

Node Measure: ○ Degree ● Average Shortest Path Length ● Betweenness Centrality

Edge Measure: Correlation Coefficient ○ Pearson

Connectivity Thd. (-1~1): 0

☐ Show Binary

☐ Show Reject

Network Measure

Density : 0.9406

Characteristic Path Length : 0.57878

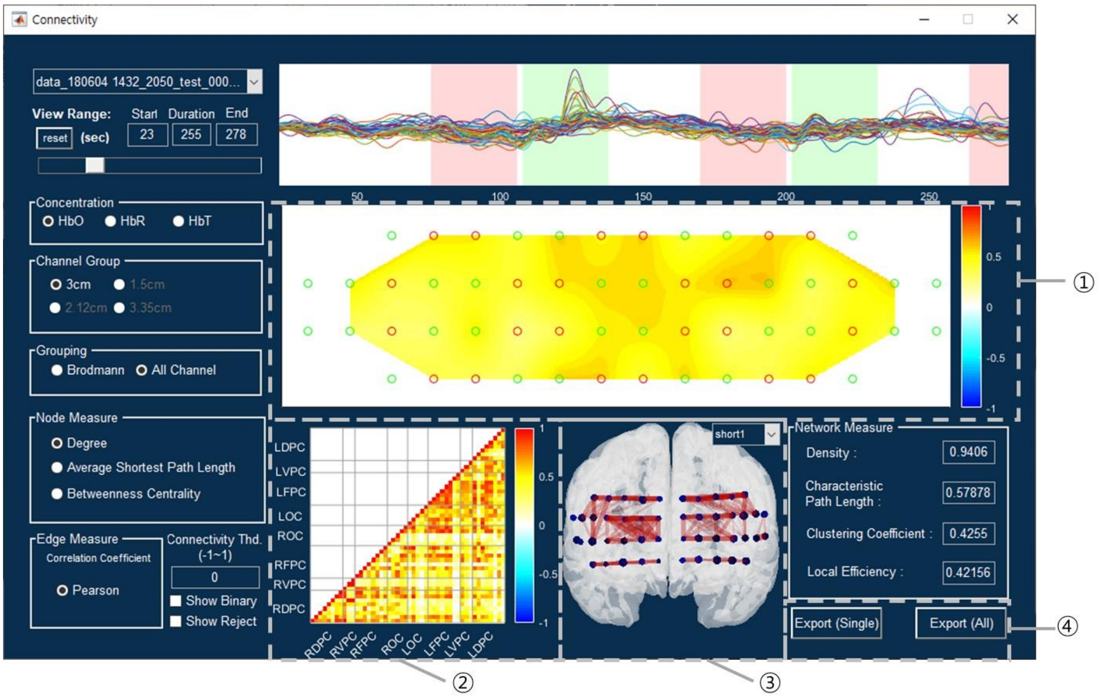
Clustering Coefficient : 0.4255

Local Efficiency : 0.42156

Connectivity will be calculated with below options.

No.	Description
1	**Concentration** Hemoglobin concentration type
2	**Channel Group** You can select only 3cm option for now.
3	**Grouping** The Brodmann function is applied to generate representative time series data by averaging the time series data of the channels belonging to each area defined in section 3.4.2, and then calculates the correlation between the representative data of each areas and displays them on the screen.
4	**Node Measure** Degree / Average Shortest Path Length / Betweenness Centrality
5	**Edge Measure** Spearman / Pearson
6	**Connectivity Thd (-1~1)** Set the threshold value of correlation for displaying. Show Binary: mapping 1 with higher than threshold value and 0 for others. Show Reject: Showing connectivity except rejected channels in pre-processing step.
7	**Network Measure** It shows Density, Characteristic Path Length, Clustering Coefficient, Local Efficiency

3.6.3 Node Measure output



data_180604 1432_2050_test_000...

View Range: Start Duration End
reset (sec) 23 255 278

Concentration: ○ HbO ● HbR ● HbT

Channel Group: ○ 3cm ● 1.5cm ● 2.12cm ● 3.35cm

Grouping: ● Brodmann ○ All Channel

Node Measure: ○ Degree ● Average Shortest Path Length ● Betweenness Centrality

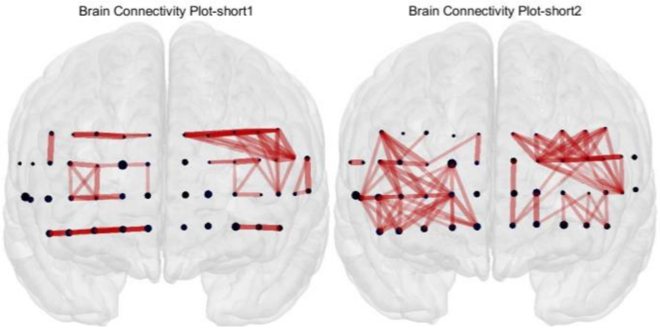
Edge Measure: Correlation Coefficient ○ Pearson

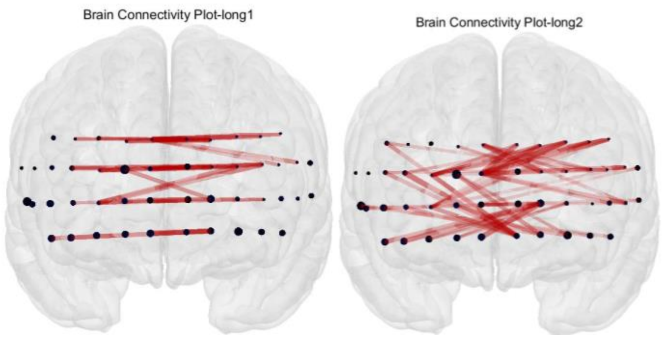
Connectivity Thd. (-1~1): 0

☐ Show Binary
☐ Show Reject

Network Measure
Density : 0.9406
Characteristic Path Length : 0.57878
Clustering Coefficient : 0.4255
Local Efficiency : 0.42156

Export (Single) Export (All)

No.	Description
1	It shows connectivity node measure result for each data as a 2-dimensional image (Degree, Average Shortest Path Length, Betweeness Centrality)
2	It shows correlation matrix for calculating connectivity. It is replaced in order that Brodmann area with gray grid line not channel numbers.
3	It provides 4 view modes. (when All channel selected) It is divided according to the left and right of each brain area and between areas. same areas (left), different ares (right) in each side of right and left 

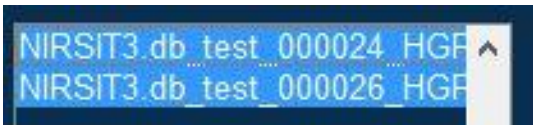
No.	Description
	same areas (left), different ares (right) between right and left 
4	You can export all result such as images and features with Export button. If you select path for saving data, a folder with the selected data name is created in the path and files as shown below are created. ▪ Data name_[Correlation_parameter].csv ▪ Data name_[Degree, Average Shortest path-length, Betweenness Centrality].csv ▪ Data name_[Density, Characteristic Path-length, Clustering Coeff, Local Efficiency].csv ▪ Data name_1.Connectivity_Node_Measure.jpg (fig) ▪ Data name_2.Connectivity_Edge_Measure.jpg (fig) ▪ Data name_3.Brain_Connectivity_Network (Hemosphere).jpg (fig) ▪ Data name_4.Brain_Connectivity_Network (Interhemispheric).jpg (fig) **Export (Single)** button will export currently selected data, and **Export (All)** button will export all of the result for your data.

3.7 Data Export

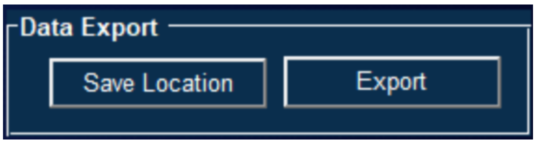
Export data files after signal processing and calculate concentration processes.

3.7.1 Save Location

1 Use the **Data Selection** panel to select one or more data files to export, and then click **Save Location** button in the **Data Export** panel to set the destination folder where the exported files will be saved.

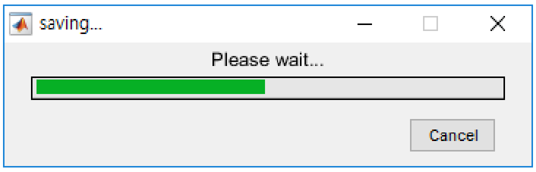


NIRSIT3.db_test_000024_HGF
NIRSIT3.db_test_000026_HGF



3.7.2 Export

If you click **Export** in the **Data Export** panel, selected data files are exported and saved to the specified destination folder under the file name “data_data name”.



Please wait...

- The files can be loaded and imported as raw data.
- If an exported file is loaded again, the Block Average & Analysis option becomes available.

OBELAB