

Optical Topography System

Topo Signal Processing type-G

Ver.2.05

Instruction Manual

Notes for operators and responsible maintenance personnel

- ★ Please read through this Instruction Manual carefully prior to use.
- ★ Keep this Instruction Manual together with the system to ensure it is available at all times.

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Tokyo, Japan

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1. Introduction

1.1 Topo Signal Processing type-G

Topo Signal Processing type-G (hereinafter called “TSP-G”) is a software package, which runs on MATLAB® provided with ample signal processing functional capabilities and analyzes measurement data obtained from the optical topography system.

TSP-G processes the hemoglobin text data output from the optical topography system using media such as DVD-RAM and calculates the averaged waveforms in the external PC in which MATLAB® is installed.

Also, it is possible to conduct topographic image display processing, frequency analysis processing, principal component analysis processing, spectrogram analysis processing, difference t analysis processing, waveform superimposed display processing and difference display processing of the averaging results.

It is possible to use all signal processing functions that MATLAB has since TSP-G retains all signal data in MATLAB.

TSP-G software allows you to easily analyze and evaluate signal data for your research, presentations for scientific meetings and so on.

TSP-G is a product of Hitachi Medical Corporation and only available for users who sign the leasing contract.

It is necessary for users to prepare and install MATLAB on computers.

*MATLAB is a trademark of The Math Works, Inc.

® mark is not shown in the following text.

1.2 Major Contents of Leasing Agreement

The following shows the major contents of the leasing agreement.

For details, refer to the leasing agreement.

*Risk bearing

Damage or loss of the analysis software or its duplication occurring after delivery shall be born by Hitachi Medical Corporation except those occurred intentionally or accidentally.

*Prior announcement of publication, advertisement, etc

When analysis results obtained from using the analysis software are to be presented to academic meetings or published in advertisements, newspapers or any other media, Hitachi Medical Corporation shall be informed in advance.

*Handling of patent application

When any patent based on analysis results obtained from using the analysis software is to be applied, the user and Hitachi Medical Corporation shall mutually discuss its property.

Also, when property is to be shared by both parties the patents shall be applied by both parties upon making agreement of joint application that specifies equity and so on.

However, when the user succeeds the right of patent application from Hitachi Medical Corporation, the user shall have the right of sole application.

*Priority implementation

When the sole application as a result of discussion above is patented, Hitachi Medical Corporation or any party Hitachi Medical Corporation appoints shall exclusively have the right of priority implementation within a period not exceeding 10 years. However, this period can be updated as necessary. Joint application shall be handled in the same way. Analysis results not subject to patent application shall be handled in the same way.

*Compensation for loss

When either party infringes any clause provided in this agreement, the other party shall have the right to claim compensation for damage or loss and any action the other party agrees as necessary.

*Exemption from responsibility

In the event of any damage or loss occurred is caused by using the analysis software, Hitachi Medical Corporation shall have no obligation for the damage or loss.

2. Operation Environment

2.1 Computer

- 1) Main Unit : DOS/V PC on which MATLAB can be installed and operated

For more information, please visit the MATLAB website below.

<http://www.cybernet.co.jp/matlab/support/install/>

- 2) OS : Microsoft Windows (XP or 2000 is recommended)

- 3) MATLAB : R11.1(Version5.3) or later

The Signal Processing Toolbox is necessary

*Signal Processing Toolbox is used when using the Filter, moving average or spectgram functions.

*It is necessary for users to prepare and install MATLAB on computers.

2.2 Input data format and conditions

Data format and conditions that can be processed using this software are described below.

- ◆ The hemoglobin text data output from the optical topography system using the Fileout function (with the header and comma separated value)
Note: Do not edit the output data using software such as Excel.
- ◆ Store the output hemoglobin text data (Oxy, Deoxy and Total file) in the same folder as one set.
- ◆ The measurement device, the analysis condition, the measurement time and probe mode of the read data are to be the same.
- ◆ The measurement position and rotative direction of the probe are to be the same (Channel 1 is to be displayed in the upper left part of the screen when analyzing and displaying)
- ◆ Do not use “space”, 2 bytes of code letter or special characters (¥ / : * ? “ < > |) as a folder name or a file name.
- ◆ Do not mix data obtained from different devices in the same folder and same sorting condition.

* “Type” in the sentence shows averaged data group.

2.3 Corresponding Optical Topography system

The system type, the system software version and the probe mode that can be processed using this software are described below.

System Type	System Software Version	Probe Mode
ETG-100	Ver2.02L, Ver3.06 ^a , Ver4.00 or later	3x3, 4x4, 3x5
ETG-4000	Ver1.41 or later	3x3, 4x4, 3x5, 3x11
ETG-7000	Ver2.05 or later	4x4, 3x5
ETG-7100	Ver3.02 or later	4x4, 3x5, 3x10

3. MATLAB

For more information about MATLAB, please see the MATLAB help or visit the website below.

<http://www.cybernet.co.jp/matlab>

4. Operation Flow and Sorting

4.1 Operation Flow

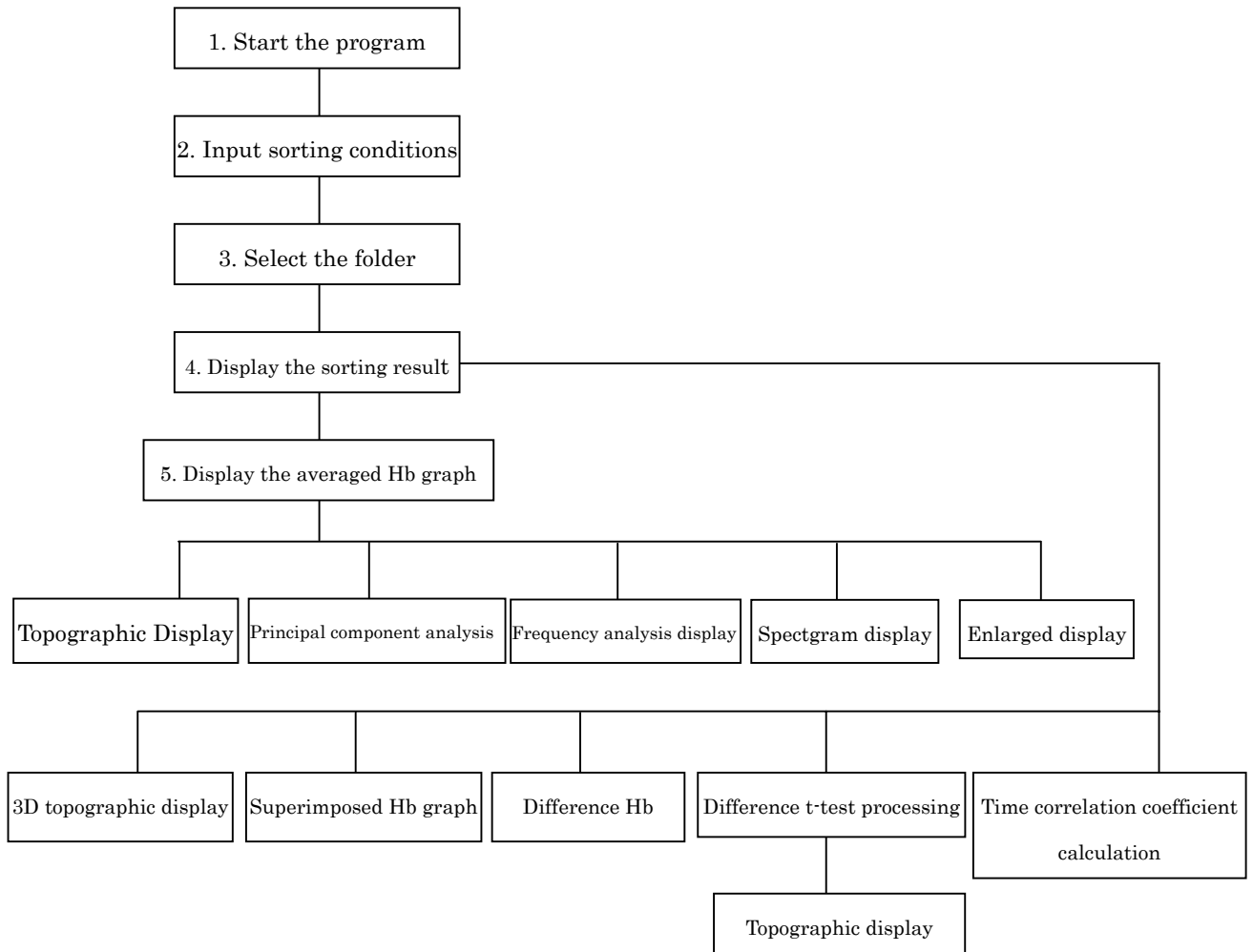


Fig 4.1.1 Operation Flow

1. Start the program and select the device.
2. Set the sorting conditions.
3. Specify the folder in which the hemoglobin text data to be sorted is stored (It is possible to select more than one folder).
4. The sorting results will be displayed by Type.
5. Pressing the [Type Average] button conducts averaging and displays the results.
6. It is possible to conduct those functions such as the topographic display, the principal component analysis, the time correlation coefficient calculation, the spectrogram display, the zooming channel display, the superimposed Hb graph display and the difference t-test processing after displaying the averaged graphs.

4.2 Sorting Examples by Type

4.2.1 Example 1; Sorting by ID or Name

- 1) Select the folder in which data to be sorted is stored.

Table 4.2.1 Conditions of hemoglobin text data in the folders

Folder A			Folder B		
File Name	ID	Name	File Name	ID	Name
Hbdata_A.csv	001	NC	Hbdata_E.csv	003	DP
Hbdata_B.csv	001	NC	Hbdata_F.csv	003	DP
Hbdata_C.csv	002	NC	Hbdata_G.csv	004	DP
Hbdata_D.csv	002	NC	Hbdata_H.csv	004	DP



- 2) Input the folder sorting conditions of each Type

Table 4.2.2 Sorting Conditions

Type	ID	Name
Type1	001	—
Type2	002	—
Type3	—	NC
Type4	—	DP
Type5	004	—



- 3) Displays the sorting results

Table 4.2.3 Sorting Results

Type	File Name
Type1	Hbdata_A.csv、 Hbdata_B.csv
Type2	Hbdata_C.csv、 Hbdata_D.csv
Type3	Hbdata_A.csv、 Hbdata_B.csv、 Hbdata_C.csv、 Hbdata_D.csv
Type4	Hbdata_E.csv、 Hbdata_F.csv、 Hbdata_G.csv、 Hbdata_H.csv
Type5	Hbdata_G.csv、 Hbdata_H.csv

4.2.2 Example 2; Sorting by Comments (“or” sorting)

If the sorting conditions in the comment field are specified separating each comment with a space, the data file that corresponds with one of the conditions will be sorted.

- 1) Select the folder in which data to be sorted is stored.

Table 4.2.4 Conditions of hemoglobin text data in the folders

Folder A		Folder B	
File Name	Comment	File Name	Comment
Hbdata_A.csv	Right Tapping 1try	Hbdata_E.csv	Right Tapping 2try
Hbdata_B.csv	Right Tapping 1try	Hbdata_F.csv	Right Tapping 2try
Hbdata_C.csv	Left Tapping 1try	Hbdata_G.csv	Left Tapping 2try
Hbdata_D.csv	Left Tapping 1try	Hbdata_H.csv	Left Tapping 2try



- 2) Input the folder sorting conditions of each Type.

Table 4.2.5 Sorting Conditions

Type	Comment
Type1	1try
Type2	2try
Type3	Right 1try
Type4	Left 2try
Type5	1try 2try



- 3) Displays the sorting results

Table 4.2.6 Sorting Results

Type	File Name
Type1	Hbdata_A.csv, Hbdata_B.csv, Hbdata_C.csv, Hbdata_D.csv
Type2	Hbdata_E.csv, Hbdata_F.csv, Hbdata_G.csv, Hbdata_H.csv
Type3	Hbdata_A.csv, Hbdata_B.csv, Hbdata_C.csv, Hbdata_D.csv, Hbdata_E.csv, Hbdata_F.csv
Type4	Hbdata_C.csv, Hbdata_D.csv, Hbdata_E.csv, Hbdata_F.csv, Hbdata_G.csv, Hbdata_H.csv
Type5	Hbdata_A.csv, Hbdata_B.csv, Hbdata_C.csv, Hbdata_D.csv, Hbdata_E.csv, Hbdata_F.csv, Hbdata_G.csv, Hbdata_H.csv

4.2.3 Example 3; Sorting by Comments (“and” sorting)

If the sorting conditions in the comment field are specified separating each condition with a space, the data file that corresponds with all conditions will be sorted.

- 1) Select the folder in which data to be sorted is stored.

Table 4.2.7 Conditions of the hemoglobin text data in the folders

Folder A		Folder B	
File Name	Comment	File Name	Comment
Hbdata_A.csv	Right Tapping 1try	Hbdata_E.csv	Right Tapping 2try
Hbdata_B.csv	Right Tapping 1try	Hbdata_F.csv	Right Tapping 2try
Hbdata_C.csv	Left Tapping 1try	Hbdata_G.csv	Left Tapping 2try
Hbdata_D.csv	Left Tapping 1try	Hbdata_H.csv	Left Tapping 2try



- 2) Input the folder sorting conditions of each Type.

Table 4.2.8 Sorting conditions

Type	Comment
Type1	Tapping 1try
Type2	Tapping 2try
Type3	Right 1try
Type4	Left 2try
Type5	1try 2try



- 3) Displays the sorting results

Table 4.2.9 Sorting Results

Type	File Name
Type1	Hbdata_A.csv、 Hbdata_B.csv、 Hbdata_C.csv、 Hbdata_D.csv
Type2	Hbdata_E.csv、 Hbdata_F.csv、 Hbdata_G.csv、 Hbdata_H.csv
Type3	Hbdata_A.csv、 Hbdata_B.csv
Type4	Hbdata_G.csv、 Hbdata_H.csv
Type5	—

5. Explanations of each window & how to use TSP-G

5.1 Starting TSP-G

1) Copy the TSP-G folder on the CD-ROM to the computer in which MATLAB is installed (Do not delete the copied file as the file is necessary to start the software).

Example: Copy the TSP-G folder to the folder directly below the C drive.

2) Start MATLAB.

3) Input the command on MATLAB to move to the copied TSP-G folder.

Example: `>> cd c:\TSP-G`

4) Input “topo” and press the [return] key.

5) The [Welcome to TSP type G] window shown in fig 5.1 will be displayed. Select the system from which data were obtained and will be analyzed.

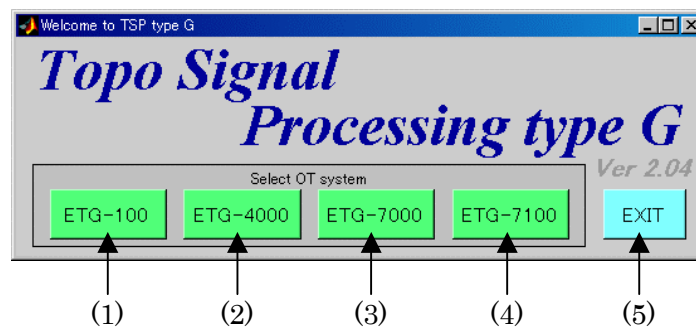


Fig 5.1.1 [Welcome to TSP type G] window

- | | |
|---------------|--|
| (1) ETG-100: | Analyzes the data obtained from the ETG-100 system. |
| (2) ETG-4000: | Analyzes the data obtained from the ETG-4000 system. |
| (3) ETG-7000: | Analyzes the data obtained from the ETG-7000 system. |
| (4) ETG-7100: | Analyzes the data obtained from the ETG-7100 system. |
| (5) EXIT: | Ends the program. |

5.2 Inputting the Type sorting conditions

Selecting the system button in the [Welcome to TSP type G] window displays the [Input search condition] window shown in Fig 5.2.1.

It is possible to categorize the hemoglobin data into 5 groups from Type 1 to Type 5 by a keyword such as ID, Name and Comment (if the conditions apart from “Probe” are not specified, sorting will not be conducted).

It is necessary that the target data be obtained from the same system type and in the same condition.

It is also necessary that the probe mode, layout and directions of the probes be the same (All are displayed in the same direction).

Click the [(9) Search Start] button after defining the sorting conditions.

Figure No. 2
ファイル(F) 編集(E) 表示(V) 挿入(I) ウィンドウ(W) ヘルプ(H)
Input search condition (ETG-4000)

(1) ID (2) Name (3) Probe
(4) Comment (5) Age (6) Male Female
(7) Type 1 Type 2 Type 3 Type 4 Type 5
(8) Comment Search Mode OR (9) Search Start

Fig 5.2.1 [Input search condition] window

- | | |
|-------------|--|
| (1) ID | : Input the ID as a keyword. |
| (2) Name | : Input the name as a keyword. |
| (3) Probe | : Select the probe (This function is available only when data is obtained from ETG-4000, ETG-7000 and ETG-7100). |
| (4) Comment | : Input the comment as a keyword. |
| (5) Age | : Input the age range (Specify the age range such as 20-40 years). |

- (6) Male or Female : Select the gender (Select one gender).
- (7) Type : It is possible to sort the data into 5 groups from Type 1 to Type 5.
- (8) Comment Search Mode : Select comment keyword-sorting method (and/or)
(Separate each comment with a space).
- (9) Search Start : Determine the sorting conditions and select the folder in which the data to be sorted is stored.

5.3 Selecting the folders for Type sorting (to be sorted)

Clicking the [Search Start] button in the [Input search condition] window displays the [Select Folder] window shown in Fig 5.3.1.

Select the folders in which the hemoglobin data to be sorted are stored and then check the box for [(4) Select]. Click the [(5) OK] button to start sorting. Sorting will be conducted for all hemoglobin data in the selected folders.

NOTE: If a space is selected in the folder name or the file name, sorting cannot be conducted

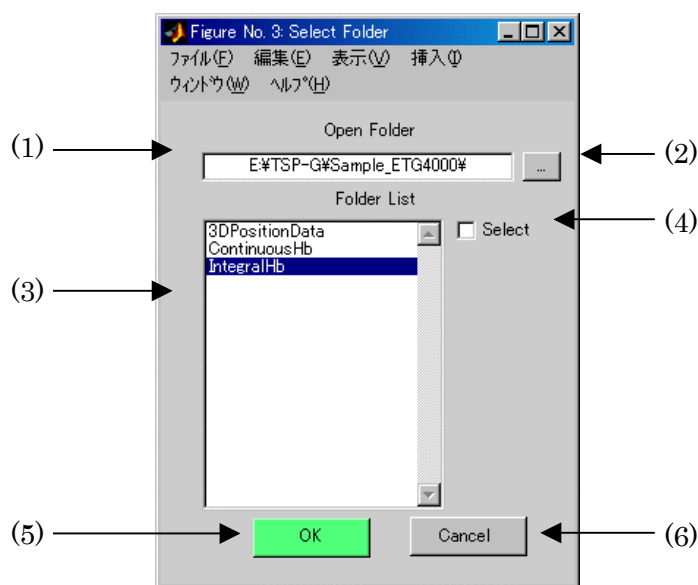


Fig 5.3.1 [Select Folder] window

- (1) Open Folder: Displays the folder directly above the target folders for sorting in the file hierarchy.
It is also possible to input the folder name.
- (2) : Select the files in the target folders for sorting (The folders that contain the selected files are selected).
- (3) Folder List : Displays folders in the same hierarchy as the target folders for sorting (It is possible to select more than one folder in the same hierarchy by checking the box for “Select”).
- (4) Select : Check the [Select] box after selecting the target folder for sorting.
- (5) OK : Click the [OK] button to start sorting.
- (6) Cancel : Click the [Cancel] button to close the [Select Folder] window.

5.4 Sorting Results by Type

Clicking the [OK] button in the [Select folder] window starts sorting.

The “HIT” results and how much data has been read are displayed on the MATLAB command line.

After the read operation has ended, the [Sorting Results by Type] window shown in Fig 5.4.1 will be displayed. The hemoglobin file name (Oxy file name) sorted by Type will be displayed.

Click the [(6) Type Average] button to display the averaged hemoglobin graphs by Type.

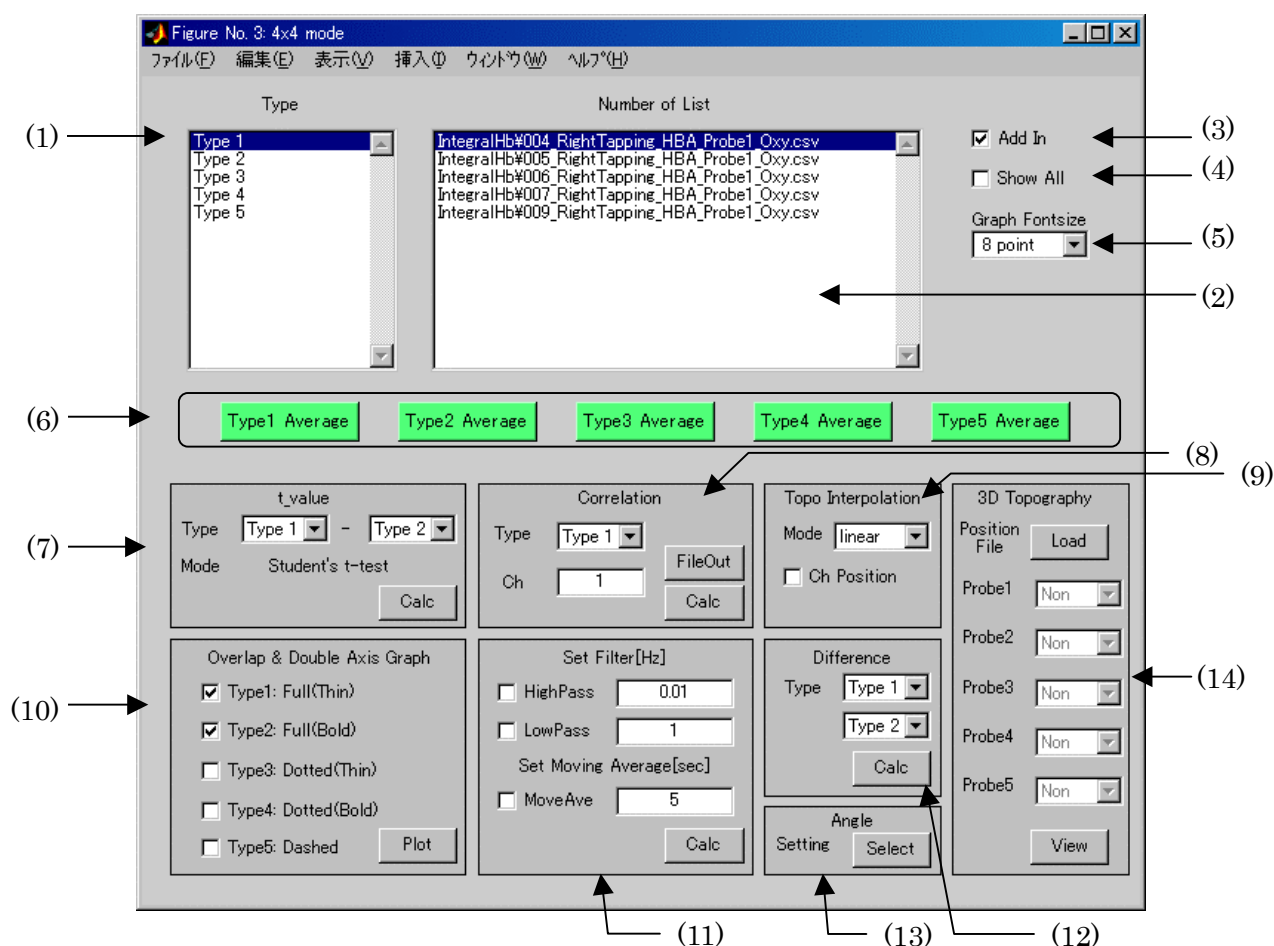


Fig 5.4.1 [Sorting results] window

- (1) Type : Displays the sorting results by Type.
- (2) Number of List : Displays the file list sorted by Type.
(Selecting the file displays the Hemoglobin graph)
- (3) Add In : Select the files to be averaged.
(Select the files to be averaged and check the [Add In] box. All files are selected in default)
- NOTE: If the selection is changed, recalculate the averaged hemoglobin graph.
- (4) Show All : Displays all hemoglobin graphs sorted by Type simultaneously.
(The graphs of the selected files are displayed in black)
- (5) Graph Fontsize: Select the font size for the graph display.
- (6) Type Average : Displays the averaged hemoglobin graph of the selected Type.

- (7) t_value : Conducts the difference t-test in the specified Types.
- ✧ Type: Specify the Types to be subtracted.
 - ✧ Mode: Select the t value calculation formula (homoscedasticity or non-homoscedasticity).
 - ✧ Calc: Conducts the t value calculation.
- (8) Correlation : Calculates the time correlation coefficients for measurement channels of all averaged hemoglobin graphs as the basis of the specified Type and measurement channel.
- ✧ Type: Specify the reference Type.
 - ✧ Ch: Specify the reference measurement channel.
 - ✧ FileOut: Outputs the calculation results in the CSV format.
See **Chapter 6 Output Format** regarding the file format.
 - ✧ Calc: Conducts the calculation.
- (9) Topo Interpolation: Select the interpolation method when a topographic image is to be created.
- ✧ Mode: Linear interpolation method (Linear)
Nearest point interpolation method (Nearest)
Spline interpolation method (Spline)
 - ✧ Ch Position: Checking the [Ch Position] box displays the measurement channel positions on the topographic image.
- (10) Overlap&Double Axis Graph: Superimposes and displays the averaged hemoglobin graphs of the specified Type. Enables range adjustment of the Oxy and Deoxy graphs separately.
- Type: Select the Types to be superimposed and displayed.
- Plot: Displays the superimposed graphs
- (11) Set Filter: Set the filter and the moving average.
- ✧ HightPass: Set the value of the high pass filter.
 - ✧ LowPass: Set the value of the low pass filter.
 - ✧ MoveAve: Set the moving average value.
 - ✧ Calc: Conducts the calculation.
- (It is necessary to refresh the screen after the calculation)
- NOTE: If the filter setting is changed, it is necessary to conduct calculation in order to display the Hemoglobin graphs, averaged graphs, difference t-test graphs, superimposed graphs and difference graphs.
- (12) Difference: Calculates the difference between the specified Types.
- ✧ Type: Select the target Types.
 - ✧ Calc: Displays the difference between the Types.

(13) Angle: Rotates the graph layout by the specified degrees.

Select: Displays the rotation angle setting window.

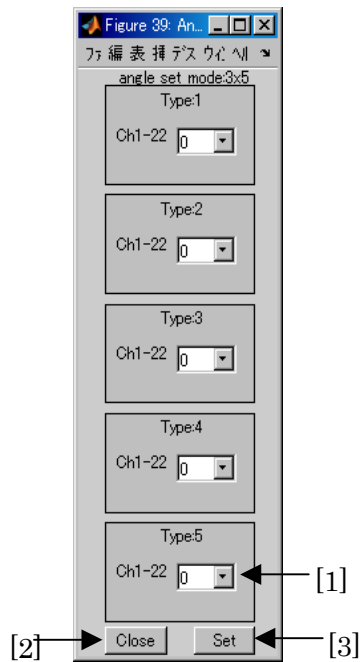


Fig 5.4.2 [Rotation angle setting] window

[1] Set the rotation angle with respect to each Type (0, 90, 180, 270).

[2] Close the window without enabling the new setting.

[3] Close the window enabling the new setting.

(14) 3 D Position: Displays 3D Topography.

Position File: Loads the probe position data.

Probe: Select the waveform to be displayed with respect to each probe position.

View: Displays "3D Topography" images.

5.5 Hemoglobin graphs

Clicking the file in the [Number of List] in the [Sorting results] window shown in fig 5.4.1 displays the hemoglobin graphs of the selected data. If [Show All] is selected, all data in the Type will be displayed (The graphs of the selected data are displayed in black).

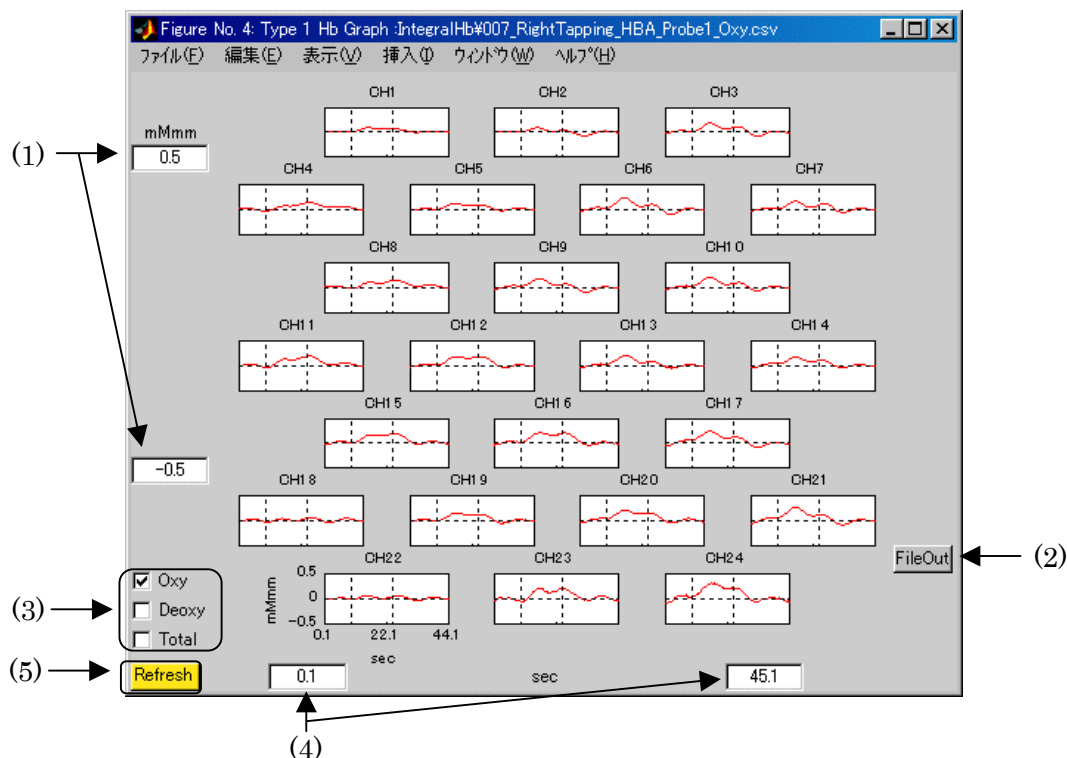


Fig 5.5.1Hb Graph window (Example: 4x4 mode)

- (1) Hb Graph range: Set the Hb graph range (mMmm).
(Specify the graph range within -1000 to 1000. Round off the values to two decimal positions)
- (2) File Out: Outputs the graph data of [oxy], [deoxy] and [total] separately in the csv file format. See Chapter 6 Output Format regarding the file formats.
- (3) Oxy, Deoxy, Total: Displays the Hb graphs of the selected data.
- (4) Time Range: Set the time range of the graphs.
(Specify the time range within the measurement time. Round off the value to one decimal positions)
- (5) Refresh: Resets the screen.

5.6 Averaging

5.6.1 Averaged hemoglobin graphs

Clicking the [Type Average] buttons in the [Sorting results] window displays the averaged hemoglobin graph window. Averaging will be carried out on the channels on which the Exception Channel function in the optical topography system is set to OFF. Averaging will not be applied to the channels on which the Exception Channel function is ON. As such, the channels on which the Exception Channel function is ON will not be considered for averaging. If an identical channel in all hemoglobin data is ON, the averaging waveform will be zero.

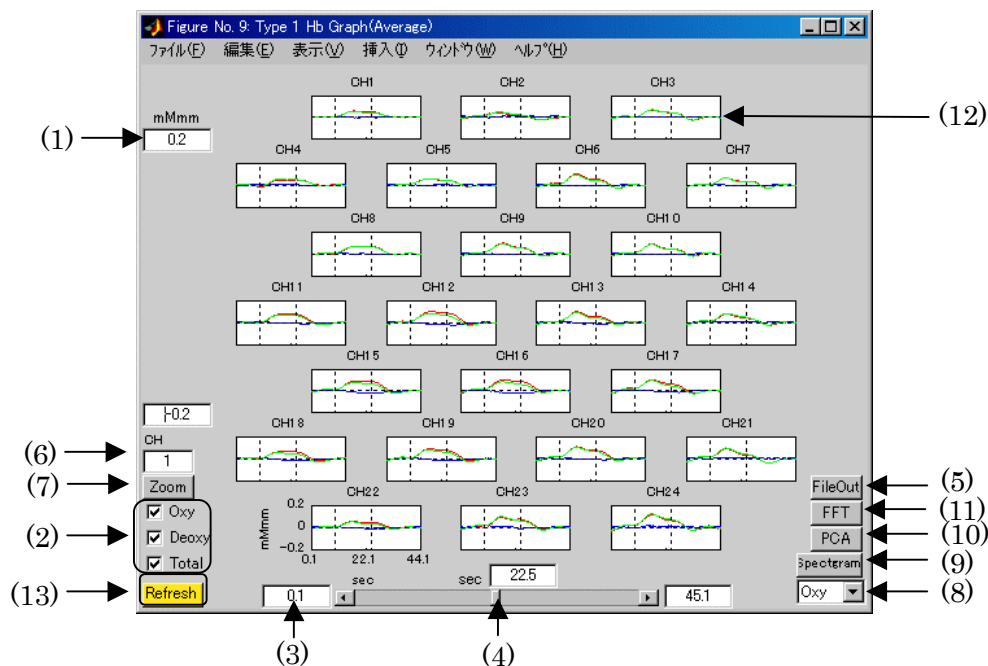


Fig 5.6.1 Averaged Hb graph (Example: 4x4 mode)

- (1) Hemoglobin graph range: Set the graph range (mMmm).
(Specify the graph range within -1000 to 1000. Round off the values to two decimal positions)
- (2) Oxy, Deoxy, Total: Select the hemoglobin type to be displayed.
- (3) Time range: Set the time range of the graph.
(Specify the time range within the measurement time. Round off the values to one decimal place)
- (4) Slider bar: Sets the time position of the topographic image display.
- (5) File Out: Outputs the graph data of [oxy], [deoxy] and [total] respectively in the csv file format. See Chapter 6 Output Format regarding the file formats.
- (6) CH: Specify the measurement channel to be zoomed in on.
- (7) Zoom: Displays the window in which the graph of the specified channel is zoomed in on.
- (8) Selecting hemoglobin type: Select the hemoglobin type with which Principal Component Analysis is to be conducted.
- (9) Spectrogram: Carries out frequency analysis continuously in terms of time and displays the intensity, frequency and time by showing intensity using a color key.

- (10) PCA: Conducts Principal Component Analysis.
- (11) FFT: Displays frequency analysis graphs (Fast Fourier Transformation graphs).
- (12) Hemoglobin graph: Clicking on the graph displays the topographic image at a particular time.
- (13) Refresh: Resets the screen.

Table 5.6.1 Corresponding device version for the Exception Channel function

	Software Version	File Version
ETG-100	4.04 or later	4.04 or later
ETG-4000	1.41 or later	1.06 or later
ETG-7000	2.06 or later	2.03 or later
ETG-7100	3.02 or later	2.05 or later

5.6.2 Topographic image display

Clicking anywhere on the averaged Hb graphs displays the topographic images at a particular time.

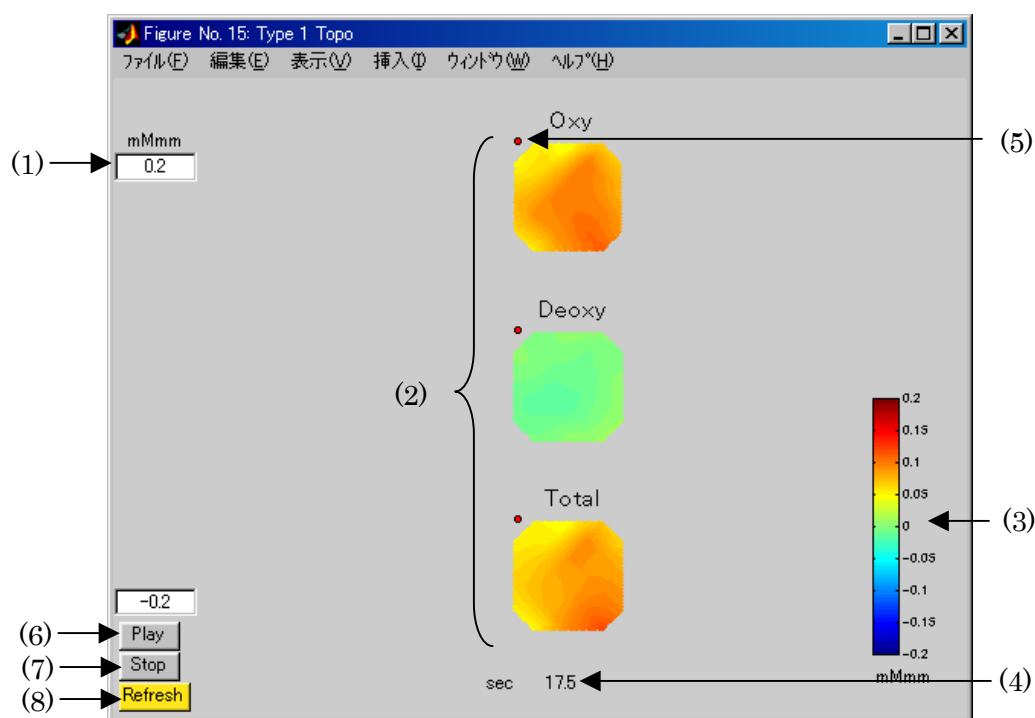


Fig 5.6.2 Topographic image (Example: 4x4 mode)

- (1) Topographic image range: Set the topographic image range (mMmm).
(Specify the range within -1000 to 1000. Round of the value to two decimal places)
- (2) Topographic image: Displays the topographic images of Oxy, Deoxy and Total.
- (3) Range bar: Displays the color range bar.
- (4) Time of topographic image display: Displays the topographic images at a particular time.
- (5) Channel reference position: Displays the reference position.
- (6) Play: Plays animated topographic images.
- (7) Stop: Stops animated topographic image playback.
- (8) Refresh: Resets the screen.

The position in which the tip of the incident fiber of channel 1 touches the skull is displayed as the reference position. In the 3x3 probe mode, the positions in which the tips of the incident fibers of channel 1 and channel 13 touch the skull are displayed as the reference positions.

In the 3x3 mode, the left probe is displayed as measurement channels 1-12 and the right probe is displayed as measurement channels 13-24. Therefore, the measurement channels in the left probe and the measurement channels in the right probe can be reversed depending on the actual position on the head.

5.7 The zoom window of a specified channel

Clicking the [Zoom] button in the [Averaged Hb graph] window displays the zoom window of the specified channel. Clicking anywhere on the graph displays the hemoglobin value, the standard deviation value (SD value) and the standard error value (SE value) of a particular time. The clicking point will be displayed as a red-purple color bar.

Checking the [SD] and [SE] boxes displays each graph (mean value plus or minus SD or SE) as thin lines. Checking the [Tilt & Area] box displays “Tilt” and “Area” on the graph and displays the values in (9) Value display area. The calculation interval of Tilt and Area can be set in (6) Tilt & Area time range.

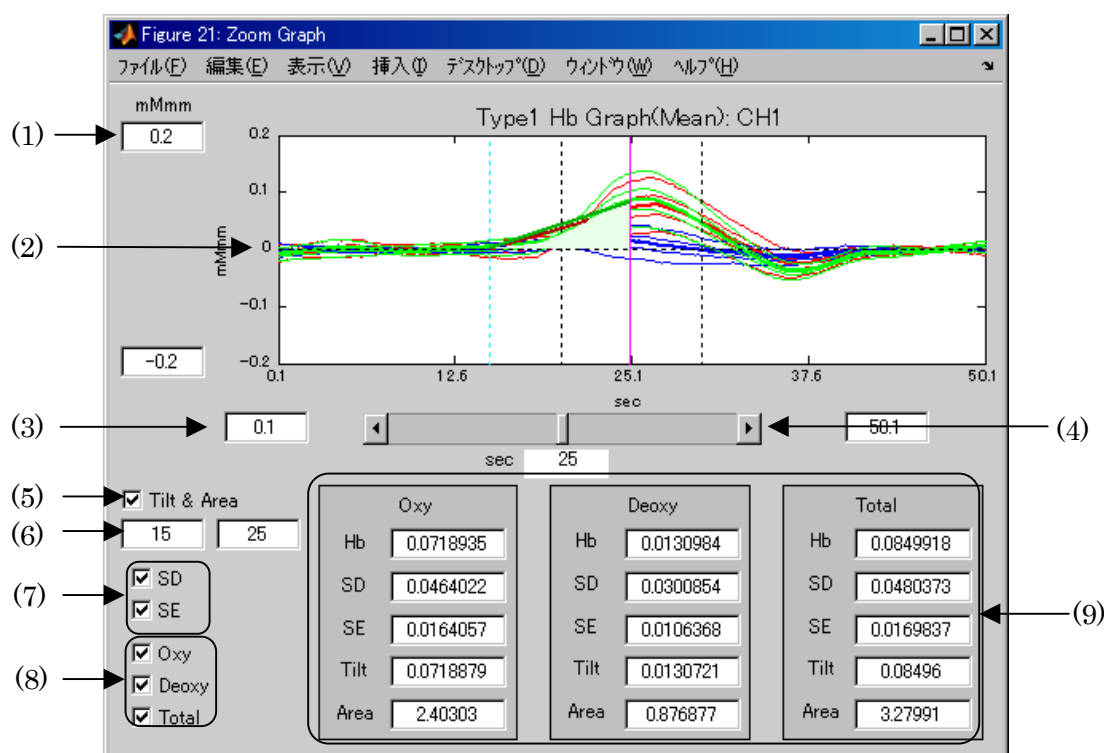


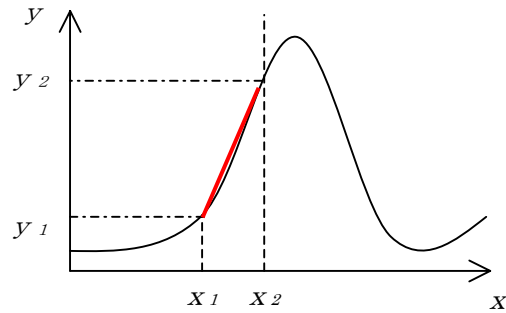
Fig 5.7.1 The zoom window of the specified channel

- (1) Hemoglobin graph range: Set the graph range (mMmm)
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (2) Graph: The hemoglobin graph and the mean value plus or minus SD or SE graph
- (3) Time range: Set the time range of the graph.
(Specify the time range within the measurement times. Round off the value to one decimal place)
- (4) Slider bar: Specifies the time position to display the values.
- (5) Tilt & Area: Calculates “Tilt” and “Area”, and displays them in the graph.
- (6) Tilt & Area time range: Specify the time range for Tilt and Area.
- (7) SD, SE: Calculates SD and SE and displays them in the graph.
- (8) Oxy, Deoxy, Total: Select the hemoglobin type to be displayed.
- (9) Value display area: Displays the Hb values, the SD values, the SE values, the Tilt values and the Area values.

Tilt calculation method

The tilt in the interval (x1 - x2) set in (6) will be displayed in “Tilt” of the (9) Value display area.

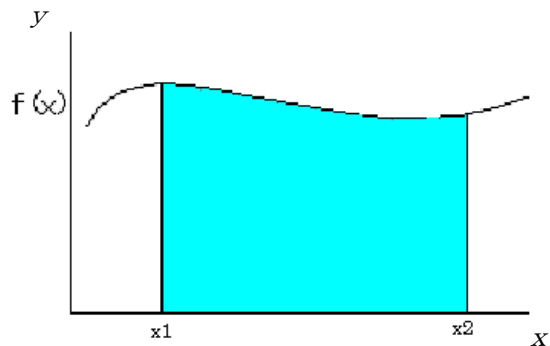
$$Tilt = \frac{y_2 - y_1}{x_2 - x_1}$$



Area calculation method

The area (integration value) in the interval (x1 – x2) set in (6) will be displayed in “Area” of (9) Value display area.

$$Area = \sum_{x=x1}^{x2} f(x)dx$$

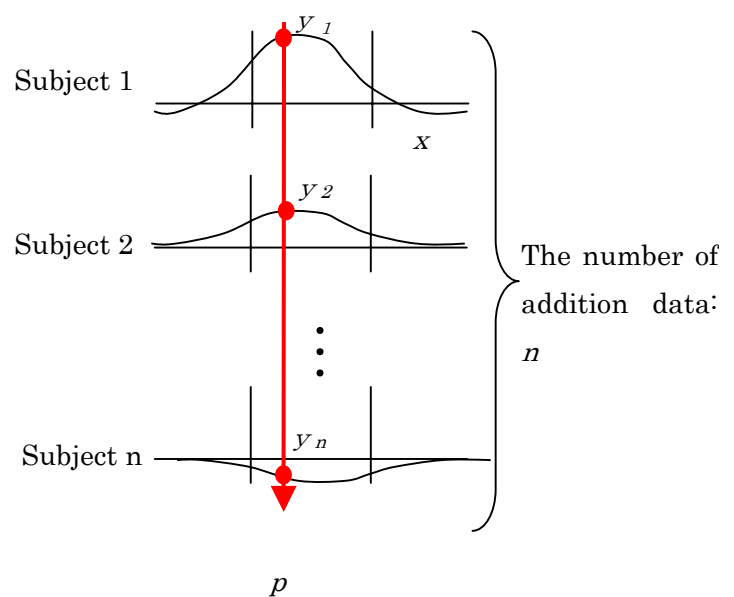


Standard deviate (SD) calculation method

The hemoglobin standard deviation value of the addition data n at the time point specified in (4) will be displayed in “SD” of (9) Value display area (The hemoglobin standard deviation value at the time point p will be calculated following the figure below).

$$SD = \left(\frac{1}{n-1} \sum_{i=1}^n (y_i - \bar{y})^2 \right)^{\frac{1}{2}}$$

	Hb value at the time of p
Subject 1	$y_1=0.55$
Subject 2	$y_2=0.32$
:	
Subject n	$y_n=-0.21$
Average \bar{y}	0.35
Standard Deviation value SD	0.14



Standard Error (SE) calculation method

The hemoglobin standard error value calculated based on the SD value will be displayed in “SE” of (9) Value display area.

$$SE = SD / \sqrt{n}$$

5.8 FFT (Fast Fourier Transformation) graph window (Frequency analysis)

Clicking the [FFT] button in the [Averaged Hb graph] window displays the [FFT Graph] window for the selected hemoglobin type. The frequency characteristic of the raw Hb waveform is displayed in black lines. The frequency characteristic of the waveform after carrying out the “moving average” or “Filter” processing is displayed in colored lines.

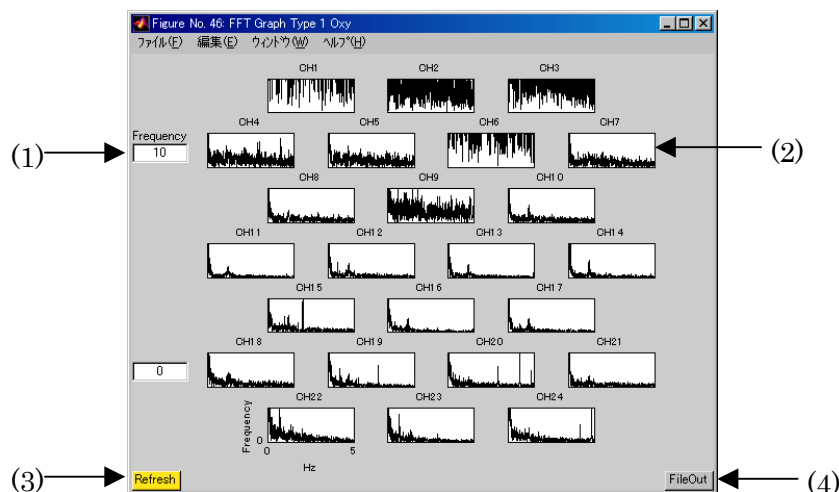


Fig 5.8.1 FFT Graph (Example: 4x4 mode, Oxy Hb)

- (1) Graph range: Set the graph range (Frequency).
(Specify the range within 0 to 1000. Round off the value to two decimal places)
- (2) FFT graph: Displays the FFT graph for the selected hemoglobin type.
- (3) Refresh: Resets the screen.
- (4) File Out: Outputs the graph data of [oxy], [deoxy] and [total] respectively in the csv file format. See Chapter 6 regarding the file formats.

5.9 Principal Component Analysis

5.9.1 Principal Component Analysis Result

Clicking the [PCA] button after selecting the [Hb type] in the [Averaged Hb graph] window displays the principal component analysis window. Principal component analysis allows you to separate and extract the biological and noise signals from measurement signals statistically and objectively.

The eigenvalues and eigenvectors are used in this principal component analysis.

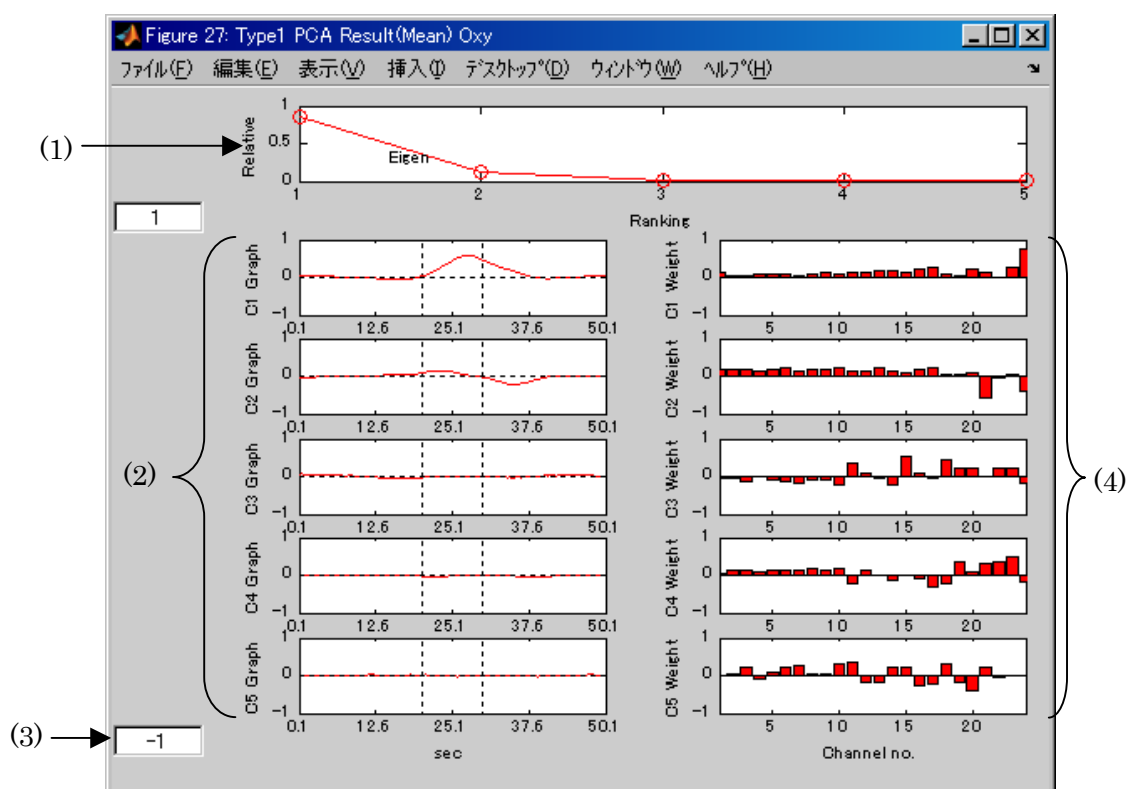


Fig 5.9.1 Principal component analysis window (Example: 4x4 mode, Oxy Hb)

- (1) Relative contribution (Eigen value): Displays the relative contribution of each component.
- (2) Principal component waveform: Displays Principal component waveform of each component.
- (3) The graph range of the principal component waveform: Set the statistic range of the graphs.
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (4) Weighting factor (Eigen vector): Displays the weighting factors (existence frequency) of each principle component waveform for each channel.

5.9.2 Weighting factor topographic image

Clicking the [PCA] button after selecting the [Hb type] in the [Averaged Hb graph] window displays the weighting factor topographic image window shown in Fig 5.9.2. The weighting factors of each principle component waveform for each channel are displayed as a topographic image.

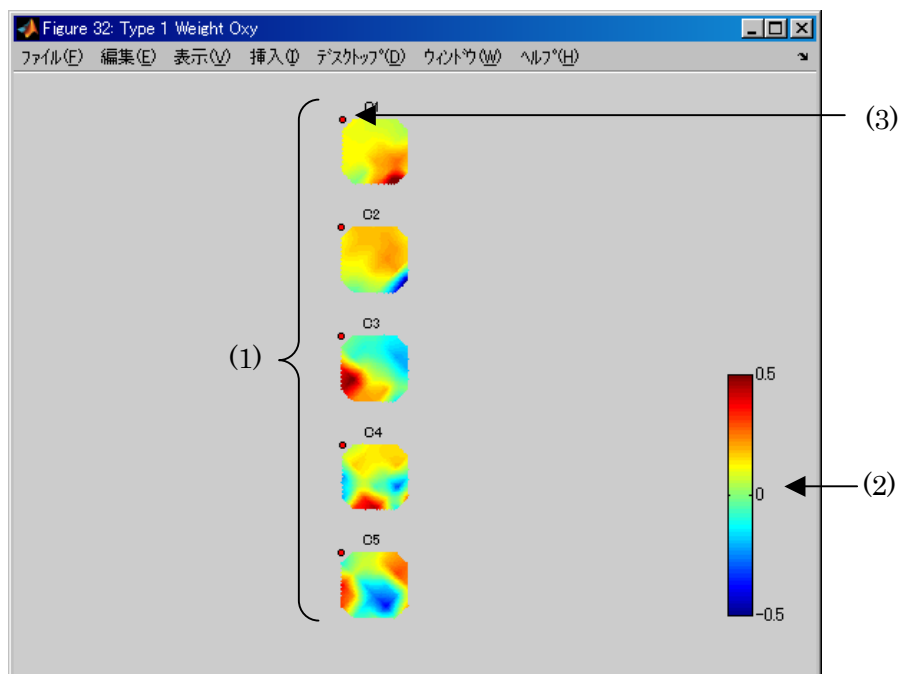


Fig 5.9.2 Weighting factor topographic image window (Example: 4x4 mode, Oxy Hb)

- (1) Topographic image: The weighting factors of each component are displayed as a topographic image.
- (2) Range bar: Displays the color range bar.
- (3) Channel reference position: Displays the reference position.

The position in which the tip of the incident fiber of channel 1 touches the skull is displayed as the reference position. In the 3x3 probe mode, the positions in which the tips of the incident fibers of channel 1 and channel 13 touch the skull are displayed as the reference positions.

In the 3x3 mode, the left probe is displayed as measurement channel 1-12 and the right probe is displayed as measurement channels 13-24. Therefore, the measurement channels in the left probe and the measurement channels in the right probe can be reversed depending on the actual position on the head.

5.10 Spectrogram processing

Clicking the [Spectrogram] button after selecting the [Hb type] in the [Averaged Hb graph] window displays the [Spectrogram] window shown in Fig 5.10.1.

The spectrogram is expressed by the short-time Fourier transformation with respect to each window size. This spectrogram analysis uses the SPECTGRAM function in the MATLAB Signal Processing Toolbox.

Spectrogram window size = the number of measurement data / 10

(The number of measurement data = Measurement time / Sampling rate)

The spectrogram display may not be conducted if points in the last interval of data are not secured depending on the spectrogram window size (displayed as white).

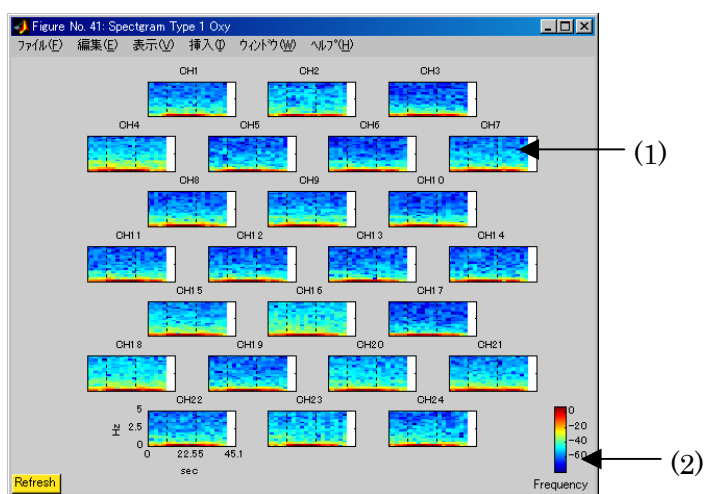


Fig 5.10.1 Spectrogram window (Example: 4x4 mode, Oxy Hb)

(1) Spectrogram

Carries out frequency analysis continuously in terms of time and displays the frequency characteristics with respect to each time using a color key.

(2) Color bar

Displays the intensity of the frequency in the [Spectrogram] window.

5.11 Difference t-test processing

5.11.1 T value graph display

Clicking the [Calc] button after selecting [Type] and [Mode] to be analyzed at [t_value] in the [Sorting results] window displays the [difference t-test graph] window. The red horizontal lines show a 1% significance level and the blue horizontal lines show a 5% significance level. Student's t-test is used for the difference t-test calculation and the t-value is calculated with respect to each measurement point.

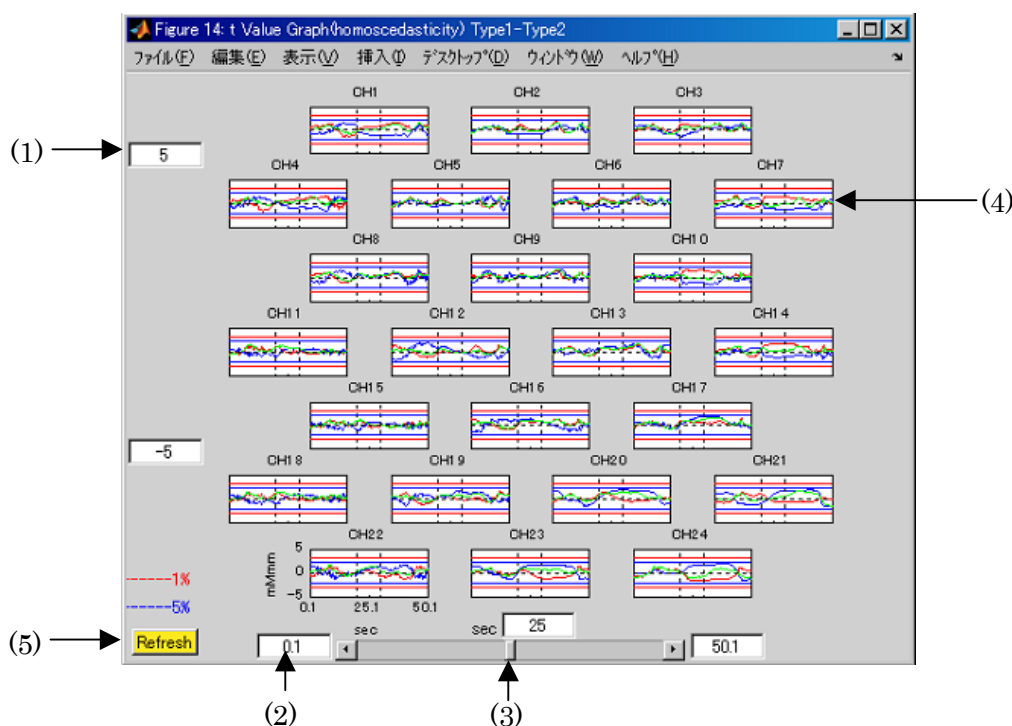
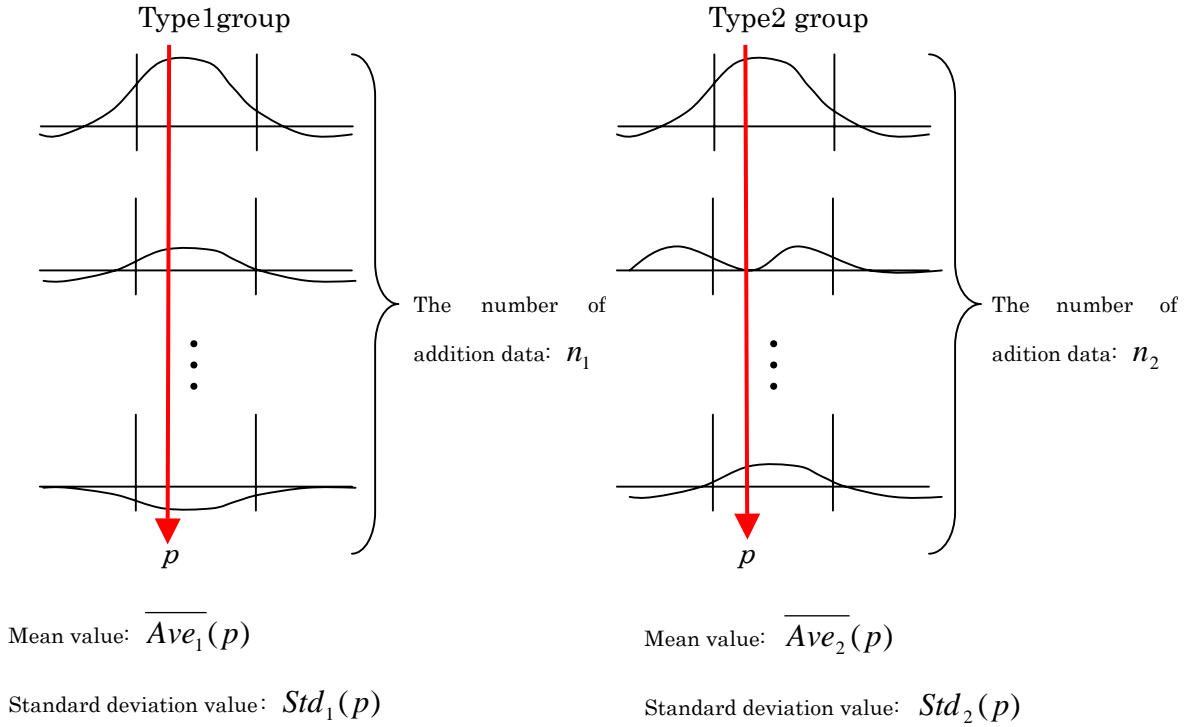


Fig 5.11.1 Difference t-test graph window (Example: 4x4 mode)

- (1) Hemoglobin graph range: Set the statistic range of the graphs.
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (2) Time range: Set the time range of the graph.
(Specify the time range within the measurement time. Round off the value to one decimal place)
- (3) Slider bar: Set the time position of the topographic image display.
- (4) Difference t-test graph: Clicking on the graph displays the topographic image of a particular time.
- (5) Refresh: Resets the screen.

The calculation method of the difference t value (at the time point “p”)



$$\text{Differential t value } (p) = \frac{\overline{Ave}_1(p) - \overline{Ave}_2(p)}{\sqrt{\frac{Std_1^2(p)(n_1 - 1) + Std_2^2(p)(n_2 - 1)}{n_1 + n_2 - 2}} \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

The above calculations are carried out at each time point in all hemoglobin graphs.

More than three data in each Type are required as the significance line is calculated from the t distribution of the degrees of freedom ($n_1 + n_2 - 2$).

If the time point at which the standard deviation value is 0 exists, the calculation of differential t cannot be conducted.

5.11.2 t value topographic image display

Clicking anywhere on the difference t-test graphs displays the topographic images of a particular time.

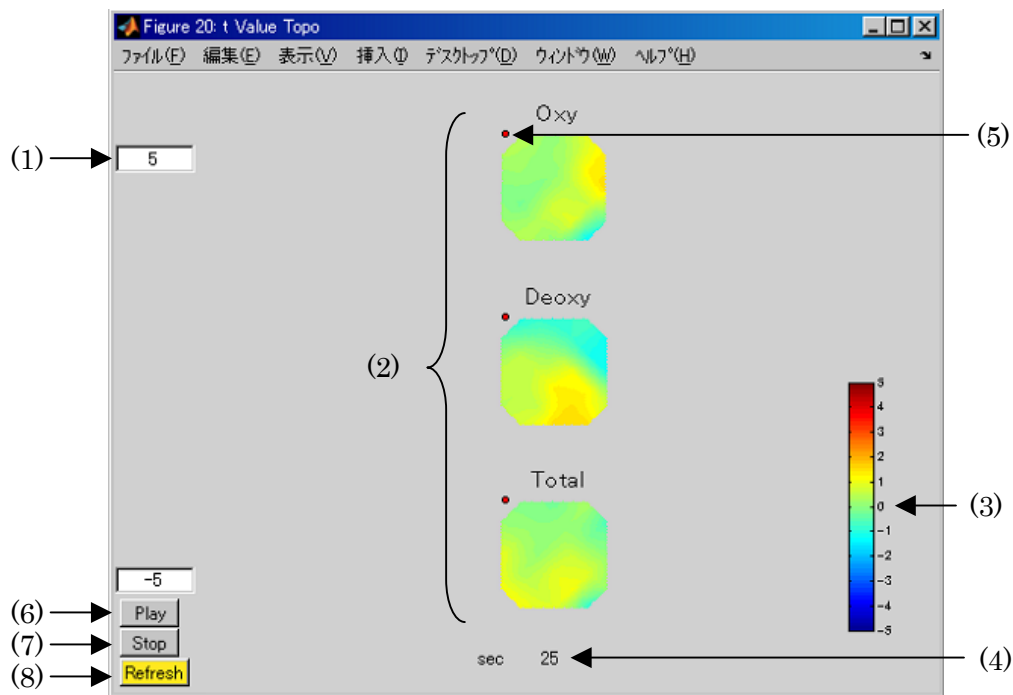


Fig 5.11.2 t Value topographic image window (Example: 4x4 mode)

- (1) Topographic image range: Set the statistic range of the topographic image.
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (2) Topographic image: Displays the topographic images of Oxy, Deoxy and Total.
- (3) Range bar: Displays the color range bar.
- (4) Time of topographic image display: Displays the topographic image of a particular time.
- (5) Channel reference position: Displays the reference position.
- (6) Play: Plays animated topographic images.
- (7) Stop: Stops animated topographic image playback.
- (8) Refresh: Resets the screen.

The position in which the tip of the incident fiber of channel 1 touches the skull is displayed as the reference position. In the 3x3 probe mode, the positions in which the tips of the incident fibers of channel 1 and channel 13 touch the skull are displayed as the reference positions.

In the 3x3 mode, the left probe is displayed as measurement channel 1-12 and the right probe is displayed as measurement channels 13-24. Therefore, the measurement channels in the left probe and the measurement channels in the right probe can be reversed depending on the actual position on the head.

5.12 Time Correlation Coefficient

Display the averaged graphs, select “Type” and “Ch” at [Correlation] in the [Sorting results] window and click the [Calc] button. The time correlation coefficient of All Type averaged graph Ch is calculated and displayed based on the specified channel (Ch) of the specified Type averaged graph.

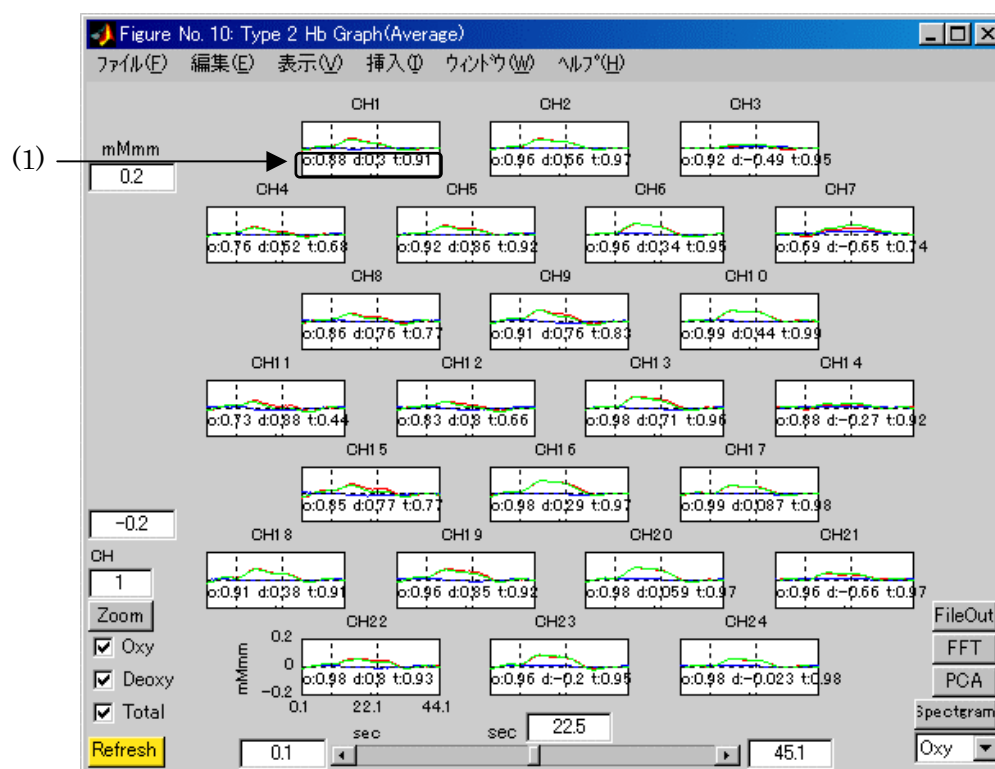


Fig 5.12.1 Time correlation coefficient window (Example: 4x4 Mode)

- (1) Time Correlation Coefficient: Time Correlation Coefficient with the reference Ch (the specified channel)(o: oxy, d: deoxy, t: total)

5.13 Superimposed Hemoglobin Graph

Select [Type] to be displayed from [Overlap & Double Axis Graph] and then click the [Plot] button in the [Sorting results] window to display the [Superimposed Hemoglobin Graph] window. The averaged Hb graphs of the specified Types will be superimposed and the ranges of Oxy and Deoxy can be adjusted respectively.

Each averaged waveform will be displayed as a line type below depending on “Type”.

Type1: thin solid line	————
Type2: thick solid line	—————
Type3: thin dotted line
Type4: thick dotted line
Type5: thin dashed line	- - - - -

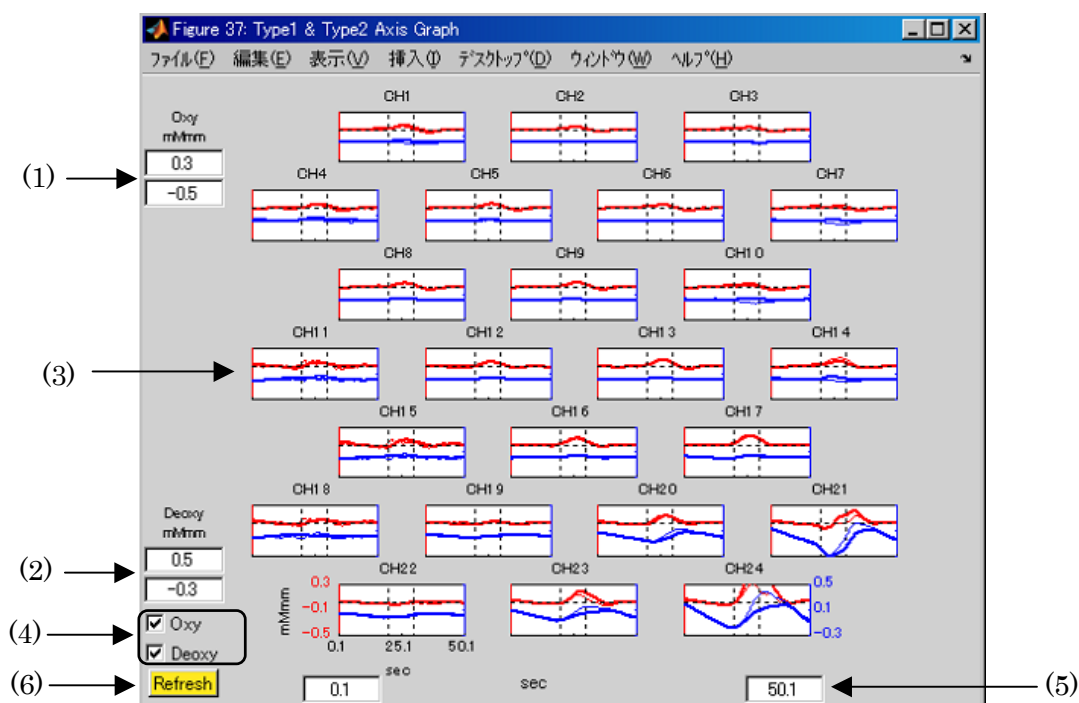


Fig 5.13.1 Superimposed Hemoglobin Graph window (Example: 4x4 Mode)

- (1) Hemoglobin graph range: Set the Oxy graph range (mMmm).
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (2) Hemoglobin graph range: Set the Deoxy graph range (mMmm)
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (3) Superimposed hemoglobin graph: The averaged graphs of the specified Types will be superimposed.
- (4) Selecting the data to be displayed: Select the hemoglobin type to be displayed.
- (5) Time range: Set the time range of the graphs.
(Specify the time range within the measurement times. Round off the value to one decimal place)
- (6) Refresh: Resets the screen.

5.14 Difference graph display

Select “Types” to be analyzed from [Difference] and click the [Calc] button in the [Sorting results] window to display the [Difference graph] window.

The “Type” data in the lower combo box will be subtracted from the “Type” data in the upper combo box at [Difference] in the [Sorting results] window.

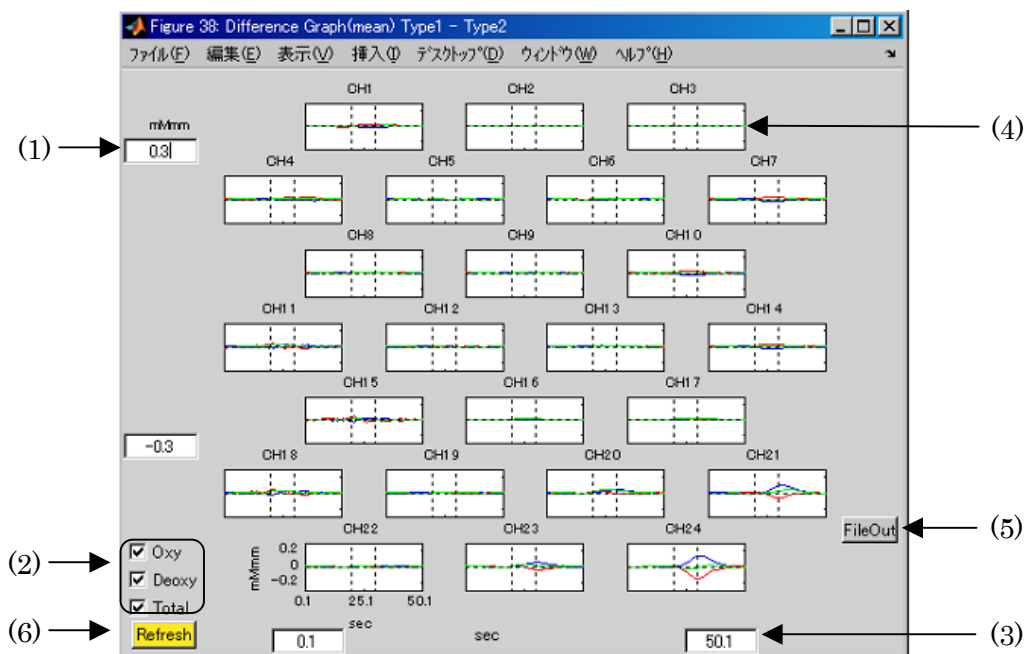


Fig 5.14.1 Difference Graph window (Example: 4x4 mode)

- (1) Hb graph range: Set the graph range (mMmm).
(Specify the range within -1000 to 1000. Round off the value to two decimal places)
- (2) Oxy, Deoxy, Total: The selected data is to be displayed as a “Difference” graph.
- (3) Time range: Set the time range of the graph.
(Specify the time range within the measurement times. Round off the value to one decimal place)
- (4) Difference Graph: The Difference graph of the specified Types will be displayed.
- (5) File Out: Outputs the graph data of [oxy], [deoxy] and [total] respectively in the csv file format. See Chapter 6 regarding the file formats.
- (6) Refresh: Resets the screen.

5.15 3D topographic image display

The topographic images are displayed on the 3D wireframe of a simulated head based on the position data obtained from the 3D Probe positioning unit (optional unit of the optical topography system).

Clicking the [Load] button at [3D Topography] in the [Sorting Results] window displays the [Pos Data Load] window. Select the probe position information file (pos file) corresponding to the loaded NIRS data.

* The [pos] file is the probe position information file obtained from the 3D Probe positioning unit.

Export the [pos] file from the optical topography system in advance following the procedures below.

1. Start the optical topography system and open the [File manager] window.
2. Export the target data to media such as DVD-RAM (Ensure that the symbol ○ is in the 3D field of the target data).
3. When conducting [Export], the [.pos] (4-digit figure) file will be exported in the output folder. For details regarding the function, see the instruction manual of the optical topography system.

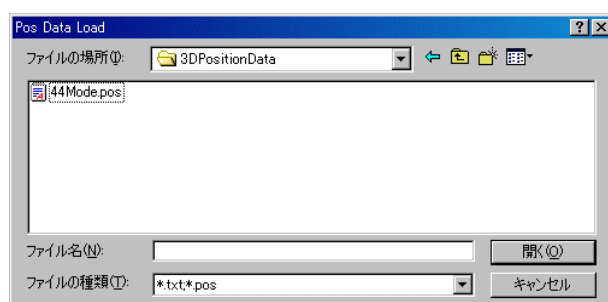
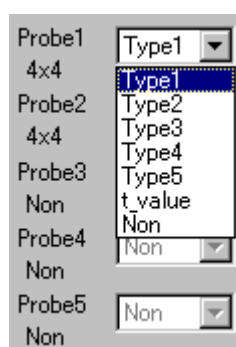


Fig 5.15. 1 Pos Data Load window

After loading the probe position information file, the probe mode will be displayed in the [Probe] field and it will be possible to select the waveforms to be displayed.



Type1-5: Displays the averaged waveform

t_value: Displays the t-value waveform

Fig 5.15.2 3D Position window

After selecting the waveform to be displayed, click the [View] button to display the [3D Topography] window.

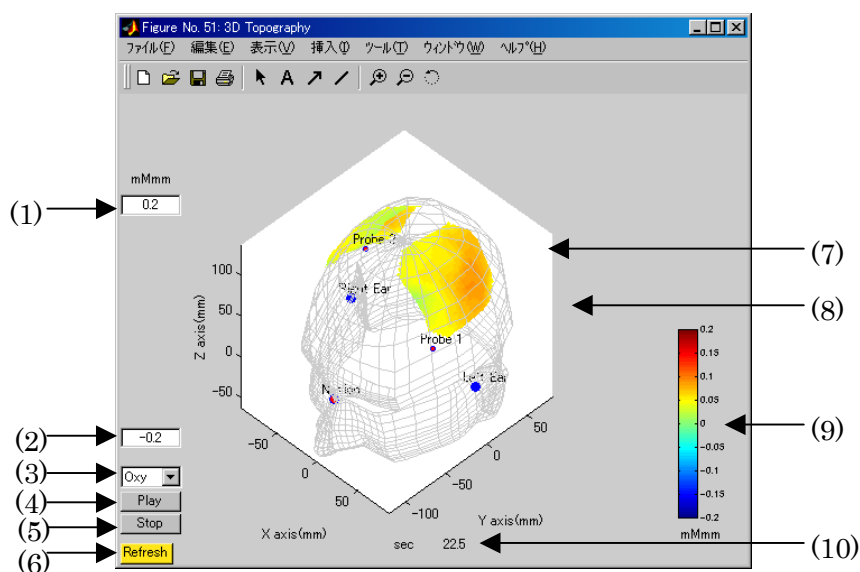


Fig 5.15.3 3D Position window

- (1) Graph maximum range (Unit: mMmm)
Set the upper limit of hemoglobin in the topography window.
- (2) Graph minimum range (Unit: mMmm)
Set the lower limit of hemoglobin in the topography window.
- (3) Hemoglobin type
Select the hemoglobin type to be displayed.
- (4) Play button
Displays the topography window and plays the animated images (Rate: Sampling time x 2)
- (5) Stop button
Stops playing animated images in the topography window.
- (6) Refresh button
Resets the screen.
- (7) 3D image data
Creates the head polygon and displays the topography images.
- (8) Channel position
Displays the position of Channel 1.
- (9) Color bar
Displays the color range bar.
The top of the color range bar shows the maximum value of hemoglobin concentration and the bottom of the color range bar shows the minimum value of hemoglobin concentration.
- (10) Topography window display time
Left-clicking the Hb mapping graph or shifting the scroll bar changes the display time of the topography window.

6. Output Format

The output format for each file is described below.

[#] denotes a user-specified name and [*] denotes a Type number.

Hb data types are [oxy], [deoxy] and [total].

Correlation file (Output file name: #_type*_corr.csv)

Correlation			
Type: TypeNo.			
Base Type (Reference Type): Channel (Reference channel)			
	Oxy	Deoxy	Total
Ch 1	Data	Data	Data
Ch 2	Data	Data	Data
:	:	:	:
:	:	:	:
	Data	Data	Data
Channel number	Data	Data	Data

Hb Data (Output file name: #_Hb data type_row.csv)

Name: File name					
Mode: Probe mode					
Sampling Period: Sampling rate (ms)					
Total Time: Total time (s)					
Time(s)	ch1	ch2	Channel number	Mark
0	Data	Data	Data	Data	0
0.1	Data	Data	Data	Data	0
0.2	Data	Data	Data	Data	0
:	:	:	:	:	:
:	:	:	:	:	:
Total time	Data	Data	Data	Data	0

Averaged Hb Data (Output file name: #_Hb data type_mean.csv)

Type: TypeNo.					
Mode: Probe mode					
Sampling Period: Sampling rate (ms)					
Total Time: Total time (s)					
Time(s)	ch1	ch2	Channel number	Mark
0	Data	Data	Data	Data	0
0.1	Data	Data	Data	Data	0
0.2	Data	Data	Data	Data	0
:	:	:	:	:	:
:	:	:	:	:	:
Total time	Data	Data	Data	Data	0

Difference Data (Output file name: #_Hb data type_diff.csv)

Difference: TypeNo - TypeNo.					
Mode: Probe mode					
Sampling Period: Sampling rate (ms)					
Total Time: Total time (s)					
Time(s)	ch1	ch2	Channel number	Mark
0	Data	Data	Data	Data	0
0.1	Data	Data	Data	Data	0
0.2	Data	Data	Data	Data	0
:	:	:	:	:	:
:	:	:	:	:	:
Total time	Data	Data	Data	Data	0

Frequency Analysis Data (Output file name: #_Hb data type_fft.csv)

FFT Power (data type)				
Type: Type				
Mode: Probe mode				
Sampling Period: Sampling rate (ms)				
Total Time: Total time (s)				
HighPass filter, Setting value				
LowPass filter, Setting value				
Moving Average, Setting value				
Frequency[Hz]	ch1	ch2	Channel number
0	Data	Data	Data	Data
:	Data	Data	Data	Data
:	Data	Data	Data	Data
:	:	:	:	:
:	:	:	:	:
:	:	:	:	:

7. Function Processing Flowchart

The flow of the major modules is shown below.

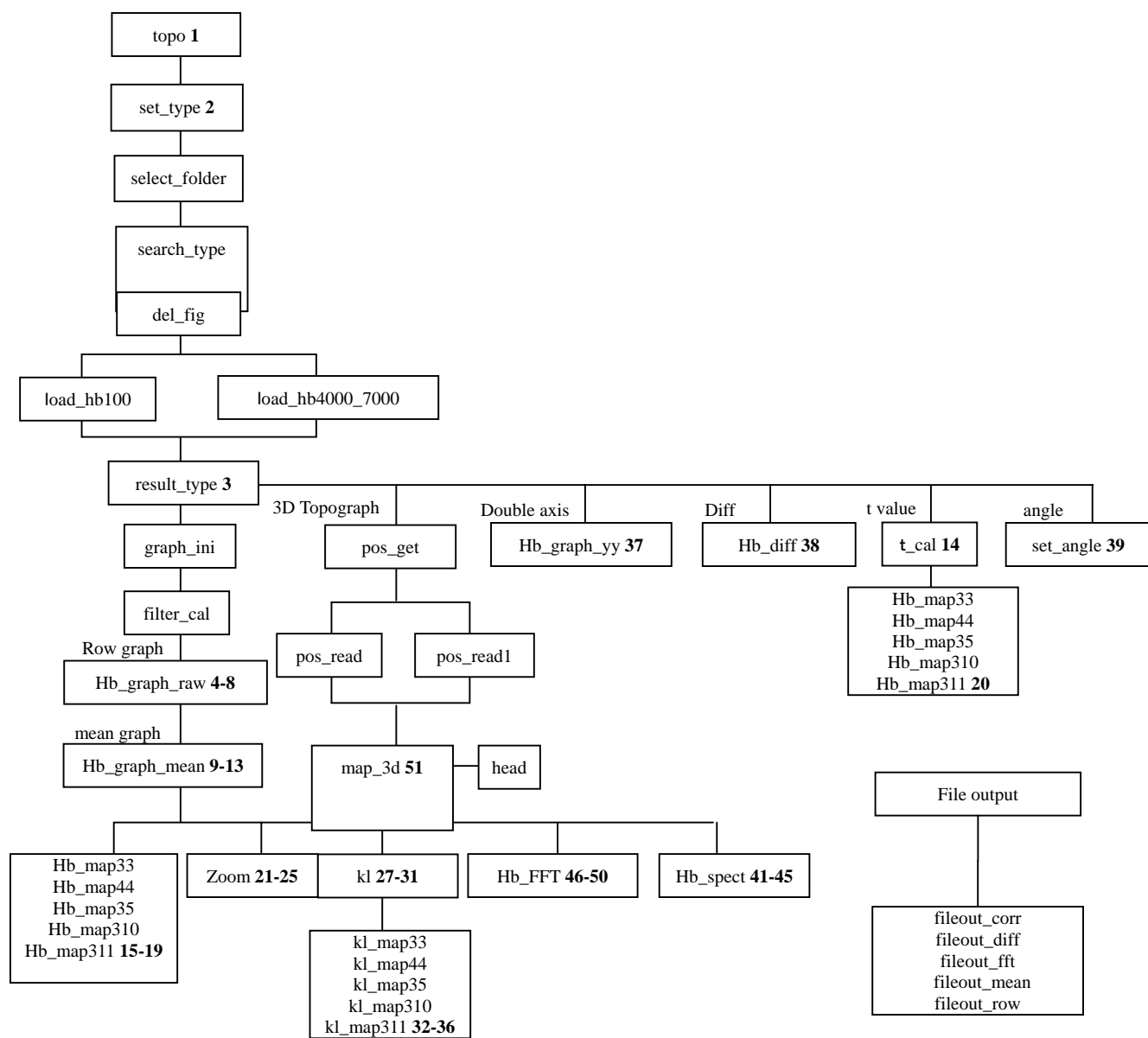


Fig 7.1 Processing Flow

8. Figure Number List

The figure numbers of each window are shown below.

Table 8.1 Figure Number List

Screen or Window	Figure Number
Main Screen	1
Input search condition	2
Sorting results	3
Hb graph	4~8
Averaged graph	9~13
Difference t-test graph	14
Topo graph	15~20
Zoom graph	21~25
PCA (analysis)	27~31
Weighting factor topographic image	32~36
Superimposed graph	37
Difference graph	38
Display angle setting	39
Spect	41~45
Frequency analysis graph	46~50
3D Topo graph	51

9. Function List

- del_fig: Window deletion processing (Function)
Input: fig1,fig2
Output: -
Example of use: function del_fig(fig1,fig2);
- fileout_corr: correlation data file output (Script)
Input: -
Output: -
- fileout_diff: Difference data file output (Script)
Input: -
Output: -
- fileout_fft: FFT data file output (Script)
Input: -
Output: -
- fileout_mean: averaging data file output (Script)
Input: -
Output: -

- fileout_row: hb data file output (Script)
 - Input: -
 - Output: -
- filter_cal: filter processing (Script)
 - Input: -
 - Output: -
- graph_ini: Returning graph display to default (Script)
 - Input: -
 - Output: -
- Hb_diff: Difference data graph creation (Script)
 - Input: -
 - Output: -
- Hb_fft: Frequency analysis graph creation (Script)
 - Input: -
 - Output: -
- Hb_graph_mean: averaging hb graph creation (Script)
 - Input: -
 - Output: -
- Hb_graph_row: hb graph creation (Script)
 - Input: -
 - Output: -
- hb_graph_yy: Superimposed hb graph creation (Script)
 - Input: -
 - Output: -
- Hb_graph_zoom: Zoomed hb graph creation (Script)
 - Input: -
 - Output: -
- Hb_map_310: 3x10 topo map creation (Script)
 - Input: -
 - Output: -
- Hb_map_311: 3x11 topo map creation (Script)
 - Input: -
 - Output: -
- Hb_map_33: 3x3 topo map creation (Script)
 - Input: -
 - Output: -
- Hb_map_35: 3x5 topo map creation (Script)
 - Input: -
 - Output: -
- Hb_map_44: 4x4 topo map creation (Script)
 - Input: -
 - Output: -

- Hb_spect: Spectgram window (Script)
 - Input: -
 - Output: -
- head: Head polygon image creation (Script)
 - Input: -
 - Output: -
- kl: Principal Component Analysis processing (Script)
 - Input: -
 - Output: -
- kl_map310: Principal Component Analysis topo map creation (Script)
 - Input: -
 - Output: -
- kl_map311: Principal Component Analysis topo map creation (Script)
 - Input: -
 - Output: -
- kl_map33: Principal Component Analysis topo map creation (Script)
 - Input: -
 - Output: -
- kl_map35: Principal Component Analysis topo map creation (Script)
 - Input: -
 - Output: -
- kl_map44: Principal Component Analysis topo map creation (Script)
 - Input: -
 - Output: -
- load_hb100: ETG-100 data load (Script)
 - Input: -
 - Output: -
- load_hb4000_7000:ETG-4000 & ETG-7000 data load (Script)
 - Input: -
 - Output: -
- map_3d: 3D topography window creation (Script)
 - Input: -
 - Output: -
- pos_get: 3D position data determination (Script)
 - Input: -
 - Output: -
- pos_read: 3D position data acquisition (Script)
 - Input: -
 - Output: -
- pos_read1: 3D position data acquisition for ETG-100 (Script)
 - Input: -
 - Output: -

- result_type: Sorting result creation (Script)
 - Input: -
 - Output: -
- search_type: Sorting target setting (Script)
 - Input: -
 - Output: -
- select_folder: Sorting folder setting (Script)
 - Input: -
 - Output: -
- set_angle: Angle setting window (Script)
 - Input: -
 - Output: -
- set_type: Sorting condition setting (Script)
 - Input: -
 - Output: -
- strchknum: Character string check (Function)
 - Input: sel,title,initial_path
 - Output: folder,sel_folder
 - Example of use: function [folder,sel_folder] = uigetfolder(sel,title, initial_path);
- strdel: Deleting the specified character at the end of a string of characters (Function)
 - Input: str,char,
 - Output: str
 - Example of use: dum=strdel(dum,delm);
- t_cal: Creating equality of variance (Script)
 - Input: -
 - Output: -
- topo: Software start (Main script)
 - Input: -
 - Output: -
- uigetfolder: Sorting folder display (Function)
 - Input: sel,title,initial_path
 - Output: folder,sel_folder
 - Example of use: function [folder,sel_folder] = uigetfolder(sel,title, initial_path);

10. Variable List

Reads information from Hb data output using “Fileout” and stores it as the variables below.

Variable Name	Class	Structure	Contents
data_para	struct array		Measurement information
	double	ana_mode	Measurement mode
	double	ch_num	The number of channels
	double	datanum	The number of data
	double	mark	Mark position
	double	measmode	Measurement mode
	double	ope_mode	Operation mode (1:stim 2:event)
	double	smpl_period	Sampling interval
fft_data	struct array		FFT graph data information
	double	fft_w	Frequency range
	double	fft_mean	FFT data
fft_graph_h	struct array		FFT graph information
	double	chk_val	Calculation type determination
	double	fft_fig	Window number
	double	fft_mean	FFT graph part number
	double	fft_ref	Refresh button part number
	double	fout	FileOut button part number
	double	lenge_max	Y axis maximum range part number
	double	lenge_min	Y axis minimum range part number
	double	y_max	Y axis maximum range value
	double	y_min	Y axis minimum range value
	double	y_unit	Y axis unit label part number
file_list	struct array		Target data information
	char	name	Target file name
	double	add	Averaging addition determination
	double	sel_list	File selection determination
folder_list	char		Display folder list
folder_list_add	double		Selection folder determination
graph_h	struct array		Screen information
	double	angle_type	Angle setting window number
	struct array	corre_h	Time correlation of the Hb graph
	struct array	dimen	3 D topography selection information
	double	g_list	Sorting result window Type list part number
	double	Hb_fig	Hb graph window number
	struct array	hb_graph	Graph window data
	double	kl_fig	PCA window number
	struct array	kl_graph	PCA window graph range information
	double	kl_topo_fig	Weighting factor topographic image window number
	double	l_check	Sorting result window averaging addition check part number
	double	l_list	Sorting result window file list part number
	double	label_point	Graph label drawing position
	double	label_point2	Graph label drawing position
	struct array	map	Topo map display position information
	double	map_col	Color bar part number

Variable Name	Class	Structure	Contents
	double	map_x	Display size constant x
	double	map_xi	Display size interpolation constant xi
	double	map_y	Display size constant y
	double	map_yi	Display size interpolation constant yi
	double	point_h	Selected position text part number
	struct array	pos	Graph drawing position information
	struct array	result	Sorting result window part information
	double	result_type	Sorting result window number
	double	scrsz	Screen size
	double	sel_folder	Folder selection window number
	struct array	set	Sorting condition information
	double	set_type	Sorting condition window number
	double	show_all	All data display selection flag
	double	sl_h	Slider bar part number
	double	sl_val_h	Selected position input part number
	struct array	spct	Spectgram information
	double	spect_fig	Spectgram window number
	struct array	t_cal	Difference t window information
	double	topo_fig	Topo map window number
	struct array	topo_graph	Topo window information
	struct array	yy	Superimposed graph part information
	struct array	zoom	Zoomed graph window information
	double	zoom_fig	Zoomed graph window number
corre_h	struct array	graph_h	Time correlation of the averaged graphs
	double	mean	Time correlation part number of the averaged graphs
dimen	struct array	graph_h	3D Topo graph selection information
	double	lab	Position mode label part number
	double	menu	Position selection menu part number
	double	val	Position selection menu selection value
hb_graph	struct array	graph_h	Graph window data
	double	mean	Averaged graph part number
	double	mean_ch	Averaged graph Zoom channel part number
	double	mean_fft	Averaged graph fft button part number
	double	mean_fout	Averaged graph FileOut button part number
	double	mean_pca	Averaged graph PCA button part number
	double	mean_pm	Averaged graph PCA type pull-down menu part number
	double	mean_ref	Averaged graph Refresh button part number
	double	mean_spect	Averaged graph Spectgram button part number
	double	mean_t2	Averaged graph time label part number
	double	mean_t3	Averaged graph range label part number
	double	mean_t_max	Averaged graph end position part number
	double	mean_t_min	Averaged graph start position part number
	double	mean_tch	Averaged graph channel label part number
	double	mean_y_max	Averaged graph maximum range part number
	double	mean_y_min	Averaged graph minimum range part number
	double	mean_zoom	Averaged graph Zoom button part number
	double	raw	Hb graph part number
	double	raw_fout	Hb graph FileOut button part number
	double	raw_l1	Hb graph range label part number
	double	raw_l2	Hb graph time label part number
	double	raw_mean	Hb graph Calc Mean button part number
	double	raw_ref	Hb graph Refresh button part number

Variable Name	Class	Structure	Contents
	double	raw_t_max	Hb graph end position part number
	double	raw_t_min	Hb graph start position part number
	double	raw_y_max	Hb graph maximum range part number
	double	raw_y_min	Hb graph minimum range part number
map	struct array	graph_h	Topo map display position information
	double	m	Hb map display position
	double	ml	Hb map 3x3 A display position
	double	mr	Hb map 3x3 B display position
	double	w	Kl map display position
	double	wl	Kl map 3x3 A display position
	double	wr	Kl map 3x3 B display position
pos	struct array	graph_h	Graph drawing position information
	double	p	Graph drawing position
result	struct array	graph_h	Sorting result window part information
	double	ch	Sorting result window channel part number
	double	high_val	Sorting result filter High pass part number
	double	low_val	Sorting result filter Low Pass part number
	double	move_val	Sorting result Move Ave part number
set	struct array	graph_h	Sorting condition information
	double	age1	Sorting condition age 1
	double	age2	Sorting condition age 2
	double	male	Sorting condition male
	double	female	Sorting condition female
spct	struct array	graph_h	Spectgram window information
	double	chk_val	Selection value for each type
	double	spect_color	Color bar part number
	double	spect_lab	Color bar label part number
	double	spect_ref	Refresh button part number
t_cal	struct array	graph_h	Difference t window information
	double	sl_h	Slider bar part number
	double	sl_val_h	Selected position input part number
	double	t2	Difference t time label part number
	double	t_cal_ref	Refresh button part number
	double	t_max	Difference t maximum range part number
	double	t_min	Difference t minimum range part number
	double	v_max	Difference t maximum range part number
	double	v_min	Difference t minimum range part number
yy	struct array	graph_h	Superimposed graph window information
	double	t1	Superimposed graph time label part number
	double	t2	Superimposed graph range label part number
	double	t3	Superimposed graph range label part number
	double	t_max	Superimposed graph end position part number
	double	t_min	Superimposed graph start position part number
	double	tdeoxy	Superimposed graph Deoxy label part number
	double	toxy	Superimposed graph Oxy label part number
	double	y_max1	Superimposed graph Oxy maximum range part number
	double	y_max2	Superimposed graph Deoxy maximum range part number

Variable Name	Class	Structure	Contents
	double	y_min1	Superimposed graph Oxy minimum range part number
	double	y_min2	Superimposed graph Deoxy minimum range part number
zoom	struct array	graph_h	Zoomed graph window information
	double	area_h1	Zoomed graph Oxy fill area part number
	double	area_h2	Zoomed graph Deoxy fill area part number
	double	area_h3	Zoomed graph Total fill area part number
	double	deo_area	Zoomed graph Deoxy-Area text part number
	double	deo_check	Zoomed graph Deoxy check part number
	double	deo_flg	Deoxy selection value
	double	deo_hb	Zoomed graph Deoxy-Hb text part number
	double	deo_sd	Zoomed graph Deoxy-SD text part number
	double	deo_se	Zoomed graph Deoxy-SE text part number
	double	deo_tilt	Zoomed graph Deoxy-Tilt text part number
	double	hb	Zoomed graph part number
	double	oxy_area	Zoomed graph Oxy-Area text part number
	double	oxy_check	Zoomed graph Oxy check part number
	double	oxy_flg	Oxy selection value
	double	oxy_hb	Zoomed graph Oxy-Hb text part number
	double	oxy_sd	Zoomed graph Oxy-SD text part number
	double	oxy_se	Zoomed graph Oxy-SE text part number
	double	oxy_tilt	Zoomed graph Oxy-Tilt text part number
	double	sd	Zoomed SD graph part number
	double	sd_check	Zoomed graph SD check part number
	double	sd_flg	SD selection value
	double	se	Zoomed SE graph part number
	double	se_check	Zoomed graph SE check part number
	double	se_flg	SE selection value
	double	sl_h	Zoomed graph slider part number
	double	sl_val_h	Zoomed graph display position part number
	double	til1	Zoomed graph Tilt&Area start position part number
	double	til2	Zoomed graph Tilt&Area end position part number
	double	til_are	Zoomed graph Tilt&Area check part number
	double	til_flg	Tilt&Area selection value
	double	tilt_h1	Zoomed graph Oxy line part number
	double	tilt_h2	Zoomed graph Deoxy line part number
	double	tilt_h3	Zoomed graph Total line part number
	double	tot_area	Zoomed graph Total-Area text part number
	double	tot_check	Zoomed graph Total check part number
	double	tot_flg	Total selection value
	double	tot_hb	Zoomed graph Total-Hb text part number
	double	tot_sd	Zoomed graph Total-SD text part number
	double	tot_se	Zoomed graph Total-SE text part number
	double	tot_tilt	Zoomed graph Total-Tilt text part number
	double	x_max	Zoomed graph start position
	double	x_min	Zoomed graph end position
	double	y_max	Zoomed graph maximum range
	double	y_min	Zoomed graph minimum range
topo_graph	struct array	graph_h	Topo map window information
	double	mMmm_t1	Unit part number 1
	double	mMmm_t2	Unit part number 1
	double	play	PLAY button part number
	double	point_h	Time part number
	double	point_t1	Time unit part number

Variable Name	Class	Structure	Contents
	double	stop	STOP button part number
	double	topo_ref	Refresh button part number
	double	v_max	Range part number Low
	double	v_min	Range part number Hi
kl_graph	struct array	graph_h	PCA graph information
	double	v_max	PCA maximum graph range
	double	v_min	PCA minimum graph range
hb_data	struct array		Hb data information
	double	add	File averaging addition determination information
	double	area	Area value
	double	corre	Correlation coefficient based on the channels of the specified Type
	double	fil	Filter processed data
	double	mean	Averaged data
	double	raw	File data
	double	sd	SD value
	double	se	SE value
graph_diff	struct array		Difference graph range information
	double	fig	Difference graph range window number
	double	fout	Difference graph FileOut button part number
	double	hb_range1	Difference graph range minimum value
	double	hb_range2	Difference graph range maximum value
	double	mean	Difference graph data
	double	t1	Difference graph time label part number
	double	t2	Difference graph range label part number
	double	t_max	Difference graph range end value part number
	double	t_min	Difference graph range start value part number
	double	time_range1	Difference graph range start value
	double	time_range2	Difference graph range end value
	double	y_max	Difference graph range maximum value part number
	double	y_min	Difference graph range minimum value part number
graph_yy	struct array		Superimposed graph window display information
	double	fig	Superimposed graph window number
	double	h1	Superimposed graph 1 part number
	double	h2	Superimposed graph 2 part number
	double	h3	Superimposed graph 3 part number
	double	h4	Superimposed graph 4 part number
	double	h5	Superimposed graph 5 part number
	double	hb_range11	Superimposed graph Oxy range maximum value
	double	hb_range12	Superimposed graph Oxy range minimum value
	double	hb_range21	Superimposed graph Deoxy range maximum value
	double	hb_range22	Superimposed graph Deoxy range minimum value
	double	time_range1	Superimposed graph time range start value
	double	time_range2	Superimposed graph time range end value
hb_map	struct array		Topo data
	double	intp	Data after interpolating the selected positions
	double	raw	Topo data at the selected position
hb_map_h	struct array		3D topography window information
	struct array	map3d	3D topography window part information3D

Variable Name	Class	Structure	Contents
	double	map3d_col	Color bar part number
	double	map_3d_fig	Window number
	double	topo3d_max	Range maximum value part number
	double	topo3d_min	Range minimum value part number
	double	map3d_oxy	Selection number by each type
	double	map3d_suf1	3D topography part number
map3d	struct array	hb_map_h	3D topography window part information
	double	chk	Selection part number by each type
	double	lab1	Range label part number
	double	lab2	Color bar label part number
	double	max	Maximum range part number
	double	min	Minimum part number
	double	play	Play button part number
	double	ref	Refresh button part number
	double	stop	Stop button part number
	double	t_lab	Time label part number
	double	time	Reproducing time part number
hb_range	struct array		Topo map range data
	double	kl	Kl map range value
	double	mean	Averaging Topo map range value
	double	raw	Topo map range value
	double	zoom	Zoom range value
kl_data	struct array		PCA data
	double	eigen	Contribution ratio of each channel
	double	graph	Representative waveform
	double	weight	Weight of each channel
match_num	double		The number of data with matched conditions by Type
pname	char		Selected folder path
sel	struct array		Selected information
	struct array	angle	Rotation angle setting information
	double	calc_diff1	Difference graph Type 1 calculation determination
	double	calc_diff2	Difference graph Type 2 calculation determination
	double	calc_high	High pass filter calculation determination
	double	calc_high_val	High pass filter calculation value
	double	calc_low	Low pass filter calculation determination
	double	calc_low_val	Low pass filter calculation value
	double	calc_move	Move filter calculation determination
	double	calc_move_val	Move filter calculation value
	double	calc_t_flg	t value calculation flag
	double	call_flg	3D topography call determination flag
	double	ch	Zoomed graph selected channel
	double	corr_ch	Correlation reference channel
	double	corr_type	Correlation reference type
	double	d_type1	Difference selected probe number 1
	double	d_type2	Difference selected probe number 2
	double	flg	
	double	fsize	Font size

Variable Name	Class	Structure	Contents
	double	graph_yy1	Type1 superimposed graph display determination
	double	graph_yy2	Type 2 superimposed graph display determination
	double	graph_yy3	Type 3 superimposed graph display determination
	double	graph_yy4	Type 4 superimposed graph display determination
	double	graph_yy5	Type 5 superimposed graph display determination
	double	high_flg	High pass filter determination
	double	high_val	High pass filter value
	double	kl_hb	PCA selection type
	double	list	Selection list number
	double	list_back	Previous selection list number
	double	low_flg	Low pass filter determination
	double	low_val	Low pass filter value
	struct array	menu	Selection type information
	double	move_flg	MoveAve determination
	double	move_val	MoveAve value
	double	old_sel_t	Previous selection Type number
	double	para	Comment sorting conditions (or:1,and:2)
	double	point	Selected position
	double	sel_fsize	Font size selection number
	double	system	Read file type
	double	t_mode	t_value calculation method
	double	t_type1	t_value target type 1
	double	t_type2	t_value target type 2
	double	topo	Topo image display type
	double	topo2	Topo image channel position display determination
	double	type	Selection Type number
angle	struct array	sel	Rotation angle setting information
	double	a_type1	Probe rotation angle
	double	a_type2	Probe rotation angle (for 3x3B)
	double	ch_a	Probe rotation angle part number
	double	ch_b	Probe rotation angle part number
menu	struct array	sel	Selection type information
	double	kl_hb	Selection type
sel_folder	char		Selection folder
set_para	struct array		Sorting condition information
	double	age1	Sorting condition age 1
	double	age2	Sorting condition age 2
	char	comm	Sorting condition comment
	double	female	Sorting condition female
	double	id	Sorting condition subject ID
	double	male	Sorting condition male
	char	name	Sorting condition subject name
	double	probe	Sorting condition probe
move_stop	double		Animation replay state
system_ver	double		MATLAB version
t_data	struct array		t value data information
	double	alpha1	Display 1 significance value % (1%)

Variable Name	Class	Structure	Contents
	double	alpha2	Display 2 significance value % (5%)
	double	thre1	Coefficient of significance value 1
	double	thre2	Coefficient of significance value 2
	double	type1_fcnt	The number of data of selected Type 1
	double	type2_fcnt	The number of data of selected Type 2
	double	value	Difference t data
thre1	double		1% standard deviation
thre5	double		5% standard deviation
tilt_range	struct array		Tilt & Area information of the zoom graphs
	double	zoom	Tilt & Area range of the zoom graphs
time_range	struct array		Hb graph information
	double	mean	Averaged graph time range
	double	raw	Hb graph time range
	double	zoom	Zoom graph time range
topo_range	struct array		Topo map range information
	double	mean	Averaged Topo map range
view_flg	double		Topo map part display setting flag
pattern_flg	double		3D position data format section
position	struct array		3D position data information
	double	angle_x	Angle x
	double	angle_y	Angle y
	double	angle_z	Angle z
	double	back_x	Occipital x
	double	back_y	Occipital y
	double	back_z	Occipital z
	double	ch_a	Channel information
	double	ch_cnt	The number of channels
	double	ch_e	Channel information
	double	ch_nx	Channel information
	double	ch_ny	Channel information
	double	ch_nz	Channel information
	double	ch_r	Channel information
	double	ch_x	Channel position x
	double	ch_y	Channel position y
	double	ch_z	Channel position z
	double	file_id	ID
	double	file_probe	Probe mode
	double	file_product	Product name
	double	file_type	File type
	double	file_ver	File version
	double	left_x	Left antilobium position x
	double	left_y	Left antilobium position y
	double	left_z	Left antilobium position z
	double	mode	Mode
	double	nasion_x	Nasal position x
	double	nasion_y	Nasal position y

Variable Name	Class	Structure	Contents
	double	nasion_z	Nasal position z
	double	pos_name	Position file name
	double	probe_no	Probe number
	double	right_x	Right antilobium position x
	double	right_y	Right antilobium position y
	double	right_z	Right antilobium position z
	double	top_x	Parietal position x
	double	top_y	Parietal position y
	double	top_z	Parietal position z
	double	user_age	Age
	double	user_comment	Comment
	double	user_id	ID
	double	user_name	Name
	double	user_sex	Sex

11. Message List

No	Message	Description	Action to be taken
1	Please perform an addition average first	Conduct the averaging processing first.	Conduct the averaging processing.
2	None Hit File!	The file cannot be found.	Change the sorting conditions.
3	Sampling Period is different!!	The sampling intervals are different.	Specify the data whose sampling intervals are the same.
4	Data length is different!! Please check	The data lengths are different Please check.	Specify the data whose measurement times are the same.
5	Mark data is not found.!	The Mark data cannot be found.	Specify the data with Mark.
6	There is no standard deviation.	There is no standard deviation.	Increase the number of the data.
7	None Add In File!	There is no addition file.	Turn the list data into an addition target by checking the [Add In] box in the [Sorting Results] window.
8	None list of type!	There in no list in the Type.	Select another Type.
9	The number of Ch is inaccurate.!	The channel number is incorrect.	Specify the correct channel number.
10	Please Select Folder!	Please select a folder.	Please select a folder.
11	Selected data Type is different!!	The selected data types are different.	Change the system type.
12	Probe mode is different!! Please check	The probe modes are different Please check.	Specify the files of the same probe mode.
13	Probe mode is different(Between Type)!! Please check	The probe modes are different (between Types). Please check	Specify the files of the same probe mode.
14	Probe mode is different(Inside of Type)!! Please check	The probe modes are different (in the Type). Please check.	Specify the files of the same probe mode.
15	Oxy t_data.value is NaN.	The data has an indefinite value in Oxy calculation of t_value.	There is no data of the standard deviation. Reselect the data.
16	Deoxy t_data.value is NaN.	The data has an indefinite value in Deoxy calculation of t_value.	There is no data of the standard deviation. Reselect the data.
17	Total t_data.value is NaN.	The data has an indefinite value in Total calculation of t_value.	There is no data of the standard deviation. Reselect the data.
18	It is over the input range	It is over the input value.	Enter the correct input value
19	Measure mode err:	Measurement mode error	Standardize the measurement modes.
20	Analyze mode err:	Analysis mode error	Standardize the analysis modes.
21	A selection file is different:	Incorrect data has been selected.	Select the correct data.
22	File open err.Please check disk or file.	File open error.	Check the disk or the file.
23	File out err.Please check disk.	File output error.	Check the disk.
24	Data format err!! Type:	Data format error.	Check the file.

No	Message	Description	Action to be taken
25	sel.t There is no standard deviation.	There is no standard deviation.	Specify the data in order to create the standard deviation.
26	Please check ID. : Type	Check the ID.	Check the set ID.
27	Please check Name. : Type	Check the name.	Check the set name.
28	Please check Comment. : Type	Check the comment.	Check the set comment.
29	Please check Age. : Type	Check the age.	Check the set age.
30	Please check Sex. : Type	Check the sex.	Check the set sex.
31	The file of the same name already exists.	The file that has the same name already exists.	Change the file name.
32	Please perform filter calculation.	Please conduct the filter calculation.	Please conduct the filter calculation.
33	Please input reference conditions.	Please input the reference conditions.	Please input the reference conditions.
34	There is too little data.	There is too little data.	Increase the target data.
35	Please push a stop button.	Press the [Stop] button.	Press the [Stop] button to stop the reproduction.
36	Please select Type.	Select the Type.	Select the Type of the overlap graph.

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