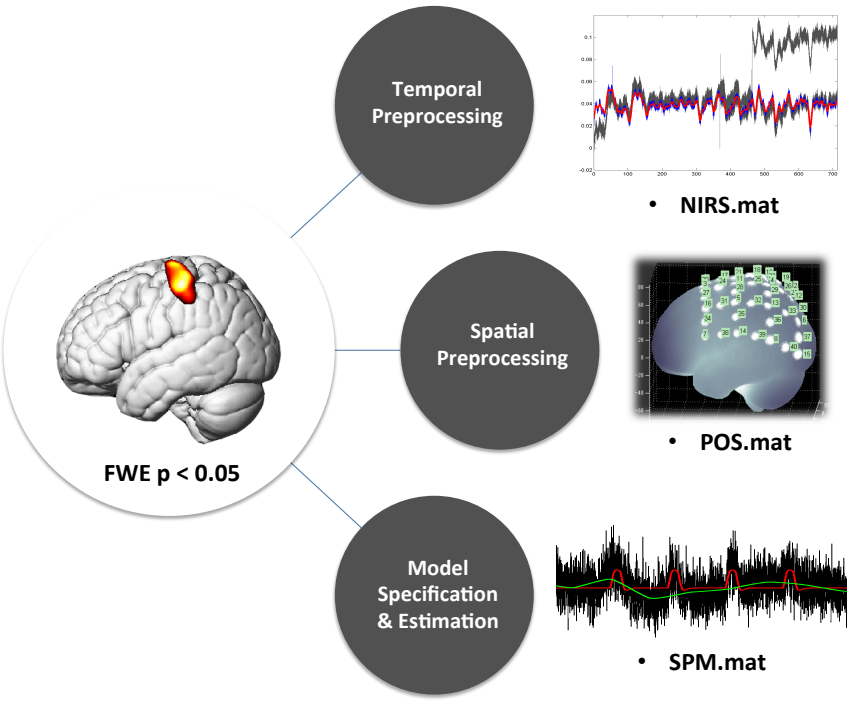
SPM-fNIRS toolbox

The SPM for fNIRS toolbox is the SPM12 (1) - based software for statistical analysis of functional near-infrared spectroscopy (fNIRS) signal. The toolbox allows for inferences about regionally specific hemodynamic effects with superresolution, by applying the general linear model (GLM) and random field theory to fNIRS data (2; 3; 4). In this manual, we provide an illustrative statistical parametric mapping (SPM) analysis using fNIRS data acquired during Stroop task, and then describe detailed information about functions implemented in the toolbox.

Specific features of the SPM-fNIRS toolbox are as follows:

- **Conversion to Hb Changes**:
  Read data acquired using fNIRS system, and calculate hemoglobin concentration changes using the modified Beer-Lambert law (5).
- **Spatial Preprocessing**:
  Transform fNIRS channel positions in the subject space into the corresponding positions in the Montreal Neurological Institute (MNI) space (6).
- **Temporal Preprocessing**:
  Preprocess time series of hemodynamic changes, to (i) reduce motion artifact (7), (ii) reduce cardiac and respiration noise (8), (iii) downsample the data for computational efficiency, and (iv) reduce slow drifts (1).
- **Model Specification**:
  Specify the design matrix in the GLM for the first level analysis (2). The design matrix consists of regressors of interest (eg, canonical hemodynamic response) and confounds (eg, systemic physiological noise) (9).
- **Estimation**:
  Estimate GLM parameters to produce statistical parametric maps (SPMs) (10; 11).
- **Inference of Activation**:
  Make inference about regionally specific effects in SPMs. The random field theory allows for identifying the activated region where the T or F statistic exceed a threshold given by corrected p-value (3).



Installation

1. Download the SPM12 and SPM for fNIRS toolbox.

2. Start MATLAB, and add directories of SPM12 and SPM-fNIRS toolbox into your path:
   » addpath('C:\spm12');
   » addpath('C:\spm_fnirs');

3. Enter 'spm_fnirs' at the MATLAB command window.
   » spm_fnirs;

   The main panel of the toolbox will then open, as shown in Figure 1.

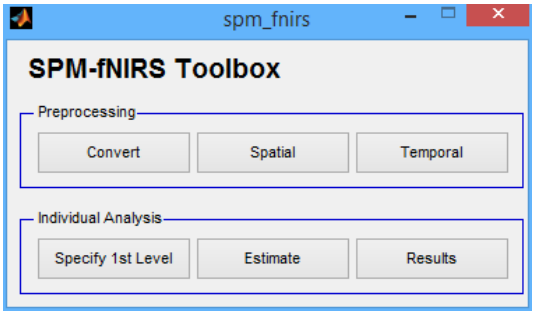


Figure 1: Main panel of the SPM for fNIRS toolbox.

Example: Stroop Task fNIRS Data

This section presents an illustrative SPM analysis using fNIRS data acquired during a color-word matching Stroop task in an event-related design. This data was collected by Minako Uga and Ippeita Dan in the functional brain science laboratory, Jichi Medical University.

- Data acquisition
  A continuous wave fNIRS instrument (Hitachi ETG 4000, Hitachi Medical Corporation, Japan).
  - 52 channels for bilateral placements
  - 10 Hz sampling frequency
  - 3 cm distance between the optical source and the detector
- Experimental protocol
  The subject was instructed to determine whether the color of the top row letters corresponded to the color name written on the bottom row. Figure 2 shows an example of congruent and incongruent conditions of the color-word matching stroop task. One of the objectives of this study was to understand how humans perform a task by suppressing automatic responses. Previous fMRI studies showed activations in middle frontal gyrus (MFG), inferior frontal gyrus (IFG), and anterior cingulate cortex while performing the Stroop task (12).

The data set (sample_fnirs.zip) containing fNIRS measurements and optical probe positions can be downloaded from our website. To analyze the data, start up MATLAB and type spm_fnirs at the MATLAB prompt.

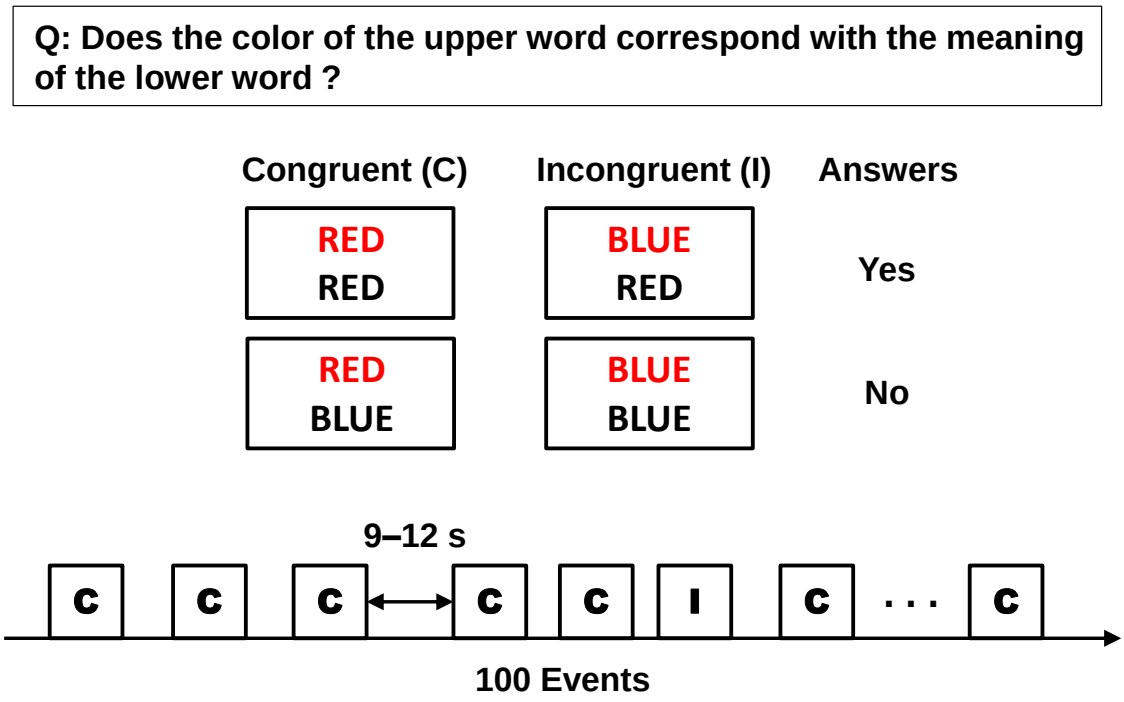


Figure 2: Example of congruent and incongruent conditions of the color-word matching Stroop task. The inter-stimulus interval was randomly selected to be between 9 and 12 seconds.

Data Conversion to Hb Changes

This routine calculates hemoglobin concentration changes using measurements of light intensity or optical density changes, according to the modified Beer-Lambert law (5).

1. **Conversion of Hitachi ETG 4000 data format to SPM-fNIRS data format**

   (a) Enter 'spm_fnirs_read _hitachi' at the MATLAB command window.
   » spm_fnirs _read _hitachi;

   (b) Select a CSV text file which includes measurements of light intensity changes, using the SPM file selector eg, ...\stroop\meas\stroop_fnirs.csv.

   (c) Data will be read and written to NIRS.mat file eg, ...\stroop\meas\NIRS.mat.

2. **Conversion to hemoglobin concentration changes**

   (a) Press the Convert button from the SPM-fNIRS main window.

   (b) Select the NIRS.mat file generated in the step 1 (c) eg, ...\stroop\meas\NIRS.mat.

   (c) Enter age of subject [years] to be used in estimation of differential pathlength factor (DPF) eg, 25.

   (d) Enter distance between source and detector [cm] eg, 3.

   (e) Highlight molar absorption coefficients [$\mathrm{mM}^{-1}\mathrm{cm}^{-1}$] of oxy-hemoglobin (HbO) and deoxy-hemoglobin (HbR) at wavelength 1 and wavelength 2. Accept the default values, 0.72053 4.5269; 2.4187 1.7965.

   (f) Highlight DPF at wavelength 1 and wavelength 2.
   Accept the default values, 6.1718 5.5374.

   (g) Hb changes will be calculated and then overwritten to the NIRS.mat file eg, ...\stroop\meas\NIRS.mat (See Figure 3).

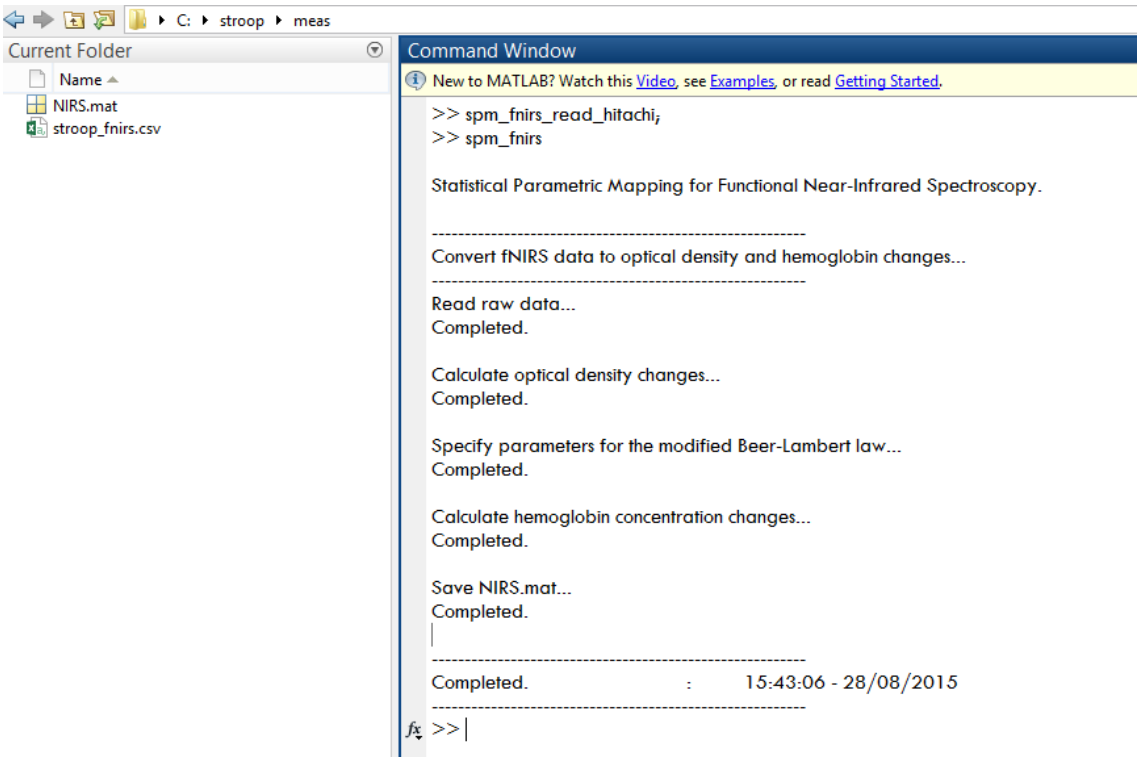


Figure 3: Results of data conversion.

We also provide functions to read fNIRS data acquired using other systems (see below for more details).

- **Conversion of TEXT files to hemoglobin concentration changes**
  Text files (.txt or .csv format) include channel measurements of light intensity or optical density changes at wavelength λ_1 and wavelength λ_2.

  File structure: matrix with M rows of temporal samples and N columns of channels

Wave1.txt				**Wave2.txt**			
Ch 1	Ch 2	...	Ch N	Ch 1	Ch 2	...	Ch N
$y_{1,1}(\lambda_1)$	$y_{1,2}(\lambda_1)$	...	$y_{1,N}(\lambda_1)$	$y_{1,1}(\lambda_2)$	$y_{1,2}(\lambda_2)$	...	$y_{M,N}(\lambda_2)$
$y_{2,1}(\lambda_1)$	$y_{2,2}(\lambda_1)$	...	$y_{2,N}(\lambda_1)$	$y_{2,1}(\lambda_2)$	$y_{2,2}(\lambda_2)$	...	$y_{M,N}(\lambda_2)$
$\vdots$	$\vdots$	$\ddots$	$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
$y_{M,1}(\lambda_1)$	$y_{M,2}(\lambda_1)$	...	$y_{M,N}(\lambda_1)$	$y_{M,1}(\lambda_2)$	$y_{2,2}(\lambda_2)$	...	$y_{M,N}(\lambda_2)$

  y is either light intensity or optical density changes.

  Example of using this function:
  We illustrate this function using data from a motor task (13).

  - Press the Convert button from the SPM-fNIRS main window.
  - Select two text files of measurements at wavelength 1 and wavelength 2, using the SPM file selector. eg, ...\motor\txt\wave1.txt and wave2.txt.
  - You will then be prompted with 'Measurement type? [Light Intensity/Optical Density]'. Select type of measurements included in the text files eg, Light Intensity.
  - Enter sampling frequency [Hz] eg, 10.4167
  - Enter wavelengths [nm] of the first and second text files, respectively. eg, 760 850.
  - Enter age of subject [years] to be used in estimation of DPF eg, 43.
  - Enter distance between source and detector [cm] eg, 2.5.
  - Highlight molar absorption coefficients of HbO and HbR at wavelength 1 and wavelength 2. Accept the default values, 1.4033 3.8547; 2.6694 1.8096.
  - Highlight DPF at wavelength 1 and wavelength 2. Accept the default values, 6.658 5.5957.
  - Hemoglobin changes will be calculated and then written to NIRS.mat file eg, ...\motor\txt\NIRS.mat.

- **Conversion of NIRx NIRScout data format to SPM-fNIRS data format**

  - Enter 'spm_fnirs_read_nirscout' at the MATLAB command window.
    » spm_fnirs_read_nirscout;
  - Select *.wl1, *.wl2, and *.hdr files which include measurements of light intensity changes eg, ...\motor\meas\execution.wl1, execution.wl2, execution.hdr.
  - Data will be read and written to NIRS.mat file eg, ...\motor\meas\NIRS.mat.
    Note that stimulus events and channel configuration are read from *.hdr file and written in ch_config.txt and multiple_conditions.mat files, respectively. You could use these files as input for spatial preprocessing and model specification. See pages 9 and 13 for more details.

  Conversion to hemoglobin concentration changes can then be performed using the same procedures described in the previous page (**'2. Conversion to hemoglobin concentration changes'**):

  - Press the Convert button from the SPM-fNIRS main window.
  - Select the NIRS.mat file created in the last step eg, ...\motor\meas\NIRS.mat.
  - Enter wavelengths [nm] of the *.wl1 and *.wl2 files, respectively eg, 760 850.

- Enter age of subject [years] to be used in estimation of DPF eg, 43.
- Enter distance between source and detector [cm] eg, 2.5.
- Highlight molar absorption coefficients [$\mathrm{mM}^{-1}\mathrm{cm}^{-1}$] of HbO and HbR at wavelength 1 and wavelength 2. Accept the default values, 1.4033 3.8547; 2.6694 1.8096.
- Highlight DPF at wavelength 1 and wavelength 2.
  Accept the default values, 6.658 5.5957.
- Hb changes will be calculated and then overwritten to the NIRS.mat file eg, ...\motor\meas\NIRS.mat.

- **Conversion of Artinis Oxymon MK III data format to SPM-fNIRS data format** (14)
  - Enter 'spm_fnirs_read _artinis' at the MATLAB command window.
    » spm_fnirs_read_artinis;
  - Select a *.oxy3 file which includes measurements of optical density changes eg. ...\artinis\motor.oxy3.
  - Data will be read and written to NIRS.mat file eg. ...\artinis\NIRS.mat.

  Conversion to hemoglobin concentration changes can then be performed using the same procedures described in the previous page (**'2. Conversion to hemoglobin concentration changes'**).

- Note: default values of DPF and molar absorption coefficients are calculated using results reported in (15; 16; 17).

Spatial Preprocessing

Channel Positions in MNI Space $\Rightarrow$ on the Surface of the Standard Brain

1. Press the Spatial button from the SPM-fNIRS main window.
2. Select two files containing the following information
   (a) MNI coordinates of optical source (S) and detector (D) positions
   eg, ...\stroop\pos\optode_positions_MNI.csv

optode_positions_mni.csv			
Optode (MNI)	X	Y	Z
S1	63.9	-38.8	41.4
D1	68.7	-32.6	16.0
S2	70.7	-25.3	-10.3
$\vdots$	$\vdots$	$\vdots$	$\vdots$
S17	-69.8	-23.4	-11.4

   (b) Channel configuration which relates a pair of source and detector to a channel
   eg, ...\stroop\pos\ch_config.csv

ch_config.csv		
Ch	Source	Detector
1	1	2
2	4	2
$\vdots$	$\vdots$	$\vdots$
52	17	15

   This example file specifies that S1 and D2 are paired up to form channel 1; S4 and D2 are paired up to form channel 2; and S17 and D15 are paired up to form channel 52.
3. Select NIRS.mat file to make a file of fNIRS channel positions (POS.mat) be paired up with a file of fNIRS time series (NIRS.mat) eg, ...\stroop\meas\ NIRS.mat.
4. Spatial registration results will be written to a POS.mat file eg, ...\stroop\pos\POS.mat, and appear in the 'spm_fnirs_viewer_ch' window, as shown in Figure 4(a).

- As a default, all channels are used in the SPM analysis. However, you could change channels of interest using the Specify ROIs button. This produces an interactive tool in which you press the left mouse to identify sides of a region, double-clicking at end, then entering eg, 0 if selected channels are of no interest. The POS.mat file will be overwritten with the specified channels of interest, by selecting the Update button. See Figure 4(b).

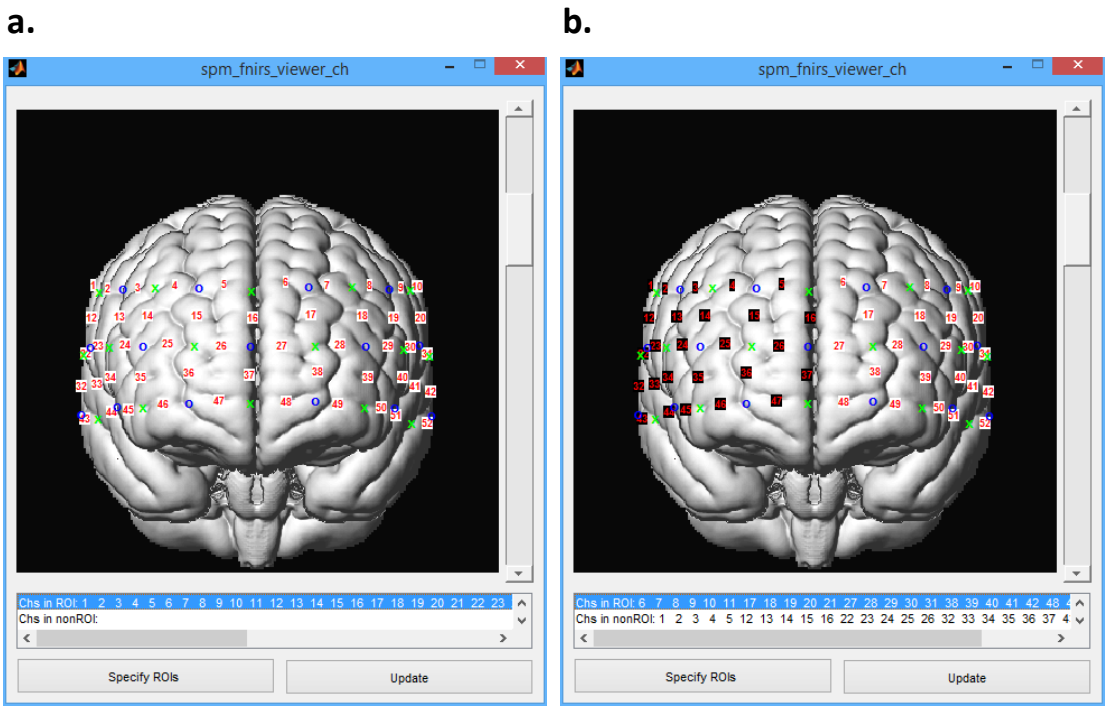


Figure 4: Results of spatial preprocessing. ‘o’ and ’x’ indicate optical source and detector positions, respectively. ‘number’ on white and black background indicate channel positions of interest and non-interest, respectively. Different views can be selected using the vertical slider.

Channel Positions in Subject Space ⇒ MNI Space ⇒ on the Surface of Standard Brain

We also provide functions to transform fNIRS channels in the subject space into the corresponding positions in the MNI space (6; 18). The channel positions are then projected onto the surface of a volume rendered brain (1). An example of using these functions is described as follows:

1. Press the Spatial button.
2. Select three files containing the following information
   (a) Anatomical landmarks and positions of the 10-20 system measured using a 3D digitizer.
   eg ...\motor\pos\reference_positions.csv

reference_positions.csv			
Reference	X	Y	Z
NzHS	111.6	2.3	0.5
IzHS	−92	−0.7	21.4
ARHS	0.1	−76.7	2.4
ALHS	−0.9	81.8	−1.8
⋮			
CzHS	4.1	−3	129.5
⋮			
O2HS			

   At least four reference positions are required. It is recommended to use measurements of reference positions, including nasion (Nz), inion (Iz), Cz, left preauricular point (AL), and right preauricular point (AR). For more details, see NFRI toolbox user's guide (19).

   (b) Positions of optical source and optical detector measured using a 3D digitizer.
   eg ...\motor\pos\optode_positions.csv

optode_positions.csv			
Optode	X	Y	Z
S1	14.4	59.8	104.8
⋮	⋮	⋮	⋮
S4	−11.3	−62.2	97.4
D1	36.2	−68.7	77.4
⋮	⋮	⋮	⋮
D12	−36.9	40.4	108.6

   (c) Channel configuration which relates a pair of source and detector to a channel.
   eg ...\motor\pos\ch_config.txt. See page 7 for more details about this file format.
3. Select NIRS.mat file to make a file of fNIRS channel positions (POS.mat) be paired up with a file of fNIRS time series (NIRS.mat) eg, ...\motor\meas\NIRS.mat (See the section of 'conversion of NIRx NIRScout data format to SPM-fNIRS data format' in page 5, to create this NIRS.mat file).
4. Spatial registration results will be written to the POS.mat file eg, ...\motor\pos\POS.mat, and appear in the 'spm_fnirs_viewer_ch' window.

Temporal Preprocessing

This routine separately preprocesses time series of HbO, HbR, and HbT, (i) to reduce motion artifact (7), (ii) reduce cardiac and respiration noise (8), (iii) downsample the data for computational efficiency, and (iv) reduce slow drifts (1). An example of using this function is described as follows:

1. Press the Temporal button from the SPM-fNIRS main window.

2. Select NIRS.mat file using the SPM file selector eg, ...\stroop\meas\NIRS.mat.
   Time series of optical density, HbO, HbR, and HbT changes will then appear in the 'spm_fnirs_viewer_timeseries' window. This window plots (i) signal intensity and its standard deviation in the time domain, and (ii) signal amplitude in the frequency domain. This can be used for determining optimal parameters for subsequent movement and physiological noise correction steps, respectively.

3. **Highlight 'Motion artifact correction? [MARA/No]'** in the SPM window.
   Select the MARA button to reduce motion artifact using a method based on moving standard deviation and spline interpolation (7; 20).

   (a) Highlight 'specify parameters using a file?' and then select 'No'.

   (b) Highlight 'channels to be analyzed: [All/Selected]' and then select 'All'.

   (c) Highlight 'moving window length [sec]' and then accept the default value '1'.

   (d) Highlight 'threshold factor-motion detection' and then accept the default value '3'.

   (e) Highlight 'smoothing factor-motion artifact' and then accept the default value '5'.

   See below for a description of each of these parameters.

4. **Highlight 'Physiological noise removal? [Band-stop filter/No]'.**
   Select the Band-stop filter button to reduce physiological noise eg, cardiac pulsation and respiration (8).

   (a) Highlight 'stopband frequencies Hz [start end]'. In the sample data (\stroop\meas\NIRS.mat), frequencies of cardiac pulsation have a broad peak, centered around 1.5 Hz. Therefore, you could change the default values [0.12 0.35; 0.7 1.5] to [0.12 0.35; 0.7 2.0].

5. **Highlight 'Change sampling rate from 10.00 Hz?'**.
   This function downsamples hemoglobin changes acquired at a high sampling rate to any sampling rate (eg, 1 Hz). This can often be advisable that we make inferences about activations from measurements of slow-varying hemoglobin changes. Note that (i) high-frequency physiological noise is removed before downsampling, and (ii) high sampling rate is exploited in the dynamic causal modelling (DCM) for fNIRS analysis (13).

   (a) Highlight 'new sampling rate [Hz]:' and then accept the default value '1'.

6. **Highlight 'Detrending? [DCT/no]'.**
   Select the DCT button to reduce very low-frequency confounds using a high-pass filter based on a discrete cosine transform set (1).

   (a) Highlight 'cut-off period [sec]:' and then accept the default value '128'.

7. **Highlight 'Temporal smoothing? [Gaussian/HRF/no]'**
   Select 'no' for the sample data (\stroop\meas\NIRS.mat).
   High frequency noise can be reduced using a low-pass filter based on a Gaussian or hemodynamic response function (1; 21). This is often useful if the fNIRS data is simultaneously acquired with fMRI, as the signal-to-noise ratio (SNR) is relatively low in this context (4).

8. The specified temporal preprocessing steps will then be applied to fNIRS data, and results will appear in a window, as shown in Figure 5. Bad channels can be selected by turning off the radio button (below the vertical bar). The channels will be excluded from further analysis. Parameters specified in this step will be overwritten to the NIRS.mat file.

Parameters of motion artifact removal algorithm (MARA) (7; 20)

- Moving window length [sec], L, for calculating moving standard deviation:
  Moving standard deviation, $s(t)$, is obtained by calculating standard deviation of samples within moving window.

- Threshold factor, k for detecting movement artifact segments:
  Motion artifact segments are identified on a channel-by-channel basis by comparing the moving standard deviation with threshold: $th = k \cdot \mathrm{mean}\left(s\left(t\right)\right)$.

- Smoothing factor, α, for removing movement artifacts:
  Motion artifacts are reduced from the signal, by subtracting smoothed motion artifact segments from the original signal.

  Channel-specific parameters of motion artifact correction (eg, threshold) will be calculated using values specified in the step 3, and then written to motions_params.mat file. This mat file includes the following cell arrays and variables:

  – L: moving window length, th: threshold, alpha: smoothing factor (α).
    The first, second, and third elements of cell arrays include channel-specific parameters for HbO, HbR, and HbT, eg, L$\{1\}$, th$\{1\}$, and alpha$\{1\}$ contain the required parameters of motion correction of HbO signal.
  – chs: channels where motion artifact correction is applied.

  If you want to change motion correction parameters on specific channels, modify values in certain variables of the motions_params.mat file. You could use this mat file in the step 3.(a).

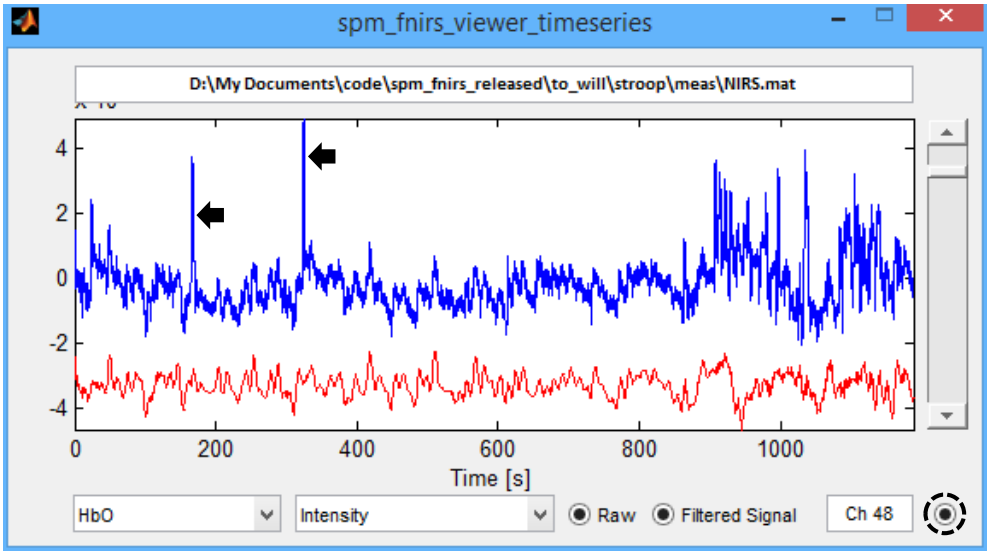


Figure 5: Results of temporal preprocessing. Blue plot indicates oxy-hemoglobin (HbO) concentration changes at channel 48. The channels can be selected using the vertical slider. Bad channels can be selected by turning off the radio button (highlighted by black dotted circle). The channels will be excluded from further analysis. Red plot indicates the corresponding signal after motion correction, physiological noise correction, and downsampling. Arrows indicate motion artifacts that result in rapid changes (such as sharp spikes) in HbO.

Model Specification

This routine specifies the GLM design matrix for the first level analysis of fNIRS data. The design matrix consists of regressors of interest (eg, canonical hemodynamic response) and confounds (eg, systemic physiological noise) (2; 9). The design matrix can vary according to experimental protocol and form of hemoglobin responses including HbO, HbR, and HbT. An example of using this function is described as follows:

1. Press the Specify 1st Level button from the SPM-fNIRS main window.
2. Select NIRS.mat file using the SPM file selector eg,...\stroop\meas\NIRS.mat.
3. Select a directory, eg. ...\stroop, in which to place the results of your analysis.
4. Highlight 'Hb signal to be analyzed?[HbO/HbR/HbT]', and then select which form(s) of hemoglobin that you want to analyse eg, HbO, HbR, and HbT.
5. **Experimental Design**
   (a) Highlight 'specify design in [scans/secs]', and then select the unit for experimental design eg, 'secs'. The onsets of events or blocks will then be specified in seconds.
   (b) Highlight 'specify conditions using a file? [yes/no]'.
   An array of experimental input functions is constructed, specifying occurence of events or epochs (or both):
   - Name: Condition name
   - Onsets: A vector of onset times for this condition type.
   - Durations: The event or epoch durations. If you enter a single number for the durations, it will be assumed that all trials conform to this duration.

   These parameters can be specified by entering values into the SPM window or loading a *.mat file which is useful for specification of multiple conditions.

   For the event-related fNIRS data (eg, \stroop\meas\NIRS.mat), select 'yes', and then specify a multiple condition file using the SPM file selector eg. ...\stroop\multiple_conditions.mat. We have prepared this file to contain information about congruent and incongruent events.
   (c) Highlight 'Other regressors (eg, systemic confounds). user specified [0/1/2/3/4]', and then select '0'.
   Responses that would not be convolved with a basis set of hemodynamic response (eg, systemic physiological noise) can be included in the design matrix:
   - Name: Regressor name
   - Value: Values that the regressor take. This could also be the name of a variable in MATLAB's work space.
6. **Highlight 'Correct for serial correlations? [none/AR(1)]'**
   Select 'AR(1)' to estimate autocorrelations in the time series of hemoglobin changes using a pre-whitening method (22; 11). We also provide a pre-colouring method for estimation of autocorrelation (see below).
7. **Highlight 'Hemodynamic Basis functions... Select basis set...'.**
   Select a single basis function or a set of basis functions to be used for modelling canonical HbO response eg, 'hrf (with time and dispersion derivatives)'. SPM-fNIRS will create a subdirectory HbO, and then write a SPM.mat file to the directory eg, ...\stroop\HbO. It will also plot the design matrix, as shown in Figure 6. Repeat this procedure to generate SPM.mat files for HbR (inverse of canonical hrf) and HbT.

- You can enter the experimental design in the SPM window, instead of using the multiple_conditions.mat file. For a block design with a functional run containing 5 blocks of 30 seconds finger tapping interspersed with 30 seconds rest, the experimental design can be entered in step 5 above as follows:
  - Highlight 'specify conditions using a file? [yes/no]', and then select 'no'.
  - Highlight 'number of conditions/trials [0/1/2/3/4]', and then enter '1'.
  - Highlight 'name for condition/trial 1?', and then enter 'finger tapping task'.
  - Highlight 'vector of onsets - finger tapping task', and then enter '0 60 120 180 240'.
  - Highlight 'duration[s] (event = 0)', and then enter '30'. If you have multiple different durations, then the number of durations should match the number of onset times.
- Format of multiple_conditions.mat file: This mat file should include the following cell arrays: names, onsets, and durations eg, names$\{2\}$ = 'SSent-DSpeak', onsets$\{2\}$ = [3 5 19 222], durations$\{2\}$ = [0 0 0 0] contain the required details of the second condition.
- Estimation of temporal autocorrelations:
  - Pre-colouring:
    - If a low-pass filter is applied in the temporal preprocessing step, temporal autocorrelations are estimated by using multiplication of filter matrices (10).
    - Low-pass filters derived from a Gaussian smoothing kernel with full width at half maximum (FWHM) of 4-6 s, or derived from the canonical HRF have been suggested as optimal filters for pre-colouring.
    - Pre-colouring method would be suitable for relatively low SNR fNIRS data (eg, simultaneously acquired fNIRS and fMRI data) (4).
  - Pre-whitening: If a low-pass filter is not applied, temporal autocorrelations are estimated by using a 1st-order autoregressive (AR(1)) plus white noise model (22). The model parameters are estimated using a restricted maximum likelihood (ReML) method (11).
- Basis functions for modelling canonical HbO, HbR, and HbT responses (9):
  - Canonical hemodynamic response function (HRF)
    - The canonical HRF with time and dispersion derivatives allows the peak and the width of response to vary by plus or minus a second, respectively.
  - Other basis sets
    - Fourier Set
    - Fourier Set (Hanning)
    - Gamma Functions
    - Finte Impulse Response (FIR)
- Main structure of this routine is identical to fMRI model specification in SPM12. For more details, see Chapter 8 in (23).

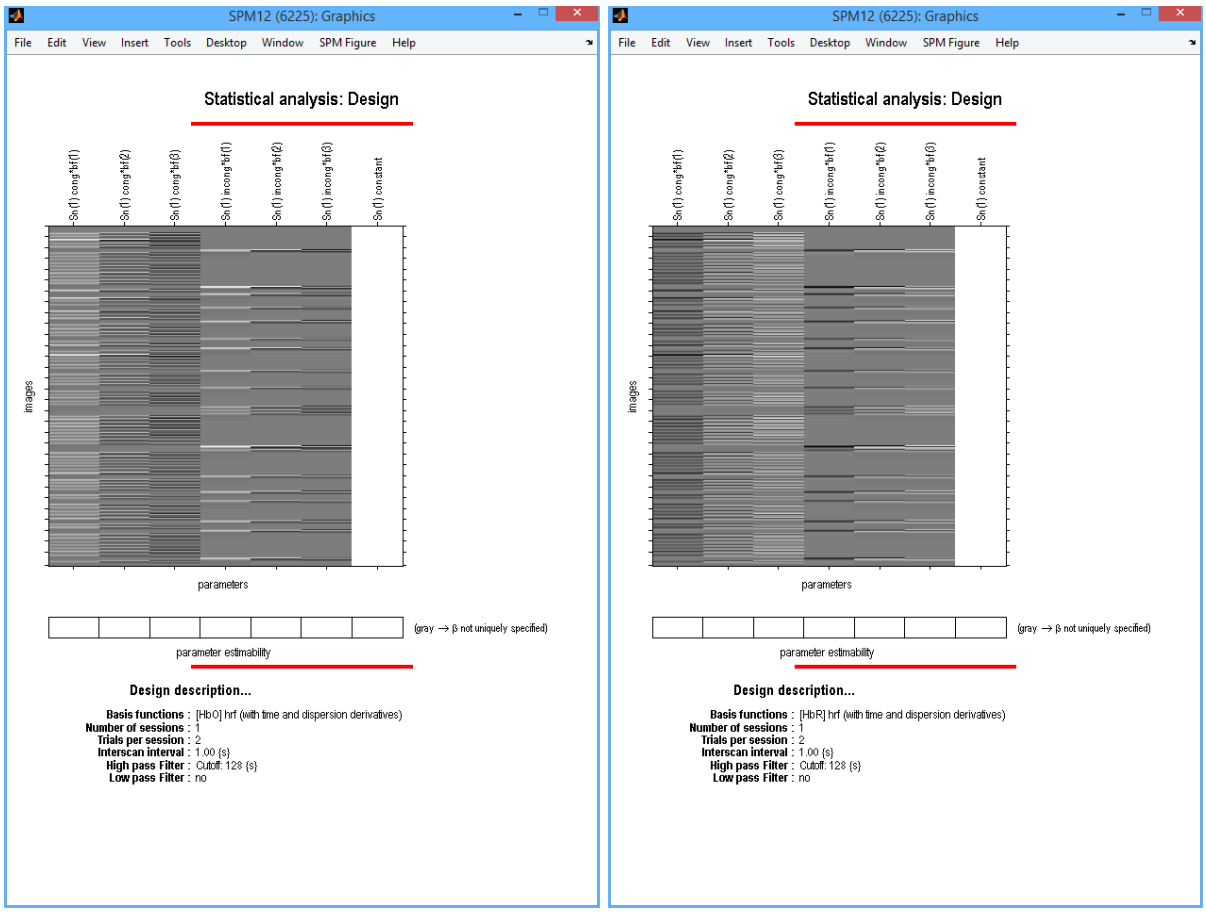


Figure 6: Results of model specification.
Left: design matrix for oxy-hemoglobin (HbO) signal. Right: design matrix for deoxy-hemoglobin (HbR) signal. The first three columns model the first experimental condition (congruent task) and columns 4 to 6 model the second experimental condition (incongruent task). Each of three regressors is the result of the convolution of the stimulus onsets with the (i) canonical HRF, (ii) its temporal, and (iii) dispersion derivatives.

Estimation

This routine estimates GLM parameters on a channel-by-channel basis (10; 11).

1. Press the 'Estimate' button from the SPM-fNIRS main window.
2. Select SPM.mat file(s) to be estimated eg, ...\stroop\HbO\SPM.mat, ...\HbR\SPM.mat, and ...\HbT\SPM.mat.
3. Parameter estimation will start, and its result will then be overwritten to the SPM.mat file(s).

Results

This routine performs interpolation on channel-specific estimates of GLM parameters, to compute a map of values on the surface of a volume rendered brain (24). Classical inference about the experimentally induced effects proceeds using the voxel-specific T or F statistics. Random field theory then allows us to assess the significance of regionally specific hemodynamic effects (3).

1. Press the 'Results' button from the SPM-fNIRS main window.
2. Select the SPM.mat file created in the last section eg, ...\stroop\HbO\SPM.mat.
   This will invoke the 'spm_fnirs_viewer_stat' window.
3. Press the 'Contrast' button from the 'spm_fnirs_viewer_stat' window. The SPM contrast manager displays the design matrix in the right panel and lists specified contrasts in the left panel. To examine statistical results for condition effects (eg, incongruent condition effects),
   (a) Select 'Define new contrast...'
   (b) Enter the contrast name eg, 'incongruent condition effects'.
   (c) Select either 't-contrast' or 'F-contrast' eg, 't-contrast'.
   (d) Highlight 'contrast - contrast weights vector', and then enter '0 0 0 1 0 0 0', and press 'submit'. Note that the first column of design matrix models the congruent condition effects, and the fourth column of design matrix models the incongruent condition effects, as shown in Figure 6.
   (e) Press 'OK'. Select the '001 {T}: incongurent condition effects' from the SPM contrast manager and then press 'Done'.
   (f) A t-statistic map will then appear in the 'spm_fnirs_viewer_stat' window
4. Press the 'Activation' button. You will then be prompted with
   (a) p value adjustment to control [FWE/none]. Select 'FWE'.
   (b) Highlight 'p value (FWE)' and then accept the default value '0.05'.
5. Regionally specific effects (eg, cortical activation during incongruent task detected using HbO) will then be identified, as shown in Figure 7. The current figure in the 'spm_fnirs_viewer_stat' window can be saved using the 'S' button.

- As a result of this step, the following files will be created:
  - Vbeta.mat: interpolated parameter β in GLM
  - VResMS.mat: interpolated error covariance
  - VRpv.mat: resels (resolution elements) per voxel in search region
  - con_0001.mat: channel specific effects of interest ($c^T\beta$) in GLM
  - spmT: voxel specific T statistic
  - spmF: voxel specific F statistic
- Note:
  - Significantly activated voxel positions can be identified using the 'P' button. This reveals the t-value and anatomical locations of selected positions. The position can be used as a hemodynamic source in dynamic causal modelling (DCM) for fNIRS (13). DCM for fNIRS enables us to infer directed interactions in the brain mediated by neuronal dynamics from measurements of optical density changes.

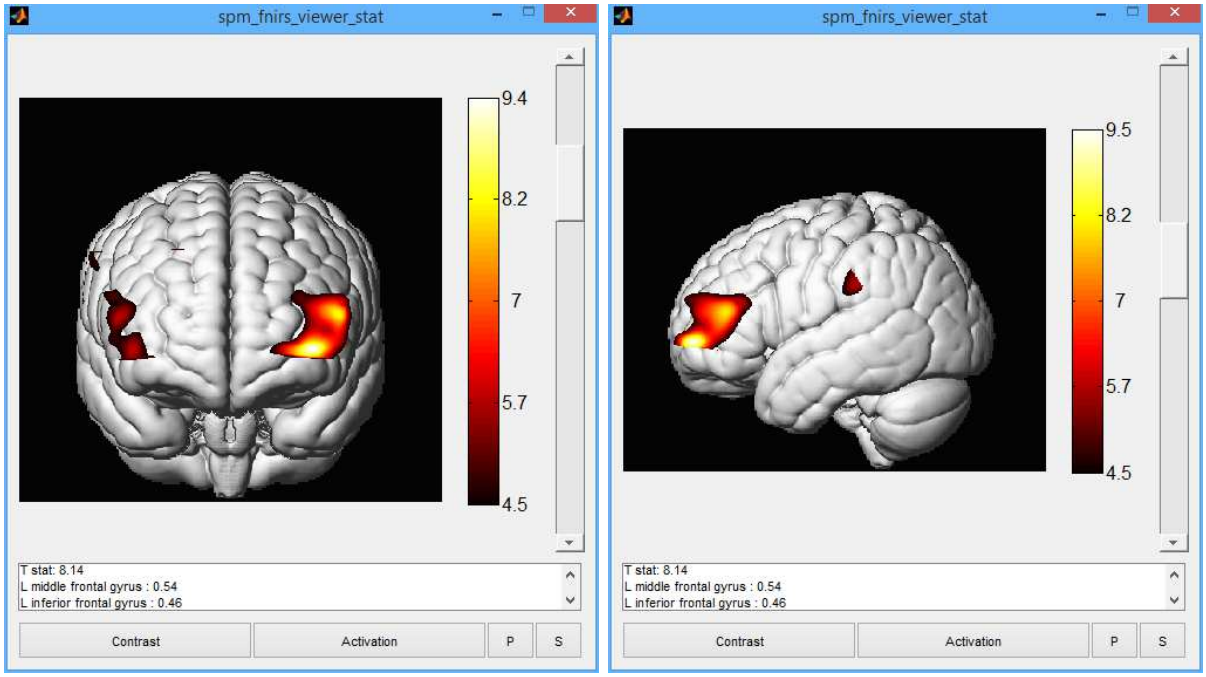


Figure 7: Inference of activation eg, cortical activation during incongruent task detected using oxy-hemoglobin response ($p < 0.05$, FWE-corrected). Different views can be selected using the vertical bar.

Computation of Individual Contrast Images

This routine generates individual contrast images containing the experimental effects of interest either on a 2D regular grid (25) or on a 3D triangular mesh (26; 27), both representations of a canonical scalp surface (28). The contrast images of all subjects from the first-level are then analysed as a random-effects analysis via summary-statistics implemented in SPM12 (29). The random-effects analysis allows for making inference about the population from which subjects are drawn.

- Computation of 2D contrast images
    1. Enter 'spm_fnirs_con_2d' at the MATLAB command window.
       » spm_fnirs_con_2d;
    2. Select con_*.mat files created in the Results step.
    3. 2D contrast images will then be generated on a 2D regular grid and saved in standard NIfTI-1 data format eg, con_*.nii.
- Computation of 3D contrast images
    1. Enter 'spm_fnirs_con_3d' at the MATLAB command window.
       » spm_fnirs_con_3d;
    2. Select con_*.mat files created in the Results step.
    3. 3D contrast images will then be enerated on a 3D triangular mesh and saved in standard surface-based data format GIfTI eg, con_*.gii.
- Sensor-space contrast images can then be analysed using SPM12 in the usual way (30; 31).

References

[1] SPM software. Wellcome Trust Centre for Neuroimaging, University College London. http://www.fil.ion.ucl.ac.uk/spm/.

[2] K. J. Friston, A. P. Holmes, K. J. Worsley, J.-B. Poline, C. D. Frith, and R. S. J. Frackowiak. Statistical parametric maps in functional imaging: A general linear approach. *Hum. Brain Mapp.*, 2:189–210, 1995.

[3] J. E. Taylor and K. J. Worsley. Detecting sparse signals in random fields, with an application to brain mapping. *J. Am. Statist. Assoc.*, 102(479):913–928, 2007.

[4] J. C. Ye, S. Tak, K. E. Jang, J. Jung, and J. Jang. NIRS-SPM: statistical parametric mapping for near-infrared spectroscopy. *NeuroImage*, 44:428–447, 2009.

[5] D. T. Delpy, M. Cope, P. Van der Zee, S. Arridge, S. Wray, and J. Wyatt. Estimation of optical pathlength through tissue from direct time of flight measurement. *Phys. Med. Biol.*, 33(12):1433–1442, 1988.

[6] A. K. Singh, M. Okamoto, H. Dan, V. Jurcak, and I. Dan. Spatial registration of multichannel multi-subject fNIRS data to MNI space without MRI. *NeuroImage*, 27:842–851, 2005.

[7] F. Scholkmann, S. Spichtig, T. Muehlemann, and M. Wolf. How to detect and reduce movement artifacts in near-infrared imaging using moving standard deviation and spline interpolation. *Physiol. Meas.*, 31(5):649, 2010.

[8] FieldTrip Toolbox. Donders Institute for Brain, Cognitive, Behaviour, Radboud University. http://www.fieldtriptoolbox.org/.

[9] R. Henson and K. Friston. *Statistical Parametric Mapping: The Analysis of Functional Brain Images*, Chapter 14. Convolution Models for fMRI. Academic Press, 2007.

[10] K. J. Worsley and K. J. Friston. Analysis of fMRI time-series revisited–again. *NeuroImage*, 2(3):173–181, 1995.

[11] K. J. Friston, W. Penny, C. Phillips, S. Kiebel, G. Hinton, and J. Ashburner. Classical and Bayesian inference in neuroimaging: theory. *NeuroImage*, 16(2):465–483, 2002.

[12] H.-C. Leung, P. Skudlarski, J. C. Gatenby, B. S. Peterson, and J. C. Gore. An event-related functional MRI study of the Stroop color word interference task. *Cerebral cortex*, 10(6):552–560, 2000.

[13] S. Tak, A. M. Kempny, K. J. Friston, A. P. Leff, and W. D. Penny. Dynamic causal modelling for functional near-infrared spectroscopy. *NeuroImage*, 111:338–349, 2015.

[14] FieldTrip Toolbox for fNIRS. Artinis Medical Systems, Netherlands. http://www.fieldtriptoolbox.org/development/nirs/.

[15] A. Duncan, J. H. Meek, M. Clemence, C. E. Elwell, P. Fallon, L. Tyszczuk, M. Cope, and D. T. Delpy. Measurement of cranial optical path length as a function of age using phase resolved near infrared spectroscopy. *Pediatric research*, 39(5):889–894, 1996.

[16] F. Scholkmann and M. Wolf. General equation for the differential pathlength factor of the frontal human head depending on wavelength and age. *J. Biomed. Opt.*, 18(10):105004–105004, 2013.

[17] Tissue Spectra. Biomedical Optics Research Laboratory, University College London. http://www.ucl.ac.uk/medphys/research/borl/intro/spectra/.

[18] NFRI toolbox. Functional Brain Science Laboratory, Jichi Medical University. http://www.jichi.ac.jp/brainlab/tools.html#GroupSp/.

[19] NFRI toolbox user's guide. Functional Brain Science Laboratory, Jichi Medical University. http://www.jichi.ac.jp/brainlab/download/ReadMe091114.doc.

[20] MARA functions. Felix Scholkmann. Biomedical Optics Research Laboratory, Univeristy of Zurich.

[21] K. J. Friston, O. Josephs, E. Zarahn, A. P. Holmes, S. Rouquette, and J.-B. Poline. To smooth or not to smooth?: Bias and efficiency in fMRI time-series analysis. *NeuroImage*, 12(2):196–208, 2000.

[22] P. Purdon and R. Weisskoff. Effect of temporal autocorrelation due to physiological noise and stimulus paradigm on voxel-level false-positive rates in fMRI. *Hum. Brain Mapp.*, 6:239–495, 1998.

[23] SPM12 manual: fMRI model specification. Wellcome Trust Centre for Neuroimaging. University College London. http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf.

[24] H. Li, S. Tak, and J. C. Ye. Lipschitz-Killing curvature based expected Euler characteristics for p-value correction in fNIRS. *J. Neurosci. Meth.*, 204:61–67, 2012.

[25] S. J. Kiebel and K. J. Friston Statistical parametric mapping for event-related potentials: I. Generic considerations. *Neuroimage*, 22:492–502, 2004.

[26] J. Mattout, R. N. Henson, and K. J. Friston Canonical source reconstruction for MEG. *Comput. Intell. Neurosci.*, 2007.

[27] R. Oostenveld, P. Fries, E. Maris, and J. M. Schoffelen FieldTrip: open source software for advanced analysis of MEG, EEG, and invasive electrophysiological data. *Comput. Intell. Neurosci.*, 2011.

[28] S. Tak, M. Uga, G. Flandin, I. Dan, and W. D. Penny. Sensor space group analysis for fNIRS data. *J. Neurosci. Meth.*, 264:103–112, 2016.

[29] W. D. Penny and A. J. Holmes. *Statistical Parametric Mapping: The Analysis of Functional Brain Images*, Chapter 12. Random Effects Analysis. Academic Press, 2007.

[30] SPM12 manual: Factorial design specification Wellcome Trust Centre for Neuroimaging. University College London. http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf.

[31] SPM12 manual: Face group fMRI data Wellcome Trust Centre for Neuroimaging. University College London. http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf.