



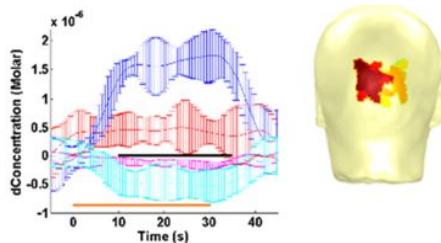
Laboratoire d'imagerie optique
en neurodéveloppement



User manual

LIONirs toolbox

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LIONirs

LIONirs is a toolbox designed for the analysis of functional near-infrared spectroscopy (fNIRS) data. It includes basic tools of analysis such as normalization, filter, Beer-Lambert Law, average, a semi-automatic artifact detection. A graphical interface helps to visualize and manually review the artifact rejection. It applies data decomposition (PCA, PARAFAC, ICA) on the data as well as the general linear model estimation (GLM). Topographical representation of the 3D helmet over the scalp or cortex anatomical MRI is available at each step of the analysis. The 3D helmet is built using Matlab GUI interface (.prj) and links the positions of the source and detector fibers, registered on a template or a subject's MRI, it is used to read the raw data.

Installation requirement

The project has been developed under the GNU General Public License. You can download the toolbox at the link <https://github.com/JulieTremblay3/LIONirs>. It is shared for research purposes without any warranty. Source code has been developed under Matlab MathWorks, it has been tested with the version of SPM12.

Download the source code and define the root folder in Matlab set path (menu set path & add with subfolder or path tool command) to try it. Add the LIONirs toolbox as SPM toolbox extension i.e. simply copy and paste the LIONirs toolbox folder in the .\spm12\toolbox\ folder.

Compatibility with SPM12 Matlab 2014 to 2018a

Toolbox Matlab

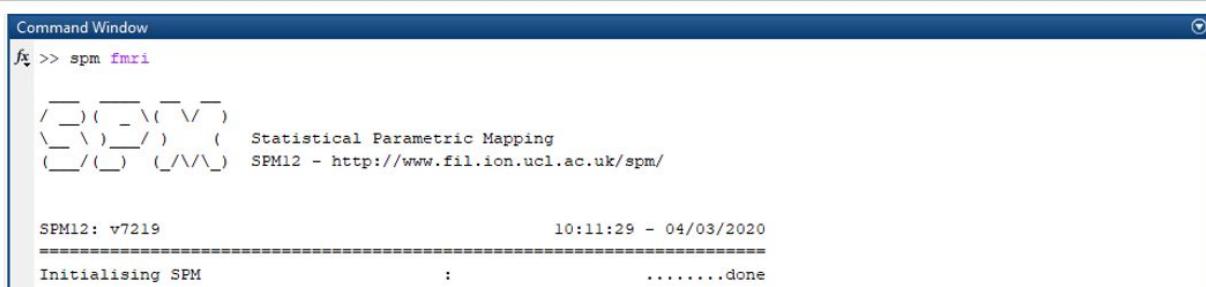
Statistics and Machine Learning Toolbox™

External package used

NWAY toolbox, FastICA_25, mmread function for the video compatibility

Launch the batch editor :

From the command window in Matlab, use spm fMRI to run spm12.

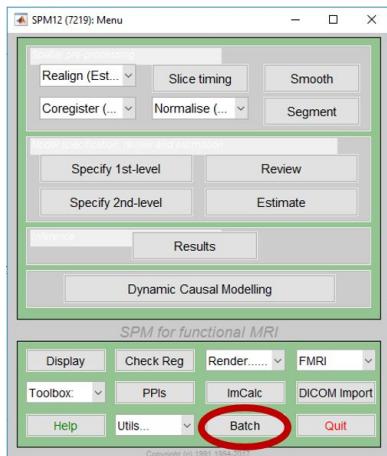


```
Command Window
fx >> spm fmri

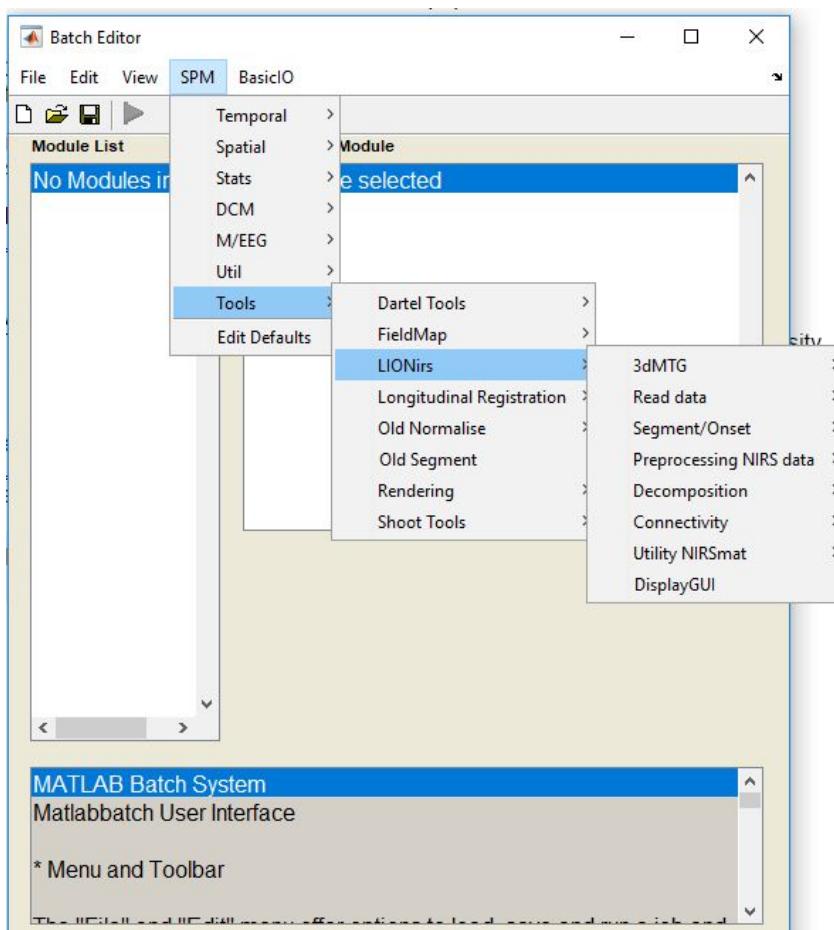
/ \ ) ( _ \ ( \ / \
\ _ \ ) _ / ) (   Statistical Parametric Mapping
( _ / ( _ ) ( _ \ / _ ) SPM12 - http://www.fil.ion.ucl.ac.uk/spm/

SPM12: v7219                               10:11:29 - 04/03/2020
=====
Initialising SPM : .....done
```

This GUI will appear, localize the batch editor and open the batch editor window by pressing "Batch" from the SPM Menu window.



Localize in the batch editor menu the LIONirs toolbox: 'SPM/tools/LIONirs'. This menu access all functions of the LIONirs toolbox. The present documentation describes all the functions. Refer to introduction tutorials for a quick introduction with examples of data.



General data organization

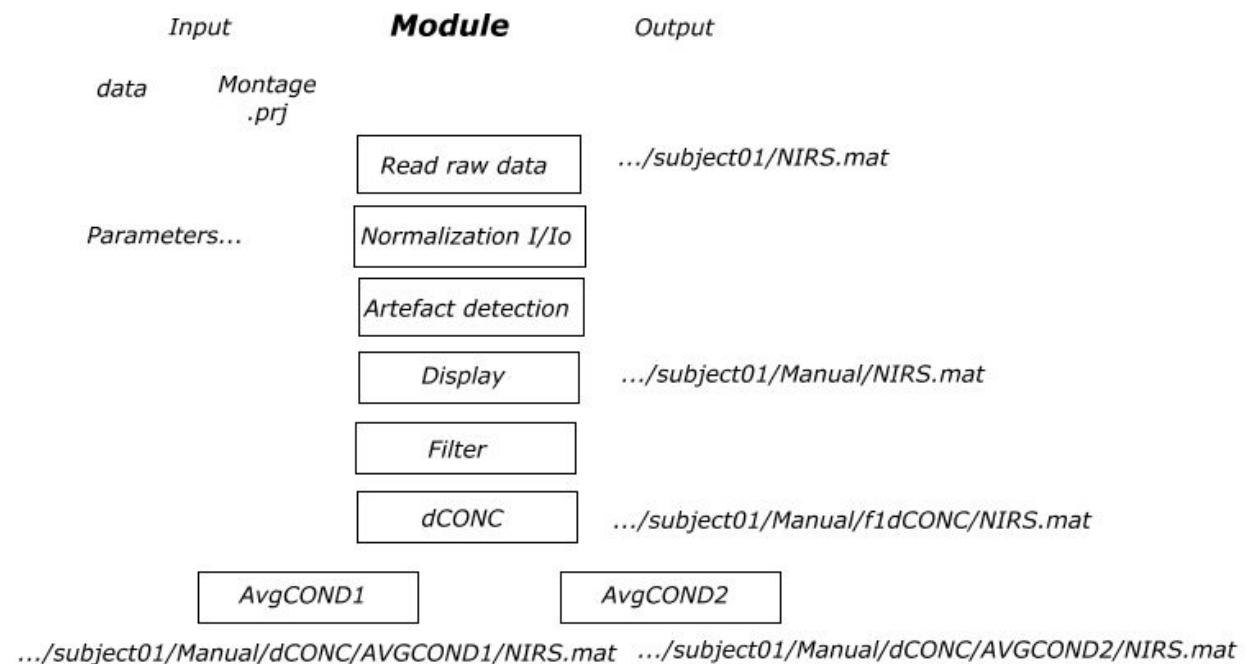
Montage .prj: This structure is created and edited by the graphical interface (GUI) 3dMTG. This structure handles all positions of the source and detector configuration to read the raw data and to visualize optode over and cortical or head surface.

NIRS.mat: This structure is created by the toolbox and is used as the main structure to keep track of all the operations performed and to visualize and analyzed data. Most of the functions of the toolbox need this structure as input to perform an operation to the data. Each step of operation will be performed sequentially, it means that you can only edit or perform an operation on the last module. To create a parallel branch of analysis, you need to use the utility **NIRSMat create a new branch**. The structure contains the location of the analyzed data in the file directory, similar to SPM. If you need to move this folder location please keep the subfolder dependency and use the function **folder adjustment** to adjust dependency to the new current location. For more information about this structure see appendix 1 file format NIRS.mat data structure.

Module: Step of operation accessible through the Batch editor menu. The operations will always be applied sequentially on the last module of data. To avoid unnecessary intermediate data on the drive set 'Delete previous .nir data file' to option 'true'. Keep the step strategic to inspect. The data from any module can be accessed to be visualized by the DisplayGUI. However, only the last one could be edited.

Data analyzed: Binary data in the analyzed folder with 3 extensions, .nir (binary data), .vhdr (header information), .vmrk (trig and bad interval information).

Subfolder: Creates parallel branches of analysis, for example clean data, could be average for condition 1 and condition 2. Choose the option NIRSMat to create a new branch to separate the module and create parallel branches to try several data processing.



Flow chart of analysis, each module of operation could be visualized by the DisplayGUI. To create a parallel branch, use the option ***NIRSmat create a new branch*** and save the NIRS.mat in a different subfolder.

Batch you can save a series of modules in a batch to keep track of the preprocessing applied to the data.

Template example of batch that could be applied on multiple subjects

Datainfo.xls file used to summarize individual batch analysis.

Optional multimodal files:

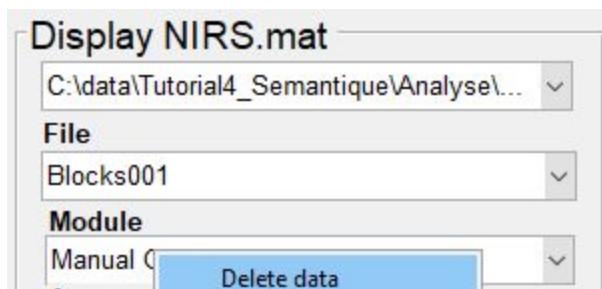
Auxiliary data all auxiliary could be visualized and used in the GLM model see appendix 1 for the data format of the auxiliary (.dat (binary data), .vhdr (header information), .vmrk (trig and bad interval information)) could be created using the generic data export from BrainVision analyzer.

EEG data (same format as Auxiliary)

Video simultaneous recording (to fNIRS or EEG trigger). If they have a lag with the fNIRS or EEG recording indicating offset to be synchronized to the field who received the trigger information.

Delete previous .nir data file

This function is available in each module. If it is set to true, it will delete the data of the previous operation. It is important to use it to avoid filling up your hard drive with all intermediary steps. However, when deleted, the module will not be available for visualization. Set the option to false to conserve and see all intermediate steps in the DisplayGUI. You could also delete them afterward in the DisplayGUI by using the right-click (delete data) on the module information selected.



Hands on tutorial

Several tutorials are available to help you to start with the toolbox. They provide examples of data and template batch to show the main feature you could use in this toolbox. You could adapt those batches to your data to build your pipeline of analysis.

[Tutorial 0 introduces 3dMTG project construction with a template MRI.](#)

[Tutorial 1 introduces how to read multimodal data using NIRScout equipment \(NIRx\).](#)

[Tutorial 2 introduces semi-automatic artifact rejection and manual revision in the displayGUI.](#)

- Open and read fNIRS and multimodal data acquired using NIRScout equipment.
- Apply automatic artifact rejection and correction.
- How to review the corrected data using DisplayGUI.
- Short distance regression

[Tutorial 3 introduces task based analysis.](#)

- Read data and convert them in hemodynamic concentration HbO, HbR
- Data average
- GLM
- Stats (One sample, unpaired t-test, anovan)

[Tutorial 4 resting coherence.](#)

[Tutorial 5 how create a template to automatise batch pipeline.](#)

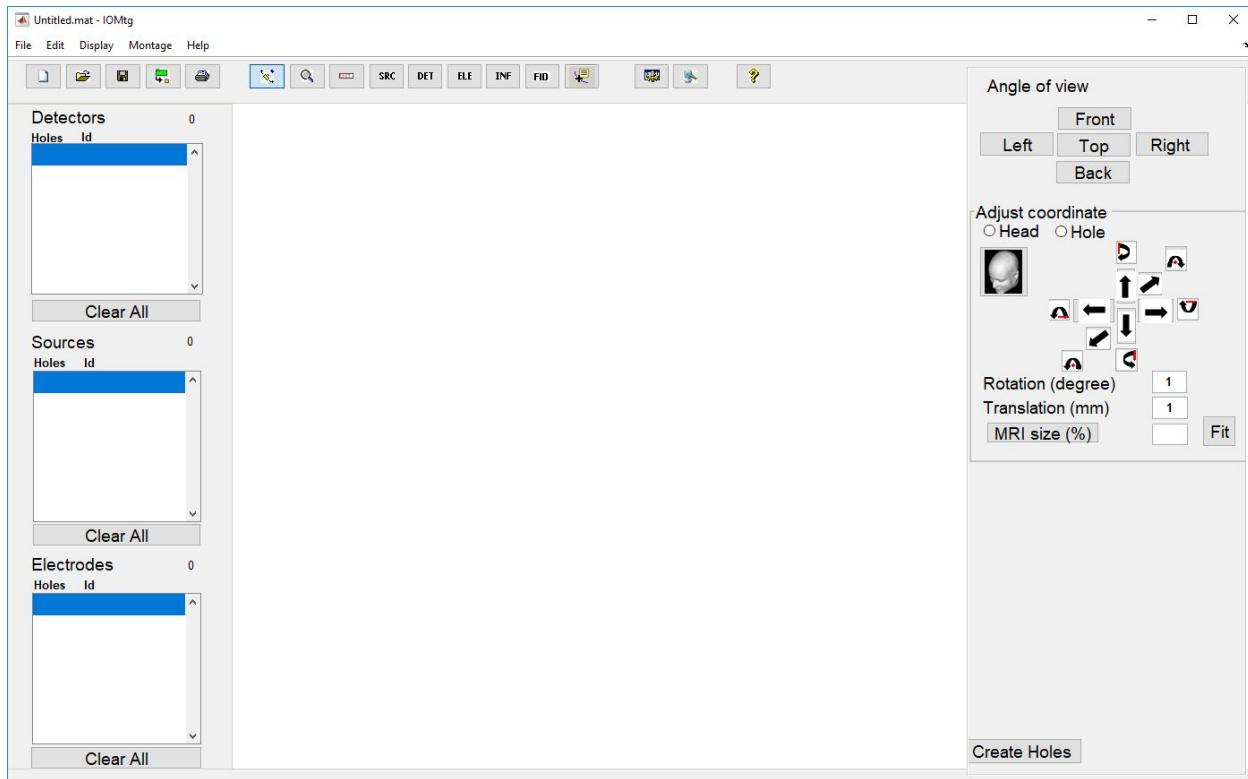
3dMTG

This module helps to prepare the 3d anatomic reconstruction to represent all pairs of sources and detectors (also called optodes) used for the fNIRS recording experiment. The 3d representation could be the head skin, the cortical surface or the cortical surface atlas. The anatomy can be defined by the subject's individual MRI or a template. Tutorial 0 provides examples of data using an MRI template and coordinates to construct a project (.prj). In case individual MRI images are available, the anatomy of the brain and skin surface can be extracted using an external image processing software such as Neuronic Image Processor (<http://www.neuronicsa.com>), Brainsuite (Dogdas et al., 2005). See appendix 1 for some examples, as the segmentation is done using external software it will not be covered in detail here. The optodes' localization is read from the .elp files created by a stereotactic system such as BrainsightTM Frameless 39 (Rogue Research Inc., Montreal, QC, Canada) or Polhemus (Polhemus, Colchester, Vermont, USA). The correspondence between optodes localization and anatomical representation is done with a rigid body transform method using anatomical markers (nasion, left and right pre-auricular points) identified on the subject's MRI images (Penny et al., 2011). In either case, the user has the flexibility to manually refine the optode's position in the GUI if appropriate. Talairach atlas visualization helps the user to ensure that the montage is adequately covering the regions of interest in the cerebral cortex.

Required data preparation :

1. Coordinates of the source and detector on the helmet .elp.
2. Fiducial marked on the MRI for registration.
3. MRI segmentation brain and head surface.
4. Anatomical atlas (optional)

The following GUI appears when you open the 3dMTG module.



Coordinates of the source and detector

You need a file with the position and distance of the source and detector as well as the anatomical fiducial marker on the subject head (Nasion, Left preauricular marker, right preauricular marker). You can acquire this data with a commercial system of localization such as Polaris or Brainsight. It is also possible to measure and create your own .elp file see .elp file format in appendix 1.

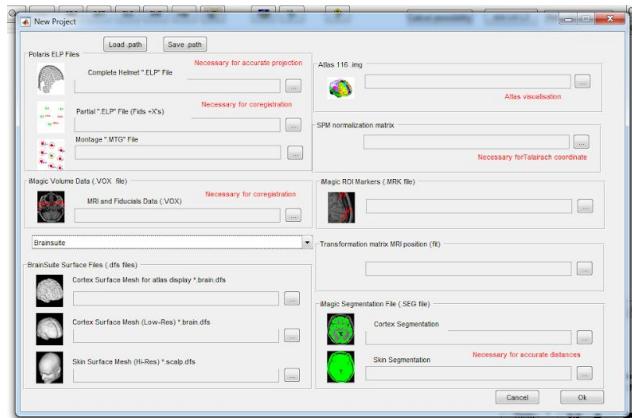
Get familiar with the interface shortcuts

	Creation of a new project (.prj)
	Open .prj
	Save .prj
	Export project data. Export .elp,

	Print the screen as an Encapsulated PostScript (.esp) vector graphic.
	Rotate to change the helmet orientation, Select point of view short cut point or view left, right could
	Zoom
	Rules to measure distance between 2 holes.
	Insert new source position in a hole.
	Insert new detector position in a hole.
	Insert new electrode position in a hole.
	Display hole information and coordinates.
	Display fiducial information and distance from selected hole.
	Identify the atlas projection area or add a hole on the skin surface.
	Montage parameters
	Display options
	Open help file.

Creation of a new project

To create a .prj file go in menu: File/ New Project, you have to complete the information.



Complete helmet ELP File: Polaris position measured on the helmet you used. Fiducial positions are not accurate so registration will be approximate.

Partial ELP helmet: Polaris position measured on the subject head which contains accurate fiducial position for registration.

MTG file (optional): If it isn't the first project you made with the same helmet and hole configuration, you may use a previous mtg file that contains holes and optodes association.

VOX file: MRI volume, with fiducial left preauricularis (LPA), right preauricularis (RPA) and nasion (NAS) manually indicated. If necessary, voxel may need to be interpolated in isotropic format (1x1x1 mm) before.

Surface file: Mesh that contains a 3d representation of the tissue.

Cortex surface: Hi Res & Lo Res. Used to display the atlas.

Skin surface: (Head shape where source and detector are set)

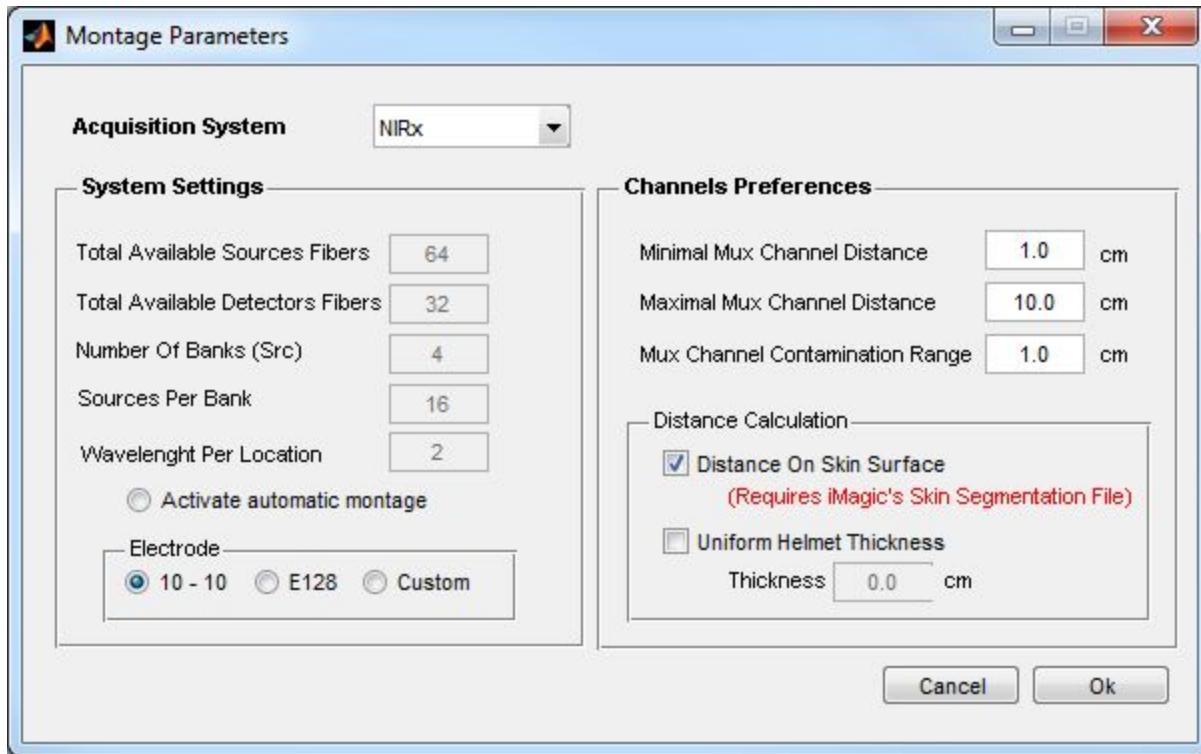
Segmentation file: Mask that contains tissue associated with the surface file.

Atlas: Volume segmented with standard atlas (should be in the same referential as the previous file).

SPM normalization matrix: Transformation file .mat that needs to be used to bring the MRI volume in the mni standard space.

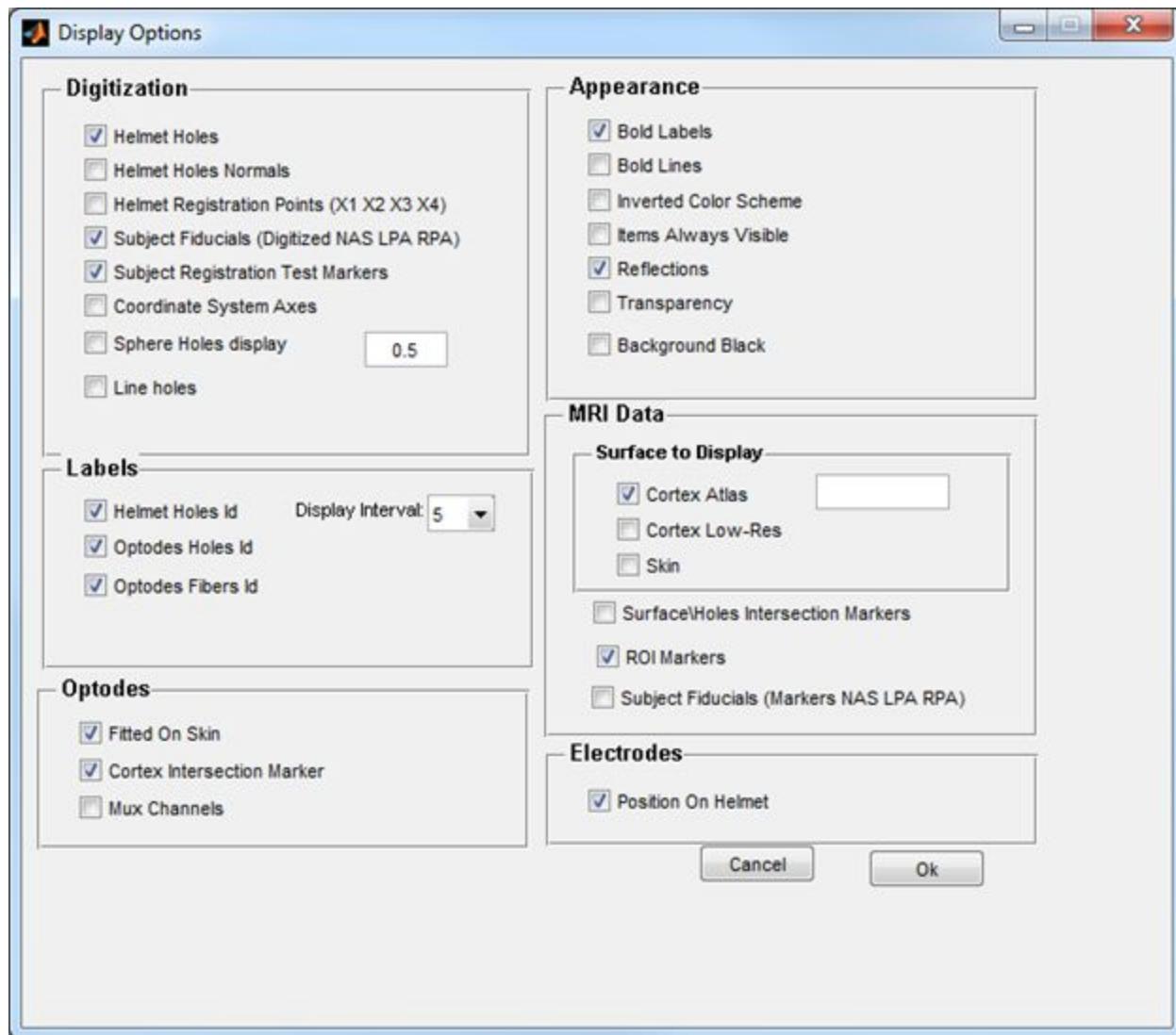
After entering the locations of the files, you could save the location using the button save path and load path to help to reconstruct your project quickly.

Montage parameters



The montage parameters window lets you select the hole nomenclature as according to your recording equipment. Please refer to the appendix 1 to see details on hole nomenclature for ISS or NIRx recording system.

Display options



Digitalization options	Description
Helmet Holes	Show the helmet's holes.
Helmet Holes Normals	Show normal to the center of the head, are used for the projection to the scalp or the brain surface.
Helmet Registrations Points (X1, X2, X3, X4)	Additional registration points used to register rigid helmets.
Subject Fiducials	Anatomical point for registration.

Subject Registration Test Markers	Additional markers, region of interest.
Coordinate System Axes	Display the axis x, y, z on the visualization.
Sphere Holes Display	Holes are displayed as spheres instead of circles.
Line Holes	Links holes DA1 DA2 to facilitate visualization.

Labels is the name of each hole perforated in the helmet. You may use our own convention. Our convention is:

- **DA1:** D to indicate the Right hemisphere of the subject, first Row A, Hole 1.
- **DB1:** D to indicate the Right hemisphere of the subject, second Row B, Hole 1.
- **Z1:** Z to indicate midline, Hole 1.
- **GA1:** G to indicate the Left hemisphere of the subject, first Row A, Hole 1.
- **GB1:** G to indicate the Left hemisphere of the subject, second Row B, Hole 1.

Labels options	Description
Helmet holes Id	Display the hole identification.
Display Interval	Set the space between two hole ID for example set to 1 to show all whole id or to 5 to show 1 label holes ID over 5 holes.
Optodes Holes Id	Display hole identification on optodes holes, i.e. holes occupied by a source or a detector.
Optodes Fibers Id	Display source or detector identification on the holes occupied by a source or a detector.

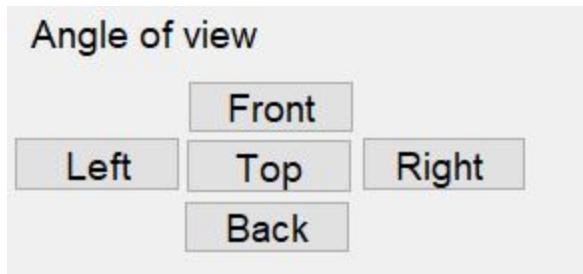
Optodes options	Description
Fitted On Skin	Show optodes projection on the skin surface.
Cortex Intersection Marker	Show optodes projection on the cortex surface.
Mux Channels	Combinaison of channels close to a source or a detector.

Appearance options	Description
Bold Labels	Bold font on the labels.
Bold Lines	Show optodes projection on the cortex surface.
Inverted Color Scheme	Use black background color and white label color.
Items Always Visible	Display graphical elements even if they are on the other side of the head.
Reflections	View light reflection for 3d appearance.
Transparency	View scalp or brain transparency.

MRI Data	Description
Cortex Atlas	Atlas segmentation surface display
Cortex Low-Res	Display a cortex surface with a lower resolution for faster rendering.
Skin	Display a scalp surface.
Surface\Holes Intersection Markers	Display the intersection point between the surface and the normals.
ROI Markers	Add a manual region of interest as defined in Neuronic Image Processor marker.
Subject Fiducials (Markers NAS LPA RPA)	Add manually in the MRI Neuronic Image Processor.

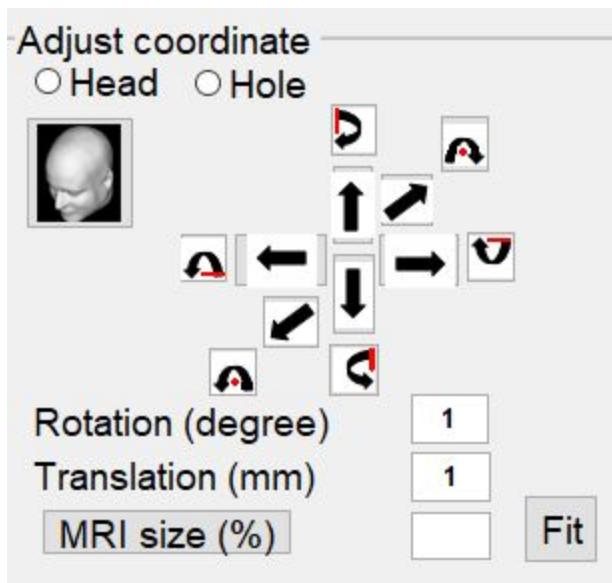
Electrodes	Description
Position On Helmet	Show the electrode labels

Angle of view



Front	Front view
Left	Left view
Top	Top view
Right	Right view
Back	Back view

Adjust the coordinate of MRI and helmet position



Translation (mm) : adjust the length of the translation to apply.

Rotation angle (degree) : adjust the angle of rotation to apply.

MRI size (%): decrease or increase the scaling factor of the head proportion.

	Move the head/hole on the top
	Move the head/hole on the bottom
	Move the head/hole on the back
	Move the head/hole on the front
	Move the head/hole on the left
	Move the head/hole on the right
	Rotate head left (yes)
	Rotate head right (yes)
	Rotate head down (no)
	Rotate head up (no)
	Move head on the left side
	Move head on the right side

Insert new source, detector or electrode

Please refer to montage parameters to get the correct label identification according to your equipment. Appendix, holes nomenclature contains additional information about the convention used by our different equipment.

1. Press on the interface shortcut Src (source), Det (detector) or Ele (electrode).
2. Click on a holes to attribute a new hole.
3. On the left panel choose the label identification corresponding to your experiment.
4. Once the setting is complete save the .prj file and use this information for the following steps of the data analysis.

Read NIRS data

The first step of the analysis is often to read the raw data. The menu NIRS data offers few options to support your data format.

Read NIRSCOUT

Description : Read data from commercial NIRx [NIRScout](#).

Inputs:

Select NIRx NIRScout data Recorded data files (.evt, .hdr, .wl1, .wl2, .inf, .tpl, .set) are placed in the same folder during recording sessions. Indicate the .hdr file containing the raw data, then the trigger, wavelengths and parameters will be read and associated with the helmet project .prj. Please do not rename the files, or if you must, rename them all to the same name and keep them in the same folder.

Helmet .prj Associate recording helmet configuration. See 3dMTG.

Analyzed files directory Indicate the location where the analyzed files will be saved. NIRS.mat structure is created and could be open in the display or used for any further operation. Analyzed data file .nir will be saved in the folder.

STD deviation criteria can be used to reject channels with a higher standard deviation than a fixed criteria.

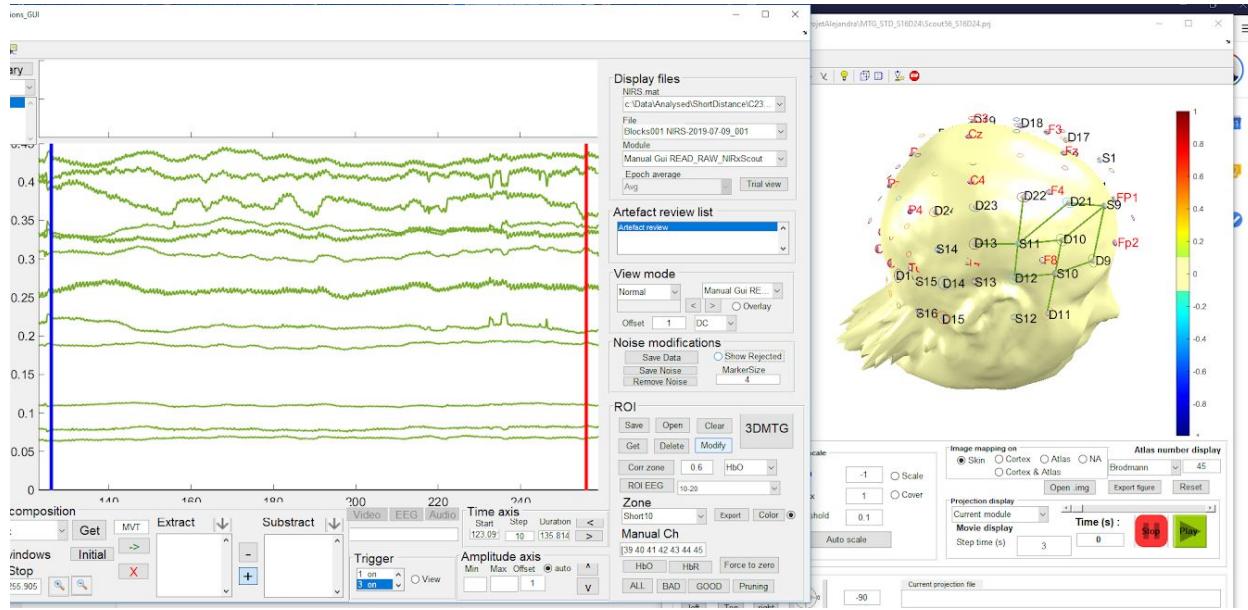
DC intensity criteria can be used to reject channels with a lower DC intensity than a fixed criteria.

Minimum distance defines a minimal geometric distance between a source and a detector to keep the data.

Maximum distance defines the maximal geometric distance between a source and a detector to keep the data.

Short distance probe NIRx provides a short distance probe with multiple short distances placed in the source location. If you use the probe to indicate the source number, you insert the probe. A zone file will be created to associate the

short distance channels to the closest channels. They could be used as a regressor in the GLM. Use the zone as a regressor in the Component extract list.



Example of zone identify close to the NIRx short distance S10.

Read .nirs (HoMER)

Description : Read HoMER .nirs format.

Matlab structure with the .nirs extension that contains the following field

d	Nirs data Sample x Channel
ml	Channel information Source x Detector x weight x wavelength
t	Time vector
s	Trig vector
SD.SrsPos	Source id x position (x,y,z)
SD.DetPos	Detector id x position (x,y,z)
SD.Lambda	Equipement wavelength (nm)

Inputs:

Select .nirs locate .nirs file to open.

Subject age enter subject age

Helmet .prj locate the project optional could be created

Analyzed files directory Location where analyzed data will be located.

Options:

Each file (put each .nirs is a blocks)

Merge files (put all file after the other to create one block)

Merge and detrend (put one file after the other and apply a detrending for each block.)

Read SNIRF file

Description: Read [Shared Near Infrared File Format Specification](#) file and import the data into this toolbox.

Inputs:

Select SNIRF data The SNIRF file containing the desired data.

Create or import a project file? Decide whether to import or create a project file. To import a project, the .prj file must be selected using the file selector. No further actions are required to create a new project file. It will be created in the output folder.

Path to output folder Where the analyzed files (NIRS.mat), data files (.vhdr, .nir, .vmrk) and created project will be created. The NIRS.mat can then be selected to be the starting point for further analysis.

STD deviation criteria: Same function as for Read NIRx scout.

DC intensity criteria: Same function as for Read NIRx scout.

Minimum distance: Same function as for Read NIRx scout.

Maximum distance: Same function as for Read NIRx scout.

Short distance probe: Same function as for Read NIRx scout.

Read BOXY ISS

Description : Read data from commercial [ISS imagent system](#).

Inputs:

Select boxy files

Subject age enter subject age

Helmet .prj : Associate recording helmet configuration. See 3dMTG

Analyzed files directory:

STD deviation criteria: Same function as for Read NIRx scout.

DC intensity criteria: Same function as for Read NIRx scout.

Minimum distance: Minimal distance between a source and a detector to include channels.

Maximum distance: Maximal distance between a source and a detector to include a channel.

Multimodal

Read EEG

Description: Add link to EEG data and synchronize it with NIRS using common markers.

Compatibility format generic data export BrainVision analyzer.

The same trig needs to be recorded in EEG and fNIRS to synchronize them. You must add the EEG file in your pipeline just after the read fNIRS data. It is good practice to keep one long block for both modalities before segmenting. If you have many sessions, use the concatenate function to merge them all. The data will be synchronized only when you use the operation ‘segment’. Be careful to have the same trig before the segmentation to avoid misinterpretation.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

EEG_files: identify the EEG data file.

Import EEG marker information (E_readEEGMarker)

Description: Import EEG markers as fNIRS triggers. fNIRS uses trigger information (i.e. integer value) to identify the event. The toolbox uses trigger information segmentation, to model a hemodynamic response or to average fNIRS data. When you edit the marker in BV analyzer ensure that they are also exported in the .VMRK file definition. You need to re-export (Generic Data Export including all markers) the EEG file to include manual marking edition. Please apply a first segmentation to synchronize EEG and fNIRS before importing these manual markers.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

EEGMarker=NIRSTrigger: You must enter the label you want to import and specify the trigger value that will be used to identify this marker. For example, use the identification MARKER1:1, MARKER2:2 to find all events called MARKER1 and give them the fNIRS trigger definition 1 and all events called MARKER2 and give them the fNIRS trigger definition 2. You can find many different markers, but separate them by a comma.

Read Video

Description: Identify a simultaneous video recording, to be synchronized to fNIRS.

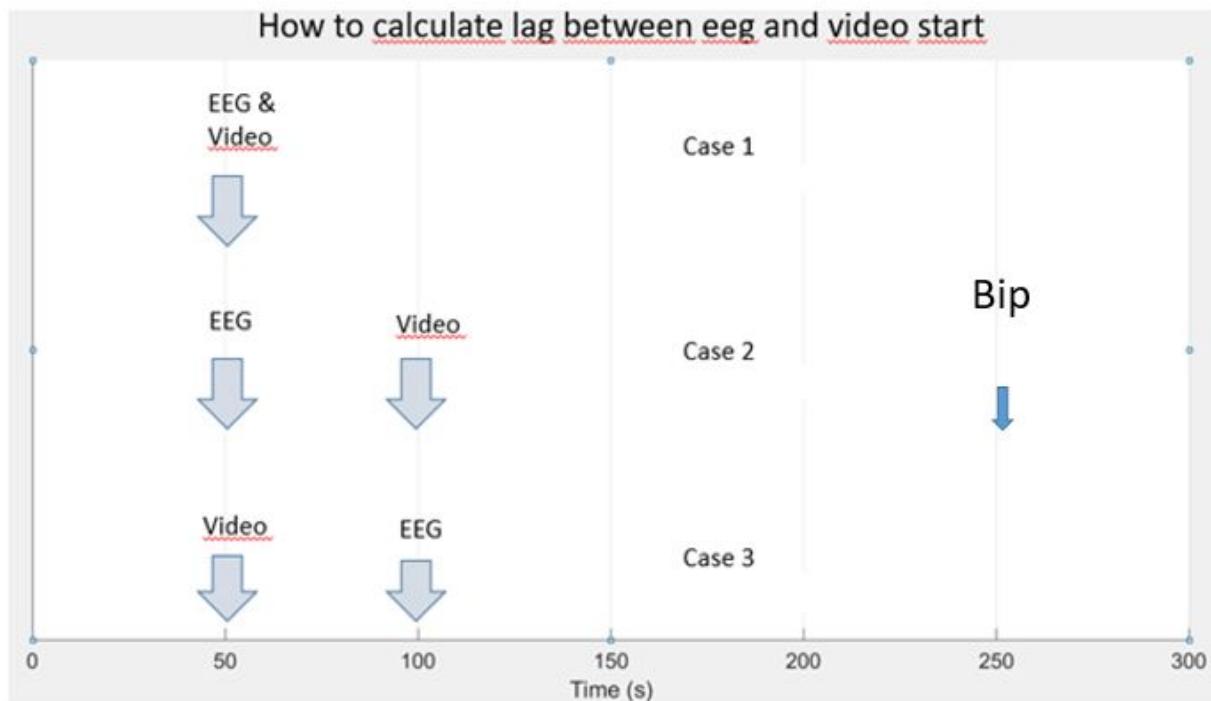
Inputs:

NIRS.mat: Select NIRS.mat for the subject.

Video file: Identify the video data file.

Reference to synchronization trigger: Indicate if the trig are common to NIRS, EEG or AUX data. The trig will be used for the segmentation to keep all data in the same time line.

Offset (yes no): No, the start of the video is perfectly synchronized with modality indicated as reference. Yes, a lag exists between those recordings. It is possible to enter the delay manually if you add some time reference to synchronize the video with some trigger.



Case 1: EEG and Video start at the same time therefore they are perfectly synchronized so the delay is 0.

Case 2: EEG recording starts before the video recording. We measured a bip mark at 200 sec EEG and you can hear the same bip in the video after 150 sec. The lag between EEG and the video will be

$$\text{Video lag} - \text{EEG lag} = \text{offset}$$

$$150 - 200 = -50$$

Case 3: EEG recording starts after the video recording. This triggered will occur at 150 sec EEG and you can hear the same bip in the video after 200 sec. The lag between EEG and the video will be

$$\text{Video lag} - \text{EEG lag} = \text{offset}$$

$$200 - 150 = 50$$

Warning: Reading problems in Matlab could be related to the codec ensuring that you have the right codec installed. If a specific codec is only available in 32 bits, that could be an issue with Matlab 64 bits version.

Read Audio

- Same as video for audio file. Matlab supports the following audio format. All platforms WAVE (.wav), OGG (.ogg), FLAC (.flac), AU (.au), AIFF (.aiff, .aif), AIFC (.aifc). Windows® 7 (or later), Macintosh, and Linux®MP3 (.mp3) MPEG-4 AAC (.m4a, .mp4).

Read AUX

- Same as EEG but auxiliary data available directly for GLM regression. And visible in the upper panel of the DisplayGUI.
- Compatibility format generic data export BrainVision analyzer.
- If the trigger is present in NIRS and AUX files, add this module in your pipeline just after the read fNIRS data and before the ‘segment’ module. The data will be segmented in the same pretime and post time trigger to be homologous as the NIRS file.
- Multiple different auxiliary files using different sampling rates could be added but all of them will be treated as independent files and need their own trigger.

Create AUX

This function helps to generate auxiliary files such as HRF response to further be used in the GLM modelisation.

HRF trigger onset

Description: Create and HRF in the data HRF parameter Glover, NeuroImage, $9.416-429 \text{ gamma1}/\max(\text{gamma1}) - \text{DIP}^*\text{gamma2}/\max(\text{gamma2})$ scaled so that its total integral is 1.

Options:

Replace AUX: Erase previous multimodal AUX file and add the new create HRF signal.

Add AUX: Keep previous multimodal AUX file definition and add the new create HRF signal.

Inputs:

Trigger onset: Trigger to used

Duration (s):

HRF label: HRFtask

Time to peak: of the first gamma density

FWHM1: approximate FWHM of the first gamma density

Time to peak: of the second gamma density

FWHM2: approximate FWHM of the second gamma density

DIP: coefficient of the second gamma density

Multimodal folder: Where to save the HRF created as an auxiliary file.

GUI_AUXEdit

This is a utility GUI to create auxiliary information for GLM regression or visualization.

- The auxiliary file corresponds to a whole data recording (unsegmented)
- Triggers need to match the recorded NIRS .nir data or EEG .dat to be segmented adequately.
- We recommend adding all auxiliary in a separate folder.

It helps to create auxiliary data such as

- Hemodynamic response function model (HRF)
- Mel coefficient from speech voice
- Muscular component (using high frequency from EEG)
- Global data
- One channel data

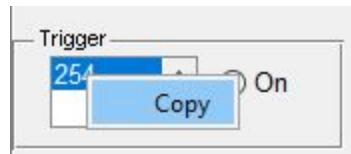
Create HRF using onset duration xls file

HRF based on event onset. In excel, first create an onset file, use time onset, duration and weight of the event as follows. The HRF will be convoluted with these responses. Indicated the .nir file to keep the same trigger information of the current recording.

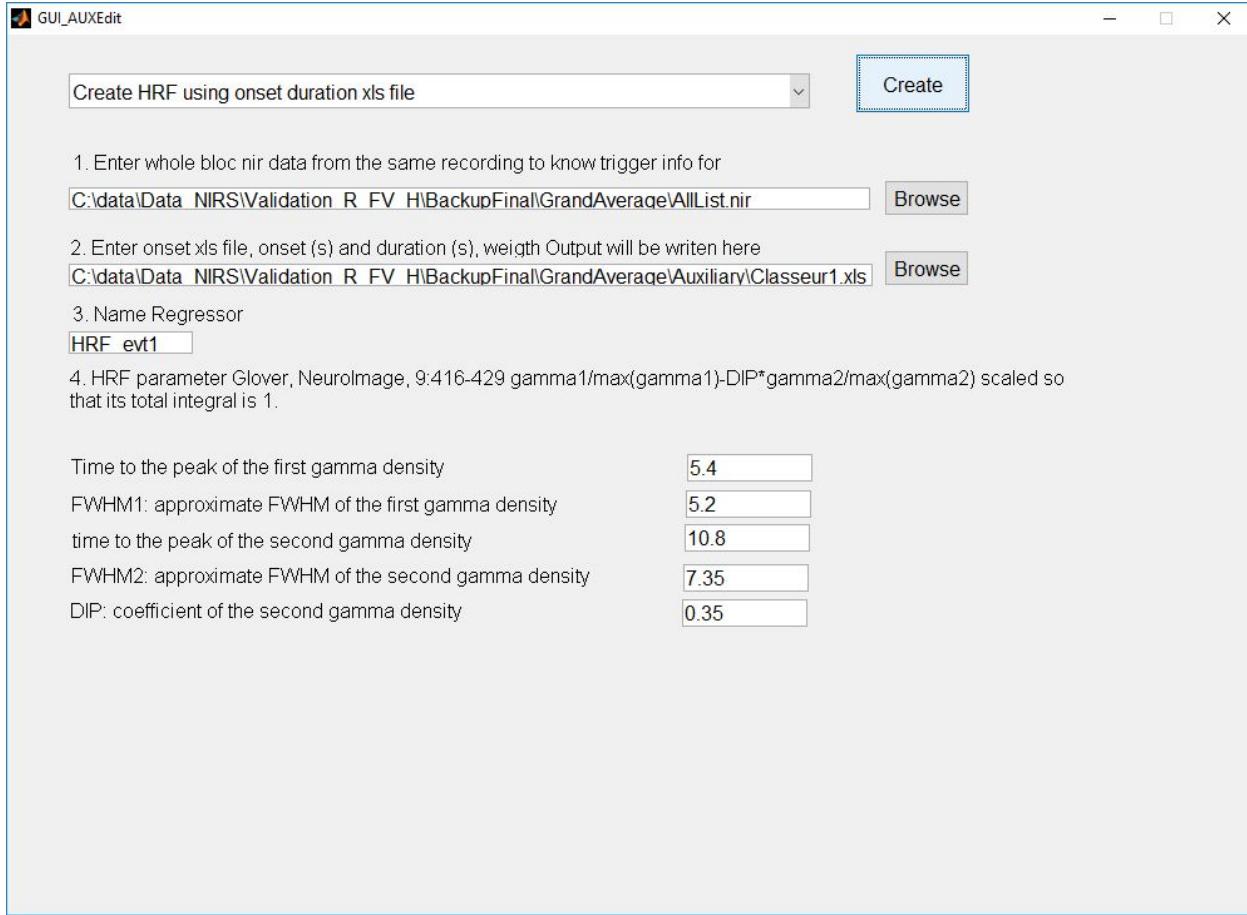
1. Create an excel file such as event onset, duration and weight information about the hemodynamic response function are indicated (Glover et al, 1999).

	A	B	C
1	Time (s)	Duration (s)	Weight
2	47.36	29.952	1
3	102.4	29.952	1
4	158.336	29.952	1
5	215.296	30.08	1
6	274.304	30.08	1
7	332.288	30.08	1

Tip: To obtain the onset time of the trigger use the copy function in the GUI_DISPLAY you can access by right-click on the trigger.



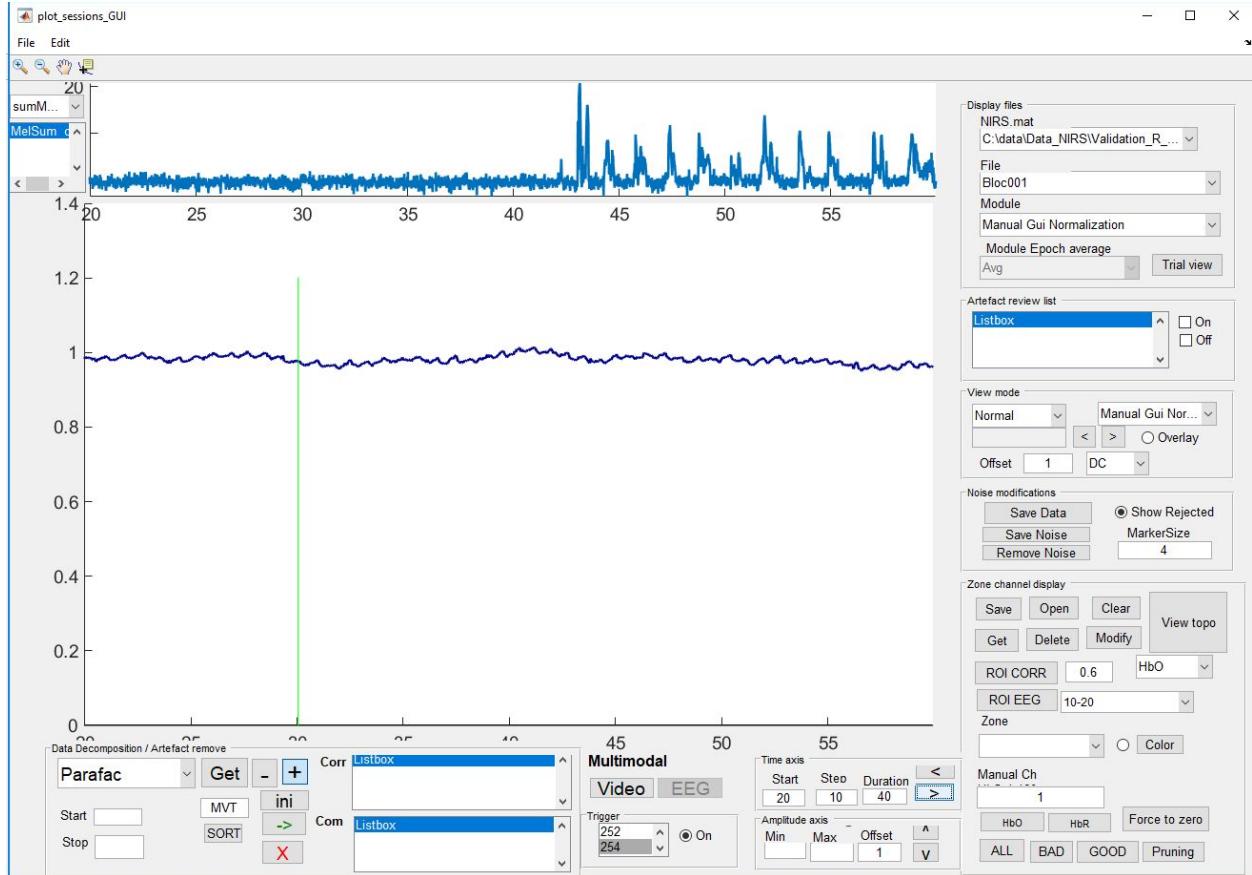
2. Define file and parameter of the HRF in the GUI :

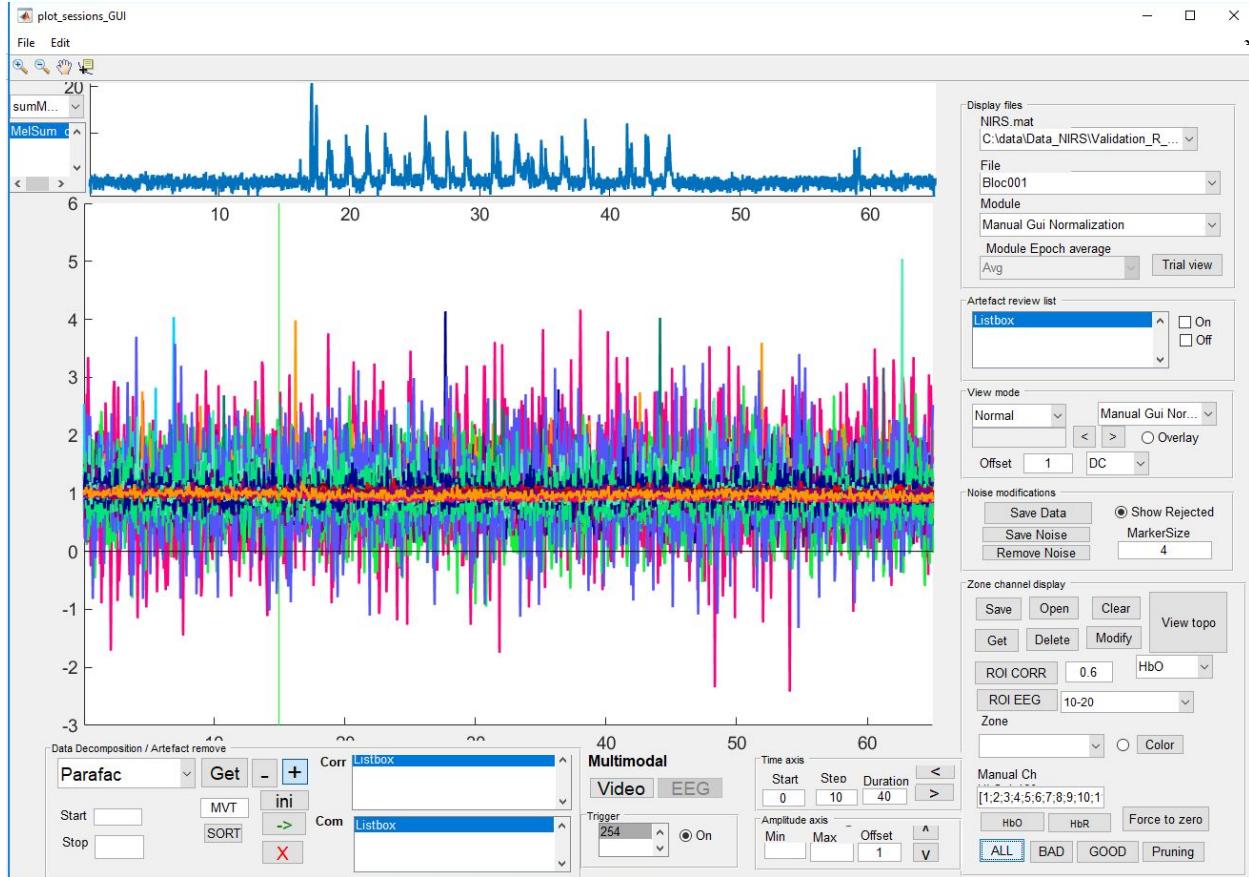


Trigger info

```
C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M01KM\Pre\M01KM_FV_001.vmrk - Notepad+
[Marker Infos]
[Comment Infos]
Codepage=UTF-8
MarkerFile=M01KM_FV_001.nir
[Marker Infos]
; Each entry: Mz-Marker number->Type<Comprition>->Position in data file(s).
; Fields are separated by commas, some fields might be omitted (empty).
; Commas in type or description text are coded as "\,".
Mz-New Segment,1,1,C
Mz-trigger,255,1,0,M
Mz-trigger,254,587,0,M
Mz-trigger,252,1173,0,M
Mz-trigger,254,1173,0,M
Mz-trigger,255,1,M

```





Global average

Use the average of all channels from a NIRS.mat data and create an auxiliary data. Use the NIRS.mat at the stage you want to create the auxiliary global average data. As an example, use the HbO and HbR concentration after filtering if you want to use it as a regressor with the HRF.

Short distance

Use a particular channel from a NIRS.mat data and create an auxiliary data. Write the channel as A a1b2 ISS format or NIRSx. For example, use the HbO and HbR concentration after filtering if you want to use it as a regressor with the HRF. However, it is recommended and more efficient to use the zone directly in the regression.

Audio .wav (Sum mel coefficients) (Matlab version 2014 and higher)¹

In sound a signal decomposition procedure named as Mel Frequency Cepstral Coefficient is used to identify relevant parts of the speech (Davis, Mermelstein, 1980).

¹ Davis, Mermelstein, 1980. The toolbox [MFCC](#) by Kamil Wojcicki is used to compute the MEL coefficient (base on the work ok of Ellis, D., 2005).

The toolbox [MFCC](#) by Kamil Wojcicki is used to compute the MEL coefficient². We do the sum of the mel coefficient to determine where the words are pronounced during the experiment as an auxiliary channel.

As preprocessing

1. Get the sound in a wav format could be done in Matlab.

Set the current directory at the position of the audio file

filename = 'M01KM'

```
[speech,Fsaudio] = audioread([filename,'.m4a']);
audiowrite([filename,'.wav'],speech,Fsaudio)
```

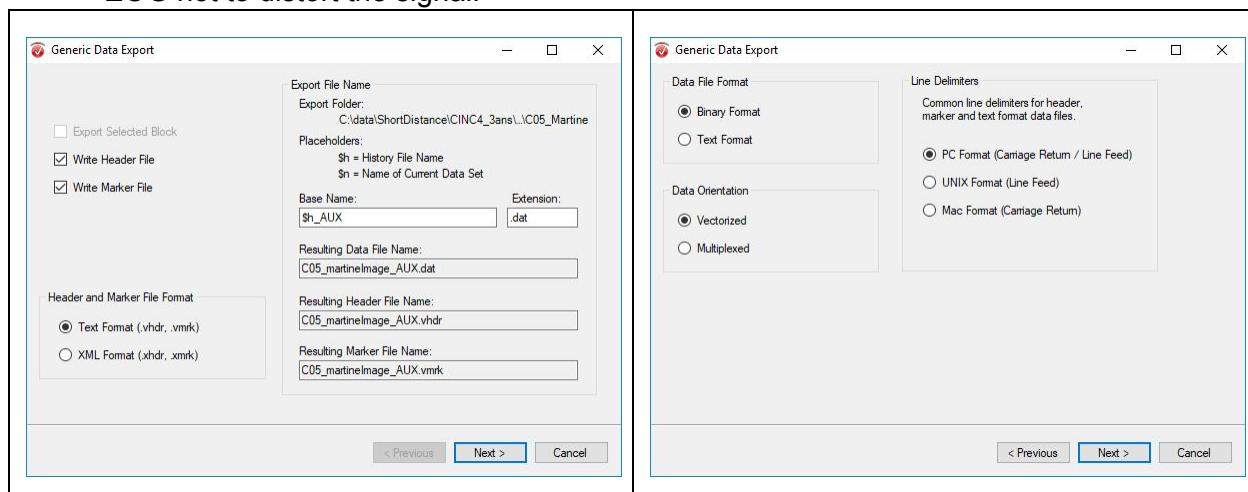
2. Identify the delay between the sound and the beginning of the nirs data or EEG data file (used to identify an associate trigger in the auxiliary file). You could use the software Audacity and calculate the delay using a sound marker in the file, or clean noise in the room that is not voice content. Usually, the sound recording starts before the NIRS or EEG data and the irrelevant part of the beginning will be cut.

Concatenate AUX or EEG file

The rule to segment and synchronize NIRS, EEG, AUX and Video on the same time line is to keep one long file with identical triggers on each of them. The segment module will handle each trigger to keep the segments synchronized in the GUI (NIRS, EEG, AUX and video). It is possible to merge them in the GUI_AUXEdit to combine multiple sessions of recording in one long file. YOU MUST KEEP THE RECORDING ORDER WHEN YOU OPEN THEM AND USE SEGMENT TO SYNCHRONIZE THEM.

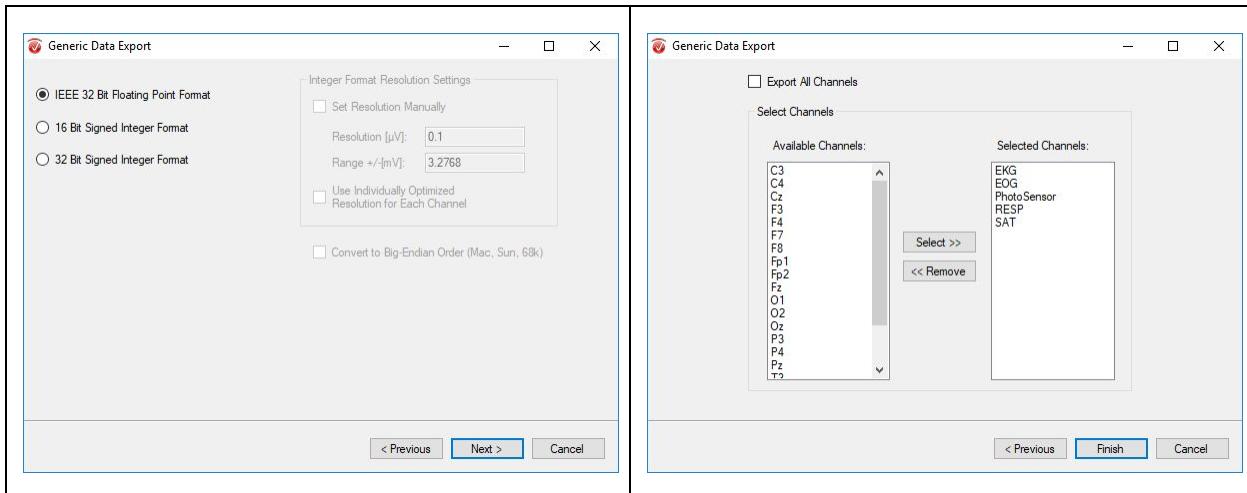
Prepared auxiliary EEG as multimodal data in the toolbox

Use BrainVision analyzer, and use Export/Generic data export/ to save EEG or AUX data. A filter is advised for EEG (notch 60Hz or 50Hz; 0.1 to 200 Hz), to remove dc drift that will affect visualization. We do not recommend applying filters on the respiration and EOG not to distort the signal.



² Kamil Wojcicki (2020). HTK MFCC MATLAB

(<https://www.mathworks.com/matlabcentral/fileexchange/32849-htk-mfcc-matlab>), MATLAB Central File Exchange. Retrieved April 3, 2020.



Segments / Onsets

To configure the analysis data onset need to identify the event during an experiment through the auxiliary trigger (AUX Trig). It is a numerical value that is usually recorded from an external trig and marks the time when starting a specific task. In further analysis, this auxiliary trigger value could be used to segment the event belonging to the same category.

Segments

Description: Segment data around trigger (defining pretime and post time). This step is essential to synchronize multimodal data such as EEG, auxiliary (AUX) or video.

If the acquisition is recorded in many sessions, use the option Concatenate to merge blocks. Trigs must be homologous in each data file (fNIRS, EEG, AUX). Please test the correct synchronization of your files, as sample rates are different a long period could induce a small lag between both files, the use of simultaneous multiple triggers could help to avoid lagging.

Inputs:

Delete previous .nir data file: set true delete previous data files set false to keep them.

Trigger: Enter the trigger value to use for the segmentation. Integer value.

PreTime: Enter the time before the trig to use for the segmentation in seconds.

PostTime: Enter the time after the trig to use for the segmentation in seconds.

Concatenate blocks in a nirs.mat

Description: Group file one after the other, each file usually corresponds to a trial or block of the experiment. Concatenate AUX file and EEG if they are included in the NIRS.mat structure. See Read EEG and Read AUX. Concatenate Video is not supported. Enter one nirs.mat.

Options:

Merge only groups files without any additional operation.

Merge and detrend groups files and detrend each file before, such as the start point and stop point of each file is adjusted to zero.

Create NIRS.mat then group the NIRS.mat data to create one long continuous segment.

Blocks number: Enter the numbers of the blocks to be considered.

Concatenate nirs.mat (multi subjects time series).

Description: Group all data from different NIRS.mat. Create a new folder as an example .../Grand_Average and put the list.xls inside as well as the channelist.txt which identify the channel to keep for the average, a new NIRS.mat will be created in /Grand_Average folder for visualization. Once they are grouped, you could use the average module.

Inputs:

Enter NIRS.mat list to group (xls): Identify subject to group and channel as list write as an xls file.

	Sujet path	Channel List (same location xls file)
1	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M05GM\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
3	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M06MC\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
4	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M07IG\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
5	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M08LF\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
6	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M09EA\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
7	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M10ST\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
8	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M11SF\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt
9	C:\data\Data_NIRS\Validation_R_FV_H\BackupFinal\PARAFAC\M13AL\Data_FV\SimpleNormalisation\Batch_1\dCONC\AVG	M07IG_AVGseedlist.txt

It is important to identify the channels having the exact same localization on the scalp for an average, i.e. the same montage. In the case NIRS.mat file recording is performed using a slightly different montage, you must ensure that the localization is identical across subjects. The channel list needs to ensure that participants have the same channel order, it lists the source and detector labels. See **create channel list** to create a channel list automatically for a participant. If they have any helmet difference the order will be kept according to the first subject in the list. Use the first subject montage to visualize the result correctly.

Or

Identify subject to group and zone to use list write as an xls.file

A	B
1 Sujet path	Zone List (same location xls file)
2 C:\data\Analysed\Histoire\M01MK\Clean\dCONCfilter\AVG	ROI_V2.zone
3 C:\data\Analysed\Histoire\M02CL\Clean\dCONCfilter\AVG	ROI_V2.zone
4 C:\data\Analysed\Histoire\M03YP\Clean\dCONCfilter\AVG	ROI_V2.zone
5 C:\data\Analysed\Histoire\M04LC\Clean\dCONCfilter\AVG	ROI_V3.zone
6 C:\data\Analysed\Histoire\M06MC\Clean\dCONCfilter\AVG	ROI_V3.zone
7 C:\data\Analysed\Histoire\M07IG\Clean\dCONCfilter\AVG	ROI_V3.zone

The zone is a group of channels to use for each region of interest. You must ensure that the zone contains the same identification label as example TemporalRight. All the channels belonging to the temporal right zone will be average. Once again the first subject in the list is kept as reference.

Options:

Merge only groups file without any additional operation.

Merge and detrend groups file and detrend each file before, such as the start point and stop point of each file is adjusted to zero.

Set exclude channel to NAN:

Exclude: rejected channel will be set to NAN.

Keep: no special process concerning the rejected channels will be applied.

Normalization: Apply normalization operation on each NIRS.mat to reduce individual variability³. Only apply using the channel list.

No normalization: do not apply any normalization.

Min-Max Normalization: Apply min max normalization fixing boundary between 0 and 1.

Z-score Normalization: Apply z-score normalization.

AuxTrig to ManualTrig

Description: Trigger is usually recorded by the equipment in the raw data. This trigger information is kept in the structure and could be visualized or used to segment, normalized or averaged the data. Create a file to export the time (in second) of the trigger onset. The export will be saved in a Matlab file .m that could be edited manually. The file is located in the NIRS.mat current folder and is named ‘Manualtrig_2trig.m’. In the following example, the Manual Trig is the onset for the trigger 2.

Trigvalue = 2;

```
filename{1} = ['mnAllNIRS-2018-07-20_006b01'];
timingfile{1} = [1.152,2.56,3.712,4.992]; %time seconde
filename{2} = ['mnAllNIRS-2018-07-20_006b02'];
timingfile{2}=[0.384,1.664,2.816];
```

File output: indicate a name for the output file

³ Moeller, J., 2015. A word on standardization in longitudinal studies: don't. Front Psychol 6. <https://doi.org/10.3389/fpsyg.2015.01389>

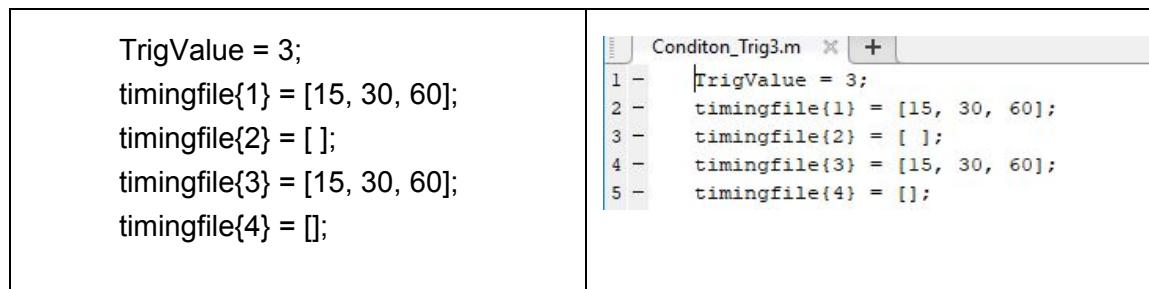
If you want to modify the trigger you must import a manual version using '*ManualTrig to AuxTrig*' or edit them in the DisplayGUI, see trigger section in the DisplayGUI to do so.

ManualTrig to AuxTrig

Description: Use the manually edited file to enter trigger information. Triggers are used to identify the onset of the events to be segmented, normalized, model HRF or average the data. They are almost essential to data analysis.

Inputs:

Enter new trig definition: Open ManualTrig file. The manual trig is a .m Matlab script that defines the new TrigValue=X an integer used for the trigger identification and the timingfile{1}=[15,30]; which indicate the timing of the trig event in seconds for the file 1. As the NIRS.mat structure could contain one or many files, you must define a timingfile for each of the files present in your data. If as an example the file 2 does not have any trig events defined the timingfile as empty value : timingfile{2} = [];. Be aware that .m file names do not support space or accent in the name definition. Example :



```
TrigValue = 3;
timingfile{1} = [15, 30, 60];
timingfile{2} = [];
timingfile{3} = [15, 30, 60];
timingfile{4} = [];
```

In tutorial 3 you can find an example of batch using manual trig.

Options:

Replace completely trig: Remove old trigger information and replace it completely with the new trig definition.

Add trig: Add trigger information to the current trig definition.

Preprocessing NIRs data

Artifact detection

Artifact detection and correction with the LIONnirs toolbox is structured as a two-step semi-automatic process including an automatic and a manual processing of the signal. First, several criteria of the signal's variation allows it to automatically detect changes in the signal, potentially related to an artifact. Based on these intervals, the user can subsequently apply an automatic artifact correction (extract and subtract). Depending on the signal's quality, the automatic detection and correction may in some cases be too severe. There may also be other reasons that could lead to over- or undercorrection of the signal, which is why we strongly

recommend to manually verify and, if required, to adjust the results of the automatic detection and correction.

Description: Automatic artifact detection modules can be applied on either raw or normalized unfiltered data to detect abrupt variations, potentially related to an artifact. The user has the option to consider several criteria to improve detection. These four criteria are: ‘Artifact detection using moving average’, ‘Minimal percentage of bad channels to be marked as artifact’, ‘Minimal subinterval’ and ‘Correlation between channels for artifact’. A more detailed description of each criterion is presented above.

Inputs:

NIRS.mat: Select NIRS.mat for the subject where you would like to apply artifact detection.

Save general report: Allows the user to generate a figure summarizing the percentage of detected channels over time for each criterion applied. These are saved as .\ArtifactDetection_Report in the home folder of the NIRS.mat file. Each criterion: ‘Artifact detection using moving average’, ‘Minimal percentage of bad channels to be marked as artifact’, ‘Minimal subinterval’ and ‘Correlation between channels for artifact interval’ will save a summary report if they are applied. This means for instance that the user receives an individual report for the artifacts detected based on the moving average and those detected based on the minimal percentage of bad channels during a period.

Artifact detection using moving average: Moving average allows to identify discontinuity or strong perturbations in the signal. It is a criterion based on the signal’s mean variation for two subsequent time intervals: M1 from X_n to X_{n+step} and M2 from X_{n+1} to X_{(n+1)+step}. The step is defined by the user and defines the period of time for the moving average from sample n to sample n+step according to the time window. Changes of light intensity between M1 and M2 are then specified as the difference (D) between both means: D = M₂-M₁. Difference D is transferred into z-scores normalized over the entire dataset to determine which periods have increased signal variations. The threshold, i.e. the z-score above which abnormal variations in the signal are identified as artifact intervals, is to be defined by the user.

Apply: Yes or No. Use the artifact detection using moving average.

Z-score threshold: The difference (D) between M1 and M2 over time is converted into a standardized z-score distribution. A z-score threshold determines which variations in the moving average difference of two subsequent intervals are considered abnormal, thus representing artifacts. Depending on the value defined by the user, variations higher than this z-score are identified.

Moving average step (seconds): Defines the duration (sec) of the time interval (step) to calculate moving average M1 and M2. Depending on the smoothing the user wants to apply, i.e. how sensitive the detection of the signal’s variation should be, a higher or lower value should be indicated.

Ignore intervals shorter than x seconds: This specifies the minimal duration (seconds) of an abnormal variation in the signal, as defined by the z-score threshold of the moving average, in order to be considered as an artifact. Intervals where the z-score threshold appears for a period shorter than this time are ignored.

Print threshold report for each channel: Select if you want to save a figure that displays the threshold detection made for each channel. The figure will be saved in ...\\ArtifactDetection_Report\\EachCh folder at the NIRS.mat home location.

Minimal percentage of bad channels to be marked as artifact: In some cases, only a few channels are detected as having artifacts. Based on the premise that a true artifact usually affects several neighboring channels, it may be recommended to restore an interval when very few channels are detected during a period. For example, if based on previous criteria less than 10% of all channels have been identified as showing abnormal variations in a specific period, this interval is unmarked.

Apply: Yes No. Use Minimal percentage of bad channels to be marked as artifacts.

Minimal percentage of bad channels: Define a minimal number of bad channels percentage to be marked at the same interval. Max value 100, Min value 0

Minimal subinterval : This criterion helps to consider small artifacts as one event instead of two subparts. For each detected interval, ensure that more than 2 seconds separates it from the previous or next detected interval, otherwise consider them as one event.

Apply: Yes No. Use minimum subinterval.

Minimum sub-interval duration (seconds) : Select the minimum duration (in seconds) for a good subinterval.

Correlation between channels for artifact interval: Finally, artifact detection is based on a correlation coefficient between channels. It determines the Pearson's correlation coefficient threshold of channels to be considered as being affected by the same event. For each artifact interval that has previously been detected, channels that have a correlation equal or above the threshold with the time course of this artifact are detected as well. This means that for each artifact, this tool marks the channels showing the same signature, but that have not been detected based on the previous criteria.

Apply: Yes No. Use Correlation between channels for artifact interval

Correlation threshold: Set the minimal correlation threshold between the channels. If the correlation is stronger than this threshold the time course will be marked as an artifact.

Output: Example of summary reports

1. Summary report is saved for first criteria Artifact detection using moving average:
.\\ArtifactDetection_Report\\ReportsC28b01__01zscore_tr3.fig
2. Summary report is saved for second criteria Minimal percentage of bad channels to be marked as artifact:
.\\ArtifactDetection_Report\\ReportsC28b01__02percentagemin_10.fig
3. Summary report is saved for third criteria Minimal percentage of bad channels to be marked as artifact:
.\\ArtifactDetection_Report\\ReportsC28b01__03minsubinterval_2.fig
4. Summary report is saved for fourth criteria Correlation between channels for artifact interval: .\\ArtifactDetection_Report\\ReportsC28b01__04correlation_0.95.fig

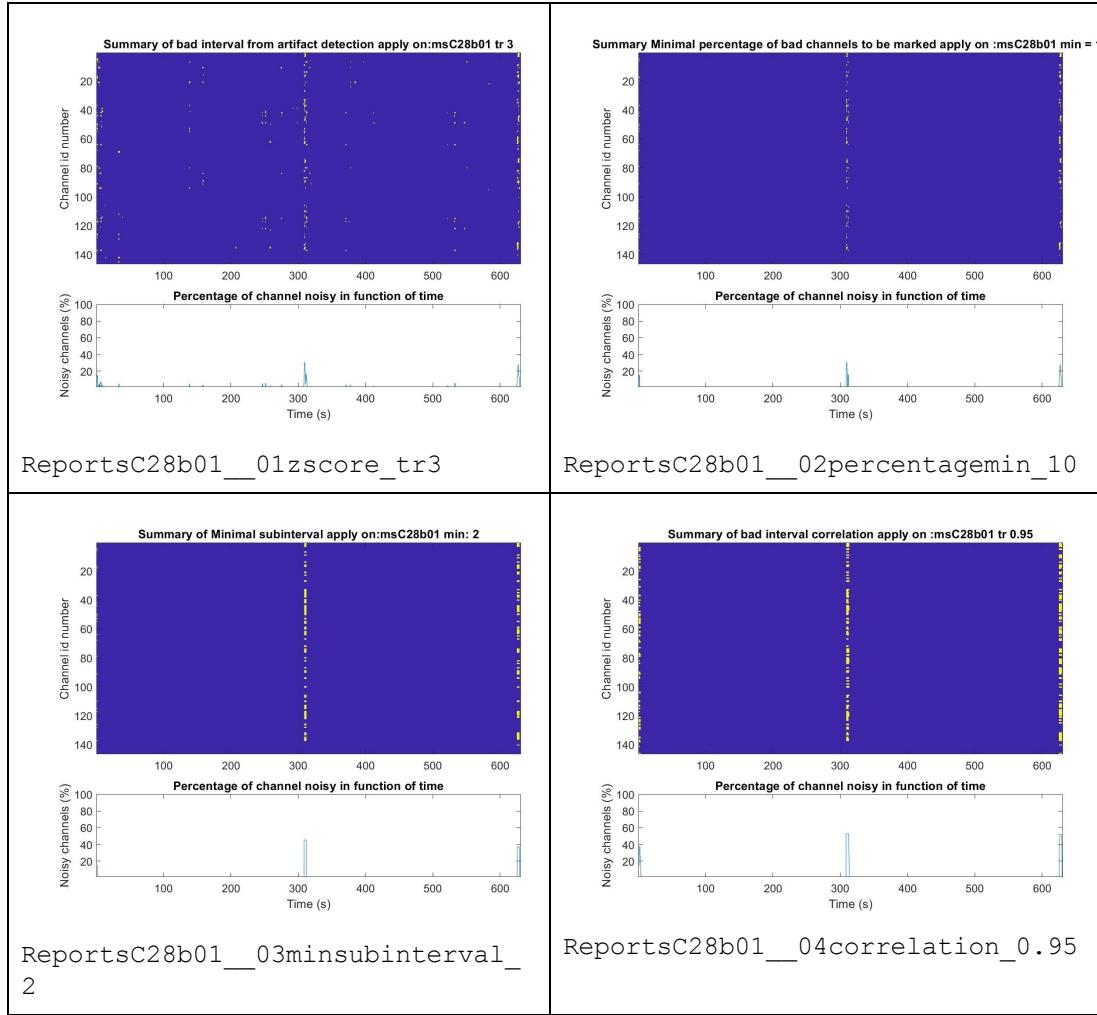
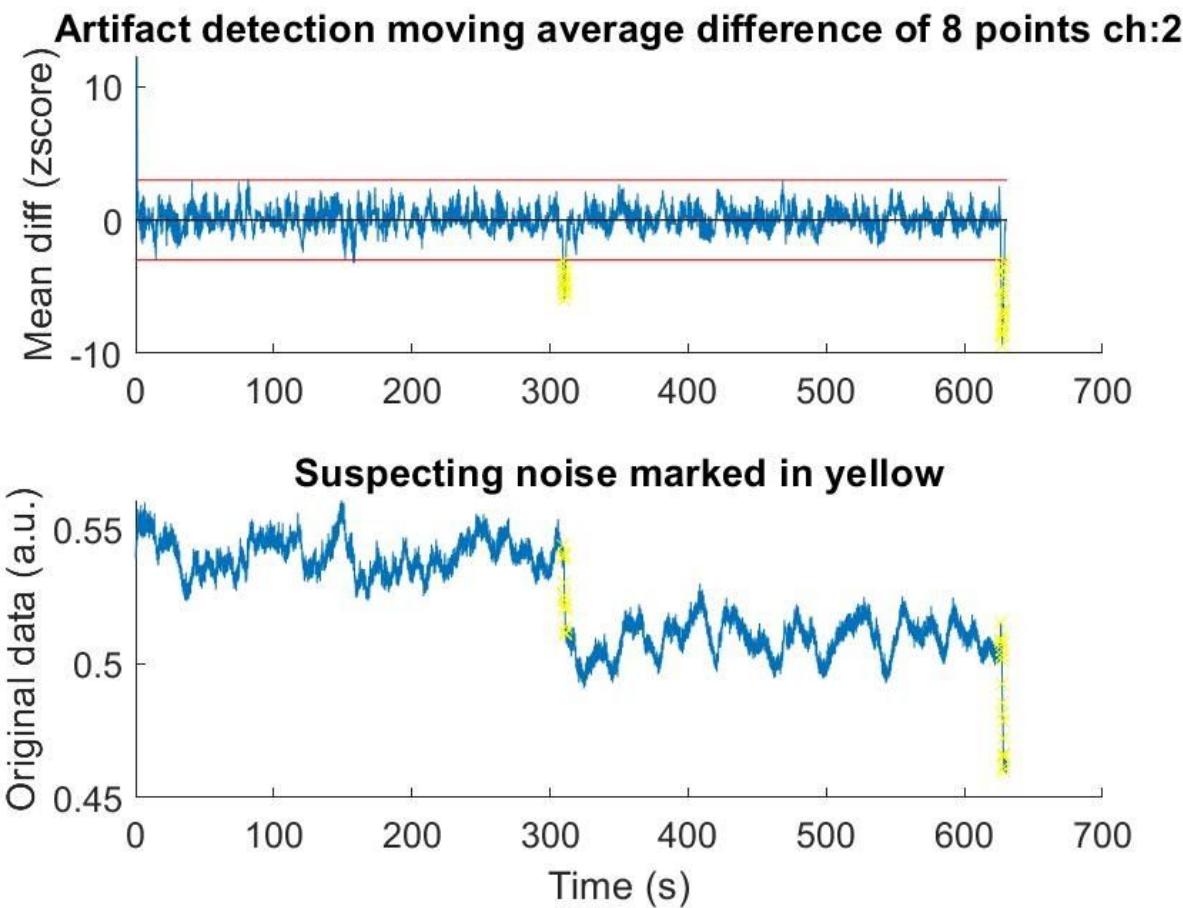


Figure by channel for the first criteria detected. To verify if the z-score threshold and moving average step is adapted to the data. The segment identified as artifacts are in yellow.

```
. \ArtifactDetection_Report\EachCh\sC28b01\sC28b01_ch_146tr3.fig
```



Cardiac detection

Description: Detects cardiac beat in signal using the coherence measure among channels and rejects channels without any cardiac beat. This physiologic signal could be absent when light intensity is too low, due to a poor contact with the skin or a too large distance between source and detector. Sometimes, light intensity is high but the detector is not touching the skin, therefore it measures contaminating light from external light sources from the brain and does not measure physiology.

Inputs:

NIRS.mat: Select NIRS.mat for the subject

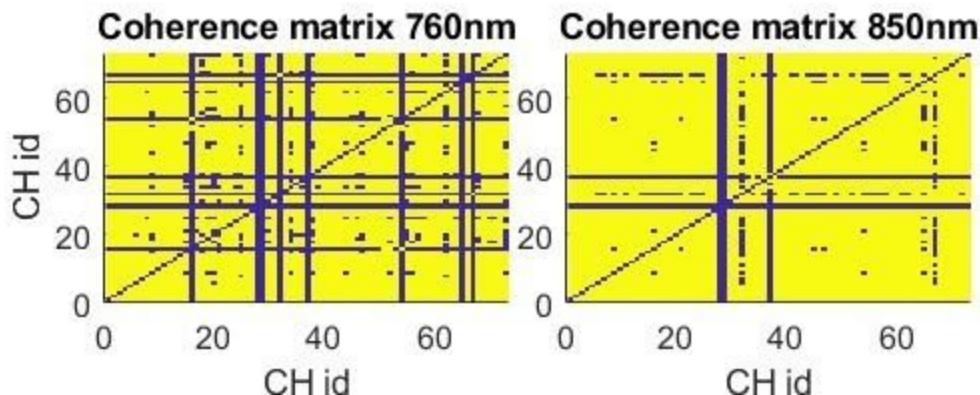
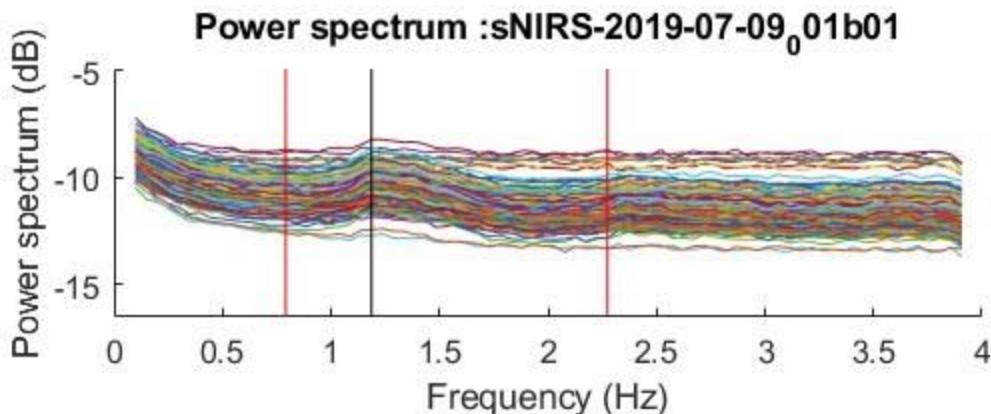
Frequency range to detect cardiac peak: Define the range of frequency for cardiac detection. Select a large range of frequencies to ensure that your cardiac peak is captured. Normal cardiac pulse will vary around 1Hz in the adult population and 2Hz in babies. Verify the output figure to ensure that the peak is well selected. (Mortensen et al., 2017, <https://doi.org/10.1177/1367493516689166>, Fekete et al., 2011 <https://doi.org/10.1371/journal.pone.0024322>).

Minimal coherence: Threshold to determine if the cardiac coherence is sufficient or not.

Minimal percentage of channel: Reject the channel if less than 10 % of the other channels obtain the minimal coherence value.

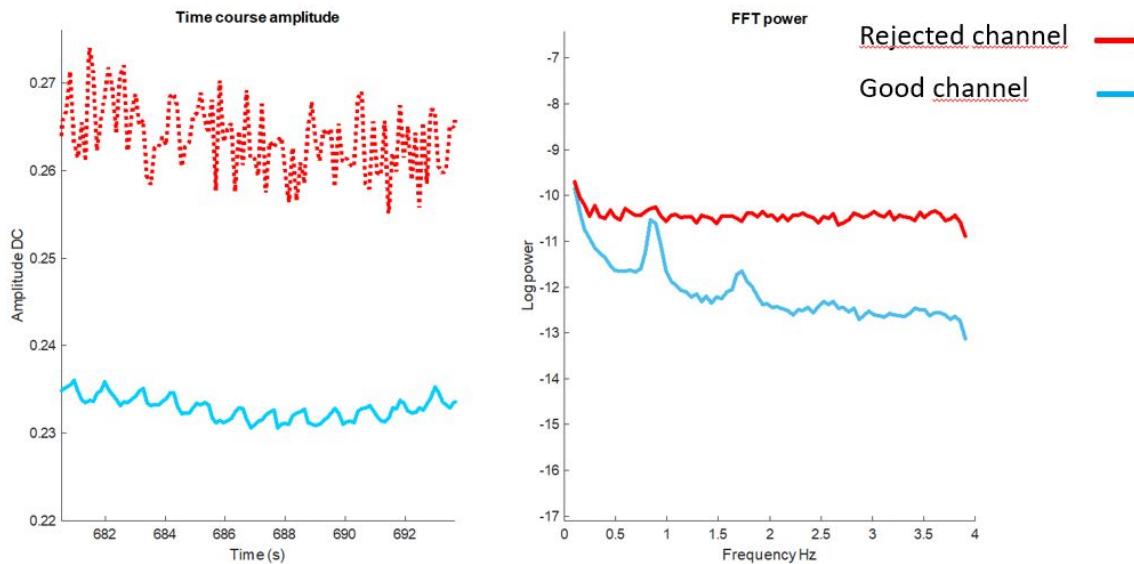
Range around the peak: Define the range to compute the coherence around the peak.

Output: A figure named cardiacCHCOH.tif is saved in the same folder as the NIRS.mat. This figure displays the power spectrum of all channels and lets the user verify if the peak of the cardiac pulse is correctly identified.



The figure reports the FFT power spectrum for each channel, the two red lines are the interval used to detect the peak caused by heart beat pulsations. The heart beat frequency peaks are detected automatically between this interval and marked by a black line. These peaks are used to measure coherence among channels. The peaks could be detected with a stronger or a milder intensity. However it should be coherent with other channels as it came from the same cardiac pulse. The two lower figures, we observe a threshold connectivity matrix for each wavelength. Channels without evidence of cardiac coherence are seen as blue lines as the coherence is poor among other channels.

Example of channels



Here is an example of a rejected channel (in red) and a good channel (in blue). The cardiac pulse is barely visible on the excluded channel in red. A poor coupling with the skin and thick hair could explain this poor quality. If there are many channels presenting a poor coupling, it is a good idea to double-check the source and detector configuration in your montage. If it is always the same source or detector, test your equipment. In the matrix, blue lines are below the threshold for cardiac coherence, they will be found as rejected channels.

A xls file named cardiacCHCOH.xls in the NIRS.mat folder helps to summarize the channels removed and the peak of the cardiac frequency. A figure named cardiaccCHCOH.tif is also saved to plot the power spectrum and the matrix of cardiac coherence. When you open the data using the displayGUI, rejected channels will be excluded and plotted in dotted lines if you choose to display rejected channels.

	A	B
1	sNIRS-2019-07-09_001b01	
2	PEAK cardiac=	1.2362
3	D07E6	28
4	D08E6	29
5	D24E6	32
6	D07E8	37
7	D16E14	65
8	D24E14	67

cardiacCHCOH.xls

Normalization dOD

Description: Delta optical density (dOD) is an essential operation to calculate the Modified Beer Lambert Law. It measures the variation of light absorption between 2 states as an example before and after a cognitive task, we measured the variation of oxygenated or deoxygenated blood concentration between these two distinct states. The way to define the initial state (I_0) could be different according to the experiment's goals. The intensity measured during the experiment relates to movement or other recording so a piecewise normalization could be advantageous.

Delete Previous .nir data files: False keep previous file for visualization, True delete previous file.

$$dOD = \log_{10}(I/I_0)$$

Apply the normalization defining I_0 as

Normalization by files: Define I_0 as each file average. Apply on the whole file.

Exclude artifacts from the I_0 calculation: Yes exclude all yellow marks from the calculation or No just take the average without artifact marking.

Normalization around trigger: Apply on each identified trigger between the PreTime and PostTime Period.

Trigger: (identification number)

PreTime: stimulus time in second (time before trigger)

PostTime: stimulus time in second (time after trigger)

How define I_0 :

$I_0=PreTime$ to 0: Define I_0 in the period between the pretime and the trig.

$I_0=PreTime$ to $PostTime$: Define I_0 in the period between the pretime before the trig and the post time after the trig.

Exclude artifacts from the I_0 calculation: Yes to exclude all yellow marks from the calculation or No to take the average without artifact marking.

Normalization inter-artifacts: Normalize each segment by its mean, segment are separated by artifacted periods.

Selection of the periods between artifacts identification (yellow marker):

Normalization will be done between each period

Filter

Description: Design a Butterworth digital filter and apply using a zero-phase digital filtering (filtfilt).

Inputs:

Delete Previous .nir data files: False keep previous file for visualization, True delete previous file.

Low pass : Low pass frequency set to zero if you do not want to apply any low pass filter.

High pass : High pass frequency set to zero if you do not want to apply any high pass filter.

Filter order : Generally, the larger the filter order, the better the frequency magnitude response performance of the filter.

Symmetric padding : Symmetric padding pads with the reflection of the mirrored signal to avoid deformation caused by the border effect.^{4 5 6}

Interpolate bad interval : you must set this option to yes to interpolate artifact marks in yellow. Each yellow segment is set to nan and then replaced by the interpolation before and after the artifact.

T. W. Parks and C. S. Burrus, Digital Filter Design, John Wiley & Sons, 1987, chapter 7, section 7.3.3.

Oppenheim, Alan V., Ronald W. Schafer, and John R. Buck. Discrete-Time Signal Processing. 2nd Ed. Upper Saddle River, NJ: Prentice Hall, 1999.

Modified Beer Lambert law

Description: Continuous wave NIRS used Beer Lambert Law to deduce hemoglobin concentration changes using light absorption from dual wavelength information. Hemoglobin concentration affects mainly the light absorption property in the tissues (Delpy 1988). Therefore, by measuring light variation between two states and using two wavelengths, it is possible to deduce the concentration by solving a linear equation with two unknowns. Use the wavelength extinction coefficient from W. B. Gratzer, Med. Res. Council Labs, Holly Hill,London, N. Kollias, Wellman Laboratories, Harvard Medical School, Boston. The modified (MBLL) version includes the L distance between source and detector and a differential pathlength factor ($DPF(\lambda, Age)$) to cover the extra distance traveled by NIR light as well as a medium geometry constant $G(\lambda)$ to calculate an accurate concentration. An additional correction will adjust the concentration to the spatial extent of the activation partial volume factor (PVF) i.e. amplify the concentration if the activation is counted for only a small volume of the activation. It is set between 0 and 1. Partial volume correction factor (Strangman et al. 2003, Strangman et al. 2014 and Selb et al. 2014) is more difficult to implement as it depends on knowledge of the activation spatial extent. You could adjust it or let it by default to 1. The estimated concentration changes will always be smaller than the real concentration changes. The real concentration change is affecting a smaller area than the whole measured volume. This is generally known as a partial volume effect.

⁴ (Lyons, Richard. 2011. Understanding Digital Signal Processing ISBN: 013702741-9)

⁵ S. Leske & S. Dalal,2019. Reducing power line noise in EEG and MEG data via spectrum interpolation. Neuroimage. doi: [10.1016/j.neuroimage.2019.01.026](https://doi.org/10.1016/j.neuroimage.2019.01.026)

⁶ Pacola E et al, 2016. Influences of the signal border extension in the discrete wavelet transform in EEG spike detection. <https://doi.org/10.1590/2446-4740.01815>

$$\Delta[\text{HbR}] = \frac{\varepsilon_{\text{HbO}_2}(\lambda_2)\Delta\mu_a(\lambda_1) - \varepsilon_{\text{HbO}_2}(\lambda_1)\Delta\mu_a(\lambda_2)}{\varepsilon_{\text{HbR}}(\lambda_1)\varepsilon_{\text{HbO}_2}(\lambda_2) - \varepsilon_{\text{HbO}_2}(\lambda_1)\varepsilon_{\text{HbR}}(\lambda_2)}$$

$$\Delta[\text{HbO}_2] = \frac{\varepsilon_{\text{HbR}}(\lambda_1)\Delta\mu_a(\lambda_2) - \varepsilon_{\text{HbR}}(\lambda_2)\Delta\mu_a(\lambda_1)}{\varepsilon_{\text{HbR}}(\lambda_1)\varepsilon_{\text{HbO}_2}(\lambda_2) - \varepsilon_{\text{HbO}_2}(\lambda_1)\varepsilon_{\text{HbR}}(\lambda_2)}.$$

Inputs:

Delete Previous .nir data files: False keep previous file for visualization, True delete previous file.

Partial Volume Factors: Adjust manually 1 1

DPF: DPF is a parameter to adjust it is estimated from the wavelength and the age of the subject from different methods. Choose one of the following methods:

Scholkmann et Wolf 2013

$$DPF(\lambda, A) = 223.3 + 0.05624A^{0.8493} - 5.723*10^{-7}\lambda^3 \\ + 0.001245\lambda^2 - 0.9025\lambda.$$

Duncan et al. 1996

$$DPF^{690} = 5.38 + 0.049*(A^{0.877})$$

$$DPF^{744} = 5.11 + 0.106*(A^{0.723})$$

$$DPF^{807} = 4.99 + 0.067*(A^{0.814})$$

$$DPF^{832} = 4.67 + 0.062*(A^{0.819})$$

Manual

Acceptable range of DPF value in adult humans is from 3 to 6 (Duncan et al. 1995, Kamran et al. 2018). You could fix your own value.

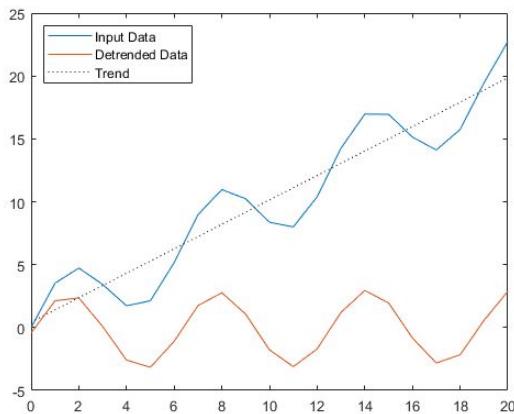
N.B. Concentration unit is displayed in the micromolar directly.

Detrend

Description: Subtract linear trends on the data. The trend is estimated using the beginning and end of the bloc.

Input:

Delete Previous .nir data files: False keep previous file for visualization, True delete previous file.



Epoch averaging

Description: Average all block files segmented.

Inputs:

Delete Previous .nir data files: False keep previous file for visualization, True delete previous file.

Save in .nirs format: yes a .nirs format will also be saved in the current NIRS.mat directory or no do not save additional files.

Averaging options:

Average over Multiple files: Use all the files in the NIRS.mat

Trigger: Use specific triggers to use only segments belonging to the condition to average, you can identify one or many triggers.

PreTime: Define the period to use before the trig.

PostTime: Define the period to use after the trig.

Reject trial ratio: Reject the trial if more than xx % of its duration is marked as a bad interval, set to 1 to keep trial

Reject channel ratio: Reject the channel if less than xx % of the trials are rejected, set to 0 to keep all channels

Data type: DC, default use both wavelengths or concentration HbO HbR to average the data. AC and PH (phase) are available only for ISS equipment.

Baseline Correction:

Subtract preTime: Subtract pretime to trig mean to each event.

Manual: Subtract value: use Mean or Median

PreTime baseline correction: enter the PreTime baseline correction.

PostTime baseline correction: enter the PostTime baseline correction.

No baseline corr: Do not apply any correction.

Reject outlier trial:

Keep trial: Keep all trials, except if the trial is more noisy than the reject trial ratio

Reject outlier trial z-score

Threshold z-score: exclude trial outliers based on the z-score compute in comparison to other trials

Print report

Tvalue option:

Against 0: Simple t-test against 0

Against mean baseline: Simple t-test against mean baseline value.

Nullify bad intervals

Description: replace all artifacts identified in the data (yellow part) by a missing value (nan).

Inputs:

NIRS.mat: Select NIRS.mat for the subject

Delete previous .nir data file: set true delete previous data files set false to keep them.

Padding time: Time (in seconds) padded with NaN before and after the nullified intervals.

Decomposition (data)

Tools to perform data decomposition automatically.

Extract component

Description: Identify data components using several data decomposition methods on target data. The component will be added to a list that could be visualized in the DisplayGUI (extract), subtract in case of an artifactual component using 'Subtract component' or export as a relevant activity for further statistics using 'Export component'. The component list is stored in 'SelectedFactors.mat' in the same folder as the NIRS.mat.

Identify PCA for artifact period

Description: First, identify noisy intervals using artifact detection or a manual revision. This function runs a PCA decomposition (targetPCA) on each bad interval (yellow segment in the DisplayGUI). The decomposition is performed on identified channels during a continuous bad interval. PCA decomposition sort components according to the explained variance. The component(s) explaining the highest variance during the artifactual interval is assumed to be mainly related to the artifact event. They will be stored in the component list with the label MVTPCA. We recommend using the module 'Subtract Components' that will subtract all the components identified with a specific label.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

Extract: MVTPCA serves as a label of identification to recognize extracted PCA components in the subtract or export function.

Figure: yes no display figure output

Percentage minimal noisy channel to be a new component: Consider this event to extract components if they have at least 5% of noisy channel for this time window.

Components to remove up to XX% of the variance in the data: Find number of components to identify as an artifact, one or more, in order to explain up to 97% of the variance in the data.

Minimal percentage of variance to explain XX%: to be rejected in the up to 97% the component must explain at least XX% of the variance.

Identify PARAFAC for artifact period

Description: First, identify noisy intervals. This function runs a PARAFAC⁷ decomposition on each pre-identified bad interval (yellow segment in the DisplayGUI). The decomposition is performed on the noisy channel during this interval as a Target PARAFAC. The decomposition explaining the most of variance in the data will save as the one representing the artifact will be stored in the component list with the label MVTPARAFAC. The component list is stored in 'SelectedFactors.mat' in the same folder as the NIRS.mat. You could visualize them in the DisplayGUI before subtracting them. We recommend using the module 'Subtract Components' that will subtract all the components identified with the same label.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

Extract: MVTPARAFAC serves as a label of identification to recognize extracted PARAFAC components in the subtract or export function.

Figure: yes no display figure output

Percentage minimal noisy channel to be a new component: Consider this event to extract components if they have at least 5% of noisy channel for this time window.

Nb component to try: Find the optimal number of components using highest Concordia and lowest residual error. Try components from one to the user's defined number of components to optimise Concordia and error. The wavelength and time course help to find the component to be removed when the distance between wavelengths is lower than the average distance

- a. Reject highest time course than the average time course

⁷ Andersson, C.A., Bro, R., 2000. The N-way Toolbox for MATLAB. Chemometrics and Intelligent Laboratory Systems 52, 1–4. [https://doi.org/10.1016/S0169-7439\(00\)00071-X](https://doi.org/10.1016/S0169-7439(00)00071-X)

Physiology regression

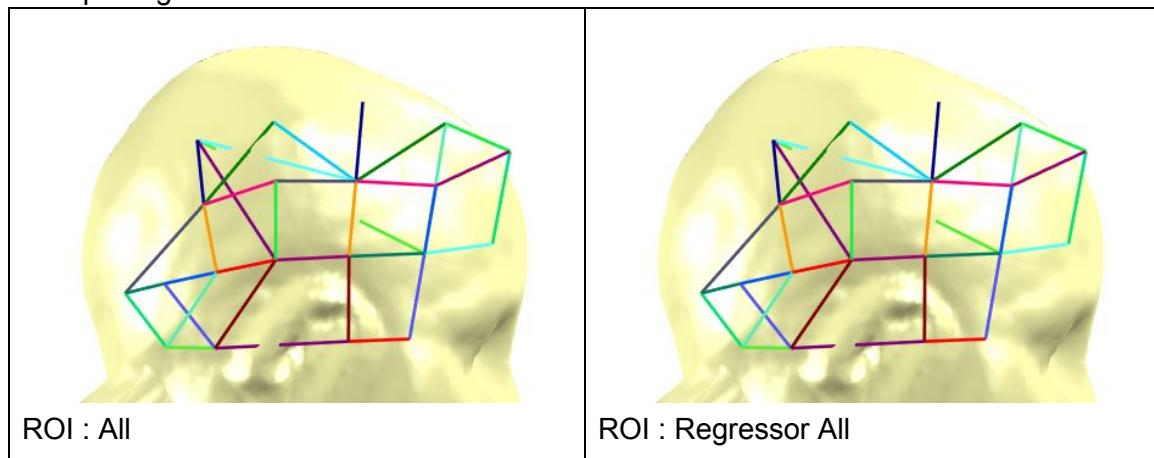
Description: Apply short distance physiology regression as described in Saager and Berger 2008 [https://doi.org/10.1117/1.2940587](https://doi.org/10.1111/1.2940587). The short distance channel is scaled to fit the other using least square estimation. Use a zone definition such as Regressor zone1 will be applied on zone1. When you use NIRx short distance channel, a zone is created by default when you read the data for the first time and contain the SD channel and the closest channel association. The zone is in the data folder under the name 'SHORTDISTANCE.zone'. It is possible to use all short distances and get the principal component or the mean to be used in the regression. Components will be identified as **GLMSHORT**. You could visualize them in the DisplayGUI before subtracting them. We recommend using the module 'Subtract Components' that will subtract all the components identified with the same label **GLMSHORT**.

Inputs:

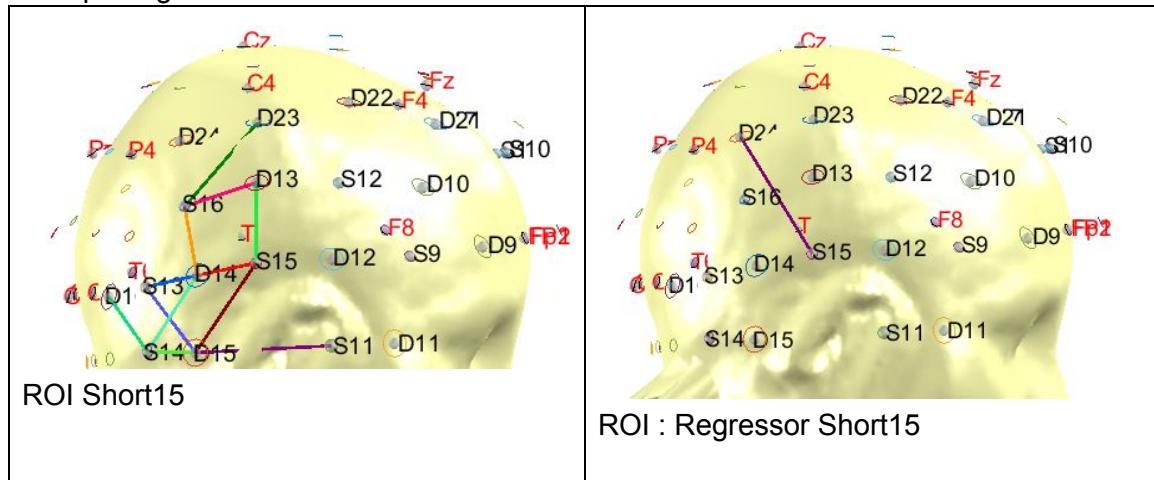
Select .nirs locate .nirs file to open.

Enter Regressor zone : enter a zone containing the channel used as regressor (short distance channel or larger area)

Example regressor Global.zone

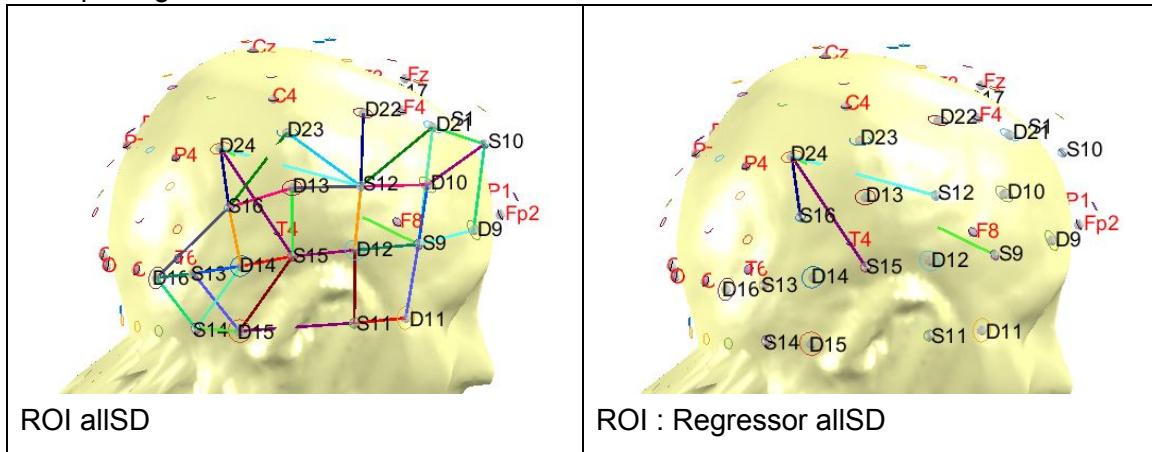


Example regressor SHORTDISTANCE.zone



(integrate NIRx short distance probe integrates a detector in the source probe) These short distance channels are virtually recorded as the last detector in the acquisition system detector 24 here. Be careful to use them as a rejected channel for the topography.

Example regressor AllShortDistance.zone



(NIRx short distance probe integrates a detector in the source probe) This short distance channel is virtually recorded as the last detector in the acquisition system detector 24 here. All Short distances are regrouped as one zone.

Use: PCA or mean if many channels identify as regressor use the first PCA of them as regressor or the mean.

GLM (General linear model)

General linear models use a [Multiple linear regression](#) with one or many regressors. It is written under the form $y = Xb + e$, where y is the vector data to model, X are the explanatory variables, b is the estimation and e the error. Regressor X has to be defined among the auxiliar or the data using a zone definition to model short distance channel as an example. This function uses a list of intervals and a regressor in the data to estimate the model. If we are inspired from fMRI literature, the model hemodynamic response function could be convolved to our paradigm [Glover et al] to create your auxiliary data. The model could include the physiological measurement such as additional short distance measurements or a combination of all of them. The component list is stored in 'SelectedFactors.mat' in the same folder as the NIRS.mat. You could visualize them in the DisplayGUI.

Create an excel file that contains all these columns of information, please use the column label as described above.

Input columns:

NIRS.mat folder (location of the data file, usually after preprocessing and transfer in hemodynamic concentration.)

File NIRS.mat could have many file sessions after segmentation. You have to identify which file session you want to use for the estimation by writing the number.

tStart Time start to define the beginning of the period where the GLM will be applied

tStop Time stop to define the end of the period where the GLM will be applied

Label Label identification to write in the event (useful to manage the export)

X0 first regressor 1

X1 second regressor

X.. add as many regressors as you want, up to 100.

NIRS.mat folder	File	tStart	tStop	label	X0
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	1	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	2	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	3	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	4	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	5	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	6	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	7	5	40	HRFSymbol	C28_HRFSymbole
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	8	5	40	HRFSentence	C28_HRFsentence
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	9	5	40	HRFSentence	C28_HRFsentence
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	10	5	40	HRFSentence	C28_HRFsentence
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	11	5	40	HRFSentence	C28_HRFsentence
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	12	5	40	HRFSentence	C28_HRFsentence
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	13	5	40	HRFSentence	C28_HRFsentence
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	14	5	40	HRFSentence	C28_HRFsentence

Regressor could be

1. AUX

Use the label name as written in the auxiliary identification.

2. Zone

In case you want to use a channel in the data as regressor, for example a short distance channel to model the physiology effect, you must define regressor as a zone of channels. Indicate as Xn regressor the full directory of the zone file C:\data\Tutorial4_Semantique\Analyse\C28b\Global.zone or ensure the zone files are in the same folder of the extract xls files.

The label of the zone indicates which one is the regressor and on which channel it will be applied. As an example:

Zone label	Use as
regressor zone1	Regressor channel
zone1	The channel for which the regressor is apply

3. Global average

In case you want to apply global average as regressor:

Zone label	Use as
regressor global	Select all channels. The mean of all channels will be used as regressor.
global	Select against all channels this regressor will be applied on all channels.

Average

Description: Identify the average time window for each channel, in the selected window.

Input columns:

NIRS.mat folder: Directory to locate the data to extract.

File: 1 : block in the NIRS.mat data file

tStart: to get the curve start point

tStop: to get the curve stop point

tStartavg: to get the average starting point

tStopavg: to get the average stopping point

Label: Write label in the component name

ZoneDisplay: use the first zone channel to plot the average. Keep the zone file in the same folder as the excel ExtractAVG setting.

	File	Conc	Trig	tstart	tstop	tstartavg	tstopavg	Label	ZoneDisplay
1	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	1 HbO		10	10	54	15	25 M001p01p	Wer
2	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	2 HbO		10	10	54	15	25 M001p02p	Wer
3	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	3 HbO		10	10	54	15	25 M001p03p	Wer
5	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	4 HbO		10	10	54	15	25 M001p04p	Wer
6	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	5 HbO		10	10	54	15	25 M001p05p	Wer
7	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	6 HbO		10	10	54	15	25 M001p06p	Wer
8	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	7 HbO		10	10	54	15	25 M001p07p	Wer
9	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	8 HbO		10	10	54	15	25 M001p08p	Wer
10	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	9 HbO		10	10	54	15	25 M001p09p	Wer
11	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	10 HbO		10	10	54	15	25 M001p10p	Wer
12	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	11 HbO		10	10	54	15	25 M001p11p	Wer
13	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	12 HbO		10	10	54	15	25 M001p12p	Wer
14	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	13 HbO		10	10	54	15	25 M001p13p	Wer
15	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	14 HbO		10	10	54	15	25 M001p14p	Wer
16	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	15 HbO		10	10	54	15	25 M001p15p	Wer
17	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	16 HbO		10	10	54	15	25 M001p16p	Wer
18	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	17 HbO		10	10	54	15	25 M001p17p	Wer
19	C:\data\NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	18 HbO		10	10	54	15	25 M001p18p	Wer

Parafac

Description: Create an excel file that contains all these columns of information, please use the column label as described above.

Input columns:

NIRS.mat folder: location of the data file, usually after preprocessing and transfer in hemodynamic concentration.

File: NIRS.mat could have many file sessions after segmentation. You have to identify which session file you want to use for the estimation by writing the number.

tStart: Time start to define the beginning of the period where the GLM will be applies

tStop: Time stop to define the end of the period where the GLM will be applied.

Label: Label identification to write in the event (useful manage the export)

Export component list

Description: This module helps to export component extract from the NIRS.mat data for further statistique. The export will be organized using the channel list order. Each subject must have a close localization on the head to be compared. Enter the list to export columns such as : 'NIRS.mat folder', 'Type' (GLM, PARAFAC,PCA), 'Label' , Component name to filter, 'Channel List' full file or .txt same folder as xls file' and 'Name' use as the output name of the export .

Input columns: Create a list in an excel file to identify the component you want to export as follow:

NIRS.mat folder: Indicated the step where the component is extracted in the GUI or using the extract function. It should contain the NIRS.mat and the SelectedFactors.mat structure.

Type: Indicated the type of component to extract: GLM, PARAFAC, AVG.

Label: Name to filter among the list of components.

Channel list: Order of the channels to export. The first list will be used as a reference if you want to open on and helmet to visualize the topography. Copy the 'Channel list' at the same location of the excel file.

See Channel list for more explanation.

Name: output name of the export.

Remove index:

You could exclude some component for the average topographic visualization mean. (D1 matrix) by writing down the number of the event to exclude. Look at the figure using the plot browser option to know which index you want to exclude.

A	B	C	D	E
NIRS.mat folder	Type	Label	Channel list	Name
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	GLM	Sentence	C28achannellist.txt	GLMC28
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	AVG	Sentence	C28achannellist.txt	AVGC28
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	PARAFAC	Sentence	C28achannellist.txt	PARAFACC28
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	GLM	Symbole	C28achannellist.txt	GLMC28
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	AVG	Symbole	C28achannellist.txt	AVGC28
C:\data\Tutorial4_Semantique\Analyse\C28a\AutoCorrect\dCONC	PARAFAC	Symbole	C28achannellist.txt	PARAFACC28

Output: Value by channel or zone will be saved in a .mat structure by component at the same location of the export.xls files.

Each component channel intensity are save as mat file:

D1matrixHbOSentenceAVG008.mat

D1matrixHbRSentenceAVG008.mat

It creates an average of each row that could be opened in as a topographic with the name: HBOmeanAVGC28.mat

Use the montage of corresponding to the channel list to visualize the Channel project on a topographic view.

An Excel file with each component will also be saved. Each subject mean.

They will be saved in the same location of the xls file.

Export component zone

Description: This module helps to export components extracted from the NIRS.mat data for further statistics. The export will be organized in the zone list order. Each subject must have a close localization on the head to be compared.

Input:

Enter list of component to export (xls): Enter the list to export in columns such as: 'NIRS.mat folder', 'Type' (GLM, PARAFAC, PCA), 'Label', Component name to filter, 'Zone List' full file or .txt in the same folder as the xls file.

1	NIRS.mat folder	Type	Label	Zone list
2	C:\data\Tutorial4_Semantique\Analyse\C28\AutoCorrect\dCONC	GLM	SentenceGLMC28	RegionInteret.zone
3	C:\data\Tutorial4_Semantique\Analyse\C28\AutoCorrect\dCONC	GLM	SymbolGLMC28	RegionInteret.zone

Identification zone to extract:

Enter zone to extract: Identify the label to identify the zones to export, separate different labels using a comma, for example zone1, zone2, zone3.

Enter .txt to list zone to extract: Use a text file to identify the zones to export

Output:

zoneExport.xlsx:

	A	B	C	D	E
1	Zone	FusiformLeft	FusiformRight	TempPostLeft	TempPostRight
2	SentenceGLMC28_HRFsentence C28_HRFsentence043	0.66	0.42	0.08	0.17
3	SentenceGLMC28_HRFsentence C28_HRFsentence045	0.35	0.11	-0.25	-0.26
4	SentenceGLMC28_HRFsentence C28_HRFsentence047	0.38	0.36	0.51	0.19
5	SentenceGLMC28_HRFsentence C28_HRFsentence049	0.35	0.48	-0.06	0.25
6	SentenceGLMC28_HRFsentence C28_HRFsentence051	0.30	0.32	0.44	0.15
7	SentenceGLMC28_HRFsentence C28_HRFsentence053	0.19	0.07	0.17	-0.20
8	SentenceGLMC28_HRFsentence C28_HRFsentence055	0.45	0.51	0.05	0.48

Subtract component

Description: Subtract the component with the name that corresponds to the name entry.

The component will be subtracted in the data and saved in the correction list.

Component identification: Label to filter among all components the ones to subtract.

Offset correction: Add an offset

Stats components

Description: Applies basic statistics on exported components. Three statistical tests are available: One sample t-test, Unpaired t-test, and Anovan. The first step is to choose which test you want to perform. More explanations on each option are presented below.

One sample t-test

Description: Apply a one-sample t-test on the selected component, apply the tests for each channel. Use the false discovery rate method to apply a correction for multiple comparisons.

Input: Open components exported using the export list function, ensure the same channel list has been used compared to the homologous channel on the head.

Result folder: Define where to save the result.

Use: 2 tails, 1 tail negative value, or 1 tail positive value

Output: Results are saved in the same folder using a default name. You could move them into a meaningful place.

ONESAMPLE_mean001fdr: Average value mask using only significant channels, using false discovery rate correction for multiple comparisons using a threshold of $q < 0.001$.

ONESAMPLE_mean001unc: Average value mask using only significant channels, using sample t-test threshold of $p < 0.001$ uncorrected for multiple comparisons.

ONESAMPLE_mean01fdr: $q < 0.01$

ONESAMPLE_mean01unc: $p < 0.01$

ONESAMPLE_mean05fdr: $q < 0.05$

ONESAMPLE_mean05unc: $p < 0.05$

ONESAMPLE_Mean: average value without any masking.

ONESAMPLE_Tmap: T value without any masking.

Unpaired t-test

Description: Apply a unpaired t-test between 2 groups of data.

Inputs:

Group 1 (component export): Identify exported components from group 1.

Group 2 (component export): Identify exported components from group 2.

Use: 2 tails, 1 tail negative value, 1 tail positive value

Result folder: define where to save the result.

Output: Results are saved in the same folder using a default name. You could move them into a meaningful place.

TWOSAMPLE_mean001fdr: average value mask using only significant channels, using false discovery rate correction for multiple comparisons using a threshold of $q < 0.001$.

TWOSAMPLE_mean001unc: average value mask using only significant channels, using sample t-test threshold of $p < 0.001$ uncorrected for multiple comparisons.

TWOSAMPLE_mean01fdr: $q < 0.01$

TWOSAMPLE_mean01unc: $p < 0.01$

TWOSAMPLE_mean05fdr: $q < 0.05$

TWOSAMPLE_mean05unc: $p < 0.05$

TWOSAMPLE_Mean: average value without any masking.

TWOSAMPLE_Tmap: T value without any masking.

ANOVAN

Description: N-way analysis of variance, the anova could be perform by channel (channelist) or by zone

Group definition: in a xlsx file or a tab space delimited .txt file, define the following column:

Dir: folder where are the exported component use as observation

Observation: file name of the export component

Zone or channelist:

Zone: if you use zone you must define a specific zone in the adjacent column.

Use a label that exists in your zone definition. The mean of that zone will be used for the calcul.

Channelist: if you use channelist define a channel list text file.

Group definition: use text label to define at which group belong each observation

If you use zones, you have to define a meaningful label to ROI to be compared.

If you use channelist, you only need to define groups for each channel.

Result folder: define where to save the result.

Output: p value anova, in the subfolder the full stat.

Connectivity

Connectivity matrix using channel list as seed

Description: Create a connectivity matrix using channels as node information or zones as node information.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

Node List: Nodes could be defined by a region of interest (zones) or each channel. Technical note, to allow subject comparison to ensure channels or zones spatial localization analogous.

List of channels as nodes: List channels to be used as a node using a text file, one node per line, example: F a1b2; To create automatically this list use the module ‘Utility/Create channel list’.

List of zones as nodes: Use a zone structure that identifies channels belonging to a region of interest. This structure could be created and saved in the DisplayGUI

Connectivity to use: Cross-correlation analysis, Hilbert joint phase probability or Coherence, detailed below.

Cross-correlation analysis

Cross-correlation analysis has been used in fMRI to describe connectivity between regions^{8 9 10}. For a fNIRS time course $Fx(k)$ and a seed $Fy(k)$. Cross-correlation analysis estimates the correlation coefficient at lag u .

$$\text{Corr}_{x,y}(\mu) = \frac{\text{Cov}_{x,y}(\mu)}{\sqrt{\text{Var}(x) \times \text{Var}(y)}}$$

where $\text{Var}(x)$ and $\text{Var}(y)$ are the variances of $Fx(k)$ and $Fy(k)$, respectively; $\text{Cov } x,y(u)$ is the cross variance of $Fx(k)$ and $Fy(k)$ at zero lag μ . $\text{Cov } x,y(\mu) = E \{ ((Fx(k)-E(Fx)) \times (Fy(k)-E(Fy))) \}$ and E means the expected value, and $E(Fx)$ and $E(Fy)$ are the expectation or the mean of $Fx(k)$ and $Fy(k)$, respectively.

Fortunately, the hemodynamic response of blood makes full-lag-space calculation of cross-correlation unnecessary and most of the studies compute only the correlation with zero lag. This method computed at lag zero is equivalent to Pearson's linear correlation coefficient, the most commonly used linear correlation coefficient. Values of the correlation coefficient can range from -1 to +1. A value of -1 indicates a perfect negative correlation, while a value of +1 indicates a perfect positive correlation. A value of 0 indicates no correlation between channel x and y. They have two implementations, the one who uses the user segmentation files or the random circular bootstrap over a long segment to compute the cross-correlation analysis.

Inputs: filtered signal

Segment

Circular bootstrap

⁸ Cao, J., Worsley, K., 1999. The Geometry of Correlation Fields with an Application to Functional Connectivity of the Brain. *The Annals of Applied Probability* 9, 1021–1057.

⁹ Bellec, P., Rosa-Neto, P., Lyttelton, O.C., Benali, H., Evans, A.C., 2010. Multi-level bootstrap analysis of stable clusters in resting-state fMRI. *NeuroImage* 51, 1126–1139.

<https://doi.org/10.1016/j.neuroimage.2010.02.082>

¹⁰ Li, K., Guo, L., Nie, J., Li, G., Liu, T., 2009. Review of methods for functional brain connectivity detection using fMRI. *Comput Med Imaging Graph* 33, 131–139.

<https://doi.org/10.1016/j.compmedimag.2008.10.011>

Trial length (s): The length of the segment will define which frequency can be computed, a short segment doesn't allow to identify slow frequency associated with hemodynamic response. The whole length of the segment needs to be artifact-free to be considered if it contains noise the segment will be rejected.

Number of random samples: Defines the number of randomly selected segments to extract from the whole bloc. Coherency will be computed as explained above using FFT of all the segments randomly defined and the segments marked as artifacts will be excluded. Use a circular bootstrap to obtain a stable measure of the coherence among the data sample.

Z-score outlier control: additional quality criteria, reject segments when the estimated value is an outlier regarding z-score segments distribution.

Hilbert joint phase probability

In order to determine the phase relation between channels, we extract the phase of the signal in each channel using the Hilbert transform¹¹. The joint probability distribution of the phases across channels to describe their connectivity. A common model for probability distribution of phase which is the circular analog of the Gaussian distribution is the Von Mises distribution use the external toolbox circstat 2012a¹². The signals were first filtered to extract spontaneous hemodynamic activities and reject other interferences. They have two implementations, the one who uses the user segmentation files or the random circular bootstrap over a long segment.

Inputs: filtered signal

Segment

Circular bootstrap

Trial length (s): The length of the segment will define which frequency can be computed, a short segment doesn't allow to identify slow frequency associated with hemodynamic response. The whole length of the segment needs to be artifact-free to be considered if it contains noise the segment will be rejected.

Number of random samples: Defines the number of randomly selected segments to extract from the whole bloc. Coherency will be computed as explained above using FFT of all the segments randomly defined and the segments marked as artifacts will be excluded. Use a circular bootstrap to obtain a stable measure of the coherence among the data sample.

Z-score outlier control: additional quality criteria, reject segments when the estimate value is an outlier regarding z-score segments distribution.

¹¹ Molavi, B., May, L., Gervain, J., Carreiras, M., Werker, J.F., Dumont, G.A., 2014. Analyzing the resting state functional connectivity in the human language system using near infrared spectroscopy. *Front Hum Neurosci* 7. <https://doi.org/10.3389/fnhum.2013.00921>

¹² P. Berens, CircStat: A Matlab Toolbox for Circular Statistics, *Journal of Statistical Software*, Volume 31, Issue 10, 2009

<http://www.jstatsoft.org/v31/i10>

Coherence

Coherence is a statistic representing the relationship between two signals and is also an extension of correlation to the frequency domain (Kida, 2016)¹³. Coherence is known as magnitude squared coherence is defined as the complex conjugate product of the Fourier transforms data $X(f)^* Y^* T(f)$. $x(t)$ and $y(t)$ are two time series, $G_{xy}(f)$ is the cross-spectral density between x and y , and $G_{xx}(f)$ and $G_{yy}(f)$ are the auto spectral densities of x and y , respectively. Cross-spectra density (CSD) is calculated in the frequency domain as:

$$C_{xy}(f) = \frac{|G_{xy}(f)|^2}{G_{xx}(f) G_{yy}(f)}$$

The coherence is implemented to use on one long continuous segment of the recording. In case you record multiple sessions, you may join them using the concatenate module. A large number of segments (*Number of random samples*) of a specific duration (*Length of the segment*) will be picked randomly (circular bootstrap). Any segments that belong to a specific¹⁴ artifact period will be excluded from the coherence calculation. The recording will be randomly segmented to calculate coherence based on many segments. An FFT is computed on each random segment and the coherence is measured based on the specified frequency range (*The frequency range to obtain Cxy(f)*) to obtain a connectivity matrix representative of the whole recording.

Inputs: unfiltered signal (FFT)

Frequency range to obtain Cxy(f): The average value of this spectrum window is used to compute the coherency.

Zone to display spectrum: Insert a zone to plot FFT over a region of interest

Trial length (s): The length of the segment will define which frequency can be computed, a short segment doesn't allow to identify slow frequency associated with hemodynamic response. The whole length of the segment needs to be artifact-free to be considered if it contains noise the segment will be rejected.

Number of random samples: Defines the number of randomly selected segments to extract from the whole bloc. Coherency will be computed as explained above using FFT of all the segments randomly defined and the segments marked as artifacts will be excluded. Use a circular bootstrap to obtain a stable measure of the coherence among the data sample.

Z-score outlier control: Additional quality criteria, reject segments when FFT power is an outlier regarding z-score distribution of other segments.

Path connectivity matrix: Output location

File name: Define the prefix of the output file

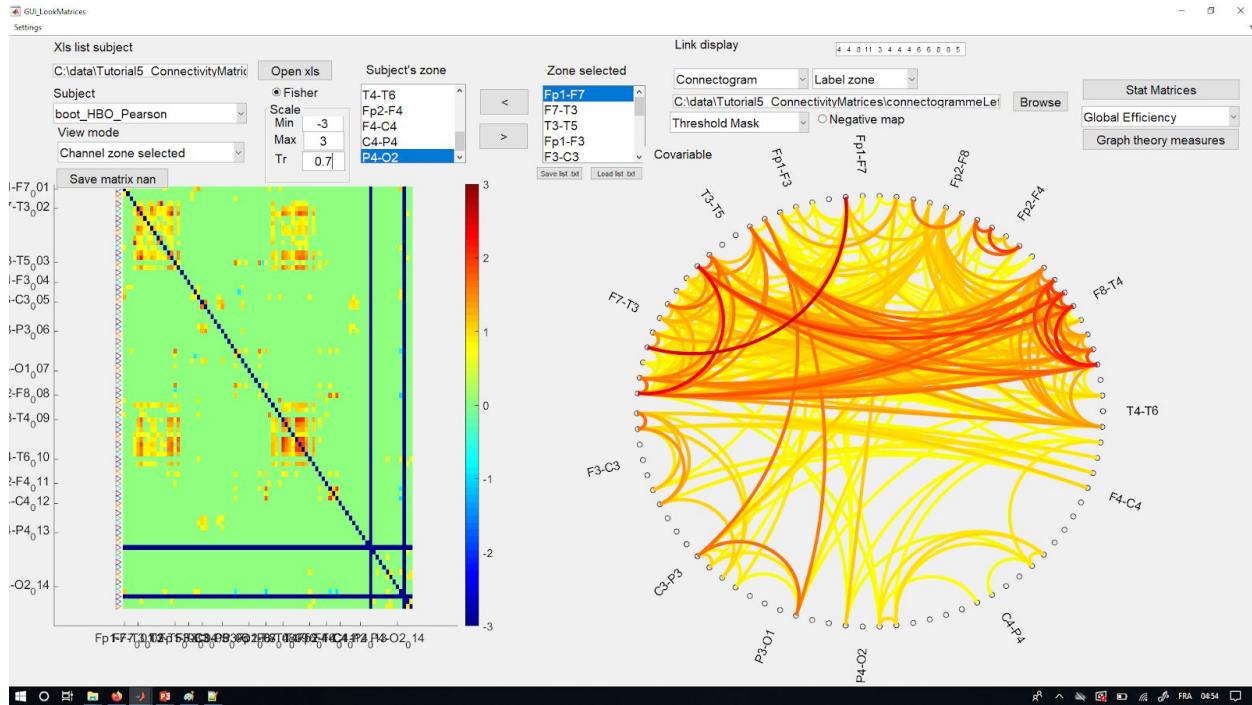
Output: Coherence matrix file for HbO and HbR

¹³ Kida, T., Tanaka, E., Kakigi, R., 2016. Multi-Dimensional Dynamics of Human Electromagnetic Brain Activity. *Front. Hum. Neurosci.* 9. <https://doi.org/10.3389/fnhum.2015.00713>

¹⁴ Politis, Dimitris Nicolas and Joseph P. Romano. "A circular block-resampling procedure for stationary data." (1992).

GUI_Lookmatrices

The interactive GUI is designed to ease the individual visualization or statistical measure of connectivity using a matrix or connectogram representation. The matrix or connectogram visualization is organized in function of the zone (channel gathered by regions of interest).



Function overview

Open xls: Select the file to localize the matrices to visualize on your computer.

You need to identify a column for : ‘the directory’, ‘the name of the connectivity matrix’, ‘the zone file’ (.zone file needs to be placed in the same directory of the connectivity matrix), ‘the groups’ to compute a first average on the data and finally one or many additional columns to be use as covariable for the statistical analysis in an xls file that you will open. The group must be defined by a positive integer. The format could be an xlsx file or a text file using a tab space delimitation.

Dir	subjectfile	zonefile	Groupe
C:\data\NIRS\BebeResting\connectivity\MAT_COH_dCONC1COH03to08	nana_C07JB_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\NIRS\BebeResting\connectivity\MAT_COH_dCONC1COH03to08	nana_C09AC_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\NIRS\BebeResting\connectivity\MAT_COH_dCONC1COH03to08	nana_C10MB_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\NIRS\BebeResting\connectivity\MAT_COH_dCONC1COH03to08	nana_C11LC_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\NIRS\BebeResting\connectivity\MAT_COH_dCONC1COH03to08	nana_C12AD_4m_001_HBO_COHFFT	ByDetector.zone	1

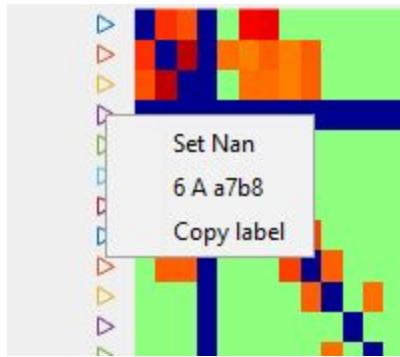
NB: Add the matrix .mat and .zone in the same directory.

You could add another column if you want to add a covariable or a regressor. The covariable must be an integer value to be considered, else it will be considered as a missing value.

Subject list: Scroll in the subject list to visualize a subject.

View mode: Visualized each channel as a node of the average of a region of interest.

Save matrix nan: You could exclude channels using right-click on the small arrow on the left side of the matrix and mark as NAN. Once you complete your selection use the button Save Matrix a copy of the original matrix with the prefix 'nan' will be created. Use this new version of the matrix to exclude channels in statistical analysis, those channels will be treated as a missing value. Create a new subject list using the nan file instead of the original one.



Fisher transform: Apply the fisher transform on the matrices prior visualization.

$$\frac{1}{2} \ln\left(\frac{1 + \rho}{1 - \rho}\right)$$

Scale colorbar: Adjust intensity for colormap visualization

Min: Minimal value for the colorbar

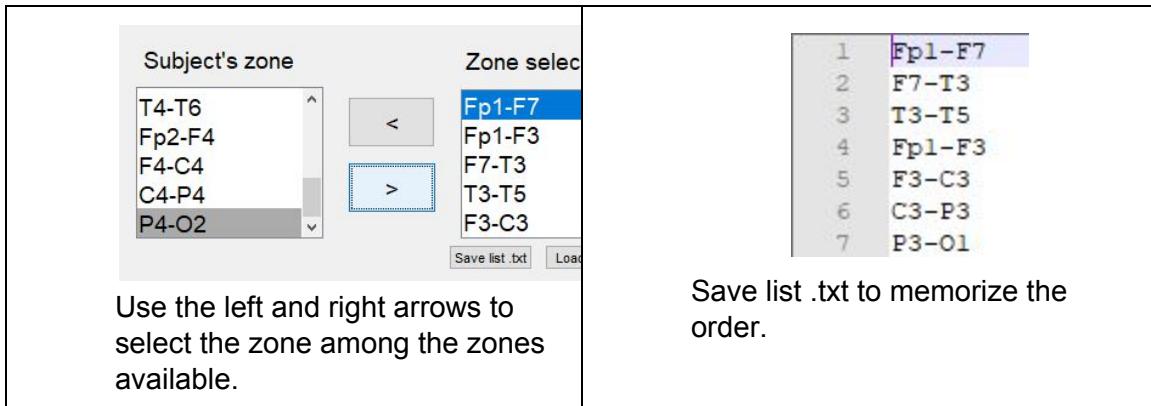
Max: Maximal value for the colorbar

Tr: adjust threshold to display only value superior or inferior to this threshold on the matrices. Display only values superior to this threshold on the connectogram (use negative map to inverse the view).

Zone selected: use the left and right arrow to select the zone in the subject's zone list to visualize on the connectivity matrices:

Save list .txt: Save in a text file the order to use to display region of interest in a specific order.

Open list .txt: Open a text file with the associate name of region of interest to display the matrices using a specific order.



Link display: Select link to display

Nothing: Do not display the link, it eases the matrix visualization speed.

Connectogram: Display the connectogram link¹⁵.

Label: Select label to display

Zone: use zone name as label

Channel: use channel name as label

Color scale: Select the color scale to display the connectivity link.

Colormap (jet): use heatmap identical as the matrix display

Colormap (jet), mask by zone: use a heatmap identical as the matrix display but use the user defined mask in the zone list.

RGB color, mask by zone: use user define color to display threshold link, plot only the region with a valid RGB definition, use mask to define the region to hide in the zone list definition.

Black: use black color for all threshold link

Open zone list: use the same txt file but to fix the order of the connectogram. The connectogram will display zones using a counter clock order, starting the zone from the left middle of part of the circle.

Example of zone list without color mask

¹⁵ Inspired from circularGraph version 2.0.0.0 (828 KB) by [Paul Kassebaum](https://github.com/paul-kassebaum/mathworks/circularGraph)
<https://github.com/paul-kassebaum/mathworks/circularGraph>

connectogrammeLeftRight.txt

```

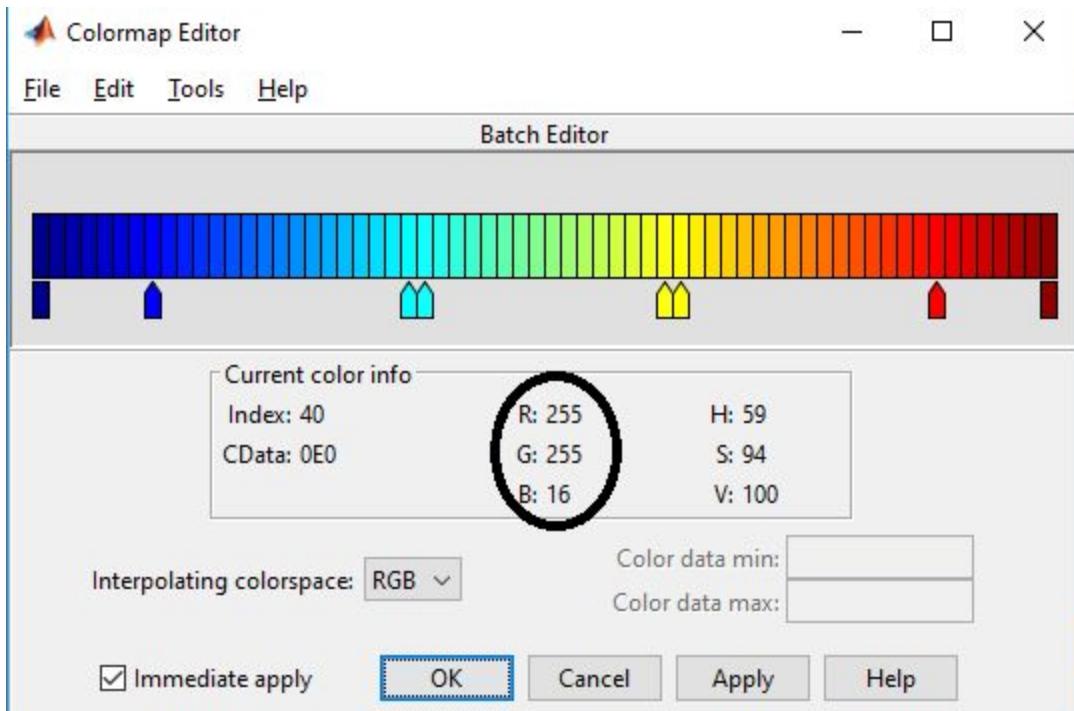
1 F3-C3
2 C3-P3
3 P3-O1
4 P4-O2
5 C4-P4
6 F4-C4
7 T4-T6
8 F8-T4
9 Fp2-F4
10 Fp2-F8
11 Fp1-F7
12 Fp1-F3
13 T3-T5
14 F7-T3

```

Example of zone list with color mask (matrix zone x zone define the RGB color or the region to mask)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1		F3-C3	C3-P3	P3-O1	P4-O2	C4-P4	F4-C4	T4-T6	F8-T4	Fp2-F4	Fp2-F8	Fp1-F7	Fp1-F3	T3-T5	F7-T3
2	F3-C3	0,255,255	mask	0,255,243	0,255,243										
3	C3-P3	0,255,250	mask	0,255,244	0,255,244										
4	P3-O1	mask	0,255,245	0,255,245											
5	P4-O2	mask	0,255,246	0,255,246											
6	C4-P4	mask	0,255,247	0,255,247											
7	F4-C4	mask	0,255,248	0,255,248											
8	T4-T6	mask	0,255,249	0,255,249											
9	F8-T4	mask	0,255,250	0,255,250											
10	Fp2-F4	mask	0,255,251	0,255,251											
11	Fp2-F8	mask	0,255,252	0,255,252											
12	Fp1-F7	mask	0,255,253	0,255,253											
13	Fp1-F3	mask	0,255,254	0,255,254											
14	T3-T5	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255
15	F7-T3	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255	0,255,255

The ‘colormapeditor’ may help you to define RGB color code



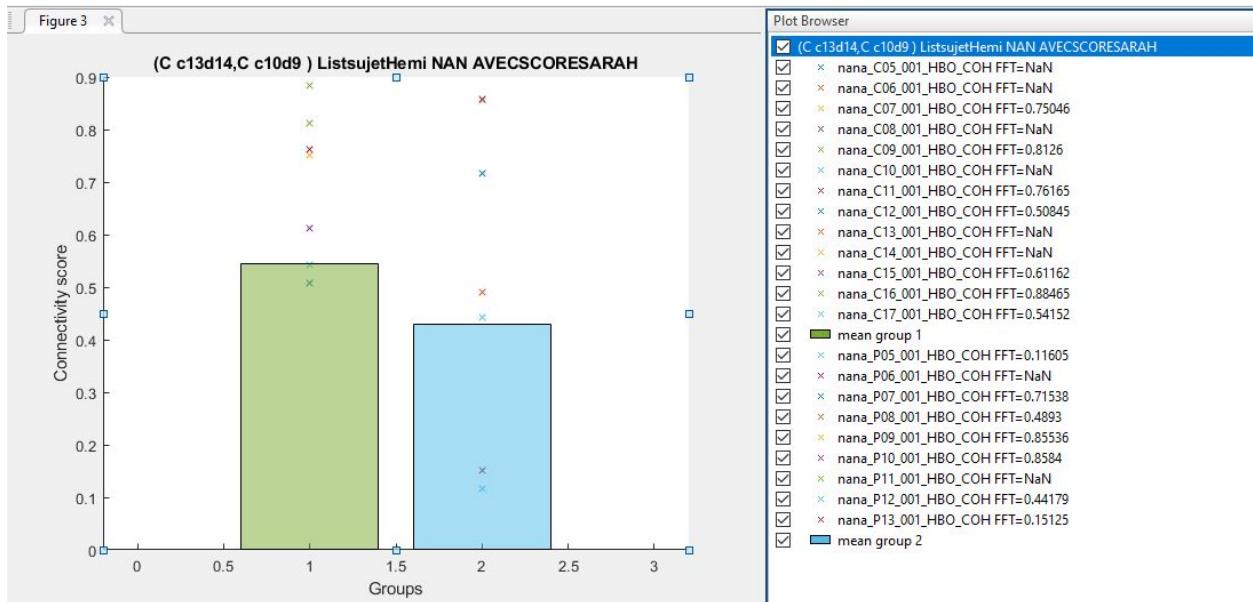
Negative map: Display value lower than zero.

Covariable: optional if you use additional covariable add extra column in your excel used to identify subjects (see open excel). The first row of this new column will be used to identify the covariable. Use the right-click on a connectogram link to plot the connectivity score in function of a covariable value.

Right-click on a connectogram link:

(i,j)=(1,3)=(A a1b2, A a3b4): identification of the link location, the position 1,3 is the position on the matrix record position (channel list order used for the matrix creation at the step Connectivity matrix using channel list as seed).

Groups histogram: display a bar histogram of the average link of each group, each subject is represented to help to visualize the data distribution.



Covariable: display connectivity score in function of the selected covariable.

Right-click on a connectogram:

Make a new figure so that a normal Matlab figure is created and allows manual edition of the connectogram using the plot browser.

Stats Matrices

The connectivity matrix has been computed each node of the matrix has connectivity value.

Enter list connectivity matrix: Enter a .xsl list of connectivity to test statistically.

Fisher transform: Yes/No, Use the fisher transform $1/2 \ln((1+p)/(1-p))$, when the transformation is applied to the sample correlation coefficient, the sampling distribution of the resulting variable is approximately normal, with a variance that is stable over different values of the underlying true correlation.

Nodes: Apply the statistic on each node. Define nodes as each channel or each average of zone channels.

Choose the statistical test: Select one of the two options detailed below.

One sample t-test

Description: Apply a one sample t-test to see if the group average is different from zero.

Group identification: use an integer to identify the subject belonging to the first group.

Unpaired permutation test

Description: This operation could be done at the channel level or the zone level. It performs permutation based on student statistic¹⁶, it produces as output a xls list of the resulting matrices : t value and p value based on permutation computation. It excludes nan value from the statistical analysis.

Nb permutation: Number of permutations to use to estimate the null distribution using randomization of both statistical groups.

Group identification: use an integer to identify the subject belonging to the first group.

Group 2 identification: use an integer to identify the subject belonging to the second group.

Dir	Subject file	Zone file	Group
C:\data\Tutorial5_ConnectivityMatrices\Analyse\Matconnectivity\	boot_HBO_Pearson	1020.zone	1
C:\data\Tutorial5_ConnectivityMatrices\Analyse\Matconnectivity\	boot_HBO_Hilbert	1020.zone	1
C:\data\Tutorial5_ConnectivityMatrices\Analyse\Matconnectivity\	boot_HBO_COH FFT	1020.zone	1
C:\data\Tutorial5_ConnectivityMatrices\Analyse\Matconnectivity\	boot_HBR_Pearson	1020.zone	2
C:\data\Tutorial5_ConnectivityMatrices\Analyse\Matconnectivity\	boot_HBR_Hilbert	1020.zone	2
C:\data\Tutorial5_ConnectivityMatrices\Analyse\Matconnectivity\	boot_HBR_COH FFT	1020.zone	2

¹⁶ Galán, L., Biscay, R., Rodríguez, J.L., Pérez-Abalo, M.C., Rodríguez, R., 1997. Testing topographic differences between event related brain potentials by using non-parametric combinations of permutation tests. *Electroencephalography and Clinical Neurophysiology* 102, 240–247. [https://doi.org/10.1016/S0013-4694\(96\)95155-3](https://doi.org/10.1016/S0013-4694(96)95155-3)

Utility NIRS.mat

Operation to adjust NIRS.mat structure.

Folder adjustment

Description: This function is used to modify the root folder of a subject analysis when the NIRS.mat file has been moved on a computer. In general, we recommend keeping the analysis at the same place to avoid confusion. The NIRS.mat structure contains the information about intermediary data analysis saved. However, if you disorganize the root analysis folder, this dependency will be lost, keep the subject as a whole folder and avoid renaming branch subfolder. This function replaces the root directory for the NIRS.mat new location. It is recommended to put all AUX and EEG files in the same folder. If the directory changes, you will have to indicate the new location. It is possible to edit the new location used when you open the file in the DisplayGUI.

Inputs:

NIRS.mat: Select NIRS.mat file that has been moved to adjust dependency

Multimodal dir: New folder used for multimodal files EEG, AUX, Video, Audio. If the location of the multimodal files has changed, enter the new directory location. This function expects all the multimodal files in the same folder. For a more specific adjustment use the DisplayGUI menu Setting/Multimodal files to define a new location.

New branch

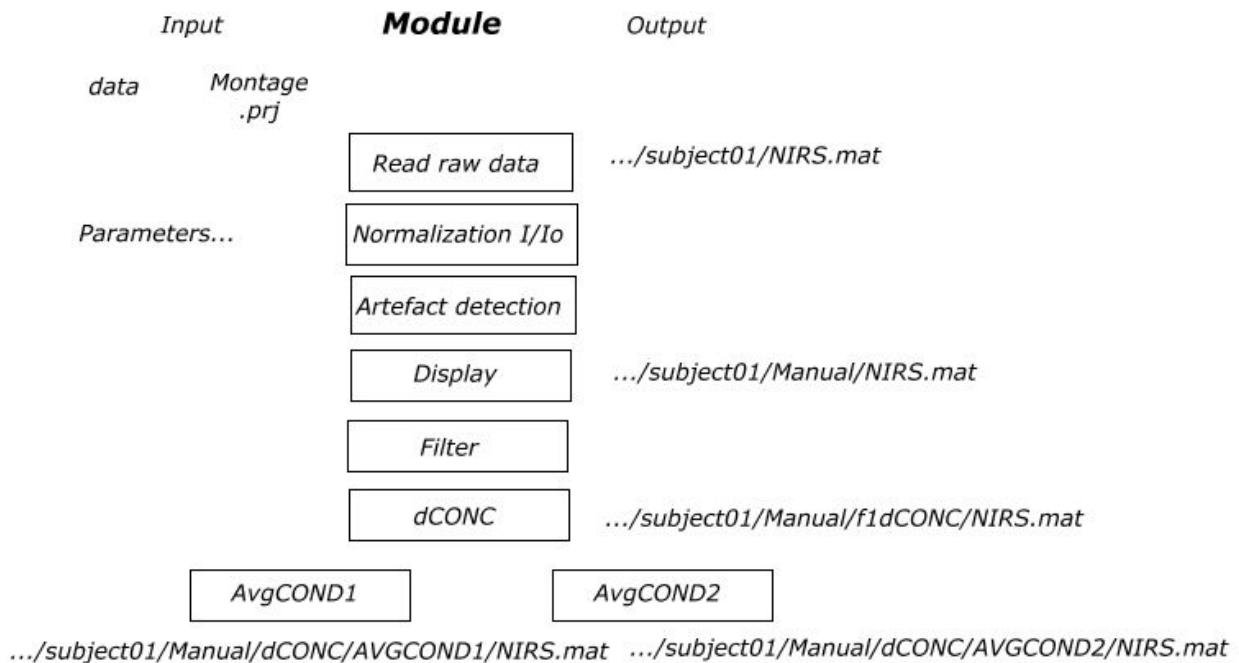
Description : This function is used to create a subfolder and copy NIRS.mat structure. It allows the creation of a parallel branch of analysis.

Inputs:

NIRS.mat: Select NIRS.mat file to be copied in the new branch.

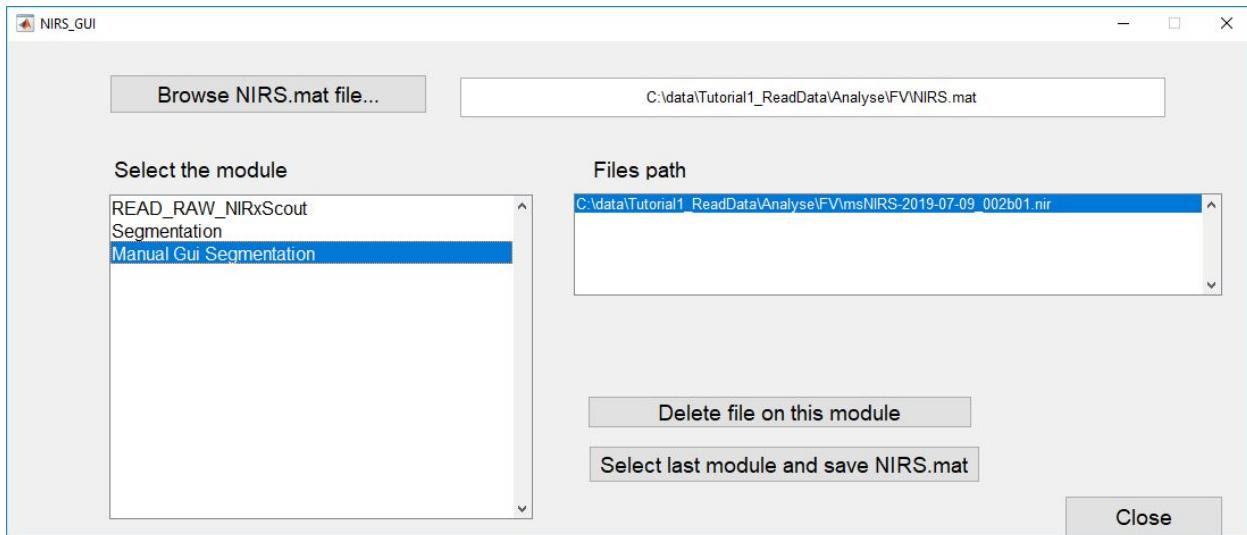
Create a new branch of analysis in the subfolder: indicate the name of the subfolder.

Components and corrections: Keep or clean components and correction.



Display NIRSmat

Open the NIRS.mat structure to see the list of operations performed and data file actual location. All the operations (module) are listed above the selected module.



Delete file on this module: Similar to the function in each module 'Delete Previous .nir data files' used to delete intermediate files (.nir, .vhdr, .vmrk).

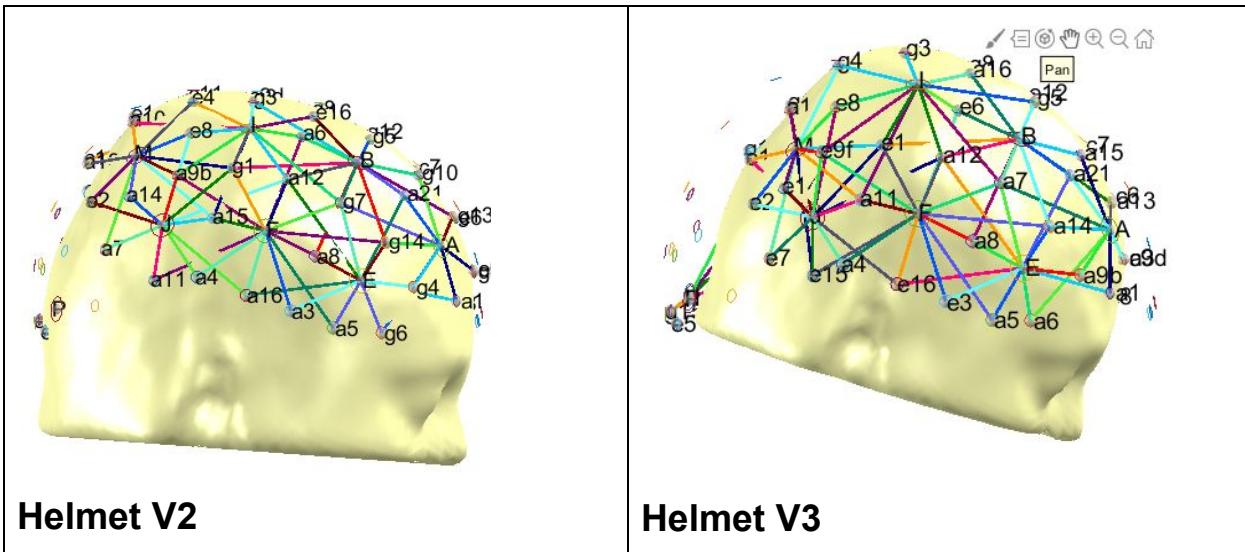
Select the last module and save NIRS.mat: Help to delete modules you run by mistake. Use this function carefully.

Create channel list (seed list)

Description: Indicate NIRS.mat structure to create a list of all channels in this subject. This file lists the channel name (or nodes) that will be used to calculate the connectivity or to group subjects and ensure analog channels. To group connectivity matrices between multiple subjects at the channel level, you have to ensure that the seed list is comparable (as an example: channel line 51 subject 1 is ordered on the same location in the scalp than channel line 51 subject 2, this condition is easy to achieve in identical montage, but could need some modifications if you change the sources or detectors position). When they could not be compared you will need to use the zone. If you have little modifications on one helmet, it is possible to adjust the list by identifying the good source or detector manually for one subject, but ensure line 1 of the seed list file is the same localization on the helmet for all subjects before you combine them for a group average.

<table border="1"><tbody><tr><td>1</td><td>A</td><td>a1b2</td></tr><tr><td>2</td><td>A</td><td>a3b4</td></tr><tr><td>3</td><td>E</td><td>a5b6</td></tr><tr><td>4</td><td>B</td><td>a7b8</td></tr><tr><td>5</td><td>E</td><td>a7b8</td></tr><tr><td>6</td><td>F</td><td>a7b8</td></tr><tr><td>7</td><td>A</td><td>a9b10</td></tr><tr><td>8</td><td>E</td><td>a9b10</td></tr><tr><td>9</td><td>F</td><td>a11b12</td></tr><tr><td>10</td><td>J</td><td>a11b12</td></tr><tr><td>11</td><td>A</td><td>a13b14</td></tr><tr><td>12</td><td>A</td><td>a15b16</td></tr></tbody></table>	1	A	a1b2	2	A	a3b4	3	E	a5b6	4	B	a7b8	5	E	a7b8	6	F	a7b8	7	A	a9b10	8	E	a9b10	9	F	a11b12	10	J	a11b12	11	A	a13b14	12	A	a15b16	Example of channel list using ISS label.	<table border="1"><tbody><tr><td>1</td><td>D01</td><td>E1</td></tr><tr><td>2</td><td>D02</td><td>E1</td></tr><tr><td>3</td><td>D03</td><td>E1</td></tr><tr><td>4</td><td>D07</td><td>E1</td></tr><tr><td>5</td><td>D02</td><td>E2</td></tr><tr><td>6</td><td>D04</td><td>E2</td></tr><tr><td>7</td><td>D02</td><td>E3</td></tr><tr><td>8</td><td>D03</td><td>E3</td></tr><tr><td>9</td><td>D04</td><td>E3</td></tr><tr><td>10</td><td>D05</td><td>E3</td></tr><tr><td>11</td><td>D01</td><td>E4</td></tr><tr><td>12</td><td>D03</td><td>E4</td></tr></tbody></table>	1	D01	E1	2	D02	E1	3	D03	E1	4	D07	E1	5	D02	E2	6	D04	E2	7	D02	E3	8	D03	E3	9	D04	E3	10	D05	E3	11	D01	E4	12	D03	E4	Example of channel list using NIRx label
1	A	a1b2																																																																									
2	A	a3b4																																																																									
3	E	a5b6																																																																									
4	B	a7b8																																																																									
5	E	a7b8																																																																									
6	F	a7b8																																																																									
7	A	a9b10																																																																									
8	E	a9b10																																																																									
9	F	a11b12																																																																									
10	J	a11b12																																																																									
11	A	a13b14																																																																									
12	A	a15b16																																																																									
1	D01	E1																																																																									
2	D02	E1																																																																									
3	D03	E1																																																																									
4	D07	E1																																																																									
5	D02	E2																																																																									
6	D04	E2																																																																									
7	D02	E3																																																																									
8	D03	E3																																																																									
9	D04	E3																																																																									
10	D05	E3																																																																									
11	D01	E4																																																																									
12	D03	E4																																																																									

Tip: Adjust channel list when some sources change during experiment. The easiest is to keep the same montage for the whole experiment but in some cases, modifications have been made for technical reasons during the experiment. A fixed optode localization is necessary to group subjects, the channel list helps to reorganize this tricky condition. The row order will be used as a reference. Ensure row line one on the channel list montage V2 have a localization comparable to row line one on the channel list montage V3, they will be used as the same optode for the average. Adjust the list to keep a consistent localization of the channels is essential, the row number will be used as the new reference to allow the average subject. We do not recommend modifying montage during the experiment.



Modify source in montage V2 g6h5 -> a6b5 to keep the sample order of channel and localization in the version V3. Use transfert source to list all changes to execute.

M03YPchannellist_V2.xlsx			Transfertsource.xlsx	M03YPchannellist_V3.xlsx
1	A	a1b2	V2	V3
2	E	a1b2	e3f4	a3b4
3	E	a3b4	g13h14	a13b14
4	F	a3b4	g10h9	a15b16
5	E	a5b6	e16f15	a16b15
6	F	a5b6	e4f3	g4h3
7	J	a7b8	a13b14	e13f14
8	M	a7b8	a6b5	e6f5
9	P	a7b8	a14f13	e14f13
10	F	a9b10	g4h3	a9b8
11	I	a9b10	g14h13	a14b13

See source a3b4 has been changed by e3f4
A9b10 has been changed by e9f10 to fit the new montage organization. The order (line row) of each optodes localization is identical for both montages.

```

[num,txt,raw] =xlsread('M03YPchannellist_V2.xlsx')
[num,txt,change] =xlsread('transfertsource.xlsx')
new = raw
for i =2: size(change,1)
    tf = find(strcmp(change(i,1),raw(:,2)))
    new(tf,2) = change(i,2)
End
Copy new to obtain file
M03YPchannellist_V3.txt

```

Data quality report

Description: Export a summary of the rejection and correction apply for the NIRS.mat structure.

Inputs:

NIRS.mat: open one or many NIRS.mat for the quality reports.

Result folder: define where to save the result.

Output: *QualityReport.xlsx*

	A	B	C	D	E	F	G	H
1	NIRS.mat	File	Duration (s)	Ratio time rejected/time total	Nb independent intervals rejected	Ratio time corrected/time total	Nb independant intervals corrected	Maximal duration interval corrected (s)
2	COHr\NIRS.mat	Cinc4_C05_001	696	32%	5	3%	3	17.8
3	COHr\NIRS.mat	Cinc4_C06_001	1741	9%	26	4%	12	11.9
4	COHr\NIRS.mat	Cinc4_C07_001	1044	14%	6	1%	1	6.8
5	COHr\NIRS.mat	Cinc4_C08_001	1444	28%	5	1%	2	9.3
6	COHr\NIRS.mat	Cinc4_C09_001	1037	16%	6	0%	0	0.0
7	COHr\NIRS.mat	Cinc4_C10_001	1444	27%	8	4%	8	19.1
8	COHr\NIRS.mat	Cinc4_C11_001	722	2%	2	4%	7	6.0
9	COHr\NIRS.mat	Cinc4_C12_001	722	3%	3	4%	4	13.4

NIRS.mat: Data structure used for the report.

File: Segment where the correction has been applied.

Duration: total length of the file segment in seconds.

Ratio time rejected/time total: percentage of time rejected (marked in yellow)

Nb independent intervals rejected: number of separate intervals rejected.

Ratio time corrected/time total: percentage of time where a PCA or a PARAFAC correction has been applied.

Nb independent intervals corrected: count the number of intervals where a correction is applied, if one or two PARAFAC corrections apply to the same interval they will be found only as one interval because they are part of the same artifactual event.

Maximal duration of the correction: among the corrections apply find the longest one.

Transfert Zone to channel list

Description: small utility to list the channels included in each region of interest (zone).

Input: fichername.zone created using the DisplayGUI.

Output: fichername.txt will be created in the same folder of the fichername.zone with the label of the zone, the RGB color identification (example 255 0 0 = red, 0 0 255 = blue, tip, use the colormap tool to find the RGB color) and finally the list of detector and source identification D07 E1 one channel by row.

Example:

Label: prefrontal_G

RGBcolor : 0 0 0

D07 E8

D02 E8

D07 E1

Label: frontal_G

RGBcolor: 0 0 0

D01 E4

D03 E4

D01 E1

D03 E1

Transfert channel list to zone list

Description: Use channel label to create a zone list

Input: Channel label text file description, NIRS.mat to be associated.

Output: Create a zone list with the description in the NIRS.mat folder associate to the subject.

Write external file

Write NIRS

Description: Export the

Inputs:

Session: Enter the session number or the module in the processing NIRS file.

NIRS.mat: Select NIRS.mat for the subject.

Options:

Separate file: Export each segment in a separated .nirs file. The output file is located in the same folder of the NIRS.mat file.

Concatenate file: Export each segment in one .nirs file with all segments one after the other.

File output: Output name, only use to name concatenate file

Write HMR

Description: Write in NIRS.mat epoch average session in session for Homer .hrm. This function will use the last epoch averaging file in the .nirs file. It will cause an error if there is any epoch averaging in the NIRS.mat session.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

File output: Output name, only used to name concatenate file. Ise initial name will be kept.

Helmet .prj: Select project of the montage HSJ for the subjects.

Write SNIRF

This toolbox enables you to export your data as SNIRF V1.10-compliant files. A description of this format is available [here](#).

Write to a newly created or to an already existing .snirf file.

Write the data of multiple subjects to the same file or multiple files.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

Choose SNIRF export type:

Create a new SNIRF file: Export the data to a new SNIRF file.

Output filename: Used to name the resulting output SNIRF file.

Folder path for output SNIRF: The path of the folder in which the file is going to be created.

Append to an existing SNIRF file: To append the data to an existing file.

Select existing SNIRF file: Select the SNIRF file to which to want to append the data.

Write NIR individual file segment

Description: Use a nir file to write a smaller segment, can be used to specify only the baseline for the PCA artifact for example.

Inputs:

NIRS.mat: Select NIRS.mat for the subject.

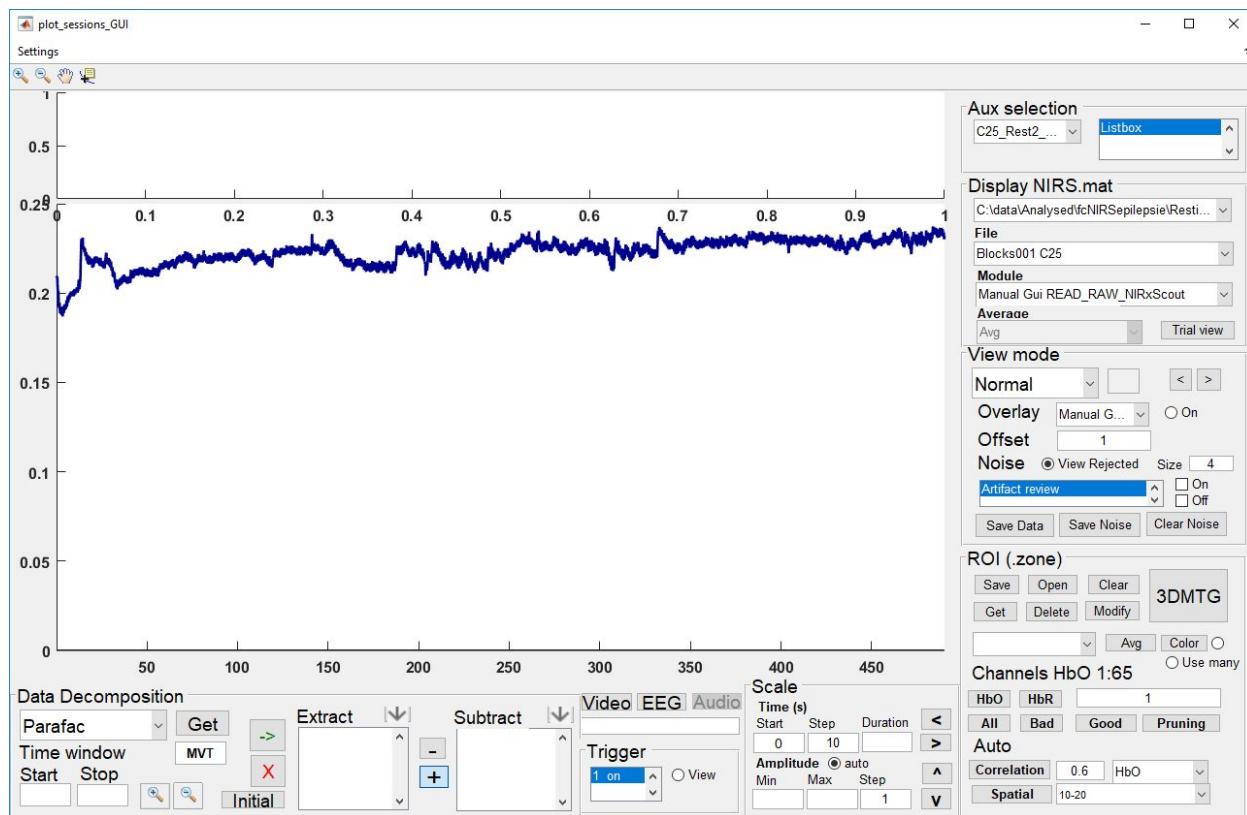
Enter .NIR to segment: Select a .NIR file to extract a smaller time segment and create a new .NIR file.

Time start: Time start selection

Time stop: Time end of the selection

DisplayGUI

Description: This function opens the NIRS.mat structure for visualization from any step of the analysis, as well as optional multimodal data. It opens this interface to display the data with many visual features. Only the last open module could be edited for manual artifact adjustments. The top panel displays the auxiliary channel and the bottom larger panel shows the fNIRS data channels. The right and bottom control are used to visualize and review the data.



AUX selection

Select the auxiliary channel to display. Multiple AUX files are accessed using the left selection tool. The one on the right shows each auxiliary channel available. Right-click to used the following options:

Select: View this channel.

Unselect: Mask this channel

Copy label: The label should be identified with the exact auxiliary name to be used in GLM regression.

Display NIRS.mat

Indicate the path of the NIRS.mat folder used to visualize the data. If you move your data analyzed folder you will need to perform a folder adjustment to be able to see the file correctly. See the annexe 'NIRS.mat structure' for a detailed description of the fields.

Files

The data can have one or many segments separated as separated files on your hard drive. As an example, if an experiment has 10 blocks of repetitions that have been recorded in a separate folder, you could segment these blocks to average them. You can select which 'blocks' you will be able to visualize.

Modules

Module or step of operation. Each step applied to the data is visible in the module list. However, if you Delete Previous .nir data files, they could not be read anymore. We recommend to delete most of the intermediate files except if you need them for verification.

Average

Only available on the epoch averaging module, allows to visualize standard deviation. T value against zero.

View mode

View options

Normal: Stack view on concentration, exact value of the data for the selected channels.

Spread : View selected channel but add and offset between each of them to show a spread view.

Normal 2 wavelengths: Stack view but show the first wavelength in full line and the second wavelength in dotted (HbO HbR in hemodynamic concentration after MBLL have been apply)

Spread 2 wavelengths : Adjust the offset of the second wavelength to see the curve superimposed.

Zone list: spread the view between each zone. You must enter the zone number to display more than one at the same time. Use the left and right arrows to navigate from a zone to another.

Overlay

Select a previous module you want to overlay to the current data. Select the option 'on' on the right to overlay the data from this module. They will be presented in a dotted line. The overlay is available only for the normal mode view.

Noise

On the manual module, you can edit ‘manually noise’ its mean channel or part of the signal that will be identified as a bad interval.

View rejected: When selected view rejected channel is dotted. Unselect to hide them.

Size: All noise marked periods are overlaid to the data in yellow, you could adjust the marker size of this overlay.

Save data: Save data modifications .

Save Noise: Save artifacts marks.

Clear Noise: Remove artifacts for the whole time window.

Right-click on the fNIRS window

Time start: indicate the time start for the interval to define

Time stop: indicate the time stop for the interval to define

New figure: Take the data out of the GUI to be a normal Matlab figure, easier for the edition using the plot browser.

Remove all selected channels interval (shortcut key ‘y’) : Set all selected channels as an artifact (in yellow); or use the shortcut key (y). This will affect all selected channels for the interval defined by time start and time stop.

Restore all selected channels interval (shortcut key ‘u’) : Restore all selected channels interval; or use the shortcut key ‘u’. This will affect all selected channels for the interval defined by time start and time stop.

Clear all artifacts (shortcut key ‘c’): Restore all marked artifacts for the whole file for all selected channels.

New trig: insert a new trig at the cursor position.

Right-click a specific channel in the fNIRS window

Unselect: Remove this specific channel from the current channel selection. The channel will not be rejected.

Remove selected interval : Set this specific channel interval as an artifact, artifact periode are displayed using a yellow overlay.

Restore selected interval: Restore this specific channel interval.

Remove the entire channel: Remove this specific channel. View rejected channel is selected in the DisplayGUI and in the 3dMTG this channel will appear in a dotted line. The topographic projection excludes the reject channels.

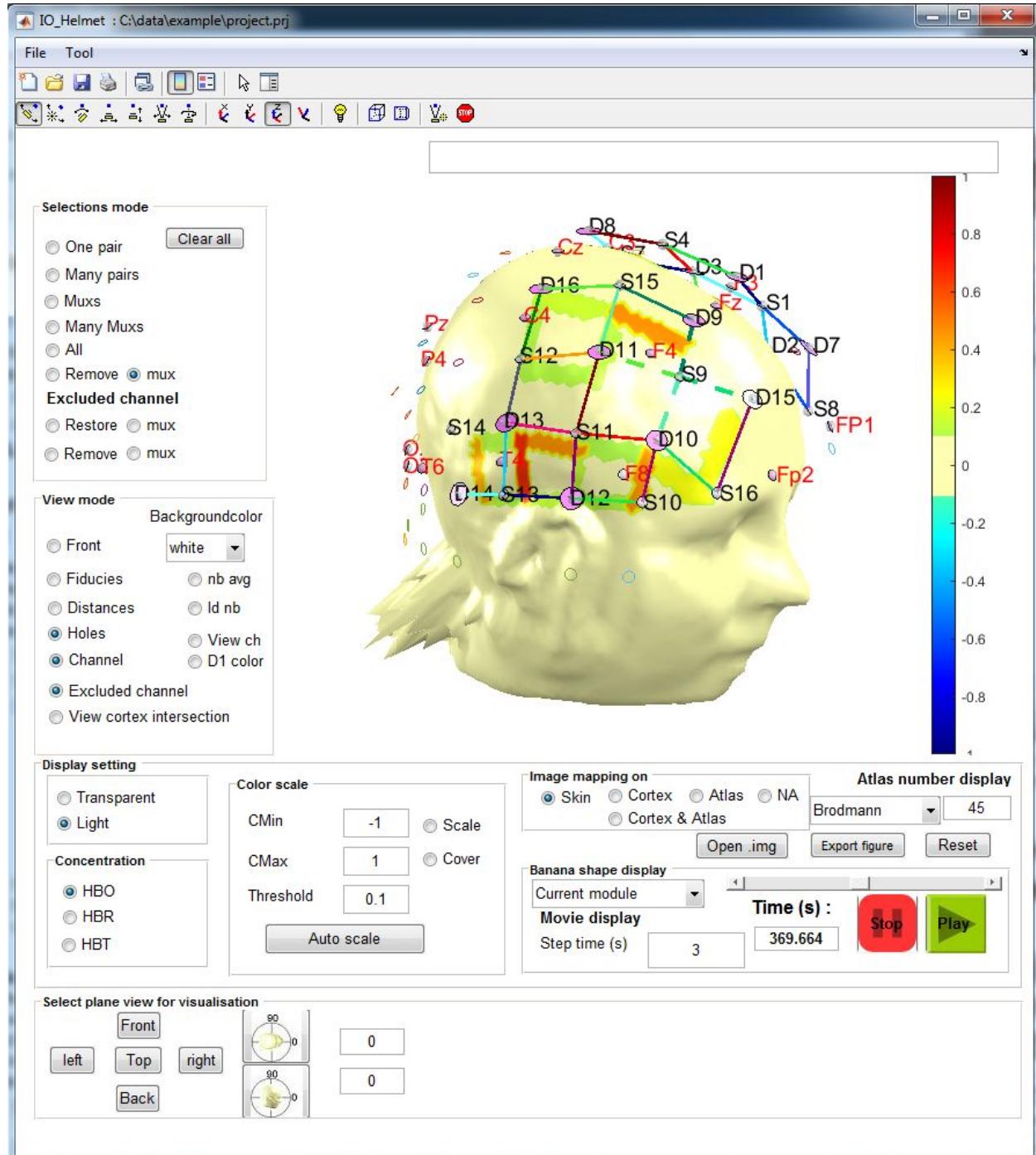
Restore the entire channel: Restore this specific channel.

chXX_Exx_Dxx: Help to identify this selected channel, it indicates the channel position in the data as well as the associate emitter and detector on the cap.

Copy data to clipboard: Copy the selected channel data to the clipboard (time amplitude) you could paste this data in the Matlab workspace or another program.

3dMTG (Topographic projection)

The 3dMTG button opens the 3dMTG interface to enable data visualization and channel selection.



Function overview

Camera control

The topo GUI uses the stock Matlab 3D camera manipulation graphical user interface. Please refer to the Matlab documentation.

Channel selection

The selection mode panel provides tools to choose which channels will be rendered in the plot_session_GUI. Here are the available tools:

One pair: Only one source-detector pair is selected (only one channel). Left-click a source then a detector or the inverse to select a pair.

Many pairs: The selected source-detector pair is added to the current selection (add one channel).

Muxs: Select a source or a detector and select all adjacent channels (a “mux”). Left-click a source or a detector to select a mux.

Many muxs: Add the selected mux to the current selection.

All: Select all channels.

Remove: Remove a channel from the current selection.

Remove mux: Remove a mux from the current selection.

Clear all: Unselect all channels.

Channel rejection is used when it is not desired in the rendering but still needs to be kept for some purposes. They will be rendered as dotted lines if the relevant view mode option is enabled. To reject data, here are the available tools:

Remove (channel rejected): Reject the selected channel.

Remove mux (channel rejected): Reject the selected mux.

Restore: Return the selected channel to the regular current selection.

Restore mux: Restore the selected mux.

View mode

The view mode panel provides rendering options for the view. Here are the options:

Holes: Display the holes and their labels.

Channels: Display the channels as colored lines.

View rejected: Display the excluded channels as dotted lines.

Labels: Select to display the required label.

Amplitude: Display the channel topographic amplitude.

Distances: Display the channel lengths.

ID number: Display the channel id numbers.

Nb avg: Display the number of observations for the average. This option is only accessible in the context that you displayed epoch average data.

Color: Select the display color of the channels. The choices are default randomized colors, black and heatmap color where the color of the channels will reflect their value according to the defined color gradient.

Rotation angle: Rotation view angle of the head, 0=front view, 90 = left view, 180=back view, -90 or 270 = right view.

Elevation angle: Elevation view angle of the head, 0= nose level, 90=top level.

Front: Front head view

Left: Left head view

Top: Top head view

Right: Right head view

Back: Back head view

Topography

Current module: Use the data in the DisplayGUI for the visualization. Enter the time in the time option.

Mean start stop time: Show mean amplitude in the current module data between time start and time stop definition.

Projection channel: Select exported topography.

PARAFAC: Show current PARAFAC spatial decomposition.

PCA: Show current PCA spatial decomposition.

GLM: Show current GLM spatial decomposition.

Component: Display current selected component.

New figure: Create a new figure with the topography.

Reset

Concentration (dCONC): Select which concentration data is going to be used to render the map between HBO, HBR and HBT.

Scale (colormap): Colormap scales are by default centered to zero. Select the scale to adjust the range from minimal value to maximal value without centered scale to zero.

Min: Enter minimal value of the color scale.

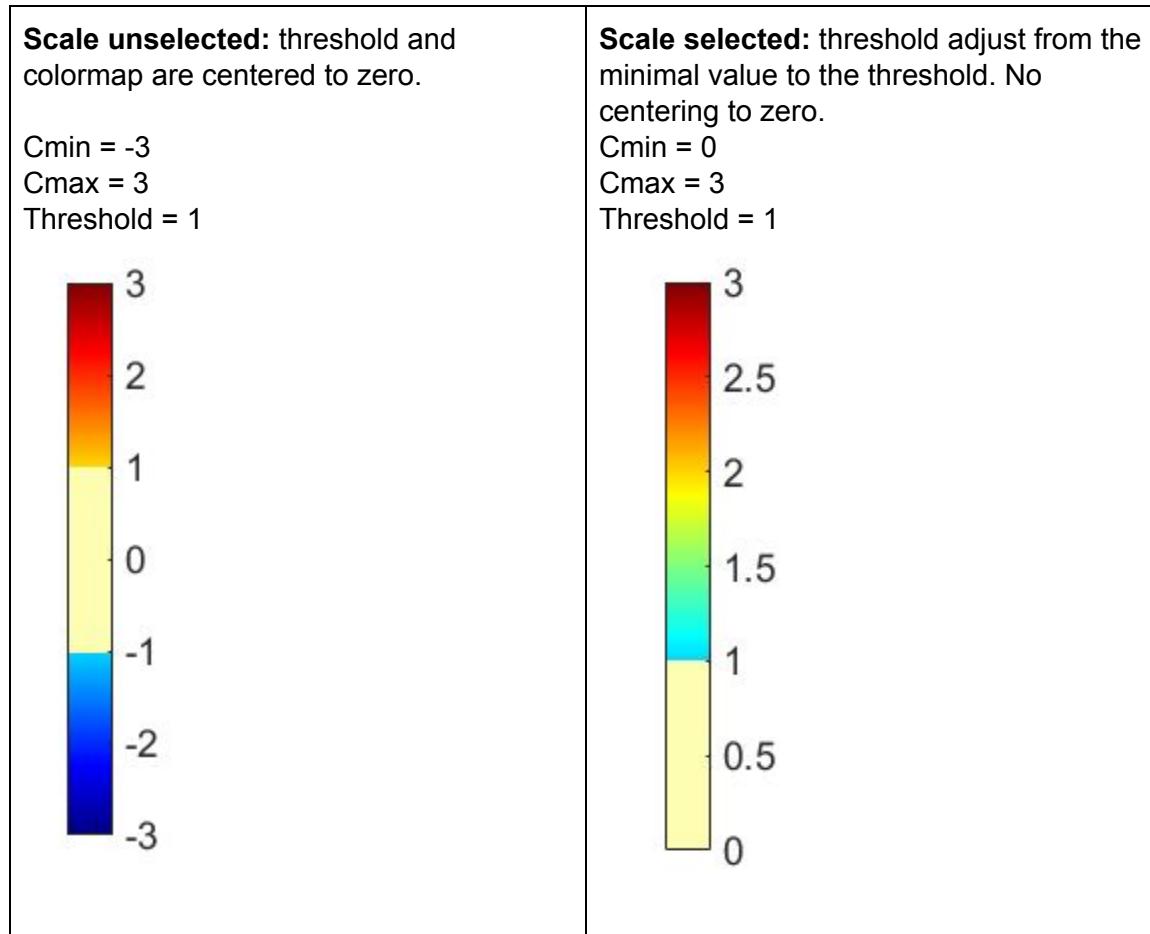
Max: Enter maximal value of the color scale.

Threshold: Enter threshold value of the color scale.

Scale: By default threshold is used to remove mask value close to zero amplitude.

Unselected: use a map to show a blue scale for negative value and a red scale for positive value, the threshold will be in absolute value close to zero to show positive or negative value.

Select: use map from the min value to the maximum value. The threshold will be adjusted from the minimum value



Cover: help to know how the head is covered, set in grey when any channel is available to be projected.

Auto: use auto to adjust range scale to the maximal intensity in the data

Anatomical surface:

Skin: display skin surface

Cortex: display cortex surface

Atlas: display atlas cortex surface use the atlas identification you use to identify atlas area associated identification label by clicking on the surface.

Atlas116: use label associate to AAL116 area¹⁷

Brodmann: use label associate to Brodmann area

Use the number associated with a region to display specific regions in color.

Time option (s): Time option to current module display time in second unit.

- **Start time:** Time to display in second
- **Step time:** step time for video increment

¹⁷ Tzourio-Mazoyer N., et al., "Automated anatomical labeling of activations in SPM using a macroscopic anatomical parcellation of the MNI MRI single-subject brain," *NeuroImage* 15, 273–289 (2002). 10.1006/nimg.2001.0978 [PubMed] [CrossRef] [Google Scholar]

- **Play:** Play current module video.
- **Stop:** Stop current module video.
- **Transparent:** Enable transparency of the 3D model.
- **Light:** Enable the light source visual effect of the 3D model. It highlights the reliefs of the 3D model at the cost of a more computationally intensive rendering.
- **Color scale panel:** The size of the color gradient is determined using the *CMin* and *CMax* textboxes and the zero threshold can be set using the *Threshold* textbox. The scale can be automatically adjusted using the *Auto scale* button.
- **Image mapping on:** Select what kind of 3D model will be used for rendering. The choices are: *Skin*, *Cortex*, *Atlas*, *Cortex & Atlas* and no 3D model (*NA*).
- **Projection display:** This panel enables you to select a module and customise its playback. You can set the step size in seconds using the *Step time (s)* textbox, see the current timestamp and jump to a specific time using the *Time (s)* textbox, move forward or backward in time using the slider and initiate or pause the playback using the green *Play* and red *Pause* buttons respectively.

Select plane view for visualization

This panel enables you to quickly select a camera orientation using the *Front*, *Top*, *Back*, etc. buttons and to precisely set the angle of the camera using the angle selection textboxes. The images next to the textboxes are useful references to determine the influence of each parameter. Also, you can see the file that is used to render the current projection in the *Current projection file* textbox.

Region of interest definition *ROI.zone*

Select the channel to form the region of interest (.zone). This region could be used for data decomposition, statistical analysis or connectivity operation.

- ROI Corr (select channel based on the correlation between channel)
- Attribute 10-20 ROI.

OVERLAY of the decomposition adjust offset

Data decomposition

Data decomposition methods and general linear model regression have proven to be a great help to separate components from multiple sources such as movement artifacts, physiological artifacts, or brain activity. The component spatial coefficient could be visualized on the topography using 3D helmet.

1. Set start and stop time
2. Select specific channels for the decomposition
3. Select the method. See below for a more detailed explanation on each method
 - a. Parafac
 - b. PCA
 - c. GLM
 - d. Offset Adjustment

e. Component

4. Review the list. Two lists of components are used to keep track of the change and the identification. The list of corrections (components subtract from the original data) and the list of components identified.

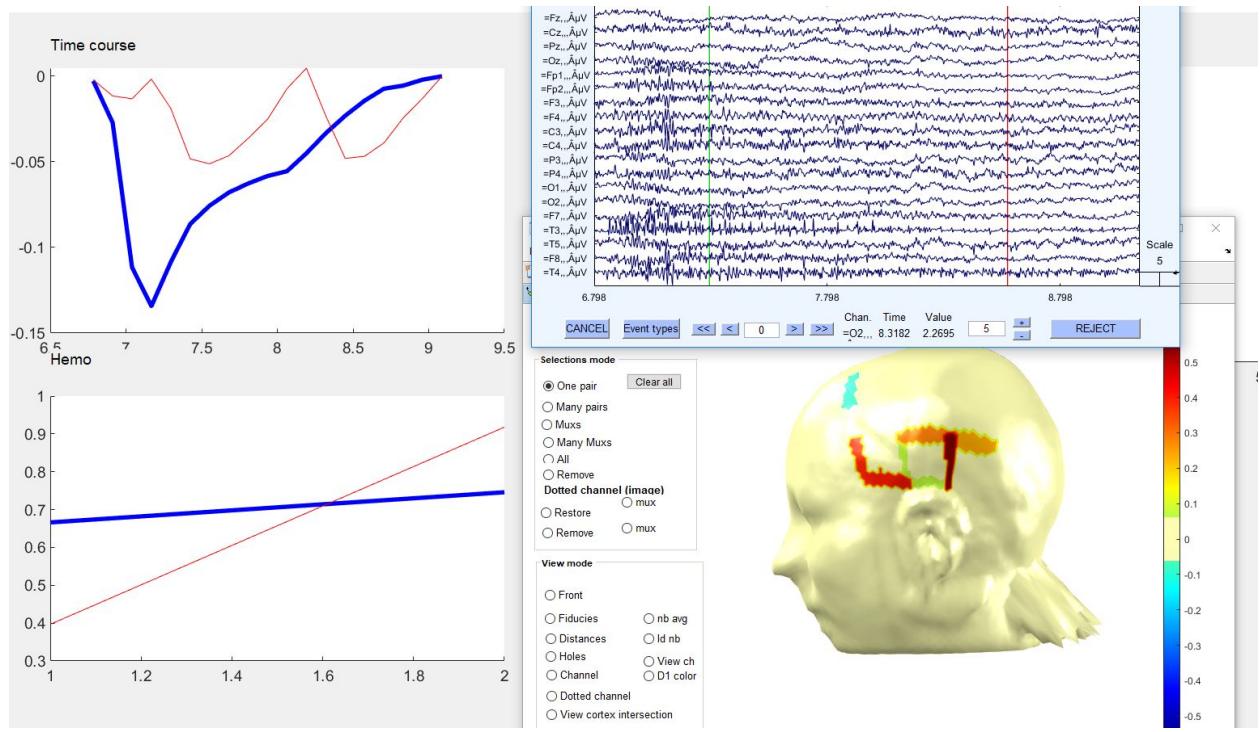
Functionality : They have two lists of data decomposition, one for subtracted components and the other to store components. All the corrections will be saved in the ‘corrections’ listbox which will be saved in the same folder as the NIRS.mat operation in a mat file name ‘CorrectionApply.mat’. All the components will be saved in ‘Comp’ listbox which will be saved in the same folder as the NIRS.mat operation in a mat file named ‘SelectedFactor.mat’.

- **Get** : get the decomposition; selected appropriate ‘start and stop time’, ‘channels’, and ‘method of decomposition’ you want to apply.
- **-** : Subtract the current selected type of component, to subtract a previously identified component you must choose the ‘component type’.
- **+** : Add the current selected correction
- **Ini** : Restore the data to the initial state (remove all correction for the whole block)
- **>** : Get the selected component to be saved in the list.
- **X** : Delete the selected component from the list.
- **Sort** : Classify all components in chronological order.

PARAFAC

Application to movement artifact in the GUI

1. In the GUI display, identify a time interval using start and stop markers and selected channels to be used for the parafac decomposition.
2. PARAFAC decomposition.
 - a. Data are centered before (first point and last point detrend)
 - b. Look at the component and adjust the number of components
 - c. Display in the topography spatial component, use the helmet and select PARAFAC as the display option, select the Topo Factor to display, the component in bold will be displayed.
 - d. Force equal wavelength



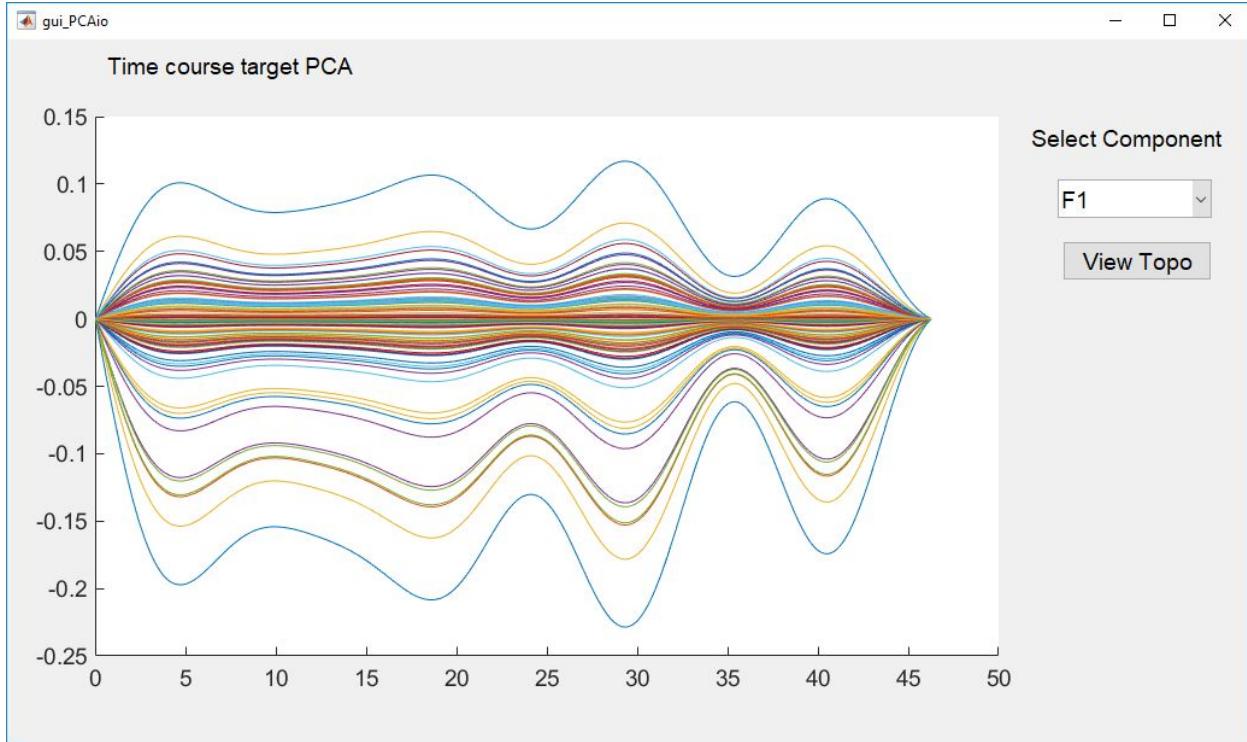
Example of muscular activity isolate in fNIRS.

PCA

Principal component analysis, use orthogonal basis to decompose the data.

Get the singular value decomposition. (Yücel et al., 2014)

$$Y = SVD$$



GLM

Select auxiliary to be regressed in a multiple linear regression to find beta and t estimation based on the general linear model. (function ‘regress’ from Matlab statistical toolbox) *Reference: Draper N. and H. Smith (1981) Applied Regression Analysis, 2nd ed., Wiley.*

$$Y = \beta_0x_0 + \beta_1x_1 + \beta_2x_2 + e$$

Component beta, regressor and t estimate value will be saved in the component.

If auxiliary does not get the same sample rate, the adjustment (resample) to the fNIRS sample rate will be made.

Offset Adjustment

Adjust the offset, it is useful when a movement changes the light intensity. The offset adjustment is applied before and after the time selection to keep as well as possible the continuity before and after the movement occurs inside the time interval rejected.

Component

List of the decomposition identified. Could be used to subtract a previously identified component.

Multimodal view

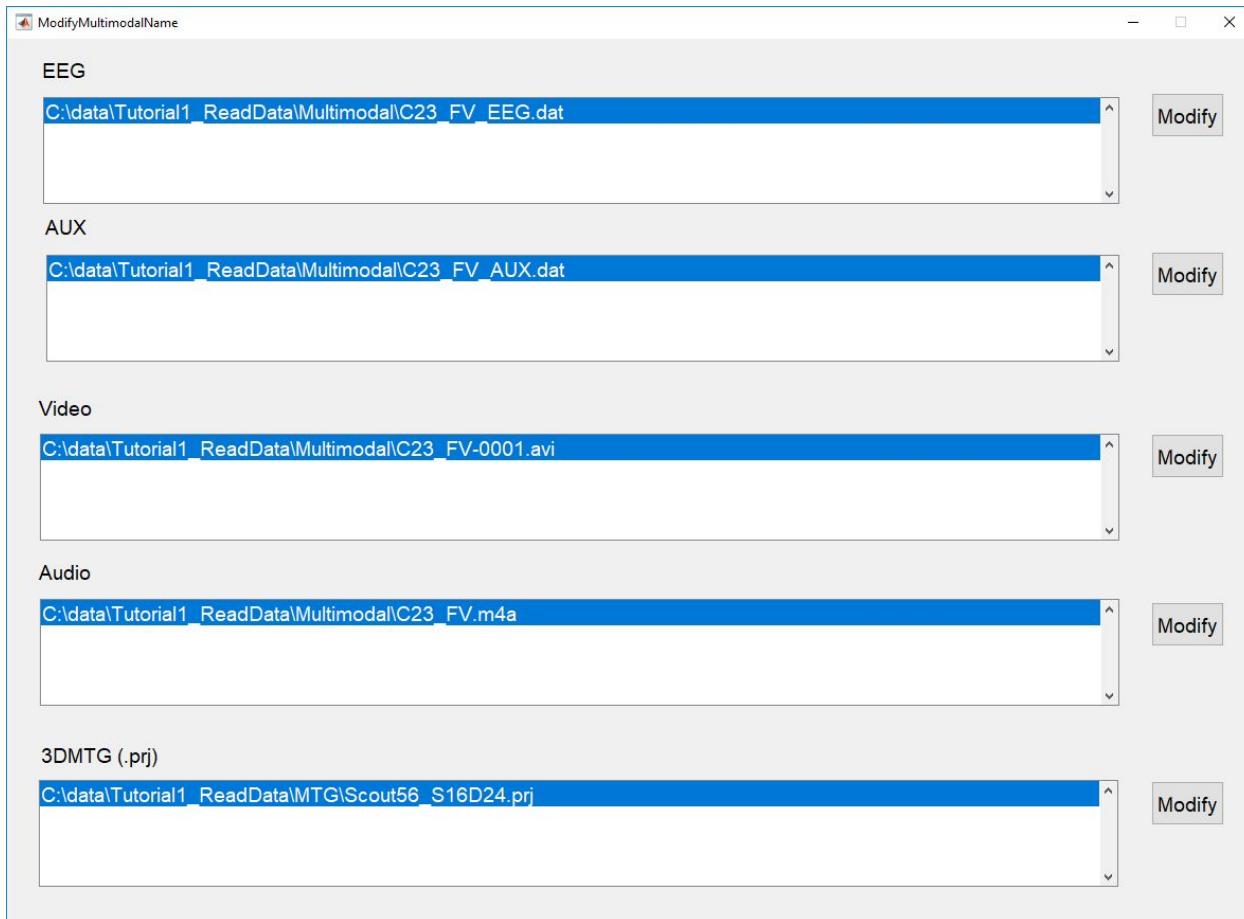
The multimodal file will be displayed for the interval time start and time stop selected. We advise to use a short duration for the selection. Press the button **EEG, VIDEO, and**

AUDIO to display these files. The original file with time start synchronized with fNIRS will be displayed in the text box below these buttons. The segmentation module is essential to synchronize fNIRS and multimodal files by using common synchronous triggers. As an example, the first trig 1 in fNIRS will be synchronized with the first trig 1 in EEG and so on. However, the error of trig or the use of a too-long segment may induce some delay. It is a good practice to verify the accuracy of this synchronization.

Settings/Multimodal files

You may adjust the path for multimodal files using the top menu **Settings/Multimodal files**.

This GUI will appear:



Use the button **Modify** to adjust the localization of the multimodal file on your computer.

Settings/Video settings

Video option (used default Matlab codec using video reader or toolbox mmread with common codec included <https://www.mathworks.com/matlabcentral/fileexchange/8028-mmread>).

Matlab enables to play audio-video, ensure the right codec is installed on your computer and you are using the version 32-bit or 64-bit of Matlab that could use the codec. However, Matlab needs to load part of the audio-video data prior to playing the

sequence. Another option is to use the time and file information to open the video with your favorite video player.

Trigger

On the bottom panel **Trigger** helps to control trigger visualization. Select the button **View** to visualize them, by default all triggers will be 'on'.

Use the right-click on the trigger number. A few options are available:

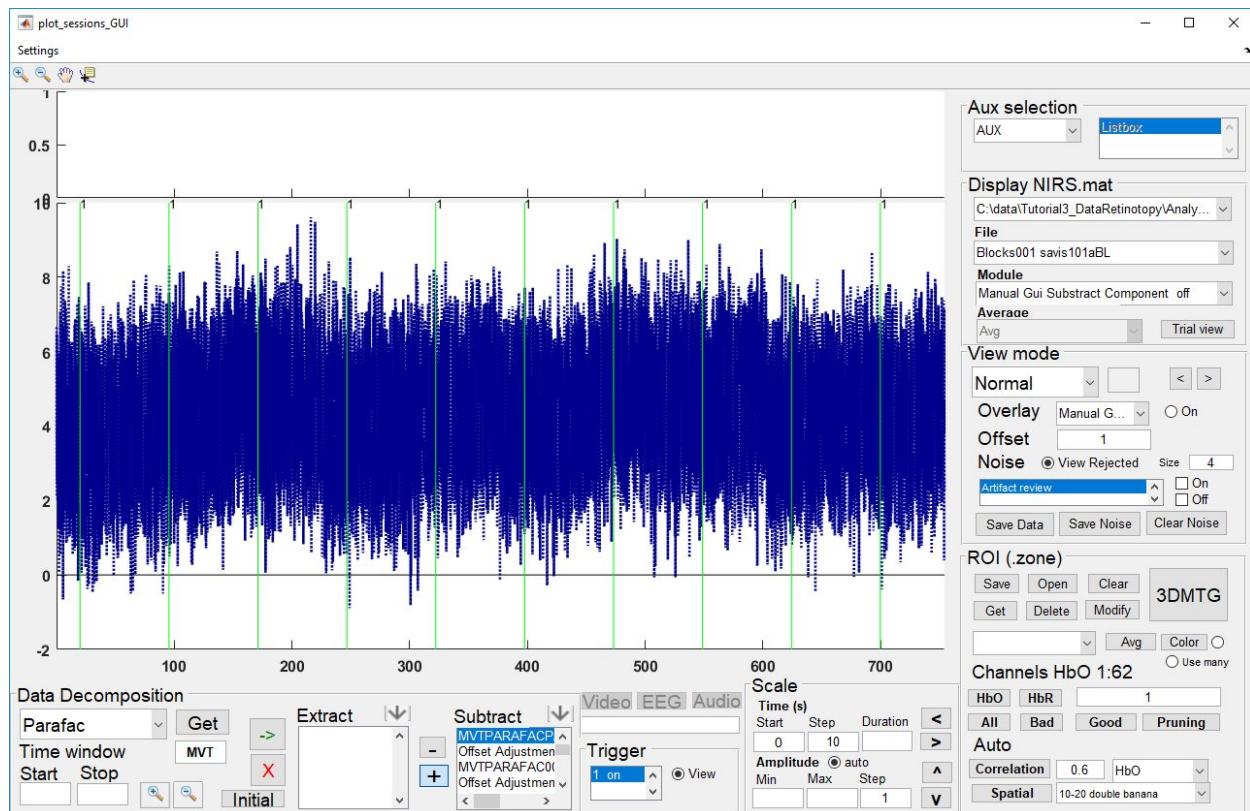
Copy: Copy in the clipboard all onset time for the selected trigger.

On: Set on the visualization for this trigger.

Off: Set off the visualization for this trigger.

Color: Set the color of the line for this trigger.

Label: Set the label name to display on the figure.



Delete a trigger: use right-click on an existing trigger. Select the option to remove the trig.

See trigger position: use right-click on an existing trigger to see the trigger position associate, as an example, if you are on the fifth trigger 1 it will indicate trigger position 5.

Add a trigger: use right-click on a specific time in the fNIRS data display window. Select the option add trigger.

Scale

Time(s): Adjust x-axis scale to select the appropriate time to display.
Start: Set to 0 to use the full windows time length. Use any other value to use a specific start time.
Step: increment to use to navigate with the left and right arrow control.
Duration: Length of the segment to display. Only valid when the start is different from zero; else the whole data set is displayed.
Amplitude: Adjust y-axis scale, use auto to adjust best scale according to the data.
Min: Minimal y-axis value (remove auto to used manual adjustment).
Max: Maximal y-axis value.
Step: Step to navigate amplitude step using up and down arrow.

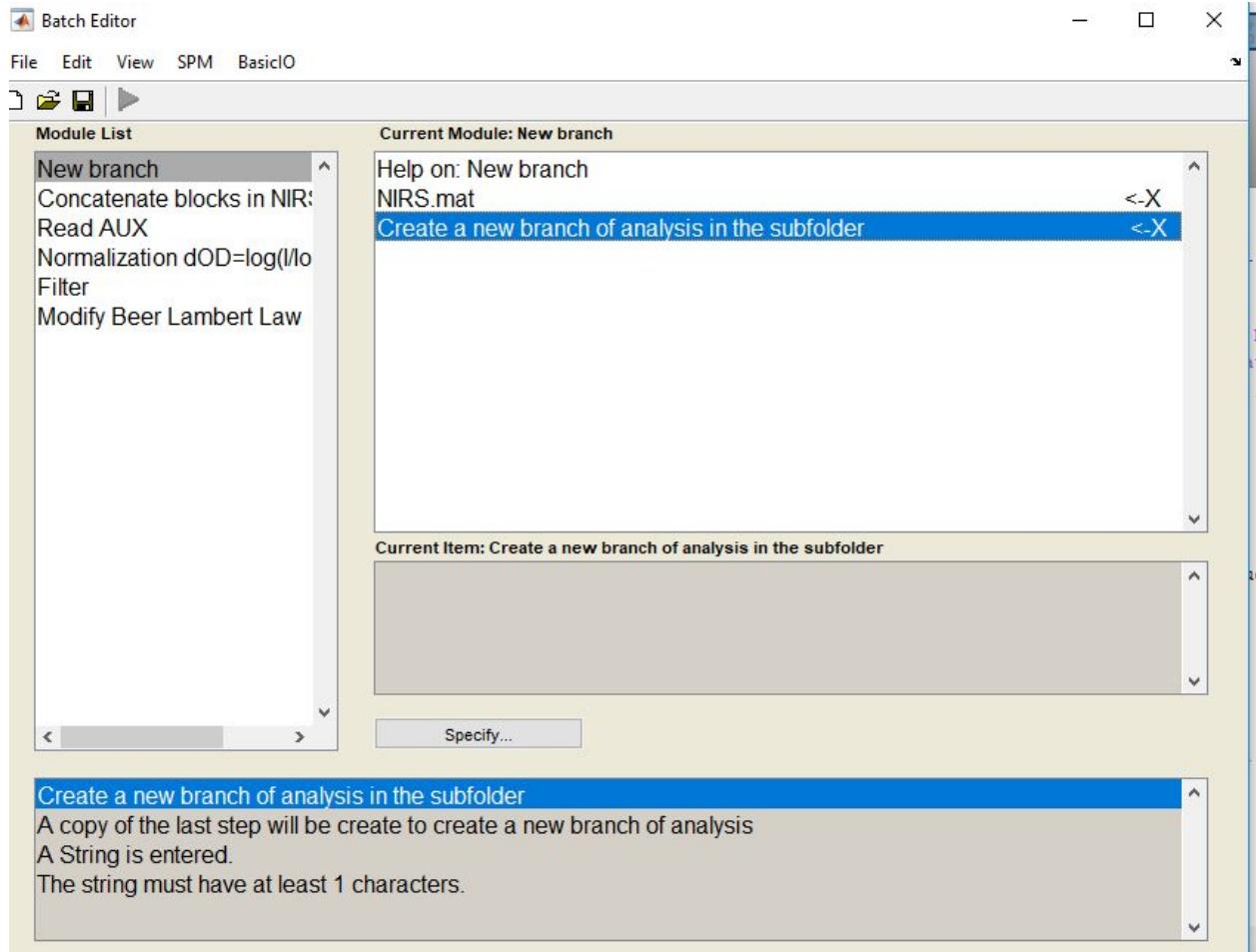
Shortcut list

Use the shortcut list to mark artifacts efficiently in the data. Place your cursor in the axes used to display fNIRS data curve to be able to use the shortcut.

- C Clear current artifact (yellow)
- U Unselect Defines the time interval between start time and stop time to be a good interval
- Y Yellow Defines, via a yellow segment, the time interval between start time and stop time to be a bad interval
- D Delete channel for this trial as long as there are at least two channels.
- R Restore (Restore all selected channel for this trial)
- A All (Remove this channel for all trials as long as there are at least two channels.)
- T Trial (Remove this trial for all channels)
- W Whole (Whole channels restore for this trial)

Create Batch Template (script using excel database to automatised multi subject pipeline)

[MATLAB Batch System](#) allows the use of Matlab script to run a Batch template modifying only a few fields, call the template script a ‘job’. This feature is useful to run multiple subjects with the same parameters. Create a ‘job’ as a normal batch but let empty the field you need to adjust for each subject. As in the following figure, the NIRS.mat is empty and the name of the New branch folder is empty. They will be considered as missing fields A and B for this example.



From the batch editor use menu view>Show .m Code
Copy in a .m file all the batch configuration and save it as
Template_Batch_dCONC_job.m, for example.

```

C:\data\Analysed\Batch_ARTICLETOOLBOX_FIGURE\Batch_pipeline\TEMPLATE_BATCHdCONC.m
1 - matlabbatch(1).spm.tools.nirsHSJ.M.Utility.E_NIRSmatcreatenewbranch.NIRSmat = '<UNDEFINED>';
2 - matlabbatch(1).spm.tools.nirsHSJ.M.Utility.E_NIRSmatcreatenewbranch.e_NIRSmatdirnewbranch = '<UNDEFINED>';
3 - matlabbatch(2).spm.tools.nirsHSJ.M_Segment.E_Concatenate_file.NIRSmat(1) = cfg_dep('New branch: NIRS.mat', substruct('.','val', '{},(1), .','val',
4 - matlabbatch(2).spm.tools.nirsHSJ.M_Segment.E_Concatenate_file.m_Concatenate_option = 0;
5 - matlabbatch(2).spm.tools.nirsHSJ.M_Segment.E_Concatenate_file.e_Concatenate_blocid = 0;
6 - matlabbatch(3).spm.tools.nirsHSJ.M_readNIRS.M_readMultimodal.E_readAUX.NIRSmat(1) = cfg_dep('Concatenate blocks in NIRS.mat: NIRS.mat', substruct('.','val', '{},(1), .','val',
7 - matlabbatch(3).spm.tools.nirsHSJ.M_readNIRS.M_readMultimodal.E_readAUX.AUX_file = {'C:\data\Analysed\Retinotopy\BG\HRF_BG.dat'};
8 - matlabbatch(3).spm.tools.nirsHSJ.M_preprocessing.normalization.NIRSmat(1) = cfg_dep('Read AUX: NIRS.mat', substruct('.','val', '{},(3), .','val',
9 - matlabbatch(4).spm.tools.nirsHSJ.M_preprocessing.normalization.DelPreviousData = 0;
10 - matlabbatch(4).spm.tools.nirsHSJ.M_preprocessing.normalization.normtype.b_choicenormstim.trigger = 254;
11 - matlabbatch(4).spm.tools.nirsHSJ.M_preprocessing.normalization.normtype.b_choicenormstim.pretime = 5;
12 - matlabbatch(4).spm.tools.nirsHSJ.M_preprocessing.normalization.normtype.b_choicenormstim.posttime = 30;
13 - matlabbatch(4).spm.tools.nirsHSJ.M_preprocessing.normalization.normtype.b_choicenormstim.m_NormType = 0;
14 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.NIRSmat(1) = cfg_dep('Normalization dOD=log(I/Io): NIRS.mat', substruct('.','val', '{},(4),
15 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.bpfilt.DelPreviousData = 0;
16 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.lowcutfreq = '0.1';
17 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.highcutfreq = 'No';
18 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.filterorder = 4;
19 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.paddingsymfilter = 1;
20 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.bpfilt.interpolatebadfilter = 0;
21 - matlabbatch(6).spm.tools.nirsHSJ.M_preprocessing.ODtoHbOHbR.NIRSmat(1) = cfg_dep('Filter: NIRS.mat', substruct('.','val', '{},(5), .','val', '{},
22 - matlabbatch(6).spm.tools.nirsHSJ.M_preprocessing.ODtoHbOHbR.DelPreviousData = 0;
23 - matlabbatch(6).spm.tools.nirsHSJ.M_preprocessing.ODtoHbOHbR.FVF = [1 1];
24 - matlabbatch(6).spm.tools.nirsHSJ.M_preprocessing.ODtoHbOHbR.C_ODtoHbOHbR_DPF.b_ODtoHbOHbR_DPF1 = struct([]);
25 -

```

The missing fields are indicated as <UNDEFINED>, you must now define in the run script. As an example a new script is created to run the batch for all subjects 'run_BatchTemplate.m' using the following instructions, most of the errors will occur if you don't use the right format (string, string cell, double...). As a tip, enter the value in the batch to know the format expected by the function and keep the same format for your entry:

```

input = {'C:\data\Analysed\Retinotopy\BG\107\NIRS.mat'} for a cell string;
input='test1' for a string;
input =4 for a double;
input = str2num('4') to convert string into double or input= num2str(4) to convert double into a string.

```

```

% fill the missing field A and B for each subject, you could add mode missing field
Subject(1).A = {'C:\data\Analysed\Retinotopy\BG\107\NIRS.mat'}
Subject(1).B = 'test1'
%LOOP for all subject
for isubject=1:numel(Subject)
    % load template batch saved as as script TEMPLATE_BATCHdCONC.m';
    jobid = cfg_util('initjob','yourpath\TEMPLATE_BATCHdCONC.m');
    %MODIFY THE SUBJECT FIELD A AND B BY YOUR VALUE
    cfg_util('filljob', jobid,Subject(isubject).A,Subject(isubject).B );
    %RUN THE JOB
    cfg_util('run', jobid)
    disp(['Subject : ', num2str(isubject)])
end

```

A convenient way is to use excel data to define each entry that has to be modified by subject.

RawNIRscout	AGE	3dMTG	AnalysisFolder	Batch_01_Read Fait (0) / À faire (1)
...\\C01\\NIRS-2018-01-16_001.hdr	18	\\C01\\MTG\\V2.prj	..\\Analysis\\C02\\	1
...\\C02\\NIRS-2018-02-16_001.hdr	16	\\C02\\MTG\\V2.prj	..\\Analysis\\C02\\	1

Adjust your script to read the excel and identify the good column for the appropriate field.

```
[num,txt,raw] = xlsread(fileXLS);
for icol=1:size(raw,2)
    if strcmp(deblank(raw{1,icol}),'RawNIRscout')
        id.RawScout = icol
    end
    if strcmp(deblank(raw{1,icol}),'AGE')
        id.AGE = icol
    end
    if strcmp(deblank(raw{1,icol}),'3DMTG')
        id.MTG = icol
    end
    if strcmp(deblank(raw{1,icol}),'AnalysisFolder')
        id.output = icol
    end
    if strcmp(deblank(raw{1,icol}),'Batch_01_Read Fait (0) / À faire (1)')
        id.doit = icol
    end
end
%Loop over all xls row
for isubject=2:size(raw,1)
    if isnan(raw{isubject,id.doit}) %skip missing row
        break
    end
    if raw{isubject,id.doit}
        %MODIFY THE SUBJECT FIELD A AND B BY YOUR VALUE
        Subject(1).NIRx = {raw{isubject,id.RawScout}};
        Subject(1).AGE = raw{isubject,id.AGE};
        Subject(1).MTG = {raw{isubject,id.MTG}};
```

Troubleshooting

- You move the data on your hard drive and they could not be read by the display

Tip: insert a module (Read NIRSdata / NIRS.mat dir adjustment) before to add another module.

- Gui dependencies are lost.

Tip: Close Matlab will fix the problem, they have some dependencies that were not correctly closed in Matlab GUI.

- Mac users could encounter some issues using excel file format, to read or write xls are not well supported in Matlab. We recommend mac users to use tab space delimited .txt files.

Glossary

Channel: Combinaison of source and detector, also called optode.

Mux: Combinaison of all sources available close to a detector, or all detectors close to a source.

Blocks: We define as block a file could be an event segment or a complete recording session.

Trigger (trig): Generated by the computer, triggers allow the separation between events, such as different cerebral activities, during the experiment. Triggers can be compared to the EEG markers.

Component: Part of the fNIRS data separated by noise events or triggers.

Regressor: It could be a channel or a grouping of several channels that cover a specific zone. It is in this zone that a regression is applied.

Raw data: Data that comes directly from the acquisition, before any processing.

Zone: a few channels on the same region of the head.

Appendix: Details about files format used

.ELP file

Description: Geometric position (in meters) of the holes of your patch or helmet where you will enter the optode. This includes the position of the patient's fiducial anatomy (LPA Left preauricular, RPA Right preauricular and NAS Nasion marker) used to register with the MRI position. ELP file format was created using Polaris equipment by Brainsight - Rogue Research. We provide an example which one could be adapted if you need to adapt your own format. Center of the coordinate axis (0,0,0) is close to the center of the head,

LPA is	0.001902	0.067339	0.000000
RPA is	-0.001902	-0.067339	0.000000

NAS is 0.089774 0.000000 0.000000

Which means :

X axis is from Back to Front

Y axis is Right to Left

Z axis is Down to Top of the head.

Example :

```
3      2
//Probe file
//Minor revision number
1
//ProbeName
%%N    Name
//Probe type, number of sensors
0      29
//Position of fiducials X+, Y+, Y- on the subject
%F    0.089774    0.000000    0.000000
%F    0.001902    0.067339    0.000000
%F    -0.001902   -0.067339   0.000000
//Sensor type
%S    400
//Sensor name and data for sensor# 1
%N    GF8
-0.005096  0.069440    0.081612
//Sensor type
%S    400
//Sensor name and data for sensor# 2
%N    GB6
0.069182   0.033833    0.084674
//Sensor type
%S    400
//Sensor name and data for sensor# 3
%N    Z6
0.077148   0.002294    0.092158
//Sensor type
%S    400
//Sensor name and data for sensor# 4
%N    DA3
0.096164   -0.011476   0.051418
```

.vox file iMagic volume format

The format is characterized by having 2 files, one for storing the image volume itself and another one for storing the minimum information (header) for describing it with .VOX and .HDR extensions respectively. The .VOX file is a binary file; the 2D slices are sequentially stored in an uncompressed way. The .HDR file is an ASCII file, where every field (text line in the file) has the following information:

FIELD DESCRIPTION

- 1 Number of columns (X) for each 2D slice
- 2 Number of 2D slices (Y)
- 3 Number of rows (Z) for each 2D slice
- 4 Amount of bytes stored for voxel
- 5 Size in mm for each pixel
- 6 Slice thickness in mm for each 2D slice
- 7 Orthogonal stored plane (axial=0, sagittal=1 and coronal=2)
- 8 Skin threshold detection
- 9 Cortex threshold detection
- 10 Left Pre Auricular (LPA) point coordinates (X, Y, Z)
- 11 Right Pre Auricular (RPA) point coordinates (X, Y, Z)
- 12 Nasion coordinates (X, Y, Z)
- 13 Vertex coordinates (X, Y, Z)
- 14 Talairach system origin coordinates (X, Y, Z)
- 15 Atlas filename associated to the image volume
- 16 MIP filename associated to the image volume
- 17 Inion coordinates (X, Y, Z)
- 18 Nose base coordinates (X, Y, Z)

The 4th field also indicates the image volume data type. 1 indicates the Byte data type; Word (16 bits integer without sign) is indicated by 2, Integer (32 bits integer with signs) is indicated by 4 and Single (floating point simple precision) is indicated by the alphanumeric chain 4F.

In the 5th field, if the pixel is not square, then it is possible to specify the two values separated by one space, first the horizontal value and, after, the vertical value in mm.

The 8th and 9th fields correspond to the thresholds used for detecting the skin and cortex in 3d visualization.

The fields from 10th to 13th and 17th, 18th are landmarks whose X, Y, Z coordinates are set interactively and will be used for coregistering with other coordinate systems. The following figure shows these points.

The image system coordinates used by iMagic is shown in the following figure. It is a left-handed system (the thumb finger indicates the X axis, the index finger Y axis and the middle finger the Z axis), very suitable for 3d visualization.

The 14th field allows reporting Talairach coordinates if the image volume is placed in that system.

The fields from 10th to 18th are optional.

.SEG file iMagic segmentation format

The format is characterized by having 2 files also, one to store the segmentation volume itself and another one to store the minimum information to describe the segmentation with .VOX and .HDR extensions respectively. The .SEG file is a binary file; the 2D slices are sequentially stored in an uncompressed way. The .HDR file is an ASCII file, where every field (text line in the file) has the following information:

FIELD DESCRIPTION

- 1 Number of columns (X) for each 2D slice
- 2 Number of 2D slices segmented
- 3 Number of rows (Z) for each 2D slice

Afterwards, many lines will appear in the file as indicated in the 2nd field, where every line indicates the slice segmented (an ordinal starting with zero) relative to the first slice in the image volume associated with the segmentation file.

NIRS.mat structure

Definition of the NIRS.mat field

NIRS.Cf.dev.n	Configuration device, name of the recording equipment Example: [ISS]
NIRS.Cf.dev.wl	Configuration device wavelength of the equipment use for Beer Lambert Law calculation Example: [830 690]
NIRS.Cf.dev.fs	Sampling frequency (Hz) Example: [19]
NIRS.Cf.H.prj	Helmet project location used for in the read data function (optional) Example: ['C:\data\Malnutrition\MTG\Scout56cm_GoNogo_v3.prj']
NIRS.Cf.H.F.r.o.mm	Fiducie matrix position coordinate, measure in meter Axis reference center of the head 0,0,0 NAS LPA RPA
NIRS.Cf.H.S.N	Number of source

NIRS.Cf.H.S.r.o.mm	Position of the source (x,y,z) in meter
NIRS.Cf.H.D.N	Number of Detector
NIRS.Cf.H.D.r.o.mm	Position of the detector (x,y,z) in meter
NIRS.Cf.H.C	Channel information
NIRS.Cf.H.C.id	Row 1 Id form the raw data index Row 2 Source Row 3 Detector
NIRS.Cf.H.C.wl	Wavelength definition for each channel Example [1,1,1,2,2,2] Channel 1 to 3 will be wavelength 1 NIRS.Cf.dev.wl(1) = 830 nm while Channel 4 to 6 will be wavelength 2 NIRS.Cf.dev.wl(2) = 830 nm while
NIRS.Cf.H.C_gp	Geometric distance between source and detector for this channel
NIRS.Cf.H.C.n	Name of the channel (S1_D1)
NIRS.Cf.H.C.N	Total number of channel
NIRS.Cf.H.C.ok	Channel rejected or not 1 valid channel 0 rejected channel
NIRS.Cf.H.C.okavg	Channel rejected or not 1 valid channel 0 rejected channel
NIRS.Dt.s.age	Subject age information
NIRS.fir.pp(idmodule)	Step of analysis Each module of operation will add as a step of analysis Example = [1];
NIRS.fir.pp(idmodule).p{ifile}	Link to the raw data record on the drive
NIRS.fir.pp(idmodule).pre	Step of preprocessing Example = ['Read Raw_NIRxScout']

NIRS.fir.pp{idmodule}.job	Detail of the parameter in the job file.
NIRS.fir.aux5{ifile}	Trigger info trig value, index of time sample Example; [2, 9; 2, 1733; 255,1] Trig 2 sample 2 et 1733, Trig 255 sample 1
NIRS.fir.sizebloc{ifile}	Nb of samples in each data file
NIRS.Dt.EEG.pp{idmodule}.p	Location of simultaneous EEG file. A new module is created when the trigs are adjusted, files are segmented around the trigger in the normalization step, the last module is always the one used
NIRS.Dt.EEG.pp{idmodule}.sync_timesec	Time ajustement to be synchronized to the NIRS blocks segmentation. In second.
NIRS.Dt.AUX(idauxfile).pp{idmodule}.p	Location of simultaneous AUX files. A new module is created when the triggers are adjusted. Files are segmented around the trigger in the normalization step, the last module is always the one used, could be many (idauxfile) if multiple files of auxiliary are defined. Each file could have its own sample rate.
NIRS.Dt.AUX(idauxfile).pp{idmodule}.syn_timesec	Time ajustement to be synchronized to the NIRS blocks segmentation. In second.
NIRS.Dt.AUX(idauxfile).label	Identification AUX label.
NIRS.Dt.Video.pp{imodule}.p	Location of the video file.
NIRS.Dt.Video.pp{imodule}.sync_timesec	Offset in the video file to be synchronized to the NIRS file segment, need the Normalization step around triggers to be synchronized.
NIRS.Dt.Video.syncref	'EEG'

	%the video needs to be synchronized to the beginning of the fNIRS file, or the EEG file to keep the synchronization.
--	--

Zone structure

A zone is a definition of a few channels on the same region.

zone.label{}	Name of the area
zone.plotLst{}	Indice number of the channel
zone.plot{}	Indice of the source and detector in the zone
Zone.color{}	Define a specific color to plot the zone
Zone.ml	Original measurement list of the recording where the zone where created use to compatibility across subject using ZoneList
Zone.pos	Position of the channel (geometric intersection between source and detector)
Zone.SD	Position of the source and detector

GUI look matrices data structure

Each subject or file corresponds to one matrix file list in the xls.

Data{isubject}.ZoneList	channel list of physical names of sources and detectors. as used in the matrix.*
.DATA{isubject}.MAT	Matrices
DATA{id}.GR	Groupe to the display
DATA{id}.System	Recording equipment 'ISS'
DATA{id}.zone	As described above, each regroupement of channels in the region of interest could be considered as one node for statistics and average.

NB *. The channel list is essential to regroup subjects and ensure that the same position on the head of the measurements. The node one in the zone list has to be the same position on the other subject.

Generic data export file format from BV analyzer use for AUX or EEG

*.dat: binary data

Binary data recorded as VECTORIZED=ch1,pt1, ch1,pt2..., or MULTIPLEXED=ch1,pt1, ch2,pt1 ...array.

*.vhdr: information about the file recording channel and time setting

Brain Vision Data Exchange Header File Version 1.0

; Data created by the Vision Recorder

[Common Infos]

Codepage=UTF-8

DataFile=G11121_2_Rest.eeg

MarkerFile=G11121_2_Rest.vmrk

DataFormat=BINARY

; Data orientation: MULTIPLEXED=ch1,pt1, ch2,pt1 ...

DataOrientation=MULTIPLEXED

NumberOfChannels=7

; Sampling interval in microseconds

SamplingInterval=2000

[Binary Infos]

BinaryFormat=IEEE_FLOAT_32

[Channel Infos]

; Each entry: Ch<Channel number>=<Name>,<Reference channel name>,

; <Resolution in "Unit">,<Unit>, Future extensions..

; Fields are delimited by commas, some fields might be omitted (empty).

; Commas in channel names are coded as "\1".

Ch1=Fz,,0.0488281, μ V

Ch2=Cz,,0.0488281, μ V

Ch3=Pz,,0.0488281, μ V

*Ch4=Oz,,0.0488281,µV
Ch5=Fp1,,0.0488281,µV
Ch6=Fp2,,0.0488281,µV
Ch7=F3,,0.0488281,µV*

[Coordinates]

; Electrode Position File: C:\Data\CMA-32_REF.bvef
Ch1=1,45,90
Ch2=1,0,0
Ch3=1,45,-90
Ch4=1,90,-90
Ch5=1,-90,-72
Ch6=1,90,72
Ch7=1,-60,-51

*.vmrk information about event and trig

Example:

Brain Vision Data Exchange Marker File, Version 1.0

[Common Infos]

Codepage=UTF-8

DataFile=G11121_2_GoNogo.eeg

[Marker Infos]

; Each entry: Mk<Marker number>=<Type>,<Description>,<Position in data points>, ; <Size in data points>, <Channel number (0 = marker is related to all channels)> ; Fields are delimited by commas, some fields might be omitted (empty). ; Commas in type or description text are coded as "\1".

Mk1>New Segment,,1,1,0,20180807130210764983

Mk2=Stimulus,S 4,11972,1,0

Mk3=Stimulus,S 12,15235,1,0

Mk4=Stimulus,S 11,22759,1,0

Mk5=Stimulus,S 2,22792,1,0

Mk6=Stimulus,S 3,23014,1,0

Mk7=Stimulus,S 2,23392,1,0

Mk8=Stimulus,S 3,23578,1,0

Mk9=Stimulus,S 2,24075,1,0

Holes nomenclature

Imaging or NIRx naming convention.

They will use E1 or D1 as identification for emitter and detector respectively. This nomenclature is available in 3d helmet, the reading raw data function will adapt the emitter and detector position indicated in our montage configuration file .prj.

Imagent ISS naming convention

Our lab configuration uses 4 ISS recording systems in parallel using mux 32 illumination sequences. Our source naming convention uses a1b2 to pair 830nm and 690nm in case of mux 16 illuminations sequence. Capital letters are used for the detector PMT recording. This nomenclature is available in 3d helmet, the reading function will adapt to the emitter position indicated in our montage configuration file .prj. Imaging or NIRx naming convention.

They will use E1 or D1 as identification for emitter and detector respectively. This nomenclature is available in 3d helmet, the reading raw data function will adapt the emitter and detector position indicated in our montage configuration file .prj.

ISS naming convention.

Our lab configuration uses 4 ISS recording systems in parallel using mux 32 illuminations sequences. Our source naming convention uses a1b2 to pair 830nm and 690nm in case of mux 16 illuminations sequence. Capital letters are used for the detector PMT recording. This nomenclature is available in 3d helmet, the reading function will adapt to the emitter position indicated in our montage configuration file .prj.

ISS 1

A	B	C	D				
a1	a5	a9	a13	b1	b5	b9	b13
a2	a6	a10	a14	b2	b6	b10	b14
a3	a7	a11	a15	b3	b7	b11	b15
a4	a8	a12	a16	b4	b8	b12	b16

ISS2

E	F	G	H				
c1	c5	c9	c13	d1	d5	d9	d13
c2	c6	c10	c14	d2	d6	d10	d14
c3	c7	c11	c15	d3	d7	d11	d15
c4	c8	c12	c16	d4	d8	d12	d16

ISS3

I	J	K	L				
e1	e5	e9	e13	f1	f5	f9	f13
e2	e6	e10	e14	f2	f6	f10	f14
e3	e7	e11	e15	f3	f7	f11	f15
e4	e8	e12	e16	f4	f8	f12	f16

ISS4

M	N	O	P				
g1	g5	g9	g13	h1	h5	h9	h13
g2	g6	g10	g14	h2	h6	h10	h14
g3	g7	g11	g15	h3	h7	h11	h15
g4	g8	g12	g16	h4	h8	h12	h16

Nomenclature transfer chart

To adapt this HSJ nomenclature to HoMer, NIRx or Imaging source number use this transfer chart.

Lasers	Detectors					
Emitter HSJ label						
830/690 nm	Emitter HSJ	IOMTG		830/690 nm	Emitter HSJ	
IOMTG						
E1	a1b2	18001	E44	E8f7	87072	
E2	a3b4	20003	E45	e10f9	89074	
E3	a5b6	22005	E46	e12f11	91076	
E4	a7b8	24007	E47	e14f13	93078	
E5	a9b10	26009	E48	e16f15	95080	
E6	a11b12	28011	E49	g1h2	114097	
E7	a13b14	30013	E50	g3h4	116099	
E8	a15b16	32015	E51	g5h6	118101	
E9	a2b1	17002	E52	g7h8	120103	
E10	a4b3	19004	E53	g9h10	122105	
E11	a6b5	21006	E54	g11h12	124107	
E12	a8b7	23008	E55	g13h14	126109	
E13	a10b9	25010	E56	g15h16	128111	
E14	a12b11	27012	E57	g2h1	113098	
E15	a14b13	29014	E58	g4h3	115100	
E16	a16b15	31016	E59	g6h5	117102	
E17	c1d2	50033	E60	g8h7	119104	
E18	c3d4	52035	E61	g10h9	121106	
E19	c5d6	54037	E62	g12h11	123108	
E20	c7d8	56039	E63	g14h13	125110	
E21	c9d10	58041	E64	g16h15	127112	
E22	c11d12	60043				
E23	c13d14	62045				
E24	c15d16	64047				
E25	c2d1	49034				
E26	c4d3	51036				
E27	c6d5	53038				
E28	c8d7	55040				
E29	c10d9	57042				
E30	c12d11	59044				
E31	c14d13	61046				
E32	c16d15	63048				
E33	e1f2	82065				
E34	e3f4	84067				
E35	e5f6	86069				
E36	e7f8	88071				
E37	e9f10	90073				
E38	e11f12	92075				
E39	e13f14	94077				
E40	e15f16	96079				
E41	e2f1	81066				

E42	e4f3	83068
E43	e6f5	85070

Detector

Detector	HSJ	IOMTG
D01	A	1000000
D02	B	2000000
D03	C	3000000
D04	D	4000000
D05	E	5000000
D06	F	6000000
D07	G	7000000
D08	H	8000000
D09	I	9000000
D10	J	10000000
D12	L	12000000
D13	M	13000000
D14	N	14000000
D15	O	15000000
D16	P	16000000

Individual anatomical MRI preparation

To create a .prj with an individual MRI. Use an individual anatomical resonance anatomical t1 weighted head scan acquired with 1 mm isotropic size voxel in axial orientation. Raw T1 Dicom images need some manipulation to be in the good format for the 3dMTG. The MRI volume could be interpolated or reorient to achieve the isotropic 1mm voxel in axial orientation if needed. Anatomical MRI needs to include the fiducial (nasion, left preauricular and right preauricular markers included in the VOX files formats) and create surface and segmentation of the skin and brain tissues. All this operation could be performed in specialized external software. We recommend MRIconvert, Neuronic Image Processor, SPM or Brainsuite.

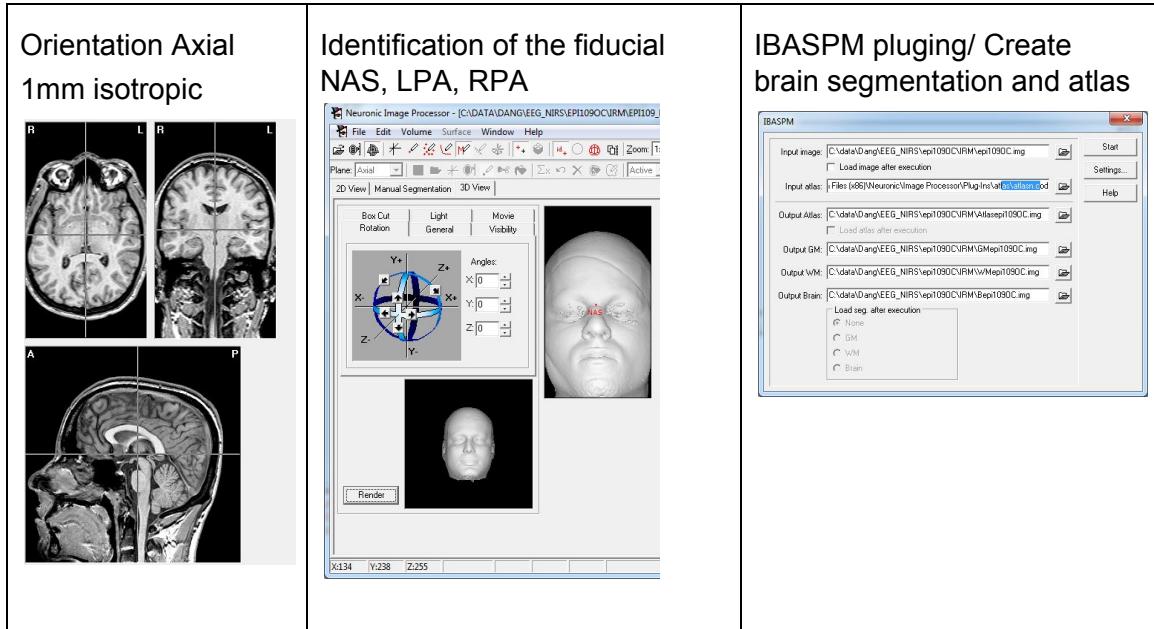
Dicom conversion to nifti

Dicom conversion to Nifti format can be handled by MRICONVERT [LCNI](#).

Preprocessing in neuronic Image Processor

1. Reorient the volume in axial
2. Interpolate volume in 1 mm voxel size menu : Volume/InterpolateImageVolume/set Isotropic
3. Mark the fiducial (NAS LPA RPA) select the marker  tool and click on the fiducial location

4. Save Image volume in .VOX file format (this format will save the fiducial as well as the binary MRI volume).
5. Create segmentation menu: Volume/plugin/Run IBASPM
6. Open pre-segmented volume to create .seg and .srx for brain and skin segmentation.
7. Adjust the threshold to highlight tissus and save the segmentation .seg. menu: File/ save segmentation as/ brain.seg
8. Menu: Volume/Create Surface /By deformation/ medium resolution
9. Menu: Save/Save surface as/ brain.srx



Brainsuite

Use the .dfs surface created in brainsuite cortical surface extraction sequence.

epi109OC.brain.dfs

epi109OC.scalp.dfs

Need external function readdfs.m

SPM12 segment

Use the spm segment function to get pre segmented scalp and skin. Create surface in Neuronic Image Processor.

Grey matter C1	White matter C2	CSF C3	Skull C4	Skin C5
----------------	-----------------	--------	----------	---------

