



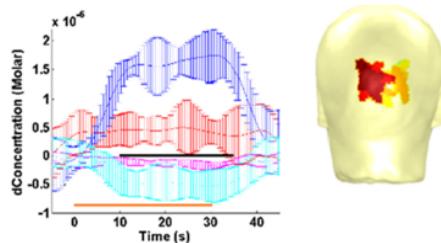
Laboratoire d'imagerie optique  
en neurodéveloppement



# 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 data analytics tools such as normalization, filter, Beer-Lambert Law, average, and semi-automatic artifact detection. A graphical interface helps to visualize and manually review the artifact rejection. It applies data decomposition (PCA, PARAFAC) and general linear model estimation (GLM) to the data. Topographical representation of the 3DMTG over the scalp or cortex anatomical MRI is available at each analysis step. The 3DMTG uses a MATLAB GUI interface to create a project (.prj) that links the positions of the source and detector to the subject's anatomy to visualize the data. Please cite the following reference in your publications if you have used our software for your data analyzes:

Tremblay, J., Martínez-Montes, E., Hüsser, A., Caron-Desrochers, L., Pouliot, P., Vannasing, P., Gallagher, A., 2021. LIONirs: flexible Matlab toolbox for fNIRS data analysis. Journal Neuroscience Methods, In review

## Installation requirements (see [Tutorial Set up](#))

The project is publicly available under the GNU General Public License. You can download the toolbox from Github: <https://github.com/JulieTremblay3/LIONirs>. LIONirs is developed for research purposes without any warranty. The source code is available in MATLAB MathWorks and it has been tested with the version of SPM12.

1. Download and install SPM12, visit <https://www.fil.ion.ucl.ac.uk/spm/software/download/> and fill out the download form with the appropriate information regarding your operating system.
2. Download LIONirs source code: <https://github.com/JulieTremblay3/LIONirs> and copy and paste the LIONirs folder as follows ./spm12/toolbox/LIONirs. It is installed as an SPM toolbox extension and use be available in the batch menu.
3. Define the root SPM folder in Matlab set path (menu set path & add with subfolder or path tool command).

Compatibility with SPM12 MATLAB 2014 to 2018a.

The following external functions have to be added to the set path in order to run some specific functionalities.

Recommended: MATLAB Toolboxes at require during MATLAB installation

- Statistics and Machine Learning Toolbox™ (Statistics function ttest, ANOVAN)
- Bioinformatics Toolbox™ (FDR correction)

External packages

- [Homer3](#) (support sNIRF format)
- [NWAY toolbox](#) (PARAFAC decomposition)
- [mmread](#) (video compatibility)
- [CircStat](#) (support Hilbert joint phase probability distribution)
- [NBS toolbox](#) (external network statistic)

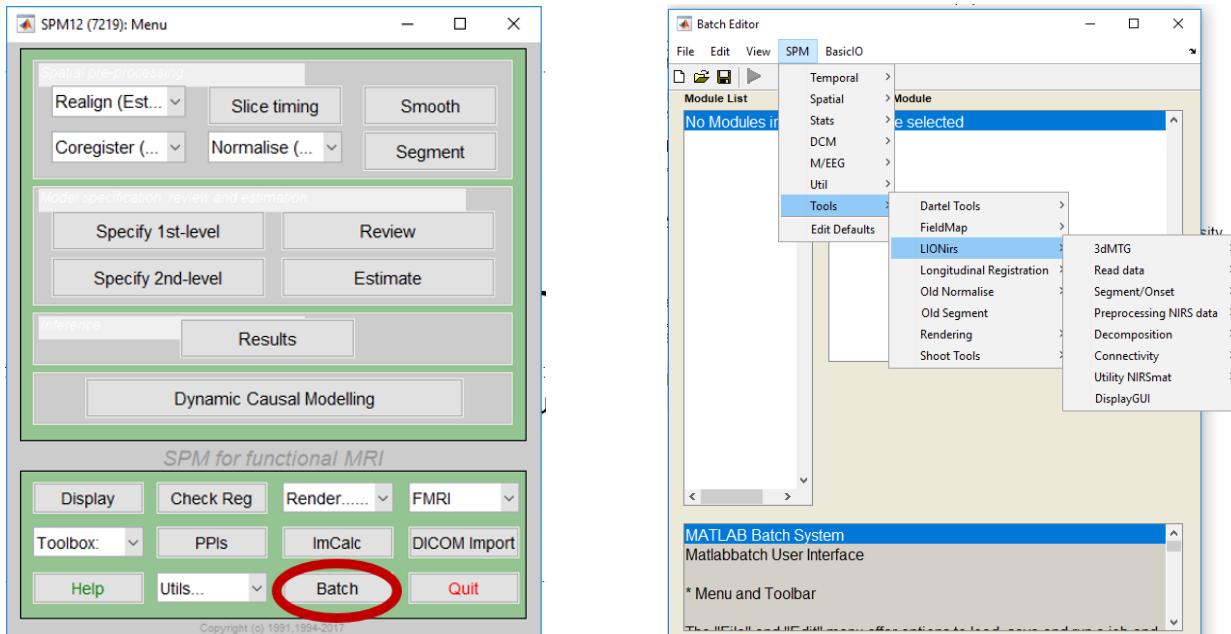
For optimal visualization of the GUIs, a screen resolution Full HD (1920\*1080p) is recommended.

## Launch the batch editor

To launch spm12, write “spm fmri” into the command window of MATLAB.

```
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
```

Once the SPM Menu window appears, open the batch editor window by pressing “Batch”.



All functions of the LIONirs toolbox can be accessed via the menu bar: SPM/tools/LIONirs. The present documentation provides a detailed description of all the modules in the toolbox. Refer to the section with hands-on tutorials for a quick introduction and examples.

## General data organization

In the LIONirs toolbox the functions (modules) are accessed via the menu bar: SPM/tools/LIONirs in the Batch editor menu. To define your analysis tree, you need to add modules in the module list.

**Module:** Select a module and define specific fields for the function. See the help and documentation for each specified module entry and function.

**Module list or Batch:** Includes all selected modules (=functions) to be applied sequentially. A series of modules ‘batch’ help to keep track of the preprocessing applied to the data and to be

reused easily on other subjects. The operations in the list will always be applied sequentially and identified in the NIRS.mat structure.

**Analyze folder:** When you read raw data using LIONirs toolbox, an analysis folder are created for each subject and contains:

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

**NIRS.mat:** This structure is created by the toolbox and is used as the main data structure to keep track of all the operations performed, to visualize and analyze data. Most of the toolbox's functionalities need a NIRS.mat file as an input to perform any operation on the data. Each step will be performed sequentially on the previous NIRS.mat (dependency), which means that you can only edit or perform an operation on the last module. Each NIRS.mat structure contains the location of the analyzed data in the file directory, similar to the SPM.mat in fMRI. If you need to move the analysis folder make sure to keep the subfolder dependency and use the utility "folder adjustment" to adjust dependencies to the new location. More information about this structure is available in the [appendix](#).

**Analyzed data:** Binary data in the analyzed folder with 3 extensions, .nir (binary data float 32), .vhdr (header information), .vmrk (trig and bad interval information).

**New branch:** Creates parallel branches of analysis, the data will be place in a *subfolder*. To create a parallel branch of analysis, you need to use the utility "new branch". For example, clean data could be averaged for two different conditions. Add the module new branch and separate the pipeline into two parallel branches to try several data processing.

#### Optional multimodal files:

**Auxiliary** data can be synchronized and visualized with the NIRS signal and integrated as variables into the GLM model (see [appendix](#) for the data format: .dat (binary data), .vhdr (header information), .vmrk (trig and bad interval information)). Auxiliary can be created via the generic data export from BrainVision Analyzer or by using a synthetic HRF model according to the data task information.

**EEG** data can be integrated in the same format as Auxiliary data (.dat, .vhdr, .vmrk files) which can for example be generated via the generic data export in BrainVision Analyzer.

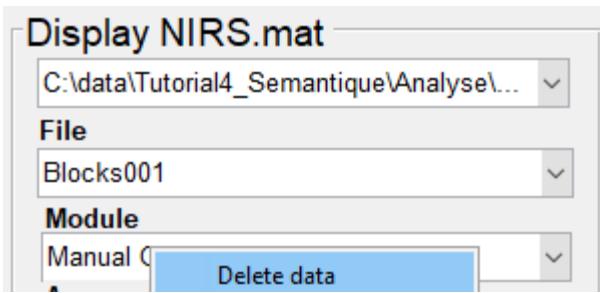
**Video** recording simultaneous to fNIRS or EEG. If there is a time lag with the fNIRS or EEG recording, you need to indicate the offset [s] to synchronize the video. Later on, trigger will be adjusted using fNIRS or EEG to be segmented.

**Audio** file simultaneous to fNIRS or EEG. Audio recordings can be synchronized similarly as video recordings by the use of offset. Later on, trigger will be adjusted using fNIRS or EEG to be segmented.

#### Delete previous .nir data file

This function is available in each module. If it is '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 can also delete them afterwards in the DisplayGUI by using the option 'delete data' accessible via right-click on the selected module. To reduce data storage, avoid saving unnecessary intermediate data and use the option: 'Delete previous .nir data file' to 'true'. Keep the step strategic to inspect. The data

from any module saved can be visualized by the DisplayGUI. However, only the last one can be edited.



## Hands-on tutorials

Several tutorials are available to help you get started with the toolbox. They provide examples of data and template batches on how to use the main features. You can adapt these batches to your data to build an individual analysis pipeline.

- [Easy SetUp](#)
- [Getting started with LIONirs toolbox](#)
  - Explanation of LIONirs toolbox menu and data structure
  - Read and visualize .nirs data.
- [Automated artifact detection](#)
  - Read .snirf dataset
  - Run automatic artifact detection and correction
  - Create a new branch
  - Apply PCA or PARAFAC correction
  - Export corrected data to .snirf
- [3DMTG introduces project construction \(.pri\) with a template MRI.](#)
- [ReadData introduces how to read multimodal data using NIRScout equipment \(NIRx\).](#)
  - Add EEG, audio, video, and auxiliary signals
- [Task related hemodynamic analysis.](#)
  - Read and convert data into hemodynamic concentration changes (HbO, HbR)
  - Data average
  - GLM
  - Statistical analysis (One sample t-test, unpaired t-test, anovan)
- [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.
  - Correct data using DisplayGUI.
  - Short-distance regression
- [Connectivity analysis](#)
- [Show how to automate batch pipelines.](#)
  - Example of script to run large dataset
- [Additional examples \(semantic task\)](#)
  - Import EEG marker
  - Quality report

## 3dMTG

This module prepares the 3d anatomic reconstruction of the head and represents all pairs of sources and detectors (also called optodes) used for the fNIRS recording experiment. The 3d representation can be the scalp, the cortical surface or the atlas of the cortex (Brodmann). The anatomical surface can be a subject's individual MRI or a template. The [Tutorial 3dMTG](#) provides examples using an MRI template, optode and landmark coordinates to construct a project (.prj). When 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>) or Brainsuite (Dogdas et al., 2005). See appendix on [individual anatomical MRI preparation](#) to find some tips. A measure of the geometric localization of the sources, detectors, and the anatomical fiducial marker on the subject's head (Nasion, Left preauricular marker, Right preauricular marker) are necessary. The optodes' localization is read from the [.elp file](#) created by a stereotactic system such as BrainsightTM Frameless 39 (Rogue Research Inc., Montreal, QC, Canada) or Polhemus (Polhemus, Colchester, Vermont, USA). Using individual MRI and subject's optode measurements give precise anatomical representation. When using an MRI template and a standard helmet measurement, it is a good practice to measure the 10-20 EEG standard, to ensure uniformity of helmet position over the subjects. The correspondence between optode localization and anatomical representation is done with a rigid body transformation method using anatomical markers (nasion, left and right pre-auricular points) identified on the subject's MRI images (Penny et al., 2011). The user has the flexibility to manually refine the optode's position in the GUI if necessary. 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. Association of coordinates with the position of each source and detector on the helmet (.elp file).
2. Identification of fiducial marks on the MRI there is used to register fiducial landmark coordinate and the MRI.
3. MRI segmentation of cortical tissue and the scalp.
4. Anatomical atlas (optional Brodmann or other predefined atlas segmentation, i.e. an MRI volume define using a specific intensity for each anatomical region).

The following graph shows the GUI of the 3dMTG module.

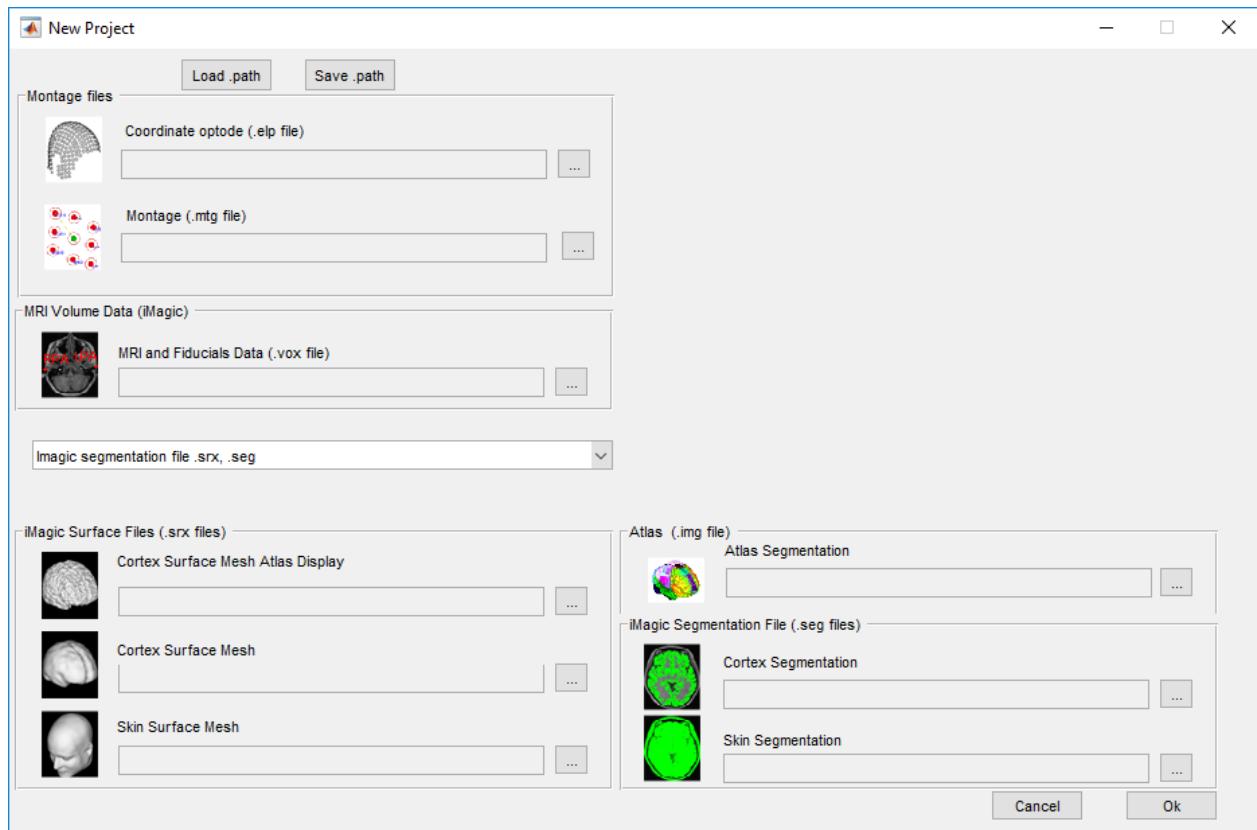
3dMTG GUI toolbar :

	Create a new project (.prj).
	Open .prj.

	Save .prj.
	Export project data (.mtg, .seq, .elp, .ele).
	Print the screen as an Encapsulated PostScript (.esp) vector graphic.
	Rotate to change the helmet orientation.
	Zoom.
	Ruler to measure the 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 a selected hole.
	Identify the atlas area or create a hole on the skin surface. Click on the skin surface to indicate the location of a new hole.
	Montage parameters.
	Display options.
	Open help file.

# Creation of a new project

To create a .prj file, go to Menu/File/New Project. Once the window opens, you can add the appropriate files as described below



## Montage files

**Coordinate Optodes (.elp file):** Polaris positions measured on a helmet which contains fiducial position for registration.

**Montage (.mtg file):** This is an optional entry. If it is not the first project with the same hole configuration, you may use a previous mtg file that contains holes and optodes association. If it remains empty, you will need to specify source and detector position. If it remains empty, you will need to specify source and detector position in the new project.

## MRI Volume Data (iMagic)

**MRI and Fiducial Data (.vox file):** MRI volume, with manual entries of fiducial left preauricular (LPA), right preauricular (RPA), and nasion (NAS). Voxels may priorly need to be interpolated into isotropic format (1x1x1 mm).

## iMagic Surface Files (.SRX files)

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

**Cortex Surface Mesh for atlas display:** Identify the mesh surface file used to display the atlas surface.

**Cortex Surface Mesh:** Identify the mesh surface file used to display the cortical surface.

**Skin Surface Mesh:** Identify the mesh surface file used to display the head shape and indicate source and detector localization.

Atlas (.img file)

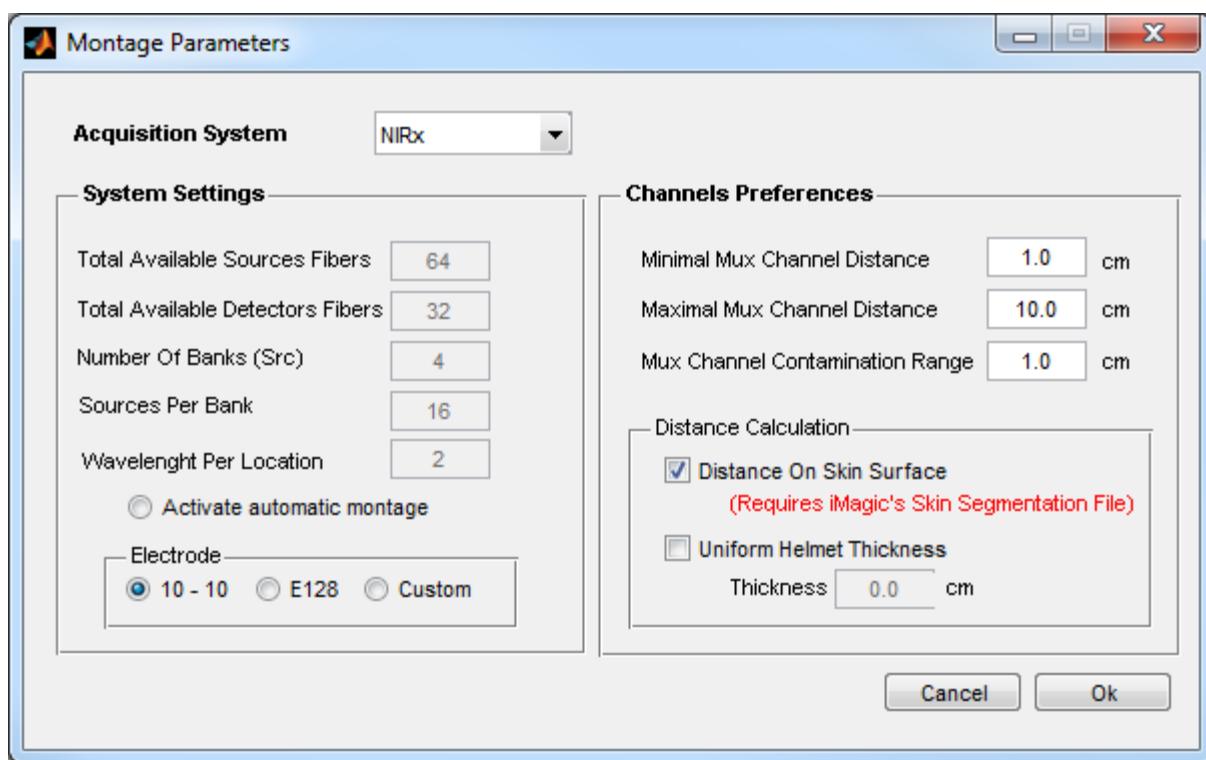
**Atlas:** Volume segmented with standard atlas (has to be in the same volume referential as the previous (.srx) file atlas surface).

iMagic Segmentation File (.seg files)

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

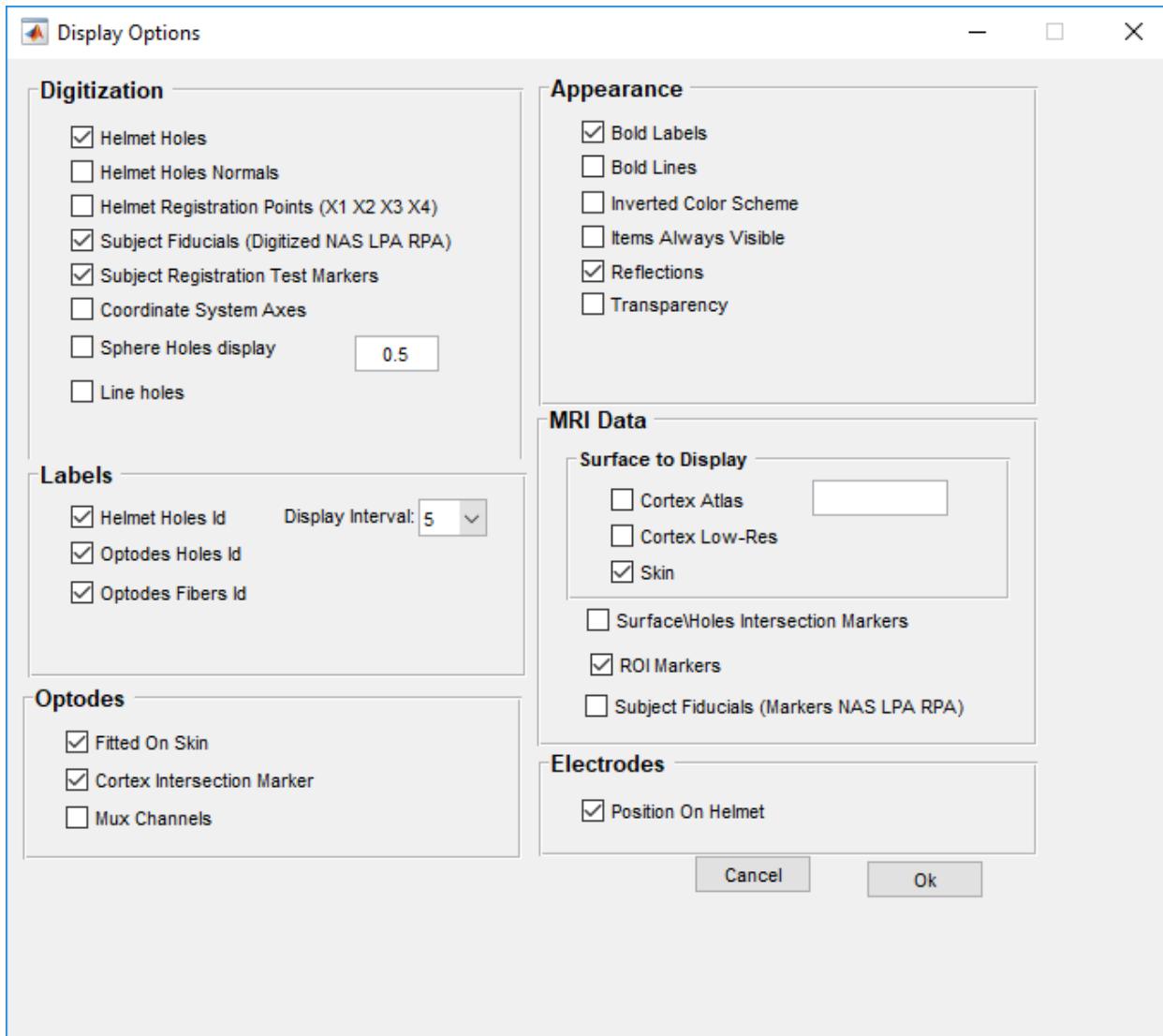
After entering the locations of the files, you can save the configuration via ‘save path’. ‘Load path’ allows you to reconstruct your project quickly.

## Montage parameters



Montage parameters can be accessed via the toolbar icon  or the menu bar ‘Montage/Parameter’ in the 3dMTG GUI. You have the option to select the acquisition system of your recording which determines the nomenclature of the holes. With the NIRx system for instance, D1,D2,D3... refer to detectors and S1,S2,S3... to sources. See [appendix](#), for the ISS hole nomenclature system.

## Display options



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

Subject Registration Test Markers	Additional markers for the region of interest.
Coordinate System Axes	Display the x, y and z axis on the visualization.
Sphere Holes Display	Holes are displayed as spheres.
Line Holes	Draws a line between holes DA1 and DA2 to facilitate visualization and installation.

Labels are the name of each hole perforated in the helmet. You may use any naming convention. Our convention specifies the hemisphere (D = right, G = left), the row (ex. A) and the hole number (ex. 1) :

- **DA1:** refers to hole 1 in the first row A of the right hemisphere.
- **DB1:** indicates 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.

Label options	Description
Helmet holes Id	Display the hole identification.
Display Interval	Set the interval between hole IDs. For example set it to 1, to show every or to 5, to show every fifth.
Optodes Holes Id	Display hole label (DA1,DB1...) on holes.
Optodes Fibers Id	Display source or detector label (S1,D1) on holes.

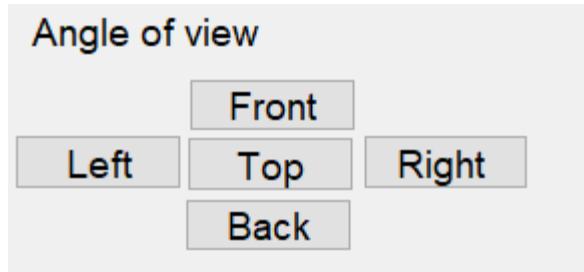
Optode options	Description
Fitted On Skin	Show optodes' projection on the skin surface.
Cortex Intersection Marker	Show optodes' projection on the cortex surface.
Mux Channels	Show a combination of source and detector close to each other.

<b>Appearance options</b>	<b>Description</b>
Bold Labels	Display labels in bold font.
Bold Lines	Show optodes projection on the cortex surface.
Inverted Color Scheme	Use a black background with white labels.
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 surface as transparent.

<b>MRI Data</b>	<b>Description</b>
Cortex Atlas	Atlas segmentation surface display. Write numbers specific to the atlas surface and show them as colored areas.
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)	Manual adding of fiducials in the MRI Neuronic Image Processor.

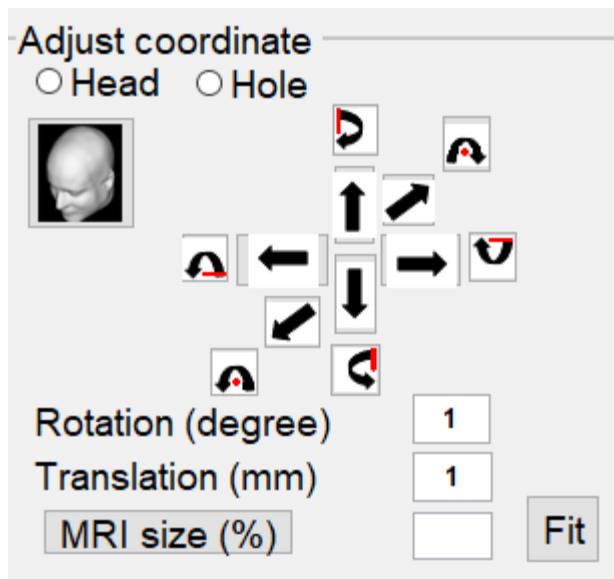
<b>Electrodes</b>	<b>Description</b>
Position On Helmet	Display the electrode labels.

## Angle of view



<b>Front</b>	Front view, front coronal plane view
<b>Left</b>	Left view, left sagittal plane view
<b>Top</b>	Top view, top axial plane view
<b>Right</b>	Right view, right sagittal plane view
<b>Back</b>	Back view, back coronal plane view

Adjust the coordinates of the MRI image or position of holes



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 towards the top.
	Move the head/hole towards the bottom.
	Move the head/hole towards the back.
	Move the head/hole towards the front.
	Move the head/hole towards the left.
	Move the head/hole towards the right.
	Rotate the head towards the left side.
	Rotate the head towards the right.
	Bend the head downwards.
	Lean the head backwards.
	Tilt the head towards the left side.
	Tilt the head towards the right side.

## Identify source, detector, or electrode

Please refer to montage parameters for the correct label identification according to your equipment (NIRx or ISS). [Appendix](#) contains additional information about the convention used by different equipment.

1. Press on the interface shortcut Src (source), Det (detector) or Ele (electrode).
2. Click on a hole of the helmet to attribute Src, Det or Ele.

3. On the left panel, choose the label identification corresponding to your experiment.
4. When 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 usually to read the raw data. The menu NIRS data offers several options to support your data format. It will transfer the data into the appropriate format for the toolbox and then create a first NIRS.mat structure.

## Read NIRSCOUT

**Description :** Read data acquired with **NIRScout** on a NIRx system.

**Inputs:**

**Select NIRx NIRScout data:** Recording 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. Trigger, wavelengths, and parameters will then be read and associated with the helmet's project .prj. Ideally you do not rename the files, or if you do, rename them all identically and keep them in the same folder.

**Subject age:** Write the subject's age in years.

**Helmet .prj:** Associate recording helmet configuration. See 3dMTG section above and [tutorial](#).

**Analyzed files directory:** Specify the location where to save the analyzed files (.nir,.vhrd,.vmrk). A NIRS.mat structure is created that can be opened/visualized in the DisplayGUI or used for subsequent operations.

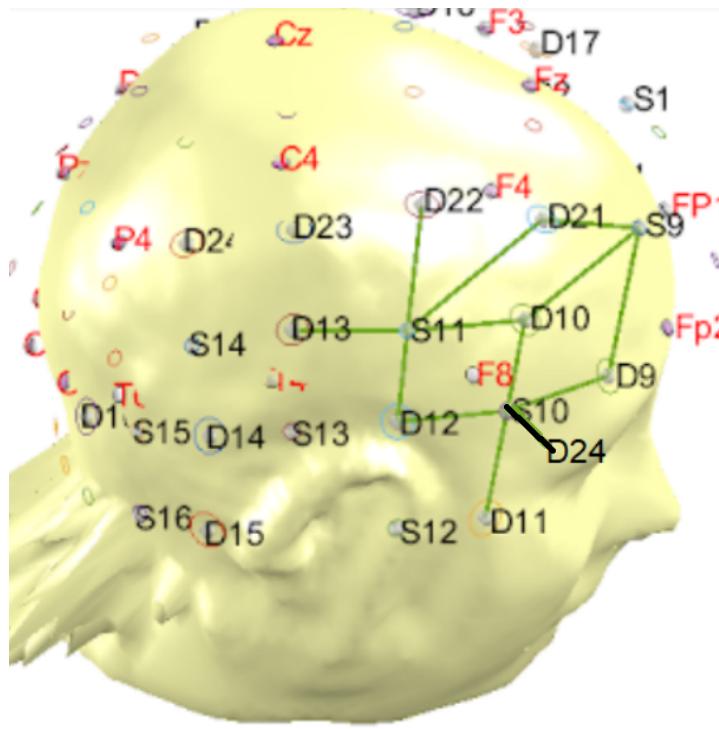
**Standard deviation (STD):** Defines STD minimal to avoid channels measuring an abnormally noisy and high variation signal in the data. High STD channels will be marked as rejected.

**Light intensity (DC):** Defines a minimal light intensity to ensure good signal detection. Low light intensity channels will be marked as rejected.

**Minimum distance:** Defines a minimal geometric distance between a source and a detector for data to be included (in centimetre).

**Maximum distance:** Defines the maximal geometric distance between a source and a detector for data to be included (in centimetre).

**Short distance probe :** NIRx provides a short distance (SD) probe with multiple detectors placed in a short distance to a source location. If you use the probe, indicate the source number(s) that you use for the probe. A zone file is created to associate the SD channels to the proximate channels. This allows the use of the SD for instance as a regressor in the GLM. To do so, use the zone file of the SD as a regressor in the Component extract list.



Example of zone identification close to the NIRx short distance S10-D24.

## Read .nirs (HoMER)

**Description :** Read HoMER .nirs format.

Matlab structure with the .nirs extension that contains at least the following information fields :

d	Nirs data Time samples x Channels
t	Time samples
s	Trig vector Time samples x Conditions
SD.SrsPos	Source id x position (x,y,z)
SD.DetPos	Detector id x position (x,y,z)
SD.Lambda	Equipment wavelength (nm)
SD.MeasList	Channel information with column Source, Detector, Weight, Wavelength define for each channel.

**Inputs:**

**Select .nirs:** File to open.

**Subject age:** Write the subject's age in years.

**Create or import a project file:** Decide whether to import or create a project file. For the import, the .prj file must be selected using the file selector. No further action is required to create a new project file. It will automatically be created in the output folder.

**Analyzed files directory:** Specify the location where to save the analyzed files ( .nir, .vhrd, .vmrk). A NIRS.mat structure is created that can be opened/visualized in the DisplayGUI or used for subsequent operations.

## Read .snirf

**Description:** Read [Shared Near Infrared File Format Specification](#) file and import the data into this toolbox. Please install Homer 3 ([https://github.com/fNIRS/snirf\\_homer3](https://github.com/fNIRS/snirf_homer3)) to support .snirf class.

**Inputs:**

**Select .snirf:** file .snirf to open.

**Subject age:** Write the subject's age in years.

**Create or import a project file:** Decide whether to import an existing or create a new project file. When you import a project, the .prj file must be selected using the file selector. No further action is required to create a new project file. It will automatically be created in the output folder (=Analyzed files directory).

**Analyzed files directory** Specify the location where to save the analyzed files (.nir,.vhrd,.vmrk). A NIRS.mat structure is created that can be opened/visualized in the DisplayGUI or used for subsequent operations.

## Read BOXY ISS

**Description :** Read data acquired with the [ISS imagent system](#).

**Inputs:**

**Select boxy files:** File to open.

**Subject age:** Write the subject's age in years.

**Helmet .prj :** Associate recording helmet configuration .prj created in 3DMTG.

**Analyzed files directory:** Specify the location where to save the analyzed files (.nir,.vhrd,.vmrk). A NIRS.mat structure is created that can be opened/visualized in the DisplayGUI or used for subsequent operations.

**Standard deviation (STD):** Defines STD minimal to avoid channels measuring an abnormally noisy and high variation signal in the data. High STD channels will be marked as rejected.

**Light intensity (DC):** Defines a minimal light intensity to ensure good signal detection. Low light intensity channels will be marked as rejected.

**Minimum distance:** Defines a minimal geometric distance between a source and a detector for data to be included (in centimetre).

**Maximum distance:** Defines the maximal geometric distance between a source and a detector for data to be included (in centimetre).

## Multimodal

### GUI\_AUXEdit

Use this utility GUI help to create auxiliary files for GLM regression or visualization.

- The files are created, but they need to be added to the analysis (see [Read AUX](#)). Prefer the option [Create AUX](#) module to embed the data directly in the project.
- The auxiliary file corresponds to a long data recording (usually unsegmented)
- Triggers need to match the recorded NIRS .nir data or EEG .dat to be segmented subsequently.

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 (physiology regression)
- One channel data (physiology regression or other example?)

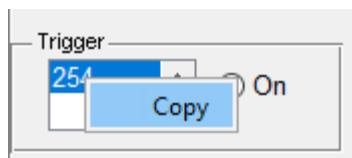
### Create HRF using onset duration .xls file

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. Indicate the .nir file to keep the same trigger information as the current recording.

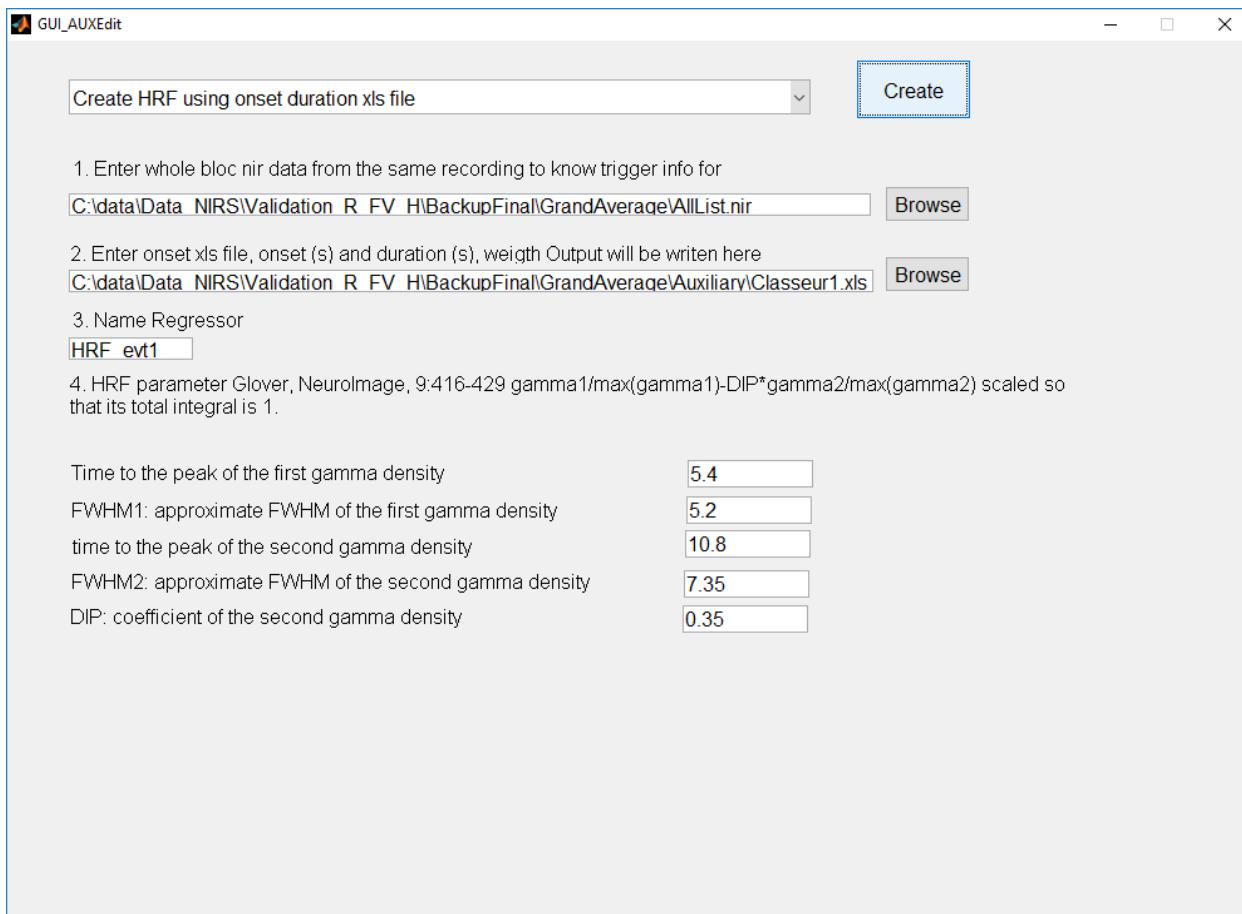
1. Create an Excel file such as event onset, duration, and weight information about the hemodynamic response function (Glover et al, 1999).

	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

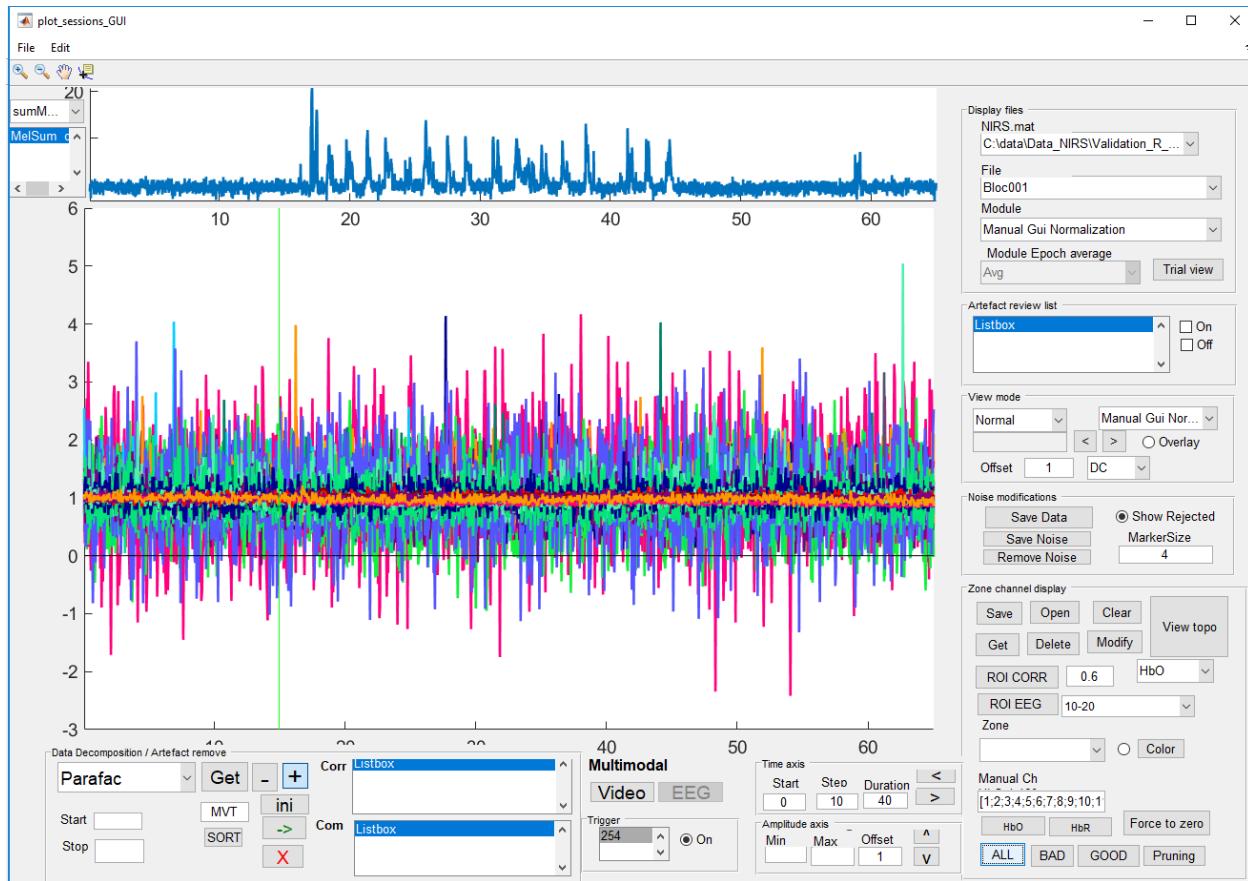
**Tip:** To obtain the onset time of the trigger use the copy function in the DisplayGUI you can access by right-click on the trigger.



Define file and parameter of the HRF in the GUI :



## Trigger info



## Global average

Use the average of all channels from NIRS.mat data to create 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 NIRS.mat data to create 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)

In speech, a signal decomposition procedure named as Mel Frequency Cepstral Coefficient is used to identify relevant parts of the speech (Davis, Mermelstein, 1980). The toolbox [MFCC](#) by Kamil Wojcicki is used to compute the MEL coefficient<sup>1</sup>. We do the sum of the mel coefficient to determine where the words are pronounced during the experiment as an auxiliary channel.

As preprocessing

---

<sup>1</sup> Kamil Wojcicki (2020). HTK MFCC Matlab (<https://www.mathworks.com/matlabcentral/fileexchange/32849-htk-mfcc-matlab>), MATLAB Central File Exchange. Retrieved April 3, 2020.

1. The sound in a wav format can be converted 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)
```

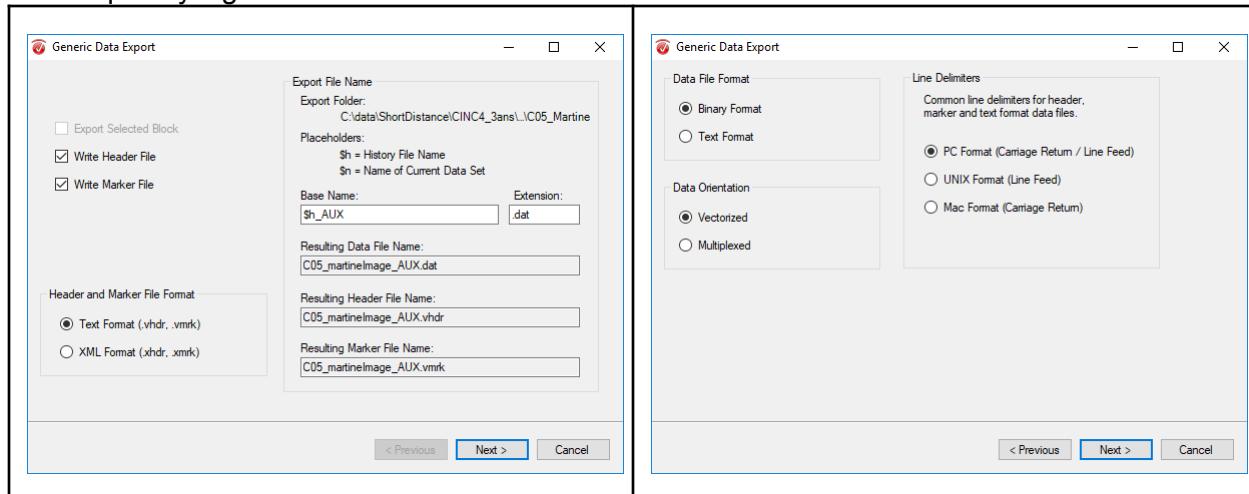
2. Identify the delay between the sound and the beginning of NIRS data or EEG data file (used to identify an associate trigger in the auxiliary file). You could use the software Audacity and calculate the delay using a marker in the file, or clean noise in the room that does not belong to participant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

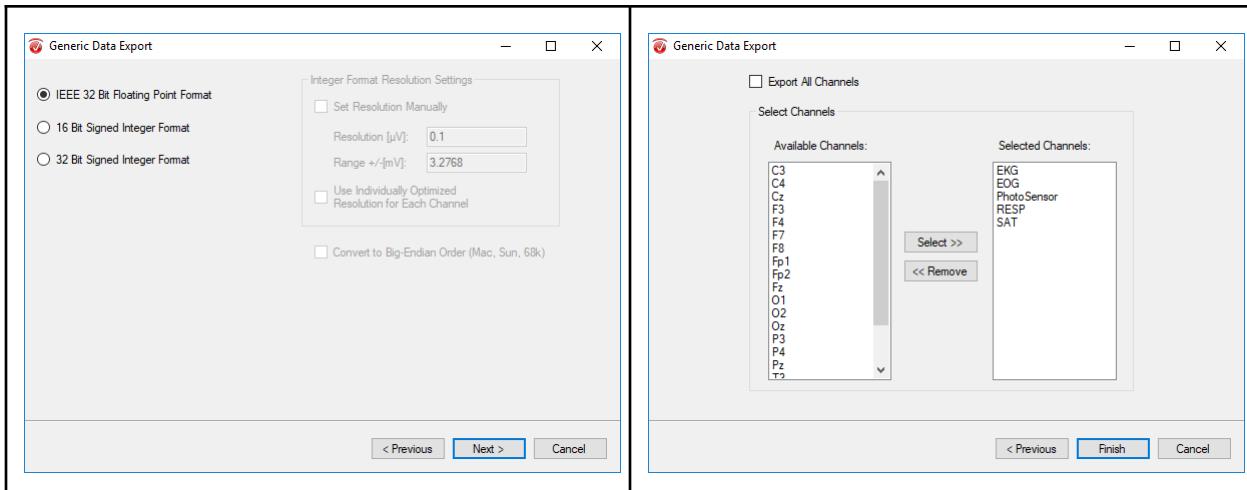
## Concatenate AUX or EEG file

The rule to easily segment and synchronize NIRS, EEG, AUX, and Video on the same timeline is to keep one long file with identical triggers on each of them. The segment module will handle each trigger to be synchronized in the GUI (NIRS, EEG, AUX, and video). It is possible to merge them in the GUI\_AUXEdit to combine multiple sessions in one long file. You must keep rigorously recording order when you open several files to ensure that all triggers are in a logical order. Be aware, verify and make sense of your data.

## Prepared EEG or AUX as multimodal data for LIONirs 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. For the AUX signal, probably no filter will be required to not distort respiration, cardiac or low-frequency signals.





## Read EEG

**Description:** Add a link to the EEG data to synchronize them with the fNIRS file using a common marker. The same trigger needs to be recorded in EEG and fNIRS to synchronize both. The appropriate data format can be generated using a generic data export in the BrainVision Analyzer program (.dat, .vhdr,.vmrk), see [appendix](#). You must add the EEG file after the read fNIRS data to add the EEG data in NIRS.mat dependency. If you have many sessions, use the concatenate function to merge them together. It is good practice to first read data from both modalities in one long block and segment at a later stage of the pipeline. The data will be synchronized only when you use the operation ‘segment’. Be careful to have the same trigger for both data sets before segmentation to avoid misinterpretation.

### Inputs:

**NIRS.mat:** Select NIRS.mat for the subject. It is expected that data was recorded simultaneously and using the same trigger.

**EEG\_files:** identify the EEG data file (.dat).

## Read AUX

**Description:** Add a link to the AUX data to synchronize them with the fNIRS file using a common marker. The same trigger needs to be recorded in AUX and fNIRS to synchronize both. The appropriate data format can be generated using a generic data export in the BrainVision Analyzer program (.dat, .vhdr,.vmrk), see [appendix](#). You must add the AUX file after the read fNIRS data to add the EEG data in NIRS.mat dependency. If you have many sessions, use the concatenate function to merge them together. It is good practice to first read data from both modalities in one long block and segment at a later stage of the pipeline. The data will be synchronized only when you use the operation ‘segment’. Be careful to have the same trigger for both data sets before segmentation to avoid misinterpretation.

- Similar to Read EEG, auxiliary data can be integrated into the analysis pipeline. They are subsequently available for GLM regression and visible in the upper panel of the DisplayGUI.
- Adequate files (.dat, .vhdr, .vmrk files) can be generated via the generic data export of BrainVision analyzer.

- If the trigger is present in NIRS and AUX files, add the Read AUX module in your pipeline after the read fNIRS data but before the Segment module. The data will be segmented using the same pre-time and post-time trigger as for the fNIRS file.
- It is possible to add several auxiliary files using different sampling rates. However, all of them will be treated as independent files and need to be segmented correctly according to the trigger.

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. It is expected that data was recorded simultaneously and using the same trigger.

**EEG\_files:** identify the EEG data file (.dat).

## Create AUX

**Description:** This function helps to generate auxiliary files such as a hemodynamic response function (HRF) that can be used as a regressor in the GLM.

**Inputs:**

**HRF trigger onset**

**Options:**

**Replace AUX:** Erase previous multimodal AUX file(s) while adding the newly created HRF signal.

**Add AUX:** Keep previous multimodal AUX file definition and add the newly created HRF signal.

**Inputs:** 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.

**Trigger onset:** Identify the trigger number to be used as onset.

**Duration (s):** Enter the duration of the task or expected response after the onset (seconds).

**HRF label:** Label for the AUX identification.

**Time to peak:** Time to peak of the first gamma density

**FWHM1:** FWHM of the first gamma density

**Time to peak:** Time to peak of the second gamma density

**FWHM2:** FWHM of the second gamma density

**DIP:** Dip coefficient of the second gamma density

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

## Import EEG marker information (E\_readEEGMarker)

**Description:** Import EEG markers as fNIRS triggers. fNIRS uses trigger information (i.e. integer value) to identify events such as the beginning/end of a task or a participant's response. The toolbox uses trigger information to synchronize and segment files, to model a hemodynamic response or to average fNIRS data. When you edit markers in Brain Vision 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. You should apply a first segmentation based on a trigger of the beginning of the acquisition to synchronize EEG and fNIRS before importing manual markers.

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. fNIRS data can be at any analysis step, but must have been acquired simultaneously with the EEG markers.

**EEGMarker=NIRSTrigger:** You must enter the marker 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 in the EEG events, and give them the trigger definition 1 in the fNIRS events. In this example, all events called MARKER2 will be identified in fNIRS by the trigger definition 2. You can find different markers, but separate them by a comma.

## Read Video

**Description:** Link a video and synchronize it with the fNIRS data. Video files do not include triggers. Indicate if the video starts conjointly to fNIRS, EEG, or AUX or if they have a time lag. fNIRS or EEG or AUX trigger will serve for the video segmentation.

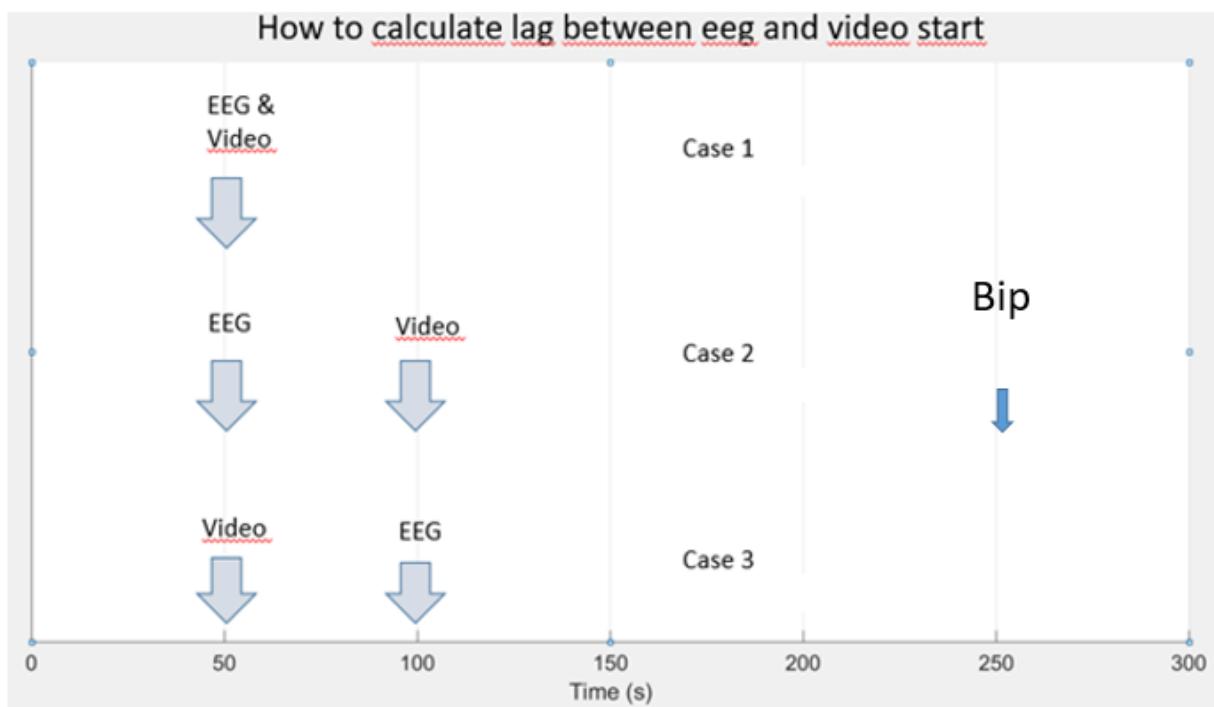
**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. Data is expected to have been recorded simultaneously with the video.

**Video file:** Identify the video data file.

**Reference to synchronization trigger:** Indicate which file will serve as a reference to segment video timing: NIRS, EEG, or AUX data. The trigger is necessary to use segmentation and keep data in the same timeline.

**Offset (yes, no):** ‘No’ means that the beginning of the video starts synchronously with the reference data (ex. NIRS, EEG or AUX data). ‘Yes’ means a lag exists between the recordings of the different modalities and you have to enter the delay in seconds between those recordings manually.



Case 1: EEG and Video start at the same time. Therefore, the delay is 0 seconds.

Case 2: EEG recording starts before the video recording. A reference mark (bip) was measured at 200 seconds for the EEG whereas in the video the same mark (bip) can be heard after 150 seconds. The lag between EEG and the video is therefore -50 seconds.

Video lag - EEG lag = offset

$$150 - 200 = -50$$

Case 3: EEG recording starts after the video recording. A reference mark (bip) was measured at 150 seconds in the EEG whereas in the video the same mark (bip) can be heard after 200 seconds. Thus, the lag between EEG and the video is 50 seconds.

Video lag- EEG lag = offset

$$200 - 150 = 50$$

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

## Read Audio

**Description:** Audio files can be integrated using the same procedure as for video files. Matlab supports the following audio format : 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).

## Segments / Onsets

A data marker is essential to identify events during an experiment using an external or manual trigger. When you read the data it can have different formats: s vector in .nirs MATLAB files, .evt in NIRx recording, aux5 field in ISS recording. It is a numerical value identifying the start time of a specific task that is recorded from an external trigger. In further analysis, these onset triggers allow segmenting the data and classify events belonging to the same category.

## Segments

**Description:** This module segments data around triggers (defining pre-time and post-time). This step is essential to synchronize multimodal data such as EEG, auxiliary (AUX), or video. If the acquisition uses several sessions, use the option Concatenate to merge blocks before segmenting. Triggers must be homologous in each data file (fNIRS, EEG, AUX). It is your responsibility to test the correct synchronization of your files. Over a long period of recording could induce a delay between files. A good practice is to use multiple triggers as a reference to avoid significant lag.

### Inputs:

**NIRS.mat:** Select NIRS.mat for the subject. It is usually expected to be raw data or dOD data with unfiltered cardiac frequency. It is recommended to add multimodal data before the segmentation and ensure they are correctly synchronized afterwards using analog trig.

**Delete previous .nir data file:** set true to 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 trigger to use for the segmentation in seconds.

**PostTime:** Enter the time after the trigger to use for the segmentation in seconds (ex. Duration of registration).

## Concatenate blocks in a nirs.mat

**Description:** This function groups files from the same subject (NIRS.mat) one after the other when different sessions have been registered. AUX and EEG files will be concatenated if they are included in the NIRS.mat structure. Concatenate video is not supported.

### Inputs:

**NIRS.mat:** Enter nirs.mat file of the specific analysis step.

**Options:**

**Merge only:** groups files without any additional operation.

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

**File number:** Enter the numbers of the blocks to be considered. Set to 0 to take them all. In the DisplayGUI, a file list will be identified as Bloc001.

## Concatenate nirs.mat (multi subjects time series).

**Description:** This function groups data from different subjects (NIRS.mat) into one NIRS.mat. Create a new folder, for instance called .../Grand\_Average and put the list.xlsx and the channelist.txt you create inside. The channelist.txt identifies the channel to use. Subsequently, a new NIRS.mat will be created in this folder using those channels. This new NIRS.mat groups the individual data of multiple subjects (NIRS.mat) and creates one long continuous segment. Once multiple subjects are grouped, you can apply further analysis, such as the average module to perform a grand average of all subjects. How to create the list.xls and [channelist.txt](#) is described beyond.

### Inputs:

**Enter NIRS.mat list to group (.xls):** Use an excel file to specify the location of the NIRS.mat of each subject and the corresponding channelist.txt as illustrated in the following example:

File List.xlsx:

	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
2	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

The channel list defines the participants' channel order and lists source and detector labels. See [create channel list](#) to automatically create a channel list for a participant. It determines the order of the channel to average together. In order to average across multiple subjects, you must ensure that channels have an identical localization on the scalp of each individual subject. In the case of recordings using a slightly different optode configuration, you must ensure that the localization is comparable across subjects. If they have any helmet differences, use the channel list order to keep constant 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. Ensure that the zone contains the same identification label for all participants. For example, ‘TemporalRight’ has to be written in the exact same way for each subject’s zone. All the channels belonging to the temporal right zone will be averaged. Once again the first subject in the list is kept as a reference.

#### Options:

**Merge only:** groups files without any additional operation.

**Merge and detrend:** groups files and detrends each of them before, such that the start and stop point of each file are adjusted to zero.

#### Set exclude channel to NAN:

**Exclude:** rejected channels will be replaced by a missing value (NAN).

**Keep:** no additional operation concerning the rejected channels will be applied.

**Normalization:** Apply normalization operation on each NIRS.mat to reduce individual variability<sup>2</sup>. Only apply using the channel list.

**No normalization:** do not apply any normalization.

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

**Z-score Normalization:** Apply z-score normalization.

## AuxTrig to ManualTrig

**Description:** A trigger is usually recorded by the equipment and saved with the raw data. This trigger information is kept in the structure and can be visualized or used to segment, normalize, or average 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 can be edited manually. In the following example, the Manual Trig is the onset for trigger 2.

```
Trigvalue = 2;
%define trigger value to 2
timingfile{1} = [1.152,2.56,3.712,4.992];
%time seconde enter trigger 2 for the file number 1
timingfile{2} = [0.384,1.664,2.816];
%time seconde to enter trigger 2 for the file number 1
```

<sup>2</sup> Moeller, J., 2015. A word on standardization in longitudinal studies: don’t. Front Psychol 6. <https://doi.org/10.3389/fpsyg.2015.01389>

#### Inputs:

**NIRS.mat**: Select NIRS.mat. The previous step can be any step if the NIRS data contains triggers to export.

**File output**: Indicate a name for the output file. The file is located in the current folder of the NIRS.mat file.

If you want to modify the trigger you have to import it manually using '*ManualTrig to AuxTrig*' or alternatively edit it in the DisplayGUI, see section on [Trigger in the DisplayGUI](#) to do so.

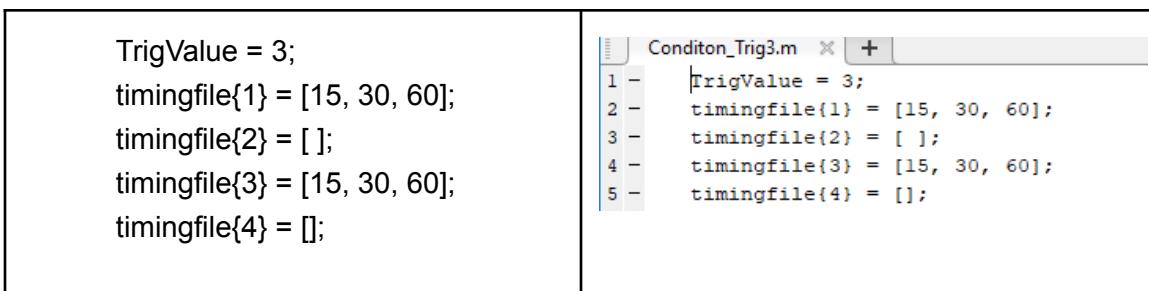
## ManualTrig to AuxTrig

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

#### Inputs:

**NIRS.mat**: Select NIRS.mat. The previous step can be any step of the NIRS data.

**Enter new trig definition**: Open ManualTrig file. The manual trig is a .m MATLAB script that defines the new trigger value (TrigValue=X) with an integer used for the trigger identification and the file number: timingfile {1} = [15,30]; indicating the timing [s] of the trigger event for the first file/block of the data. As the NIRS.mat structure can contain one or many files, you have to define a timing file for each of the files present in your data. If as an example the file 2 does not have any predefined trigger events, the timingfile has an 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](#) you can find an example of a batch using a manual trigger.

#### Options:

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

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

## Preprocessing NIRS data

### Artifact detection

**Description:** Artifact detection and correction with the LIONnirs toolbox is structured as a two-step semi-automatic process, including automatic and manual processing. First, several criteria of the signal's variation allow for an automatic detection of 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 under correction of the signal, which is why it is strongly recommended to manually verify and, if required, adjust the results of the automatic detection and correction. Automatic artifact detection and correction 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 below.

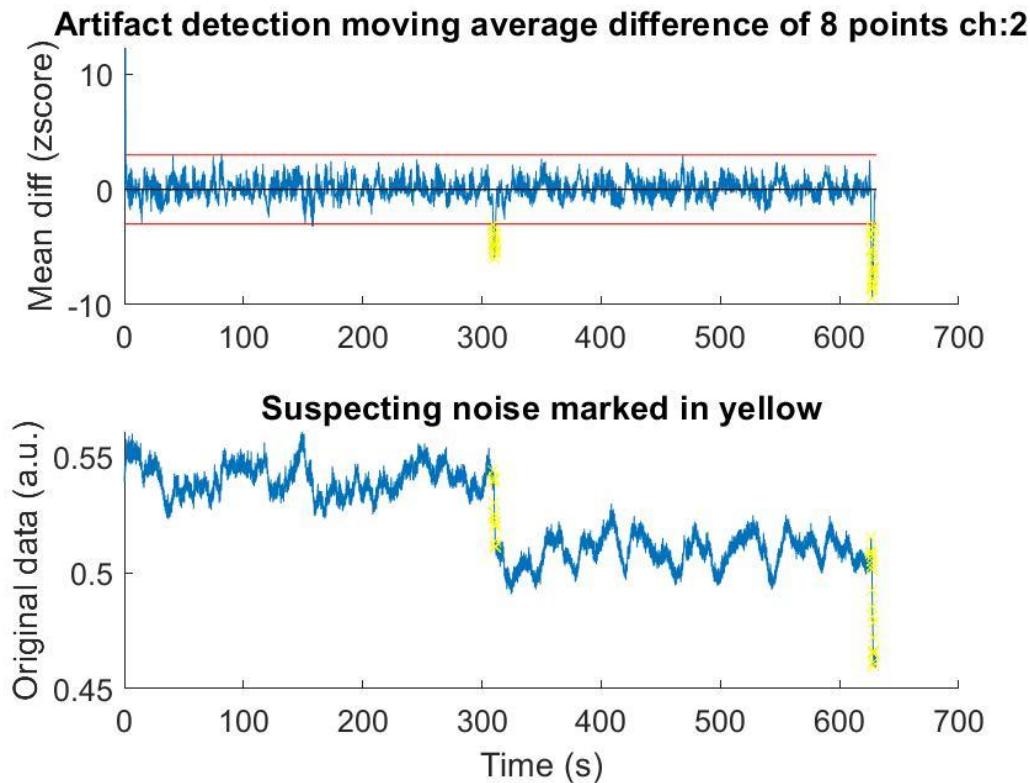
**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. It is usually expected to be raw data or dOD data with unfiltered cardiac frequency.

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

**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 selected NIRS.mat file. A summary report for each of the applied criteria: 'Artifact detection using moving average', 'Minimal percentage of bad channels to be marked as artifact', 'Minimal subinterval' and 'Correlation between channels for artifact interval'. This means that the user would for instance receive 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 ( $M$ ) for subsequent time intervals ( $X_n$  to  $X_{n+step}$ ). The new time series ( $M$ ) will be based on first sample  $M_1$  average from  $X_1$  to  $X_{1+step}$ ,  $M_2$  from  $X_2$  to  $X_{2+step}$ ,  $M_n$  from  $(X_n \text{ to } X_{n+step})$  and so on. The duration (s) of the individual time period (step) is defined by the user and determines the sensitivity of the detection for the moving average from  $X_n$  to  $X_{n+step}$ . Changes of light intensity between  $M_1$  and  $M_2$  are then specified as the difference ( $D$ ) between the means of the two subsequent time windows:  $D = M_2 - M_1$ . Difference  $D$  is transformed into z-scores and normalized over the entire dataset to determine which periods have increased signal variations. The length of the segment will affect the smoothing of the response. 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 (based on our experience we recommend a threshold around 3 z-score for a good sensibility to artifact, increase this threshold to be less sensitive or diminish this threshold to be more sensitive).



Figures show an example of artifact detection using the first criterion. The upper figure shows the moving average with the z-score scale, and the lower figure raw data on the same channel. This help you to see how the z-score selection will affect the sensibility of the detection. Segments identified as artifacts are in yellow.

**Apply:** Yes or No. Apply moving average for artifact detection.

**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 the specified z-score are identified. If identification seems too strict or too, adjust the score and rerun the module

**Z-score option:** The z-score is used to define the threshold for artifact detection. You may calculate the z-score for each channel using all-time points or using only valid time points (excluding ones identified as an artifact).

**Moving average step (seconds):** Defines the duration (s) 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 location of the selected NIRS.mat file.

**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 or No. Use a Minimal percentage of bad channels to be marked as artifacts.

**Minimal percentage of bad channels:** Define a minimal percentage of bad channels 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. Ensure that more than X seconds separate each detected interval from the previous or next detected interval, otherwise consider them as one event. Choose for instance 2 seconds as a minimum duration of the subinterval, to consider subsequent intervals that are less than 2 seconds apart as one artifact.

**Apply:** Yes or No. Use a minimum subinterval for artifact detection.

**Minimum subinterval duration (seconds) :** Select the minimum duration (in seconds) for a good subinterval, else subsequent interval will be considered as one artifacts event.

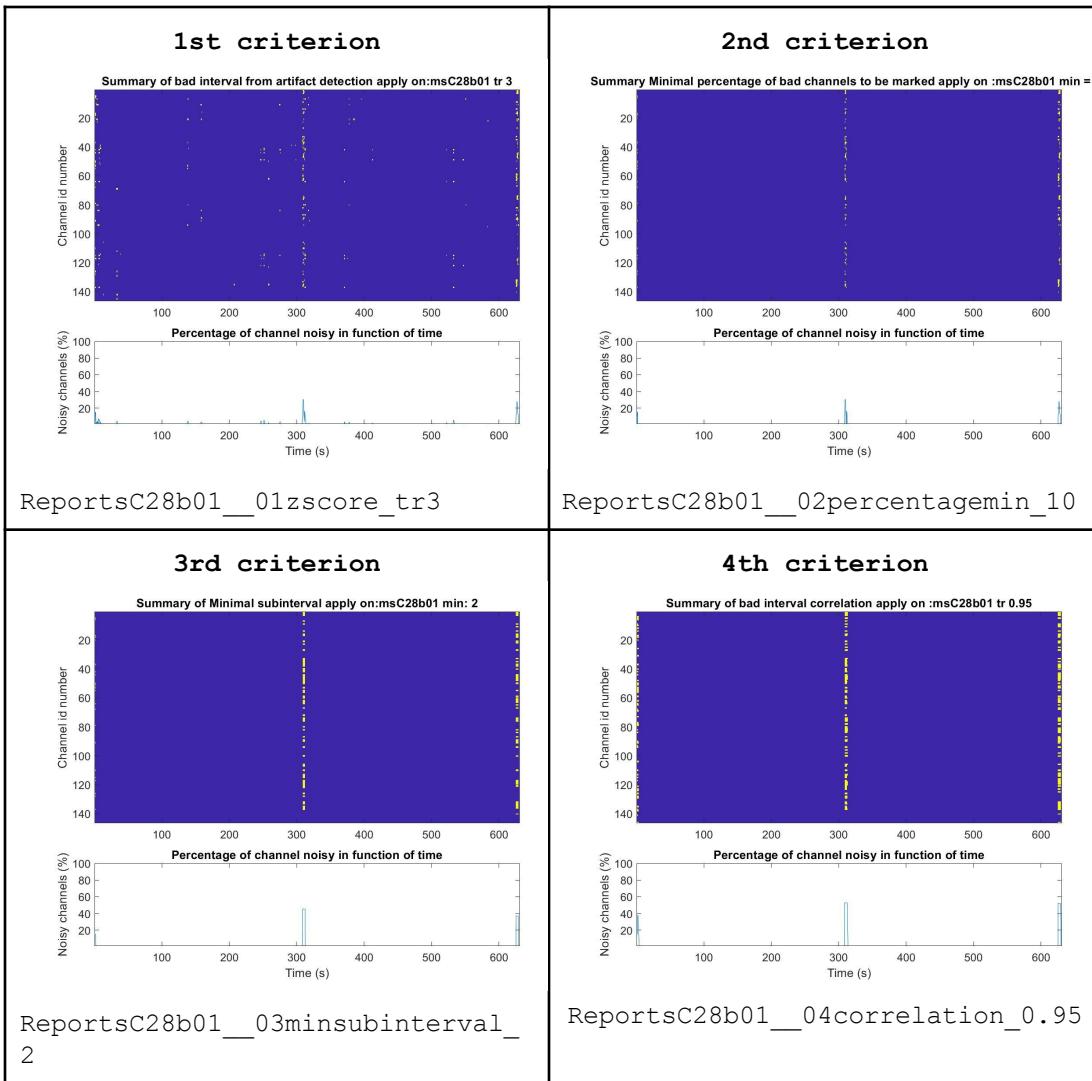
**Correlation between channels for artifact interval:** Finally, artifact detection is based on a correlation coefficient between channels. It determines the Pearson's correlation coefficient threshold of channels to be considered as being affected by the same event. For each artifact interval that has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

**Apply:** Yes or No. Use correlation coefficient between channels for artifact detection.

**Correlation threshold:** Set a minimal threshold for correlations between channels. Hence, the time course of channels showing correlations stronger than the set threshold will also be marked as an artifact.

**Output:** Example of summary reports

1. Summary report for the first criterion: Artifact detection using moving average (Fig. 1st criterion) saved as: .\\ArtifactDetection\_Report\\ReportsC28b01\_01zscore\_tr3.fig
2. Summary report for the second criterion: Minimal percentage of bad channels to be marked as artifact (Fig. 2nd criterion) saved as:  
.\\ArtifactDetection\_Report\\ReportsC28b01\_02percentagemin\_10.fig
3. Summary report for the third criterion: Minimal percentage of bad channels to be marked as artifact (Fig. 3rd criterion) saved as:  
.\\ArtifactDetection\_Report\\ReportsC28b01\_03minsubinterval\_2.fig
4. Summary report for the fourth criterion: Correlation between channels for artifact interval (Fig. 4th criterion) saved as:  
.\\ArtifactDetection\_Report\\ReportsC28b01\_04correlation\_0.95.fig



Figures showing identified artifacts for individual channels and overall percentage of noisy events based on each criterion 1-4. This help the user to verify how criteria affect the artifact detection in the data.

## Cardiac detection

**Description:** The presence of cardiac frequency in NIRS data is a well-established quality measure that allows the exclusion of channels with poor signal quality, meaning channels that did not actually capture the physiologic signal. . The physiologic signal can be absent when light intensity is too low, due to poor contact with the skin or a too large distance between source and detector. It can also be absent when the light intensity is too high because the detector is not touching the skin. In this case, contaminating light from external light sources is captured and the signal that does not represent cerebral activation. The detection of the cardiac frequency can further be affected by a low sample rate. 5Hz is a minimum requirement but you would need

a long and stable recording, else the cardiac frequency would be barely visible. Therefore, a sample rate of 10 Hz or more is recommended. The cardiac detection module in the LIONirs toolbox allows detecting the cardiac beat dominant frequency range in data using the coherence measure among channels. It subsequently allows rejection of channels without a cardiac beat.

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. It is usually expected to be raw data or dOD data with unfiltered cardiac frequency.

**Frequency range to detect cardiac peak:** Define the frequency range detection. It is recommended to select a rather wide range of frequencies to ensure that your cardiac peak is properly detected. Normal cardiac pulse varies around 1Hz in the adult population and 2Hz in babies. To verify the output figure as example below, the black line indicate the frequency interval indicated with the two red lines to ensure that the peak is well selected (Mortensen et al., 2017<sup>3</sup>, Fekete et al., 2011<sup>4</sup>).

**Minimal coherence:** Determine the threshold for the cardiac coherence between channels.

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

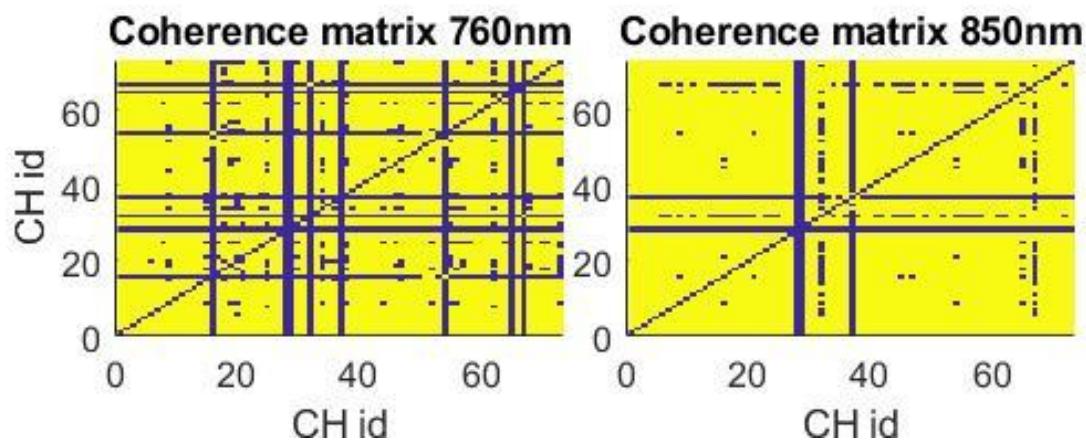
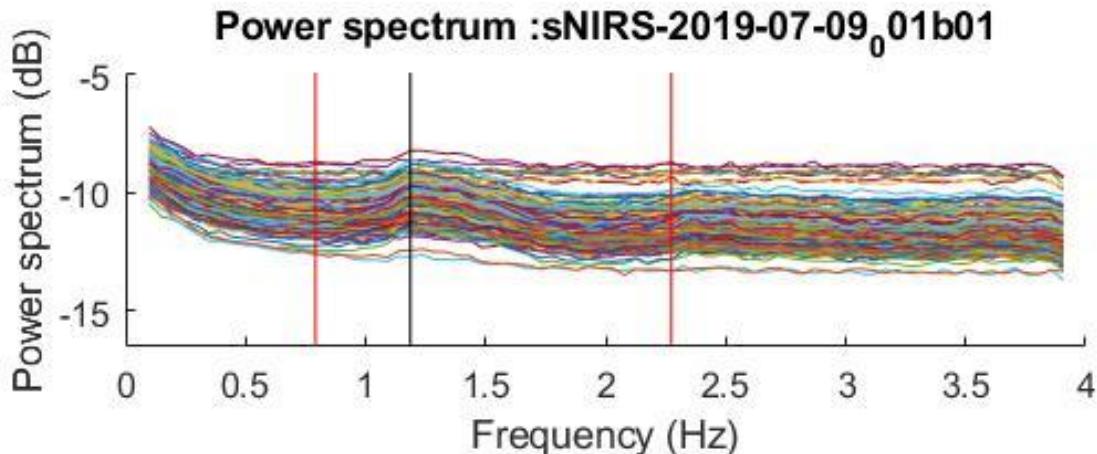
**Range around the peak (Hz):** Define a narrow range around the peak to compute the coherence. Use 0 Hz to use the peak only. If the cardiac pulse varies in time, it is possible to use a small interval around the peak (0.2 Hz).

**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 has been correctly identified.

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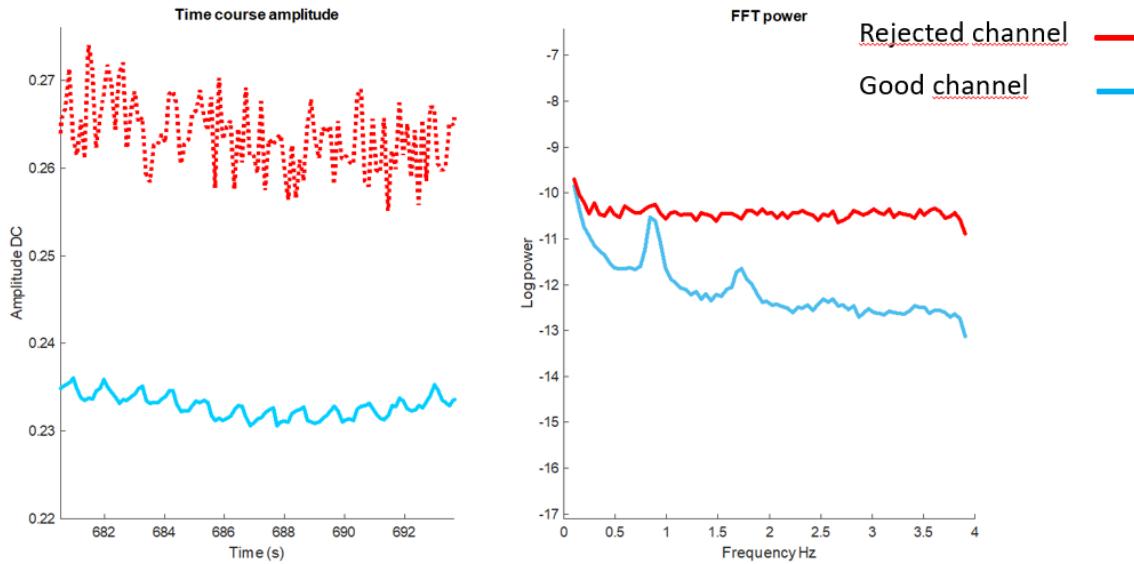
<sup>3</sup> <https://doi.org/10.1177/1367493516689166>

<sup>4</sup> <https://doi.org/10.1371/journal.pone.0024322>



The figure reports the FFT power spectrum for each channel. The two red lines limit the interval to detect the peak caused by heartbeat pulsations. The heartbeat frequency peak is identified automatically as the maximum between this interval and marked by a black line. The peak is used to measure coherence among channels. The peak can 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 show a threshold connectivity matrix for each wavelength. Channels without cardiac coherence are seen as blue lines in the coherence matrix, as the coherence measure with other channels is poor, that is below the specified threshold.

# 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 such poor quality. If many channels are 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 represent channels with a cardiac coherence below the threshold that will be identified as rejected channels.

A .xls file named cardiacCHCOH.xls is saved in the NIRS.mat folder. It helps to summarize the removed channels and the peak of the cardiac frequency. A figure (cardiacCHCOH.tif) plots the power spectrum and the matrix of cardiac coherence. When you open the data using the DisplayGUI, rejected channels are not shown. If you select 'View Rejected', they will be plotted as dotted lines.

[View Rejected](#)

	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

The file cardiacCHCOH.xls is saved in the NIRS.mat directory. In this example, the identified cardiac peak is at a frequency of 1.2362 Hz. The channels listed, represent the ones that were excluded (ex. channel #28 consisting of detector 7 and source 6, D07E6).

## 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. For example, during a cognitive task, we measured the variation of light intensity during rest and an active cognitive task to estimate the difference of hemoglobin consumption between these two distinct states. The initial state ( $l_0$ ) can be defined differently according to the experiment's goals. The intensity measured during a long experiment often varies due to movement or recording drifts. Therefore, a piece-wise normalization may be advantageous as using a resting state just before the task.

### Inputs:

**NIRS.mat:** Select NIRS.mat for the subject. It is usually expected to be raw data.

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

**Normalization type:**  $dOD = \log_{10}(I/I_0)$

Apply the normalization defining  $I_0$  as 'Normalization by files' or 'Normalization around trigger':

**Normalization by files:** Define  $I_0$  as the whole data average on each segmented file.

**Exclude artifacts from the  $I_0$  calculation:** Yes, excludes all yellow marks from the calculation. No, takes the average without considering artifact marking.

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

**Trigger:** Trigger number(identification number)

**PreTime:** pre stimulus time in seconds (=time before trigger)

**PostTime:** post stimulus time in seconds (=time after trigger)

**How to define  $I_0$ :**

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

**Io = Pretime to PostTime:** Define Io in the period between the pretime before the trig and the post time after the trig.

**Exclude artifacts from the Io calculation:** Yes, to exclude all yellow marks from the calculation. No, to take the average without considering artifact marking.

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

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

Normalization will be done between each period. This option can be useful in case of resting-state recording interrupted by a few large-scale artifacts.

## Filter

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

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. It should contain data that has been converted as DOD data.

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

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

**High pass cutoff:** Set high pass frequency 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.<sup>5 6 7</sup>

**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.*

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<sup>5</sup> (Lyons, Richard. 2011. Understanding Digital Signal Processing ISBN: 013702741-9 )

<sup>6</sup> 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)

<sup>7</sup> 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>

## Modified Beer Lambert law (MBLL)

**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. A 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.

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

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

### Inputs:

**NIRS.mat:** Select NIRS.mat for the subject. It is usually expected to be filtered dOD data.

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

**Partial Volume Factors:** Adjustment ratio of concentration changes when changes in hemoglobin occur in a focal region rather than in the entire sampling region.<sup>8</sup> Scaling could be adjusted manually, as default it is set to [1 1] i.e. equal scaling for HbO and HbR.

**DPF:** DPF is a parameter that can be adjusted. It is estimated from the wavelength and the age of the subject based on different methods. Choose one of the following methods:

**Scholkmann et Wolf 2013**

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<sup>8</sup> Strangman, G., Franceschini, M. A., and Boas, D. A. (2003). Factors affecting the accuracy of near-infrared spectroscopy concentration calculations for focal changes in oxygenation parameters. *Neuroimage* 18, 865–879.

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

### 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 can fix your own value.

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

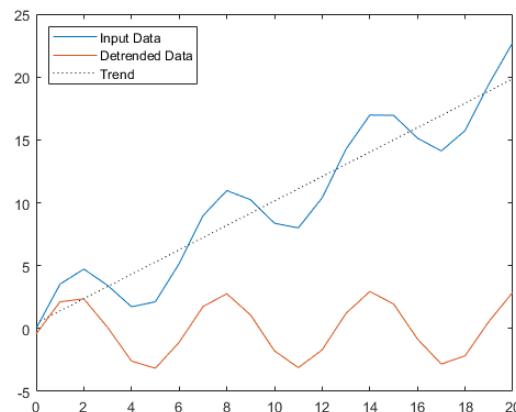
## Detrend

**Description:** Subtract linear trends on the data. The trend is estimated using the beginning and end of the block. It usually contains data that has been filtered.

### Inputs:

**NIRS.mat:** Select NIRS.mat for the subject. The data to be detrended can be at any stage of the analysis. It is typically expected to be filtered concentration data.

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



## Epoch averaging

**Description:** Average data time-window using time-locked common trigger.

### Inputs:

**NIRS.mat:** Select NIRS.mat for the subject. This is typically expected to be preprocessed data in hemodynamic concentration changes. (After artifact detection, normalization dOD, filtering, Modified Beer Lambert law)

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

**Averaging options:**

**Trigger:** Apply a specific trigger 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 trigger.

**PostTime:** Define the period to use after the trigger.

**Reject trial ratio:** Reject the trial if more than the indicated percentage of its duration is marked as a bad interval. Enter the percentage as a decimal number, for example, 0.5 for 50%. Set to 1, to keep the trial independent of the ratio of bad intervals.

**Reject channel ratio:** Reject the channel if less than the indicated percentage of the trial is rejected. Enter the percentage as a decimal number, for example, 0.5 for 50%. Set to 0, to keep all channels

**Data type:** DC is the default and uses both wavelengths or concentration changes of HbO/HbR to average the data. AC and PH (phase) are available only for ISS equipment.

**Baseline Correction:**

**Subtract preTime:** Subtract pretime to trigger from the mean of each event

**Manual:** Manual baseline correction before each events.

**Subtract value:** use the mean or median

**PreTime baseline correction:** enter the PreTime baseline correction in seconds.

**PostTime baseline correction:** enter the PostTime baseline correction in seconds.

**No baseline correction:** Do not apply any correction.

**Reject outlier trial:**

**Keep trial:** Keep all trials

**Reject outlier trial z-score:**

**Threshold z-score:** exclude outlier trials based on the z-score computation in comparison to other trials. The z-score is computed individually for each channel by using the mean and standard deviation of all trials.

**Tvalue options:**

**Against 0:** Simple t-test against 0

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

**Output:**

**Report of rejected trials per channel:** Generates a figure that expresses the percentage of blocks per channel that are used for the averaging and which channels are rejected completely after applying the Reject channel ratio. The threshold used to reject trials was defined in Reject trial ratio.

**Report of blocks used for averaging:** An xls file that indicates which blocks are rejected (0) or used (1) for averaging.

## Nullify bad intervals

**Description:** This module replaces all artifacts identified in the data (yellow part) by a missing value (NaN).

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. This is typically expected to be data where artifacts have been identified at any preprocessing step.

**Delete previous .nir data file:** set true to 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)

The following module gives the user the possibility to automatically perform data decomposition using different methods.

## Extract component

**Description:** Identify data components using several data decomposition methods on target data. The identified components are added to a list either called extract or subtract in case of an artifactual component using 'Subtract component.' These lists allow to visualize them in the DisplayGUI. Components can also be exported 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.

## Apply PCA during artifact period

**Description:** First, identify noisy intervals either using [artifact detection](#) or do 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 sorts 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. The first part of the label (ex. MVT) can be modified by the user if another nomenclature is preferred, the second part is determined by the decomposition method (ex. PCA). We recommend using the module 'Subtract Components' to subtract all identified and extracted components with a specific label (ex. MVTPCA).

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. The previous step is usually raw data where artifacts were identified.

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

**Figure:** Choose whether or not you want to display the output figure.

**Percentage minimal noisy channel to be a new component:** Consider an artifact event to extract components if noise is affecting at least 5% of the channels for this time window.

**Components to remove up to XX% of the variance in the data:** Find and extract as many components related to an artifact, so that together they 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. A component needs to explain a minimal amount of variance in order to be considered/components explaining less than this % of variance are not considered.

## Apply PARAFAC during artifact period

**Description:** This function runs a PARAFAC<sup>9</sup> decomposition on each pre-identified noise interval (yellow segment in the DisplayGUI). The decomposition is performed on the noisy channels only during this interval as a target PARAFAC. The components explaining most of the variance in the data will be saved as the one representing the artifact. Components will be stored in the component list with the label MVTPARAFAC. The component list can be accessed via 'SelectedFactors.mat' in the same folder as the NIRS.mat. You can 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. The previous step is usually raw data where artifacts were identified.

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

**Figure:** Choose whether or not you want to display the output figure.

**Percentage minimal noisy channel to be a new component:** Consider this event to extract components if they have at least 5% of noisy channels 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 (ex. 5 components) to optimise Concordia and error. The visualization of wavelengths and the time course help to find the component to be removed when the distance between wavelengths is lower than the average distance and the amplitude time course is highest.

## Physiology regression

**Description:** Apply short distance physiology regression as described in Saager and Berger 2008 <https://doi.org/10.1111/1.2940587>. The short distance channel(s) is scaled to fit the other channels using least square estimation. When you use NIRx short distance (SD) channel(s), a zone file called 'SHORTDISTANCE.zone' is created by default when you read the data for the first time. It contains the SD channel(s) and the association to the closest channels. Use a zone definition such as Regressor zone1 which will be applied to zone1. For the regression it is

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<sup>9</sup> 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)

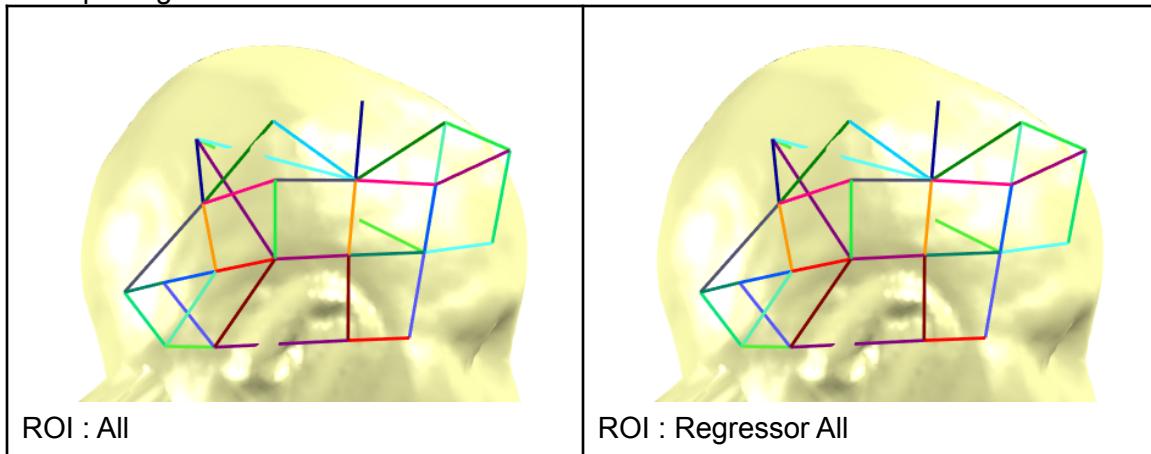
possible to use either the principal component (PCA) of all SD channels or the mean of all SD channels. By default, components related to the physiology regression will be identified as **GLMSHORT**. You can visualize them in the DisplayGUI before subtracting them. We recommend using the module ‘Subtract Components’ that will subtract all the components identified with the same label **GLMSHORT**.

#### Inputs:

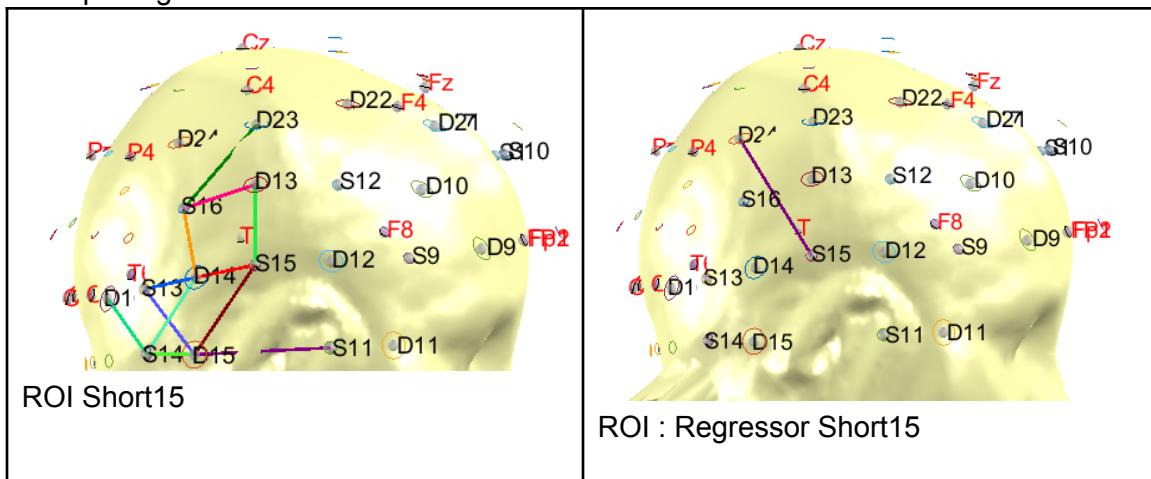
**NIRS.mat**: Select NIRS.mat for the subject. The previous step is usually hemodynamic concentration, where a filter has been applied.

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

Example regressor Global.zone

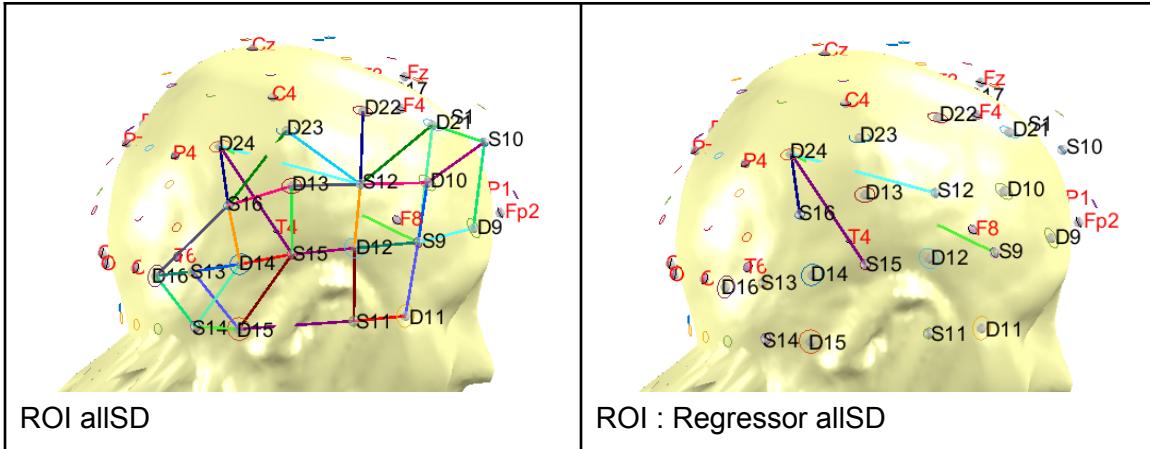


Example regressor SHORTDISTANCE.zone



(The NIRx short distance probe integrates a detector to several source probes) These short distance channels are virtually recorded as the last detector in the acquisition system, in this case detector 24. Be careful to mark 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)

**Description:** 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 auxiliary data (ex. respiration) or from the NIRS signal for instance using a zone definition to model short distance channel as an example. This function uses a list of predefined time intervals and a regressor to estimate the model. Based on the fMRI literature, the model hemodynamic response function can be convolved to our paradigm (Glover et al, 1999) to create auxiliary data. The model can further include a physiological measurement such as additional short distance measurements or respiration, or even a combination of all of them. The component list is stored in 'SelectedFactors.mat' in the same folder as the NIRS.mat. You can 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:** directory of the NIRS.mat to use as: C:\data\Analyze\C01; The data has usually been preprocessed and transformed into hemodynamic concentration changes, where artifact detection and filter have been applied.

**File:** NIRS.mat can have many file sessions after segmentation. You have to identify which session(s) 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 (task1) for the prefix to write in the component label (useful to manage the export)

**X0** first regressor

**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 can 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 a regressor, for example a SD channel to model the physiology effect, you must define the 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 to which channel it will be applied to. As an example:

Zone label	Use as
regressor zone1	Regressor channel (ex. Global.zone)
zone1	The channel to which the regressor is applied to (ex. average of all channels)

#### 3. Global average

In case you want to use the global average as a regressor:

Zone label	Use as
regressor global	Select all channels. The mean of all channels will be used as a regressor.
global	Select all channels and this regressor will be applied to 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. It is usually preprocessed data in hemodynamic concentrations, where artifact detection and filter have been applied.

**File:** 1 refer to the data file index in the NIRS.mat (see DisplayGUI)

**tStart:** to get the time course start point in seconds for visualization.

**tStop:** to get the time course stop point in seconds for visualization.

**tStartavg:** to get the average starting point in seconds.

**tStopavg:** to get the average stopping point in seconds.

**Label:** Define a name for the component

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

	A	B	C	D	E	F	G	H	I	J	K
1	Path NIRSMAT	File	Conc	Trig	tstart	tstop	tstartavg	tstopavg	Label	ZoneDisplay	
2	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	1	HbO		10	10	54	15	25 M001p01p	Wer	
3	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	2	HbO		10	10	54	15	25 M001p02p	Wer	
4	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	3	HbO		10	10	54	15	25 M001p03p	Wer	
5	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	4	HbO		10	10	54	15	25 M001p04p	Wer	
6	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	5	HbO		10	10	54	15	25 M001p05p	Wer	
7	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	6	HbO		10	10	54	15	25 M001p06p	Wer	
8	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	7	HbO		10	10	54	15	25 M001p07p	Wer	
9	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	8	HbO		10	10	54	15	25 M001p08p	Wer	
10	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	9	HbO		10	10	54	15	25 M001p09p	Wer	
11	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	10	HbO		10	10	54	15	25 M001p10p	Wer	
12	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	11	HbO		10	10	54	15	25 M001p11p	Wer	
13	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	12	HbO		10	10	54	15	25 M001p12p	Wer	
14	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	13	HbO		10	10	54	15	25 M001p13p	Wer	
15	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	14	HbO		10	10	54	15	25 M001p14p	Wer	
16	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	15	HbO		10	10	54	15	25 M001p15p	Wer	
17	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	16	HbO		10	10	54	15	25 M001p16p	Wer	
18	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	17	HbO		10	10	54	15	25 M001p17p	Wer	
19	C:\data\Data_NIRS\ELAN\ANALYSED\Martine_0m\BB027\Merge\SegmentFR\dCONC	18	HbO		10	10	54	15	25 M001p18p	Wer	
20											
21											
22											
23											
24											

## Parafac

**Description:** Create an Excel file that contains all the columns as in the Excel above Please use the very same column label as indicated.

### Input columns:

**NIRS.mat folder:** Directory to locate the data to extract. Data is typically preprocessed in hemodynamic concentration, where artifact detection and filter have been applied.

**File:** NIRS.mat can 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:** Start time to define the beginning of the period where the GLM will be applied

**tStop:** Stop time to define the end of the period where the GLM will be applied.

**Label:** Label identification (ex. PARAFAC) to write in the event (useful to manage the export).

**Case 1**

$$\sum_{t=1}^n A(t) > 0 \text{ and } C \text{ HbO} > \text{HbR}$$
$$1 \times 1 \times 1 = 1$$
$$A = A ; B = B ; C = C$$

$$\sum_{t=1}^n A(t) > 0 \text{ and } C \text{ HbO} < \text{HbR}$$
$$1 \times -1 \times -1 = 1$$
$$A = A ; B = -B ; C = -C$$

**Case 2**

$$\sum_{t=1}^n A(t) < 0 \text{ and } C \text{ HbO} > \text{HbR}$$
$$-1 \times -1 \times 1 = 1$$
$$A = -A ; B = -B ; C = C$$

**Case 4**

$$\sum_{t=1}^n A(t) < 0 \text{ and } C \text{ HbO} < \text{HbR}$$
$$-1 \times 1 \times -1 = 1$$
$$A = -A ; B = B ; C = -C$$

**Case 3**

**A = Temporal signature    B = Spatial signature    C = Hemodynamic signature**

Sign adjustment for PARAFAC components: Force HbO/HbR responses to be positive/negative by changing the sign of pairs of signatures extracted. This is due to the trivial sign indeterminacy as the trilinear multiplication in PARAFAC gives the same results for  $1 \times 1 \times 1$  as for  $1 \times (-1) \times (-1)$  so it does not discriminate between these two options in the decomposition.

## Export component list

**Description:** This module helps to export previously extracted components from the NIRS.mat data for further statistics. The export will be organized based on the order of the channel list. Each subject must have a similar localization on the head to be compared. Add the Excel file to export components and use the following columns: 'NIRS.mat folder', 'Type' (GLM, PARAFAC, PCA), 'Label' for the component name to filter, 'Channel List' and 'Name' for the output name of the export file.

**Input columns:** Create a list in an Excel file to identify the component you want to export as follows:

**NIRS.mat folder:** Indicate 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 to open a 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 can exclude some components 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 options 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 saved as a mat file:

D1matrixHbOSentenceAVG008.mat

D1matrixHbRSentenceAVG008.mat

It creates an average of each row that can be opened as a topography with the name:  
HBOmeanAVGC28.mat

Use the montage 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 output files will be saved in the same directory as 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.

### Inputs:

**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/subtracted list.

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

**Offset correction:** Add an offset

## Stats components

**Description:** Possibility to apply basic statistics on exported components. The following 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.

**Inputs:** Use exported component, see [Export component list](#).

**Alpha threshold p value <**: Define the alpha threshold of significance to mask the result map.

**Save data and parameters:** yes or no, to include or not data and parameters used to perform the test in the result file. Output file Data.mat. These data can be used in an external statistical software.

**Result folder:** Define the folder where you would like to save the results

### Choose the statistical test:

#### One sample t-test

**Description:** Apply a one-sample t-test on the selected component(s) and for each channel. This function includes the false discovery rate method to correct for multiple comparisons. It uses the ttest function from the Statistics and Machine Learning Toolbox.

**Inputs:**

**Group 1:** Open exported components using the export list function. Ensure the [channelist](#) is used for all subjects to compared to the homologous channel on the head.

**Enter list of components:** Enter the list of components to be used for the statistical test.

**Use:** 2-tailed, 1-tailed negative p-value, or 1-tailed positive p-value.

**Outputs:** Results are saved in the same folder using the following default name:

**ONESAMPLE\_mean05fdr:** Average value mask using only significant channels, using false discovery rate correction for multiple comparisons with a threshold of  $q < 0.05$ .

**ONESAMPLE\_mean05unc:** Average value mask using only significant channels, using a one sample t-test threshold of  $p < 0.05$  that is not corrected for multiple comparisons.

**ONESAMPLE\_Mean:** average value without any masking.

**ONESAMPLE\_Tmap:** T value without any masking.

## Paired t-test

**Description:** Apply a paired t-test between two groups of data. To make sure that the test is relevant, the two groups need to be paired data, which means the data has to be naturally matched between the two groups. Please make sure to pair your data in the same order between the two groups. Use the ttest.m function from the Statistics and Machine Learning Toolbox.

**Inputs:**

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

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

**Use:** 2-tailed, 1-tailed negative p-value, 1-tailed positive p-value

**Outputs:** Results are saved in the same folder using a default name. You can move them into a meaningful place.

**PAIRED\_mean05fdr:** average value mask using only significant channels, with a false discovery rate correction for multiple comparisons using a threshold of  $q < 0.05$ .

**PAIRED\_mean05unc:** average value mask using only significant channels, using one sample t-test threshold of  $p < 0.05$  uncorrected for multiple comparisons.

**PAIRED\_Mean:** average value without any masking.

**PAIRED\_Tmap:** T value without any masking.

## Unpaired t-test

**Description:** Apply an unpaired t-test between 2 groups of data. Use the ttest2.m function from the Matlab Statistics and Machine Learning Toolbox.

**Inputs:**

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

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

**Use:** 2-tailed, 1-tailed negative p-value, 1-tailed positive p-value

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

**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 can be performed by channel (channelist) or by zone. Use ANOVAN.m function from the MATLAB Statistics and Machine Learning Toolbox. Example with data is available in this [tutorial](#).

**Inputs:**

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

**Column 1st: Dir:** Folder where the exported components are for use as observation.

**Column 2nd: Observation:** File name of the exported components.

### Column 3rd: Zone or channellist

**Zone:** If you use a 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's data will be used in the statistical model.

**Channellist:** if you use channellist, define a channel list text file.

**Column 4th... : Group definition:** use a text label to define to which group each observation belongs.

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

Example for a 1x4 ANOVA 4 'Task' conditions identified by labels (BL, BR, HL, HB).

A	B	C	D
Dir	Observation	ROI zone or channellist	Task
C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLI\TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask001.mat		107_channellist.txt	BL
C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLI\TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask003.mat		107_channellist.txt	BL
C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLI\TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask005.mat		107_channellist.txt	BL

Example for an 2x2 ANOVA with condition 'High' identified by labels (Bottom and Low) and condition 'Laterality' identified by labels (Left and Right).

A	B	C	D
Dir	Observation	ROI zone or channellist	High Laterality
C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLI\TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask001.mat		107_channellist.txt	Bottom Left
C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLI\TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask003.mat		107_channellist.txt	Bottom Left

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

Example for a zone in a 2x2 ANOVA: the region 'HighLeft' in the VisualCortex.zone will be averaged for the statistical model. The contrast condition 'Laterality' with 2 labels (Ipsi and Contro) and condition 'Condition' with 2 labels (BL and BR) are used to design the 2x2 ANOVA model.

A	B	C	D	E	F
Dir	Observation	ROI zone or channelist	Region	Laterality	Condition
1 Dir					
2 C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLM_107	TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask001.mat	VisualCortex.zone	HighLeft	Ipsi	BL
3 C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLM_107	TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask003.mat	VisualCortex.zone	HighLeft	Ipsi	BL
4 C:\data\Tutorial3_DataRetinotopy\Analyse\STATGLM_107	TopoHbOBL107BLGLMHRFtaskhfnmavis107bBL-DC HRFTask005.mat	VisualCortex.zone	HighLeft	Ipsi	BL

**Outputs:** save p-value ANOVA, in the subfolder the full stat by channels.

## Connectivity

### Connectivity matrix

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

**Inputs:** NIRS.mat file with a filtered hemodynamic signal

**NIRS.mat:** Select NIRS.mat for the subject. The data at this step have been corrected for artifact and converted to hemodynamic concentration.

**Node List:** Nodes could be defined by a region of interest (zones) or each channel.

Technical note, to allow subject comparison, ensure that channels' or zones' spatial localization is 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 automatically create 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 can be created and saved in the DisplayGUI.

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

## Cross-correlation analysis

**Description:** Cross-correlation analysis has been used in fMRI to describe connectivity between regions<sup>10 11 12</sup>. 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 Var(x) and Var(y) are the variances of Fx(k) and Fy(k), respectively; Cov x,y(u) is the cross variance of Fx(k) and Fy(k) at zero lag  $\mu$ .  $\text{Cov } x,y(\mu) = E \{ ((F_x(k) - E(F_x)) \times (F_y(k) - E(F_y))) \}$  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.

This method is implemented at lag zero and 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 first uses the segmented files, and the second uses the random circular bootstrap over a long segment to compute the cross-correlation analysis.

**Inputs:** Filtered hemodynamic signal

### Segment

### Circular bootstrap

**Trial length (s):** The length of the segment will define which frequency can be computed. A short segment does not allow the identification of slow frequencies associated with a 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 block. Cross-Correlation will be computed as explained above using all the segments randomly defined, and the segments marked as artifacts will be

<sup>10</sup> 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.

<sup>11</sup> 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>

<sup>12</sup> 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>

excluded. Use a circular bootstrap to obtain a stable measure of the coherence among the sampled data.

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

## Hilbert joint phase probability

**Description:** In order to determine the phase relation between channels, we extract the phase of the signal in each channel using the Hilbert transform<sup>13</sup>. The joint probability distribution of the phases across channels to describe their connectivity. A common model for probability distribution of phase is the Von Mises distribution that use the external toolbox circstat 2012a<sup>14</sup>. The signals are first filtered to extract spontaneous hemodynamic activities and to reject other interferences. They have two implementations, one that uses the user segmentation files or the random circular bootstrap over a long segment.

**Inputs:** Filtered hemodynamic signal

### Segment

#### Circular bootstrap

**Trial length (s):** The length of the segment will define which frequency can be computed, a short segment does not allow to identify slow frequencies associated with the 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 be extracted from the whole block. Coherency will be computed as explained above using FFT of all the segments randomly defined. 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 will reject segments when the estimated value is an outlier regarding z-score segments distribution.

## Coherence

**Description:** Coherence is a statistic representing the relationship between two signals and is also an extension of correlation to the frequency domain (Kida, 2016)<sup>15</sup>. Coherence is known as magnitude squared coherence defined as the complex conjugate product of the Fourier transforms data  $X(f)^* Y^*(f)$ .  $x(t)$  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:

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<sup>13</sup> 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>

<sup>14</sup> P. Berens, CircStat: A Matlab Toolbox for Circular Statistics, *Journal of Statistical Software*, Volume 31, Issue 10, 2009

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

<sup>15</sup> 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>

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

Coherence is implemented to be used 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<sup>16</sup>). Any segment that belongs to a specific 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 predefined frequency range.

**Inputs:** Unfiltered hemodynamic signal

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

**Zone to display spectrum:** Inserts a zone to plot FFT over a region of interest.

**Trial length (s):** The length of the segment will define which frequencies can be computed. A short segment does not allow to identify slow frequencies associated with the 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 block. Coherency will be computed as explained above using FFT of all the randomly defined segments. Segments marked as artifacts will be excluded. Use a circular bootstrap to obtain a stable measure of the coherence among the data.

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

**Save FFT spectrum:** Choose whether the spectrum is saved or not.

**Path connectivity matrix:** Output location.

**File name:** Define the prefix of the output file.

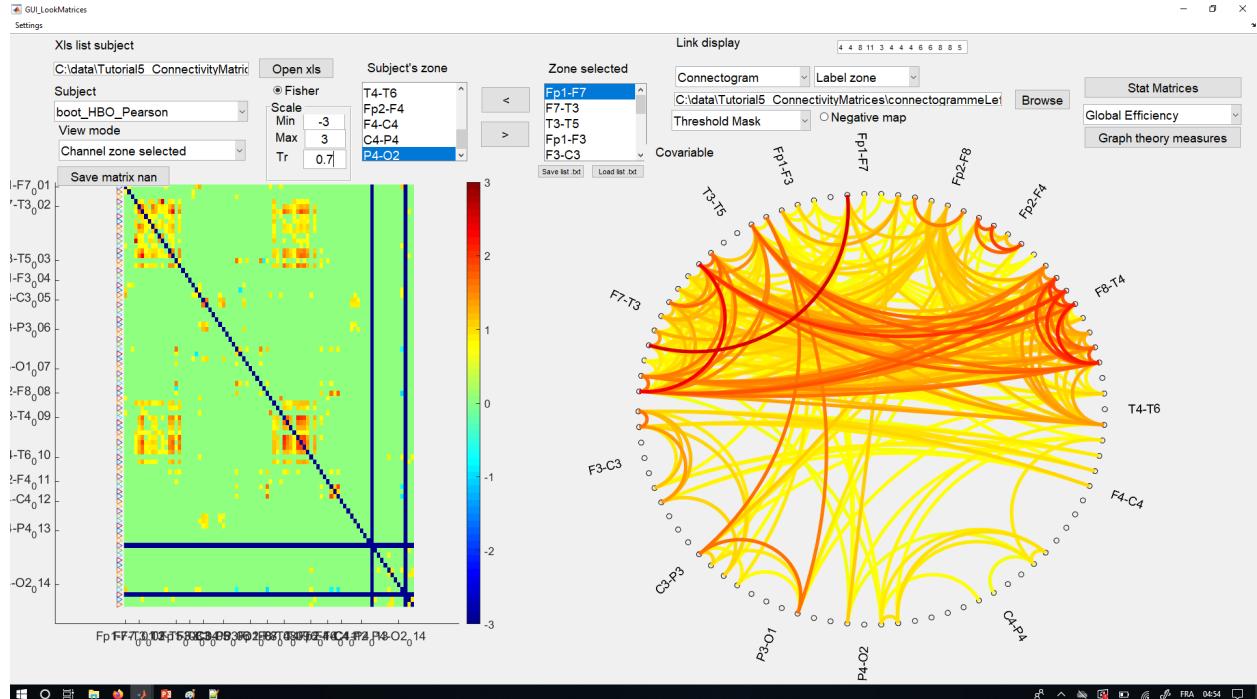
**Output:** Coherence matrix file for HbO and HbR

## GUI\_lookmatrices

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

---

<sup>16</sup> Politis, Dimitris Nicolas and Joseph P. Romano. "A circular block-resampling procedure for stationary data." (1992).



## Function overview

**Open xls:** Select the file to localize the individual or group matrices to visualize on your computer.

You need to identify the columns as follows:

1st column: write the directory to indicate where to open the matrix file

2nd column: write the name of the connectivity matrix

3rd column: write the name of zone file that needs to be placed in the same directory as the connectivity matrix.

4th column: write the number of the group to which the matrix belongs. It needs to be a positive integer number to classify the subject groups for average and statistics.

5th column and following: one or many additional columns can be used as covariate(s) for the statistical analysis. The format can be an xlsx file or a text file using a tab space delimitation.

Dir	subjectfile	zonefile	Groupe
C:\data\Data_NIRS\BebeResting\connectivityMAT_COH_dCONC\COH03to08	nana_C07JB_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\Data_NIRS\BebeResting\connectivityMAT_COH_dCONC\COH03to08	nana_C09AC_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\Data_NIRS\BebeResting\connectivityMAT_COH_dCONC\COH03to08	nana_C10MB_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\Data_NIRS\BebeResting\connectivityMAT_COH_dCONC\COH03to08	nana_C11LC_4m_001_HBO_COHFFT	ByDetector.zone	1
C:\data\Data_NIRS\BebeResting\connectivityMAT_COH_dCONC\COH03to08	nana_C12AD_4m_001_HBO_COHFFT	ByDetector.zone	1

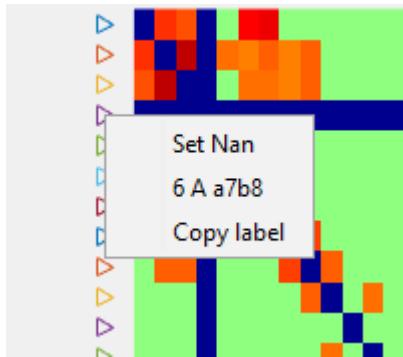
NB: Add the matrix .mat and .zone in the same directory.

You can add another column if you want to add a covariate or a regressor. The value for the covariate must be an integer value to be considered, else it will be treated as a missing value.

**Subject list:** Scroll through the subject list to visualize subject by subject.

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

**Save matrix nan:** You can exclude channels using right-click on the small arrow on the left side of the matrix and mark it as NAN. Once you complete your selection, use the button ‘Save Matrix’ and 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. As a consequence those channels will be treated as missing value(s). Create a new subject list using the nan file instead of the original one.



**Fisher transform:** Apply the fisher transform to the matrix 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.

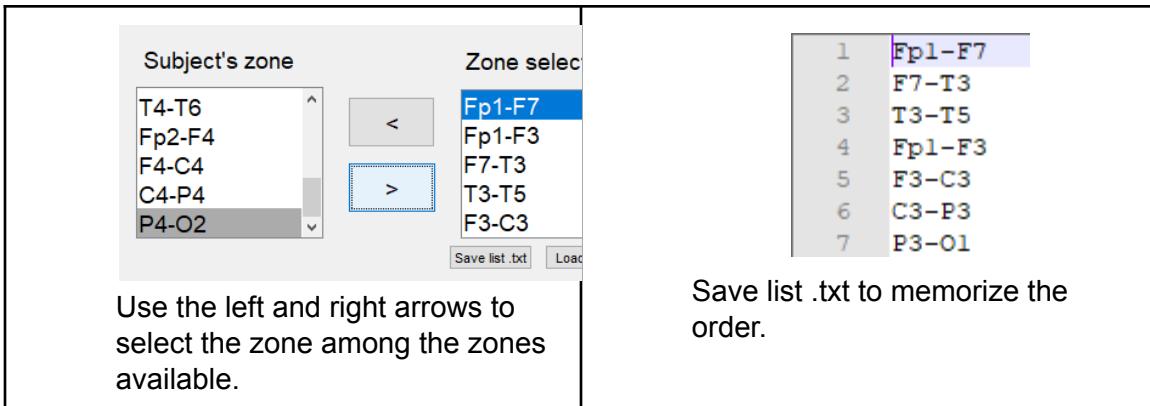
**Tr:** Adjust the threshold so that in the matrices, only values superior or inferior to this threshold are displayed. Display only values superior to this threshold on the connectogram (use a negative map to inverse the view).

**Auto:** Adjust the color scale according to the maximum and minimum values of the data.

**Zone selected:** Use the left and right arrow to select the zone in the subject’s zone list to visualize in the connectivity matrices:

**Save list .txt:** Save the list of regions in a text file. This allows modifying the order of labels to display zones of interest in a specific order.

**Open list .txt:** Open a text file with the associated names of zones of interest, to display the matrices using the label order defined in this file.



**Link display:** Select link to display

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

**Connectogram:** Display the connectogram link<sup>17</sup>.

**Label:** Select label to display

**Zone:** Use zone names as labels.

**Channel:** Use channel names as labels.

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

**Colormap (jet):** Use heatmap identical to the displayed matrix

**Colormap (jet), mask by zone:** Use a heatmap identical to the displayed matrix but use the user defined mask in the zone list.

**RGB color, mask by zone:** Use a user defined 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 links

**Open zone list:** Use the same txt file to fix the order of the connectogram. The connectogram will display zones using a counter-clockwise order, starting the first zone from the left middle of a part of the circle.

Example of zone list without color mask

---

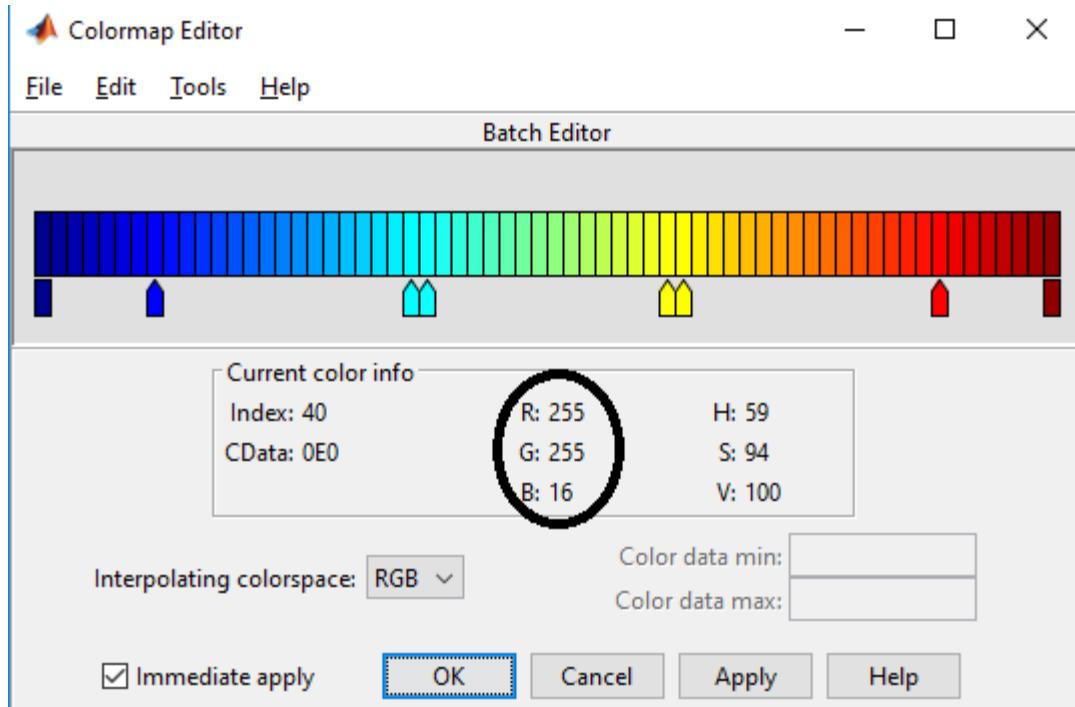
<sup>17</sup> Inspired from circularGraph version 2.0.0.0 (828 KB) by [Paul Kassebaum](#)  
<https://github.com/paul-kassebaum-mathworks/circularGraph>

```
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	T4-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 codes



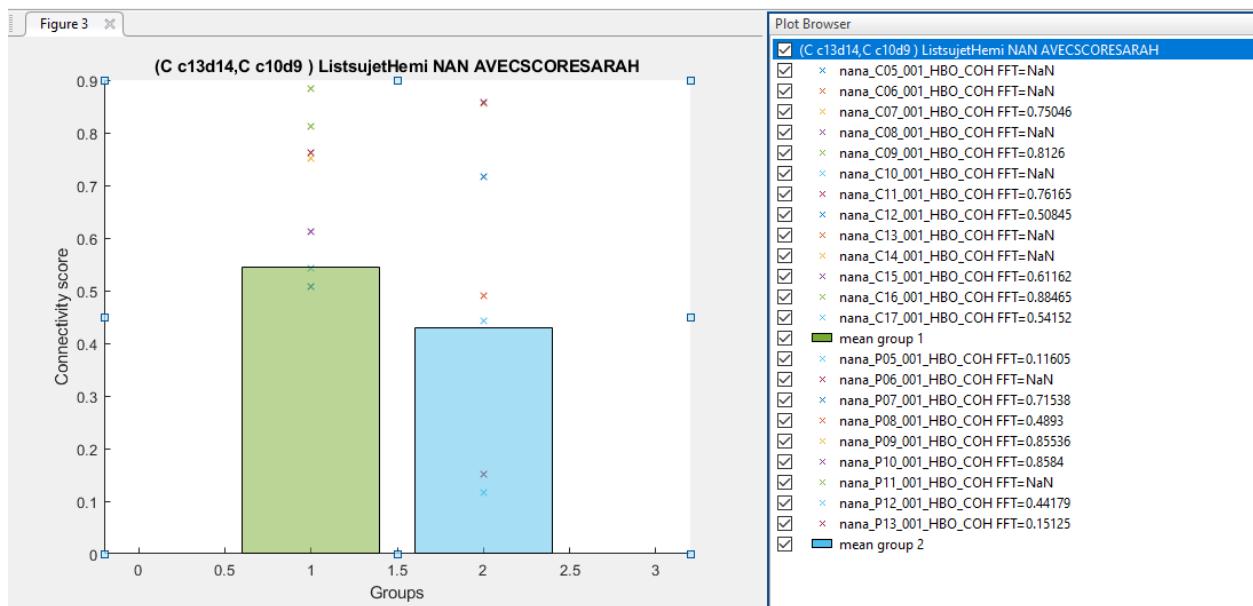
**Negative map:** Display value lower than zero.

**Covariate:** Optional, if you use additional covariates, add an extra column in your Excel to identify subjects (see open Excel). The first row of this new column is used to identify the covariate. Use the right-click on a connectogram link to plot the connectivity score as a function of a covariate 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 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 number of connectivity value for each group of the selected link. The data distribution by subject can be verified.



**Covariate:** Display connectivity scores as a function of the selected covariate.

**Right-click on a connectogram:**

**Make a new figure:** Transfer the data to a standard Matlab figure, which allows manual editing of the connectogram using the plot browser.

## Stats Matrices

**Description:** The connectivity value has been computed for each node combination to create the connectivity matrices. You can apply statistical tests on those matrices.

**Inputs:**

**Enter list connectivity matrix:** Enter a list of matrices to test statistically, as described in [GUI\\_Lookmatrices](#).

**Fisher transform:** Yes or 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 normally distributed, with a variance that is stable over different values of the underlying true correlation.

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

**Result folder:** define where to save the result

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

### One sample t-test

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

**Inputs:**

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

### Unpaired permutation test

**Description:** This operation can be done at the channel level or the zone level. It performs permutation based on student statistic<sup>18</sup> and produces a xls list of the resulting matrices including t and p values based on permutation computation. It excludes nan values from the statistical analysis. The Excel list needs to have the same columns as described in the [GUI\\_lookmatrices](#).

**Inputs:**

**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

### Pearson correlation

**Description:** This operation returns the pairwise Pearson linear correlation coefficient between the matrix connectivity score and the covariate in the Excel file. The 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 the columns. The Excel list needs to have the same columns as described in the [GUI\\_lookmatrices](#).

**Inputs:**

**Covariate:** Covariates must be added as an additional column in the Excel file that contains the subject. As an example in the following Excel chart, if you want to calculate the Pearson correlation between the connectivity score and the 'Pregnancy duration (weeks)' you have to indicate the column label 'Pregnancy duration (weeks)' as a covariate. Separate them by a comma, as an example [Pregnancy duration (weeks),

<sup>18</sup> 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)

Constant] will produce a file with the b1 estimation for the pregnancy leverage between the connectivity score and the Pregnancy duration (weeks).

Dir	subjectfile	zonefile	Group	Pregnancy duration (weeks)	Weight at birth (kg)	APGAR
C:\data\Data_	nana_C05_ByDetector.zone		1	40	3.17	9
C:\data\Data_	nana_C06_ByDetector.zone		1	41	3.4	9
C:\data\Data_	nana_C07_ByDetector.zone		1	38.43	3.915	9
C:\data\Data_	nana_C08_ByDetector.zone		1	40.14	3.365	8
C:\data\Data_	nana_C09_ByDetector.zone		1	40.29	3.815	9
C:\data\Data_	nana_C10_ByDetector.zone		1	39.57	3.44	9
C:\data\Data_	nana_C11_ByDetector.zone		1	36.86	2.7	9
C:\data\Data_	nana_C12_ByDetector.zone		1	40.57	2.655	9
C:\data\Data_	nana_C13_ByDetector.zone		1	39.29	4.14	10
C:\data\Data_	nana_C14_ByDetector.zone		1	41.43	3.37	9
C:\data\Data_	nana_C15_ByDetector.zone		1	39.14	3.82	9
C:\data\Data_	nana_C16_ByDetector.zone		1	41	4	9
C:\data\Data_	nana_C17_ByDetector.zone		1	40.57	2.88	9
C:\data\Data_	nana_C18_ByDetector.zone		1	40.43	3.055	9
C:\data\Data_	nana_C19_ByDetector.zone		1	41	3.154	10
C:\data\Data_	nana_C20_ByDetector.zone		1	39.43	3.05	9
C:\data\Data_	nana_C21_ByDetector.zone		1	37.43	2.715	9
C:\data\Data_	nana_C22_ByDetector.zone		1	40.43	3.64	9
C:\data\Data_	nana_C23_ByDetector.zone		1	40.14	3.35	9

## GLM

**Description:** This operation returns the regression coefficient between the connectivity matrix score (y) and the covariate (x) identified in the Excel. The linear equation of this:  $y = b1*x1 + b2*x2.. +e$ . You must include a constant. The Excel list needs to have the same columns as described in the [GUI\\_loomtrices](#).

**Inputs:**

**Covariate:** A covariate can be added as an additional column in the Excel file with the list of subjects. As an example, in the Excel chart if you want to calculate the Pearson correlation between the connectivity score and the 'Pregnancy duration (weeks)' you have to indicate the column label 'Pregnancy duration (weeks)' as a covariate. Separate them by a comma, as an example [Pregnancy duration (weeks), Constant] will produce a file with the b1 estimation for the pregnancy leverage between the connectivity score and the Pregnancy duration (weeks).

## Export NBS format

**Description:** This operation saves the individual connectivity matrix to be used in the statistical toolbox network-based statistic NBS<sup>19</sup>. The export is designed to compare the two-groups using a t-test. You can adjust your design matrix if you wish to explore different possibilities. The data is saved in the same order as the Excel file. However, the NBS visualization does not manage to

<sup>19</sup> Zalesky, A., Fornito, A., Bullmore, E.T., 2010. Network-based statistic: Identifying differences in brain networks. *NeuroImage* 53, 1197–1207. <https://doi.org/10.1016/j.neuroimage.2010.06.041>

easily visualize fNIRS matrices. Using the following MATLAB commands will help you to convert your NBS results and visualize them in the GUI\_LookMatrice format.

```
%find a file with the same node structure to change the result in a  
%compatible format for the GUI_LookMatrices  
dir1 = 'C:\data\Tutorial4_ConnectivityMatrices\Analyse\MatConnecvity_COH_Adult_RestHistoire\OneSampleTtest_Rest'  
file = 'ListSujet_HistoireVsRest_allcOneSampleTtest mean.mat'  
%Run NBS stat using the parameter needed and them open the results  
global nbs  
resultnbs = nbs  
newfile = 'nbs_con_mat_result.mat'  
load(fullfile(dir1,file))  
matcorr = full(resultnbs.NBS.con_mat{1})  
meancorr = full(resultnbs.NBS.con_mat{1})  
save(fullfile(dir1,newfile),'matcorr','meancorr','ZoneList')  
newfile = 'nbs_test_stat.mat'  
matcorr = resultnbs.NBS.test_stat  
meancorr = resultnbs.NBS.test_stat  
save(fullfile(dir1,newfile),'matcorr','meancorr','ZoneList')  
%add the new file nbs_con_mat_result.mat and nbs_test_stat.mat in the xls file to visualize using GUI_lookmatrices
```

## Utility NIRS.mat

Operation to adjust NIRS.mat structure.

### Folder adjustment

**Description:** This function is used to modify the root folder of a subject's analysis when the NIRS.mat file has been moved to a different folder or another computer. In general, it is recommended to keep the analysis in the same place to avoid confusion. The NIRS.mat structure contains the information about intermediary data analysis. However, if you have dislocated or reorganized the root analysis folder, this dependency will be lost. Keep the subject's data in one folder and avoid renaming the subfolders. 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 when you open the file in the DisplayGUI.

#### Inputs:

**NIRS.mat:** Select NIRS.mat file that has been moved to adjust dependency. It is essential to keep the subfolder organization and move only the root folder.

**Multimodal dir:** New folder used for multimodal files such as EEG, AUX, Video or 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

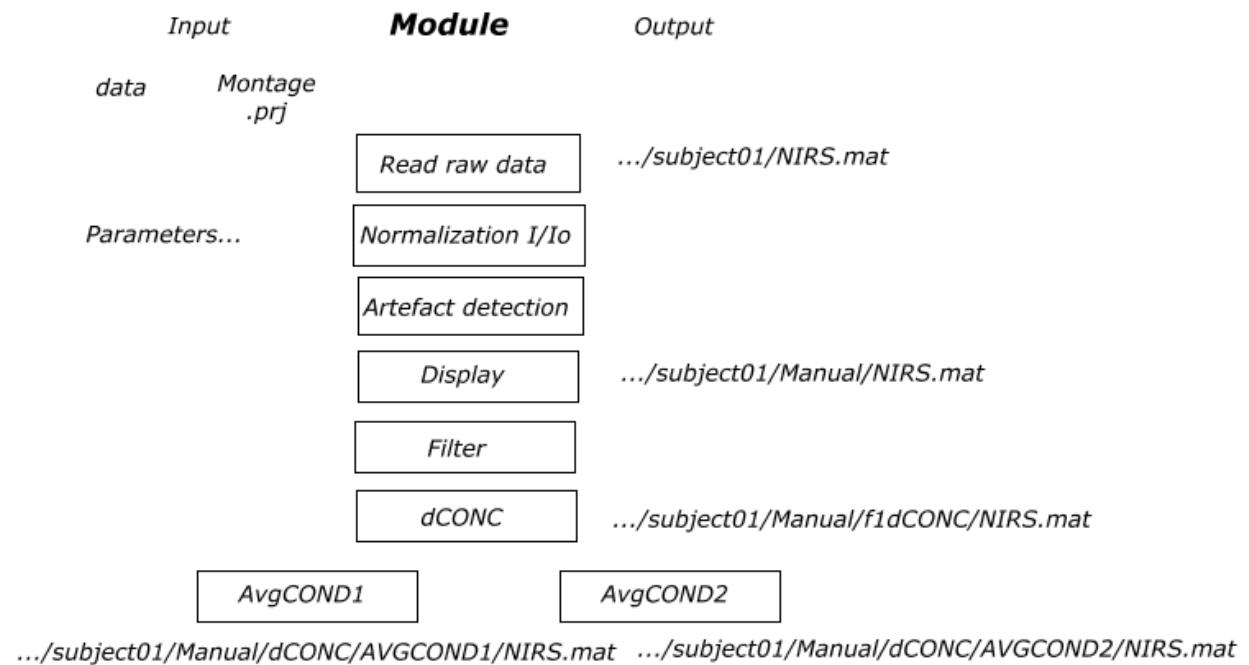
**Description :** This function is used to create a subfolder and copy the NIRS.mat structure. It allows the creation of a parallel branch of analysis.

### Inputs:

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

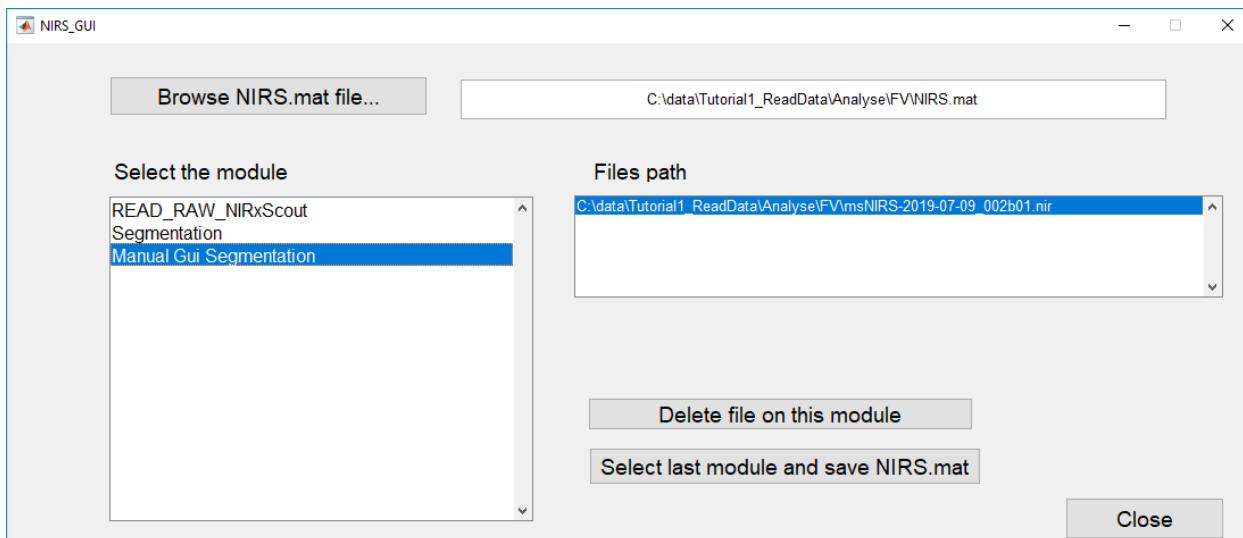
**Create a new branch of analysis in the subfolder:** indicate the name of the subfolder.

**Components and corrections:** Keep or clean components and corrections.



## Display NIRSmat

Open the NIRS.mat structure to see the list of operations performed and the file's 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.

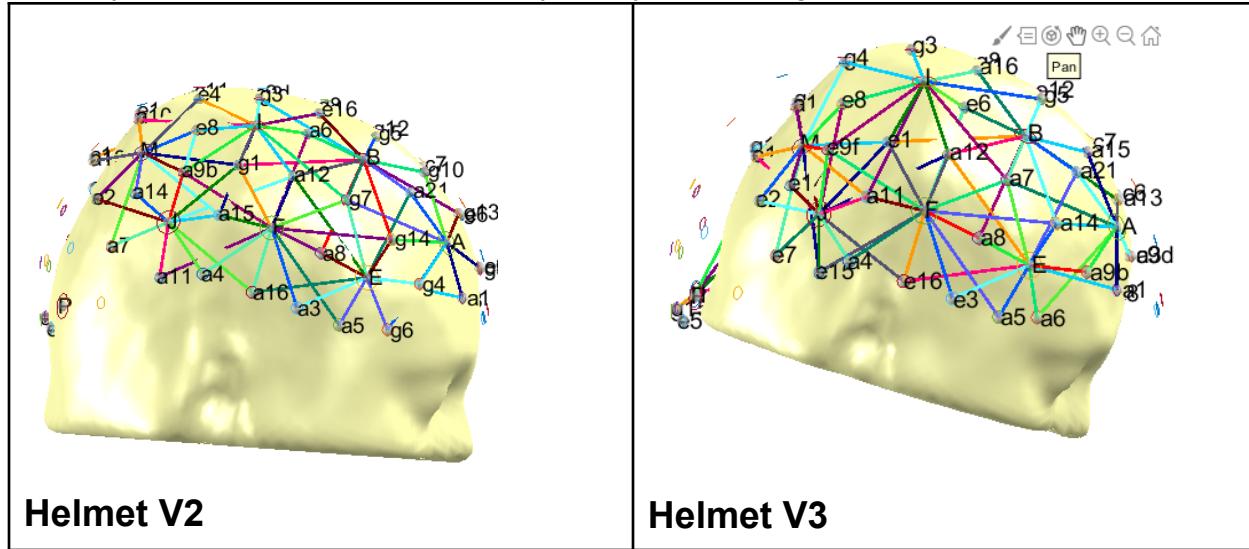
## Create channel list (seed list)

**Description:** Indicate NIRS.mat structure to create a list of all channels. This file lists channels used as nodes to calculate connectivity or as analog channels to group subjects together. To group connectivity matrices of 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 may need some modifications if you change the sources' or detectors' position). When they cannot be compared, you will need to work with zones. 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.

<pre> 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 </pre>	<pre> 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 </pre>
Example of channel list using ISS label.	Example of channel list using NIRx label

**Tip:** Adjust channel list when some helmet configuration changes during the experiment. For example, for a technical reason, a source needs to be replaced by another. A fixed localization is necessary to group subjects. The channel list helps to reorganize this channel if necessary.

The row list order will be used as a reference to list labels that are in the same position. Ensure row line one on the channel list montage V2 has a localization comparable to row line one on the channel list montage V3. They will be used as the same optode for the average. Adjusting the list to keep a consistent localization of the channels is essential. The row number will be used as the new reference to allow averaging subjects. The project of the first list is kept as a reference. Even if it is supported using an appropriate channel list, it is not recommended to modify a montage during the experiment and increase the risk of error if it is not done wrongly. Ensure you understand and counter verify what you are doing.



Modify source in montage V2 g6h5 -> a6b5 to keep the sample order of channel and localization in the version V3.

M03YPchannellist_V2.xlsx			Transfertsources.xlsx			M03YPchannellist_V3.xlsx		
1	A	a1b2	V2	V3		1	A	alb2
2	E	a1b2	e3f4	a3b4		2	E	alb2
3	E	a3b4	g13h14	a13b14		3	E	e3f4
4	F	a3b4	g10h9	a15b16		4	F	e3f4
5	E	a5b6	e16f15	a16b15		5	E	a5b6
6	F	a5b6	e4f3	g4h3		6	F	a5b6
7	J	a7b8	a13b14	e13f14		7	J	e7f8
8	M	a7b8	a6b5	e6f5		8	M	e7f8
9	P	a7b8	a14f13	e14f13		9	P	e7f8
10	F	a9b10	g4h3	a9b8		10	F	e9f10
11	I	a9b10	g14h13	a14b13		11	I	e9f10
			g7h8	a7b8				
			g1h2	e1f2				
			a9b10	e9f10				
			a7b8	e7f8				
			a11b12	e15f16				
			g6h5	a6b5				
			a15b16	a11b12				
			a11b12	e15f16				
			a16b15	e16f15				

Observed source a3b4 was changed by source e3f4 and a9b10 by e9f10. These changes fit the new montage organization. The order (line row) of each optodes localization is identical for both montages.

Use this transfer script to apply label changes among a few sources.

Transfertsource.xlsx contains the list of the sources modified. The new label is applied to the existing list M03YPchannellist\_V2.xlsx..

MATLAB script:

```
[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 variable 'new' in a file to obtain the list with the modification
M03YPchannellist_V3.txt
```

## Data quality report

**Description:** Export a summary of the rejections and corrections applied 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 results.

**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. The previous step is usually preprocessed data, where the artifact detection or correction was applied.

**File:** Segment where the correction has been applied.

**Duration:** total length of the segment in seconds.

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

**Nb independent intervals rejected:** number of separate intervals rejected.

**Ratio time corrected/time total:** percentage of time when 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 artifact event.

**Maximal duration of the correction:** among the corrections applied, find the longest one.

## Transfer Zone to channel list

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

**Inputs:** fichiername.zone created using the DisplayGUI.

**Output:** fichiername.txt will be created in the same folder of the fichiername.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 detectors and sources 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

## Transfer channel list to zone list

**Description:** Use channel label to create a zone list

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

**Output:** Create a zone list with the description in the NIRS.mat folder associated with the subject.

## Write external file

### Write .nirs

**Description:** Export the current data in .nirs format. The export will contain: data: 'd'; probe coordinates: 'SD'; sample time: 't'; stim triggers: 's'; auxiliary exports 'aux', which however are not well-supported:. Use the function 'nullify bad interval' if you want to set it as NAN missing artifact marked in yellow.

**Inputs:**

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

**NIRS.mat:** Select NIRS.mat for the subject. The previous step can be any data you wish to export in a .nirs file.

**Select output folder:** Select the output folder where to export data. Data will be placed in a subfolder with the subject name to facilitate the organization.

## Write .snirf

**Description:** This toolbox enables you to export your data as .snirf files. A description of this format is available [here](#). LIONirs uses the class developed in Homer3. To save the .snirf format, please refer to and install [https://github.com/fNIRS/snirf\\_homer3](https://github.com/fNIRS/snirf_homer3). A similar data structure as .nirs is being used to save the .snirf format. The export contains: data: 'd'; probe coordinate: 'SD'; sample time: 't'; stim trigger: 's'; auxiliary: 'aux', but auxiliary exports are not well-supported. Use the function 'nullify bad intervals' if you wish to set as NAN an artifact marked in yellow.

**Inputs:**

**NIRS.mat:** Select NIRS.mat for the subject. The previous step can be any data you wish to export in a .snirs file.

**Select output folder:** Select the output folder where to export data. Data will be placed in a subfolder with the subject name to facilitate the organization.

## Write NIR individual file segment

**Description:** Use a nir file to write a smaller segment.

**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 of the selection

**Time stop:** Time end of the selection

## 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 .nir file. It will cause an error if there is no epoch averaging in the NIRS.mat session. Old version Homer1 (obsolete)

**Inputs:**

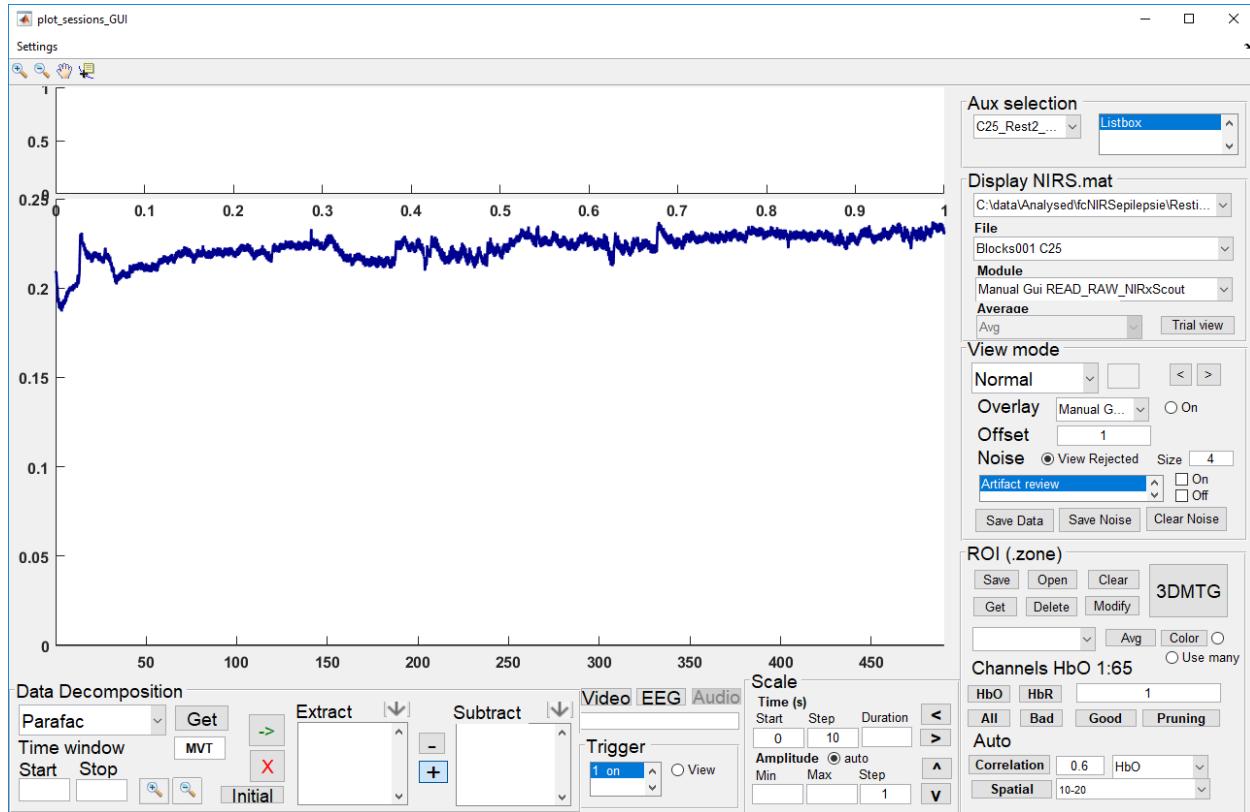
**NIRS.mat:** Select NIRS.mat for the subject. The previous step is average data to build a .hmr project in the old homer version.

**File output:** Output name.

**Helmet .prj:** Select the project of the montage for the subject.

## 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 use 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 appendix [Data structure LIONirs \(NIRS.mat\)](#) for a detailed description of the fields.

## Files

The data can have one or many segments saved as separated files on your hard drive. For example, if an experiment is recorded in many separate files, you could merge them to have them in one long file. Otherwise, it is also possible to segment them into small

separated files to ease memory access. You need to select which ‘file’ you want 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 deleting most of the intermediate files except if you need them for verification. Only the last module could be used to apply modification to the data.

## Average

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

## View mode

### View options

**Normal:** Stack view 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 (display HbO-HbR hemodynamic concentration after MBLL module)

**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.

  : The buttons allow the user to navigate through the different channels. The ID of the displayed channels is incremented so that, respectively, the previous or the following channels are displayed according to an increment value. The user can choose the increment value, 1 is the default value.

## 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 ‘view rejected’ is selected, the rejected channels are plotted in dotted. Unselect to hide them.

**Size:** Noise marked periods are overlaid to the data in yellow. Adjust the size of this noise marker 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 DisplayGUI to be a standard MATLAB figure and make the edition easier using the plot browser.

**Report noise:** Allows the user to generate a figure summarizing the percentage of artifacts data. Three graphs are generated: Artifacted data in each channel in the function of time, Channels id in the function of the percentage of artifacts time, and percentage of artifacts channels in the function of time.

**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 trigger:** Insert a new trigger 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 period is displayed using a yellow overlay.

**Restore selected interval:** Restore this specific channel interval.

**Remove the entire channel:** Remove this specific channel. When ‘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.

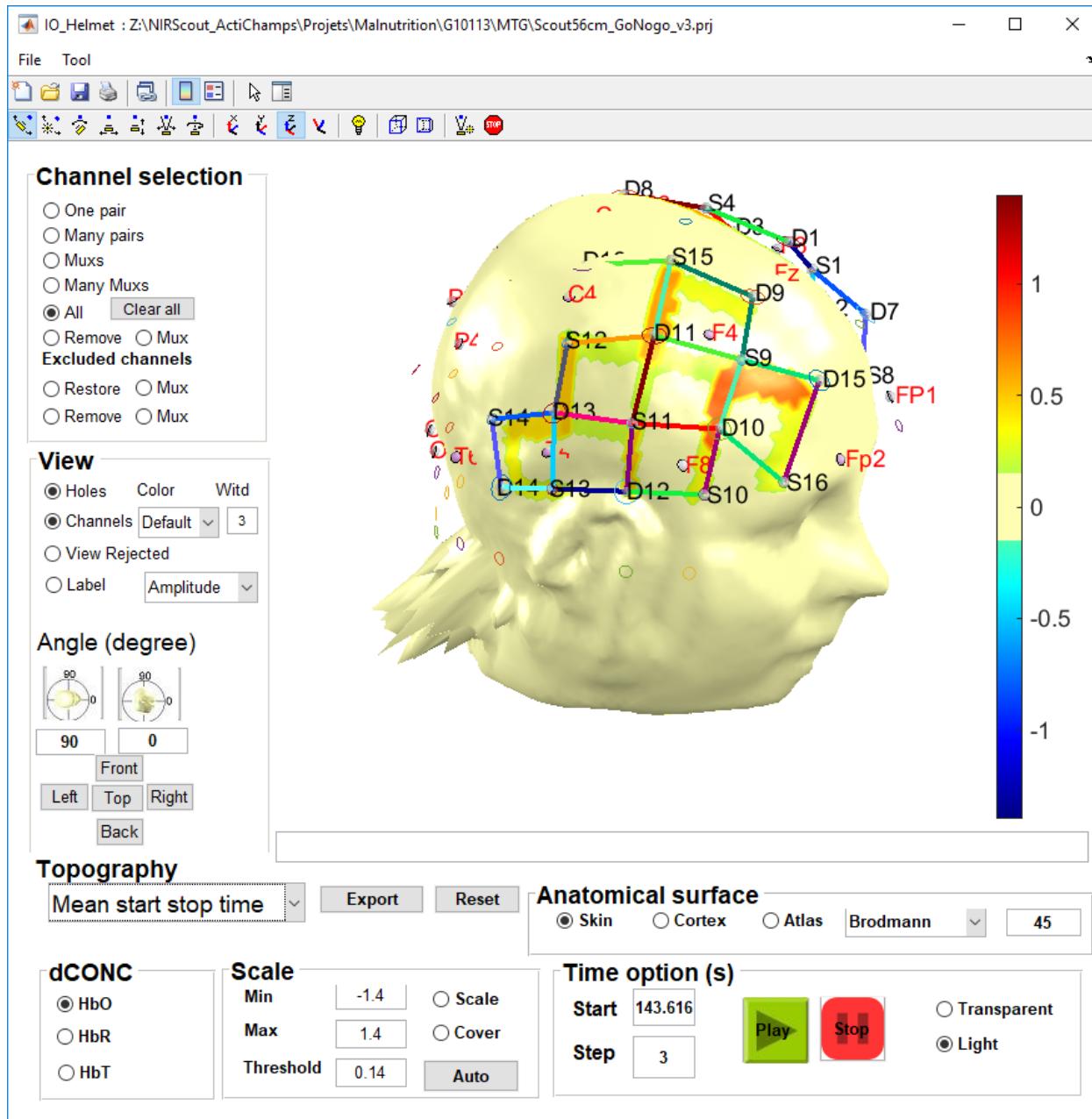
**Restore the entire channel:** Restore this specific channel.

**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 helmet.

**Copy data to clipboard:** Copy the selected channel data to the clipboard (time amplitude) and 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 3DMTG uses the MATLAB 3D camera manipulation graphical user interface. Please refer to the MATLAB documentation. The

### 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

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 channels use randomized colors for each channels, black use black color for all channels and heatmap color where the color of the channels will reflect their value according to the amplitude as the projection.

### Angle (degree) or select plane for visualization

This panel enables you to quickly select a camera orientation using the buttons: *Front*, *Top*, *Back*, Left or Right. To define a precise camera orientation, indicate the angle of the camera using the rotation angle or the elevation angle in degree.

**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

**Description:** they are two types of topography available: radial projection on the sphere or inverse weighted distance. Use right click on the topography selection to define the topography to use.

**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.

**Export:** Create a new figure with the topography.

**Reset:** Restore the topography to zero.

**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. 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.

**Min:** Enter minimal value of the color scale.

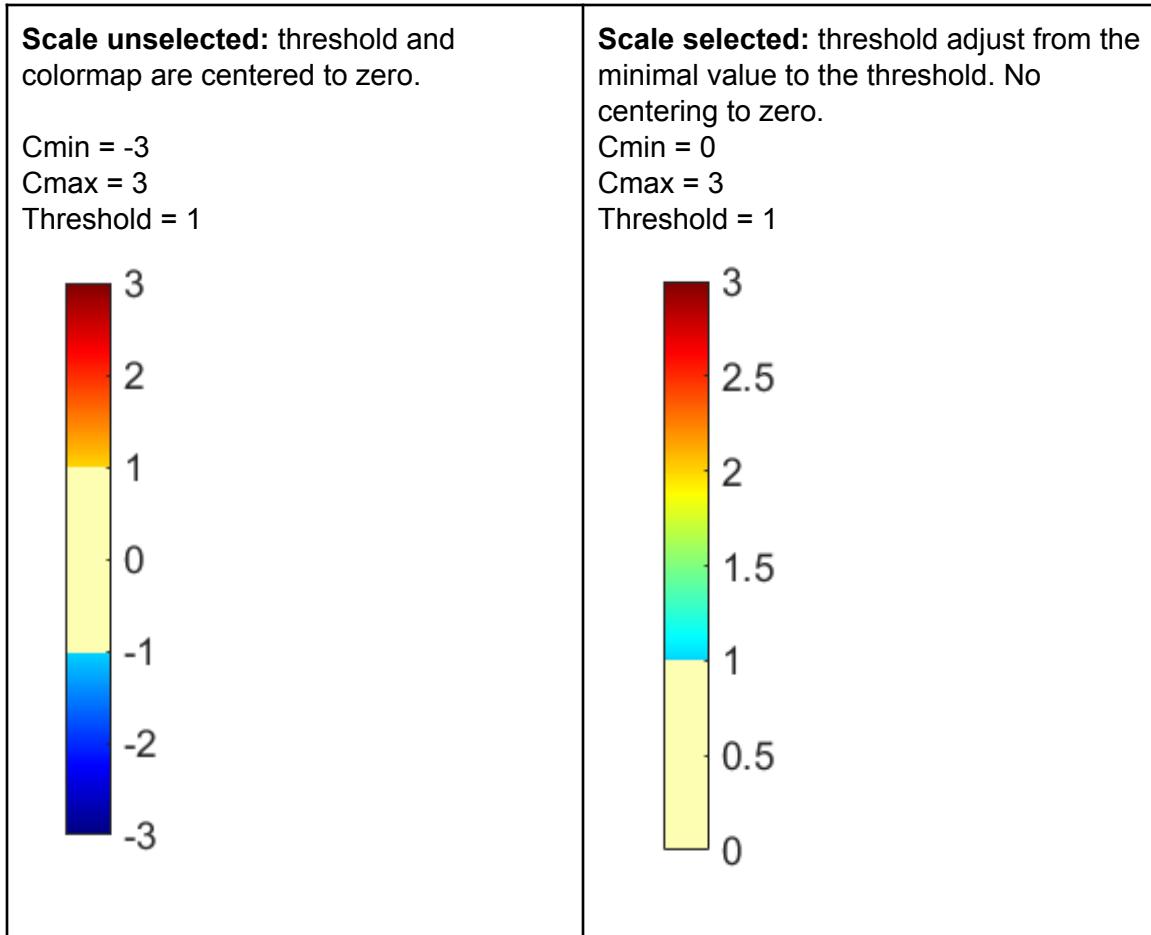
**Max:** Enter maximal value of the color scale.

**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:** Image mapping on select what kind of 3D model will be used for rendering. The choices are: *Skin*, *Cortex*, *Atlas*, *Cortex & Atlas*.

**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 area<sup>20</sup>

**Brodmann:** use label associate to Brodmann area

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

**Time option (s):** This panel enables you to select a module and customize 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. Time option to current module display time in second unit.

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

## Region of interest definition *ROI.zone*

Select the channels to form the region of interest (.zone). This region could be used for data decomposition, statistical analysis, or connectivity operation. There are a few options available to facilitate the use of regions of interest. Here are the options:

**Save:** Save a new region of interest as a .zone file.

**Open:** Open a .zone file. It's a good practice to clear the zone list before opening a new one.

**Clear:** Clears the content of the zone list.

**Get:** Create a new zone with the displayed channels. Write its name and the zone are added in the zone list.

**Delete:** Deletes the zone selected in the menu.

**Modify:** Modifies the current zone.

**Average:** Averages the current zone and illustrates it with a figure.

**Color:** Choose the color of the current zone. Every channel of the same zone is displayed with the same color.

**Use many:** Many zones is displayed at the same time. When you select this option, choose the requested zone one after the other in the menu to display them all.

## Channels

The displayed channels are listed in the plot list. It is easy to choose which channels are displayed by adding their id to the list or by choosing a predefined category of channels. The available categories are listed below:

---

<sup>20</sup> 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](#)]

**HbO:** Displays the channels using the wavelength that detects the concentration of HbO.

**HbR:** Displays the channels using the wavelength that detects the concentration of HbR.

**All:** Displays all channels.

**Bad:** Displays channels with identified artifacts. The artifact detection module must be launched before this option is available.

**Good:** Displays channels without any identified artifacts. The artifact detection module must be launched before this option is meaningful.

**Pruning:** Displays the channels, among those already displayed, with maximal or minimal values in a defined period of time. The user must define a time interval, enter the number of channels to display, and write either max or min according to their needs.

## Auto

It is possible to generate regions of interest using the DisplayGUI. To do so, the user needs to click on the label of the selected option. Indeed, two options are available to generate the list of zones automatically:

**Correlation:** It generates ROIs according to the correlation between the channels time course. The user must enter a correlation level for the regrouping of channels. As an example, 0.95 means channels with a correlation higher than 95 % will be associated in the same ROI.

**Spatial:** It generates ROIs according to the position of the optodes. The channels that are spatially near will be grouped.

## 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 3DMTG

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

For further analysis, press right-click on a selected component to access the following options:

**New figure:** Takes the component data to be a plot in a standard MATLAB figure, for further edition using the plot browser.

**Copy:** Copies the label of the selected component. It can be pasted in any other document.

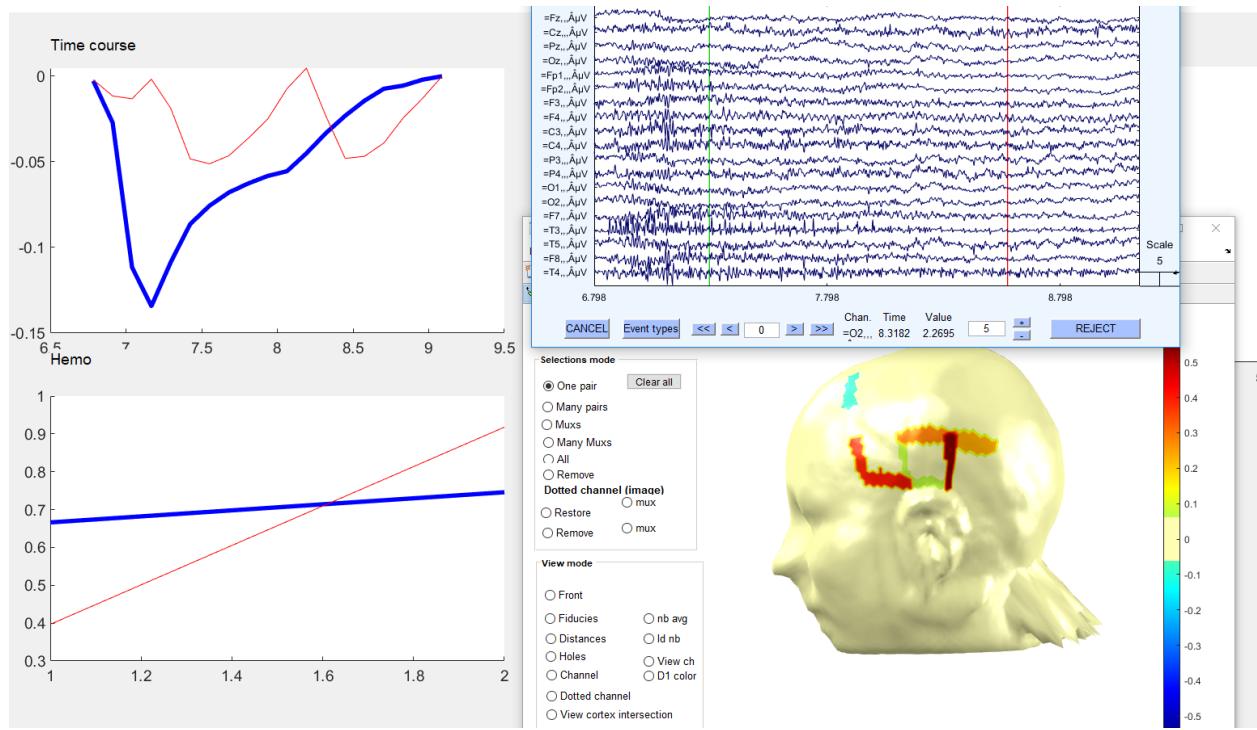
**Copy data:** Copies the data associated with the spatial component and the source, detector identification label. It can be pasted in any other document, .xls or .txt for example.

**Rename:** Allows the renaming of a component.

## PARAFAC

Application of the PARAFAC decomposition in the DisplayGUI.

1. In the DisplayGUI, 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 to zero (first point and last point detrend).
  - b. Look at the component and adjust the number of components.
  - c. Display in the topography the spatial component. In 3DMTG select PARAFAC as the display option. The component selected in bold will be projected.



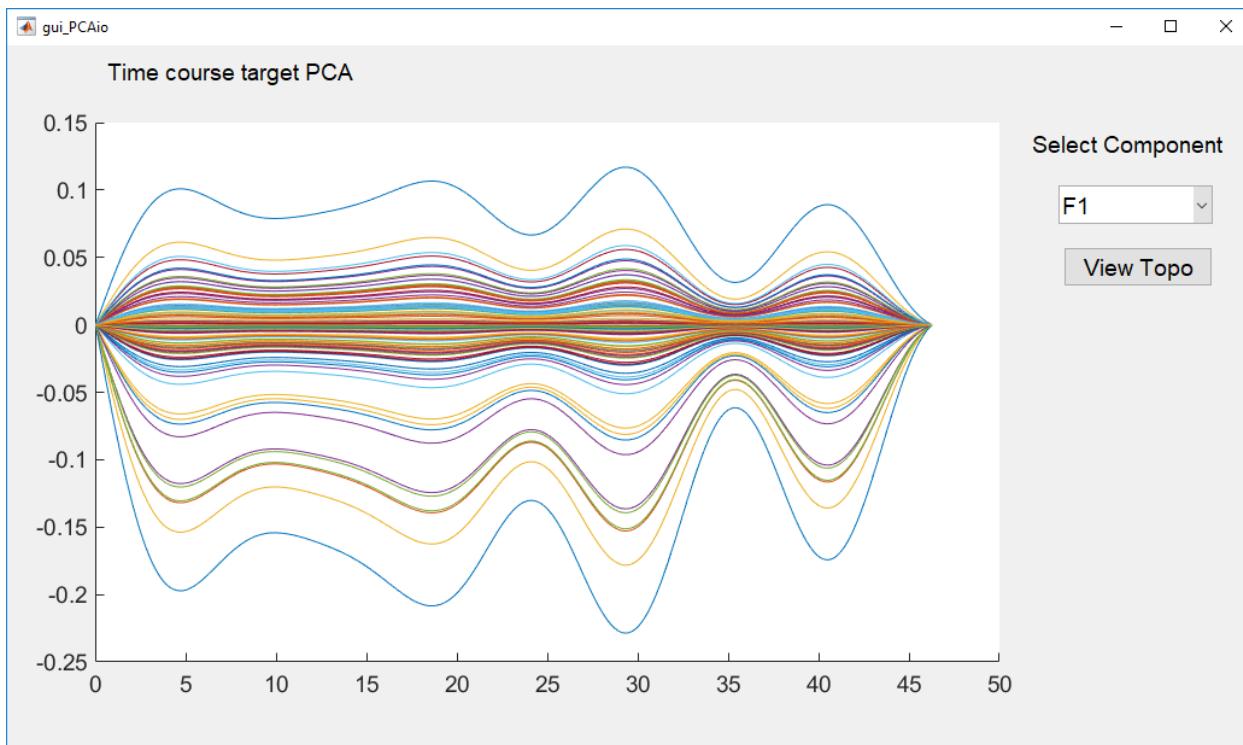
Example of muscular activity isolates in fNIRS.

## PCA

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

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

$$Y = SVD$$



## GLM

GLM function selects auxiliaries 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 amplitude (beta), regressor model, and t value will be saved in the component.

When the auxiliary does not get the same sample rate, an adjustment is done to resample the AUX to the fNIRS sample rate (resample.m).

## Offset Adjustment

Adjust the intensity after a movement that causes abrupt changes in the light intensity. The offset adjustment is applied after the artifact selection. It keeps the intensity continuity before and after the time interval reject.

## Component

List of the decomposition identified. Components could be subtracted or exported.

## Multimodal view

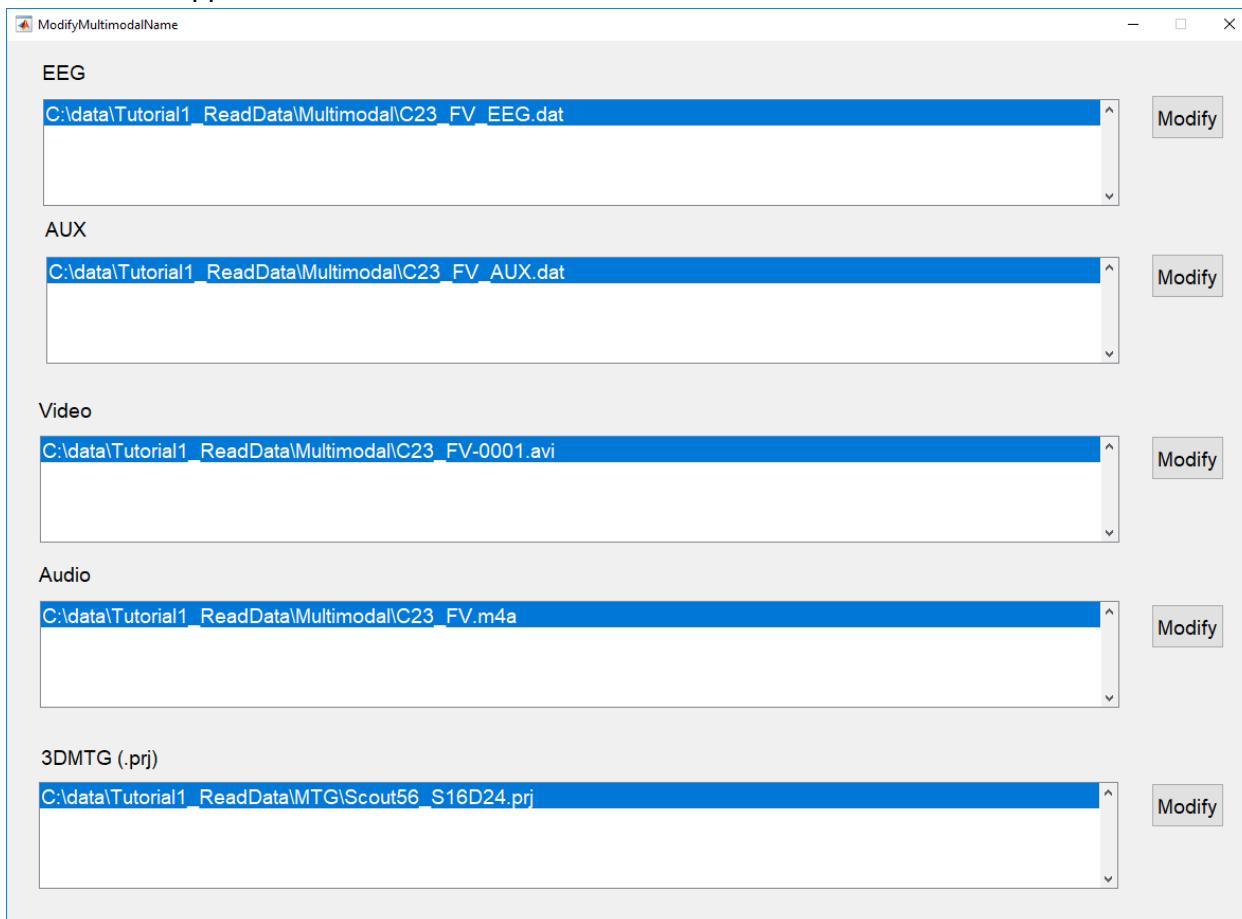
The multimodal file displayed for the interval time start and time stop selected. We advise using a short duration for the selection. Press the button **EEG, VIDEO, or AUDIO** to display these

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 trigger 1 in fNIRS will be synchronized with the first trig 1 in EEG and so on. However, the error of trigger 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 that includes several codecs <https://www.mathworks.com/matlabcentral/fileexchange/8028-mmread>).

MATLAB enables to play audio-video. Verify that the right codec is installed on your computer, and use a MATLAB version the same as the codec (32-bit or 64-bit). However, MATLAB needs to load part of the audio-video data before playing the sequence, is therefore not purpose to be a video player. Another option is to use the time (in the DisplayGUI video info) and file information to open the video at the right time in a classic 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:

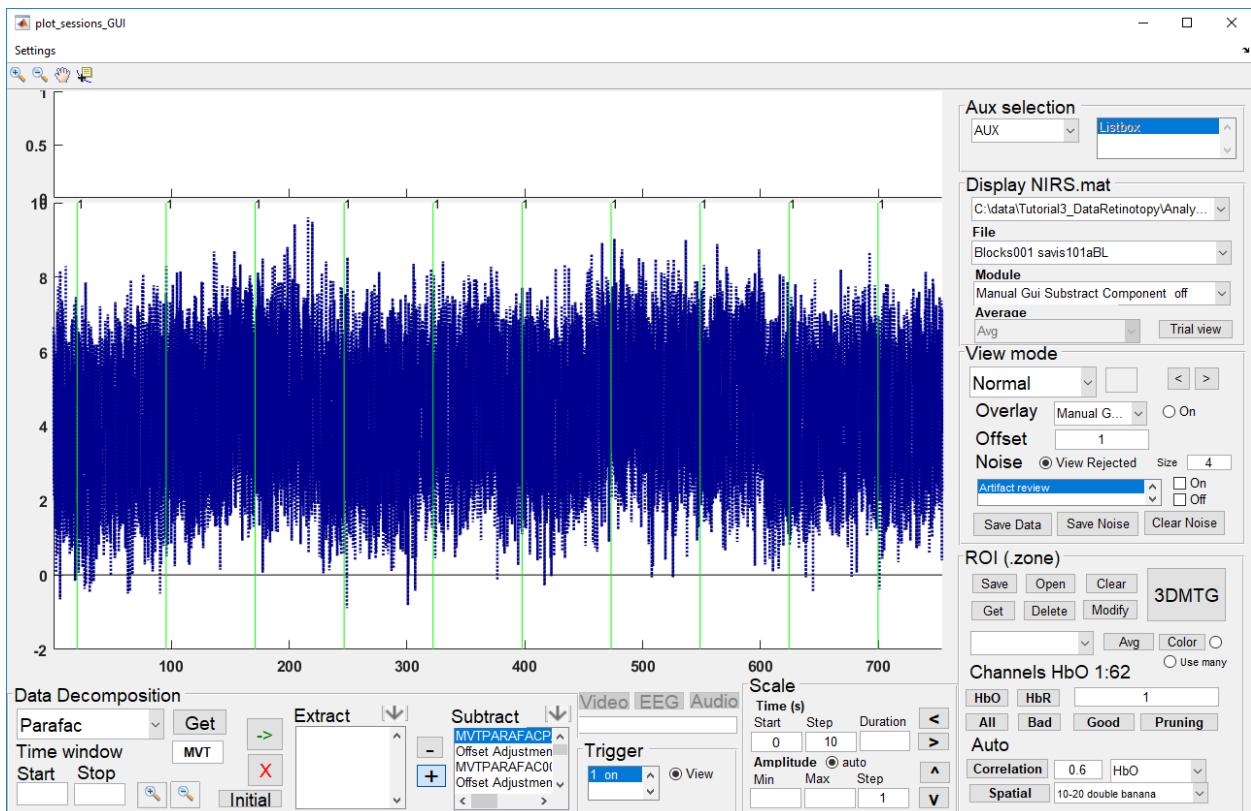
**Copy:** Copy in the clipboard all onset time for the selected trigger.

**On:** Activate the visualization for the selected trigger.

**Off:** Deactivate the visualization for the selected trigger.

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

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



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

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

**Add a trigger:** Press a right-click on a specific time in the fNIRS data display window. Select the option to add a trigger. Note that the trigger, is only added in the current step. To use them to create HRF AUX you will need to start from this new definition.

## Scale

**Time(s):** Adjust the x-axis scale to select the appropriate timeline to display.

**Start:** Set to 0 to use the full window's 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 to control the timeline x-axis.

**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 the y-axis scale, use auto to adjust the best scale according to the data.

**Min:** Minimal y-axis value (remove auto to use manual adjustment).

**Max:** Maximal y-axis value.

**Step:** Step to navigate amplitude step using up and down arrow.

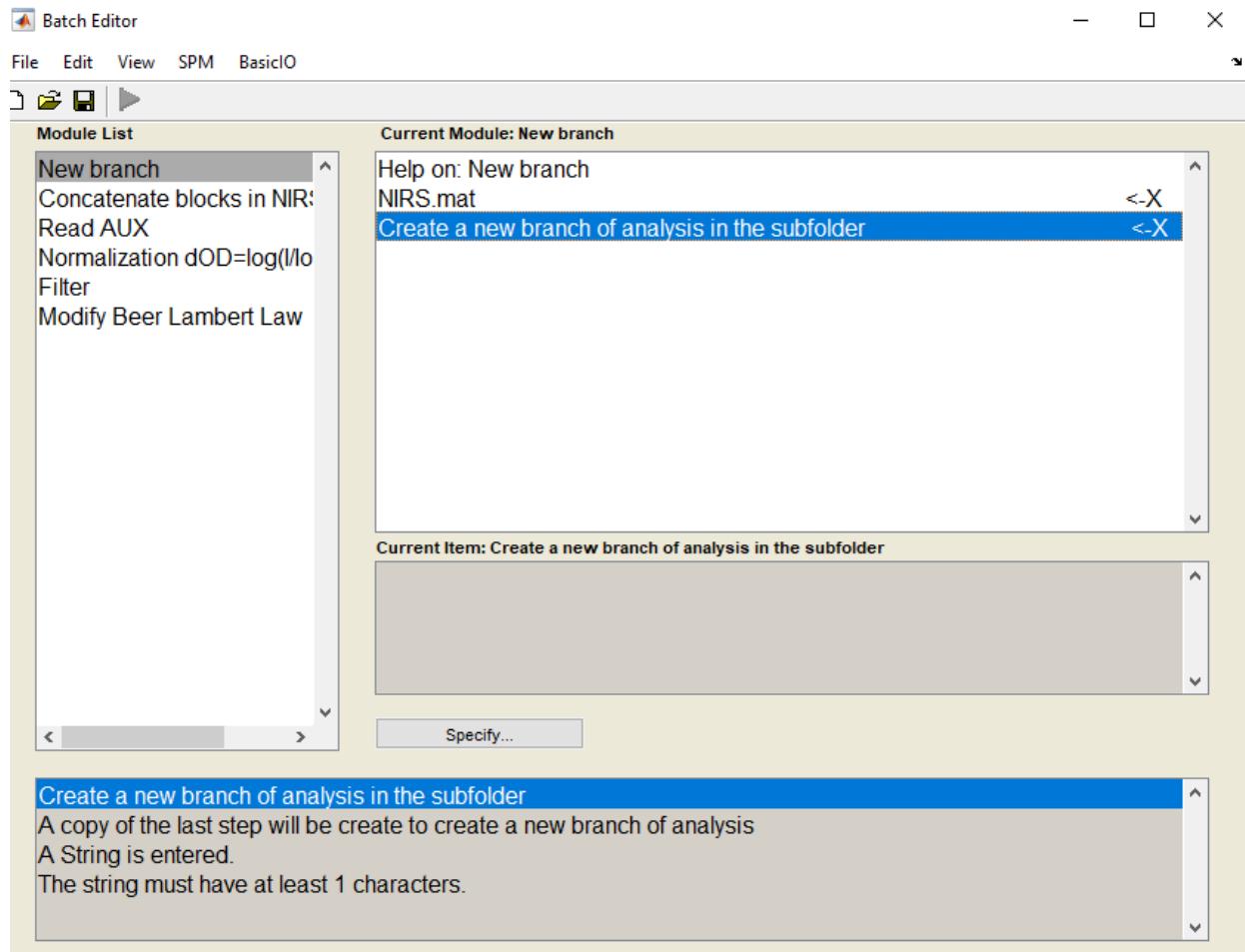
## Keyboard shortcuts list

Use the shortcuts 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 channels for this trial).
- A All (Remove this channel for all trials).
- T Trial (Remove this trial for all channels).
- W Whole (Whole channels restored for this trial).

## Create a Batch Template script using Excel database to automate pipeline

[Matlab Batch System](#) allows the use MATLAB script to run a Batch template modifying only a few fields. The system calls the template script a 'job'. This feature is useful to run processing and analysis commands on multiple subjects with the same parameters. Create a 'job' as a normal batch but leave empty the field that needs to be adjusted for each subject. As in the following figure, the NIRS.mat is empty and the name of the New branch folder is empty, <UNDEFINED>. They will be considered as missing fields A and B for this example.



Create your batch by adding all the modules you need for your pipeline.

From the batch editor use menu view>Show .m Code to visualize the script.

Copy in a .m file all the batch configuration and save it as Template\_Batch\_dCONC\_job.m, for example.



```

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_files = {'C:\data\Analysed\Retinotopy\BG\HRF_BG.dat'};
8 - matlabbatch(4).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/O): NIRS.mat', substruct('.','val', '{},{4},
15 - matlabbatch(5).spm.tools.nirsHSJ.M_preprocessing.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({});

```

The missing fields are indicated as <UNDEFINED>. Define them in the script. As an example, a new script is created to run the batch for all subjects 'run\_BatchTemplate.m' using the following instructions.

```

% fill the missing field A and B for each subject, each <UNDEFINED> in the script will
be replaced by these values.

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 );

    %first <UNDEFINED>, %second <UNDEFINED> ...
    %RUN THE JOB
    cfg_util('run', jobid)
    disp(['Subject : ', num2str(isubject)])
end

```

A convenient way is to use an Excel spreadsheet to define each entry that has to be modified <UNDEFINED> in a row for each subject.

RawNIRscout	AGE	3dMTG	AnalysisFolder	Batch_01_Read
-------------	-----	-------	----------------	---------------

				Fait (0) / À faire (1)
...\\C01\\NIRS-2018-01-1 6_001.hdr	18	\\C01\\MTG\\V2.prj	..\\Analysis\\C02\\	1
...\\C02\\NIRS-2018-02-1 6_001.hdr	16	\\C02\\MTG\\V2.prj	..\\Analysis\\C02\\	1

Adjust your script to read the Excel file and identify the appropriate column for each <UNDEFINED> 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}};
```

Most errors occur when you run the script if you don't use the right format expected (cell array, string, double, etc...). As a tip, enter a value in the batch for each module, save it as a MATLAB script and observe the expected format in the MATLAB script, ensure to keep the same format for your entry as example use:

```
% to enter a cell array with string;  
input = {'C:\data\Analysed\Retinotopy\BG\107\NIRS.mat'};  
% to enter a string of char  
Input = 'test1';  
% to enter a number as double  
input = 4;  
% to convert a string into a number double  
input = str2num('4')  
% to convert double into a string  
input= num2str(4).
```

## Troubleshooting

Here is a list of familiar problems you may face during your analysis.

### Wrong files

**Problem:** The data file you try to open in the batch is not at the expected location on your computer.

#### Error message:

```
Failed 'Read .nirs (HoMER)'  
Error using load  
Unable to read file  
'C:\data\TutorialsNIRF\snirf_homer3-master\snirf_homer3-master\Snirf\Examples\Simple_Probe.nirs'. No such file or directory.
```

```
Command Window  
Failed 'Read .nirs (HoMER)'  
Error using load  
Unable to read file 'C:\data\TutorialsNIRF\snirf_homer3-master\snirf_homer3-master\Snirf\Examples\Simple_Probe.nirs'. No such file or directory.  
In file "C:\data\ProgramMatlab\CurrentSetPath2018\spm12\toolbox\LIONirs\3dMTG\IO_FileFuncs\Createproject_fromsnirf.m" (??), function "Createproject_fromsnirf"  
In file "C:\data\ProgramMatlab\CurrentSetPath2018\spm12\toolbox\LIONirs\nirs_run_readhomerfile.m" (??), function "nirs_run_readhomerfile" at line 41.  
  
The following modules did not run:  
Failed: Read .nirs (HoMER)
```

**Solution:** Double-check the spelling, the file location, and if the file is corrupt on your computer.

### Bad multimodal synchronization

**Problem:** Multimodal data do not have a matching number of triggers to achieve synchronization. The segmentation to synchronize multimodal files could not be achieved.

#### Error message:

File processed

AUX could not be segmented

C:\data\Tutorial1\_ReadData\Analyse\FV\sNIRS-2019-07-09\_002b01.nir

**Solution:** Verify the trigger in the AUX file and in the .nirs file. Ensure they are from the same acquisition, and the first trigger in NIRS are matched with the first trigger in AUX. To do so, you can visualize the file in Analyzer or open the file .vmrk which lists all the markers. Ensure the delay between two triggers is identical in both files. Pay attention at the acquisition to start all multimodal recording before starting the task who sends the trigger. Both files need to receive the same trigger to be synchronized.

## Use a wrong project to read data

**Problem:** The read NIRx and Read ISS functions use the project (.prj) to read the raw data. If you use a project that does not correspond to the recording, the data will be associate with the wrong position.

**Error message:** no error message will be displayed, but you will find more data with bad signals and low intensity than usual. If you read data with a project and look at the result with another project, the channels will appear strangely configured. In short, channels with abnormally long distances appear instead of the usual closest source and detector configuration.

**Solution:** Ensure you always use the proper montage according to your acquisition. Double-check optodes placement before the testing. Keep clear notes on data capture performed.

## Move or rename the analysis folder

**Problem:** You move the analysis folder on your hard drive, and they could not be found by the toolbox.

**Error message:** Verify file: C:\data\Analysed\DATASET\_II\subj100\mnullmnullmaresting.vmrk could not be open.

**Solution:** Insert a module (Read NIRSdata / NIRS.mat dir adjustment) before adding the DisplayGUI module. The new directory location is adjusted in the NIRS.mat field, but you need to keep the file organization in the new folder location.

## Excel table on a macOS

macOS could encounter some issues using Excel file format, read or write .xls are not well-supported in MATLAB. We recommend Mac users use tab space-delimited .txt files for the configuration.

## Glossary

**Channel:** Combination of source and detector, also called optode.

**Mux:** Combination 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:** 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 for the synchronization.

**Component:** Mathematic decomposition of a part of fNIRS data, could be noise or relevant information obtain by GLM, PCA, PARAFAC or average operation.

**Regressor:** It could be a model response, a channel or a grouping of several channels that cover a specific zone. It is used as regressor in the GLM model.

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

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

**Event:** Different cerebral activities, such as sleeping or reading, that are separated by triggers.

## Appendix: Additional information about files format

### Optodes spatial coordinate .ELP file

**Description:** Geometric position (in meters) of the holes over the head where you will insert the optodes. This includes the position of the patient's fiducial anatomy (LPA Left preauricular, RPA Right preauricular and NAS Nasion marker) used in the registration 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 to your own format. Center of the coordinated 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

```

## MRI volume iMagic volume format (.vox file)

**Description:** 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.

## Tissues segmentation format iMagic (.SEG file)

This segmentation format have 2 files. One to store the segmentation volume itself (binary data .seg) and another to store the information to describe how to read the binary format (header .hdr). 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.

## Tissues surface format iMagic (.srx file)

The Image Processor surface format defines how the surfaces created with Image Processor are stored. The surfaces are stored in only one binary file with extension .SRX. The file has the following structure:

BYTES	DATA TYPE	DESCRIPTION
4	Integer 32 bits	Number of vertices (NV)
4	Integer 32 bits	Number of triangles (NT)
NV*4*3	Float 32 bits	X,Y,Z coordinates for all vertices
NT*4*3	Integer 32 bits	Sequence of three indices to constituting vertices of each triangle

OPTIONAL		FROM HERE
2	Integer 16 bits	Number of triangles connected to vertex 0 (NTC)
NTC*4	Integer 32 bits	Indices to triangles connected to vertex 0
.	.	.
.	.	.
.	.	.
2	Integer 16 bits	Number of triangles connected to vertex NV-1 (NTC)
NTC*4	Integer 32 bits	Indices to triangles connected to vertex NV-1

The vertex coordinates are in the same coordinates system of image volumes. All indices are relative to 0.

## Data structure LIONirs (NIRS.mat)

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 for averaging

	1 valid channel 0 rejected channel
NIRS.Dt.s.age	Subject age information
NIRS.Dt.fir.pp{idmodule})	Step of analysis Each module of operation will add as a step of analysis Example = [1];
NIRS.Dt.fir.pp{idmodule}).p{ifile}	Link to the raw data record on the drive
NIRS.Dt.fir.pp{idmodule}).pre	Step of preprocessing Example = ['Read Raw_NIRxScout']
NIRS.Dt.fir.pp{idmodule}).job	Detail of the parameter in the job file.
NIRS.Dt.fir.aux5{ifile}	First column trigger value, Second column time sample value Example; [2, 9; 2, 1733; 255,1] Trigger 2 sample 2 et 1733, Trigger 255 sample 1
NIRS.Dt.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 triggers 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_time sec	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.synref	'EEG' %the video needs to be synchronized to the beginning of the fNIRS file, or the EEG file to keep the synchronization.

## Zone structure to create channels ROIs (.zone)

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\_LookMatrices data structure

Each subject corresponds to one line list in the xls definition to be open.

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

NB \*. The channel list is essential to regroup subjects and ensure that the same position on the head of the measurements. The channels in the homologous zones has to be the same position on a subject or another subject.

## Multimodal data format (EEG, AUX)

Generic data export file format use by BrainVision analyzer use to store AUX or EEG

Description: This export contains 3 files with the same name. A .dat file use to store binary data, a .vhdr to give information about how data are saved and a .vmrk to store event markers.

### \*.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,µV*  
*Ch2=Cz,,0.0488281,µV*  
*Ch3=Pz,,0.0488281,µV*  
*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 trigger

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

### .nirs, NIRx or imaging naming convention

They will use E1 or D1 as identification for emitter and detector respectively. This nomenclature is available in 3DMTG, the reading data function will associate raw data to the appropriate emitter or and detector position indicated in your montage configuration file .prj.

### Imaging or ISS naming convention.

ISS recording systems use one or more devices in parallel. The illumination could be multiplexed in time using mux16 or mux32 illumination sequences. Mux 16 turn light a1 (830 nm) and b1(690) on simultaneously. Mux 32 turn light a1 to b16 on one after the other, and synchronize multiple device simultaneously. The source naming convention uses a1b2 to pair 830nm and 690nm wavelength to avoid simultaneous wavelength illumination at mux 16 and was therefore conserve to facilitate ISS data handling. Capital letters are used for the detector PMT recording. This nomenclature is available in 3DMTG, 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

This transfer chart define the 3DMTG sources identification number and the associate label Emitter (NIRx, .nirs) or ISS (a1b2). 3DMTG label identification was initially designed to support ISS dual wavelength multiplexing, as describe above. Likewise, for the detector identification.

Emitter	ISS	3DMTG	Emitter	ISS	IOMTG
E1	a1b2	18001	E29	c10d9	57042
E2	a3b4	20003	E30	c12d11	59044
E3	a5b6	22005	E31	c14d13	61046
E4	a7b8	24007	E32	c16d15	63048
E5	a9b10	26009	E33	e1f2	82065
E6	a11b12	28011	E34	e3f4	84067
E7	a13b14	30013	E35	e5f6	86069
E8	a15b16	32015	E36	e7f8	88071
E9	a2b1	17002	E37	e9f10	90073
E10	a4b3	19004	E38	e11f12	92075
E11	a6b5	21006	E39	e13f14	94077
E12	a8b7	23008	E40	e15f16	96079
E13	a10b9	25010	E41	e2f1	81066
E14	a12b11	27012	E42	e4f3	83068
E15	a14b13	29014	E43	e6f5	85070
E16	a16b15	31016	E44	E8f7	87072
E17	c1d2	50033	E45	e10f9	89074
E18	c3d4	52035	E46	e12f11	91076
E19	c5d6	54037	E47	e14f13	93078
E20	c7d8	56039	E48	e16f15	95080
E21	c9d10	58041	E49	g1h2	114097
E22	c11d12	60043	E50	g3h4	116099
E23	c13d14	62045	E51	g5h6	118101
E24	c15d16	64047	E52	g7h8	120103
E25	c2d1	49034	E53	g9h10	122105
E26	c4d3	51036	E54	g11h12	124107
E27	c6d5	53038	E55	g13h14	126109
E28	c8d7	55040	E56	g15h16	128111

E57	g2h1	113098	E61	g10h9	121106
E58	g4h3	115100	E62	g12h11	123108
E59	g6h5	117102	E63	g14h13	125110
E60	g8h7	119104	E64	g16h15	127112

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

## 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. Usually, 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.

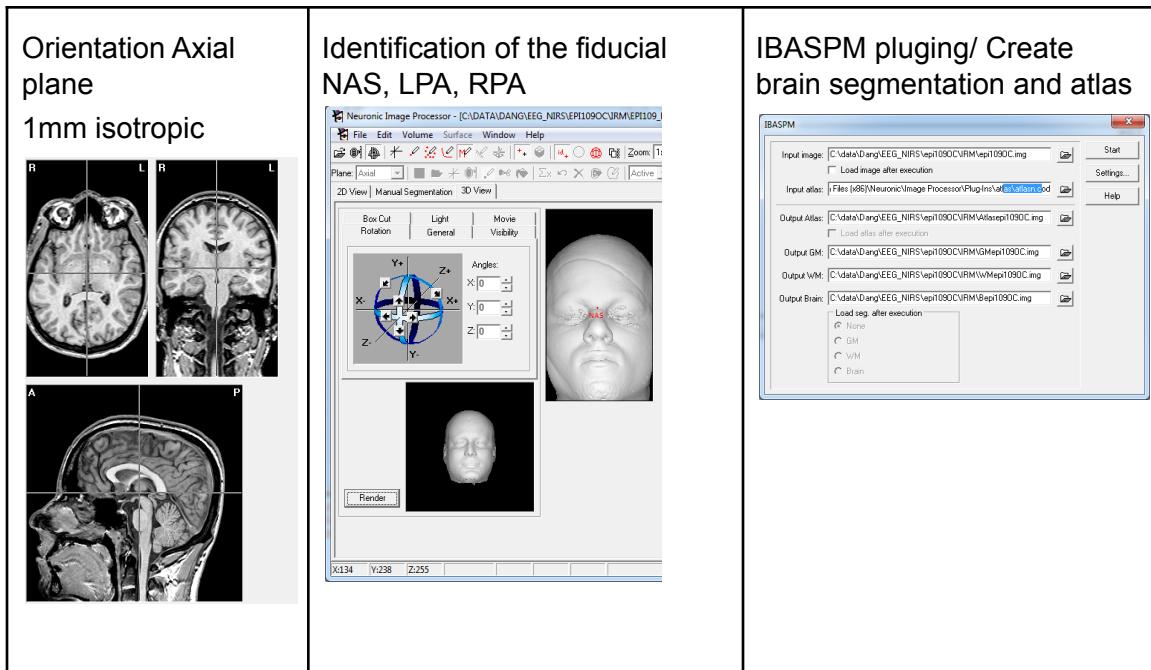
### Dicom conversion to nifti

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

### Preprocessing in neuronic Image Processor

1. Reorient the volume in axial plane.  
Menu : Volume/Rebuilt plane/Axial
2. Interpolate volume in 1 mm Isotropic 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 information 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 selected tissues and save the segmentation .seg. Menu: File/Save segmentation as/ brain(seg)
8. Create and save a surface segmented tissue (.srx)  
Menu: Volume/Create Surface /By deformation/ medium resolution  
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`, [http://brainsuite.org/matlab\\_scripts/readdfs.m](http://brainsuite.org/matlab_scripts/readdfs.m).

## SPM12 tissue segment

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

