USER TUTORIAL

– version 10.2023 –

TABLE OF CONTENTS

Download the software

To start analyzing your data with NET, download the software from https://github.com/bind-group-kul/net and make sure that the folders "external" and "template" (available from https://osf.io/jngwd/?view_only=0b776bad1bbb473ba839d8b5e7656be9) are saved in the main folder of NET. At the same link you can find also a test dataset.

As a general rule, do not rename or move any excel file and/or directory created by NET, unless otherwise stated in this manual.

Launch NET

In MATLAB®, first select the path with the main folder of NET, then either:

- run the script **net_start_gui.m** to run the toolbox with the GUI
- run the script **net_start_no_gui.m** to run NET through the main script (only for programmers)

When using the GUI, the following window will appear:
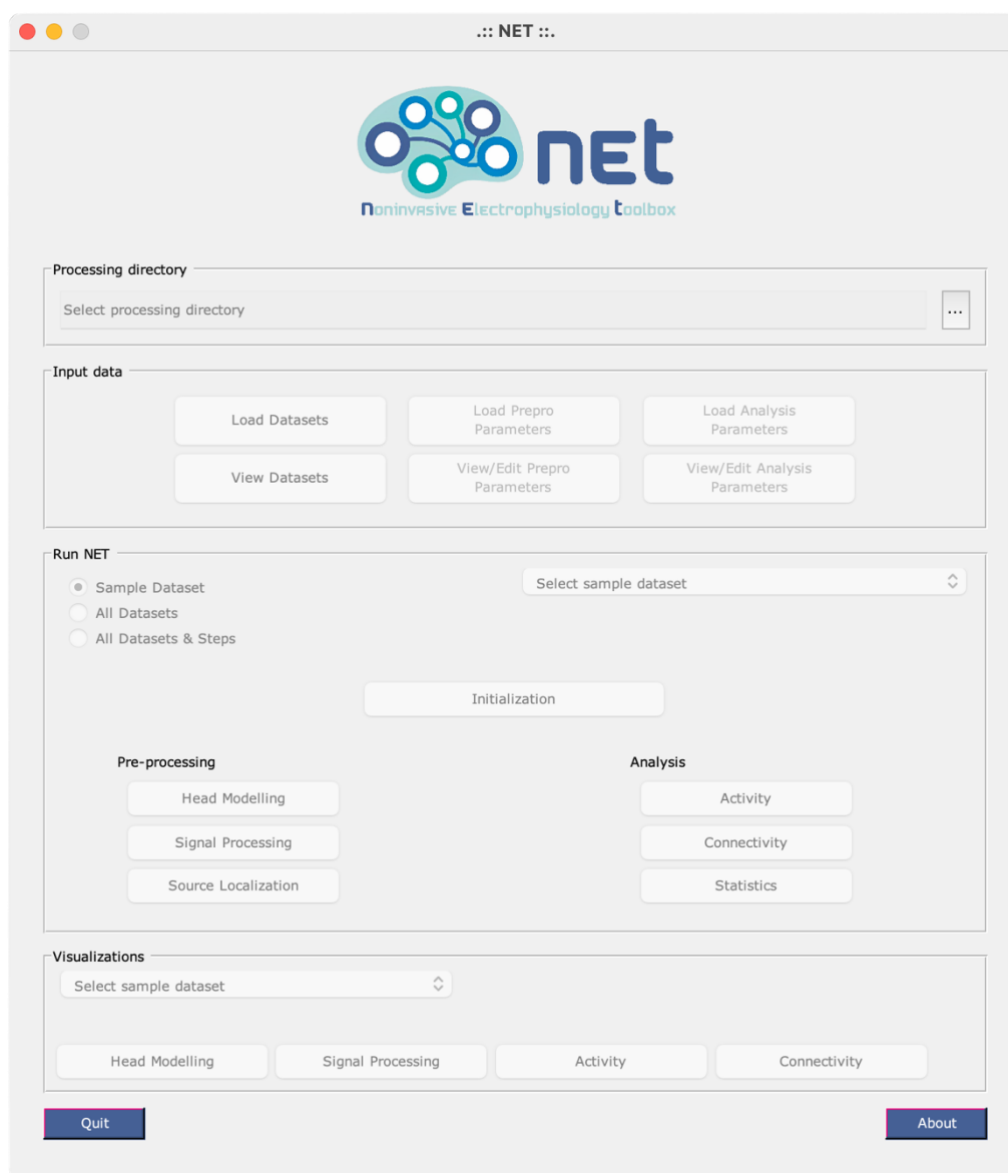
Run NET with the GUI
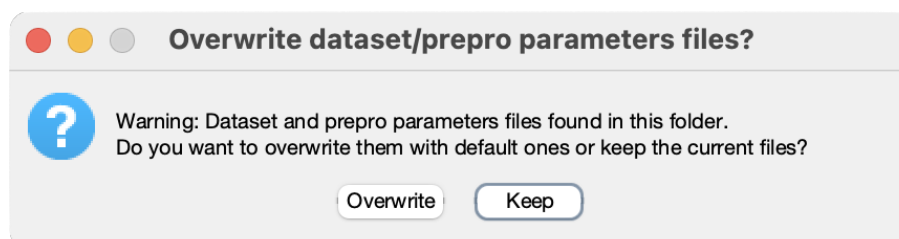
Processing directory

By selecting the three dots on the right of the Processing directory pane you can choose where NET will save the output of the analyses.

Once the directory (e.g. *myprocessingdirectory*) is selected, two excel files will be automatically copied there from the *net/template_files* folder:
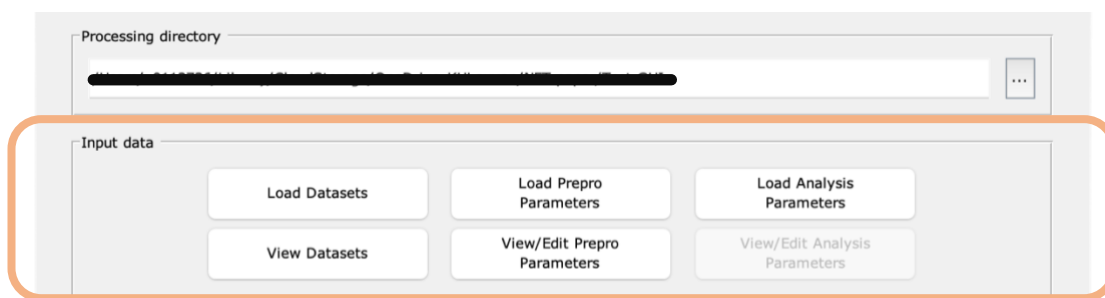
- *myprocessingdirectory_dataset.xlsx* > list of input filenames
- *myprocessingdirectory_parameters_prepro.xlsx* > parameters for conversion, head modelling, signal processing, source localization

If xlsx files with these same filenames are already present in the chosen processing directory, NET will ask you whether to keep the existing files or to overwrite them with blank templates.

Input data

In the Input data pane, you can load/edit the input data and the parameters used for the analyses.

Load or View Datasets

In *myprocessingdirectory_dataset.xlsx* file you will need to specify the file path and file name of the EEG data, the MRI image and the sensors position file for every dataset.
You can either edit the excel file directly or select the file paths through the GUI by clicking on the View Datasets button.
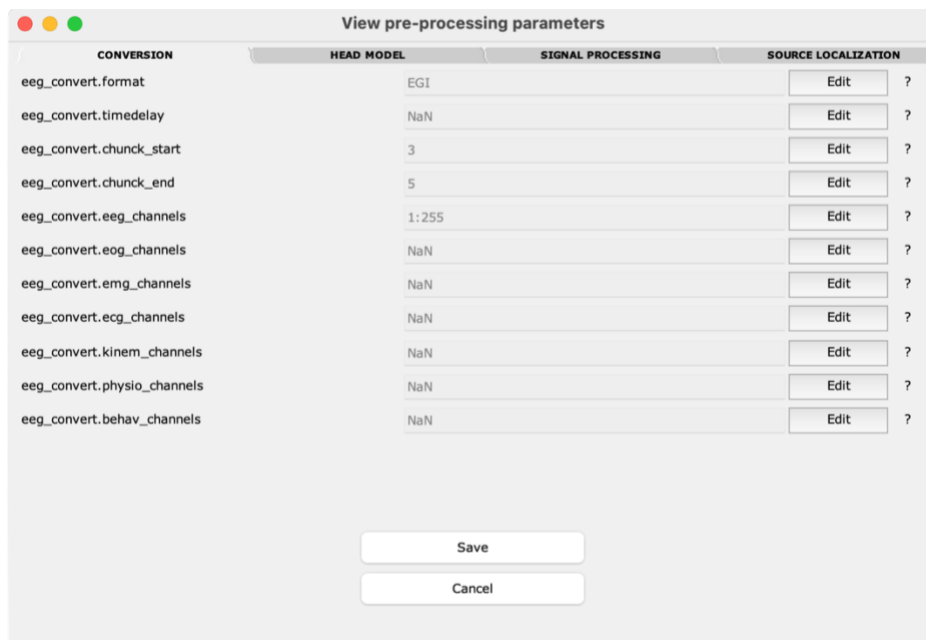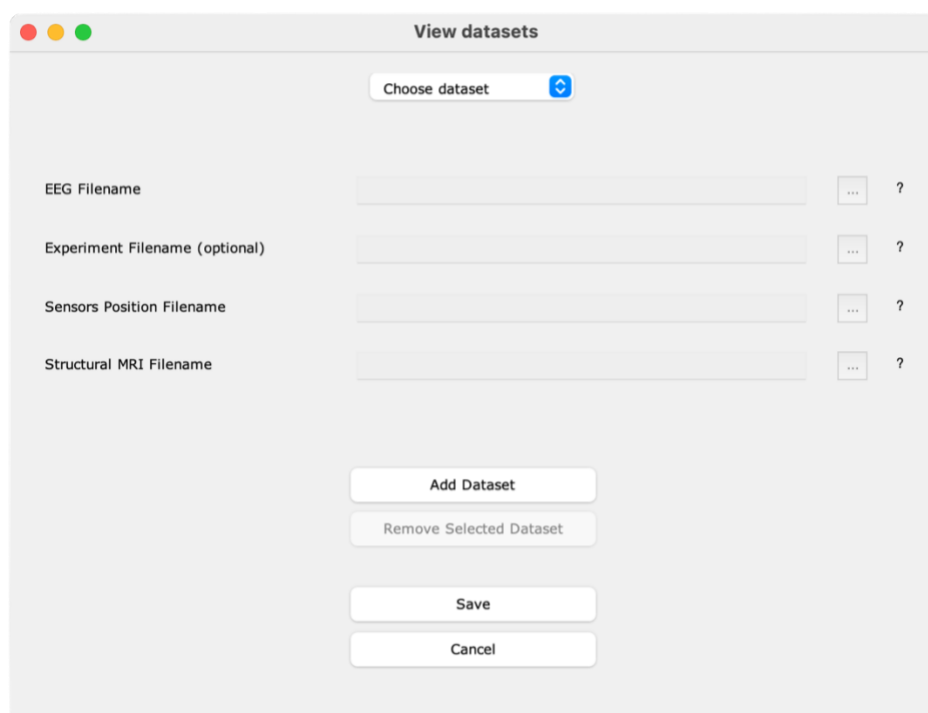

From the drop-down menu, choose one dataset at a time and select the corresponding files with the three dots on the right of each line. In order to be able to run NET, you will need to define the EEG, the sensor position and the MRI filenames. The experiment filename is required only for task-related data. By hovering over the question mark on the right, you can see the accepted file formats.
Once the dataset details are filled in, click on Add Dataset. You will then be able to define another new dataset, if necessary. When all datasets will have been added, click on Save.

Load or View/Edit Prepro Parameters

In *myprocessingdirectory_parameters_prepro.xlsx* file you will need to specify the parameters for the pre-processing analyses.
You can either edit the excel file directly or click on the View/Edit Prepro Parameters button.
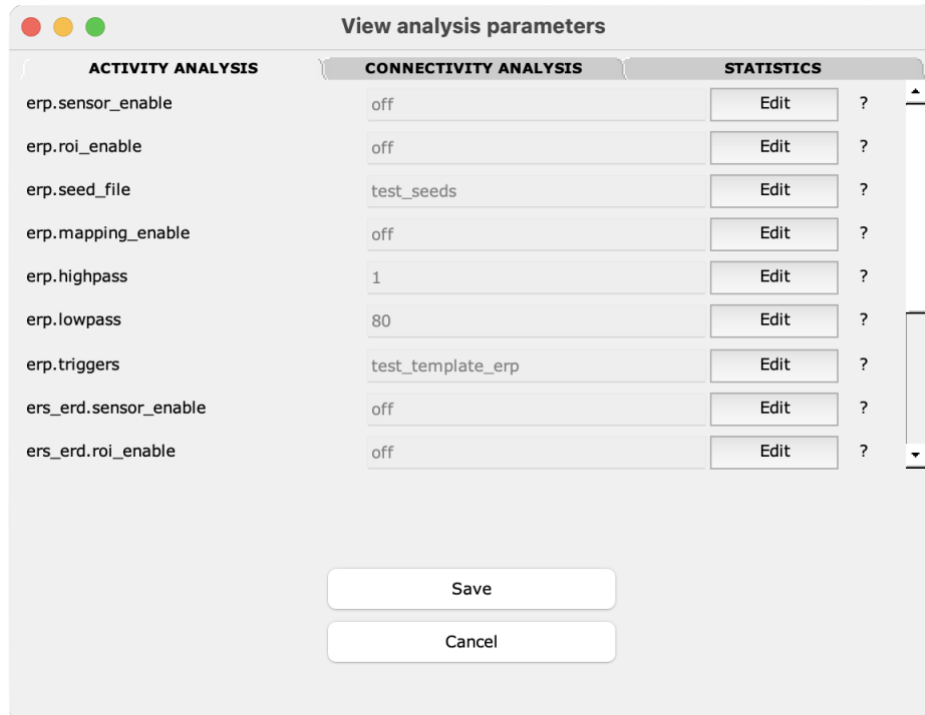

In each tab – CONVERSION , HEAD MODEL , SIGNAL PROCESSING , SOURCE LOCALIZATION – you can edit any of the parameters by clicking on the Edit button. By hovering over the question marks on the right, you can see more information about each parameter. You can move through the four tabs by clicking on the titles on the top row. The pre-filled values in the template files are the default ones. When all parameters are set, click on Save.

Load or View/Edit Analysis Parameters

In order to specify the custom parameters for your analysis, click on Load Analysis Parameters button and select the *net/template_files/template_parameters_analysis.xlsx* file from the pop-up window. Once you have edited the parameters in the GUI, an updated copy of the spreadsheet will be automatically saved in *myprocessingdirectory* and renamed as *myprocessingdirectory_parameters_analysis.xlsx*.
To change the parameters again, you can either edit the excel file directly or click on the View/Edit Analysis Parameters button.

In each tab – ACTIVITY ANALYSIS , CONNECTIVITY ANALYSIS , STATISTICS – you can edit any of the parameters by clicking on the Edit button. By hovering over the question marks on the right, you can see more information about each parameter. You can move through the three tabs by clicking on the titles on the top row. The pre-filled values in the template files are the default ones. When all parameters are set, click on Save.

Depending on your data and analysis, you might need to define some customized files:

- *seed_file.mat* > MATLAB® file defining the region(s) of interest (ROI(s)), used for source-level ERP and ERS/ERD analysis, or for seed-based connectivity analysis

  To create your own seed file, please make a copy of one of the template files inside *net/template/seeds* folder: open and edit it in MATLAB® and save it in the same folder.

- *triggers_file.mat* > MATLAB® file defining the triggers used in the experiment, used for ERP and ERS/ERD analysis, or for connectivity analysis on task data

  To create your own triggers file, please open in MATLAB® the *net/template/triggers/triggers_template_generator.m* file, edit it according to your experiment (instructions are written in the file) and run the code. Your triggers file will be saved in the same folder.

Run NET

Once the processing parameters are correctly set, you can start analyzing the data.
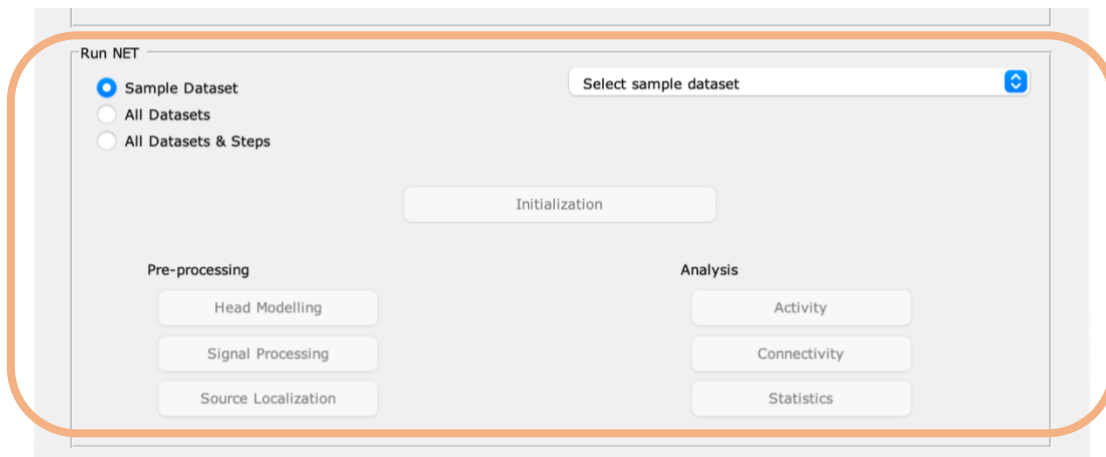
NET can be run in three modalities:

A. <u>Sample Dataset</u> > one dataset, chosen from the drop-down menu, and one processing step at a time
B. <u>All Datasets</u> > one processing step at a time on all datasets
C. <u>All Datasets & Steps</u> > all processing steps on all datasets (each dataset is fully processed before moving to the next one)

After choosing the modality, click on Initialization. In *myprocessingdirectory*, NET will create one subdirectory for each dataset containing three folders:

eeg_signal   >   contains processed channel data, ERP and ERS/ERD results at channel level

eeg_source   >   contains source reconstructed EEG data, ERP and ERS/ERD results at cortical level and connectivity results

mr_data   >   contains the files generated during the head modelling step, including processed MRI image, electrode positions and leadfield matrix

If the subdirectories are already present in the chosen processing directory, NET will ask you whether to overwrite the existing folders or to erase them and re-initialize them with empty ones. <u>Overwriting the folders will not modify their content</u>.
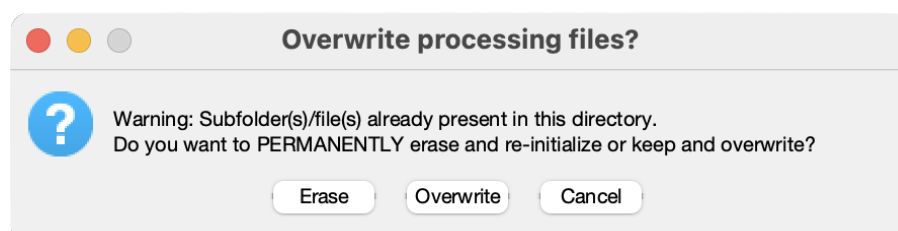
The pipeline runs through the pre-processing steps first, and then proceeds to the analyses enabled in *myprocessingdirectory_analysis.xlsx* file. **When choosing modality A or B, the button of a processing step won't be enabled for clicking if the required outputs from previous steps are not available**.
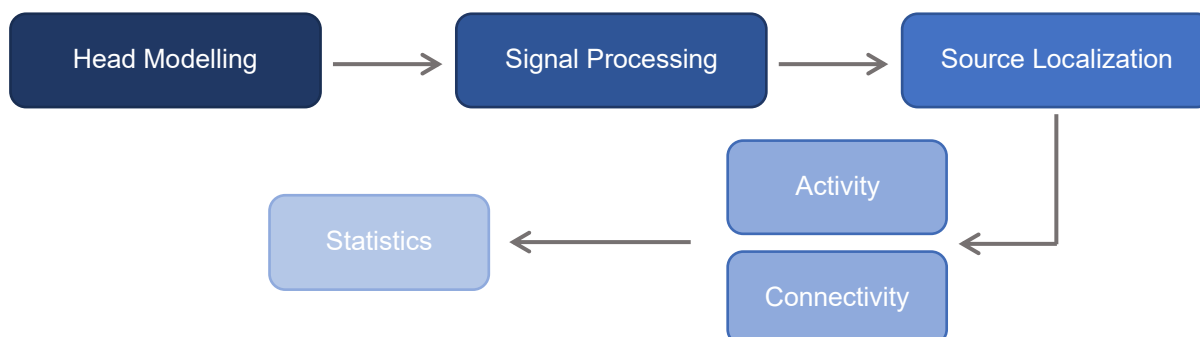

When modality C is selected, the analyses will start automatically, with no need to click on any step button.

In modality B, the [Statistics button] is enabled when individual activity or connectivity results are available. In modality C, the statistics are computed automatically if enabled in *myprocessingdirectory_parameters_analysis.xlsx* file. The statistical results are saved in the *myprocessingdirectory/group* folder, containing the same structure of subdirectories as the other datasets. Modality A doesn't provide any statistics, as at least 2 datasets are required to perform group analysis.

Visualizations

It's possible to visualize the output of the several processing steps through the Visualizations pane.
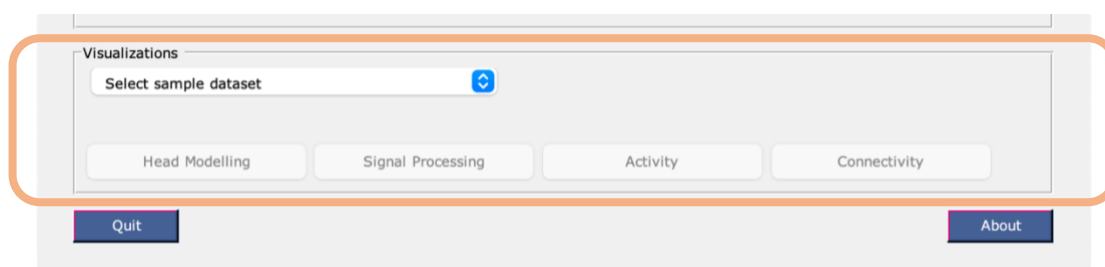

From the drop-down menu it is possible to select the results either for a single dataset or at group level by choosing the *group* option.

Only activity and connectivity results are available at the group level.

Head Modelling

For each dataset you can visualize the pre-processed MRI (Pre-processed MRI), the results of the head tissues segmentation step (Segmented MRI) and the co-registered and inflated electrode positions overlapped with the subject's head (3D MRI + electrodes).
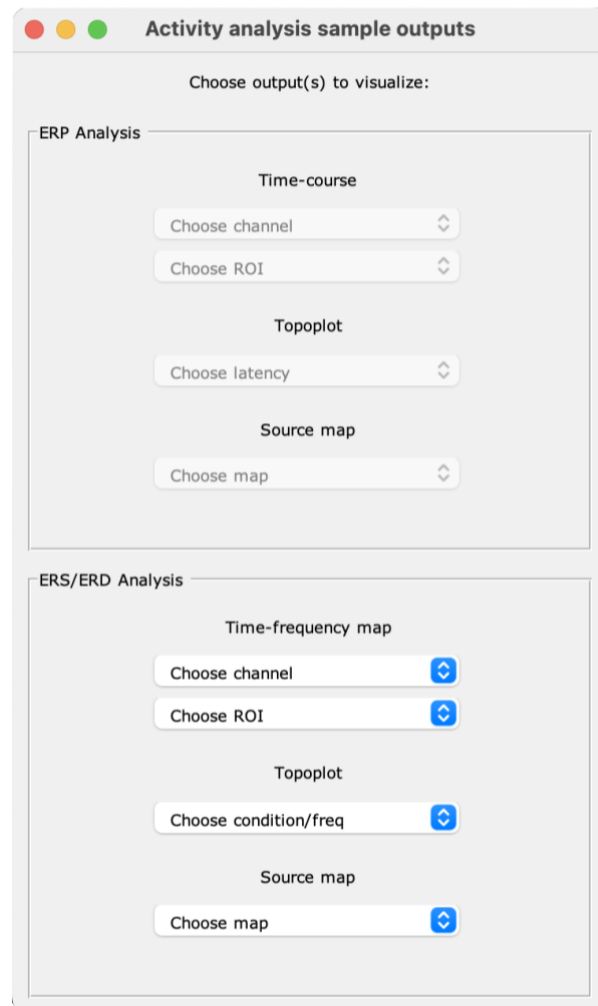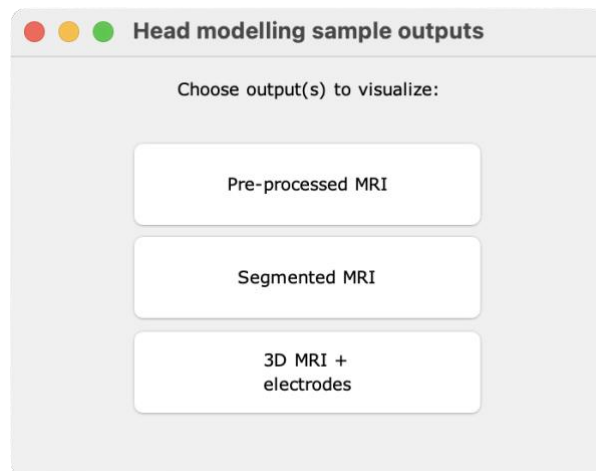

Signal Processing

For each dataset you can visualize the raw and pre-processed time-courses and the power spectra of a single EEG channel or of all channels together.
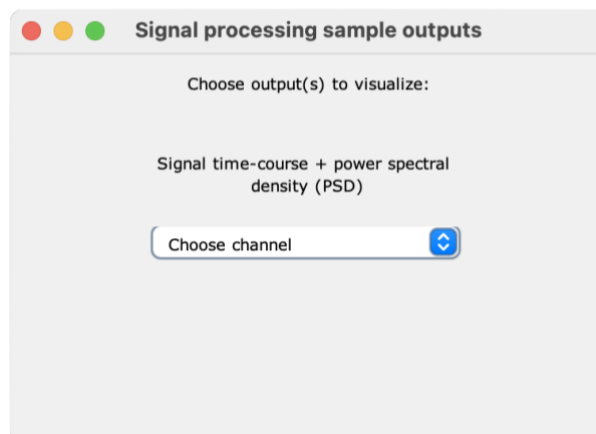
Activity

Depending on the activity analysis performed, ERP and/or ERS/ERD, the following options are available:

Connectivity

According to the method used for connectivity analysis, different visualization options will be available. The connectivity maps are calculated with both the ICA- and the seed-based methods, whereas the connectivity matrices are generated only with the seed-based connectivity.
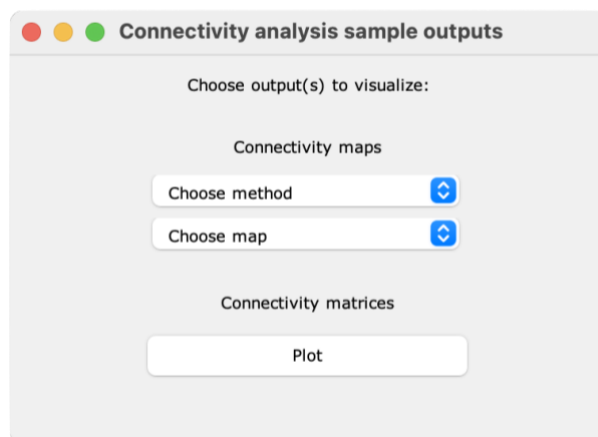
Quit the toolbox

To quit NET, click on the Quit button. More information about the toolbox can be found by clicking on About.
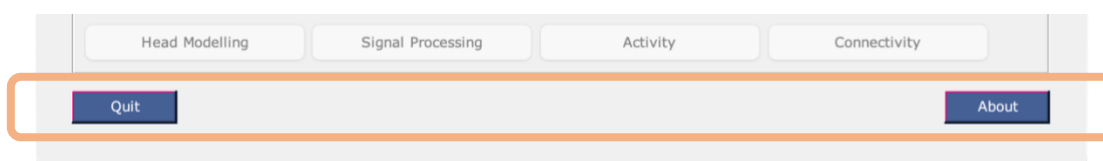
Run NET through the main script

Copy the *template_dataset.xlsx*, *template_parameters_prepro.xlsx* and *template_parameters_analysis.xlsx* files from *net/template_files* folder to *net/net_results*. *net_results* is the processing directory in which the output of NET for each dataset will be saved.

Fill in the files with the information about the datasets and the correct processing parameters. For every dataset (i.e. for each line of the *data* sheet in *template_dataset.xlsx*) set to "on" or "off" the processing steps of the pipeline you want to execute. Please consider that the steps are executed in serial order and they require the output(s) of the previous step(s) to be available, as clarified by the scheme below.
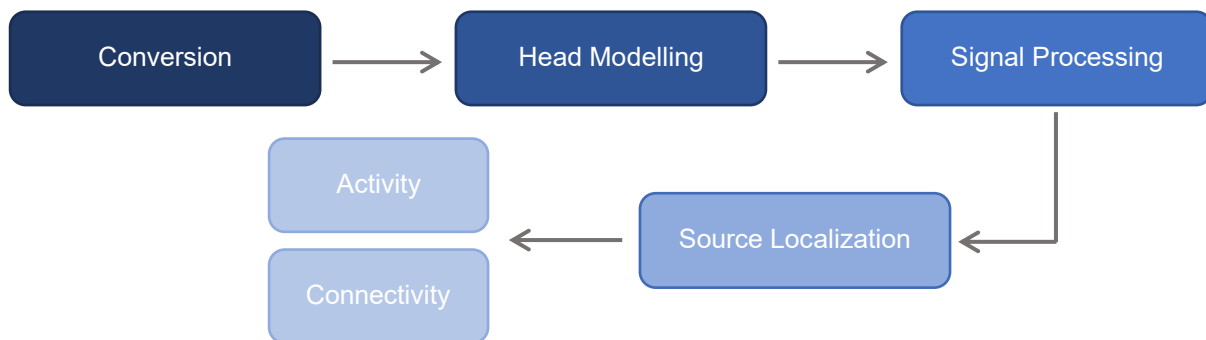
When the spreadsheets are ready, run **net_start_no_gui.m**. NET will automatically read the spreadsheets mentioned above and go through the steps you set to "on". The statistical analysis will be performed for the subjects indicated in the *statistical_analysis* sheet in *template_parameters_analysis.xlsx*.

In *net_results* folder, NET will create one directory for each dataset, containing three subfolders:

eeg_signal   >   contains processed channel data, ERP and ERS/ERD results at channel level

eeg_source   >   contains source reconstructed EEG data, ERP and ERS/ERD results at cortical level and connectivity results

mr_data   >   contains the files generated during the head modelling step, including processed MRI image, electrode positions and leadfield matrix

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    To create your own triggers file, please open in MATLAB® the *net/template/triggers/triggers_template_generator.m* file, edit it according to your experiment (instructions are written in the file) and run the code. Your triggers file will be saved in the same folder.

Using the GUI, it is possible to visualize the results of the automated process by selecting *net_results* as processing directory and then following the instructions above concerning the Visualizations pane.