Instructions for how to submit your analysis scripts

Please submit the scripts in **one of the following formats** depending on the analysis software you used:

● If you used any **self-written scripts**, please provide all those scripts (for software-specific details, see the list below). If these scripts in turn used functions from publicly available software packages or toolboxes, do not submit these toolboxes! It is enough that you tell us which toolboxes and versions you used. Please make sure that your code clearly indicates **the order** in which your scripts were called (e.g. in a separate text file or by numbering the scripts, (e.g. 01-filtering, 02-ica, etc.). Given that we may have to work with your code for our own analyses, we would appreciate it if your scripts were coded as transparently as possible. Please pay special attention to documenting how you did the time-frequency decomposition.

● If you use (mainly) the **Graphical User Interface (GUI)** of the analysis software, you should provide a text file (e.g. .docx, .pdf) in which you describe your steps. You can use both free text and screenshots. Such a text file should contain the values chosen for each entry field of a given preprocessing step. Explicitly report which parameters you decided to leave empty ('default values'), see Figure 1 and 2. It can be useful to include descriptive pictures/ screenshots with the details of the graphical windows, as illustrated in Figure 1 and 2.

Also, many software packages allow you to export and include an ordered list of functions (with all the input settings). Such files can easily be generated by most EEG analysis software through a "history" command or script generator. Please see below for software specific guidelines, and refer to the documentation for the software you are using, on how to export history scripts.
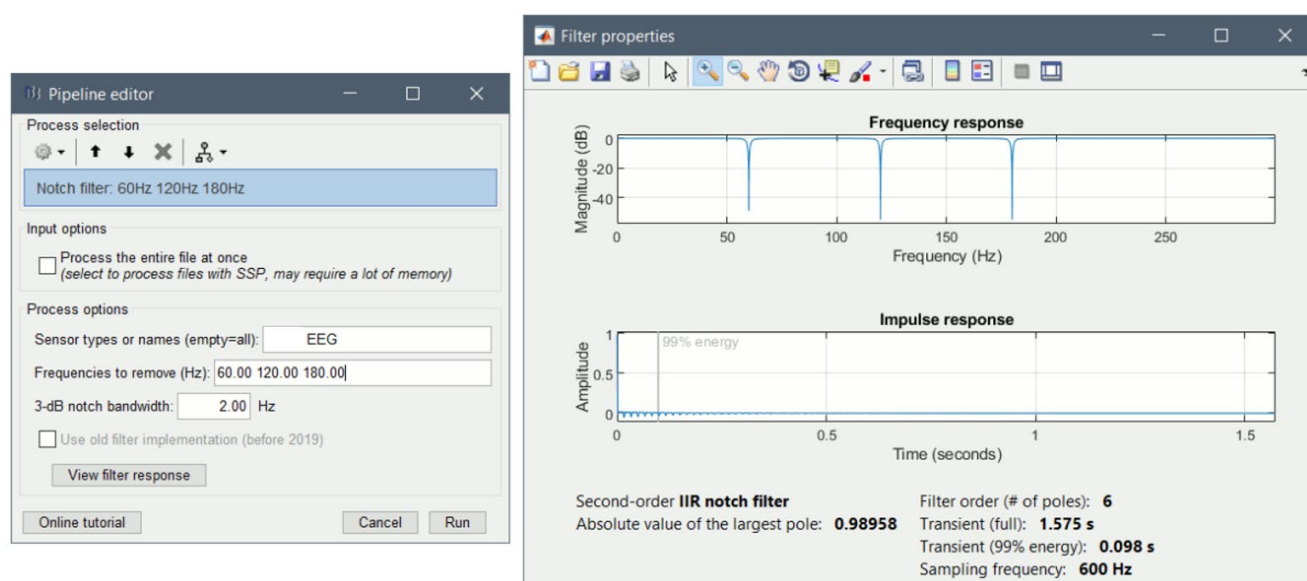

Figure 1. An example of the "notch filter" editor as implemented in Brainstorm software
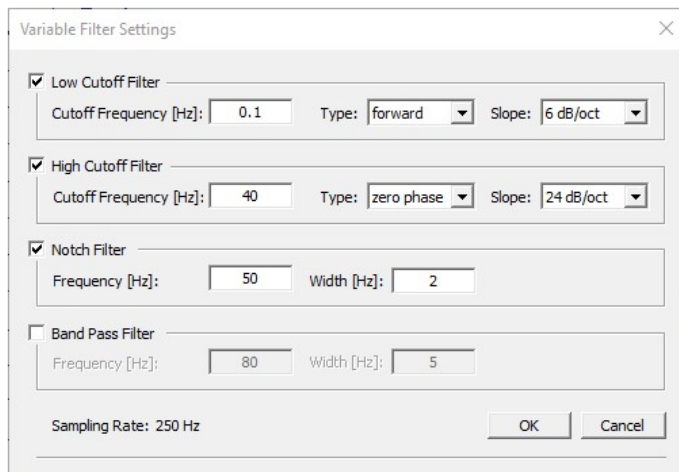
Figure 2. An example for the "Variable Filter Settings" window as implemented in BESA software.

Below are toolbox specific guidelines for code submission for some of the most commonly used EEG analysis software:

● **Brainstorm**: please use the script generator in the pipeline editor to extract the sequence of functions applied to the data. Alternatively, you can provide a clear description with pictures (screenshots) of each step parameters applied into a .doc or .txt file (as in the example above, see Figure 1).

● **BrainVision Analyzer**: for each operation (i.e., pre-processing step), please copy and paste the respective log files into a .txt file. You can retrieve this log information by right-clicking on the operation and selecting "Operation infos". Note that the operation infos will not be saved and written to the log file until after the processing is completed.

● **EEGLAB (GUI)**: EEGLAB, LIMO, and ERPLAB use command history functions that automatically store any mouse clicks in the GUI as equivalent script functions. If your analysis was exclusively GUI based, please check that the command history was recorded accurately and completely. Please share the complete command history with us (.set or .txt file).

● **EEGLAB (scripts)**: please provide all your custom scripts (.m files) and specify whether other plugins or toolboxes are required to run your scripts. If you use a combination of automatic code-based analysis and manual GUI-based analysis, make sure to provide your code as well as the automatically recorded command history in the data files.

● **Fieldtrip**: Please provide all your analysis scripts (.m files), including any custom scripts.

● **MNE-python**: please provide all your analysis scripts (.py and/or .ipynb), including any custom scripts.

● **SPM-EEG**: once you have analyzed the dataset with the GUI or batch system, use the "spm_eeg_history" function to automatically generate the script with the list of all the processing steps and input arguments.

● **Custom Matlab code**: provide all Matlab custom scripts used.

● **Custom Python code**: provide all Python custom scripts used.

● **Custom R code**: provide all R custom scripts used.

If none of the above applies to your analysis's procedure, please contact us via email at committee@eegmanypipelines.org.