Instructions for how to submit your pre-processed data

Please keep data in a format where each subject is assigned a folder containing four subfolders as shown in **Figure 1**. Do this for all subjects in the dataset, even if you excluded subjects for the final analysis, in this case, the folder could be kept empty.
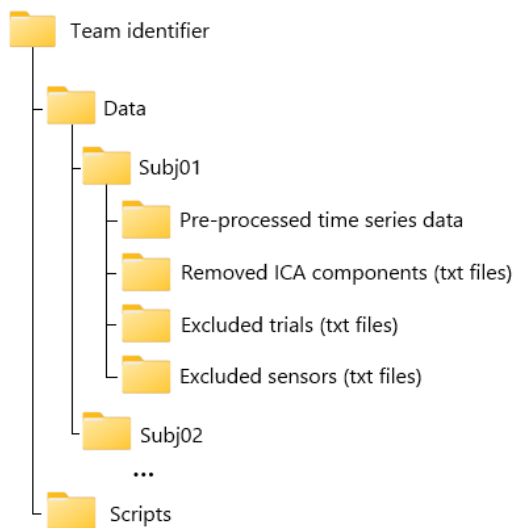

Figure 1. Structure of folders

Folders should contain:

- *Pre-processed time series data*. The single-subject time-domain data at the end of the pre-processing steps (i.e. after any data cleaning and preprocessing steps, but before any averaging and inference). The data will in most cases be a 3D structure with channels x samples x trials. If your analysis is based on continuous data (i.e. without segmentation in trials or 'epoching'), please submit your data in a 2D format with channels x samples. All pre-processed data of one subject should be stored within one single file. The data should also include the trigger value for each trial (see data documentation). This information is stored within the data structure or data file as a default for many analysis software. You therefore just have to make sure the data is in the right format and submit the data in the native format used by your analysis software (e.g., .fif, .set., .mat, etc.).

  If the trigger values are not contained in the output file of your analysis software, you have to generate a text file (.txt or .csv) with one column reporting the corresponding trigger value for each epoch. This list with trigger values should have the same length as the number of trials in your preprocessed data.

- *Removed ICA components*. In case you performed an Independent Component Analysis, please provide a full-text description (e.g., .txt, .docx, .pdf) for each subject with the following information:

  a. The total number of ICs obtained from ICA decomposition

  b. The overall number of ICs that you selected for removal

c. A breakdown with the number of components you identified as pertaining to a given class of non-brain signal. Report only the classes you decided to identify and remove. Please use the following suggested classes: a) eye blink; b) eye-movement (e.g. lateral eye-movement); c) muscular artifact; d) channel noise; e) line noise; f) heart; f) other (please specify in a few words).

An example of a report should be: "For subject 1, our ICA decomposition yields 42 components. From those, we rejected a total of 6 components, with 2 being eyeblinks; 3 muscle artifacts, and 1 being heart-related".

If possible, please provide the original ICA mixing/unmixing matrices for each subject. This should be also stored in a "Removed ICA components" folder. If you don't exclude any ICA components, please leave this folder empty.

- *Excluded trials*. A text file (.txt or .csv) with the indices of the trials rejected during the pre-processing for each subject (e.g. Epochs rejected: 2, 5, 9, etc.). Important note: if you rejected epochs in two or more separate steps, you should report in the first row the indices of the epochs rejected during the first step (by specifying the analysis step), in the second row the epochs rejected in a second step, and so on.
  Example:
  > (line 1): Trial indices rejected at step 1 (before ICA): 2, 5, 9, ….
  > (line 2): Trial indices rejected at step 2 (after ICA): 2, 23, 48, ….
  > Please report the trial indices relative to all trials (i.e., not separated by conditions) and retain consistent trial indices across preprocessing steps. For example, if you reject trial 1 at an early step, the index of trial 2 should remain 2 (and not get updated to 1).

If data were analyzed in a continuous format without segmentation or "epoching" in trials, create a plain text file (.txt or .csv) with two columns: the first with the sample index corresponding to the beginning of the removed segment, and the second column with the sample index corresponding to the end of the removed segment.

Example:
> (line 1): 5362, 9678
> (line 2): 25641, 35414
>
> …

- *Excluded sensors*. A text file (.txt or .csv) with the number/label of channels that you identified as "bad channels" in the data analysis (e.g. channels you removed and/or eventually interpolated) for each subject. The channels not reported as "bad channels" are assumed to be included in the following pre-processing and further analysis.