# User Manual for EMG Cleaning

## Prerequisite

* The following steps are included in the example\_EMGcleaning.m in the project folder ‘2100\_00 TEMPLATE Projec\EMGcleaningFunctions’. The functions can also be used separately if only one or a few of them are needed.
* The order of the steps is set such that the functions work the best if the previous steps were first completed.
* Before running the steps below, you should have loaded the data from the raw data file, epoched them, e.g., within [-1 s … 1 s]
  + Note that the sampling frequency is assumed to be 5000 Hz in the trendline fitting.

## Several EMG channels

* You can clean all EMG channels at once or perform the following steps separately over the channels, depending on if you want to define the same set of bad trials for all channels or not, respectively.

## 1 Correcting drifting in the signal baseline

Function: bnp\_detrendEMG

* Drifting is identified by Laplacian fitting. Slow drifts have very low values as given by the Laplacian operator, based on which they get separated from the signal.
  + The fitting is performed outside of the time interval defined by the user.
* Select the right boundary (green) such that the time window in between the red and the green one contains the TMS artifact and the MEP response.
  + Initial guesses for these boundaries are first shown. Left-click to redefine, right-click to confirm.

## 2 Removing 50-Hz oscillation

Function: bnp\_detrendEMG

* 50-Hz noise is identified by fitting a cosine and sine curve at 50 Hz, and projecting out these curves from the data. The fitting is performed outside of the time interval defined previously.
* This step is automatically executed after drift removal.
* After detrending and 50-Hz removal, the resulting EMG signals over all the epochs are visualized. Right-click to proceed.

## Setting pre-innervation threshold

Function: bnp\_detrendEMG

* Having completed the previous steps, the function automatically proceeds to identifying the range limit of detecting the pre-innervation: if the range of the pre-stimulus signal exceeds this limit, the respective trial is set as a susceptible trial.
  + Left-click to define the threshold in the top-right panel. Right-click to confirm.
  + Typically a threshold of 20-25 microV works well with good-quality data set
* If the data set has multiple channels, the function automatically proceeds to the step 1 of the following channel

## 4 Removing bad trials

Function: bnp\_detectPreinnervation

* All the susceptible trials are visually inspected to identify pre-innervation.
  + All channels for these trials are shown simultaneously
  + User input defines whether the trial is marked as bad
* Even if there is no pre-innervation, the range may be high due to bad-quality data, these trials are recommended to be removed as well if possible in practice.
* Alternatively, the user may automatically reject all trials where the threshold was exceeded without visual checking

## 5 TMS artifact removal

Function: bnp\_removeTMSartifact

* An exponential-decay curve is fitted to the artifact and subtracted from the signal. This is performed separately for each trial separately
* The fitting is based on two time windows: 1. the exponential decay signal after the artifact maximum and preceding the MEP response (boundaries B1 and B2) 2. the steady baseline period after the MEP (boundaries B3 and B4).
* In the first pop-up window, choose the boundaries for these time periods from the left (earliest) to the right (latest), i.e., B1, B2, B3, B4. For each boundary, left-click to define/redefine the latency, right-click when done.
* The function automatically plots 10 responses at a time where the curve is fitted. The user may re-define the time windows in each figure to improve the fits if needed.
  + RMSE is given in the title to check how well the curve is fitted. RMSE is the highest one among the shown signals. RMSE of below 10 is excellent and below 20 acceptable.
  + Sometimes RMSE is high due to unexpected deflection in the signal. You can change the time interval to exclude this deflection. However, if the resulting pink curve seems reasonable, the high RMSE value itself is nothing to worry about.
  + Typically, the needed time windows gradually change if lots of trials were recorded.
* RMSE values are given as outputs. If required, you can set further bad trials based on this output if there are some excessively high RMSE values.
* If the TMS artifact is clearly before MEP or it does not exist in your data, consider skipping this step.

## 6 Aligning the EEG and EMG trials

Function: bnp\_alignEEGandEMGtrials

* After setting the bad EEG trials, the EEG and EMG trials must be matched if your analysis involves single-trial statistics/correlations/causalities between EEG and EMG data
* If you defined bad trials separately for several EMG channels, the alignment needs to be separately performed for each EMG channel.

## 7 Saving

* Take care of saving all the variables you may need in further analysis

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