

README File for the basic CDA scripts

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Tested for versions 13.2.2 of EEGLAB and 4.0.2.3 of ERPLAB

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The aim of our two scripts is to provide an easy way to analyze EEG data from visual working memory experiments, and track the CDA component. The scripts use EEGLAB & ERPLAB functions and follow common practices in the field (see the ERPLAB documentation for more information: <http://erpinfo.org/erplab>).

- "Analyze_CDA" includes full processing of a single subject's data. It produces EEG and ERP sets, plots of the subject's waves, and a text file containing useful values such as the percentage of rejected trials.
- "Analyze_GA" averages across subjects. It produces an averaged ERP set, plots of the averaged set, and mean amplitude values for statistical analyses.

Please note that the importing phase is implemented **only for BioSemi systems**. For other systems, you must first import your data and create an EEG set (e.g. "Subject_EEG.set"). note that for all other system, **all preprocessing stages (e.g. downsampling the data) are not included in the script**.

Good luck!

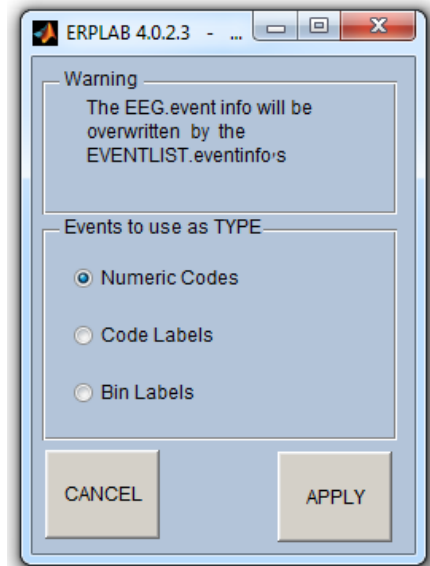
The "Analyze_CDA.m" script – analyzing EEG data of one subject

Steps to follow when using "Analyze_CDA.m":

1. Download and install EEGLAB and ERPLAB. The code was written for version 13.2.2 of EEGLAB and version 4.0.2.3 of ERPLAB.
2. Create a new folder (in a path accessible to MATLAB) which would contain all of the current experiment's files (the "Experimental_Folder" parameter).
3. Save the "Analyze_CDA.m" and "Analyze_GA.m" files directly in the experimental folder.
4. Within the experimental folder, create a unique folder for each subject in your experiment. **The name of the subject folder and subject EEG data file should be the same.**
5. Save each subject's data set within their folder.
 - i. BioSemi users: **make sure that the name of the file matches the name of the folder.** For example, if the folder is "01", then the data file should be named "01.bdf".
 - ii. Non-BioSemi users: import the data file, and **save the data file with the name of the folder and a "_EEG" suffix.** For example, if the folder is "01", then the subject's set should be "01_EEG.set".
6. Create 3 text files:
 - i. Event-list: this list should contain the important event codes of your experiment (usually conditions, left/right cue, correct/incorrect response, etc.), and their labels. See the "Eventlist_CDA.txt" example for details. Update the "Elist_File" according to your list name and location.
 - ii. Bins: this list should define the initial categorization of events to bins. **There should be two bins for each experimental condition, one for left-cue trials and the other for right-cue trials.** That way, you can later on separate contralateral and ipsilateral activity. **Hence, the total number of bins should be twice the number of experimental conditions.** See the ERPLAB documentation and the "Bins_CDA.txt" file for details (in this example, the condition code is sent when the memory array is presented, to allow for time-locking, and it is preceded by a right/left code, and followed by a correct/incorrect code). Update the "Bins_File" according to your list name and location.
 - iii. Difference waves computation: this list should contain the equations that convert the initial bins to ipsilateral activity, contralateral activity, and difference waves. Define the relevant electrodes in the left and right

hemisphere, and then use this division to define contralateral and ipsilateral activity and compute difference waves for each condition. See the "Difference_Waves.txt" example and the ERPLAB documentation for details. **The final number of bins should be three times the number of experimental conditions. Define ipsi- and contralateral bins for all conditions first, and then define the CDA bins** (e.g. if there are 3 conditions, the order is condition 1 contra, condition 1 ipsi, condition 2 contra, condition 2 ipsi, condition 3 contra, condition 3 ipsi, condition 1 CDA, condition 2 CDA, condition 3 CDA). Update the "Diff_File" according to your list name and location.

7. Specify how many channels you recorded from (the "Channel_Number" parameter), the number of the reference electrodes (only for BioSemi users; the "Reference_Channel" parameter), and what type of baseline you want for epoching (the "Baseline" parameter).
8. Update the artifact rejection, filtering and plotting parameters (see below for details and default values).
9. Update the "Subject_ID" parameter to the subject you wish to analyze. **This is the only part of the script you need to update after the first subject of the current experiment is successfully analyzed.**
10. Run the script.
11. A pop-up window labeled "" would appear, with "Code Labels" selected for "Events to use as TYPE". Choose "Numeric codes" and click on the "Apply" button.
12. The script would continue to run. When it finishes, you can open the "Subject_details.txt" file, where you would find a summary of the artifact rejection parameters and number of trials per bin, for later use. Note that ERPLAB shows the number of trials contributing to a certain bin, **which means that the CDA bins would show twice the number of actual trials**, and so the relevant numbers are those belonging to the ipsi- or contralateral bins.



Summary of parameters to modify in "Analyze_CDA.m":

1. Subject & Experiment parameters

- a. **Subject_ID**: identification number of the current subject (which should be the same as the name of the file's folder). For BioSemi users, this is the name of the ".bdf" file. For non-BioSemi users, this is the prefix of the imported file (e.g. enter '01' if the set name is "01_EEG.set"). **After successfully analyzing the first subject of the experiment, you can leave the other parameters unchanged and only change the ID according to each new subject.**
 - b. **Experimental_Folder**: specifies the full name and location of the folder containing all of the current experiment's files.
 - c. **Elist_File**: specifies the full name and location of the event-list text file.
 - d. **Bins_File**: specifies the full name and location of the bins text file.
 - e. **Diff_File**: specifies the full name and location of the difference waves equations text file.
 - f. **Epoch_Time**: defines the time window for epoching, relative to the time-locking point (i.e. memory array onset). For CDA waves, the epoch should usually include the full length of the memory array and retention interval. The first number should be the span of the baseline period (e.g. if you want a baseline of 200 ms, enter -200.0). This should include the final part of the blank display following the arrow-cues (that precede the memory array). The second number should state the end of the retention interval (e.g. if the memory array is presented for 200 ms and the retention interval is 900 ms long, enter 1100.0).
 - g. **N_Conditions**: specifies the number of experimental conditions.
2. Importing parameters:
- a. **Channel_Number**: specifies the number of EEG channels recorded.
 - b. **Reference_Channel**: specifies the number of the electrode/s to which the data would be offline referenced. **Relevant only for BioSemi users.**
3. Artifact detection parameters
- a. **Artifact_Rejections**: defines the number of moving window pick-to-pick artifact rejection procedures which would be performed. 1 procedure (on the EOG channels) can be used to remove trials containing eye movements and blinks, and the 2nd can be used to remove trials with other sources of noise.
 - b. **Moving_Window_Threshold_1**: defines the threshold (in μV) for the pick-to-pick procedure.
 - c. **Moving_Window_Width_1**: defines the size (in ms) of the moving window.
 - d. **Moving_Window_Step_Size_1**: defines the step-size (in ms) for the moving window.

- e. **Moving_Window_Electrodes_1**: specifies on which electrodes to perform the artifact detection on (usually the EOG channels).
- f. **Moving_Window_Threshold_2**: defines the threshold (in μV) for the second pick-to-pick procedure (this should be addressed only if the "N_Artifact_Rejections" parameter is set to 2).
- g. **Moving_Window_Width_2**: defines the size (in ms) of the second moving window (this should be addressed only if the "N_Artifact_Rejections" parameter is set to 2).
- h. **Moving_Window_Step_Size_2**: defines the step-size (in ms) for the second moving window (this should be addressed only if the "N_Artifact_Rejections" parameter is set to 2).
- i. **Moving_Window_Electrodes_2**: specifies on which electrodes to perform the second artifact detection on (this should be addressed only if the "N_Artifact_Rejections" parameter is set to 2, and can be set to include the to-be-analyzed electrodes).

4. Filtering parameters:

- a. **Highpass_Filter**: specifies whether a highpass filter is required (when set to 1, the EEG data would be bandpass filtered). If set to 0, only a lowpass filter would be applied to the epoched data.
- b. **Lowpass_Cutoff**: defines the cutoff frequency (in Hz) of the lowpass filter that would be applied.
- c. **Lowpass_Type**: defines the type of lowpass filter that would be applied ('butter' means IIR Butterworth, see the ERPLAB documentation for more details).
- d. **Lowpass_Order**: defines the length of filter in points.
- e. **Highpass_Cutoff**: defines the highpass cutoff frequency (in Hz) of the bandpass filter that would be applied (this should be addressed only if the "Highpass_Filter" parameter is set to 1).
- f. **Bandpass_Type**: defines the type of bandpass filter that would be applied (this should be addressed only if the "Highpass_Filter" parameter is set to 1).
- g. **Bandpass_Order**: defines the length of filter in points (this should be addressed only if the "Highpass_Filter" parameter is set to 1).

5. Plotting parameters:

- a. **Plot_Types**: specifies the number of plots that would be produced. If this parameter is set to 1, only a plot of the difference waves would be displayed. If set to 2, a plot of the contra- and ipsi-lateral waveforms would also be displayed.

- b. **Bins_to_Plot_1:** specifies the relevant bin numbers of the first plot (the CDA bins, computed by the "N_Conditions" parameter).
 - c. **Bins_to_Plot_2:** specifies the relevant bin numbers of the second plot (the contra- and ipsi-lateral bins, computed by the "N_Conditions" parameter).
 - d. **Channels_to_Plot:** specifies the relevant channels in the plot, out of the channels specified in the "Diff_File" text file.
6. Saving & Warnings parameters:
- a. **Save_All:** when this is set to 1, the sets of all processing stages would be saved. When set to 0, only the first and last set would be saved.
 - b. **Warnings:** when set to "off", none of the ERPLAB warnings would be displayed. When set to "on", warnings would be displayed.

Analysis steps for "Analyze_CDA.m":

1. Import (BioSemi systems only) or load (non-BioSemi systems) the data file.
2. Create an event-list, and save it as a text file (e.g. "Subject_elist.txt").
3. If applying a highpass filter as well as a lowpass filter (i.e. the "Highpass_Filter" parameter is set to 1), bandpass filter the data.
4. Sort bins according to the descriptions of the "Bins_File" parameter.
5. Perform a moving window pick-to-pick artifact detection (either one or two), according to the parameters specified in the "Filtering Parameters" section. Report the percentage of rejected trials.
6. Create an ERP set (average across trials, excluding trials detected as containing artifacts).
7. If applying only a lowpass filter (i.e. the "Highpass_Filter" parameter is set to 0), lowpass filter the data.
8. Create difference waves according to the equations in the file specified by the "Diff_File" parameter.
9. Plot the waveforms.
10. Create a text file containing different details of the current analysis ("Subject_ID_details.txt").

The "Analyze_GA.m" script – averaging across multiple subjects

Steps to follow before using "Analyze_CDA.m":

1. Analyze each subject's data, and save a final ERP set (with the name "Subject_ERPs_filt_diff.erp": e.g. for subject "01", inside the "01" folder there should be a final ERP set called "01_ERPs_filt_diff.erp"). Make sure all sets have the same bin names.
2. Specify the subject names in the "Subjects" parameter, separated by commas.
3. Update the different parameters (see details below).
4. Define the time window for the mean amplitude measurements in the "CDA_Time" parameter, and the channels you wish to analyze in the "Chan_CDA" parameter.
5. Run the code.

Summary of parameters to change before running "Analyze_GA.m":

1. Files & Folders:
 - a. **Subjects:** a cell array containing all of the subjects you wish to include in the grand average (separated by commas). Make sure each of the names is associated with a folder of the same name, and contains a final ERP set, with the same name and a "_ERPs_filt_diff.erp" suffix.
 - b. **Experimental_Folder:** specifies the full name and location of the folder containing all of the current experiment's files.
 - c. **GA_Folder:** specifies the name and location of the folder that would contain the grand average set and mean amplitude text files.
2. Experiment parameters:
 - a. **N_Conditions:** specifies the number of experimental conditions.
 - b. **Time_MA:** defines the time window for the mean amplitude (usually the CDA stabilizes after around 300 ms from memory array onset, and persists throughout the retention interval).
 - c. **Bin_MA:** defines the bins whose mean amplitude would be extracted, usually the final CDA bins.
 - d. **Chan_MA:** defines the channel numbers from which the mean amplitude would be extracted (the CDA is usually most pronounced at the PO7/PO8 electrodes).
 - e. **Warnings:** when set to "off", none of the ERPLAB warnings would be displayed. When set to "on", warnings would be displayed.
 - f. **Highpass_Filter:** set to 1 if a highpass filter was applied, set to 0 otherwise.
3. Plotting parameters:

- a. **Plot_Types:** specifies the number of plots that would be produced. If this parameter is set to 1, only a plot of the difference waves would be displayed. If set to 2, a plot of the contra- and ipsi-lateral waveforms would also be displayed.
- b. **Bins_to_Plot_1:** specifies the relevant bin numbers of the first plot (the CDA bins, computed by the "N_Conditions" parameter).
- c. **Bins_to_Plot_2:** specifies the relevant bin numbers of the second plot (the contra- and ipsi-lateral bins, computed by the "N_Conditions" parameter).
- d. **Channels_to_Plot:** specifies the relevant channels in the plot, out of the channels specified in the "Diff_File" text file.

Analysis steps:

1. Load the final ERP sets for each subject
2. Average across ERP sets, and save the grand average set.
3. Plot the waveforms.
4. Extract the mean amplitude values for each subject and for the grand average set, and save the to a text file ("Mean_Amp.txt").