

# LBCN Data Visualization Tool: Quick start

## 1. Overview

This is a tool developed for easier access for data preprocessing, quality control, and result visualization/navigation.

For starters who does not have much experience in Matlab, this is a handy tool with several different “pipelines” integrated & automatically identifies the task/pre-defined parameters.

It is also a convenient tool to load & review results, generate and save figures, do data quality check, check the anatomical locations, change ways of plotting, compare between different tasks etc.

Currently the app supports the new SPM based pipeline for new data analysis.

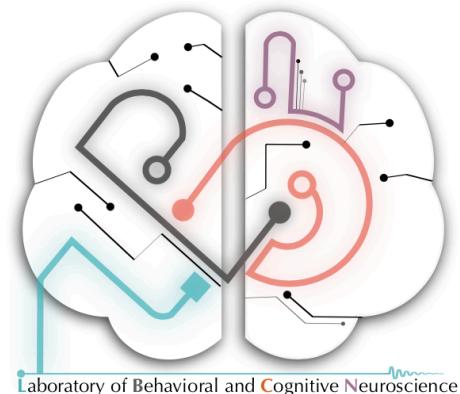
To start a new analysis, choose edf and sodataXX files. No additional parameters are required for those pre-defined tasks (e.g. emotion, VTC, race). For undefined new tasks, it uses default parameters (default\_parvizi) and can be customized as needed.

The raw data epochs and HFB signals generated by this pipeline will be automatically saved (with the names “Epoched\_TASK.mat” and “Epoched\_HFB.mat”) and can be loaded for review or re-analysis.

*\*It is recommended that the user save the data in a well organized structure, e.g. for each subject, create subfolders for different tasks, use task names as folder names, and put ECoG data + behavioral files in the same subfolder – just an example.*

*Future updates will include a input dialog for the configuration of undefined tasks.*

*The SPM independent pipeline (by Pedro and Amy) will also be included in future release.*



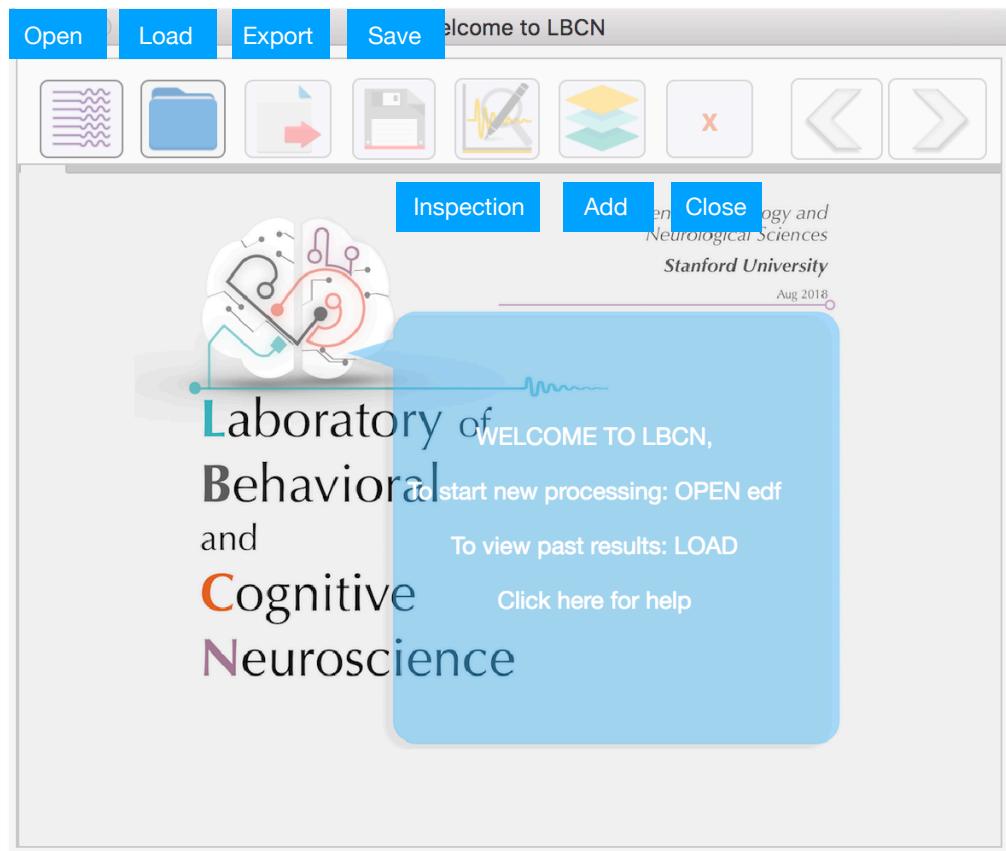
*Matlab 2017 and later versions are recommended.*

— Su Liu @ Stanford

2018 Oct.

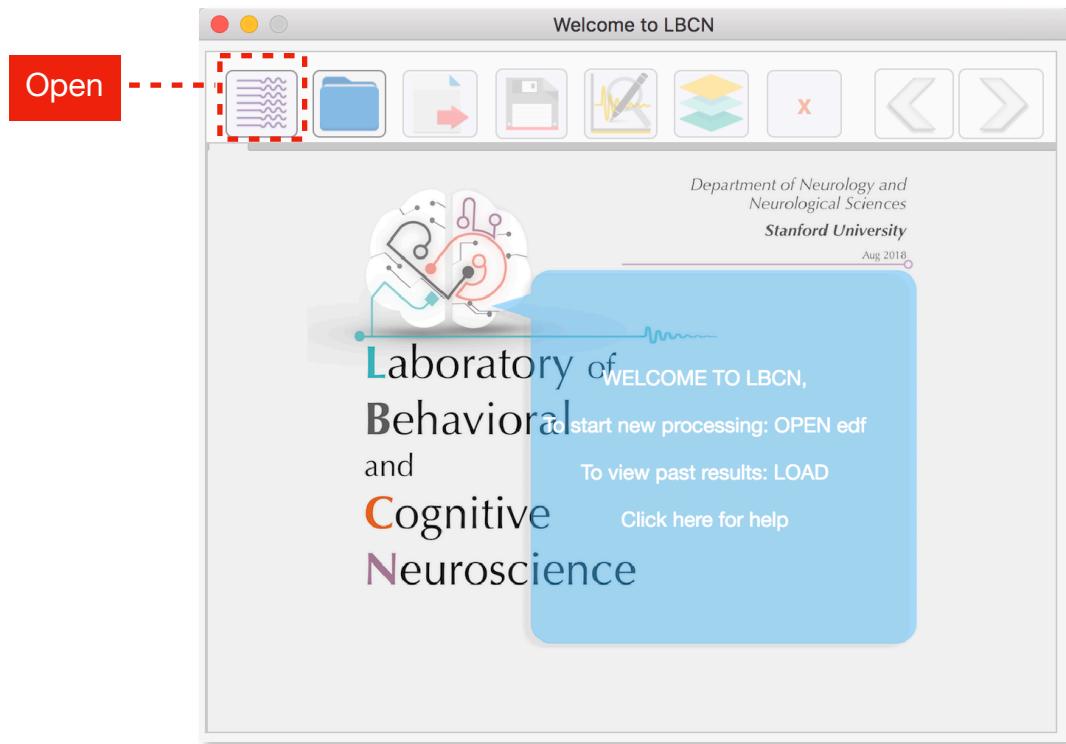
## 2. Home

Run plot\_window\_App in command window;



## 2.1. To open new EDF, click on **OPEN**.

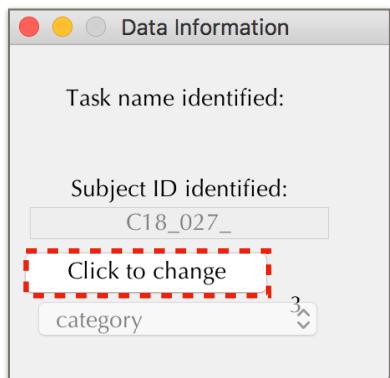
Choose EDF files and corresponding behavior files in the popup window.



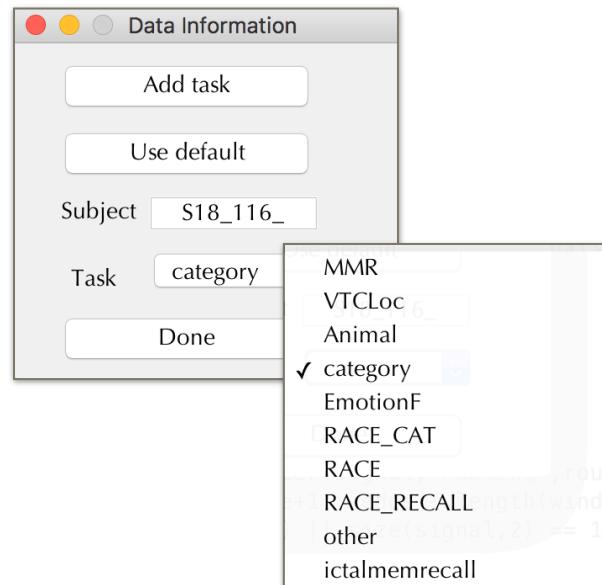
The pipeline will try to automatically identify the task and subject name.

The info window showing identified data information will stay for 5 seconds for the user to verify (i); if it fails to identify the task name and subject, another the user will need to manually choose from pre-defined task list, and type in the subject name (ii).

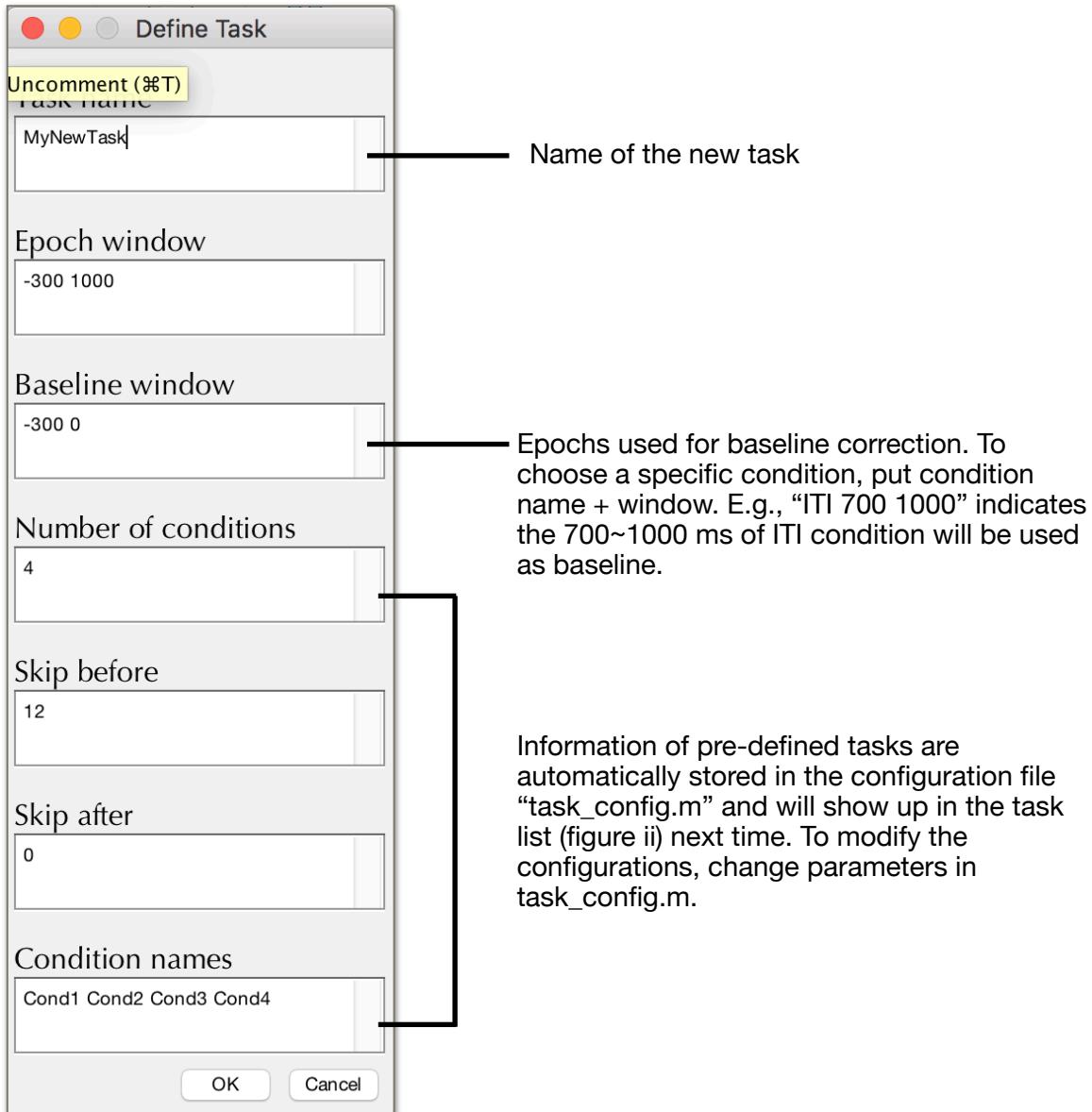
i)



ii)



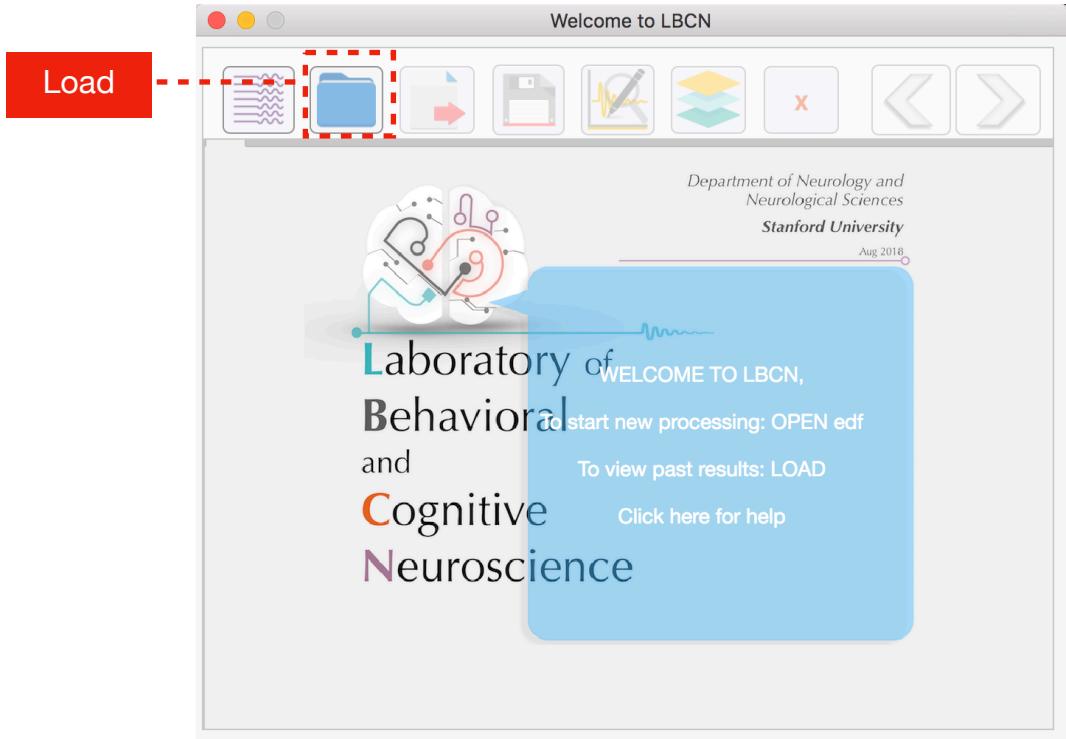
To create a new task, click on “Add task” and put parameters accordingly.



\*The pipeline will try to cover common human-caused errors (eg., mismatched diod channel, number of skipped onsets, mismatched behavioral and DC triggers, duplicating channel names, etc.), but there is always a big chance that some unexpected error will occur. To avoid errors, always be careful when recording and check behavioral data at the beginning of new analysis.

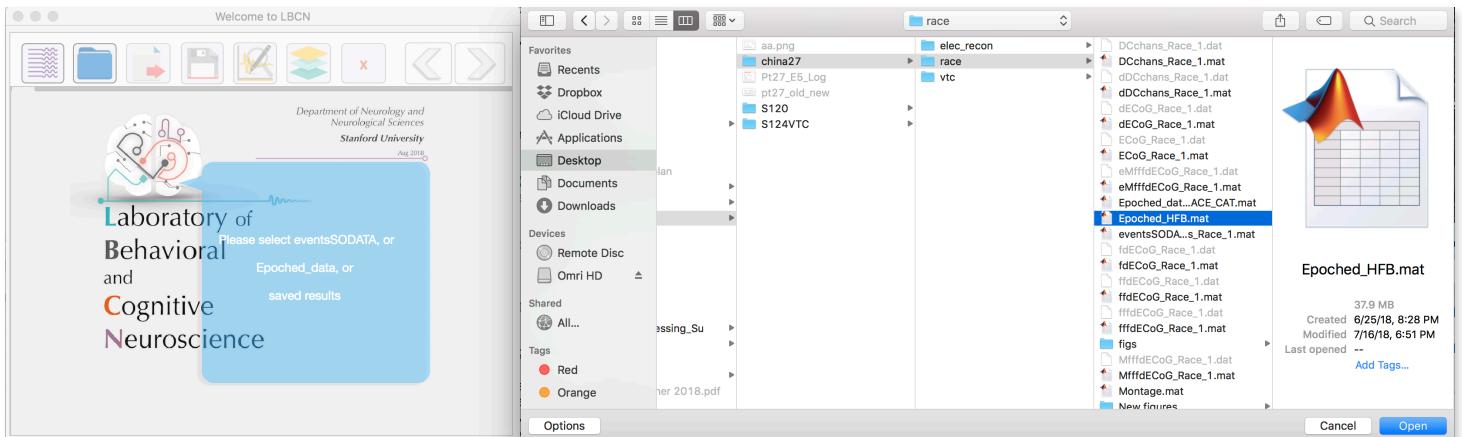
If there is mismatch in DIOD and behavioral file, a window will show up asking for further actions. If the user is aware of the causes (for example, missing DC triggers at the beginning is usually due to a late start while recording), this can be fixed easily.

2.2. To load data after the epoching step, click on **LOAD**.



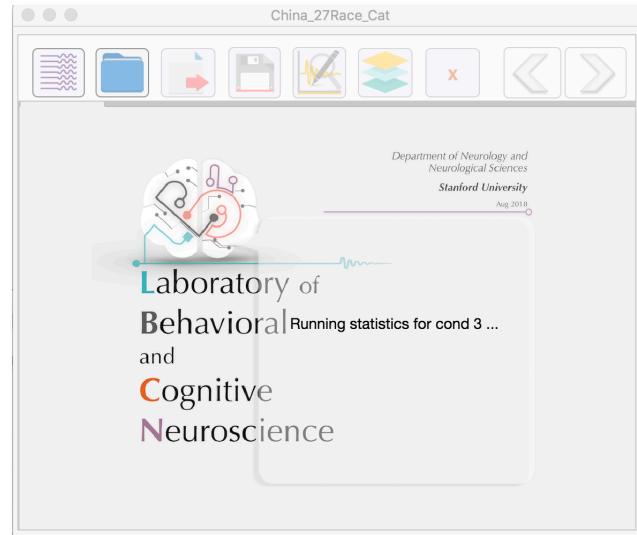
The epoched ECoG signal (eventSODATA<sup>XXX</sup>.mat by old pipeline, or Epoched\_TASK.mat by new pipeline) can be loaded for re-analysis.

To review the saved HFB data (sHFBXXX.mat for old pipeline, Epoched\_HFB.mat for new pipeline, or results generated by SPM-independent pipeline with two fields “data\_all” and “subjVar”, which can be generated by running ConcatenateAll.m).



A new window will show up while loading, and automatically runs permutation tests for all conditions.

The results for significant test will be shown (marked by colored stars) in the channel list



Artifact rejection algorithm has been integrated to the old/new/SPM independent pipelines, where the artifactual channels, trials or samples will be identified and excluded from baseline correction and common average calculation.

If more than half of the trials in a channels is identified as corrupted, a window will show up asking for user action — whether to visually review the bad epochs quickly and decide what to do next. This is an additional quality control step.

— Yes: will plot all “corrupted” epochs. After viewing the data, the user can keep all as good, eliminate all as bad, or select “don’t ask again” to repeat the last action for all further detections.

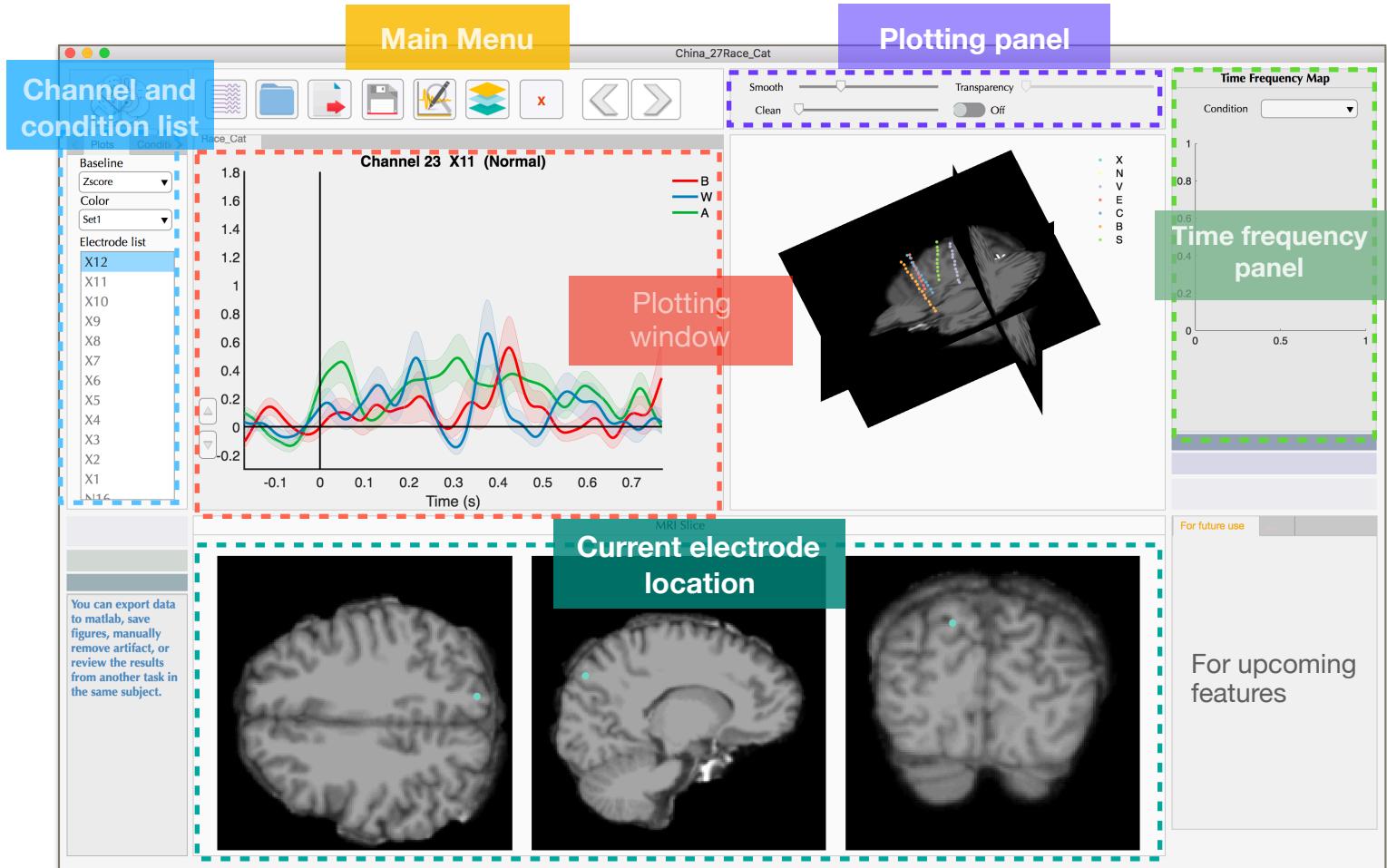
— No: will eliminate corrupted trials without plotting individual trials for review.

At the end of the pipeline, the app will try to locate the image data of the current subject. The information are stored in the elec\_con folder. User may need to choose the subject’s image folder from server [freesurfer] for the first time (folder that contains the subject’s name). App will download image data to local directory for future use.

*\*To load signal without loading image data, press cancel when the window pops out.*

*App will try to match the EDF channel names with electrode names in the image data. This is done by implementing several algorithms, but if it fails to match the names at the end, user could manually match the channels groups in the channel-relabeling window.*

# 3. Main interface



**Main menu:** export/save/visual inspection/add task/close current file.

**Channel and condition list:** switch between tabs to view result by channel, change color, or only plot a subset of conditions.

**Plotting panel:** change slider bar to change smoothing level, change the transparency for 3d cortical mech plots (when applicable), change the artifact rejection window, or switch off artifact rejection.

**Plotting window:** showing signal plots. The y axis limits could be changed using the buttons on the left.

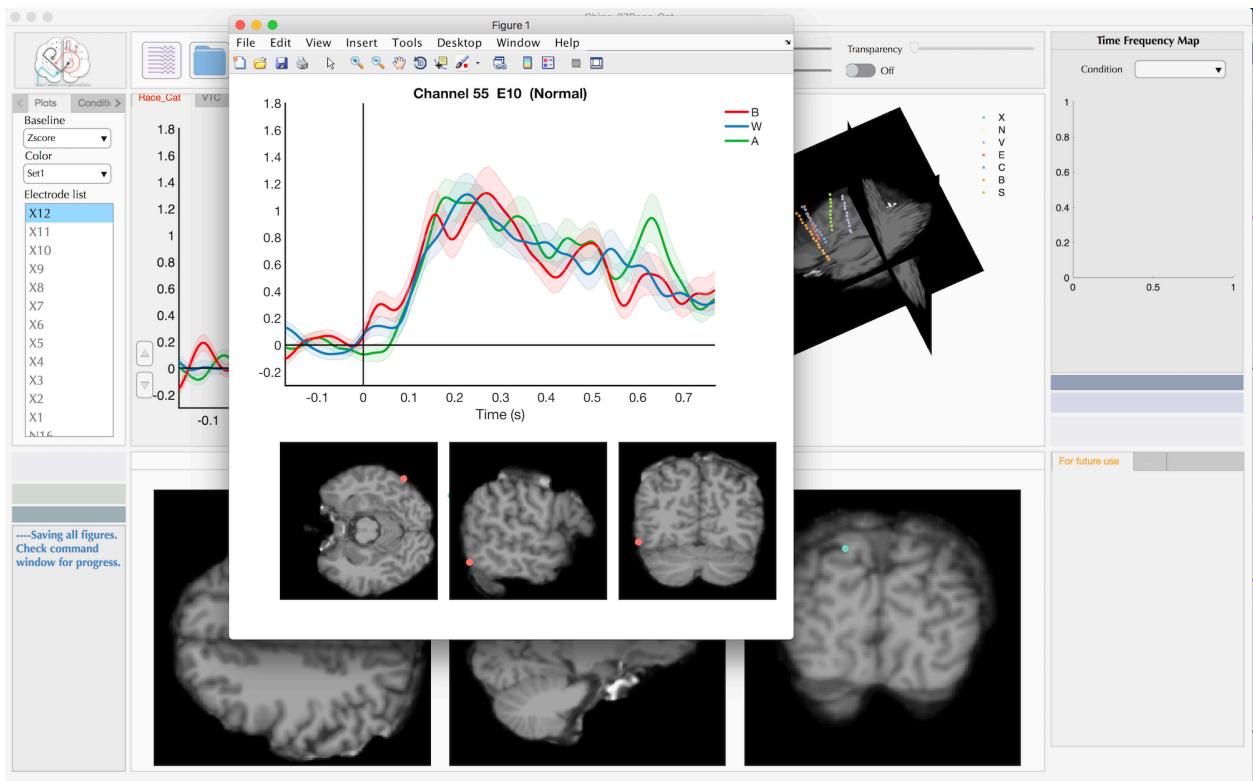
**Time frequency panel:** to plot the time-frequency map for current channel/condition.

*\*This part is skipped for now to decrease the computational burden, will find a better solution in future release to speed up the plotting.*

3.1. To save plots (with or without) electrode locations, click on **SAVE**

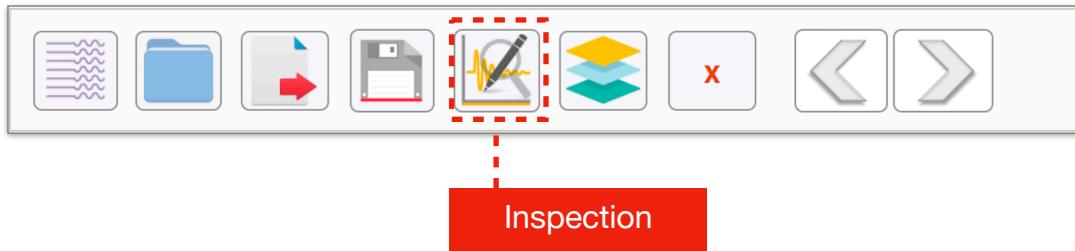


Figures will be saved in the folder “.../Results\_taskname”.



\*If no image data available, only signal plots will be saved.

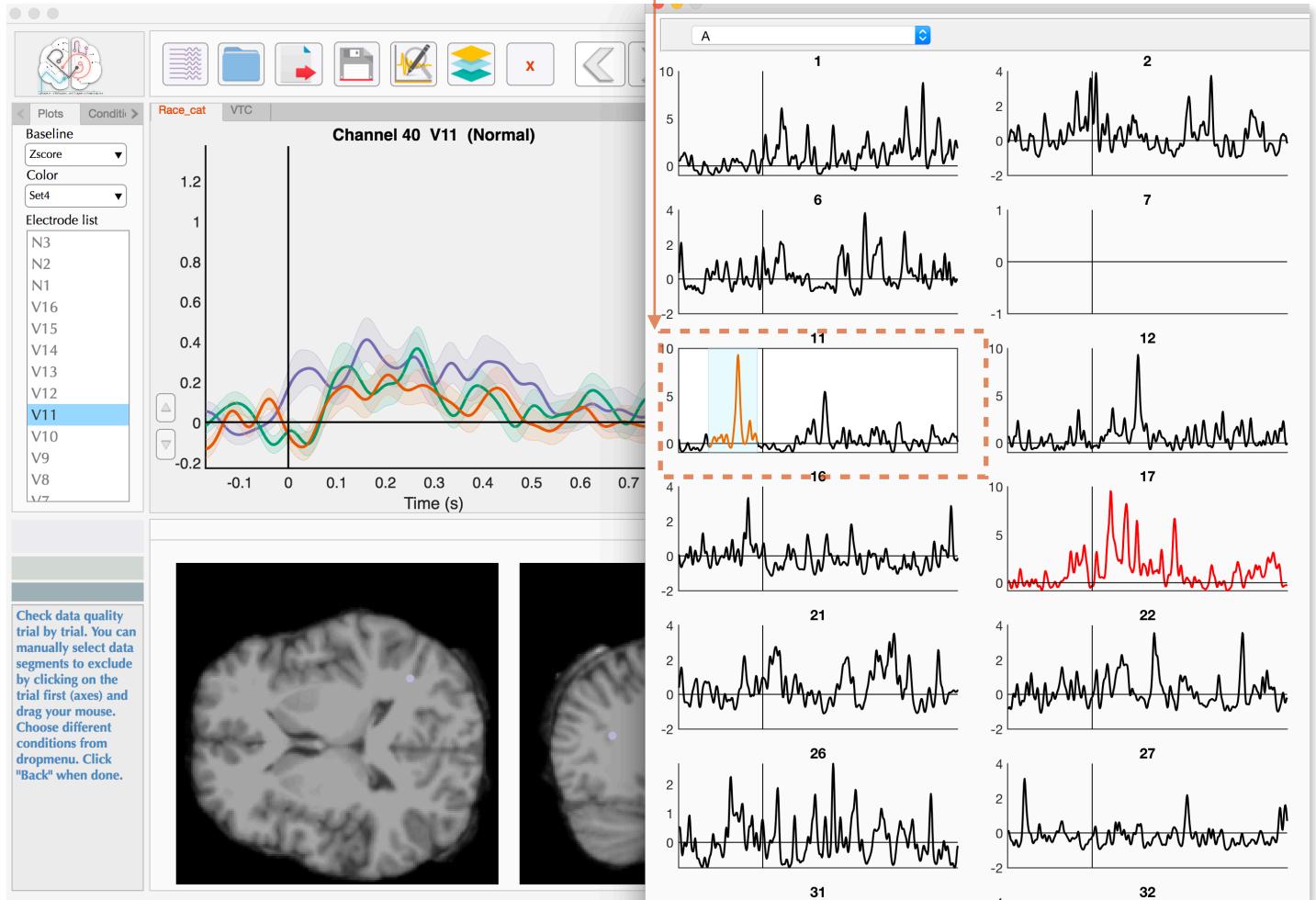
### 3.2. To review individual trials, click on INSPECTION



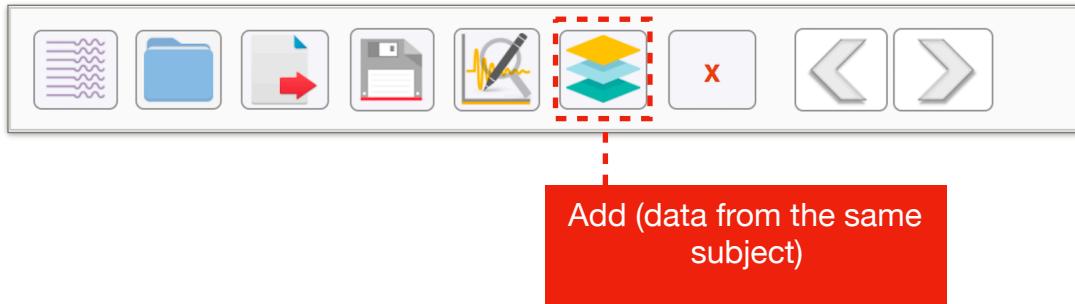
Check data quality: plot all trials for all conditions in a channel. Read points indicate the possible artifactual data that can be assigned to NAN when plotting;

On this page you could manually select bad data points to exclude. Simply [click on the trial \(axes\), and drag mouse to select a segment.](#)

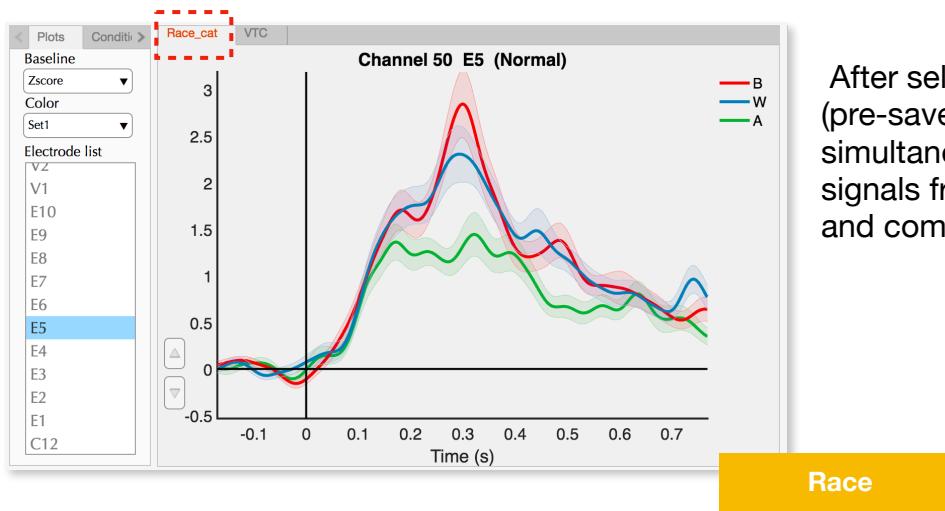
After the inspection is done, click “Back” on the right upper corner to return.



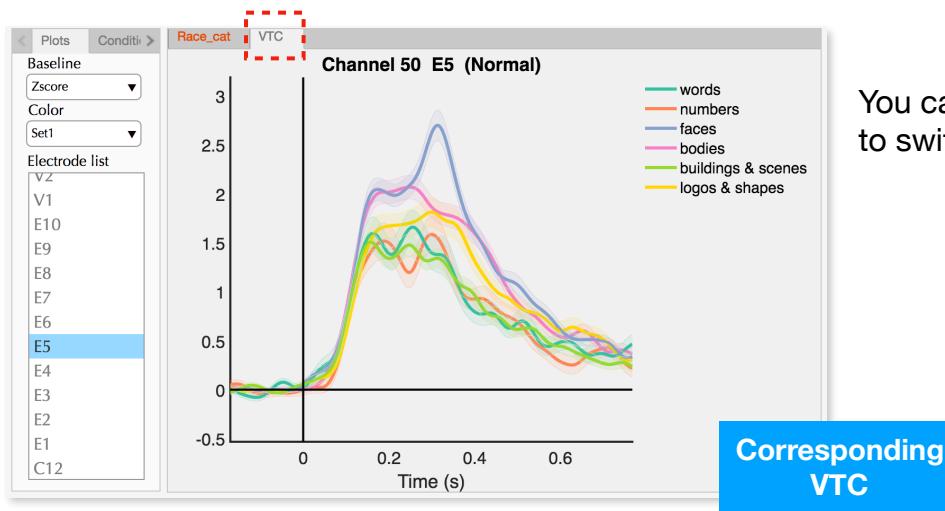
### 3.3. To add another task, click on ADD



To view another task in the same subject, use this function. Currently the tool supports reviewing 3 different tasks at the same time. More tasks will be supported in future.



After selecting another task (pre-saved results), user can simultaneously review the signals from different tasks and compare.



You can click on the tabs to switch between tasks.

*\*Currently all the operations are targeting the main task (the one that firstly being loaded, label in red).*