IN ANY OF THE FOLLWING STEPS MAKE SURE TO USE THE EXACT SAME FOLDER STRUCTURE AND NAMEING METHODS IN THE EXISTIN PATIENT FOLDERS. USE ONE PATIENT AS EXAMPLE.

* Upload the behavioral data into the server according to the existing structure
* Import the iEEG data into using Spike2, and store them on the server according to the existing folder naming and structure and save in the proper directory (use an existing patient as example)
* Inspect the imported EEG data visually and make the Block Information Excel spread sheet and save in the proper directory under **BlockInfo.xlsx** (use an existing patient as example). When inputting the start and stop of every block, make sure to give proper margin.
* Visualize the electrode positions in Slicer and identify the channels you want to analyze. Do not analyze white matter electrodes, or electrodes outside the areas of interest, to cut down computation time.
* Make the **ElectrodeInfo.xlsx** file, with the electrodes listed with the same order that shows up in the imported EEG data and save in the proper directory (use an existing patient as example). Identify the **electrode numbers** that you want to analyze by matching the names of the electrodes in the ElectrodeInfo.xlsx, and the Slicer view.
* Make the channel labels mat file under the name **ChanLabels.mat** and save in the proper directory (use an existing patient as example). It’s basically the same as **ElectrodeInfo.xlsx** inmat format.
* Make the **PathInfo.xlsx** file and save in the proper directory (use an existing patient as example). Every single mat file imported via Spike2, gets it’s own row. So the number of rows depends on how you chopped and saved the EEG data in the monitoring unit.
* Make the **BLockGroups.xlsx** and save in the proper directory (use an existing patient as example). This file now contains the 23 rows according to the participant with the highest number of block groups. Use the file for another patient as template. In Cell A, You have to enter the block numbers that match the description in cell C. If a participant doesn’t have a certain block type, leave the cell A blank, but don’t delete B.
* For every participant make a script named **seqeeg\_test\_px.m** (use an existing patient as example). In the script define the channel numbers you want to analyze, and run te seqeeg\_makeData function as follows:  
  this function will automatically load all the required files and save all the analyzed data. Takes a long time to run – overnight.

subjNum = 1; % insert the subject number here

chans = [4:12 ,14, 122:129 ,36] ;% Good Channels for this participant

seqeeg\_makeData(subjNum , chans);

* Use Visualization examples to visualize