

Lega Lab Research Introduction, How-To Guides, & Getting Started in the Lab

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Updated 3/22/2021



For more project overview, see lab website:
<https://www.utsouthwestern.edu/labs/tcm/>

UTSW Map

Lab is on South Campus

Danciger Building (H)

H1.104

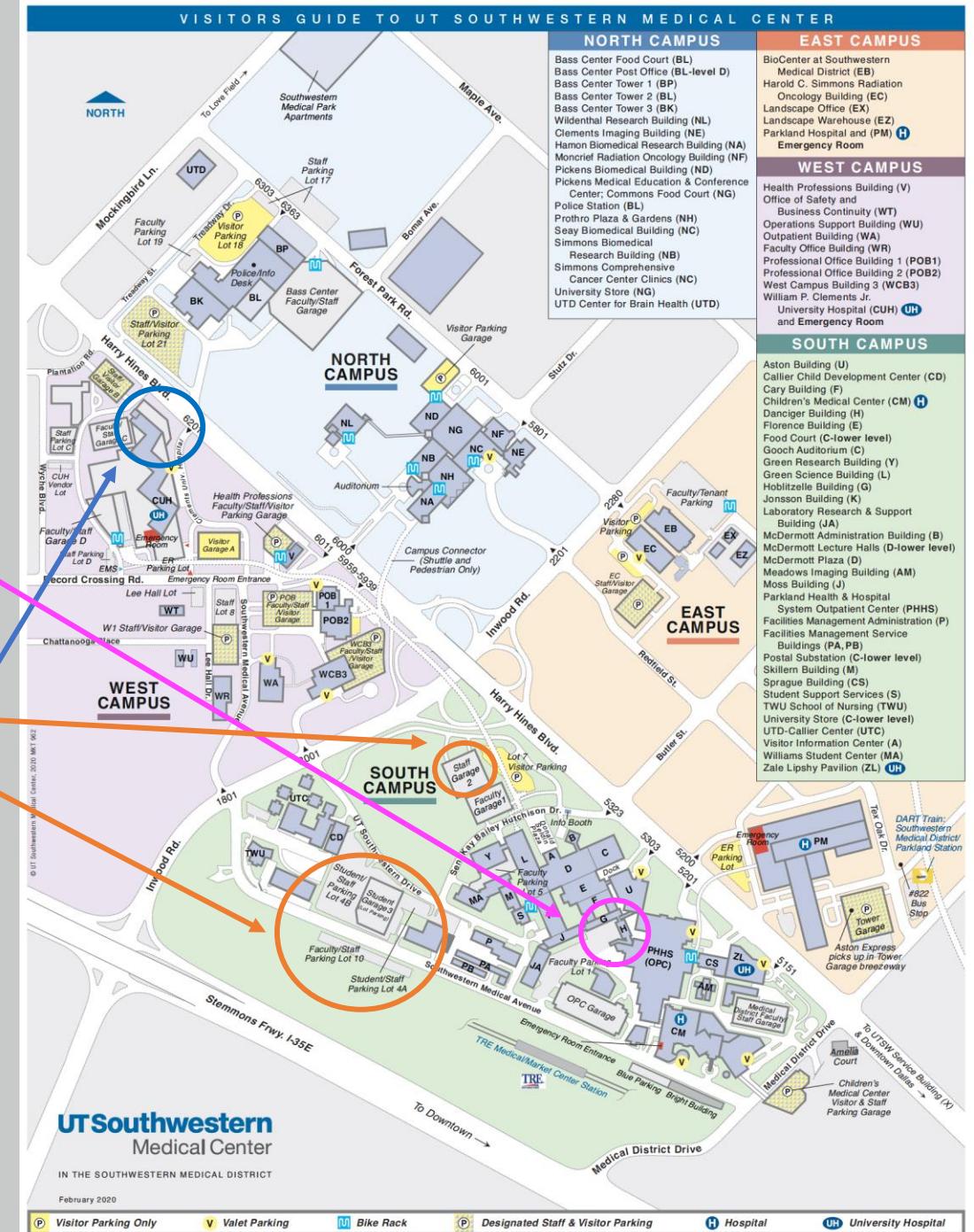
Closest Parking for Lab

Student/Staff Lot 3/4A/4B
or Staff Garage 2

Patient Testing

Clemens University Hospital
(CUH)

8th Floor (Orange Side) is
Epilepsy Monitoring Unit
(EMU)



Getting Started (Clinical Data Specialist Position)

- Parking permit
- Access to BioHPC and sign up for introductory training
- Added to IRB protocols

First, register for a BioHPC account by going to

<https://portal.biohpc.swmed.edu>

From the portal website, you can access the training calendar and register for the next available “Introduction to BioHPC” training (usually held the first Wednesday of each month).

Then send an email to biohpc-help@utsouthwestern.edu requesting access to the lega_ansir folder. If you ever encounter troubles with BioHPC, this is the email to contact them!

The introduction to BioHPC website has guides that are quite comprehensive:

<https://portal.biohpc.swmed.edu/content/guides/introduction-biohpc/>

One of the most important tools for this lab is the Web Visualization tool found under the Cloud Services tab. You can use this GUI to access Matlab from BioHPC.

Research Collaborators



Dr. Michael Rugg

Professor at UT Dallas

- fMRI, neural correlates of episodic memory and retrieval



COLUMBIA UNIVERSITY
IN THE CITY OF NEW YORK



Dr. Michael Kahana

Professor at UPenn

- Human episodic memory for verbal, visual and spatial information iEEG

Dr. Genevieve Konopka

Associate Professor at UT Southwestern

- Neurogenetics, cognitive genomics, evolution of human cognition, transcriptional networks

UT Southwestern
Medical Center

Restoring Active Memory (RAM)

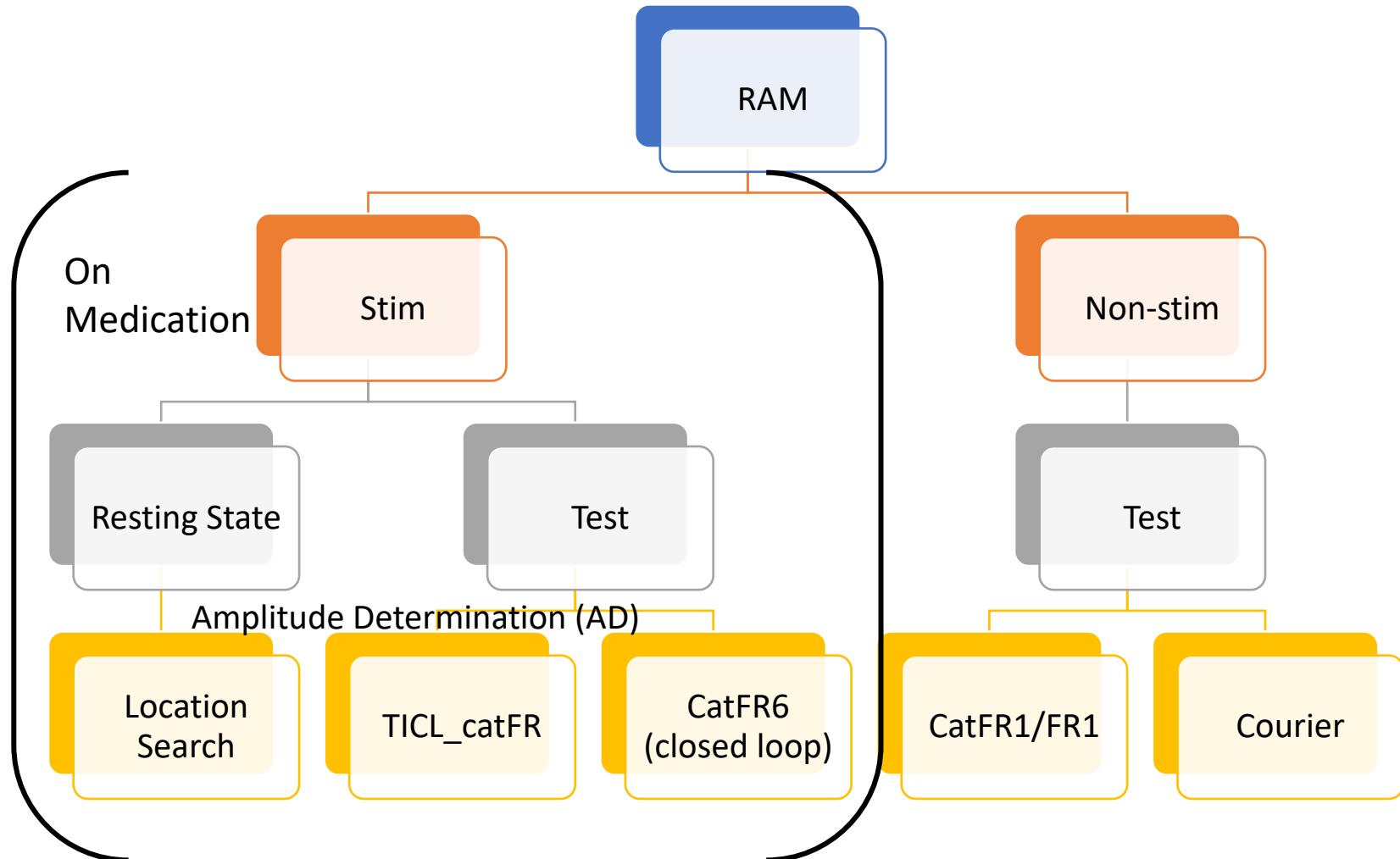
UPenn collaboration



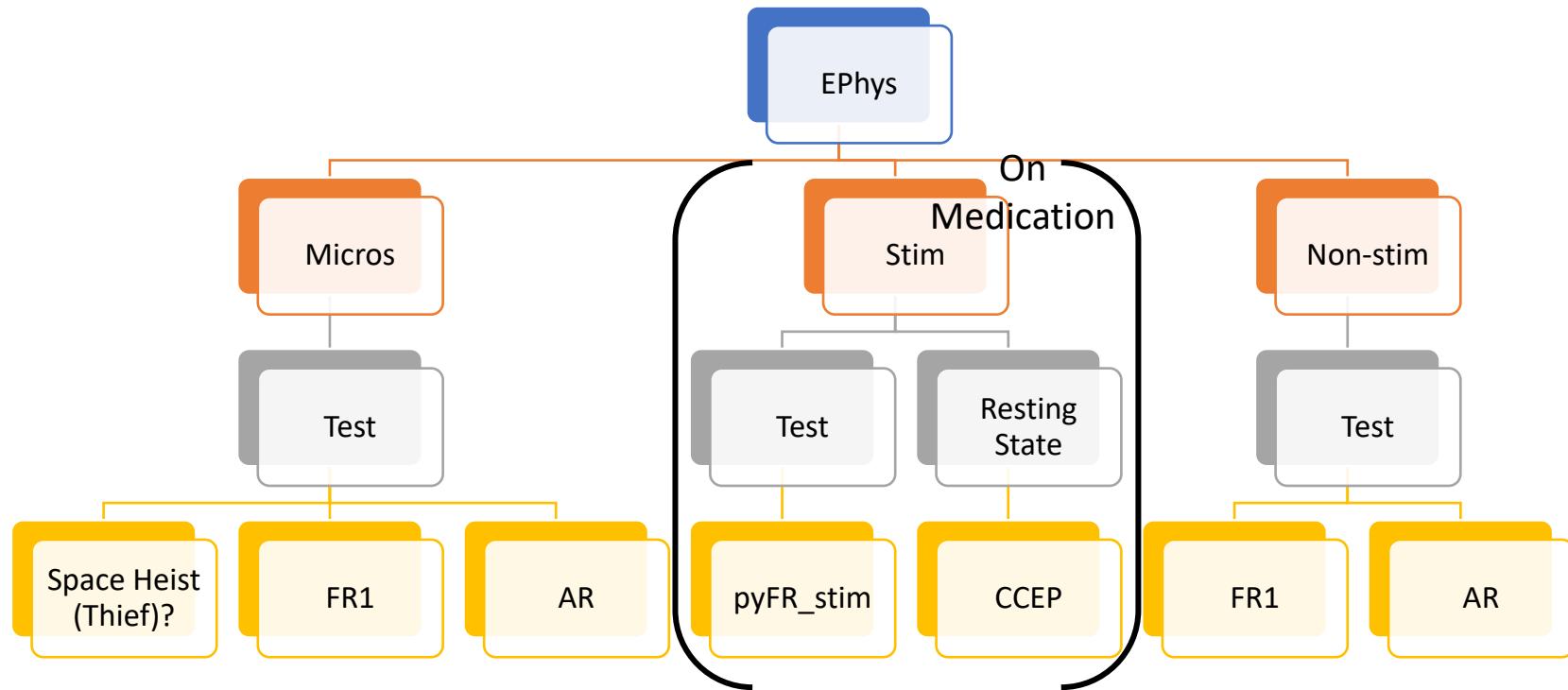
Goal: To develop a fully implantable device that can electrically stimulate the brain to improve memory function.

How: Create and use classifier to predict when you will or will not remember something → stimulate when classifier predicts you will not remember

Penn Testing Project Tree

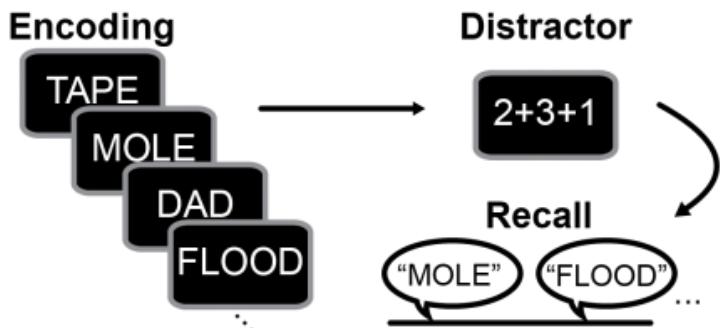


EPphys Project Tree



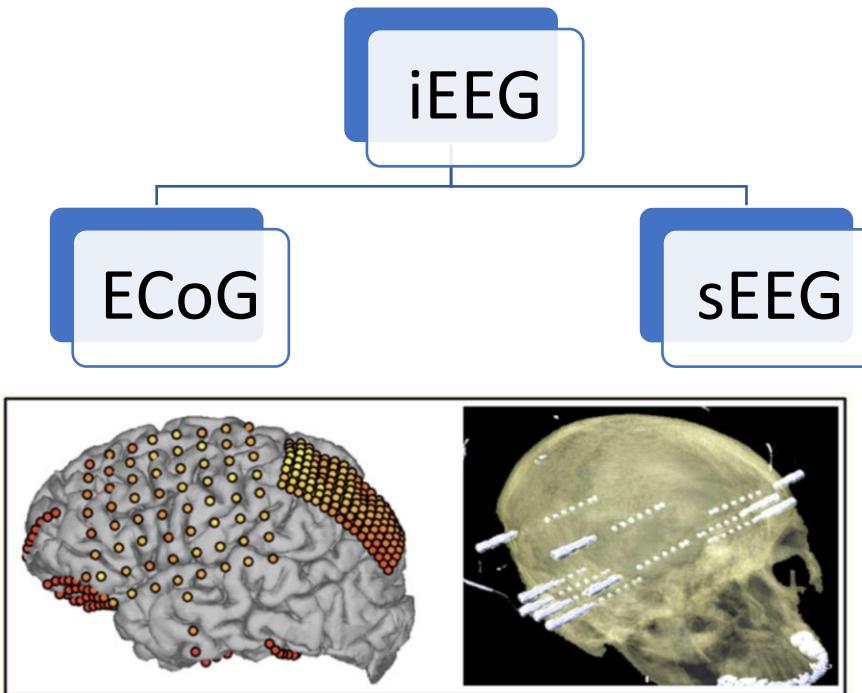
Methods | Overview |

Free Recall Task (FR)



- **Encoding:** Each trial consists of a series of word presentations that the participant tries to remember. Each word is on screen for ~1600 msec followed by a blank screen and then the next word.
- **Distractor:** After the presentation of all words in a list, a distraction task consisting of simple arithmetic problems is presented.
- **Recall (aka Retrieval)** is cued by a tone after the distractor task period. During item retrieval, the participant attempts to recall the presented words, saying them aloud in any order.

Human Intracranial EEG (iEEG)



Electrocorticography

Using strips or grids implanted in the subdural space (on the surface of the cerebral cortex)

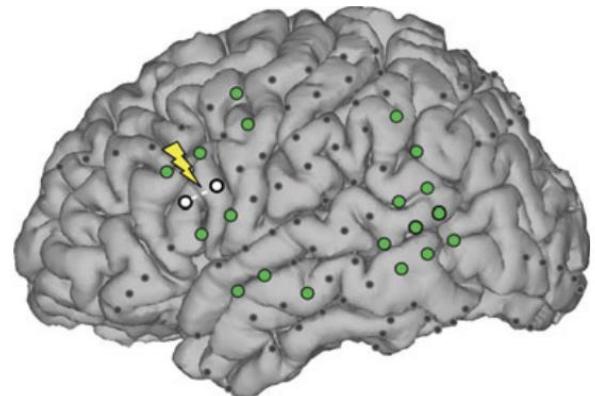
Stereotactic EEG

Using depth electrodes targeting deeper sites (e.g. hippocampus) without open craniotomy

Cortico-cortical evoked potentials (CCEP)

- CCEP is a directional and causal measure of effective connectivity between brain regions
- Bipolar stimulation is applied between the adjacent electrodes (dotted white lines).
- The strength and latency of propagating electrical activity is measured at distant sites.
- Green and grey colored electrodes represent significant and non-significant CCEPs, respectively.

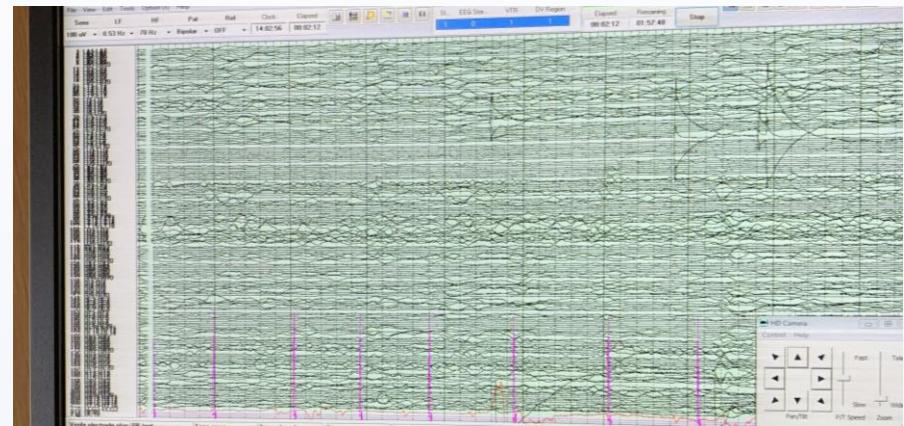
(b) cortico-cortical evoked potentials



Memory Testing Basics

- When you're about to start a test with a patient, stop and start the clinical EEG and do the same after the session is completed. This will ensure that the session EEG recording will be isolated.
- Make sure you see **sync pulses** on the clinical EEG while the test is in progress (more on sync pulses on the next slide).
- After testing, the audio files for the test session should be annotated as soon as possible by the person who administered the test using **PennTotalRecall** (more on PTR later).
- After testing, the EEG clip from the test session should be exported from the clinical EEG system (more on that later).

Sync Pulses



- Sync Pulses are timed pulses that are sent from the sync box to the clinical EEG system
- Sync pulses are the **pink pulses** that can be observed on the clinical EEG system coming from one of the **DC channels** (usually at the bottom of the screen, usually DC9 or DC10)
- If you do not see the sync pulses on the clinical EEG system, then the session cannot be aligned to the EEG, and we cannot use that session. Sometimes the EMU does not have the DC channels on. If for some reason you don't see pink lines (even flat ones), talk to an EMU tech to make sure the DC channels are turned on.



Signal Processing and MATLAB

Data Organization

/project/TIBIR/Lega_lab/shared/lega_ansir/subjFiles

 /UT###

 /behavioral

 /taskName1

 /taskName2

 /docs

 jacksheet, etc

 /eeg.noref

 /eeg.reref (average re-referenced)

 /tal (not relevant)

MATLAB Tips from Cohen Textbook

Chapter 4

- Write clean and efficient code
- Use meaningful File and Variable Names
- Make regular backups of your code
- Keep original copies of modified code
- Initialize variables
- Use the internet to aid in applying new functions or find additional help
- Be patient and embrace the learning experience

Helpful figures from Cohen Textbook

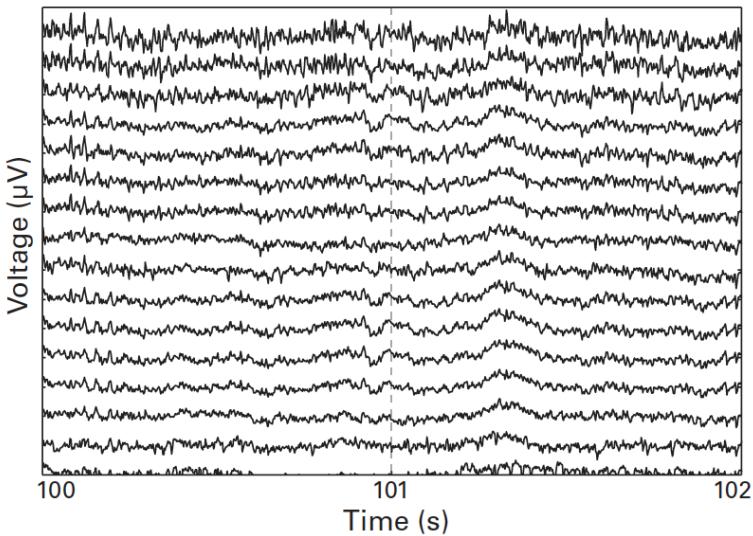


Figure 3.1

Raw EEG data (after 0.1-Hz high-pass filtering) showing oscillations at different speeds and for different lengths of time. Each line corresponds to an electrode.

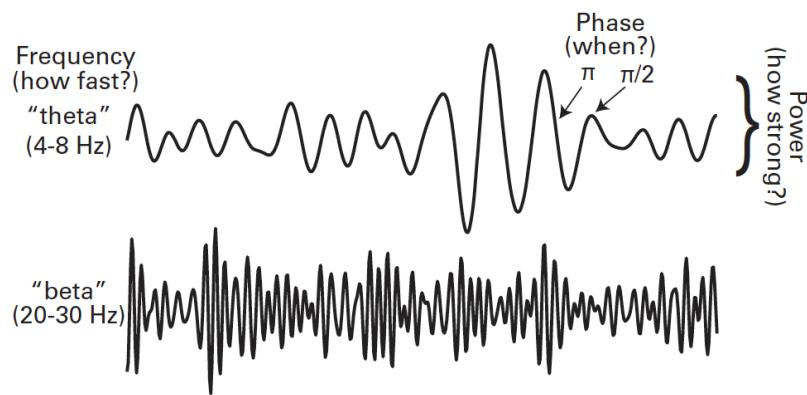
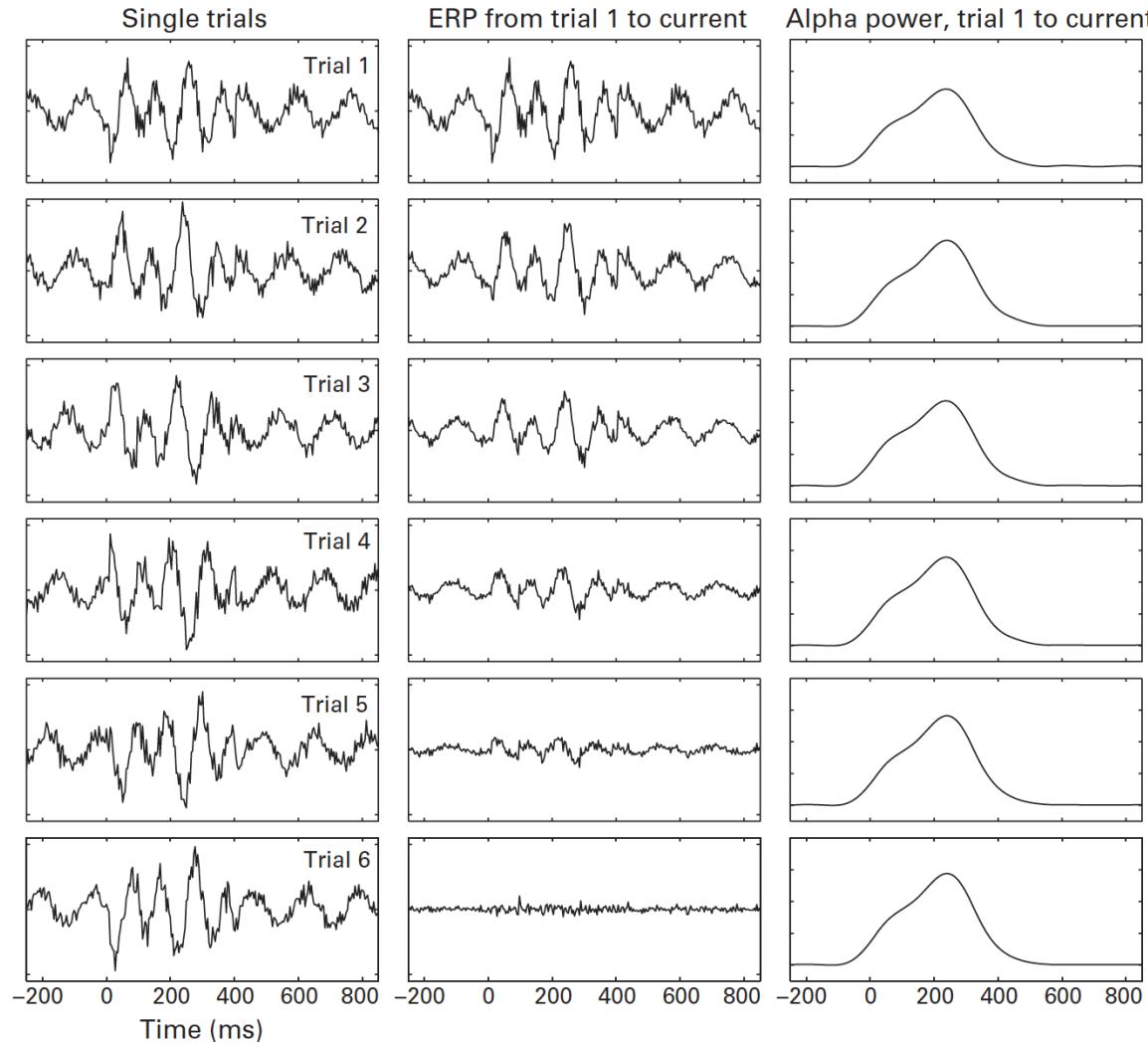


Figure 3.2

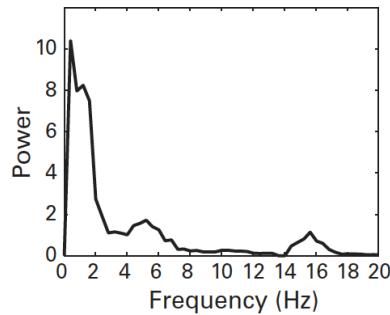
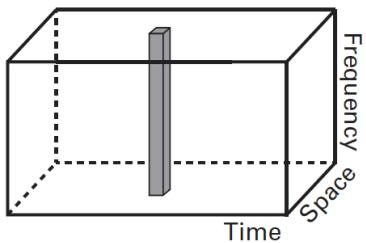
The three dimensions that define oscillations: frequency, power, and phase.

Helpful figures from Cohen Textbook

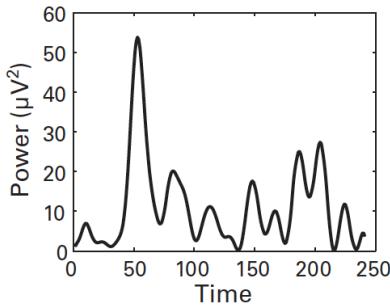
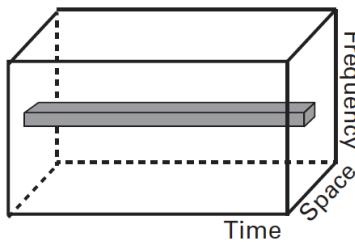


Helpful figures from Cohen Textbook

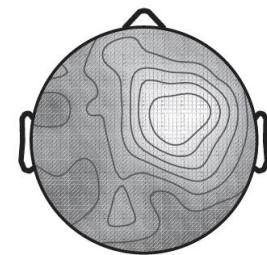
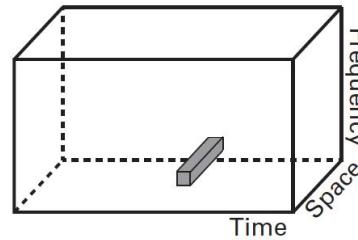
A) Frequency slice



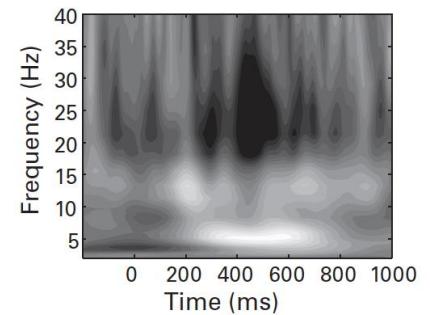
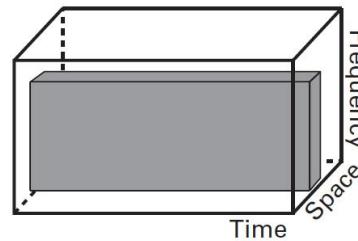
B) Time slice



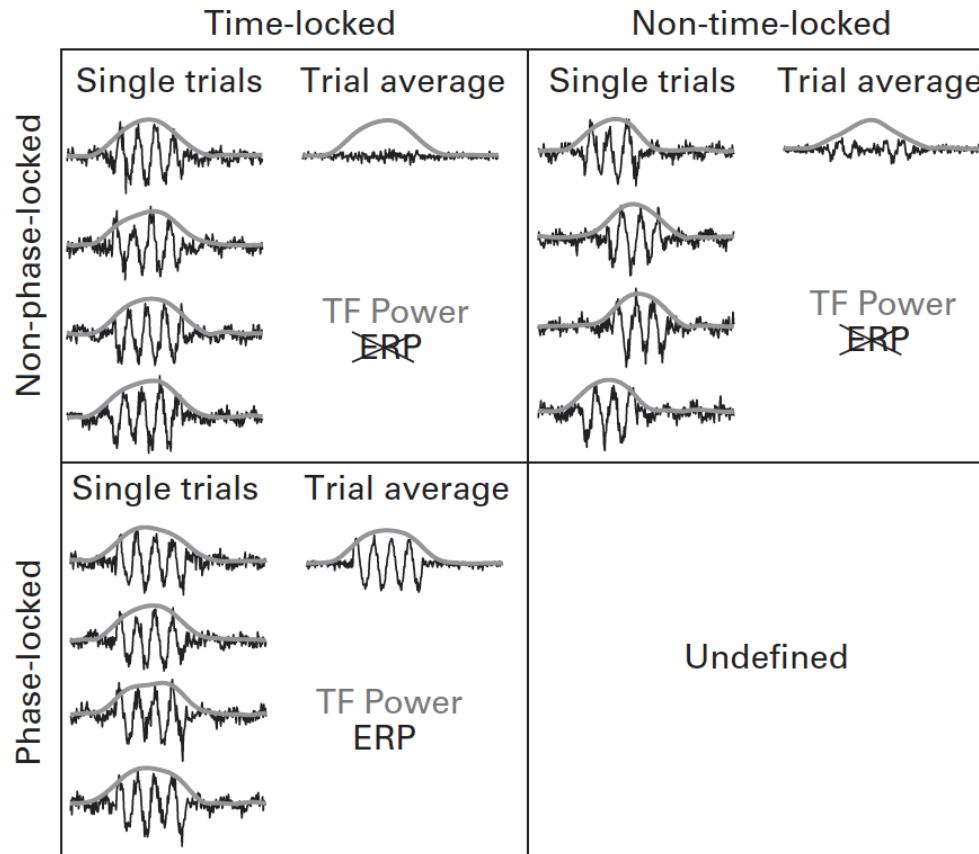
C) Space slice



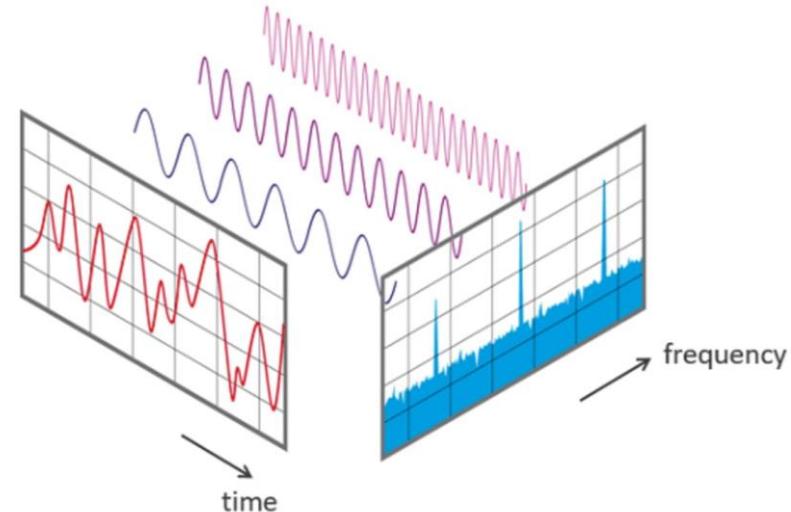
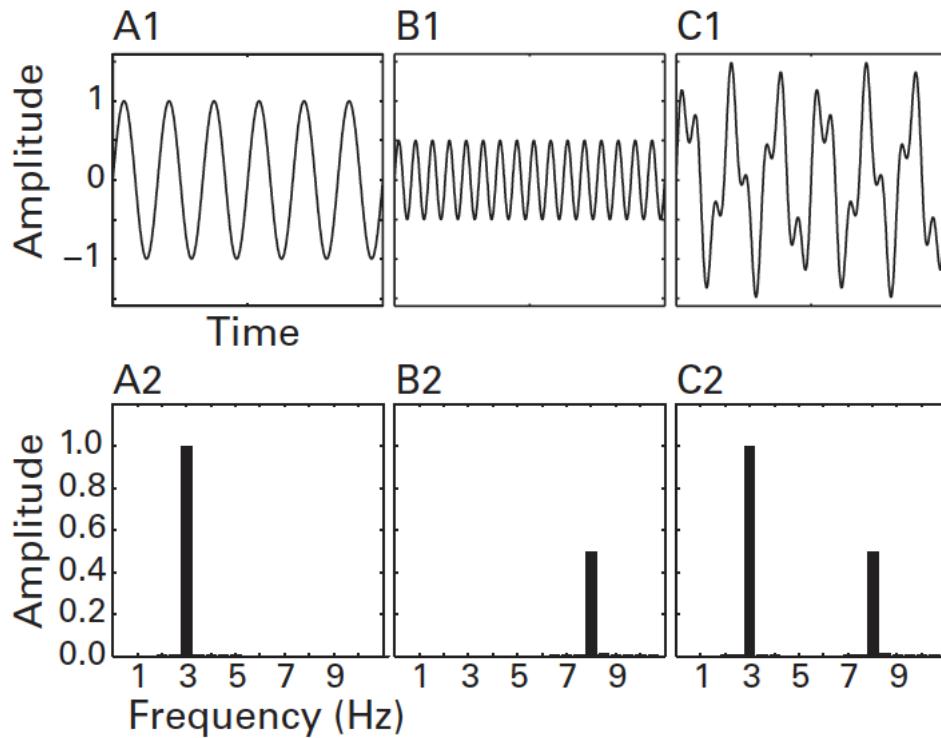
D) Time-frequency slice



Helpful figures from Cohen Textbook



Fast Fourier Transform (FFT)

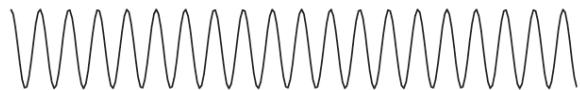


Morlet Wavelets

A) EEG data



B) No temporal weighting (Fourier transform)



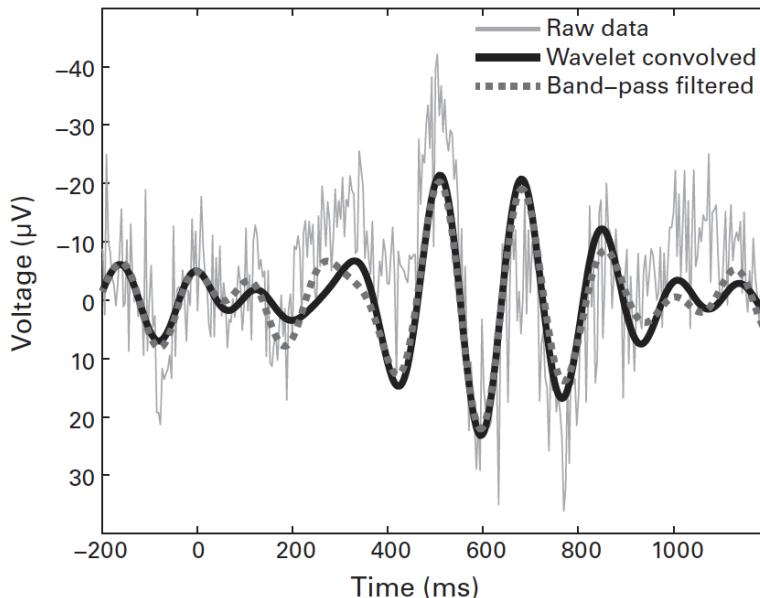
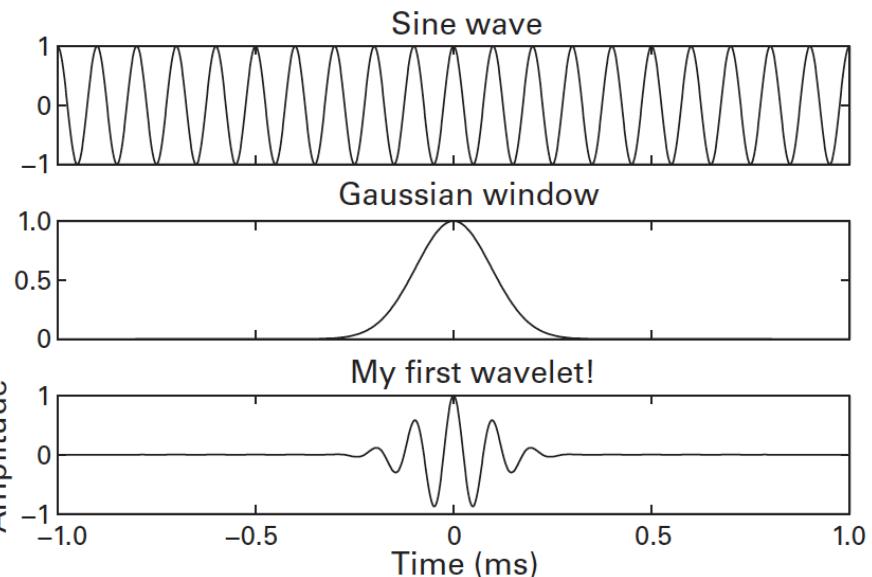
C) Strong temporal weighting



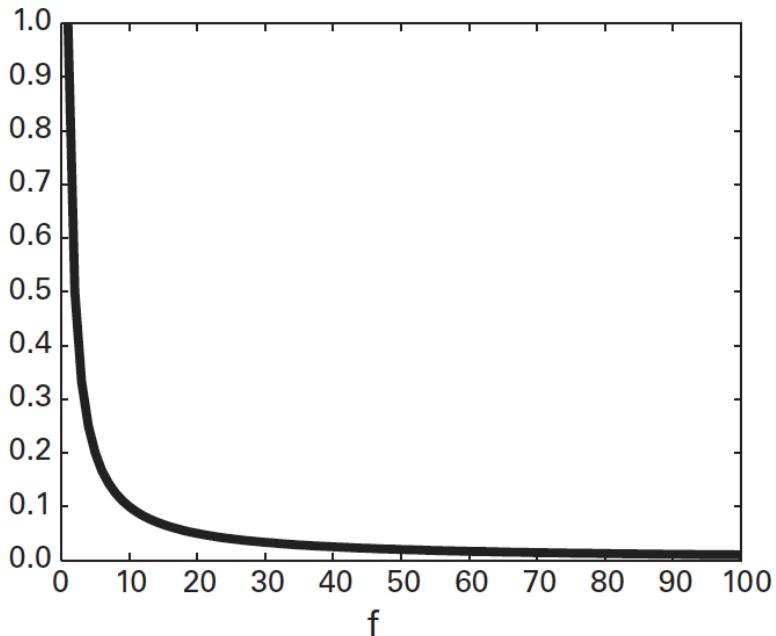
D) Boxcar temporal weighting



E) Gaussian temporal weighting



1/f Power Scaling



“EEG time-frequency power obeys a 1/f phenomenon, the power at higher frequencies (e.g. gamma) has a much smaller magnitude than the power at lower frequencies (e.g. delta)”
(page 218)

Figure 18.1

A $1/f$ function that characterizes, among other things, EEG power data.

Z-transformation

18.5 Z-Transform

The Z-transform works slightly differently from decibel or percentage change but still retains the same advantages that it corrects for $1/f$ power law scaling and transforms power data to be comparable across frequencies, electrodes, conditions, and subjects. With the Z-transform, power data are scaled to standard deviation units relative to the power data during the baseline period. The units are normal Z values and so can be easily interpreted and converted to p values (for example, $Z = 1.96$ corresponds to a two-tailed $p = 0.05$)

$$Z_{tf} = \frac{activity_{tf} - \overline{baseline}_f}{\sqrt{n^{-1} \sum_{i=1}^n (baseline_{if} - \overline{baseline}_f)^2}} \quad (18.3)$$

in which n is the number of time points in the baseline period. The denominator in equation 18.3 is the formula for the standard deviation. The Z-transform differs from decibel and percentage change because the latter two methods are based only on the average baseline power, whereas the Z-transform is based both on the average baseline power and on the standard deviation of the baseline power over time. Because of this, estimates of stimulus-related power may be adversely affected by highly variable data in the baseline period. This may be an issue if you have noisy data or few trials. An example of this is shown below.

eeg_toolbox

gete_ms()

- Matrix of voltage values
- trial x time

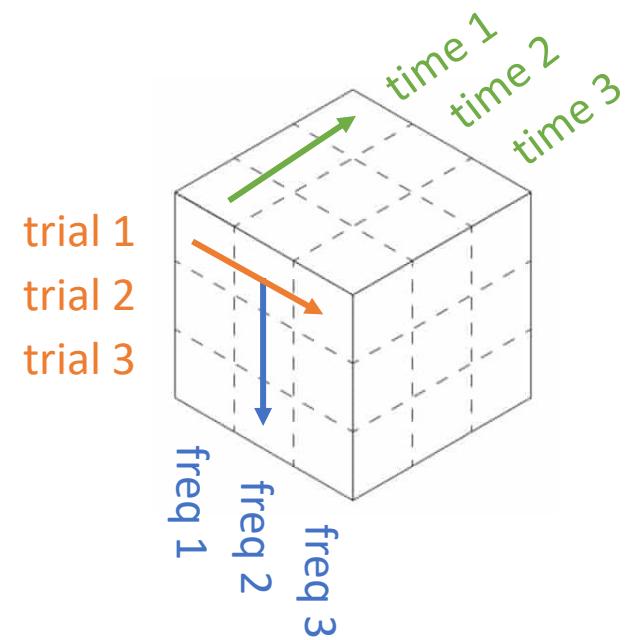
How to think about 3D matrix

eeg_toolbox

getphasepow()

- Extracts the phase and raw power values given events
- trial x freq x time

rows x columns x depth



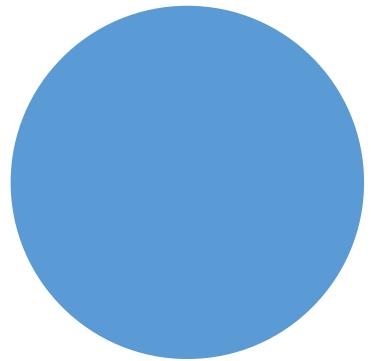
generally helpful functions

function name	purpose
dir	list folder contents
fullfile	build full file name from parts
strcmp	comparing strings
strrep	find and replace substrings
split	split strings at delimiters
sprintf	format data into string or character vector
fprintf	format data and displays the results on the screen
cellfun	apply function to each cell in cell array

Autocorrelation

A very helpful GIF

- <https://twitter.com/i/status/1355228493089361921>



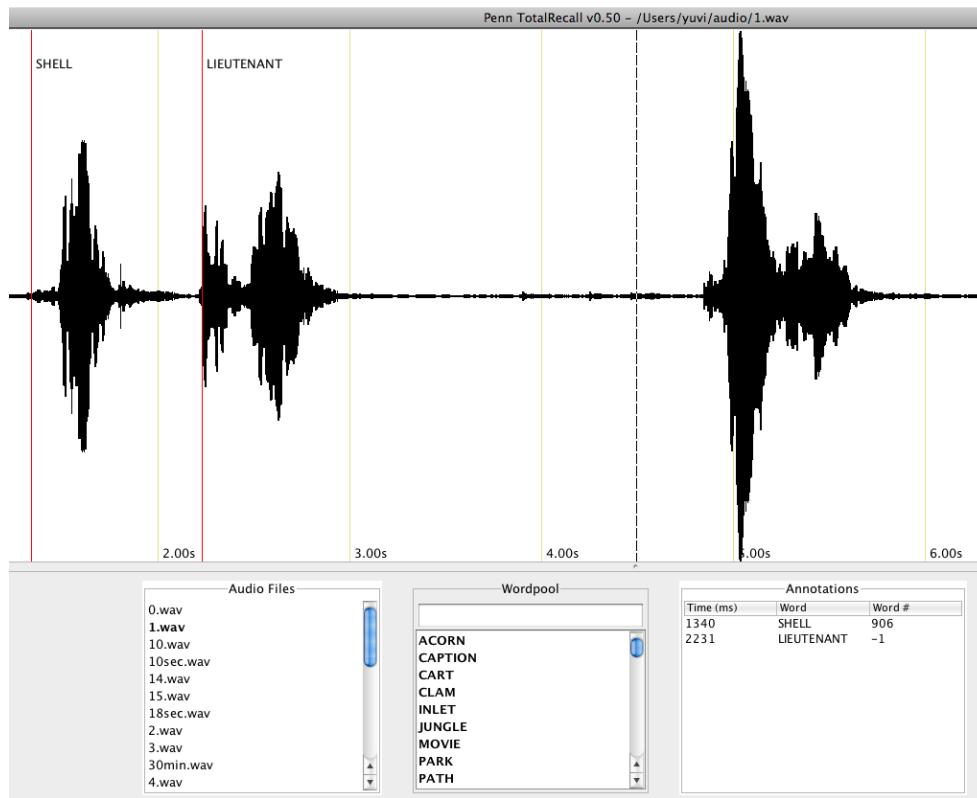
How-To Guides |
General |

“Informed consent should not be considered a one time signing of a document, but rather an ongoing dialogue between clinician/researcher and subject and a process that is revisited and re-evaluated throughout the study.”

How to obtain informed consent from a patient

- Explain the general purpose of the research
- Tasks/procedures involved
- Expected duration of task
- Risks and discomfort – task is potentially stressful
- Benefits – no direct benefits, but research will inform our understanding of the brain in general and may help others in the future
- Confidentiality – their information will be kept confidential and their data is deidentified (i.e. not traceable back to them)
- Participation is completely voluntary – they can opt not to participate and may discontinue any time
- “Any questions?”
- Contact numbers for further questions are on the informed consent form
- “Are you interested in participating?”

Annotations using Penn TotalRecall (PTR)



- “Penn TotalRecall is designed for precise scoring and timing of participant responses during verbal tasks.”
- Software can be downloaded from the UPenn Computational Memory lab website at <http://memory.psych.upenn.edu/TotalRecall>
- Load audio folder for a session
- Select Wordpool
- Annotate any recalls by typing in a word in the wordpool blank
- For any random vocalizations, don’t type in any word but add a blank annotation. This creates a ‘<>’ event for any extraneous vocalizations or undecipherable intrusions.

<http://memory.psych.upenn.edu/AnnotationGuide>

Penn TotalRecall (PTR) Keyboard shortcuts

Keyboard Combo	
Shift + Command + Return	add annotation
space bar	play
← or →	move 5 ms (small)
Command + ← or →	move 50 ms (medium)
Shift + Command + ← or →	move 500 ms (large)
Option + ← or →	listen 5 ms (small)
Shift + ← or →	move to last annotated time point

How to exit a task once it is already running on the testing laptop

Press Fn + Esc + F1 on testing laptop

If running Courier task, press Command + Q

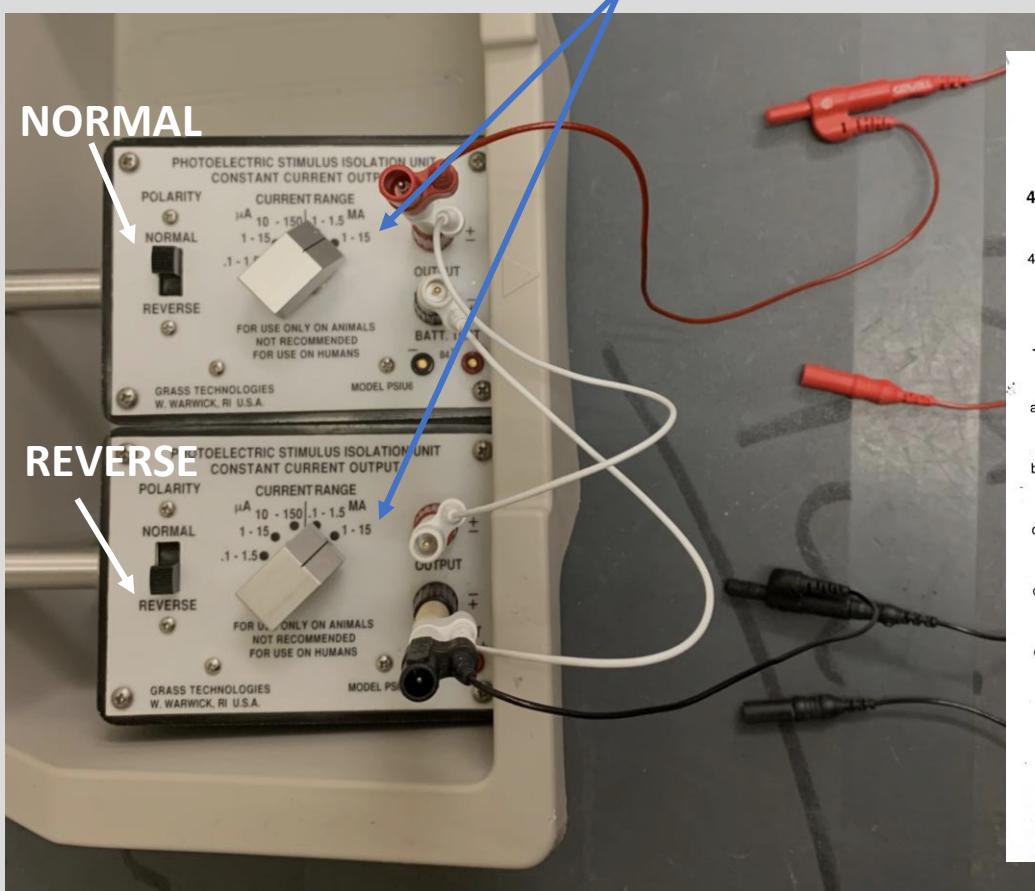
S88 GRASS stimulator



- Make the duration 2 (x.1) for both S1 and S2
- Make the delay for S2 match the duration, so 2 (x.1)
- S1 duration needs to match S2 duration, and S2 delay needs to match both of those
- S1 delay is null (<0)
- S1 rate is null (<0)
- S2 rate is null (<0)
- Make sure POWER is turned ON only when you're ready to use it

PSIU6 (Photoelectric Stimulus Isolation Unit)

Current range is currently set to 1-15 mA



OPERATION OF THE PSIU6 Section 4.5

4.5 Biphasic Constant Current Stimulation

- 4.5.1 Symmetrical biphasic, constant current pulses may be delivered to a preparation as follows:



- a. Connect one PSIU6 to the S1 output of a S11, S88 or S8800 Stimulator. See Figure 4.5.1.

- b. Connect a second PSIU6 to the S2 output of the Stimulator.

- c. Connect one electrode lead to the red (+) output binding post of one PSIU6.

- d. Connect the second electrode lead to the black (-) binding post of the second PSIU6.

- e. Connect the black (-) output binding post on the first PSIU6 to the black (-) binding post of the second PSIU6.

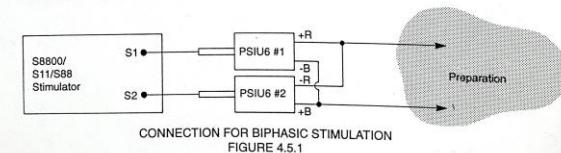
- f. Connect the red (+) output binding post on the first PSIU6 to the red (+) output binding post of the second PSIU6.

- g. Set the POLARITY switch on the first PSIU6 to NORMAL.

- h. Set the POLARITY switch on the second PSIU6 to REVERSE.

NOTE: To avoid current cancellation, the S1 and S2 pulses should not overlap.

- 4.5.2 Note: When stimulating with low currents through high impedance electrodes, the use of two PSIU6 units together at one preparation site is not recommended. Intervening tissue will affect the capacitance between electrode pairs and thus will divide the output current. Therefore, a discrepancy between the amount of current preset in each PSIU6 and actually delivered may result.



How to start AR task

Open Terminal on Task Laptop (**blue** is what to type)

- cd Desktop
- cd associative_recognition
- cd AR
- ls (first letter is a lower-case L)

Should show ar.py after Rugg_design

Click up arrow until you see a line that looks like the one below, or type in

- python ar.py -sUT### --config=config.py

Basic Terminal Commands

Command	Action
Ctrl + C	Kill whatever you're running
cd [folder]	Change directory
cd ~	Home directory
cd/	Root of the drive
pwd	Show your working directory
cd..	Move up to the parent directory
ls	Display the names of files and subdirectories in the directory
ls -l	List in a long format. Includes permissions, owner and group name, data and time file was modified, etc
mkdir FolderName	Create a new folder
Ctrl + R	Search through previously used commands
chmod -R 777 FolderName	Change the permission of a folder (and its contents) to 777
ssh username@host.com	Establish SSH connection to host with username
scp -r /path/to/folder username@host.com:/remote/pat h/	Copy folder (or file, just lose the -r) to a remote host

How to get macro EEG files from the EMU

Most important files
for macros are the
.21E and .EEG files

Before you go to grab the EEG:

- Check the notebook for the start and stop times for the EEG file(s) you need
- Make sure you have the patient's name (not just their UT###)

Use an encrypted drive to copy EEG from NeuroWorkbench

- Open NeuroWorkbench on clinical workstation
- Click on the date
- Find patient name and expand using + icon
- Scroll to find the correct date/time
- Click on the correct time
- Click copy on the right-hand side – the file should pop up in the bottom panel
- Make sure file is being copied to the correct drive (usually E)
- Right click on the file in the bottom panel and select “Exclude all DV file”
- Click “Start”
- Repeat for each file you need
- Click “Return to today” and try to leave the computer as you found it. Make sure to log out.

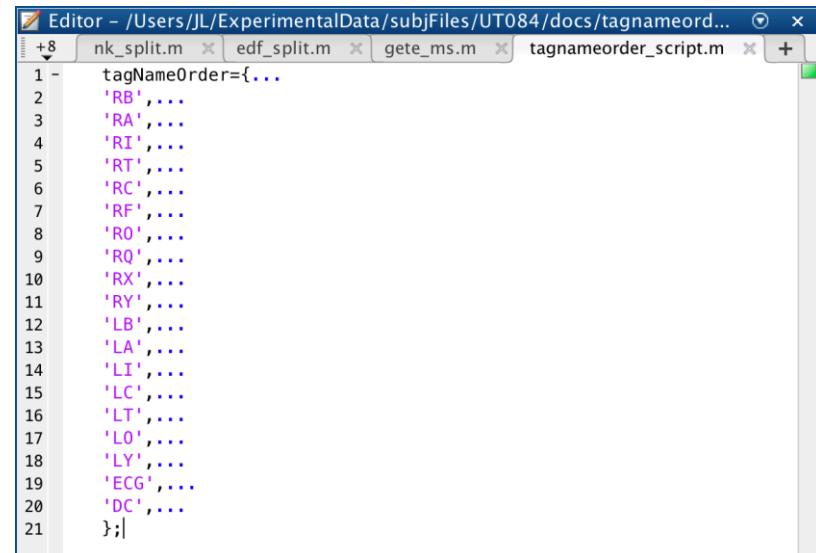
Then upload the files into the raw folder of a subject's directory on BioHPC with the format: 'MM_DD_YYYY_[task_name]'

Macro EEG Pre-Processing Steps

1. Upload task behavioral data onto BioHPC
2. Upload raw EEG data onto BioHPC
3. Split session EEG
4. Make events structure
5. fix EEG log (if there is an eeg.eeglog file)
6. Use alignTool to align the events with the EEG

How to Split EEG Recording (Parkland)

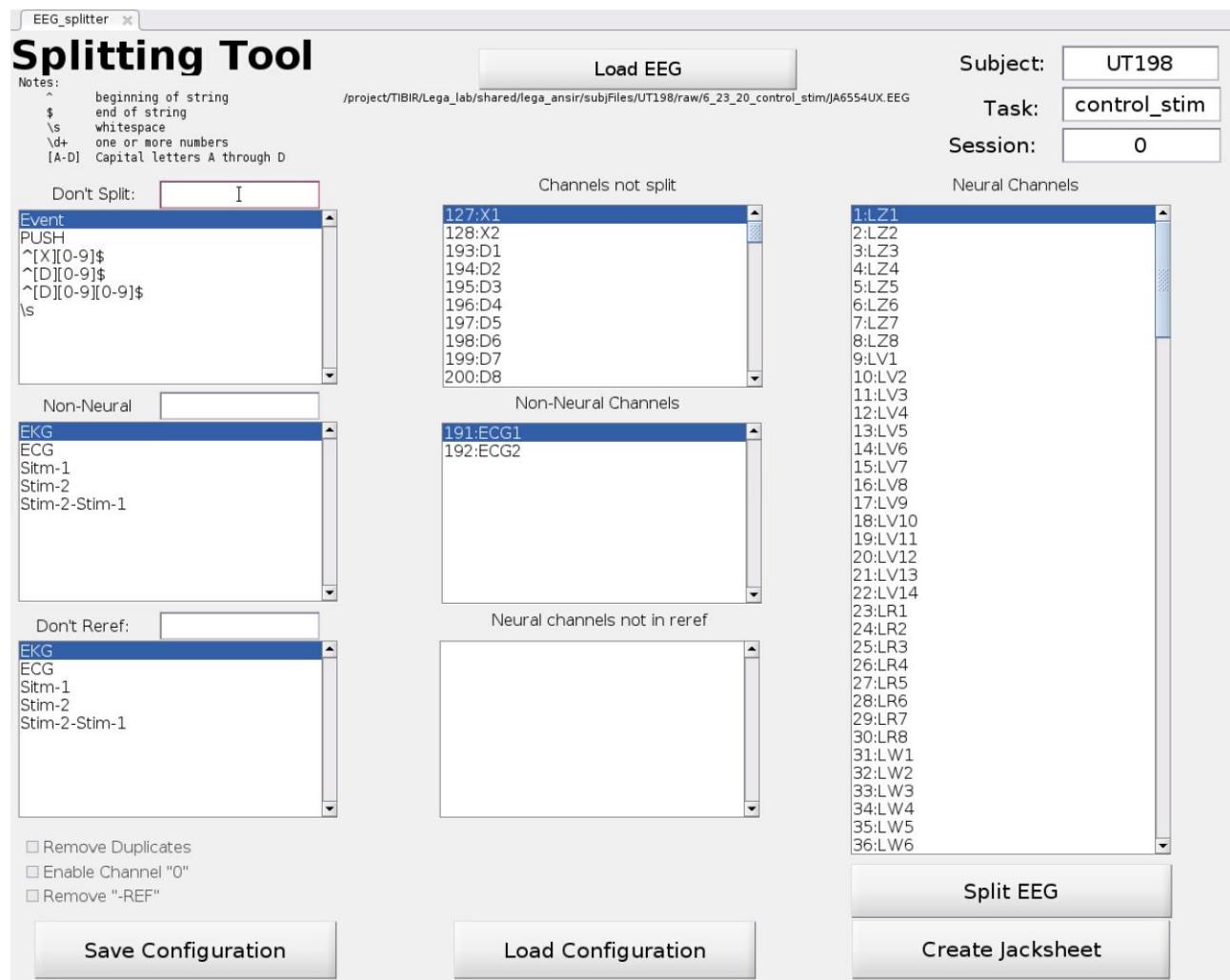
- This step splits the raw EEG recording into its individual channel components and performs a referencing step.
- For Parkland patients use:
`nk_split_wrapper.m`
- For Parkland patients, you will need to make a `tagnameorder_script` which specifies the order of the electrode labels



```
+8 nk_split.m x | edf_split.m x | gete_ms.m x | tagnameorder_script.m x +  
1 - tagNameOrder={...  
2 'RB',...  
3 'RA',...  
4 'RI',...  
5 'RT',...  
6 'RC',...  
7 'RF',...  
8 'RO',...  
9 'RQ',...  
10 'RX',...  
11 'RY',...  
12 'LB',...  
13 'LA',...  
14 'LI',...  
15 'LC',...  
16 'LT',...  
17 'LO',...  
18 'LY',...  
19 'ECG',...  
20 'DC',...  
21 };
```

How to Split EEG Recording (Zale)

- For Zale patients use `EEG_splitter`
- `EEG_splitter` is a GUI
- Once you load the EEG, enter the subject code, task name and session #
- Then you will see a list of neural channels in the rightmost column. Double-check that there are no extraneous channels in this column. If there are strange channels (like A1 or D31), you will need to add those to the 'don't split' list by entering codes like `^[D][0-9][0-9]$` to remove D channels with two digits, or `\s` to remove whitespace
- Make sure to add DC to the don't reref column



How to Make Event Structures for FR1

- To make events for FR1, use the function '**RAM_FR_CreateAllEvents.m**'
- Inputs are the subject name, path to session folder, and session folder number
 - `>> RAM_FR_CreateAllEvents('UT084', '/project/path/to/subfolder/FR1', 1)`
- If everything runs smoothly, you should see the function generate a file for both the verbal and math events

How to Make Event Structures for pyFR_stim3

- To make events for pyFR_stim_3, use the function '`extract_PYFR_STIM_wrapper.m`'
- Inputs are the subject name, path to session folder, session folder number, forceSession (just set to 0 or []), and isStim == 1
 - `>> extractPYFR_STIM_wrapper('UT084', '/project/path/to/behavioral/pyFR_stim3', 0, 0, 1)`
- Open up the session.log for this stim session, get the stim electrode, parameters (2 mA, 100 Hz, 23 secs) and refer to session.log for stim condition for every list
- Stim codes
 - 1 == ENCODING STIM
 - 3 == RETRIEVAL STIM
 - 5 == NO STIM
- If everything runs smoothly, you should see the function generate a file for both the verbal and math events

How to fix EEG Log

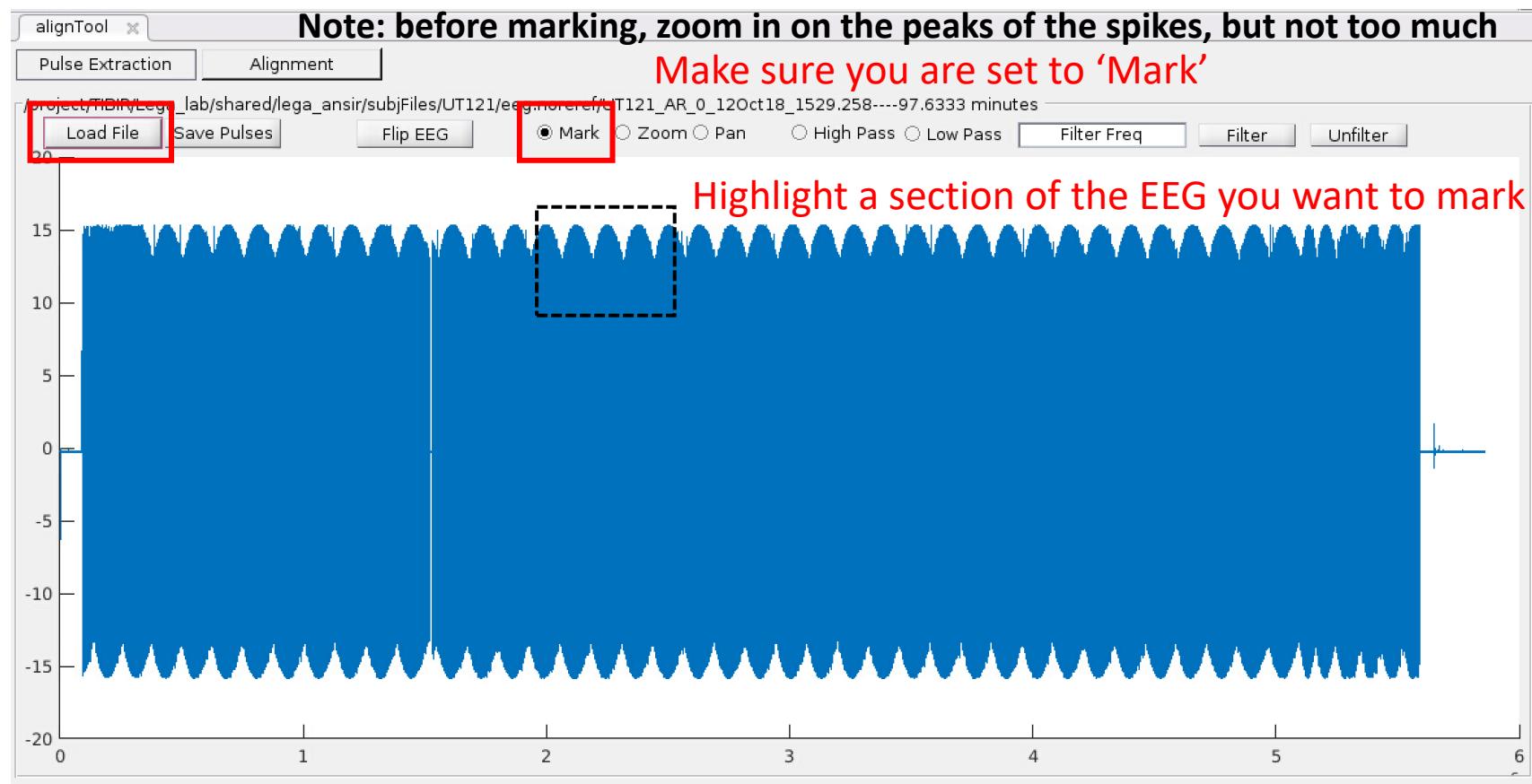
- Make sure the session folder is your current folder
- Run the fixEEGLog.m function
- `>> fixEEGLog('eeg.eeglog', 'eeg.eeglog.up')`
- This will fix the EEG log and create a file called 'eeg.eeglog.up' which you will need for aligning the events and EEG

Aligning the Events and EEG

- Event alignment involves determining the EEG recording time offset from the unix timestamps of the sync pulses generated during the memory task.
- This process is done using a GUI (Graphical User Interface) called **alignTool**
- Once you've split the EEG, made the events structure, and fixed the EEG log, you're ready to use **alignTool**
 - When using alignTool it helps to have your current directory be the subject folder
 - >> alignTool

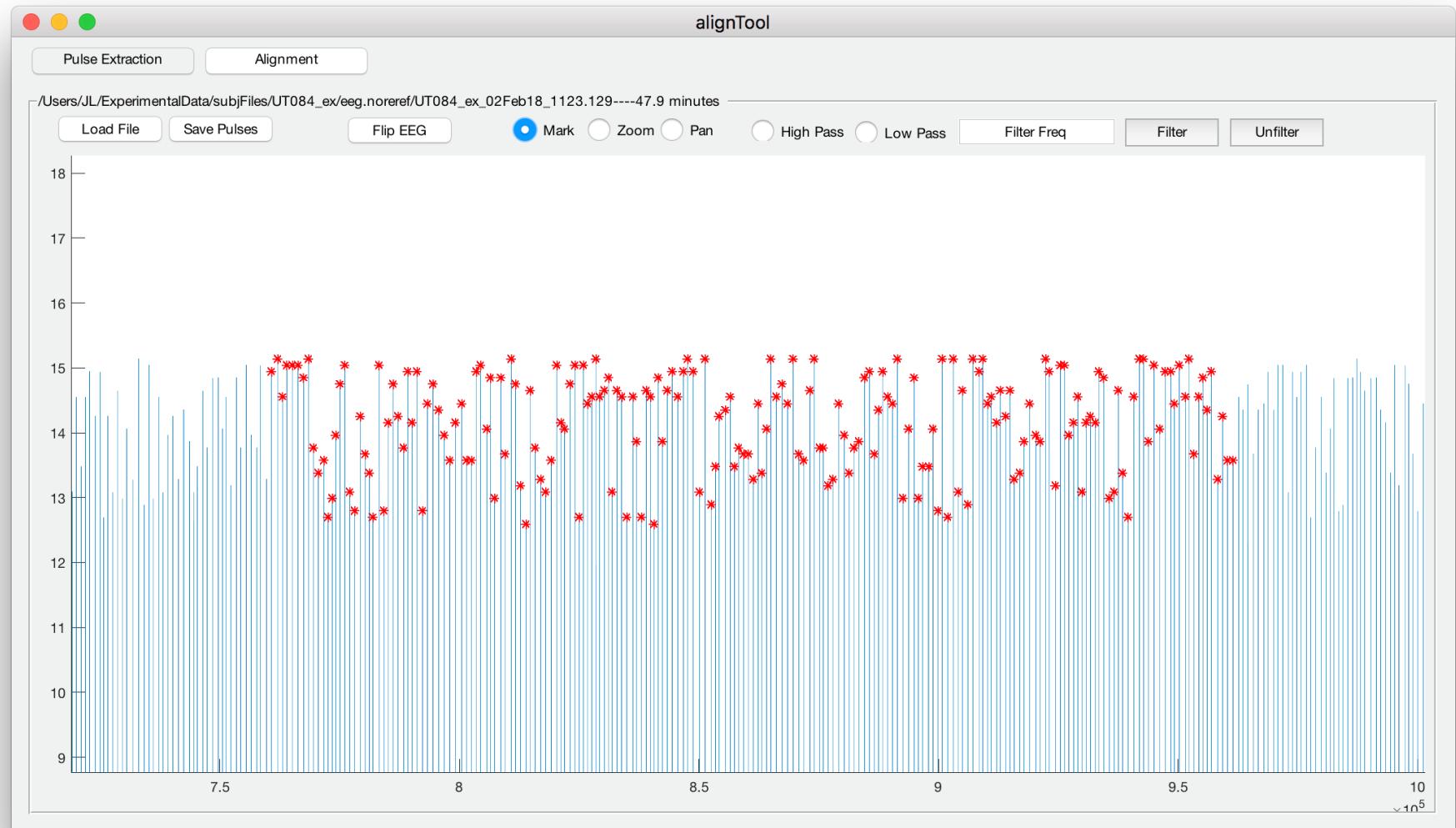
How to do pulse extraction in alignTool

Load File --> Load the DC09 channel for this session in eeg.noreref (this will be the second to last channel for the session)

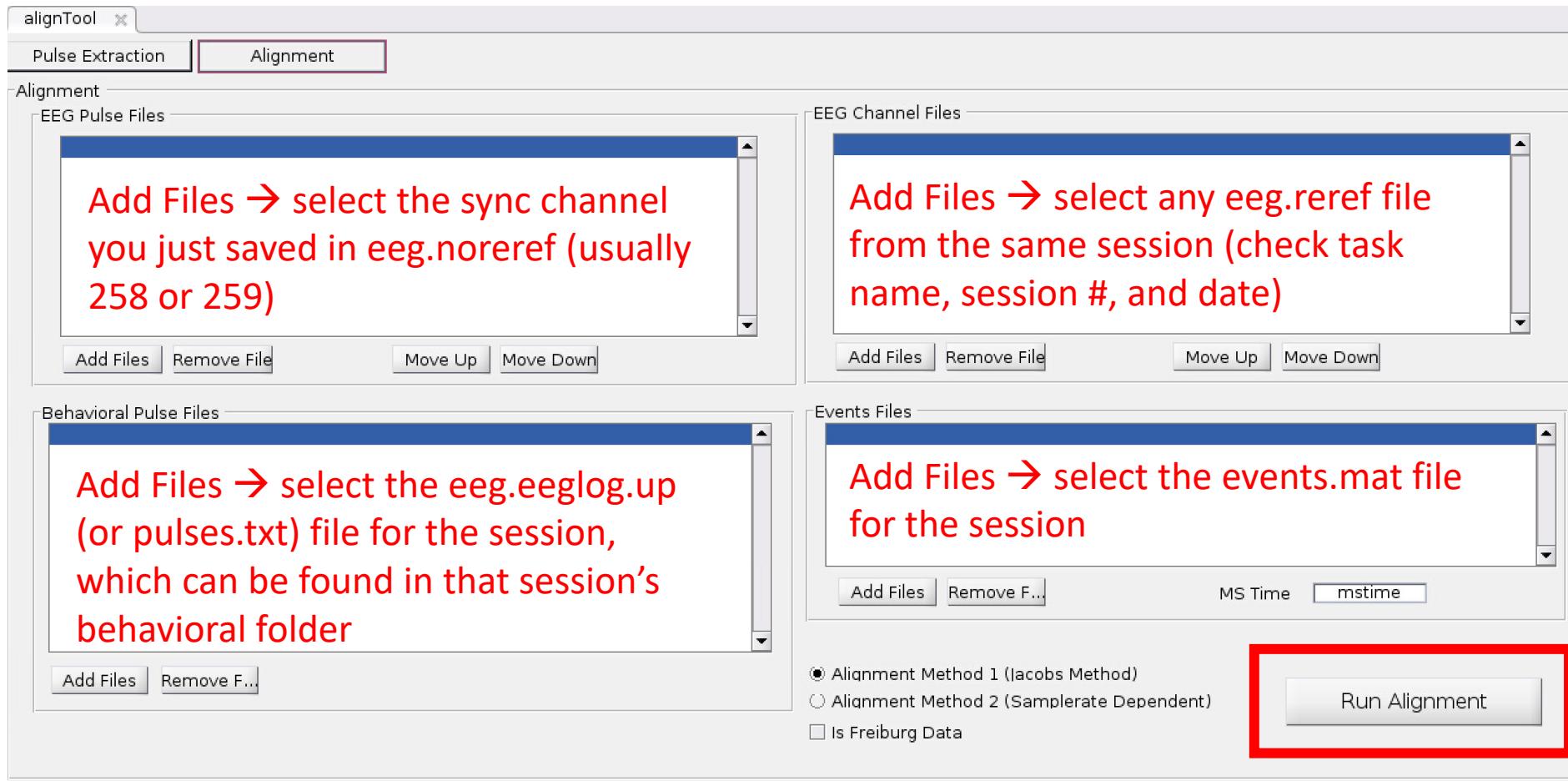


After you are satisfied with the marked pulses, click Save pulses and save the sync channel

Example of sync pulse marking from Jui-Jui Lin's Lega Lab Tutorial



How to run alignment in alignTool



then press Run Alignment

VERY IMPORTANT:

Make sure that the EEG alignment worked!

```
Running Alignment...

Samplerate: 1000
7 blocks
.....
found matches for 35 of 40 pulses
file 1, alignment method 2: 35 matches of 40 recorded pulses
/project/TIBIR/Lega_lab/shared/lega_ansir/subjFiles/UT121/eeg.reref/UT121_pyFR_stim3_0_180ct18_1103.055:
    Max. Dev. = 1.451172 ms
    Median. Dev. = 0.321533 ms
    95th pctile. = 1.080444 ms
    99th pctile. = 1.451172 ms
    R^2 = 1.000000
    Slope = 0.999936
    Pulse range = 0.548 minutes
WARNING - Out of bounds of eeg files:
WARNING - Out of bounds of eeg files:
WARNING - Out of bounds of eeg files:

ans =
    1.0e+12 *
    -1.5398
     0.0000

Done!!!
```

Double-check that these numbers are close to 1

***Note: If those numbers are crazy big, then the alignment did not work, and the events are wrong. You will have to run the alignment again!

How to use BrainNet Viewer

- Need to download BrainNet Viewer from Nitrc.org
- Save folder to /work folder or wherever you're using Matlab
- Type 'BrainNet' into the command line (no quotes)
- File, Load File
- "Surface" chose BrainMesh_ICMB152_tal.nv
- BrainNet Viewer requires your data to be in a .nodes file. Use the make_nodes script to get data formatted correctly.
- In the first "Data file" browse for your .nodes file
- You can change the layout to single view, full view, lateral/medial view, etc
- Under "Nodes" option, Draw all nodes, label if you want labels
- Make Color Modular, Size Value set to Raw, can change scale for size
- Close options before closing BrainNet Viewer



How-To Guides |
RAM |

General sequence for RAM testing

catFR1

At least 3 sessions*

*For each new day of RAM catFR1 testing, start with an EVEN numbered session

Amplitude
Determination

See instructions on next slide

(i.e. start each new day with session 0, 2, 4, etc.).

Location Search

Location search does not require the patient to do anything on the testing laptop

For example, if a patient only completed session 0 on the first day of testing, start with session 2 the next day

TICL_catFR,
catFR5, catFR6

Based on priorities sent by Penn

How to run RAM tests in Spanish



Normally we would access unity through the RAM 3.1 folder on the Desktop, but the Spanish versions are in a different folder



In exp User directory, you can access the folder RAM 3.1-languages folder, which contains unity in Spanish*

“ ”

*Note: instructions are not in Spanish, so you will have to call Parkland interpreter line to explain the task

How to set up RAM testing

(part 1 - components)

Host PC



- Runs RAMulator (System 3.0) software
- Controls stimulation
- Streams and saves data, log files (timestamps, stimulation events)

Task Laptop



- Runs behavioral tasks
- Logs behavioral responses (.wav files, task events)
- Used for annotation (Penn TotalRecall)
- Transfers and uploads session data, imaging, clinical EEG to rhino

External Neural Stimulator (ENS)



- Designed by Medtronic specifically for the RAM project
- 256 channels (4 banks) of data sensing and stimulation
- Requires a loaded configuration binary file to operate
- Powered by 3 AA batteries
- Single power button on top
- 6 LED indicator lights (blinks green in standby; solid green when connected and streaming data; 4 LEDs blue during stimulation; colored orange for low batteries; colored red for dead batteries)

Blackrock ENS Splitter Cables

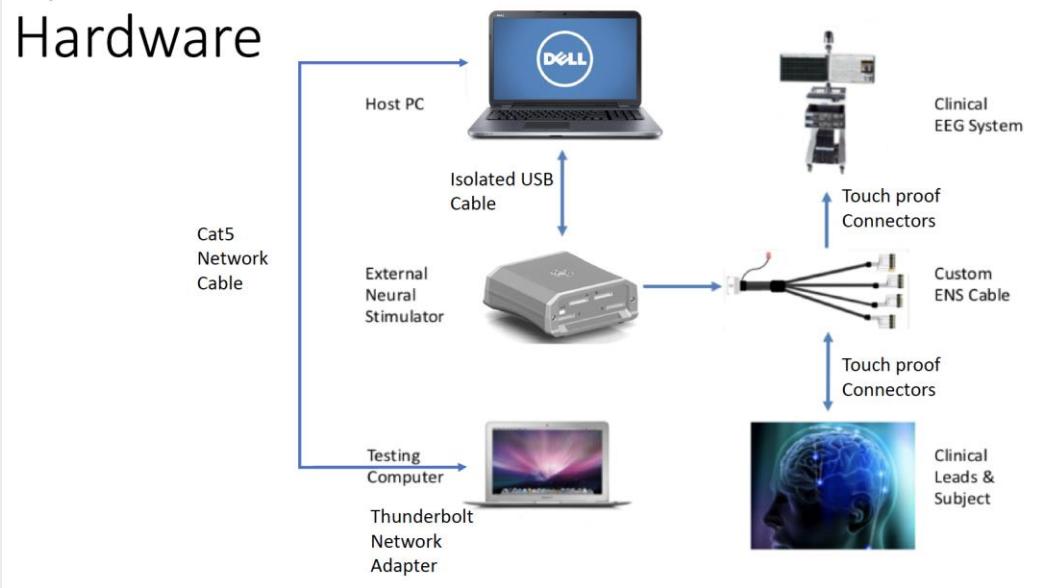


- Each cable supports 64 channels
- Connects to ENS via Omnetics connector
- Connects to patient jack box and patient leads via individual touch proof connectors
- Each touch proof connector is numbered from 1 to 256.
- Each cable has a **red REF** touch proof and a **green GND** touch proof on the jack box side.
- Each cable has a **red REF** touch proof splitter at the ENS side to tie together the references, if needed.

How to set up RAM testing

(part 2– getting connected)

System 3 Hardware



- Check that the Host PC, Task Laptop, and ENS batteries are all fully charged
- **IMPORTANT:** The ENS is connected by powering it on, connecting the USB cable to the Host PC, then powering the ENS off and on again. The ENS will also sometimes turn off if it hasn't been in use for awhile.

How to set up RAM testing

(part 3 – running the experiment)

Host PC



- Launch Ramulator software on the Host PC
- Navigate to Session >> Load Session
- Browse to Desktop and find the unzipped configuration provided by Penn
- Load the experiment_config.json file
- With the ENS powered on and in stand-by mode, press the Start button in Ramulator to connect to the ENS and begin data streaming
- LEDs on the ENS will turn a solid green color



To stop the experiment at any time:

- Press the stop button (or CTRL+X) on the Host PC or
- Press fn + esc + F1 on the Task Laptop or
- Press Command-Q to quit the Unity app



How to set up RAM testing

(part 3 – running the experiment)

Testing Laptop



Launch experiment software on Testing Laptop

- In RAM_3.1 directory, run the unityeplfr-v1.3.2 app or execute *run_experiment* script (*run_experiment* for FR5/catFR5 only)

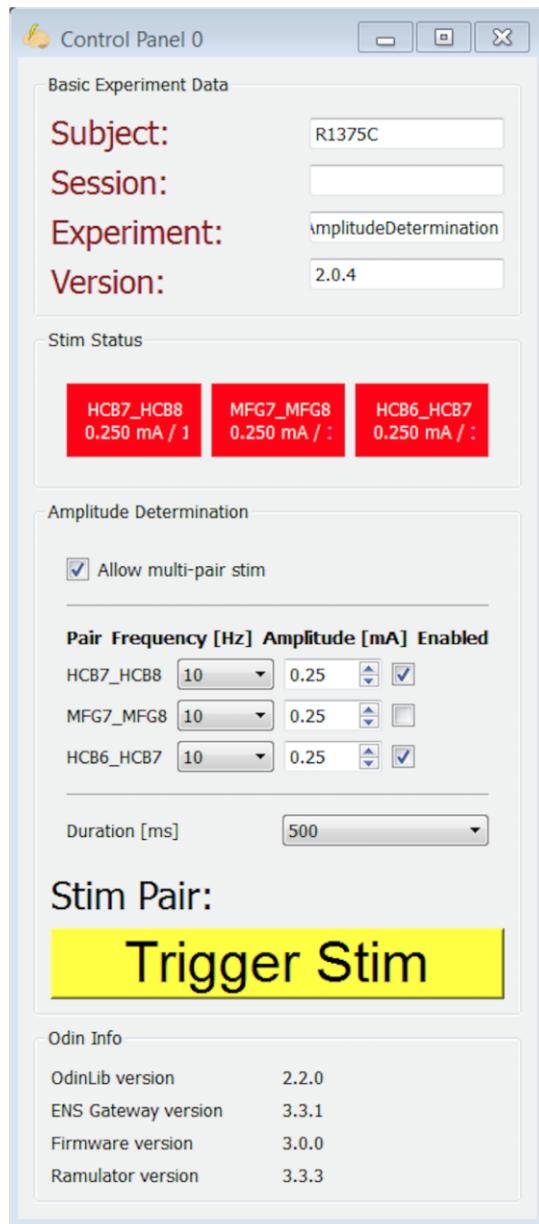
Unityeplfr application (FR1, PS4, FR6)

- Select the Task and Enter Subject Code (R*****) when prompted
- If subject has already been run, select from dropdown.
- For FR1/CatFR1, session and list numbers are selectable (to resume)

run_experiment

- Python script will launch testing GUI when connection to HostPC is established

Note: LocationSearch does not need the task laptop



How to do Amplitude Determination (AD) for RAM stimulation experiments

SAFETY: trained clinical staff must observe clinical EEG for after-discharges

- Open Ramulator on HostPC
- “Load Session”, then select the Amplitude Determination config (.json) sent by Penn that includes all electrodes and pairs you plan to test
- **Single pair amplitude determination:**
 - First check the box to enable a single pair
 - Trigger stim at 10 Hz and 0.25 mA
 - Increase frequency to 25 Hz and trigger stim
 - Increase amplitude to 0.5 mA and trigger stim
 - Increase frequency to 50 Hz and trigger stim
 - Increase frequency to 100 Hz and trigger stim
 - Increase frequency to 200 Hz and trigger stim ten times, ~1 sec apart
 - Disable current pair and enable the next pair you want to test and repeat the same process
- **Multi-pair amplitude determination:**
 - First check the box to “Allow multi-pair stim”
 - Check the boxes to enable the multiple pairs you plan to test
 - Repeat same steps as above for triggering stim

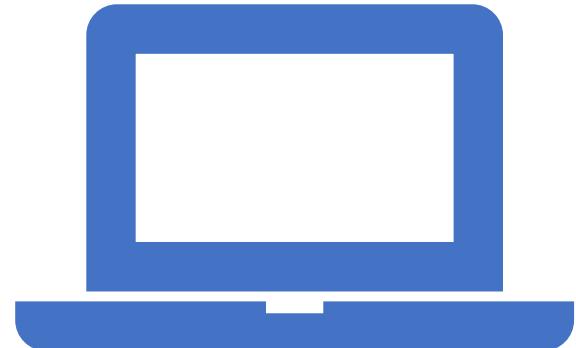
How to upload RAM data to rhino

- Connect the Host Laptop to the testing laptop via ethernet cable
- Use upload tool on testing laptop

How to connect to rhino server

username: ahassien

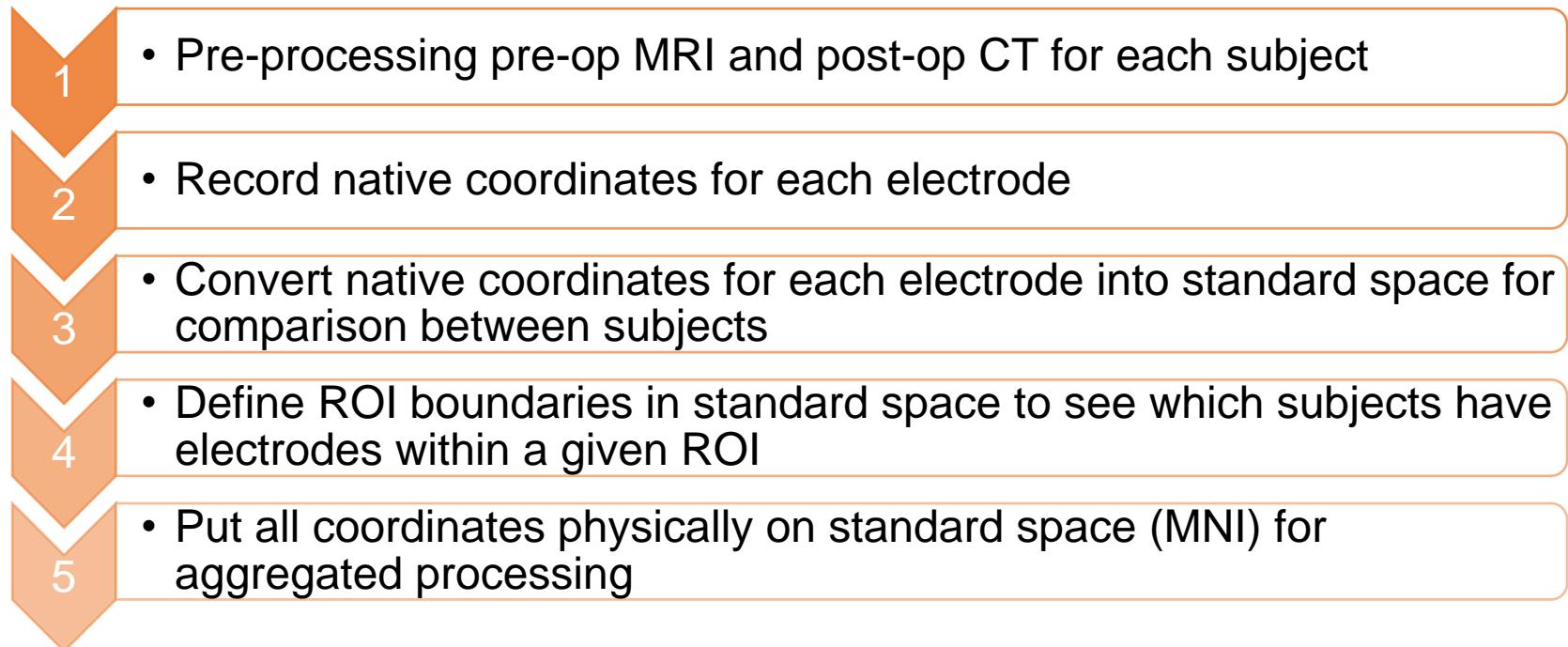
- Log in to rhino from terminal using
 - ssh ahassien@rhino2.psych.upenn.edu
- Change directories to the scratch folder
 - cd /scratch
 - Cd /scratch/lexie.hassien
- Use the command 'ls' to see contents of scratch folder
- My scratch folder name is 'lexie.hassien'
- To change your password
 - passwd
- Uploading data
 - scp -r /Users/lexie/Desktop/FolderName(space)
ahassien@rhino2.psych.upenn.edu:/scratch/lexie.hassien/
- Change permissions to Read/Write
 - chmod -R 777 FolderName
- Change group
 - chgrp -R RAM_eeg FolderName



Briefing

- Functions of Pipeline
 - Label brain regions per electrode automatically
 - Based on AAL atlas and a physician's definition
 - Positions individual labels per electrode on the standard brain (MNI2009asym)
- Pipeline Contents
 - FMRIPREP: pipeline toolbox that automatically chooses optimal settings for other tools
 - FSL: cross-modality coregistration
 - FreeSurfer: electrode localization
 - ANTs: brain standardization
 - Running platform is **Shell** on Linux, so all these tools are invisible to users

Pipeline Overview

- 
- 1 • Pre-processing pre-op MRI and post-op CT for each subject
 - 2 • Record native coordinates for each electrode
 - 3 • Convert native coordinates for each electrode into standard space for comparison between subjects
 - 4 • Define ROI boundaries in standard space to see which subjects have electrodes within a given ROI
 - 5 • Put all coordinates physically on standard space (MNI) for aggregated processing

Currently Done (subjects up to UT200)

- Codes:
`/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Pipeline`
 - Order pipeline was run:
 - Step9_STDATALAS (runs only once)
 - Now run all per subject as >> `bash Step0_FMRIPREP UT199`
 - Step0_FMRIPREP
 - Step1_COREGISTER_UT200-
 - Step2_LOCALIZE
 - Step3_NATIVEATLAS
 - Step4_LABEL
 - Step5_CROSSREF
 - Step6_FINALIZE

From Now on (subjects UT201+)

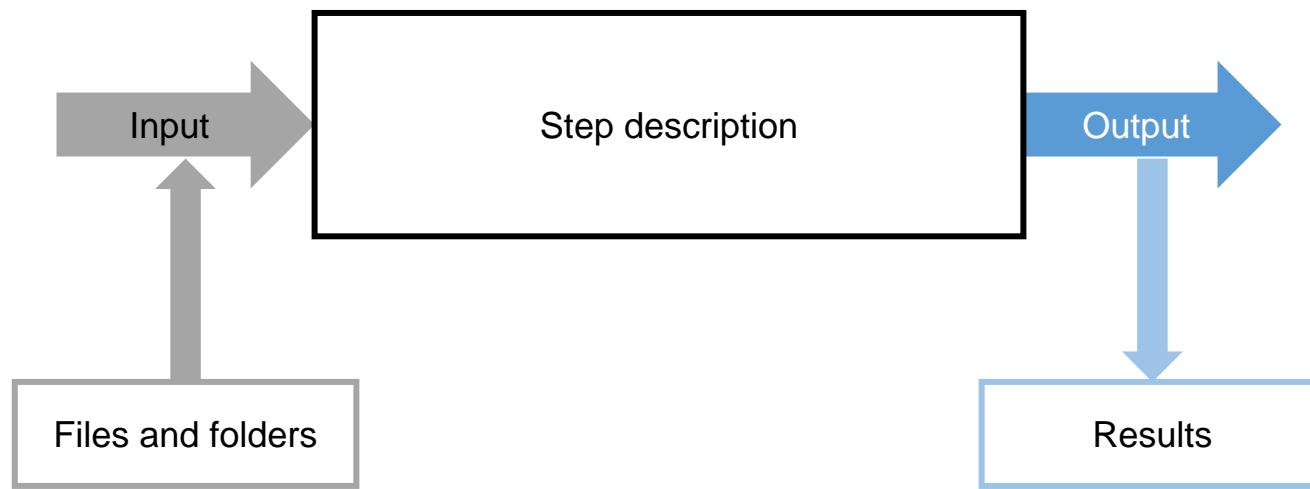
- Codes:

/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/
Pipeline

- Now run all per subject as >> **bash Step0_FMRIPREP UT201**
 - Step0_FMRIPREP
 - Step1_COREGISTER
 - Step3_NATIVEATLAS
 - Step4_LABEL
 - Step5_CROSSREF
 - Step6_FINALIZE
-
- * Step2 is no longer required

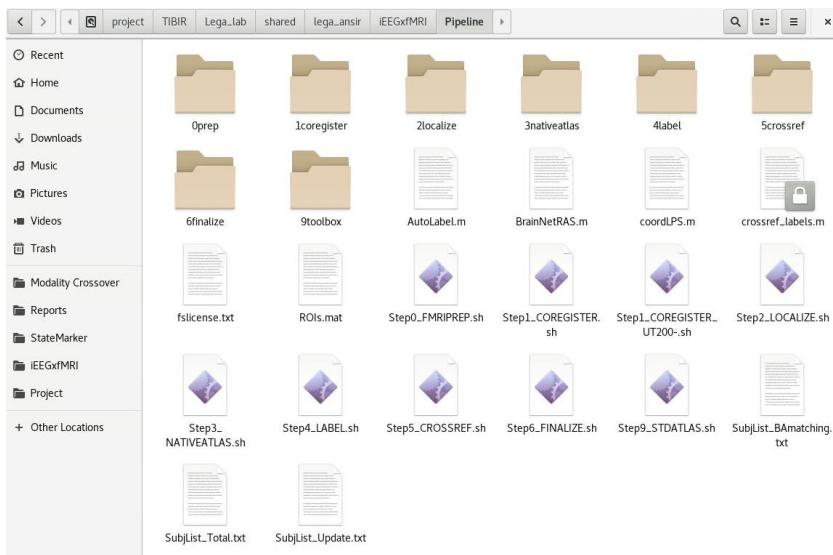
Structure of Manual

>> command on **terminal**



Detailed descriptions on next page

Workspace



/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Pipeline

Contains all steps in codes and output files in each folder

Terminal, main working platform

```
s174021@NucleusA010:/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Pipeline
File Edit View Search Terminal Help
[s174021@NucleusA010 Pipeline]$ pwd
/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Pipeline
[s174021@NucleusA010 Pipeline]$
```

Before Step0

1. Type in the following on **terminal**

```
[s174021@NucleusA106 ~]$ gedit $HOME/.bashrc
```

2. Edit the file as shown below

```
# User specific aliases and functions
module load shared
module load slurm

PATH=$PATH:$HOME/bin

export ANTSPATH=/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Pipeline/9toolbox/install/bin;
export PATH=$PATH:${ANTSPATH}

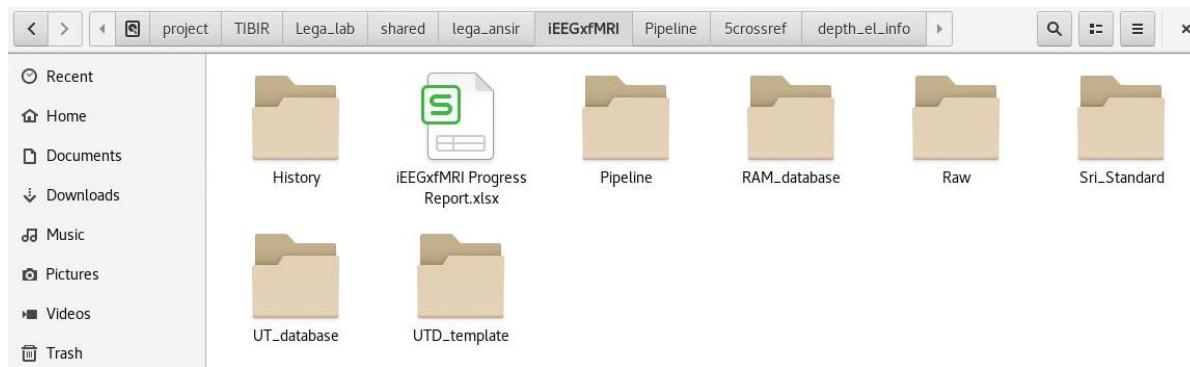
module load fsl/6.0.1
module load matlab/2019b
module load mricron/v1.0.20190902/
module load freesurfer/7.1.0

export FSLOUTPUTTYPE=NIFTI_GZ
```

3. Save and restart **terminal**

*** Personally, I find that I have trouble starting a new VNC session if I include ALL of these items in my .bashrc file. I choose to include all but mricron and load that one separately (at the start of each webGUI session).

Before Step0



Go to main project folder

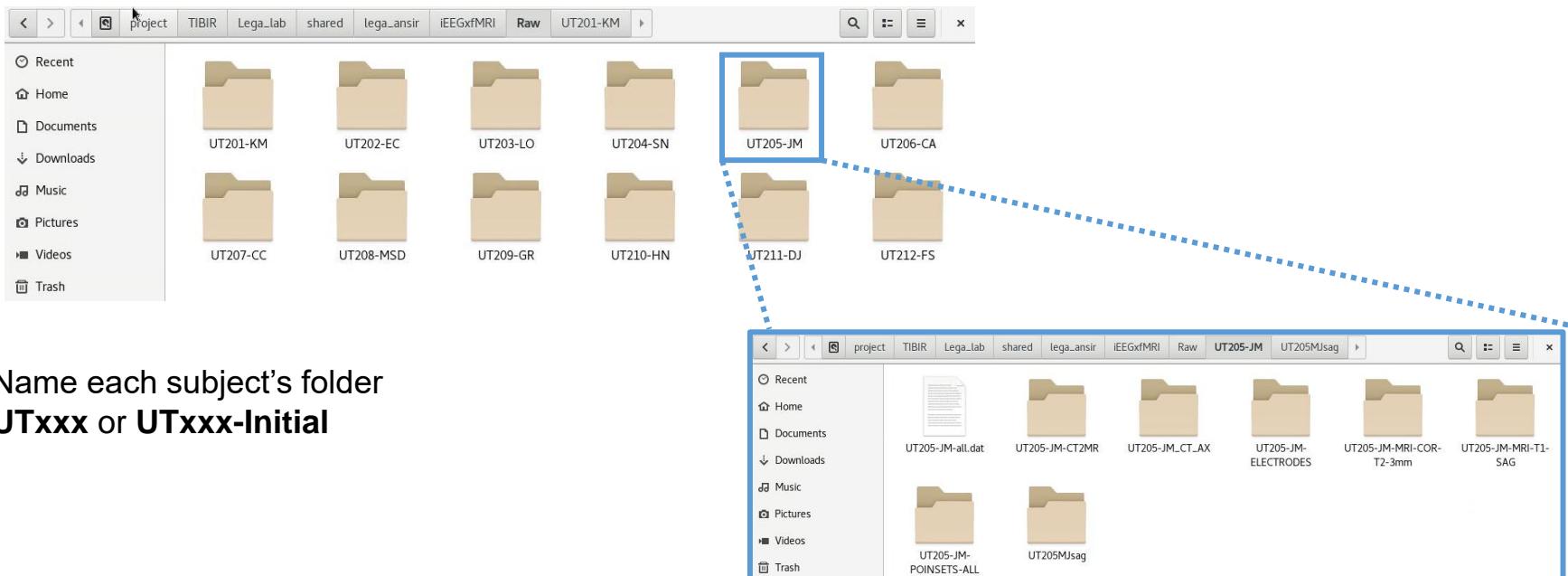
/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI

Contains all relevant files and folders

You mainly access “**Pipeline**” and “**Raw**”

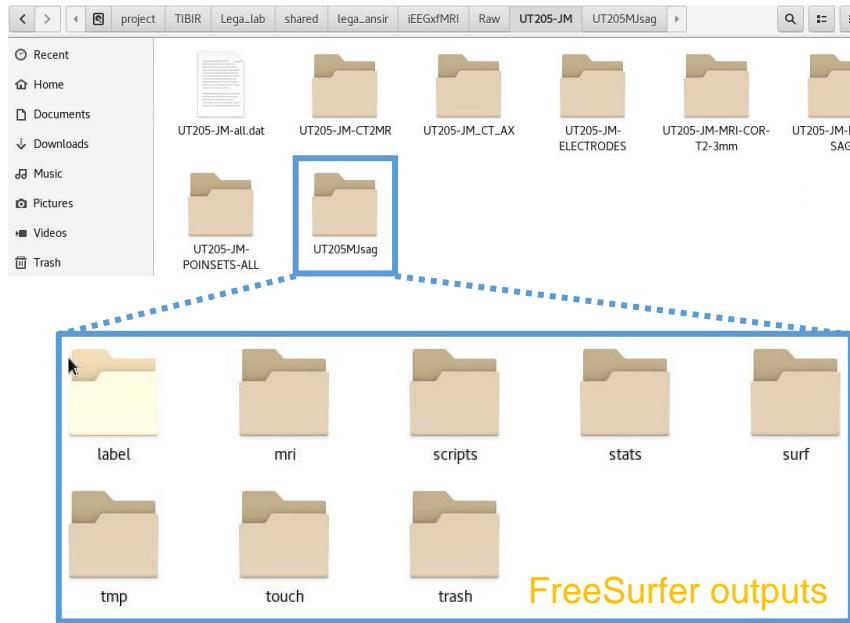
Before Step0

- Gather Required Files
 - Save them in
/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Raw



Each contains multiple folders

Before Step0



1. Find a folder that contains the following contents (folders named label, mri...)

If you get the following error:

“dcm2niix: command not found...”

Make sure you have loaded the MRIcron module (using command below):

```
module load mrircron/v1.0.20190902
```

2. Check the folder name (e.g. UT205MJsag)



3. Change to the directory of the **corresponding MRI files (most likely T1 and/or Sag/Ax)** and convert to usable format (NII) using dcm2niix



```
dcm2niix -f sub-UT###_%p *
```

```
dcm2niix -f sub-UT204_%p *
```

4. In the folder in which you created the nii file, rename the file to follow the exact format



```
sub-UT205_T1w.nii
```

* The only thing changes across subjects is the **number** after “UT”

5. Copy the file, sub-UT###_T1w.nii to the BIDS folder under /project/TIBIR/Lega_lab/shared/lega_ansir/BIDS/sub-UT###/anat Create that folder if needed.

Before Step0

1. Run the code savetoBIDS.py while in the Raw folder of iEEGxfMRI

```
[s174021@NucleusA106 Raw]$ module load python/3.6.4-anaconda 1
[s174021@NucleusA106 Raw]$ python3 savetoBIDS.py 2
Please enter a subject code (e.g. UT###):
UT205 3
```

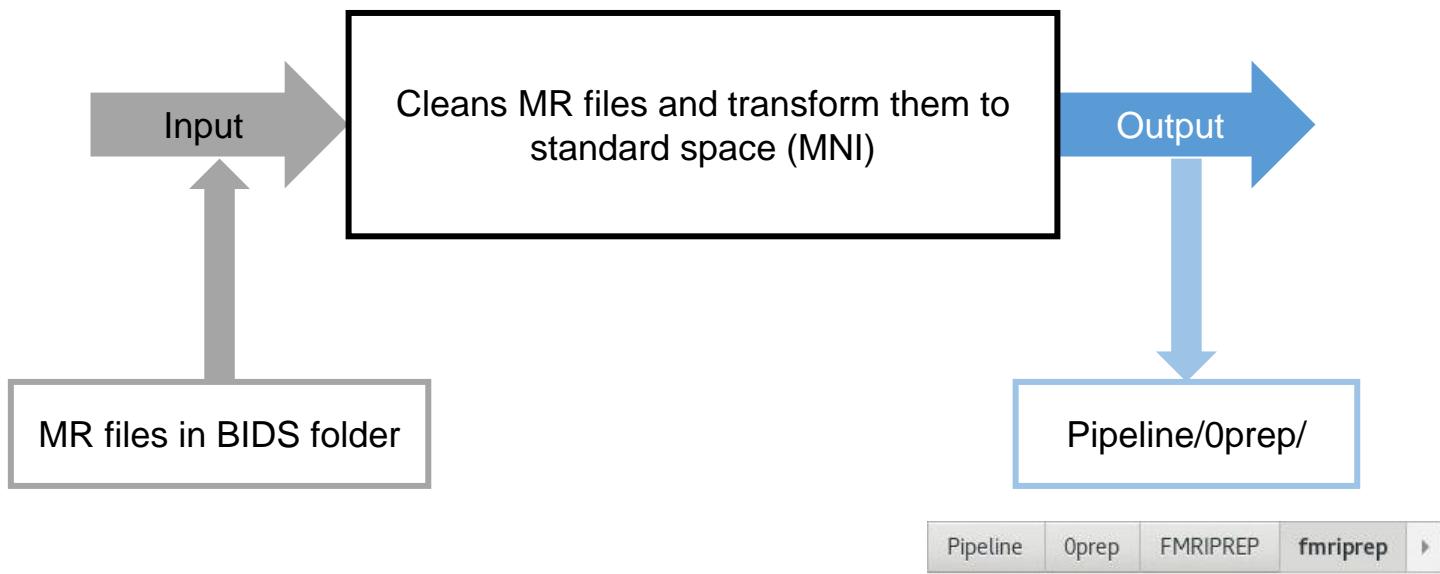
2. Copy the converted MR (T1w) file to corresponding BIDS folder

/project/TIBIR/Lega_lab/shared/lega_ansir/BIDS/sub-UTxxx/anat

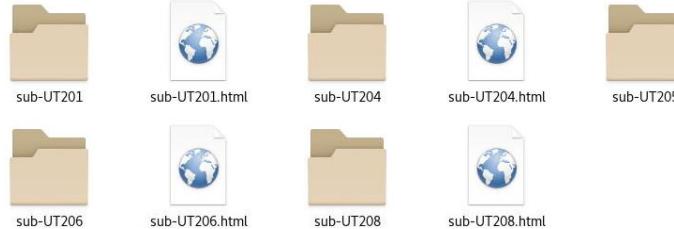


Step 0

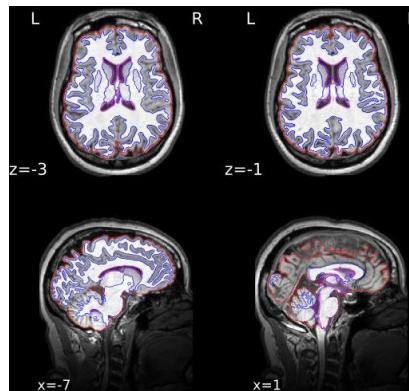
```
>> bash Step0_FMRIPREP.sh UTxxx
```



Step 0: What to Check



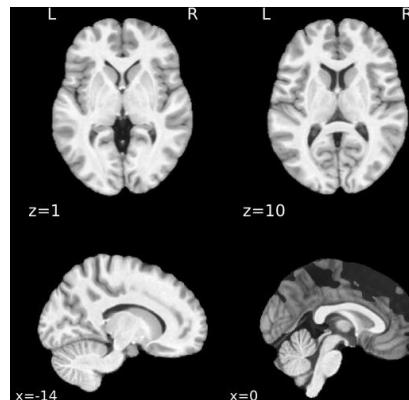
1. Check sub-UTxxx.html if there are no errors



2. Segmentation and brain masking

Errors

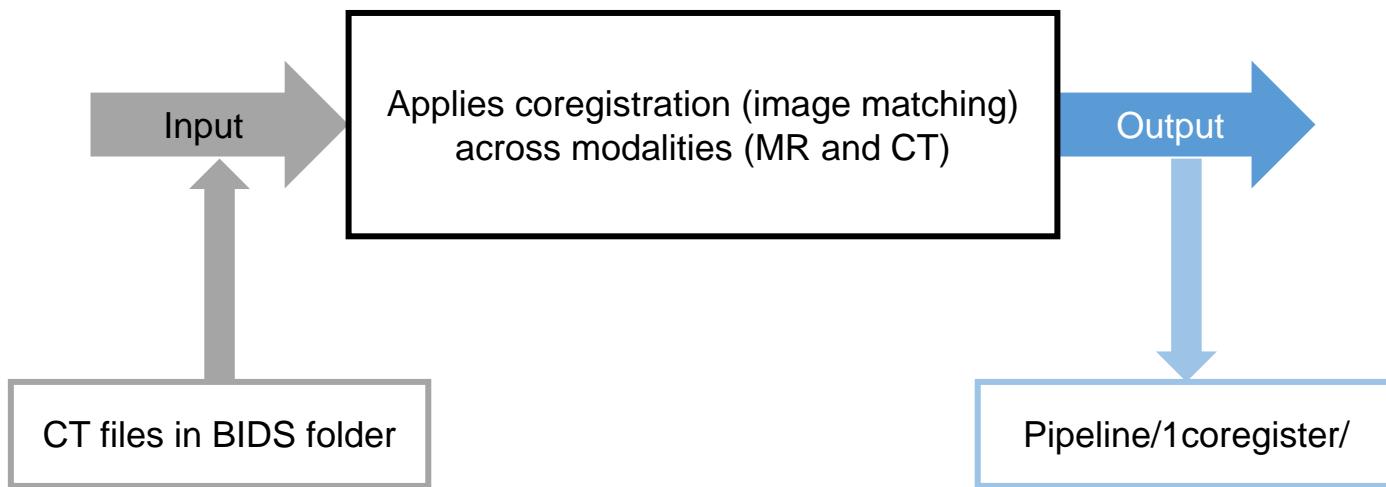
No errors to report!



3. Transformation to standard space (MNI)
Also called “normalization”

Step 1

>> bash **Step1_COREGISTER.sh** UTxxx



* You do not have to check this step

Step 2

* You do not have to run this step but files should be copied in the right folder

/project/TIBIR/Lega_lab/shared/lega_ansir/iEEGxfMRI/Pipeline/2localize/sub-UTxxx

The screenshot shows a file manager window on the left and a Microsoft Teams interface on the right.

File Manager (Left):

- Recent
- Home
- Documents
- Downloads
- Music
- Pictures
- Videos
- Trash
- Modality Crossover
- Reports
- StateMarker
- iEEGxfMRI
- Project

The current path is: project > TIBIR > Lega_lab > shared > lega_ansir > iEEGxfMRI > Pipeline > 2localize > sub-UTxxx

A list of files is shown:

- LB.dat
- LC.dat
- LP.dat
- LV.dat
- LX.dat
- LZ.dat
- RA.dat
- RB.dat

A blue box highlights the LB.dat through RB.dat files.

Microsoft Teams (Right):

1. A blue box highlights the "Freesurfer Localization" team in the "Teams" list.
2. A blue box highlights the "General" channel in the "General" tab of the team's channel list.
3. A blue box highlights the "UT207.zip" file in the "Files" section of the channel.

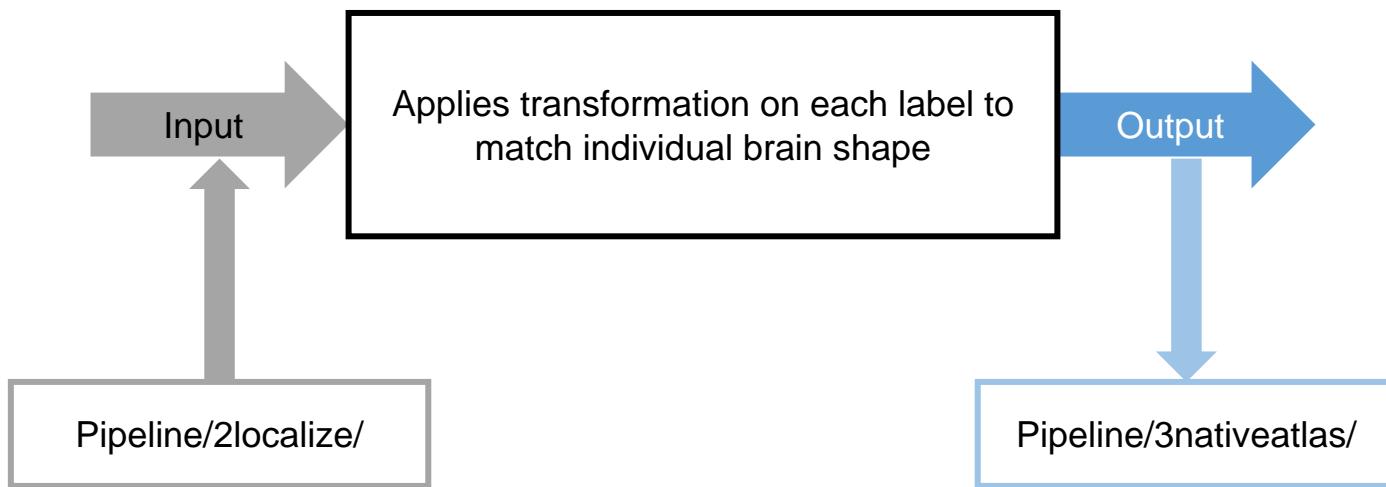
Get these files from Teams

File List (Channel Files):

Name	Modified	Modified By
Older	September 28	Hye Bin Yoo
UT192 MPRAGE Raw DICOM	April 23	Kimberly Larkin
UT207.zip	August 10	Hye Bin Yoo
UT208-SMD-POINTSETS-ALL .zip	August 15	Irina Podkorytova
UT209-GR-POINTSETS-ALL 2.zip	August 22	Irina Podkorytova
UT210-HN-COORDINATES.zip	September 13	Irina Podkorytova
UT211-DJ-COORDINATES.zip	September 7	Irina Podkorytova
UT212-FS-COORDINATES.zip	September 12	Irina Podkorytova
UT213-SJ-COORDINATES.zip	September 22	Irina Podkorytova
UT214-HC-COORDINATES.zip	September 28	Irina Podkorytova

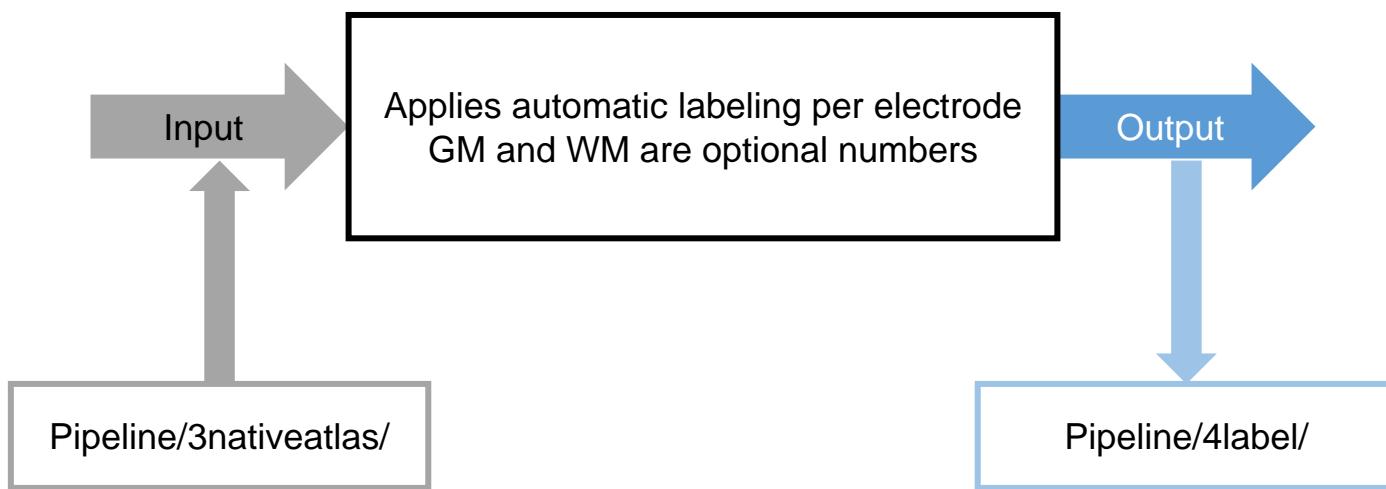
Step 3

>> bash **Step3_NATIVEATLAS.sh** UTxxx



Step 4

```
>> bash Step4_LABEL.sh UTxxx GM WM
```



If GM and WM are empty, default values are 0.75 and 0.1
Generally default values are fine

Step 4: How Output Looks Like

Variables - coordTable

coordTable 86x14 table

	1 Electrodes	2 contacts	3 x	4 y	5 z	6 ROI1	7 ROI1P	8 ROI2	9 ROI2P	10 ROI3	11 ROI3P	12 wm	13 wmP	14 label
1	'LB'	1	-12	1	-21	59	0.9759	39	0.7937	0	0	0	5.4604e-...	"ParaHip...
2	'LB'	2	-18	1	-21	39	0.9942	59	0.3581	0	0	0	1.0298e-...	"LH_Ant...
3	'LB'	3	-24	1	-20	39	0.9904	0	0	0	0	0	7.0721e-...	"LH_Ant...
4	'LB'	4	-30	1	-21	27	0.9922	0	0	0	0	0	0.4988	"Fusiform...
5	'LB'	5	-37	0	-21	87	0.9509	27	0.5472	0	0	0	0.8334	"Tempor...
6	'LB'	6	-43	0	-20	87	0.8980	89	0.7894	0	0	0	0	"Tempor...
7	'LB'	7	-54	-2	-19	87	0.8859	89	0.8508	0	0	0	0	"Tempor...
8	'LC'	1	-16	-11	-21	59	0.9982	40	0.1145	0	0	0	0.4422	"ParaHip...
9	'LC'	2	-21	-11	-20	59	0.9917	40	0.7001	0	0	0	0.8590	"ParaHip...
10	'LC'	3	-26	-11	-19	40	0.9434	59	0.8970	27	0.4135	0	0.5436	"LH_Pos...
11	'LC'	4	-31	-12	-18	27	0.9312	40	0.3745	0	0	0	0.7326	"Fusiform...
12	'LC'	5	-40	-14	-16	89	0.9939	0	0	0	0	0	0.9992	"Tempor...
13	'LC'	6	-45	-14	-15	89	0.9919	0	0	0	0	0	0.9745	"Tempor...
14	'LC'	7	-50	-14	-14	89	0.9883	0	0	0	0	0	0.9523	"Tempor...
15	'LC'	8	-56	-16	-14	89	0.9959	0	0	0	0	0	0.5863	"Tempor...
16	'LC'	9	-59	-16	-13	89	0.9633	0	0	0	0	0	0.0044	"Tempor...
17	'LF'	1	-15	-29	-22	27	0.9125	0	0	0	0	0	0.57555e-...	"Fusiform...

Electrod
e name

Location on
native brain (MR)

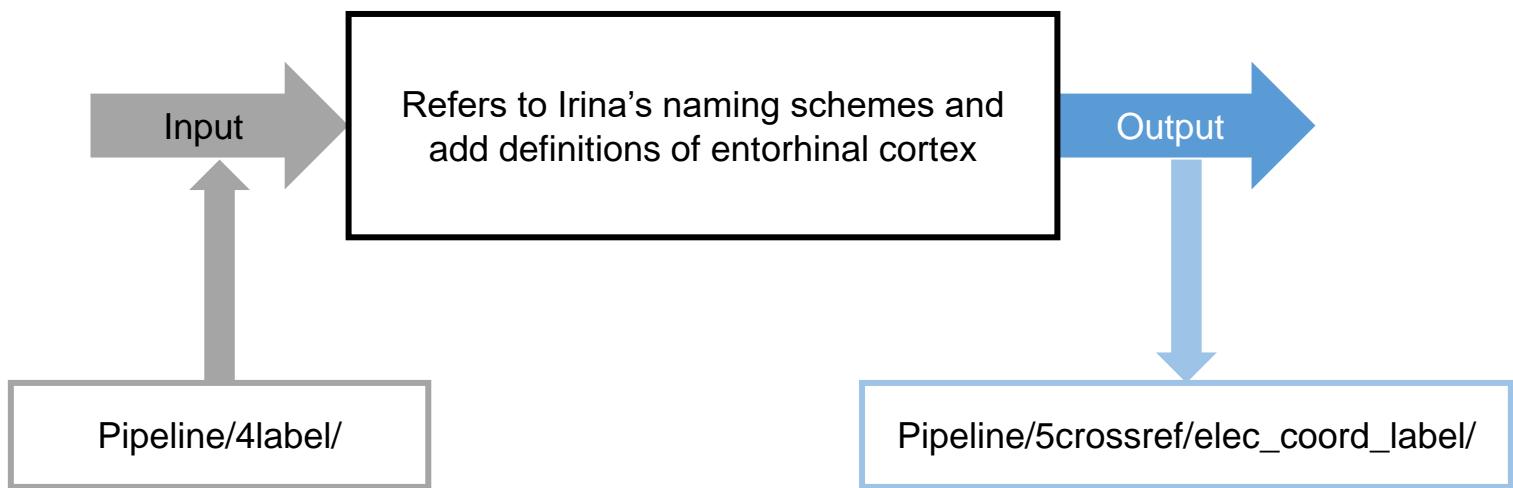
Probability of the most
probable gray matter regions

Label name

Probability of white matter

Step 5

>> bash **Step5_CROSSREF.sh** UTxxx



Step 5. Label ROIs per AAL + Irina Atlas [ANTs and FSL]

Fields	elec	contact	x	y	z	JW	label
1	1	'LB1'	-40	9	-9	'Temporal_Inf_L'	
2	2	'LB2'	-43	9	-9	'Temporal_Mid_L'	
3	3	'LB3'	-46	9	-9	'Temporal_Mid_L'	
4	4	'LB4'	-50	9	-9	'Temporal_Mid_L'	
5	5	'LB5'	-53	9	-10	'Temporal_Mid_L'	
6	6	'LB6'	-56	9	-10	'Temporal_Mid_L'	
7	7	'LB7'	-59	9	-10	'Temporal_Mid_L'	
8	8	'LB8'	[]	[]	[]	'OUT'	
9	9	'LB9'	[]	[]	[]	'OUT'	
10	10	'LB10'	[]	[]	[]	'OUT'	
11	11	'LA1'	-22	19	-4	'L_Amyg'	
12	12	'LA2'	-25	19	-4	'L_Amyg'	
13	13	'LA3'	-28	19	-4	'L_Amyg'	
14	14	'LA4'	-32	19	-4	'L_Amyg'	
15	15	'LA5'	-35	19	-5	'WM'	
16	16	'LA6'	-39	19	-5	'WM'	
17	17	'LA7'	-42	19	-5	'Temporal_Mid_L'	
18	18	'LA8'	-46	19	-6	'Temporal_Mid_L'	
19	19	'LA9'	-50	19	-6	'Temporal_Mid_L'	
20	20	'LA10'	-53	19	-7	'Temporal_Mid_L'	
21	21	'LA11'	-56	19	-7	'Temporal_Mid_L'	
22	22	'LA12'	[]	[]	[]	'OUT'	

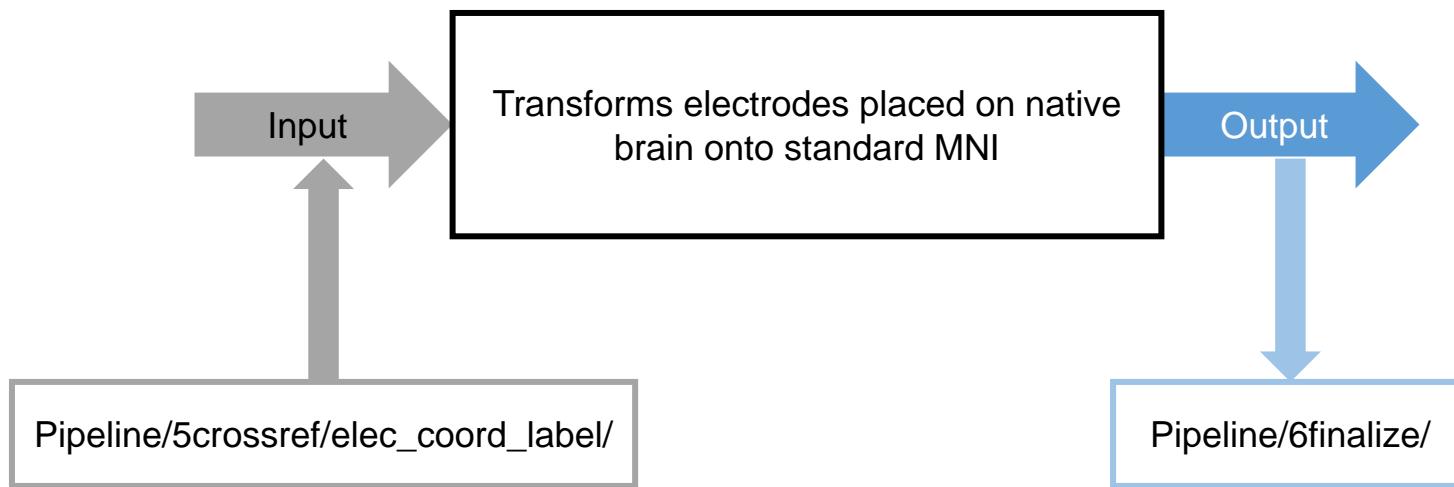
- **elec:** channel # from the jacksheet
- **contact:** unique contact name (L = left, R = right) and contact # (medial to lateral). For example, LA1 is the most medial contact of depth electrode LA, which has 12 total contacts
- **x, y, z:** MNI coordinates on native space (NOT standard space). Do not use these coordinates for plotting across subjects
- **label:** the AAL region label used to classify electrodes across subjects

Label each **electrode** by ROI name defined by AAL atlas and Irina's localization

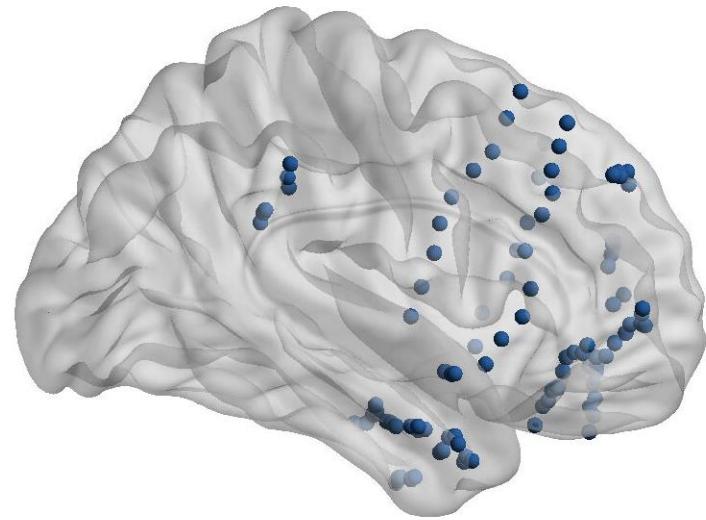
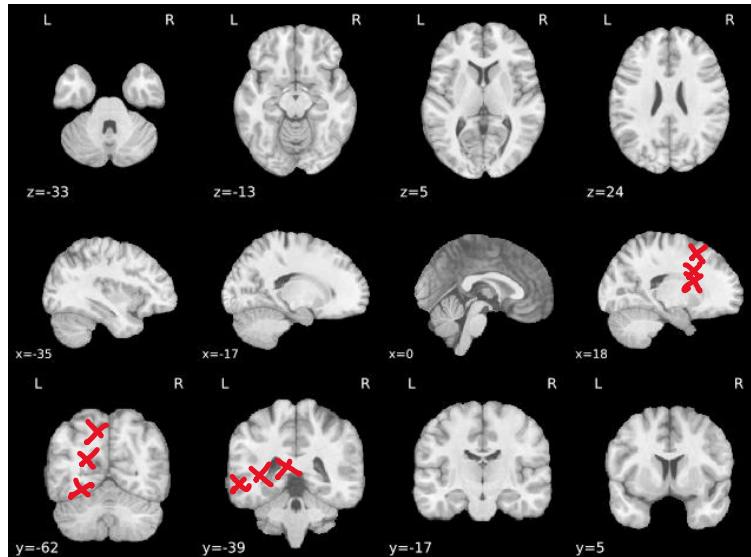
For **electrodes in most medial areas**, we follow Irina's subcortical labels

Step 6

```
>> bash Step6_FINALIZE.sh UTxxx
```

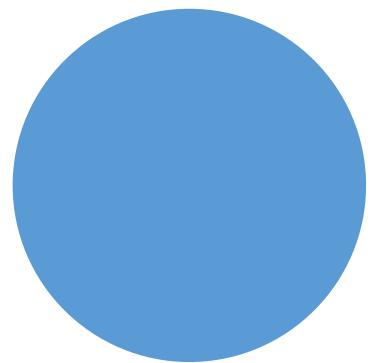


Step 6: What It Does



Move a subjects' brain from NATIVE to STANDARD space

Every coordinate will mean the same geometric location after this process



How-To Guides |
Micros |

How to set up micros testing

(part 1 – setting up the hardware)

Note: When you unplug the cart, it will start beeping. To mute, press the mute button on the power supply on the bottom shelf of the cart.

- Once the cart is in the patient's room, plug in the cart, turn on power switch to cart and to computer
- Get supplies for mastoid ground
 - Tongue depressor with dab of NuPrep (skin prep)
 - Q-tip
 - Alcohol wipes (at least two)
 - EEG pad
- Set up mastoid ground
 1. Clean with alcohol wipe
 2. Use Q-tip to apply skin prep
 3. Clean with alcohol wipe
 4. Attach white cord to EEG pad
 5. Place electrode pad on patient
- Set up headstage
 1. Connect patient electrode wire into headstage
 2. Secure headstage in place with tape (three pieces is good)
 3. Plug in white mastoid ground wire to green receiving port on the headstage
 4. Plug in blue cord (usually ch 1-16) to head stage
 5. Make sure blue light on headstage is ON. If blue light is OFF, try turning the amplifier power OFF/ON or reattaching blue cord
- Set up Jackbox ground
 - Get the green wire ready to plug into channel "z" on Bank A in the patient jackbox bag
 - Remove green wire currently in channel "z" and then quickly plug in our green wire and plug in original green wire so that the two are stacked



How to set up micros testing

(part 2 – computer stuff)

- Log in to micros computer (password is RAM)
- Copy previous patient config and rename to reflect current subject code
- Open Central → File → Load System Settings → select new config (UT...)
- Open Hardware Configuration tab – make sure correct channels are active and correctly labeled
 - *SHIFT* & select all channels you need to rename
 - Channels should match letters on the pigtail tags and jacksheet/cartoon map in binder in EMU
Check for left vs right labels (LB or RB) and anterior/posterior labels (usually B and C, respectively)
- Make sure the number of microwire channels match those implanted in the subject
- Set Signal Specifications
 - Select all channels using the *SHIFT* key
 - Right click and select “Properties”
 - Confirm settings:
 - Enable Line Noise Cancellation checked

How to set up micros testing

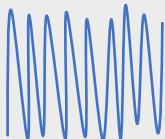
(part 2.5 – more computer stuff)

- Set Signal Specifications
 - Select all channels using the *SHIFT* key
 - Right click and select “Properties”
 - Confirm settings (**picture**):
 - Enable Line Noise Cancellation checked
 - LNC Method set to NSPIF Synch
 - Continuous Acquisition Filter set to HP 250Hz
 - Continuous Acquisition Sampling Rate set to 2 kS/s
 - Raw Data enabled
 - AC Input checked, drop-down menu Disabled
 - Enable Spike Processing checked
 - Spike Processing filter set to HP 250Hz
 - Click OK
 - Raw + spikes+ continuous should now show up on Signal Type
- In Central Window, select File → Save System Settings and replace subject config file created before

How to set up micros testing

(part 3 – troubleshooting)

Raster Plot



Bad



Great!



Okay/Good.

- Verify little blue light is on for each headstage
 - If not, try unplugging/reattaching blue cord or turning the amplifier OFF/ON
- If using both Bank A and Bank B on headstage, make sure Bank A is referenced to Bank B and Bank B is referenced to Bank A
- Try switching Line Noise Cancellation Time Constant from 10 to 1 if signal looks bad
- Try re-referencing channels on a given electrode to one of the more distant channels (e.g. referencing all RD channels to RD8 or RD7) or an earlier channel that doesn't have any units
- Try unplugging the bed and the leg compressors
- Try using a jackbox ground instead of the mastoid ground (i.e. instead of plugging the mastoid ground into the green port on the headstage, plug the green cord that was originally plugged into the amplifier directly into the headstage)

How to set up micros testing

(part 4 – starting the task)

- Once you are happy with the signal (or you have exhausted all troubleshooting options), plug in the Neurofax → micros machine and Neurofax → sync box (sync port on the left)
- Plug in the sync box to the testing laptop
- If running Thief or AR, plug in the controller → laptop
- Open the File Storage tab in Central and change path to reflect current subject “/” name of task
- Open task on testing laptop (e.g. FR1, Thief, etc)
- Stop and start the EEG
- Press “Record” on micros computer
- Start the task
- Once the task is finished,
 1. Stop micros recording
 2. Stop/start EEG

How to grab/upload microelectrode files from the BlackRock

- Make sure you have a large encrypted drive handy – either the LEGA_SUPER drive or the SEEG drive.
- Log in to the BlackRock computer and navigate to the data folder
- Copy the relevant subject/task files onto the external drive
- Most important files for micros are the .ns3 and .ns6 files

For task-specific micros recordings:

Upload the files into the raw folder of a subject's directory on BioHPC with the format:
'MM_DD_YYY_[task_name]_micros'

For no_task_micros (HFO recording):

Upload the files in the following location under the following file structure:
/project/TIBIR/Lega_lab/shared/lega_ansir/HFO_detection/subjects/UT###/
no_task_micros/YYYYMMDD-HHMMSS/raw

RippleLab & HFO Recordings

RIPPLELAB: A Comprehensive Application for the Detection, Analysis and Classification of High Frequency Oscillations in Electroencephalographic Signals

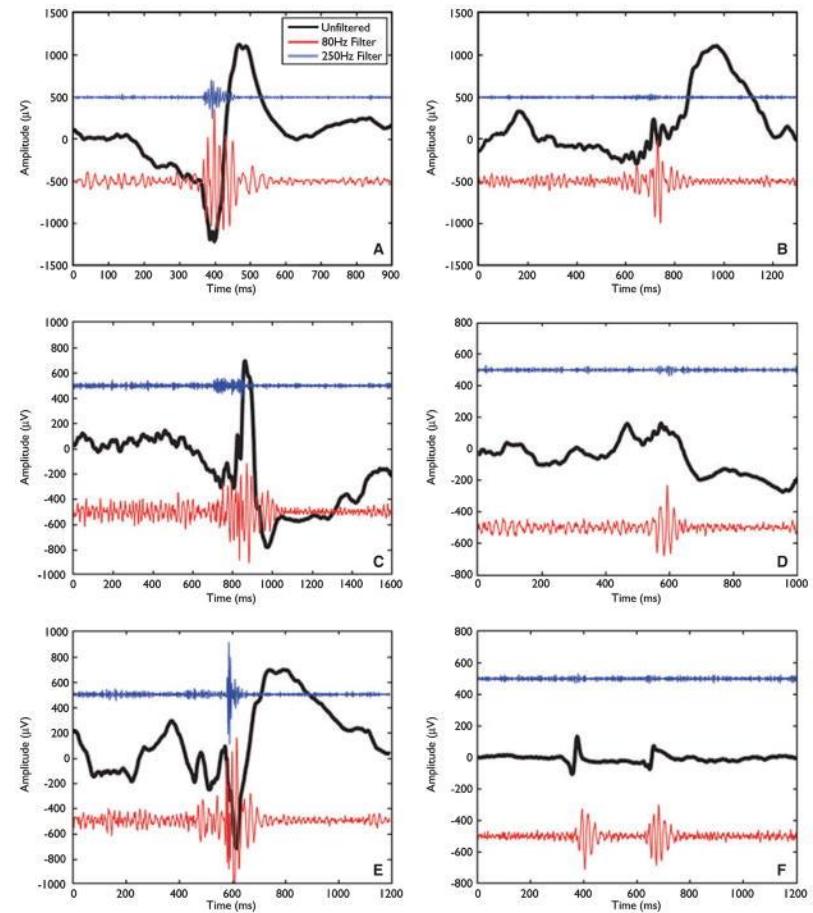
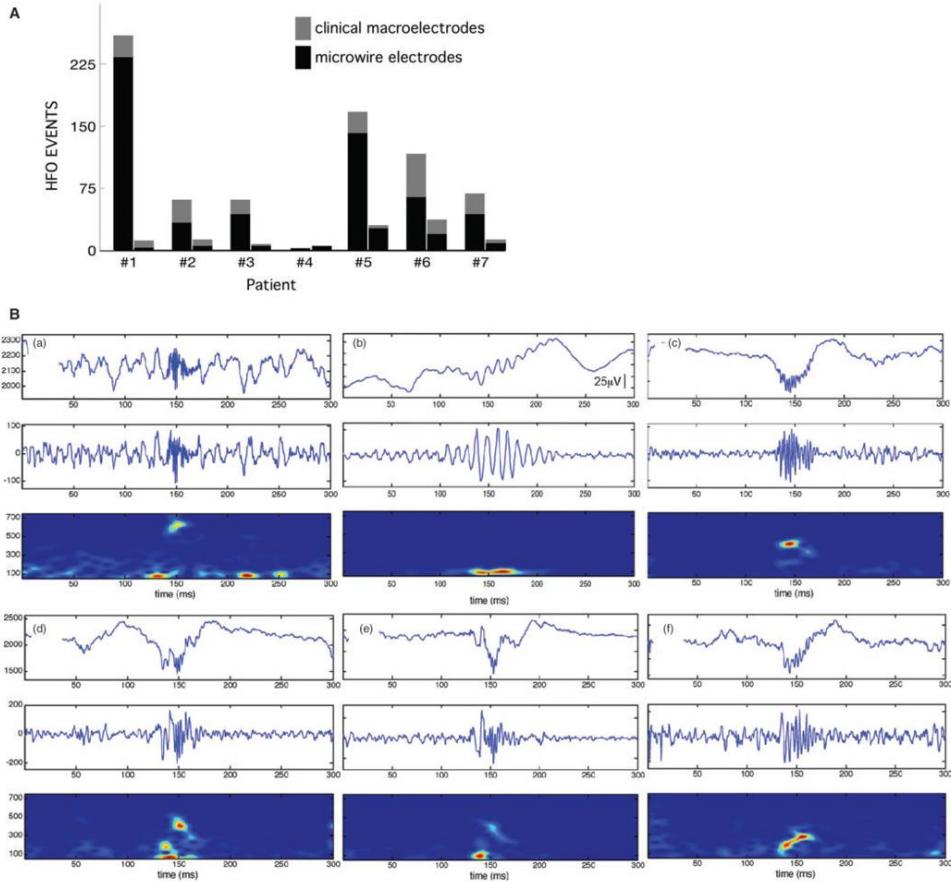
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0158276>

RIPPLELAB is a multi-window GUI developed in MATLAB for the analysis of high frequency oscillations

<https://github.com/BSP-Uniandes/RIPPLELAB>

The RIPPLELAB User Manual can be found under
RIPPLEBLAB/Documents/Help/RIPPLELAB_User_Manual.pdf

Literature examples of HFO Events

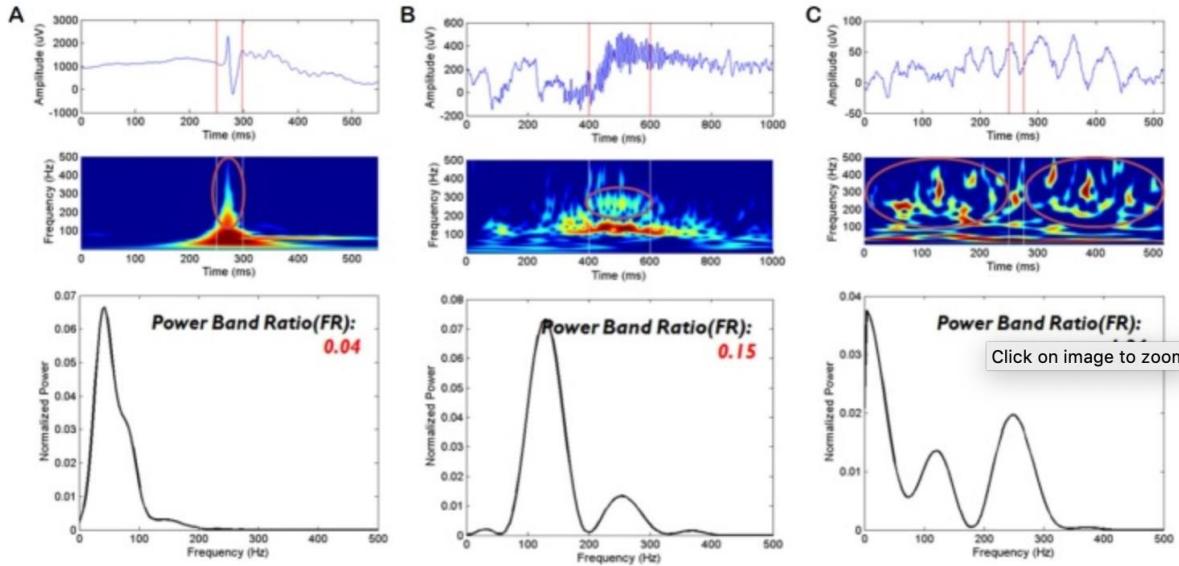


Worrell et al., 2008

Can't remember where I found this one...

Literature examples of Artifacts in HFO Detection

Figure 3



Three types of artifacts are shown. The upper most section is raw data, middle is the time-frequency plot of the same epoch above, and the lower most section is power band ratio plot. (A) Type 1: high-frequency transients due to high-pass filtering of sharp components of interictal epileptiform discharges, i.e., discharges with no visible superimposed fast oscillations in the unfiltered signal and/or with absence of isolated fast activity (“blobs”) in time-frequency decomposition plane. (B) Type 2: harmonics of low-frequency, non-sinusoidal signals. (C) Type 3: transient events with amplitudes larger than the global background but not significantly different from the local activity. Modified from reference [8](#) with permission.



Getting Access & BioHPC How-To

	User	Password
Silver Testing Laptop		Memes!14
Black Host Laptop for RAM	odinuser	MemoryExperiment
Micros cart computer		RAM
Lega Super drive		5323 5323
SEEG drive (small, Apricorn)		legalab
Main Lab		0007
5 th floor of Sprague		07*
CUH EMU		1020#

Accessing the Epilepsy O: drive

First need to request access to the O drive:

NEUROLGY ([\\SWnas\(O:\)\\NEURO](\\SWnas(O:)\\NEURO))

Once you have access, use the following to connect to the server:

smb://swnas.swmed.org/NEUROLOGY/NEURO

Path to access implantation maps and reconstructions for
Epilepsy surgery patients:

NEURO

Epilepsy_O_Drive

Neurophysiology

Test Results

Epilepsy Surgery Patients

Data back-ups

Pegasus

- Folder: rhino_backup
- Script for updating the backup:
 - updateRhinoBackup_rsync_USE.sh
- Terminal will prompt you to enter Rhino username & password
 - Username: alexa.hassien

Promise2

- Folder: lega_ansir_backup
- Before updating lega_ansir backup, make sure project folder is mounted to the computer
- Script for updating the backup:
 - backup_lega_ansir.sh

Command to run backup shell script: >> bash backup_lega_anisr.sh

First, register for a BioHPC account by going to

<https://portal.biohpc.swmed.edu>

From the portal website, you can access the training calendar and register for the next available “Introduction to BioHPC” training (usually held the first Wednesday of each month).

Then send an email to biohpc-help@utsouthwestern.edu requesting access to the lega_ansir folder. If you ever encounter troubles with BioHPC, this is the email to contact them!

The introduction to BioHPC website has guides that are quite comprehensive:

<https://portal.biohpc.swmed.edu/content/guides/introduction-biohpc/>

One of the most important tools for this lab is the Web Visualization tool found under the Cloud Services tab. You can use this GUI to access Matlab from BioHPC.

Common folder paths on the server

Where the lab data is stored:

/project/TIBIR/Lega_lab/shared/lega_ansir

Important folders within lega_ansir are ‘shared_code’ and ‘subjFiles’

Where to save your own data*:

/work/TIBIR/s193084

Where to save a custom MATLAB startup file*:

/home2/s193084

*Just substitute your person number (s#####) for mine

How to set up Lamella (Internal Cloud storage)

Information about Lamella:

<https://portal.biohpc.swmed.edu/content/cloud-services/lamella-storage-internal/>

You can use Lamella to access files in the “project” folder or your “work” folder from your web browser.

Here is the link to access Lamella – log in is the same as BioHPC

<https://lamella.biohpc.swmed.edu/index.php/login>

To connect the work and project folders to Lamella, use the instructions on the next slide.

Go to your settings

How to connect your work and project folders to Lamella:

The screenshot shows the 'External storages' configuration page in Nextcloud. On the left, a sidebar lists 'Personal info', 'Security', 'Activity', 'External storages' (which is selected), 'Mobile & desktop', 'Accessibility', 'Sharing', and 'Privacy'. The main area is titled 'External storages' and contains instructions about enabling external storage services. Below this, there are two entries in a table:

Folder name	External storage	Authentication	Configuration
home	BioHPC/Lysosome	Log-in credentials, save in database	✓
Cloud	Cloud	Log-in credentials, save in database	✓

Step 1 (orange circle at top right): Click on the 'A' icon in the top right corner to go to your settings.

Step 2 (orange circle): Click on 'External storages' in the sidebar.

Step 3 (orange circle): Add the name of the folder (e.g., 'work') in the 'Folder name' field.

Step 4 (orange circle): Select 'BioHPC/Lysosome' from the 'External storage' dropdown and choose 'Username and password' from the 'Authentication' dropdown.

Step 5 (orange circle): Enter the 'Username and password' (e.g., 'TIBIR/s193084' and 's193084') in the respective fields.

Step 6 (orange circle): Repeat the process for the 'project' folder.

Enter the:

- 1) Name of folder
- 2) Path to folder
- 3) Username
- 4) password

Where the lab data is stored:

/project/TIBIR/Lega_lab/shared/lega_ansir

To access BioHPC and start a Web Visualization Session:

1. First go to portal.biohpc.swmed.edu (*note you need to be on the UTSW network, either on campus or by VPN to access full portal homepage)
2. Log in using your UTSW ID number and BioHPC password
3. Go to Cloud Services, then select Web Visualization
4. Download TurboVNC if it is not downloaded already
5. Launch a new WebGUI – Basic GUI and use TurboVNC to access the session

The screenshot shows the BioHPC User Portal homepage. At the top, there is a header with the UTSW logo, the BioHPC logo, and user information: 'Comment on this page' and 'Logged in as: s193084'. Below the header is a navigation bar with links: Home, News, About, Status, Training, Guides, FAQs, Cloud Services (which is highlighted with a red box), BioHPC OnDemand, Software, and Careers. The main content area features a banner for a 'Monthly Online Webinar: Introduction to BioHPC – Training for New Users'. To the left of the banner is a graphic with the letters 'TRAIN' in blue. The banner text describes the webinar's purpose and content. Below the banner, the text 'Welcome to the BioHPC User Portal' is displayed, along with various system status metrics like 'Nucleus Queue' (366 pending, 273 running), 'Nodes Available' (26 GPU, 70 super), and 'Quota Usage' for different storage paths.

Welcome to the BioHPC User Portal

Nucleus Queue: 366 jobs pending 273 jobs running Nodes Available: 26 GPU 70 super Quota Usage: /home2 1 / 50 GB /work 2,380 / 5,120 GB /project 10,693 / 30,720 GB

Recently Top Used Modules: matlab gcc trimgalore python R

BioHPC is hiring - Do you want to work in HPC at UT Southwestern? See our [Careers Page](#)

Learn more about BioHPC membership. [View our Business Plan](#)

How to use modules in a BioHPC Web Visualization Session:

- 1) Go to Applications, open a Terminal Window
- 2) You can type (>> module avail) to view a list of all current available modules
- 3) Here's a few common modules and how to load them:

```
>> module load matlab/2018b
```

```
>> matlab
```

```
>> module load mrictc/v1.0.20190902
```

```
>> MRICron
```

```
>> module load combinato/20200804
```

```
>> css-gui
```

*** Note: Make sure the piece of code (with lockfiles) you are trying to run as well as the batch scripts are added to your path in your MATLAB startup.m file in your home folder.

How to run code using the cluster

You need:

- **Your piece of code** that has infrastructure for “lock files” so that the multiple computers running the code can divide and conquer.
- **Shell scripts** – need to be in the same folder as each other, must be in your path on matlab.
 - “matlabWrapper.sh”
 - “srun.sh”
- Once you have those, open a new tab on the terminal in your web visualization session, **type the following:**
 - sbatch /path/to/srun.sh
 - Example: sbatch /work/TIBIR/s193084/pyFRstim_code/srun_NeuralDrift.sh
- Then check the BioHPC homepage and you should see your submitted job

Nucleus Job Queue

Current Queue Status: 16 jobs pending 277 jobs running 0 jobs suspended 0 jobs completing

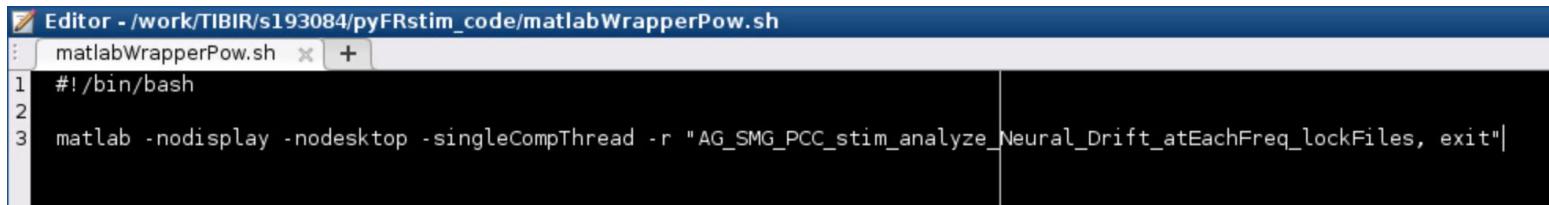
You have 2 jobs submitted to the BioHPC Nucleus cluster:

[Click to view full job queue](#)

Job ID	User	Partition	#CPUs	Job Name	Submit Time	Start Time	State	
2191853	s193084 (Alexa Hassien, Dr. Bradley Lega, Neurological Surgery)	32GB	32	webGUI	Thu Feb 25 08:13:34	Thu Feb 25 08:13:34	RUNNING	
2191976	s193084 (Alexa Hassien, Dr. Bradley Lega, Neurological Surgery)	super	224	save_pVal_shuffle	Thu Feb 25 09:33:13	Thu Feb 25 09:33:14	RUNNING	

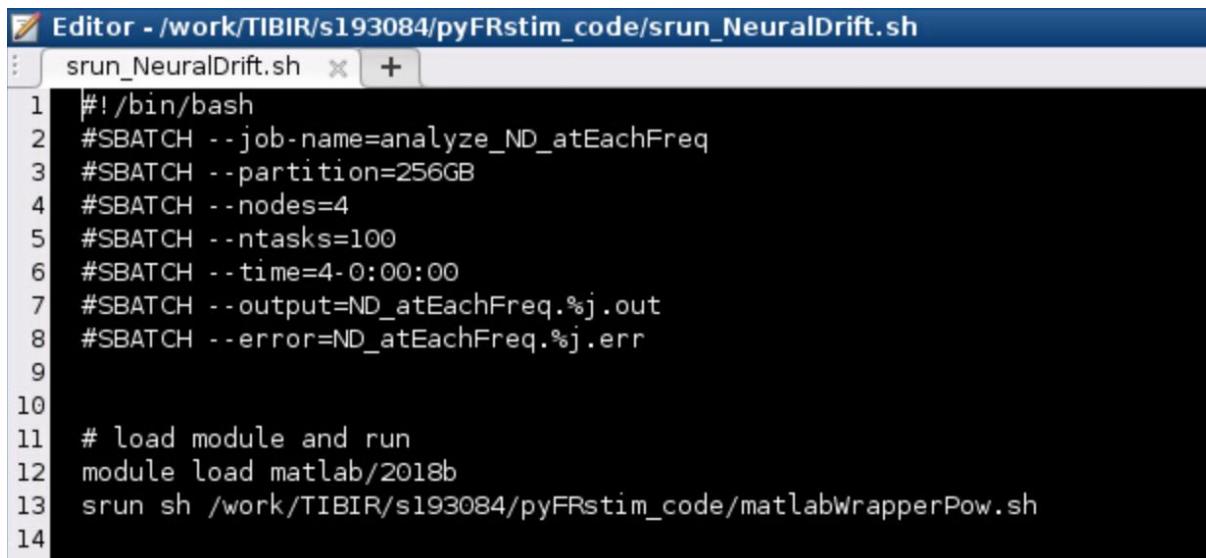
Shell scripts examples:

- “matlabWrapper.sh”



```
Editor - /work/TIBIR/s193084/pyFRstim_code/matlabWrapperPow.sh
matlabWrapperPow.sh  + 
1 #!/bin/bash
2
3 matlab -nodisplay -nodesktop -singleCompThread -r "AG_SMG_PCC_stim_analyze_Neural_Drift_atEachFreq_lockFiles, exit"
```

- “srun.sh”



```
Editor - /work/TIBIR/s193084/pyFRstim_code/srun_NeuralDrift.sh
srun_NeuralDrift.sh  + 
1 #!/bin/bash
2 #SBATCH --job-name=analyze_ND_atEachFreq
3 #SBATCH --partition=256GB
4 #SBATCH --nodes=4
5 #SBATCH --ntasks=100
6 #SBATCH --time=4-0:00:00
7 #SBATCH --output=ND_atEachFreq.%j.out
8 #SBATCH --error=ND_atEachFreq.%j.err
9
10
11 # load module and run
12 module load matlab/2018b
13 srun sh /work/TIBIR/s193084/pyFRstim_code/matlabWrapperPow.sh
14
```

SMILE

Installing SMILE:

- 1) Make sure python3 is installed
- 2) Install kivy (using conda preferably)
- 3) Install pyo, wxpython
- 4) Install libusb, libsndfile
- 5) Make sure the pennsyncbox code and .so file are in the smile folder (under site-packages)
- 6) Download smile package from <https://smile-docs.readthedocs.io/en/latest/>
- 7) Navigate to the smile-master folder
- 8) Use the following command to install smile:
`python3 setup.py install`

Some audio settings to double-check.

*** Make sure you always run smile experiments from Terminal. If you don't use Terminal, the Mac task laptop will not have access to the microphone. Then all the .wav file outputs will have no sound. ***

SMILE Audio: Recording Sound Files

*** Make sure you always run smile experiments from Terminal. If you don't use Terminal, the Mac task laptop will not have access to the microphone. Then all the .wav file outputs will have no sound. ***

Check to make sure that the number of channels = 1 (single channel audio) and the sampletype = 0 (16-bit audio). PennTotalRecall requires 16-bit audio.

You can find this code in the smile library's audio.py

```
def _start_recording(self):
    self.__rec = pyo.Record(
        pyo.Input(), filename=self._filename, chnls=1, fileformat=0,
        sampletype=0, buffering=16)
    self._rec_start = clock.now()
```

For further info about pyo audio, see the following resources:

- <http://ajaxsoundstudio.com/pyodoc/api/classes/utils.html>
- <http://ajaxsoundstudio.com/pyodoc/api/classes/server.html>

Useful Contact Information

UT Southwestern

Brad Lega – the head honcho

Bradley.Lega@UTSouthwestern.edu

Office: ext 87816

Cell: (713) 834-2497

Irina Podkorytova – neurologist who we contact frequently to monitor stim experiments

Cell: (216) 212-7689

Betsy Robertson – Neurosurgery department administration - contact about timesheets, timekeeping, etc.

Betsy.Robertson@UTSouthwestern.edu

Scott Clamp – Neurosurgery department administration - contact about technology or equipment questions

Scott.Clamp@UTSouthwestern.edu

(if in the lab, press 9 first)

CUH EMU

(214) 633-3832

Parkland EMU

(469) 419-4999

Big Room in the Lega Lab

H1.104

(214) 648 – 2332

or Ext 82332

password for voicemail:

53235323

Useful Contact Information (continued)

UPenn Computational Memory Lab

General contact for Penn testing:

kahana-clinical@sas.upenn.edu

Evan Snyder – Clinical Research Assistant

evsnyder@sas.upenn.edu

Cell: (484) 919-5994

Joseph (Joey) Rudoler – Clinical Research Assistant

jrudoler@sas.upenn.edu

Cell: (610) 787-1831

UTSW Hospital Emergency Codes

Code	Meaning
Code Red	Fire
Code Blue	Cardiac Arrest
Code Gray	Severe Weather
Code Black	Tornado (Take Cover)
Code Pink	Child Abduction
Code Yellow	Levels I-IV
Code Rush	Violence
Code Silver	Violence with a Weapon