**Data Processing**

See ‘D:\Depth electrode github example\Rat\_055\Data processing’ on harddrive or ‘eit-nas/shared/Mayo Depth electrode github example\Rat\_055\Data processing’ on eit-nas for example of output from various steps

1. **Process raw data normal data collection mode**

Overview

Processing code for Actichamp and Biosemi data using normal data collection mode. Data was collected for 8-10 repeats with source and sink switched every 30s

Code/files required

1. biosemi\_process.m
2. actichamp\_process.m
3. get\_switching\_time.m
4. get\_carrier\_freq.m
5. filter\_data.m
6. segment\_data.m
7. compute\_averages.m
8. chns\_actichamp.m
9. ScouseTom\_TrigView (‘Load-Data repository github)

Input

1. Lines 1 – 2 – change to point to correct file and directory

Ouput

1. EIT – averaged data for every repeat
2. EIT\_avg – averaged data across repeats (in my case 8 – 10)
3. Within EIT or EIT\_avg
   * dZ\_avg – impedance change
   * EP\_avg – evoked potential
   * Pair – injection pair
   * dZ\_per – impedance change in percentage
   * dZ\_std – standard deviation of impedance change across trials
   * BV0 – standing voltage on electrodes
4. Channels 1-16 are the data from the anterior depth probe
5. Channels 17-32 are the data from the posterior depth probe
6. Channels 33-64 are the data from cortical array 1 (the more posterior placed array with 27 channels) (also includes non-connected channels)
7. Channels 65-96 are the data from cortical array 2 (the more anterior placed array with 20 channels) (also included non-connected channels)

Notes

1. Can change filter settings Lines 25 – 30
2. Can change time used for baseline – Line 41 in compute\_averages.m
3. **Process raw data stim nostim mode**

Overview

Processing code for biosemi when collect data with raw EEG, EIT no stimulation and then EIT with stimulation for every injection pair

Code/files required

1. biosemi\_process.m
2. filter\_data.m
3. segment\_data.m
4. compute\_averages.m
5. ScouseTom\_TrigView (‘Load-Data repository github)

Input

1. Lines 1 – 8 – change to point to correct file and directory
2. Line 18-19 – this is changed manually (should make it so it detects is automatically)
3. Line 84 – make is point to correct file with ExpSetup
4. Line 112 – this is because whisker stimulator was set to change every 500 ms. So we are averaging back and forward triggers.
5. Line 113 and 115 – these are the trials that coincided with phase resyncing for the forward and backward deflection.

Ouput

1. EIT – averaged data for every repeat
2. EIT\_avg – averaged data across repeats (in my case 8 – 10)
3. Within EIT or EIT\_avg
   * dZ\_avg – impedance change
   * EP\_avg – evoked potential
   * Pair – injection pair
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4. Channels 1-16 are the data from the anterior depth probe
5. Channels 17-32 are the data from the posterior depth probe
6. Channels 33-64 are the data from cortical array 1 (the more posterior placed array with 27 channels) (also includes non-connected channels)
7. Channels 65-96 are the data from cortical array 2 (the more anterior placed array with 20 channels) (also included non-connected channels)
8. **Mapping depth data**

Overview

Map depth electrode data from output from Biosemi or Actichamp to the numbering used for forward solver

Code/files required

1. map\_channels\_depth\_electrodes.m
2. EIT\_avg.mat
3. depth\_recording\_map.mat
4. Protocol\_map.mat - mapped injection protocol from experiments (see forward preparation document)

Input

1. Line 1 -2 – change so they point to the file containing Prot\_map and the depth\_recording\_map.mat
2. Line 8 – change to number of depth electrodes

Output

1. dZ\_sorted – concatenated and mapped impedance changes for all protocol lines
2. BV\_sorted – concatenated and mapped BV for all protocol lines
3. keep\_sorted – index with channels used for current injection

Notes

1. The recording map is for the arrangement of electrodes that I used and the way they have been allocated in the forward solver (see pos\_depth.mat for example of numbering for forward solver)
2. **Mapping cortical data**

Overview

Map cortical electrode data from output from Biosemi or Actichamp to the numbering used for forward solver

Code/files required

1. map\_channels\_cortical\_electrodes.m
2. EIT\_avg.mat
3. cortical\_recording\_map.mat
4. Protocol\_map.mat - mapped injection protocol from experiments (see forward preparation document)

Input

1. Line 1 -2 – change so they point to the file containing Prot\_map and the depth\_recording\_map.mat
2. Line 8 – change to number of channels you have recorded from on cortical electrodes (64). The fact that there are only 47 actual channels is dealt with in the mapping

Output

1. dZ\_sorted – concatenated and mapped impedance changes for all protocol lines
2. BV\_sorted – concatenated and mapped BV for all protocol lines
3. keep\_sorted – index with channels used for current injection

Notes

1. Depending on how you have processed your data i.e whether you have saved the depth and cortical data together the index of channels for the cortical data will change in lines 17 and 34 (will be 1:n\_chan when separately or 33:n\_chan+32 when together)
2. If you have saved them separately, take 32 away from all values in Protocol\_map as this has assumed first 32 channels are for depth electrodes.
3. The recording map is for the cortical arrays I used and the way in which I have defined their positioning (see pos\_cortex.mat for an example of numbering for forward solver)
4. **Remove noisy channels**

Overview

All disconnected channels have been removed during the mapping and all injection channels are accounted for in keep\_sorted. However, there may still be some noisy channels. These are removed by looking at standard deviation of baseline

Code/files required

1. remove\_bad\_channels\_std.m
2. dZ\_sorted, keep\_sorted from previous step 3 or 4

Input

1. Change standard deviation level in line 2 to what is appropriate for data

Output

1. Updated keep\_sorted with noisy channels removed
2. **Reduce number of samples in data**

Overview

Reduce the number of samples in the data so that we don’t reconstruct too many redundant time points.

Code/files required

1. decimate\_data.m
2. dZ\_sorted, keep\_sorted, BV\_sorted from previous steps

Input

1. Line 2 – change sampling frequency to sampling frequency at which data was collected
2. Line 5 – I have decimated by a factor of 5 (change if you want to decimate more or less)
3. Line 8 – I applied a 500 Hz BW to extract impedance change so have low passed at 500 Hz
4. Line 14 – my definition of time was symmetrical about the trigger (i.e 250 ms before 250 ms after) Make this T consistent with what is output when you process the raw data (steps 1 or 2)

Output

1. EIT\_RatXX\_depth\_data – final data that needs to be used for reconstruction
   * dZ\_filt – decimated impedance change
   * T\_filt – decimated time interval
   * BV – same as BV\_sorted just renamed
   * Keep – same as keep\_sorted just renamed
2. Or EIT\_RatXX\_cortex\_data.mat
3. **Put cortex and depth data together**

Overview

When you want to reconsctruct the data from the depth and cortex simultaneously when using tikhonov 0, need to put data in same format as output from forwad

Code/Files required

1. concatenate\_depth\_protocol.m
2. EIT\_depth\_data.mat
3. EIT\_cortex\_data.mat

Input

1. Lines 2 – 5 – change to the number of protocol lines and number of electrodes used in depth and cortex

Output

1. Data in format for reconstruction (type = 4 in recon\_depth\_probes\_tik0.m)