Useful plotting tools

create\_plot\_across\_injection.m

1. **create\_plots\_BV.m**

Overview

Plots the BV distribution on the depth probes. Useful for checking which injection pairs maximise the BV on recording electrodes

Code/files required

1. Protocol\_depth.mat (unmapped protocol from experiment)
2. EIT\_depth\_all.mat (data with EIT\_avg)
3. chns\_matlab

Input

1. Line 1-2 – change the paths
2. Line 56 – if you want to save each figure automatically

Output

1. See create\_plots\_BV\_output\_example.png for example
2. **create\_plots\_BV\_normalise.m**

Overview

Plots the BV distribution on the depth probes normalized to injecting electrodes. Useful for checking which injection pairs maximise the BV on recording electrodes

Code/files required

1. Protocol\_depth.mat (unmapped protocol from experiment)
2. EIT\_depth\_all.mat (data with EIT\_avg)
3. chns\_matlab

Input

1. Line 1-2 – change the paths
2. Line 56 – if you want to save each figure automatically

Output

1. See create\_plots\_BV\_normalise\_output\_example.png for example
2. **create\_plots\_within\_injection.m**

Overview

Creates plot of dZ and EP on both probes for each injection pair. Injecting electrodes are denoted by red lines

Code/files required

1. Protocol\_depth.mat (unmapped protocol from experiment)
2. EIT\_depth\_all.mat (data with EIT\_avg)
3. chns\_matlab

Input

1. Line 1-2 – change the paths
2. Line 114 and 195 – if you want to save each figure automatically
3. Line 7 – 19 – change depending on whether data is from Biosemi or Actichamp

Output

1. See create\_plots\_within\_injection\_output\_probe1\_example.png and create\_plots\_within\_injection\_output\_probe2\_example.png
2. **create\_plots\_one\_injection.m**

Overview

Creates plot of dZ and EP on each electrode across all protocol lines. When the electrode is injecting it is denoted by a red line

Code/files required

1. Protocol\_depth.mat (unmapped protocol from experiment)
2. EIT\_depth\_all.mat (data with EIT\_avg)
3. chns\_matlab

Input

1. Line 1-2 – change the paths
2. Line 118 and 208 – if you want to save each figure automatically
3. Line 7 – 19 – change depending on whether data is from Biosemi or Actichamp

Output

1. See create\_plots\_one\_electrode\_output\_probe1\_example.png

Notes

1. At the moment can only display up to 20 protocol lines at a time
2. **create\_plots\_across\_injection.m**

Overview

Creates plot of dZ and EP averaged across all injection pairs on depth probes. Useful to understand where the activity is distributed.

Code/files required

1. Protocol\_depth.mat (unmapped protocol from experiment)
2. EIT\_depth\_all.mat (data with EIT\_avg)
3. chns\_matlab

Input

1. Line 1-2 – change the paths
2. Line 97 and 137– if you want to save each figure automatically
3. Line 7 – 19 – change depending on whether data is from Biosemi or Actichamp
4. Line 57 – remove injections with really high standard deviation (change this value if you don’t want them removed)

Output

1. See create\_plots\_across\_injection\_dZ\_output\_example.png and create\_plots\_across\_injection\_EP\_output\_example.png
2. **create\_plots\_across\_injection\_cortical1.m**

Overview

Creates plot of dZ and EP averaged across all injection pairs on first cortical array (cortical1). Useful to understand where the activity is distributed.

Code/files required

1. Protocol\_cortex.mat (unmapped protocol from experiment)
2. EIT\_cortex\_all.mat (data with EIT\_avg)
3. chns\_cortex

Input

1. Line 1-2 – change the paths
2. Line 96 and 141– if you want to save each figure automatically
3. Line 7 – 19 – change depending on whether data is from Biosemi or Actichamp
4. Line 55 – remove injections with really high standard deviation (change this value if you don’t want them removed)

Output

1. See create\_plots\_across\_injection\_cortical1\_dZ\_output\_example.png and create\_plots\_across\_injection\_cortical1\_EP\_output\_example.png
2. **create\_plots\_across\_injection\_cortical2.m**

Overview

Creates plot of dZ and EP averaged across all injection pairs on second cortical array (cortical2). Useful to understand where the activity is distributed.

Code/files required

1. Protocol\_cortex.mat (unmapped protocol from experiment)
2. EIT\_cortex\_all.mat (data with EIT\_avg)
3. chns\_cortex

Input

1. Line 1-2 – change the paths
2. Line 96 and 139– if you want to save each figure automatically
3. Line 7 – 19 – change depending on whether data is from Biosemi or Actichamp
4. Line 59 – remove injections with really high standard deviation (change this value if you don’t want them removed)

Output

1. See create\_plots\_across\_injection\_cortical2\_dZ\_output\_example.png and create\_plots\_across\_injection\_cortical2\_EP\_output\_example.png