all the stuff for plotting:

```
% functions needed: fread3.m, plot3_wrapper.m, plotsurf_wrapper.m,
read_surf_wrapper.m,
% read_surf.m, render_freesurfer_3D.m
% variables needed:  BRAIN_SCHEME.mat

load('BRAIN_SCHEME.mat'); % has what we need to plot a pretty brain without
                          % going to Gold
vL = BRAIN_SCHEME{1};vR = BRAIN_SCHEME{3};
fL = BRAIN_SCHEME{2};fR = BRAIN_SCHEME{4};

hold on;plotsurf_wrapper(vL, fL, [0.7, 0.7, 0.7]);
axis('off'); view(-90,0); camlight; zoom(1.4);
plotsurf_wrapper(vR, fR, [0.7, 0.7, 0.7]);
set(gca,'FontSize',20)

% You'll have to zoom out and choose your view
```

all the IP time things

% variables needed: patients.mat, IPtime2.mat

load('patients.mat') %key of patient identifiers
load('IPtime2.mat')

IPtime2

IPtime2 =

  Map with properties:

      Count: 139
    KeyType: char
  ValueType: any

IPtime2(patients{1})

ans =

  struct with fields:

   ip_all: [72×6×44 double] %72 electrodes, 6 frequency bands, 44 time points average
over all words
   ip_for: [72×6×44 double] % average over only forgotten words
   ip_rec: [72×6×44 double] % average over only recalled words

all the locations

% all_BA = Brodmann Areas for all electrodes. all_BA(patients{1}) will give all electrode brodmann
% areas for patient 1
% all_loc = coordinates for all electrodes. all_loc(patients{1}) will give all electrode [x y z] for patient 1
% hemispheres = Hemisphere for all electrodes. hemispheres(patients{1}) will give binary output for% hemisphere (1=Left, 0=Right) for all electrodes for patient 1

<u>Active or Inactive</u>

FINAL_AE2.mat has binary values for whether an electrode is active (1) or inactive (0).
Call a specific patient by typing FINAL_AE2(patients{1}).

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