What is changing when: Decoding visual information in movies from human intracranial recordings

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neurophysiology_data_exp1 – Contains physiology data from experiment 1

- Folder for each subject
- Sub-folder for each recording session. Data from different recording sessions were merged in the paper. IFP recordings have been shown to be stable across recording sessions (Bansal et al., 2012).
- Within each session folder, there are 4 files:
 - \circ movie_trials_bb.mat broadband voltage signals [μ V] (filtered from 0.1-100 Hz)
 - movie_trials_hg.mat high gamma frequency band signals (70-120 Hz)
 - movie_trials_lg.mat low gamma frequency band signals (30-70 Hz)
 - movie_trials_alpha.mat alpha frequency band signals (8-15 Hz)
- Each file contains 3 data variables: 1 for responses to each movie (mov1_filt_bb, mov2_filt_bb, mov3_filt_bb)
 - cell array length # trials per session
 - Each cell is #channels x time points data matrix. Each point in the matrix represents the voltage in microVolts (in the case of the broadband signals) or normalized power (in the case of the high gamma, low gamma, alpha signals) at each time point.
- Each file also contains variable sr, denoting sample rate in Hz.
- scripts/plot_fig2.m will format the data in a matrix and generate the plots in Figure 2

movie_data_exp1 – contains the 12s clip movies from experiment 1

- mov1.mat, mov2.mat, mov3.mat frame data for the three 12-s clip movies
- movie_event_times.mat contains cell arrays for the movie cut times in each clip.

eyetracking_data_exp1 -post-hoc eye tracking data for 7 subjects (a1-a7):

- Each subjects' file contains the following variables:
 - \circ frames
 - eye_targets, x (row 1) and y (row 2) positions of each eye in screen coordinates.
 - Saccades vector of time length indicating whether there was a saccade (1) or not (0) at each time
 - Blinks vector of time length indicating whether there was a blink (1) or not (0) at each time
 - screen_coords screen size
 - t_transitions_on movie onset times
 - t_transitions_off movie offset times
 - clips_list list of the five 12s movie clip names that were shown, Note: mov1a.mat, mov2a.mat, and mov4a.mat correspond to movies 1,2, and 3 in our physiology experiment
 - pseudoorder order in which the movie clips were presented

• scripts/plot_figs1.m loads the data for all subjects and generates the plots in Figure S1

neurophysiology_data_exp2 – contains physiology data from experiment 2

- For each subj and freq band there is a file
- <subjID>_movie_rasters_<freq> folder contains the data for each subject/frequency band
- Within this folder there is one file per recording channel, containing the following variables:
 - raster_data cuts x time points data file (time points span -500:2000 ms relative to cut onset, so there are 1250 time points for two subjects with sr of 500 Hz, and 5000 for subjects with sr of 2kHz).
 - raster_labels contains field 'faces' with 1/0/-1 indicating whether there was a single face on the screen, no faces on the screen, or other
 - raster_site_info channel #
 - raster_data_rand cuts x time points movie data, aligned to random inter-cut periods
- scripts/plot_fig6.m will format the data and generate the plots in Figure 6
- For more details on the raster_data format and for decoding code, visit readout.info

electrode_locations – contains files with anatomical locations for each subjects

- <subjID>_parcellation.mat contains anatomical parcel information based on freesurfer automatic parcelation for each subject. The file contains the following variables:
 - channels ordered channel number for each electrode
 - hemisphere a number indicating whether each electrode is in the right (1) or left (2) hemisphere
 - regions region name for the freesurfer parcel each electrode is in
 - region_codes numeric code for the freesurfer parcel each electrode is in
 - volume_ind 3D volume information in subjects native space for electrode location