Dear Fellow ECoG Researcher,

These are the data described in the PLoS Computational Biology manuscript titled *"Spontaneous Decoding of the Timing and Content of Human Object Perception from Cortical Surface Recordings Reveals Complementary Information in the Event-Related Potential and Broadband Spectral Change"* (e1004660. doi:10.1371/journal. pcbi.1004660).

Please keep in mind that these anonymized data are from real patients who donated time in a difficult period of their lives to advance our understanding of the brain. Any publication involving these data **MUST** include the following in the methods section of the manuscript, without modification:

> **Ethics statement:** All patients participated in a purely voluntary manner, after providing informed written consent, under experimental protocols approved by the Institutional Review Board of the University of Washington (#12193). All patient data was anonymized according to IRB protocol, in accordance with HIPAA mandate. These data originally appeared in the manuscript *"Spontaneous Decoding of the Timing and Content of Human Object Perception from Cortical Surface Recordings Reveals Complementary Information in the Event-Related Potential and Broadband Spectral Change"* published in PLoS Computational Biology in 2015 [Insert Embedded Citation for the Manuscript Here – e.g. Endnote, BibTex].

The basic face-house experiment datafiles (in MATLAB format) are named "##_faceshouses.mat" in the folder data/##, where ## denotes the 2 letter patient code. This code is not the patient's initials. The corresponding subject number for each patient from the manuscript is:

	subject	age	sex
ja	1	37	M
ca	2	31	M
mv	3	45	F
wc	4	32	M
de	5		F
zt	6	27	F
fp	7	23	M

Each datafile has 3 variables:

"stim" (time x 1): *This is what is displayed on the screen at each point in time, corresponding to the data*

-values

0: Pre-post task run
1-50: Picture of house being presented
51-100: Picture of face being presented
101: Interstimulus Interval

"data" (time x number of channels): These are the data.

- sampled at 1000Hz
- built-in band pass 0.15 to 200 Hz,
    - but a 1 pole band pass, so there is no sharp corner at 200Hz.
    -The amplitude roll-off function is in the file "ns_1k_1_300_filt.mat"

"srate": Sampling rate (1000 for all files).

In order to reproduce the analyses from the manuscript, open and examine the file "fhpred_master.m". Each step of analysis is shown clearly in the functions called from this file. I have annotated the code in a manner that should be clear if read alongside the methods of the manuscript. The function "call_fhpred_master.m" loops through all subjects, calling fhpred_master and collecting aggregate statistics.

Patient MRIs are found in subfolders "brain/##". These are .nii files. Faces have been clipped from MRI to preserve anonymity. Electrode positions (indexing voxels from the MRI matrix), as well as the anatomic locations can be found in the files "locs/##_xslocs.mat". These location files contain the following variables:

"clims":

These are reasonable upper and lower color limits for plotting the MRIs.

"elcode" (number of channels x 1):

These are anatomic location codes for each electrode. The labels of these numerical locations are detailed in the variable area_lbls in the function fhpred_master.m.

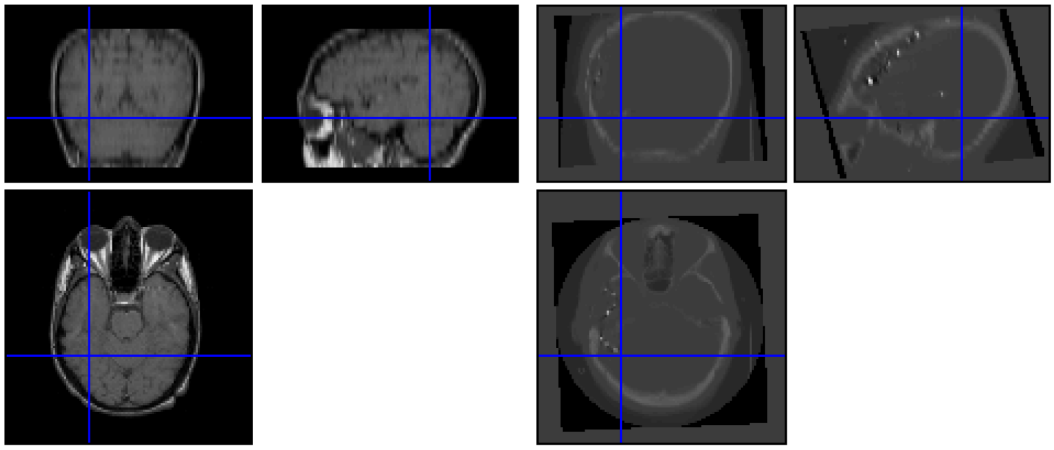
"locs" (number of channels x 3):

Electrode locations, in matrix coordinates (from the corresponding .nii file).

For plotting the data, use the functions in the folder xs_files. Start with xs_disp.m, which allows one to page through the MRI, plotting electrode locations (it calls the SPM function spm_vol to read the brain file in nifti format, so SPM should be installed and in the MATLAB path). Read through the commentary within the .m files in the folder in order to use them further.

A

Normalized Mutual information is used to co-register the pre-impant MRI and the post-implant CT



B

The CT is re-sliced into the space of the thickly-cut MRI, and then electrode positions from the CT are directly associated with locations on an MRI axial slice.

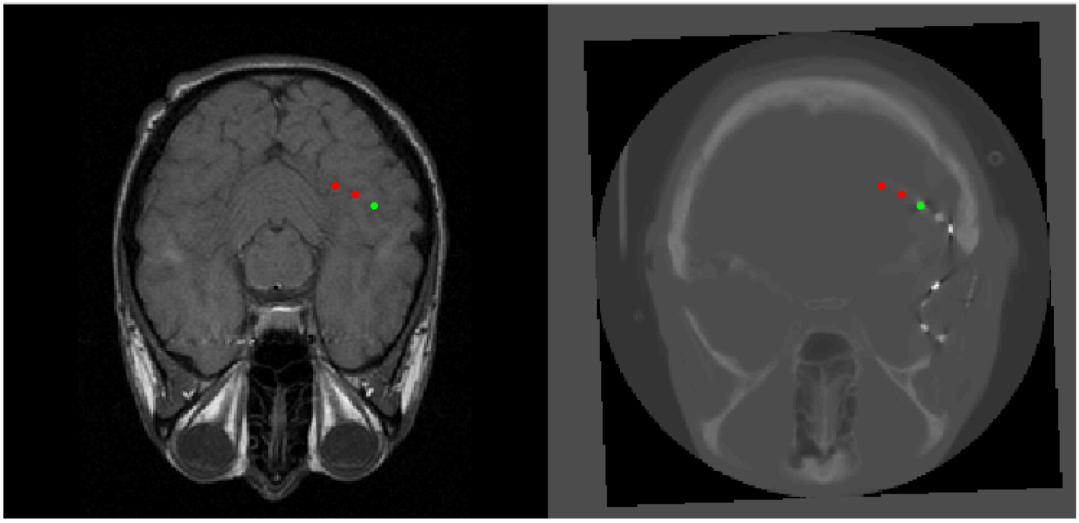


Figure: Electrode localization throughout the manuscript. The MRI slice thickness used most often with the subjects studied were by clinical protocol, and 5mm. This is generally not sufficient to render surfaces and co-register electrodes by the standard methods used in lateral fronto-parietal cortical studies. However, the clinical protocol axial T1 used most often does generate slices that are approximately parallel to the brain surface in the inferior temporal surface, a few centimeters anterior to the occipital pole. Therefore, electrode location relative to gyral surface anatomy was determined by projection of the post-implant CT to the pre-operative axial T1 in the following manner: CT is co-registered to T1 Axial MRI using normalized mutual information in SPM (SPM 5). CT is then interpolated and resliced into the T1 axial MRI. Electrodes are then identified in this mutual space on each slice so that their position is known with respect to gyral anatomy. Because of the tentorium cerebelli, there is little to no brain sag to distort the comparison of electrode position from post-op CT with the pre-operative MRI, so none of the standard correction techniques are necessary.

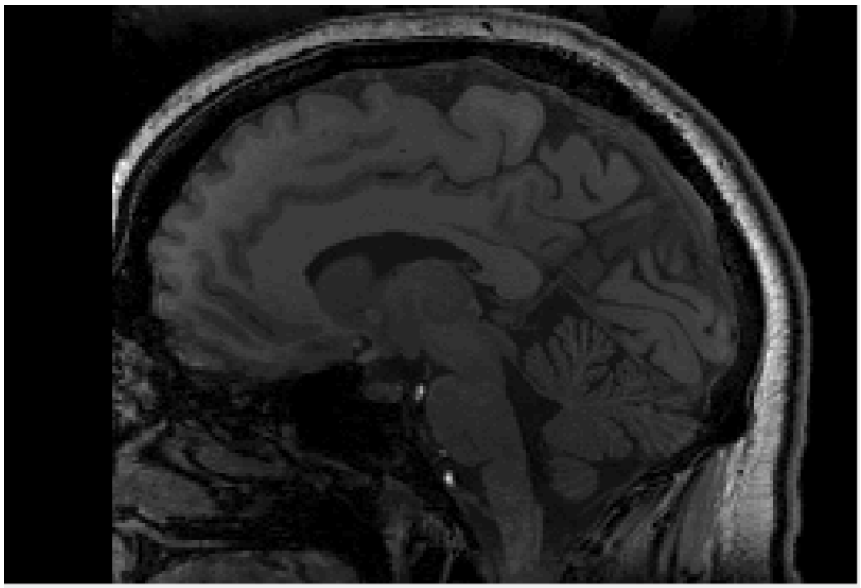


Figure: As seen here, faces have been clipped from MRI to prevent identification. Note: Subject JA has an "averaged" brain volume due to technical issue w MRI

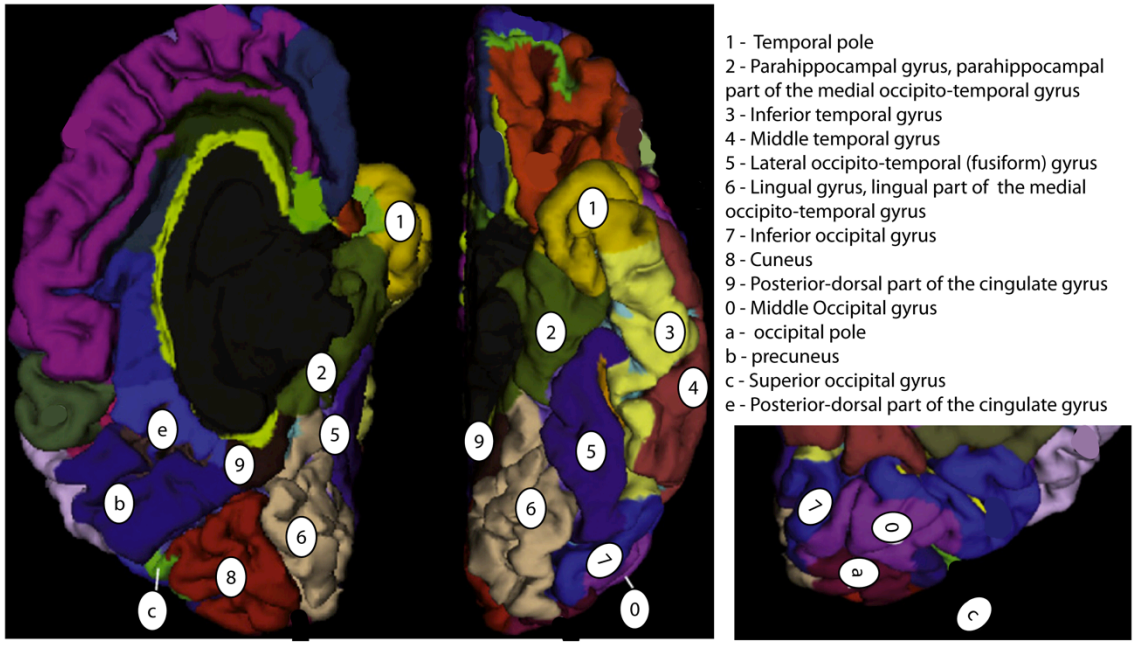


Figure: Inferior temporal (and some occipital) anatomy examined in these analyses. Electrodes were considered ventral temporal if they were localized to one of the following gyri: Temporal pole, Parahippocampal portion of the medial occipito-temporal gyrus, Inferior temporal gyrus, Middle temporal gyrus, Fusiform gyrus (Lateral occipito-temporal gyrus), Lingual portion of the medial occipito-temporal gyrus, Inferior occipital gyrus. Figure modified from (Destrieux et al., Automatic parcellation of human cortical gyri and sulci … , NeuroImage, 2010).

Best Wishes!
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