Haxby Revisited

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Abstract

The functional architecture of the object vision pathway in the human brain was investigated using fMRI imaging to measure patterns of response in ventral temporal cortex while subjects viewed categories of objects in Haxby et al. [Science 293 (2001) 2425] [3]. Haxby argued that category related responses in the VT lobe during visual object identification were overlapping and distributed in topography. At the time of Hanson et al. [Elsevier 23 (2004) 156] [2] there were prevailing views that objects codes were focal and localized to specific areas like the fusiform and the parahippocampal gyri. Hanson et al. revisited the Haxby data and provided a crucial test of the former hypothesis using a neural network classifier. The method of Hanson et al. detected more general topographic representations and illustrated that substantially the same VT lobe voxels contribute to classification of all object categories

1 Introduction

Models for the functional architecture of the ventral temporal cortex fall into three categories. One model proposes that VT contains a limited number of areas that are specialized for representing specific categories of stimuli. A second model proposes that different areas in VT are specialized for different types of perceptual processes. The third model proposes that the representations of faces and different categories of objects are widely distributed and overlapping. According to the latter model, VT has a topographically organized representation of attributes of form that underlie face and object recognition meaning that the representation of a face or object is illustrated by a unique pattern of response across a wide expanse of cortex in which primary and secondary regions (i.e. large- and small-amplitude responses) hold information about face and object appearance.

Haxby et al. tested this model by investigating the patterns of response evoked in the ventral temporal cortex by faces and multiple categories of objects (face, house, cat, bottle, scissors, shoe, chair, scrambled image) in a series of runs on six subjects. Patterns of response were defined as those voxels with response that differed significantly by category and will be referred to as POR for future purposes. The data [4] were analyzed to determine whether the stimulus category that a subject was viewing could be identified on examining the similarity between the POR evoked by each category on even and odd runs. Within-category correlations and between-category correlations were compared to determine whether a POR to one category, such as chairs, could be distinguished from the pattern of response to a different category, such as shoes, with and without the exclusion of maximally responsive voxels. For the inclusion of maximally responsive voxels, The POR in object-selective ventral temporal

cortex correctly identified the category being viewed in 96 percent of pairwise comparisons. Identification accuracy for faces, houses, and scrambled pictures was at 100 percent and identification accuracy for the small man-made objects (bottles, scissors, shoes, and chairs) was significantly better than chance for each category. For the exclusion of maximally responsive voxels, for example, within the cortex that responded maximally to houses, the POR correctly identified the category being viewed with 93 percent accuracy, 94 percent for small man made objects, and 83 percent for faces. These results demonstrate that POR in VT carries information about the type of object being viewed, even in cortex that responds maximally to other categories.

The work by Hanson et al. established Haxby et al. results while further extending the original analysis. Hanson et al. neural network classifier detected more general topographic representations and achieves an 83 percent correct generalization performance on patterns of voxel response in out-of-sample tests. Using voxel-wise analysis Hanson et al. showed that the same VT lobe voxels contribute to the classification of all object categories, suggesting that the code is combinatorial as Haxby et al. suggested. Our own analysis will adhere to the methods of Haxby et al. and Hanson et al. with the plan of reproducing the Haxby similarity method (comparisons between within-category correlation and between-category correlation) and reproducing and improving upon the POR classification rate with a neural network and homogenous methods. We will make the these studies reproducible in the sense that code used to obtain said results will be easily understandable and readable by others; any graph, statistics, etc. from these studies can be easily simplified and reproduced with the aid of well documented executable and readable code.

2 Data

The data consists of 64 slices 64 X 40 BOLD collected from a GE 3T (repetition time = 2500 ms, forty 3.5-mm-thick sagittal images, field view of = 24 cm, echo time = 30 ms, flip angle = 90 percent). Patterns of neural response were measured with functional magnetic resonance imaging (fMRI) in six subjects while they viewed pictures of faces, cats, five categories of manmade objects. Twelve time series were obtained for each subject. Each time series began and ended with 12-s rests and contained eight stimulus blocks of 24-s duration, one for each category, separated by 12-s interval of rest. Stimuli were presented for 500 ms with an inter stimulus interval of 1500 ms. Repetitions of meaningful stimuli were pictures of the same face or object photographed from different angles; stimuli for each meaningful category were four images each of 12 different exemplars. The data shape for any particular run is (40, 64, 64, 121) that can be read as 64 slices 64 X 40 BOLD for 121 contiguous slices in time (i.e. 121 volumes of time).

Due to possible subject movement and unavoidable low frequency drifts/noise we used provided preprocessed data for our analysis. Stanfords Russ Poldrack and the folks at the OpenFMRI project provided the preprocessed data. The processing applied to the scans is motion correction to partially correct for movement during the runs and between runs, high-pass filtering in time to remove low frequency drifts/noise and registration to a standard anatomical template. The old data has shape (40, 64, 64, 121) and the new preprocessed data (91, 109, 91, 121).

3 Preprocessing

3.1 Masking

Since our fMRI data is represented as a 4D block of data, we are interested in working on the voxel time-series in the brain. It is then necessary to apply a mask on the 4D brain images to subset the voxels in the brain that we will be analyzing.

3.2 Smoothing

fMRI data has a low signal-to-noise ratio. Any reduction of random noise in the image will improve the ability to detect true activation. For this reason, smoothing has become a commonly used pre-processing step in the analysis of fMRI data. Smoothing the data will improve our signal to noise ratio by applying a small blurring kernel across the image.

4 Methods

4.1 Linear Model

Ideally we want to detect any signal in relation to a task i.e. we want to determine which voxels contain high activation based on BOLD response to stimulus, (e.g. house, face, cat, shoe, house, scrambled, chair, bottle). We may detect signal by subtracting task from rest or by calculating a correlation between the task-on / task-off vector and the voxel time course. However, by using a Generalized Linear Model to fit our fMRI time series data, we will able to calculate a unique weight for each voxel that represents the different level of activation across all the voxels that we can use to distinguish BOLD response per stimulus. We will regress the BOLD time series across all voxels against the timing and duration of each stimuli (8 predictors) The GLM for our fMRI data is

$$\mathrm{Y} = \mathrm{X}\beta \pm \varepsilon$$

Y is our BOLD signal, X the design matrix with our predictors, B the that describe the relationship between the predictors and response, and E the unexplained noise in the BOLD data.

4.1.1 Design Matrix

Before we performed a regression analysis, we masked the data in order to distinguish the voxels that are in the brains versus the voxels that are outside the brain. Before applying a mask on subject001 run001, we took the mean volume (over time) (3D brain image) and plotted a histogram of the mean volume values. (Fig. 1). By selecting the correct threshold, we will be able identify the voxels inside the brain, a 3D brain mask. We first selected a threshold of 1100. We then carelessly looped through each subject and run and applied the same threshold of 1100 only to conclude that threshold will differ between subjects and their runs (Figs 1-3: histogram showing different thresholds are needed).

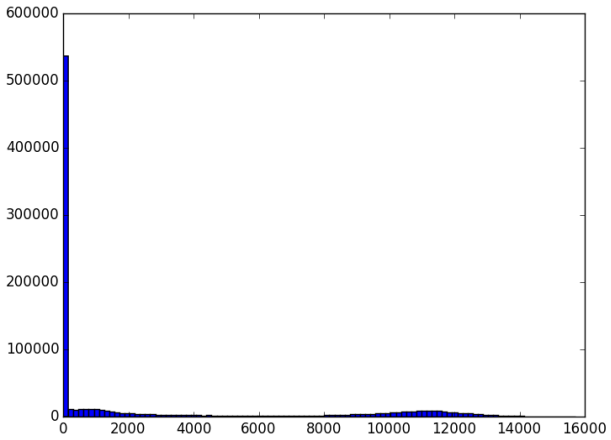


Figure 1: Sub 1 Run 1

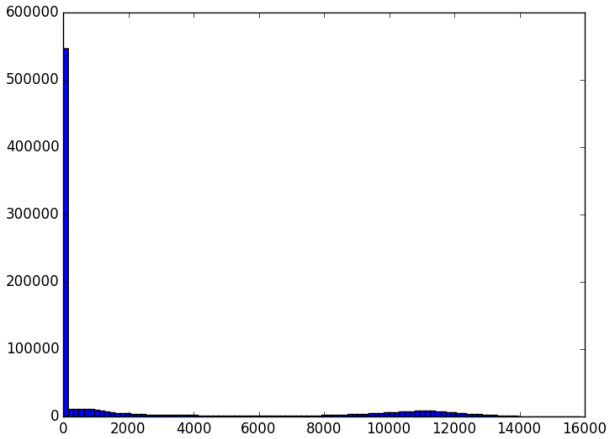


Figure 2: Sub 1 Run 3

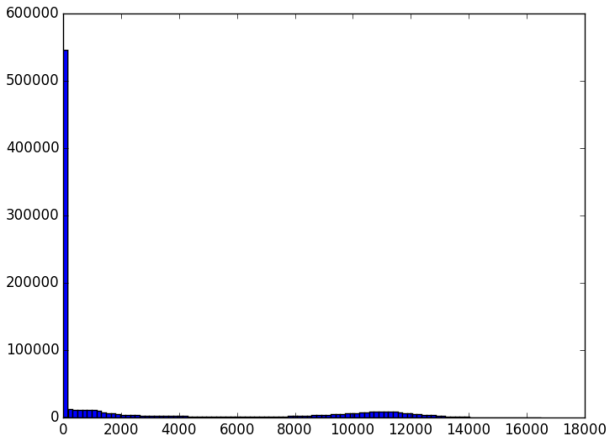


Figure 3: Sub 1 Run5

To effectively solve this problem, we used FUNCTION that provides an algorithm that computes a unique threshold, therefore a unique mask, for each subject and run. This method was more efficient and accurate as we showed that the voxels within the brain slightly vary across subjects and their runs. Now that we've removed on average 700,000 voxels per run, we can now perfomm a regression analysis on the subset of voxels that are in the brain.

4.1.2 Hemodynamic Response

Our design matrix will consist of 8 predictors, representing the ideal time series that represent what we think the response should look like to each of the eight stimulu.. Ideally we want to know the activation at the neuronal level but this is beyond the capability of fMRI, for we dont know when that signal is occurring other than the time intervals in which the subject is shown the stimuli. To account for this we have to convolve with the hemodynamic response function. Hemodynamic response (HDR) allows the rapid delivery of blood to active neuronal tissues. If a subject is shown a photo of a cat the brain will presumably receive a rapid delivery of blood to activate the neuronal tissues for identifying/processing cat. The probability density function of the gamma distribution

$$\text{Gamma}(\alpha, \beta) = \frac{\beta^{\alpha}}{\Gamma(\alpha)}.X^{\alpha-1}.e^{-\beta x}$$

can model this situation and provide us with a continuous function that is close to the hemodynamic response we observe for a single brief event in the brain.

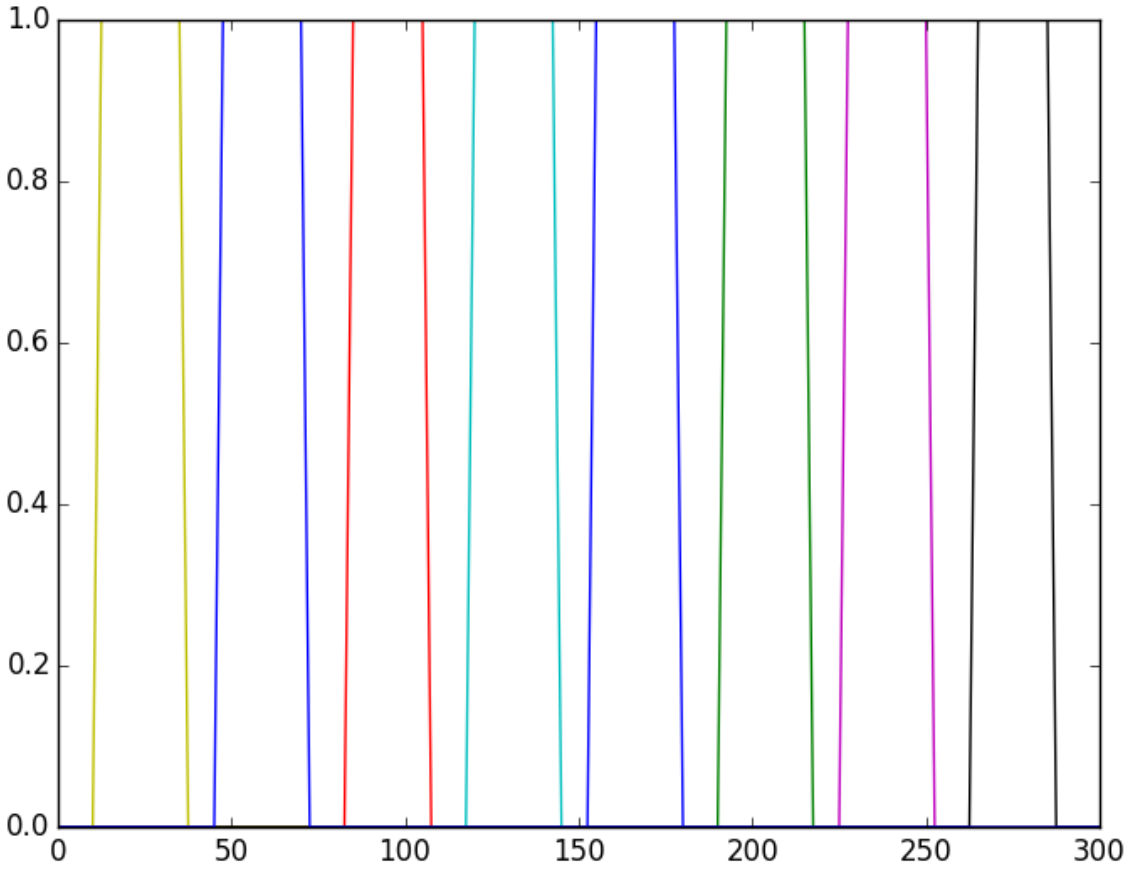


Figure 4: Onsets blocks for subject 1

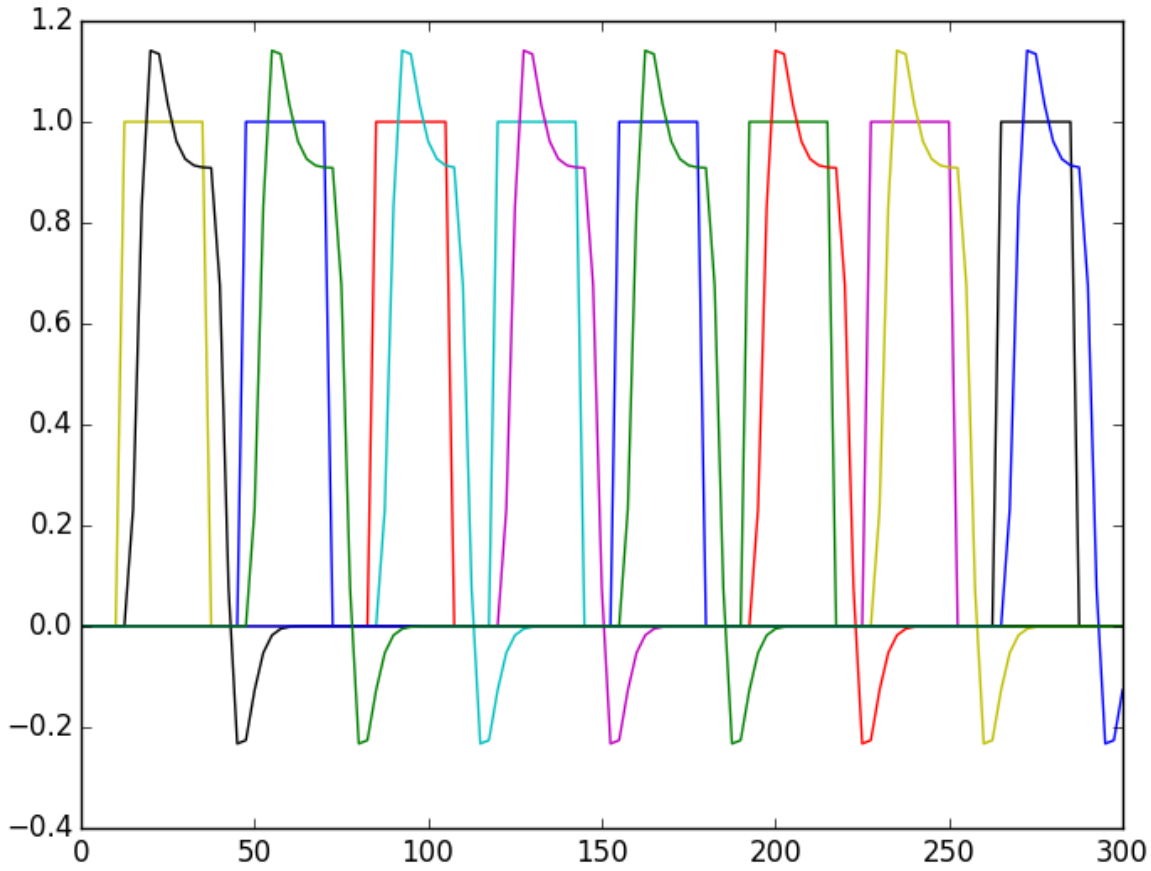


Figure 5: Onsets blocks with HDR subject 1

By using HDR to create the convolved regressors, we bridged through neural response and BOLD. These predictors will now closely simulate the onsets and allow our model to more accurately capture the changes in the BOLD activation associated with the presentation of stimulus to the subject.

This results to the following design matrix (X):

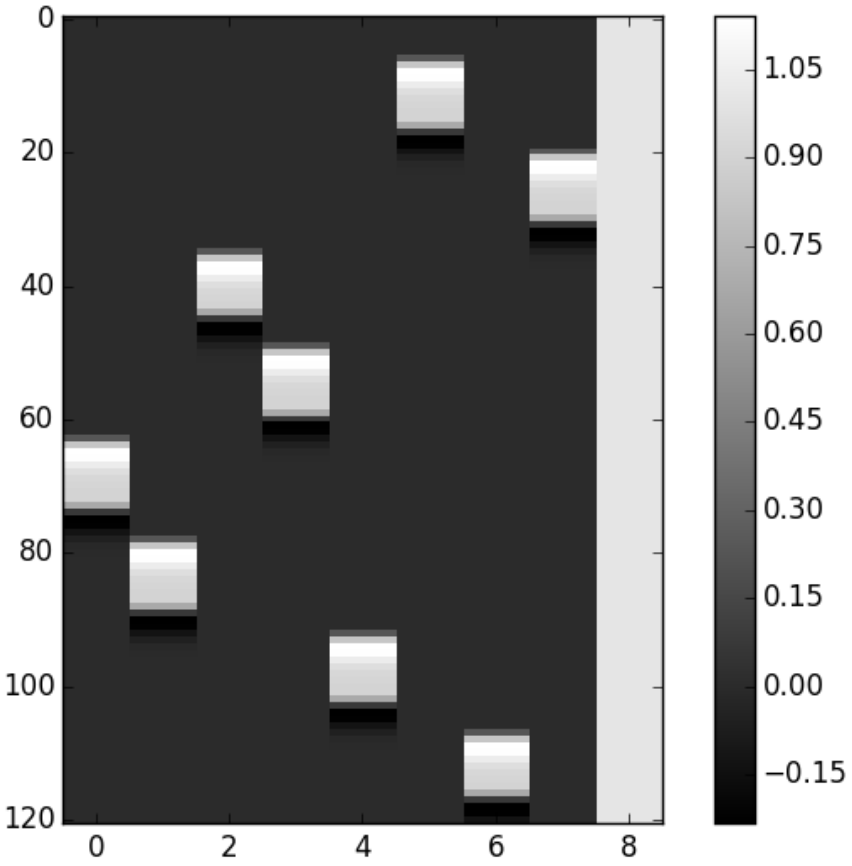


Figure 6: Design Matrix

4.1.3 Estimating Beta Values: Activation Maps

Using the design matrix, we used least squares to estimate the B (beta coeff) by:

$$\hat{\beta} = [X^T X]^{-1} X^T$$

Thus, B hat will serve as the unique weights for each voxel. The beta coefficient gives us the amplitudes of the 8 different stimulus. Small beta values, small amplitude, will represent a low level of activation, while voxels with large beta values will represent a high level of activation.

The B hat represents the parameter weight, or how much each regression factor contributes to the overall data. The B hat has the shape of (91,109, 91,8). Each slice across the fourth dimension yields a unique set of beta coefficients corresponding to that particular slice (i.e. stimuli). Additionally, slicing through the third dimension reveals the amplitude over the voxels through a transverse cut of the brain. The central slice can bee seen in Figure 7 for the first run for subject one. For example, the following activation maps represent the beta coefficients (i.e the amplitude of each voxel) produced by the viewing of the object house, face, and scissors..

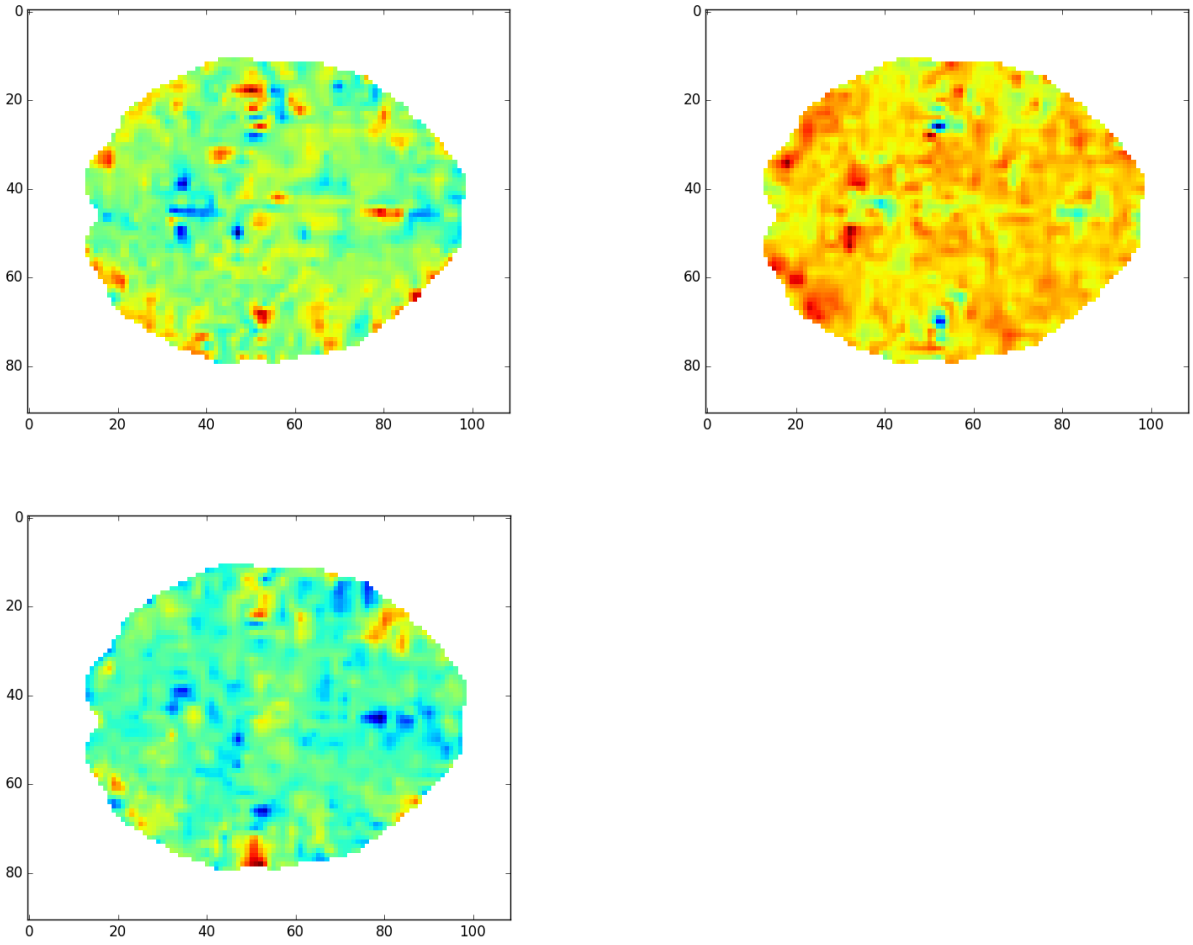


Figure 7: Beta

After analyzing many brain activation maps across subjects and runs, we need a linear drift to adjust for head movement during the scanner. We also added a quadratic drift because there is quadratic behavior present. He is the new design matrix:

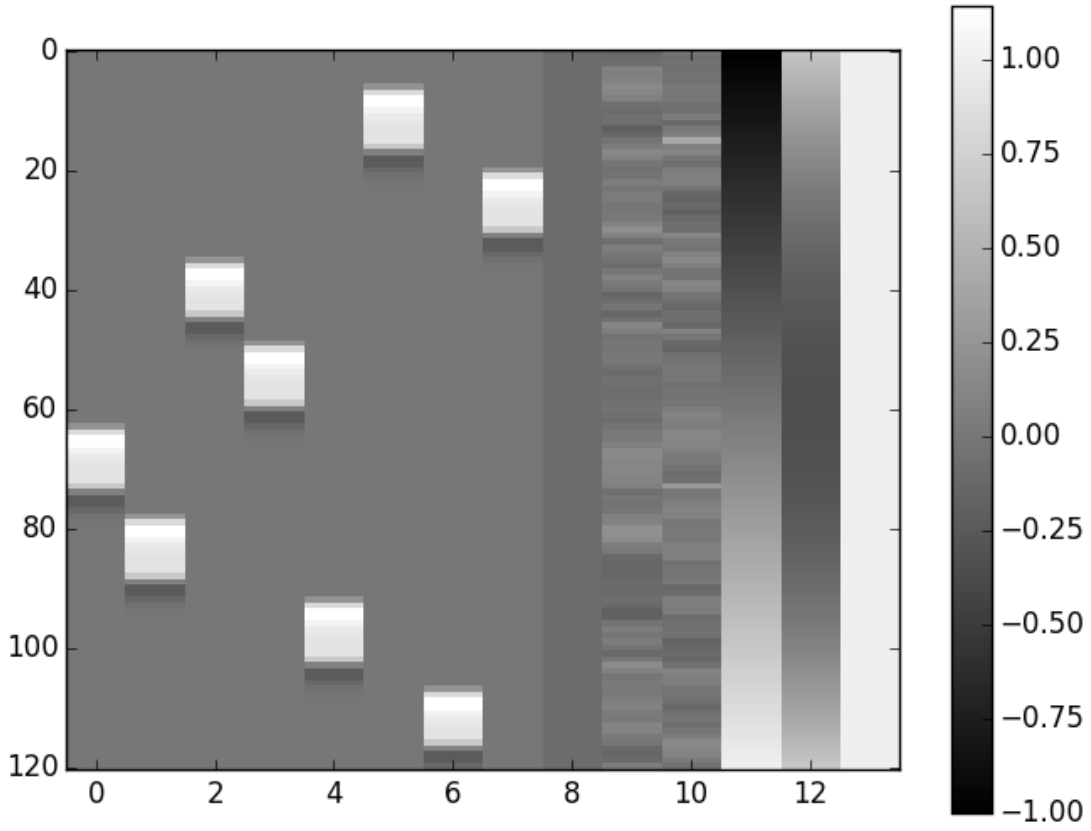


Figure 8: Design Matrix with linear and quadratic drift

We decided to go even further and applied PCA to our data to increase the accuracy of our activation levels.

4.2 PCA

Principal component analysis (PCA) is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information about abstract and rather large data sets, such as fMRI. Most import is that PCA is a significant tool for deriving a low-dimensional set of features from a large set of variables and can be used as a dimension reduction technique for regression on our design matrix. The linear and quadratic drift terms are able to model gradual drifts across the time-series but there are other patterns of noise, like brain anatomy, in our data that are undetectable by these methods. With PCA we can capture more of this noise and then remove these principle components by regression. The principle components are a sequence of projections, mutually uncorrelated and ordered in variance. In the our case the component vectors are the time-courses which provide a sequence of best linear approximations to our fMRI data. Figure 9 illustrates the mutually uncorrelated projections ordered by variance.

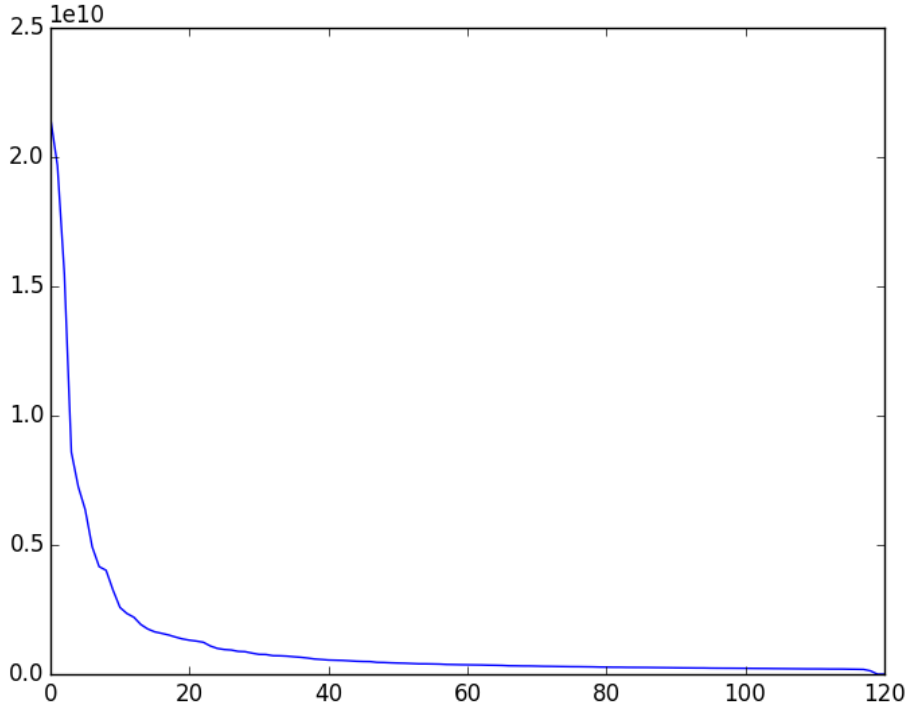
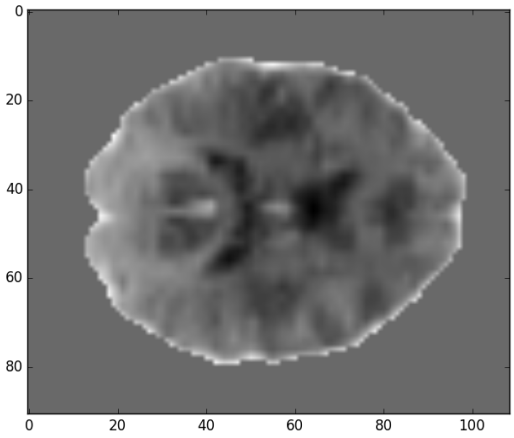
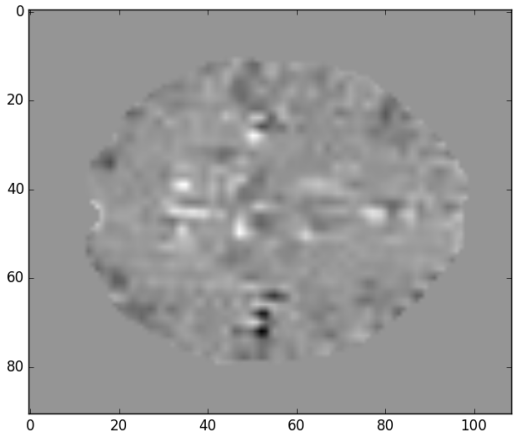
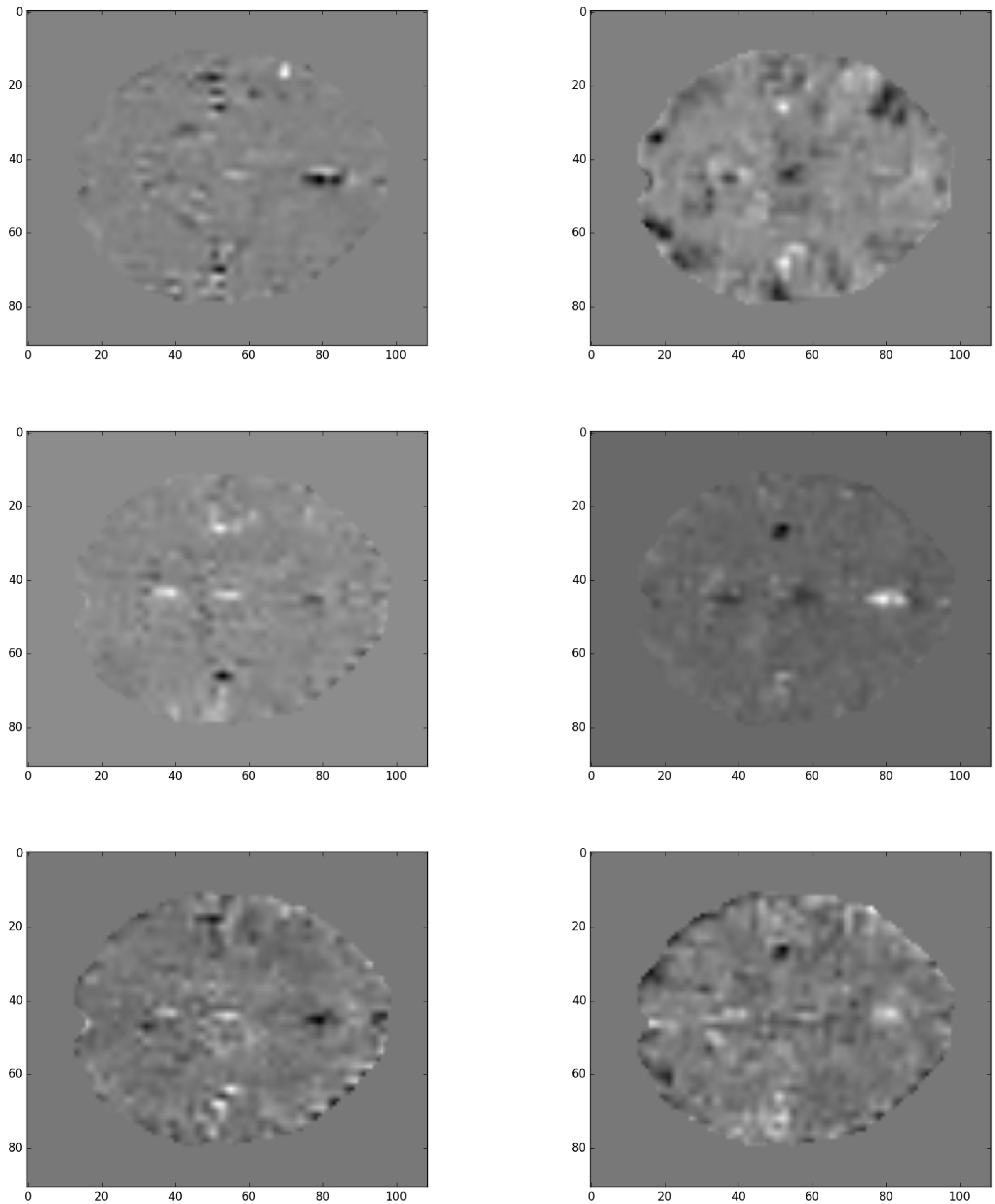


Fig. 9: Projections ordered by variance

Many of the components appear to explain much of the variance but we decided to examine the only first 10 as a rule of thumb.







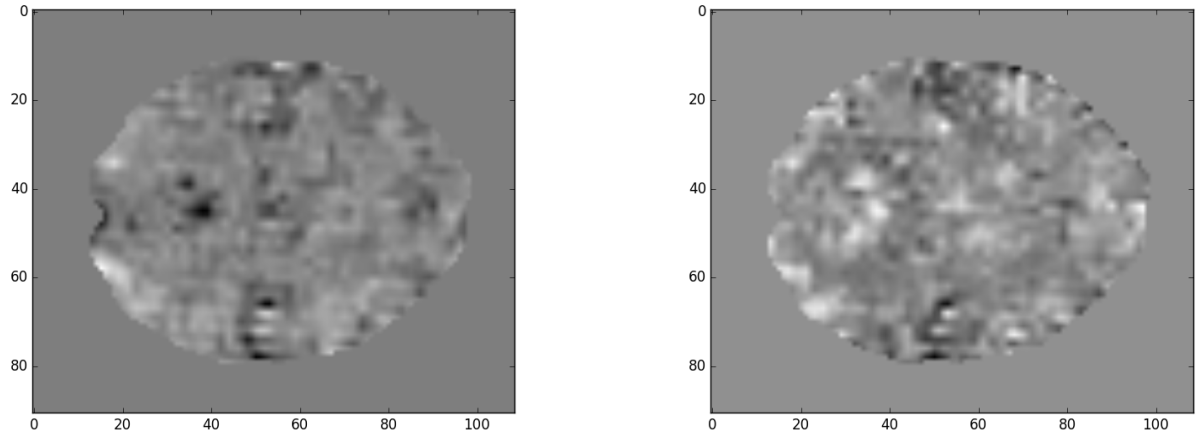


Figure 10: Projections

The first plot is the clearest and most obvious to contain brain anatomy rather than activation, for you can see the surrounding skull structure and the lateral ventricle. The other images were not so clear and for that we had to err on the side of caution. Plot 7 and 8 were on of the few images that displayed some sign of structure in the bottom right corner and top left corner, respectively.

5 Results

Now that we've applied statistical techniques on our data to improve our signal, we compared the difference of beta cofficients between two conditions to determine if two beta coefficients are significantly different. In other words, we will be comparing the difference of level of activation for a given voxel between two conditions. Using T-maps, we can infer which voxels are significantly different.

5.1 T-Map

T-map: After getting the betas hat for each run from subject 001, we applied t-statistics to look for the regions of the brain that reacts positively(red) to the one category and negatively to the other category(blue). First, we get the differences between two categories for each run and then reshape it from three dimension to one dimensions and concatenate the twelve runs. Therefore, we have runs by voxel matrix, which is two dimensional. Finally, we applied t-statistics to each voxel, and reshape the output back to three dimension. This process is called T-map. Hence, the T-map can help us investigate the regions of the brain that reacts positively(red) to the one category and negatively(blue) to the other category. We also write a function for T-map, so it is very fast to get t-map for each subject.

5.2 House vs Face

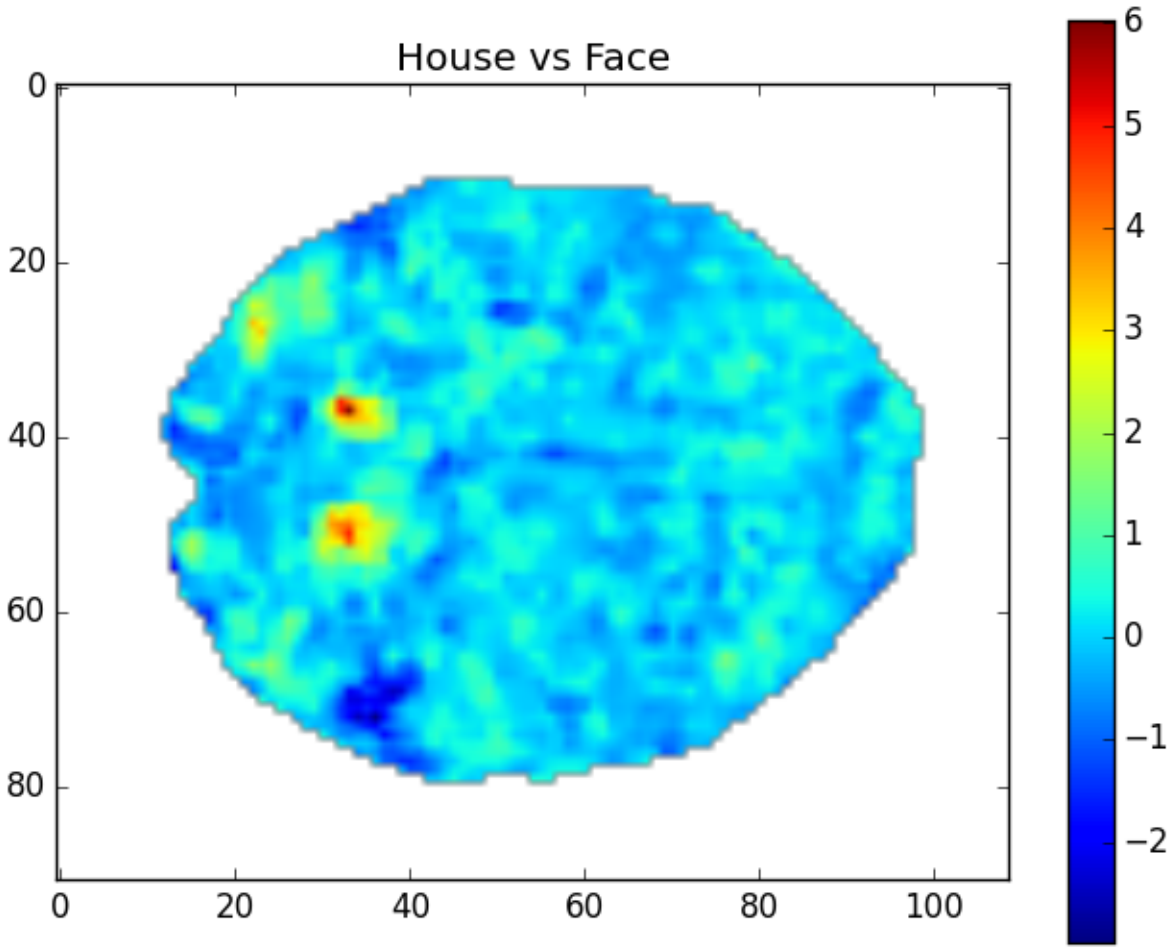


Figure 11: House vs Face

First, we investigated the house and face. According to the Figure 11 house vs face, it is not hard to see that there are two red dots in the image. The two red regions seem to react strongly to structure but not facial recognition. On the other hand, the blue region seems to react strongly to the face. Therefore, we make a hypothesis: the two regions react strongly to structure. In order to test the hypothesis, we have to compare the house regressor and every other category regressor at the same scale.

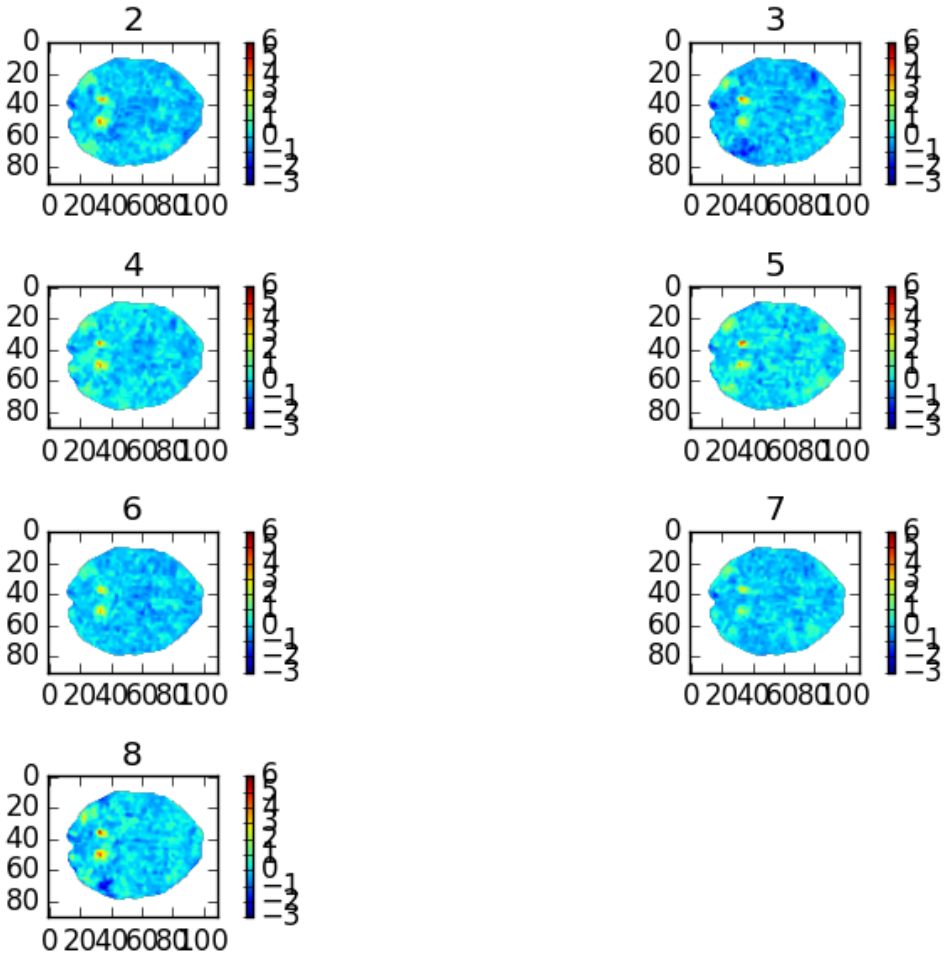


Figure 12: House vs Everything

According to the graph, the hypothesis should be accepted because all of images have two red dots at the same spot. Therefore, the all graph has same type of structure. This shows that the two red regions respond to much more house than other visual stimuli. According to the article The Parahippocampal Place Area: Recognition, Navigation, or Encoding? [1] it states that The parahippocampal place area (PPA) has been demonstrated to respond more strongly in fMRI to scenes depicting places than to other kinds of visual stimuli. Therefore, these regions are called parahippocampal place area (PPA). In conclusion, the house regressor region of activation makes it easier to visualize if the amplitude of activation in the house condition differ from that of the other 7 conditions.

Next, we want to investigate the cat and every other regressor.

5.3 Cat vs Shoe,Scram

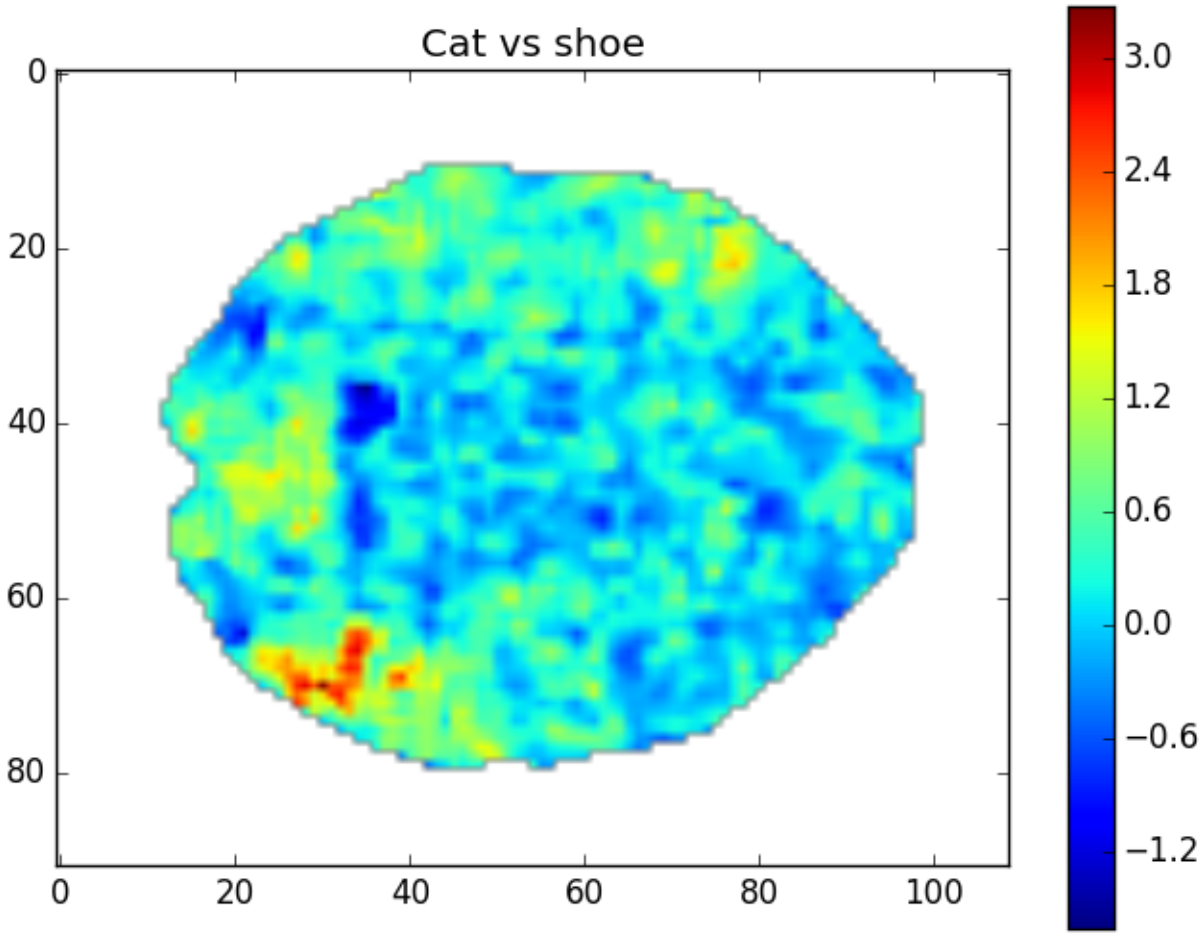


Figure 13: Cat vs Shoe

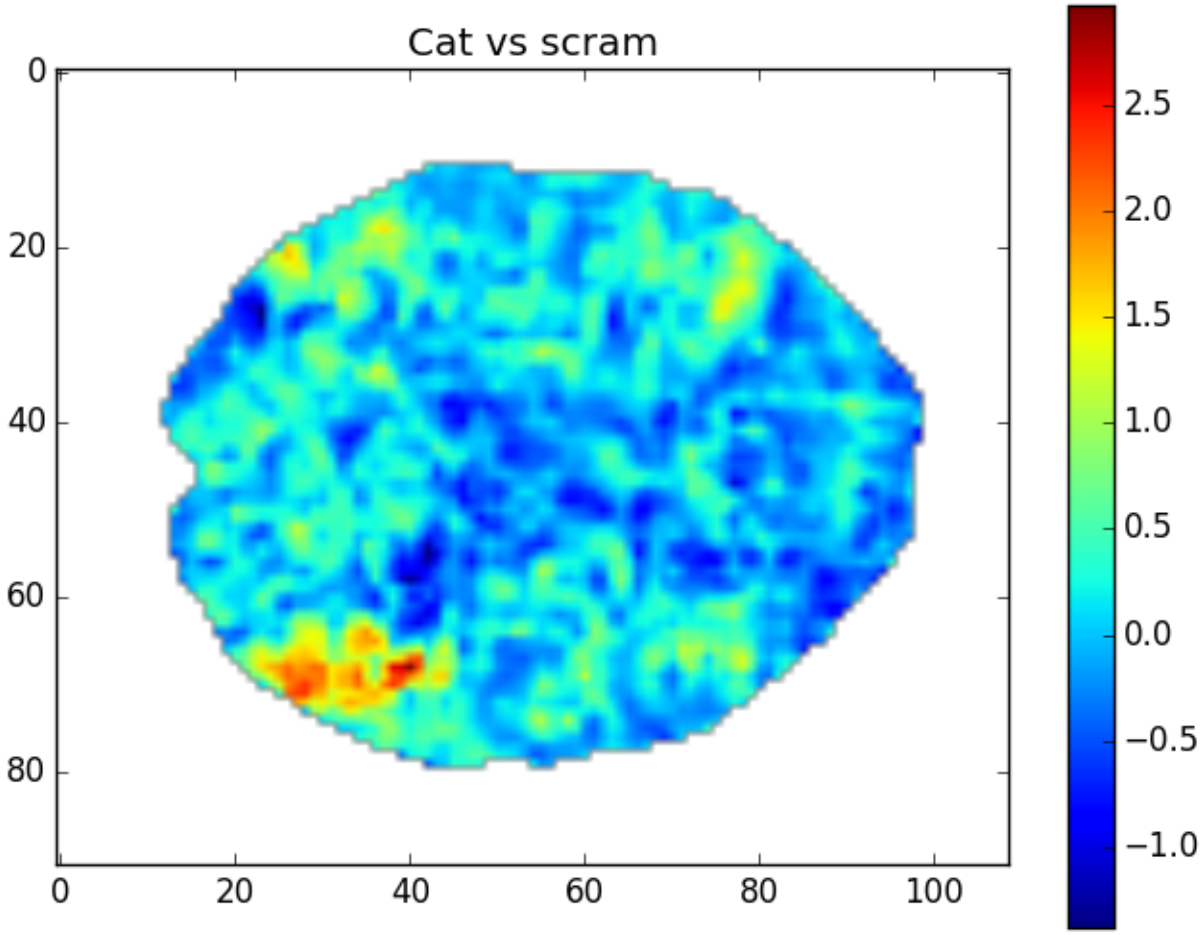


Figure 14: Cat vs Scram

5.4 Cat vs Everything

According to the two graphs, we saw the lower region of the brain seems correspond very well to cat. Therefore, we make a new hypothesis again: viewing a picture of an animal certain part of brain responds to animal. Since the two graphs have different scale, we have to compare the cat regressor and every other category regressor at the same scale.

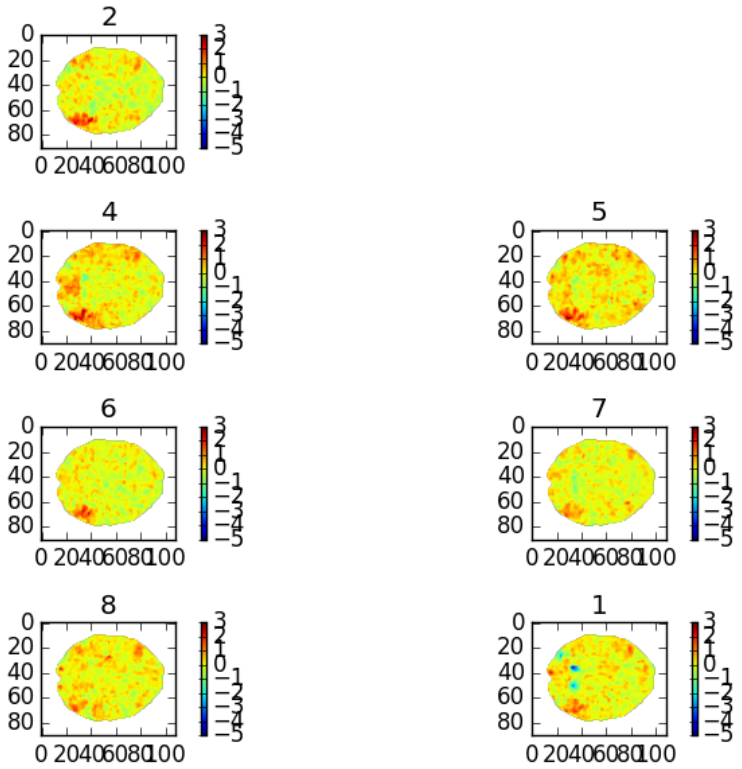


Fig 15: Cat vs Everything

According to the graph, it is clear to see that each graph has a red dot at lower region of the brain. Hence, we should accept our hypothesis, and we can make a conclusion that the regions strongly responds the animal picture.

5.5 Correlation

After getting beat from run1, we want to see the correlations between region of the brain that react strongly to one category and not to other category. Here we want to show that the correlation is exactly same interpretation of t-map.

5.6 Correlation between House vs Everything

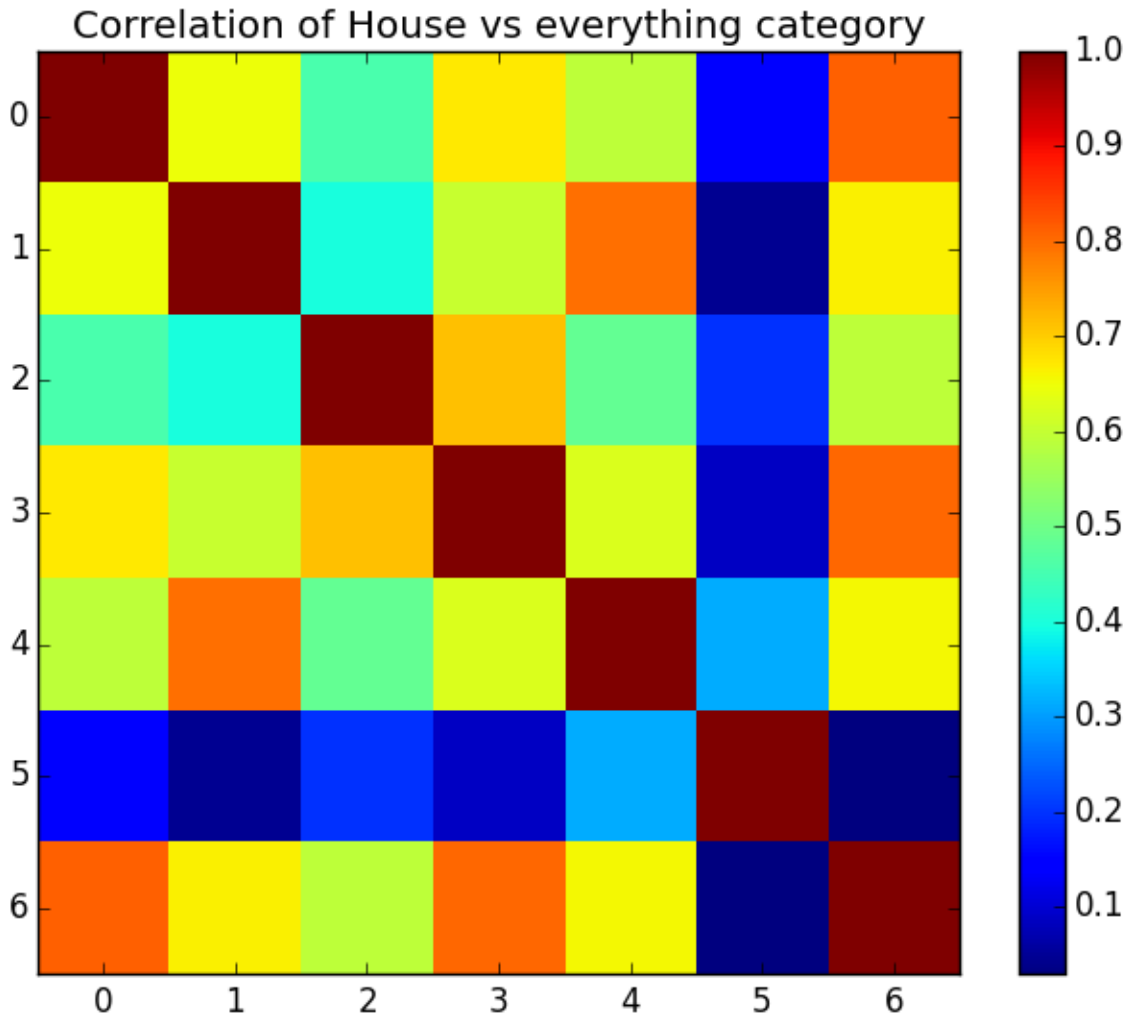


Figure 16: Correlation between House vs Everything

According to the house vs everything graph, it is harder to see the red point from t-map between house and chair than other categories. Also, Beta-chair minus Beta-house has lower correlation than other two categories according to the 1-correlation. Therefore, this shows that the correlation is exactly same interpretation of t-map.

5.7 Correlation Difference

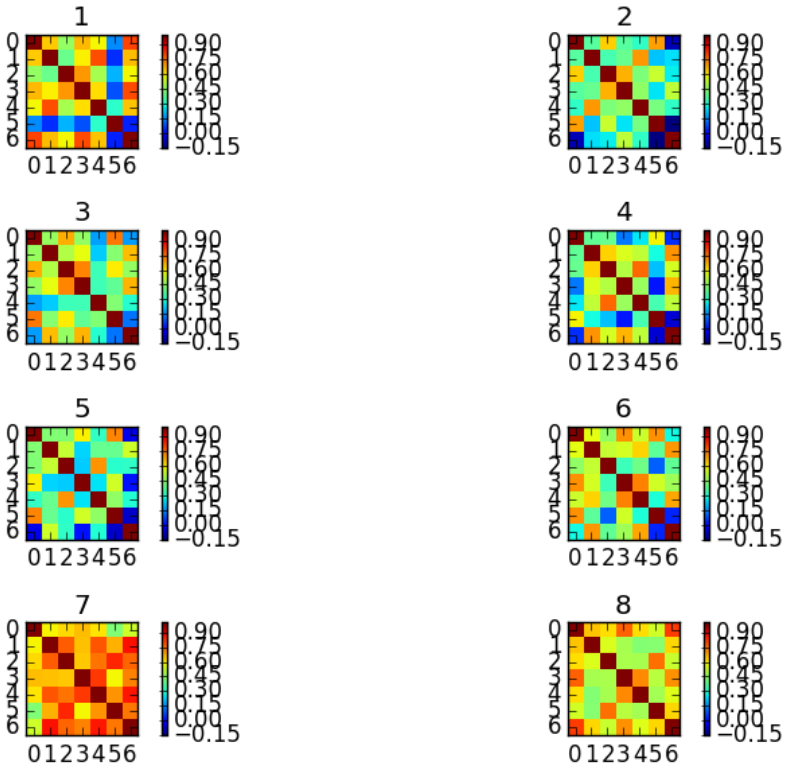


Figure 17: Correlation Difference

5.8 Discussion

We were able to identify which voxels were significantly different by comparing the difference of beta coefficients between a set of two conditions. Before reaching that point we had to prepare our data by implementing a variety of techniques and tools. Our basis tool was that of the powerful linear model which paved our work way for our analysis. We were able to provide some insight into the work of Haxby but were unable to fully delve into classification methods due to the complexity of the raw fMRI data and direction of the possibilities thereof. However, we have built a nice foundation that can and will surely guide us into the future analysis that we originally planned to execute.

References

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[2] S. J. Hanson et al., *Combinatorial codes in ventral temporal lobe for object recognition*, NeuroImage, 23 (2004), pp. 156–166.

[3] J. V. Haxby, *Distributed and overlapping representations of faces and objects in ventral temporal cortex*, Science, 293 (2001), pp. 2425–2430.

[4] J. V. Haxby et al., *Visual object recognition.* https://openfmri.org/dataset/ds000105, 2001.