

Portfolio for Mapping, Decoding and Modeling the Human Brain

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Date: February 15, 2025

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1 Introduction

Functional Magnetic Resonance Imaging (fMRI) provides a powerful tool for mapping neural activity, allowing to investigate the functional architecture of the human brain. Over the past decades, fMRI analysis techniques have evolved from traditional block-design approaches to sophisticated multivariate and encoding models.

This portfolio presents a structured exploration of fMRI data analysis, covering preprocessing, statistical modeling, and classification-based decoding techniques. Through a series of project works and homework assignments, the following core topics are addressed:

- **Project Work 1:** Understanding and visualizing the structure of the dataset, constructing design matrices, and preprocessing fMRI data.
- **Project Work 2:** Implementing the General Linear Model (GLM) to compute contrast maps and perform region-of-interest (ROI) analyses.
- **Project Work 3:** Applying multi-voxel pattern analysis (MVPA) and classification techniques to decode object categories from fMRI data.
- **Project Work 4:** Performing Representational Similarity Analysis (RSA) to explore how different stimulus categories are encoded in the brain.
- **Project Work 5:** Attempting voxel receptive field (vRF) modeling to estimate voxel-level selectivity, and discussing dataset constraints for such analyses.

The dataset (Haxby 2001) is used across all projects, providing a common framework for comparing different fMRI analysis approaches. The methods range from univariate GLM-based contrasts to multivariate decoding and similarity-based techniques, highlighting the strengths and limitations of each. By systematically exploring these methods, this portfolio aims to demonstrate how different computational tools contribute to the broader goal of mapping, decoding, and modeling human brain function.

2 Project Works

2.1 Homework 1

(1) What are the approximate spatial and temporal resolutions of fMRI data?

- The spatial resolution of fMRI data is close to 1 mm, while the temporal resolution typically ranges from 1-2 seconds per volume.

(2) What is the difference between a block and an event-related design?

- Block designs group trials of the same condition into blocks and compare the mean activity across blocks, providing robust detection power. Event-related designs randomize individual trials, and the responses to trials belonging to the same condition are averaged. The mean responses are then statistically compared. This approach avoids cognitive adaptation, allows for the estimation of a response profile, and facilitates post-hoc sorting.

(3) What is the aim of general linear modeling (GLM) of fMRI data?

- The General Linear Model (GLM) is a statistical framework used in fMRI to predict a voxel's observed BOLD signal by modeling it as a linear combination of predictors that represent experimental conditions. Each predictor is assigned a beta coefficient, indicating how strongly it explains the signal. By comparing beta coefficients, we can test whether activation in one condition is significantly different from activation in another condition.

2.2 Project Work 1: Understanding the Dataset

2.2.1 Introduction

The first project work focuses on understanding the structure of functional MRI (fMRI) data and preparing the necessary preprocessing steps for later analyses. Since Project Work 1 and Project Work 2 are closely related, I decided to separate the two by focusing this part on data exploration and preprocessing, while the next part covers the general linear model (GLM) fit.

This project includes:

- Familiarization with the dataset, including spatial and temporal properties.
- Visualization of anatomical slices and time-series data.
- Construction and visualization of the design matrix.
- Convolution of the design matrix with a sampled hemodynamic response function (HRF).

2.2.2 Exploring the fMRI Dataset

The dataset used is from Haxby 2001, consisting of fMRI recordings from six subjects performing a passive viewing task. The stimuli consisted of eight object categories presented in a block design. Each subject completed 12 runs, with 24s blocks of stimuli interleaved with rest periods. The fMRI data has a repetition time (TR) of 2.5s, with each volume containing $40 \times 64 \times 64$ voxels.

To explore the dataset, I loaded the functional data and extracted key information such as spatial transformations and anatomical orientation.

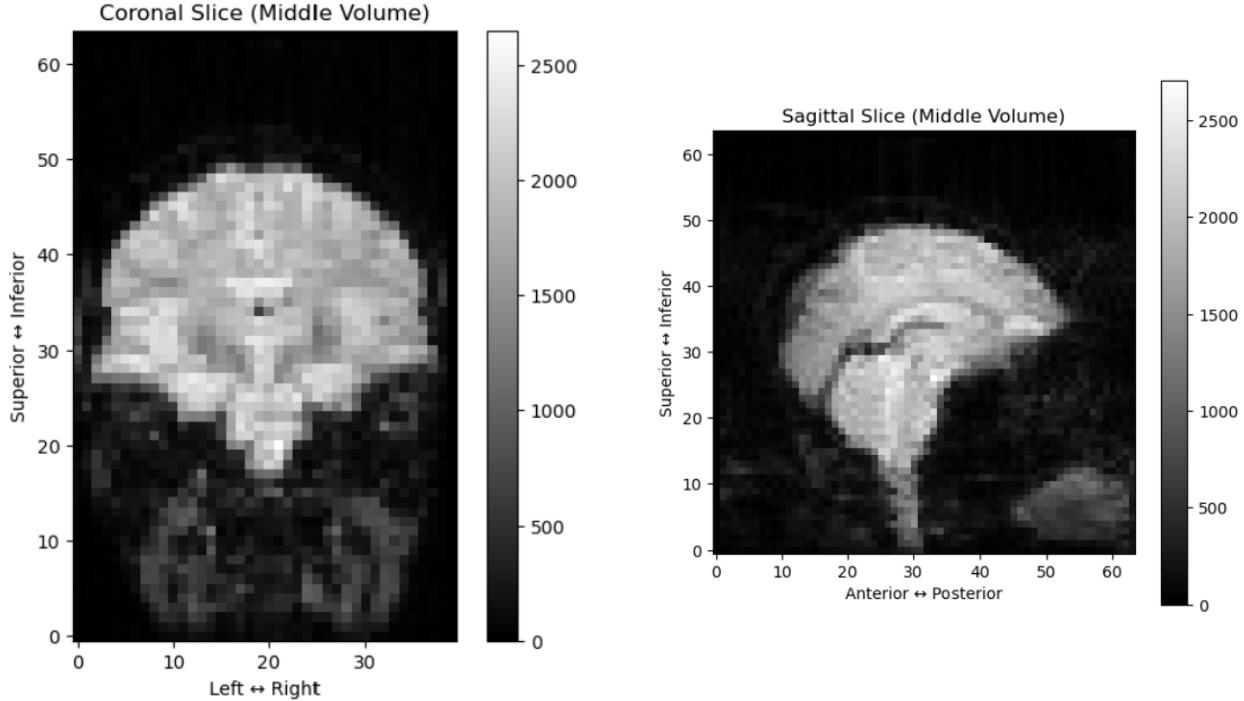


Figure 1: Visualization of anatomical slices. **Left:** Coronal slice. **Right:** Sagittal slice.

2.2.3 Voxel Activity Over Time

To understand how the fMRI signal fluctuates at the voxel level, I extracted the time-series data for three randomly selected voxels. Each voxel's signal intensity was plotted over the course of the experiment.

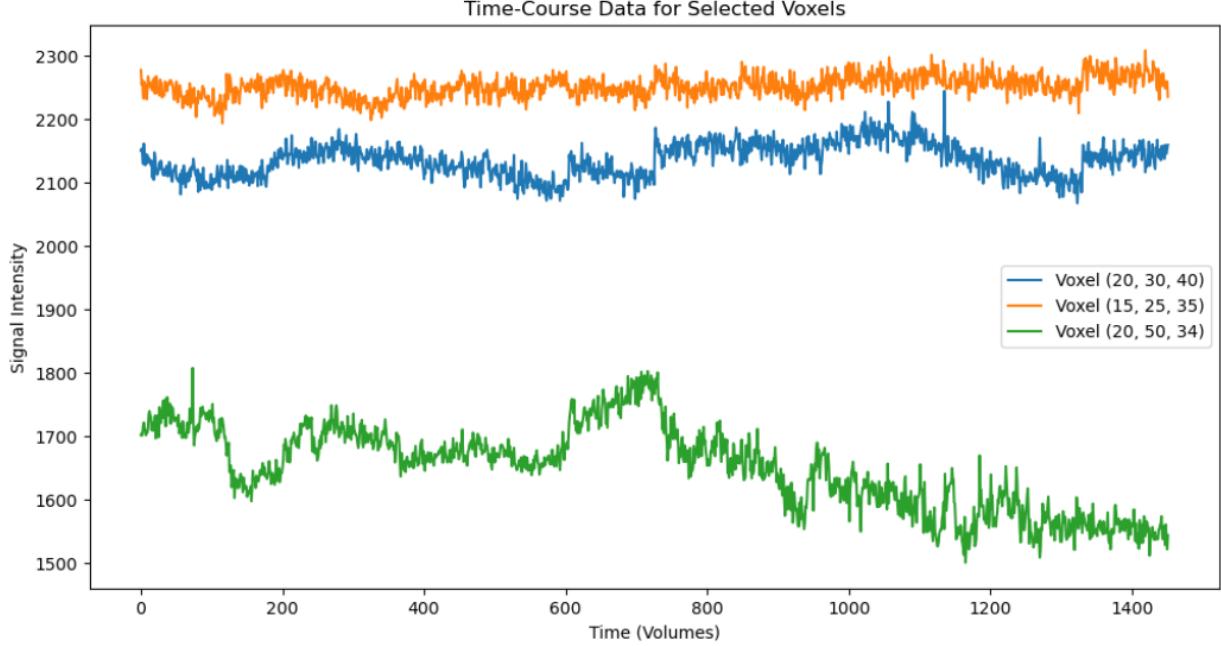


Figure 2: Time-course data for selected voxels. Each line represents the signal intensity of a different voxel over time. The variability in these signals reflects underlying neural activity and noise.

2.2.4 Stimuli Presentation and Design Matrix Distribution

The following visualizations illustrate the structure of the experimental design. The left plot represents how stimuli were presented over time, mapping each volume to its corresponding stimulus condition. The right plot shows the distribution of stimulus conditions across experimental runs, ensuring that all conditions were evenly represented.

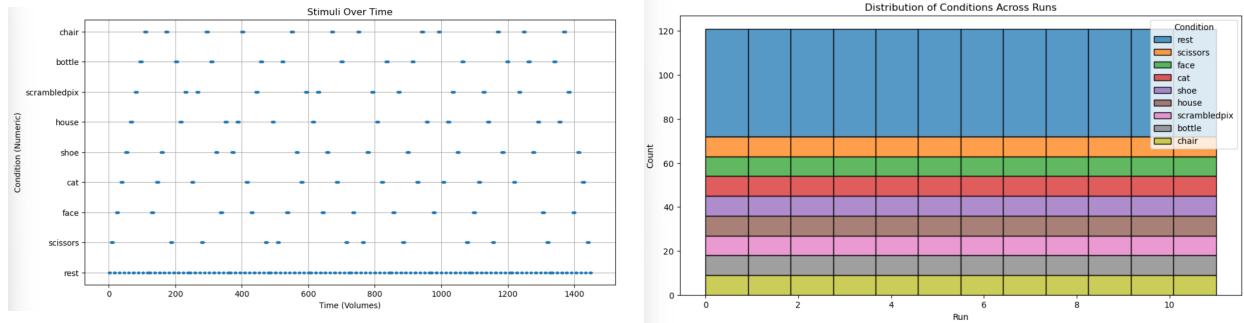


Figure 3: Experimental design visualization. **Left:** Stimuli presentation over time. **Right:** Distribution of stimulus conditions across runs.

2.2.5 Design Matrix and Convolution with HRF

To model the expected brain response, I constructed a design matrix encoding stimulus presentations.

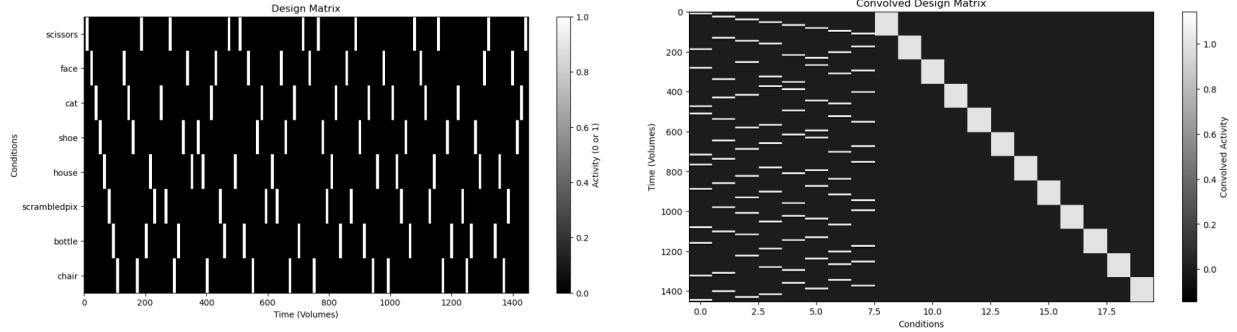


Figure 4: Comparison of the design matrix before and after convolution with the hemodynamic response function (HRF). **Left:** Original binary design matrix. **Right:** Convolved matrix with additional run intercepts.

The convolution was performed using the sampled HRF, ensuring alignment with the temporal resolution of the fMRI data. Since neural responses are not instantaneous, this step is essential to account for the delayed and dispersed nature of the BOLD response, improving the accuracy of the model.

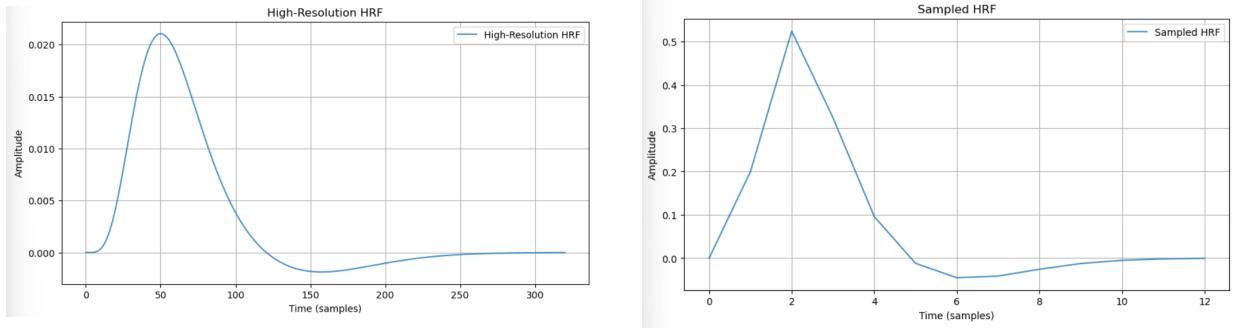


Figure 5: Comparison of HRFs. **Left:** High-resolution HRF. **Right:** Sampled HRF used for convolution.

2.2.6 Beta Map Estimation

To estimate voxel-wise activation patterns, I fitted a GLM to the data using the convolved design matrix. The resulting beta coefficient maps show how strongly each voxel is modulated by each stimulus condition.

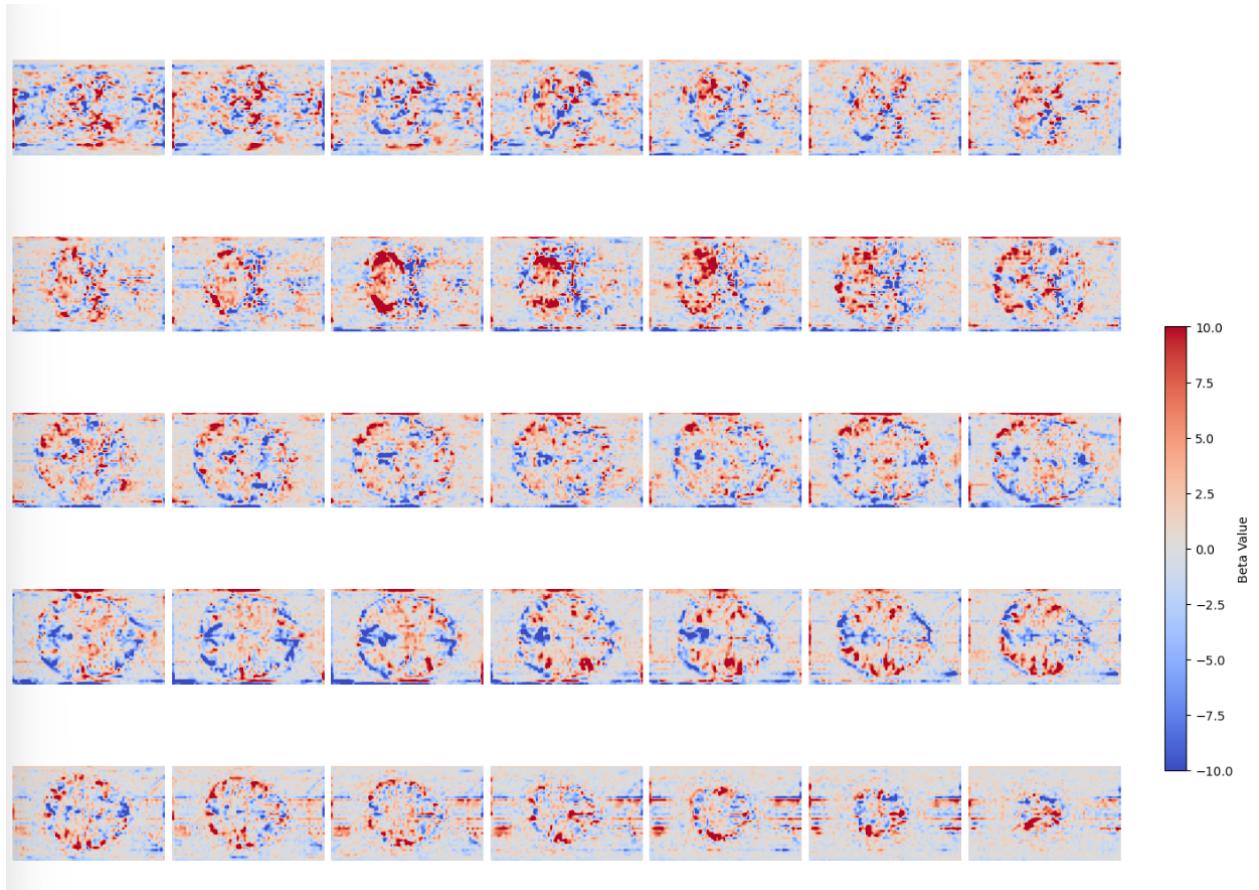


Figure 6: Beta coefficient maps visualized for different slices of the condition Cat of subject 1

2.2.7 Statistical Testing and T-Map Visualization

To determine significant activations, I computed t-maps and if necessary applied Bonferroni correction (present in the code) to control for multiple comparisons. This step ensures robust statistical inference.

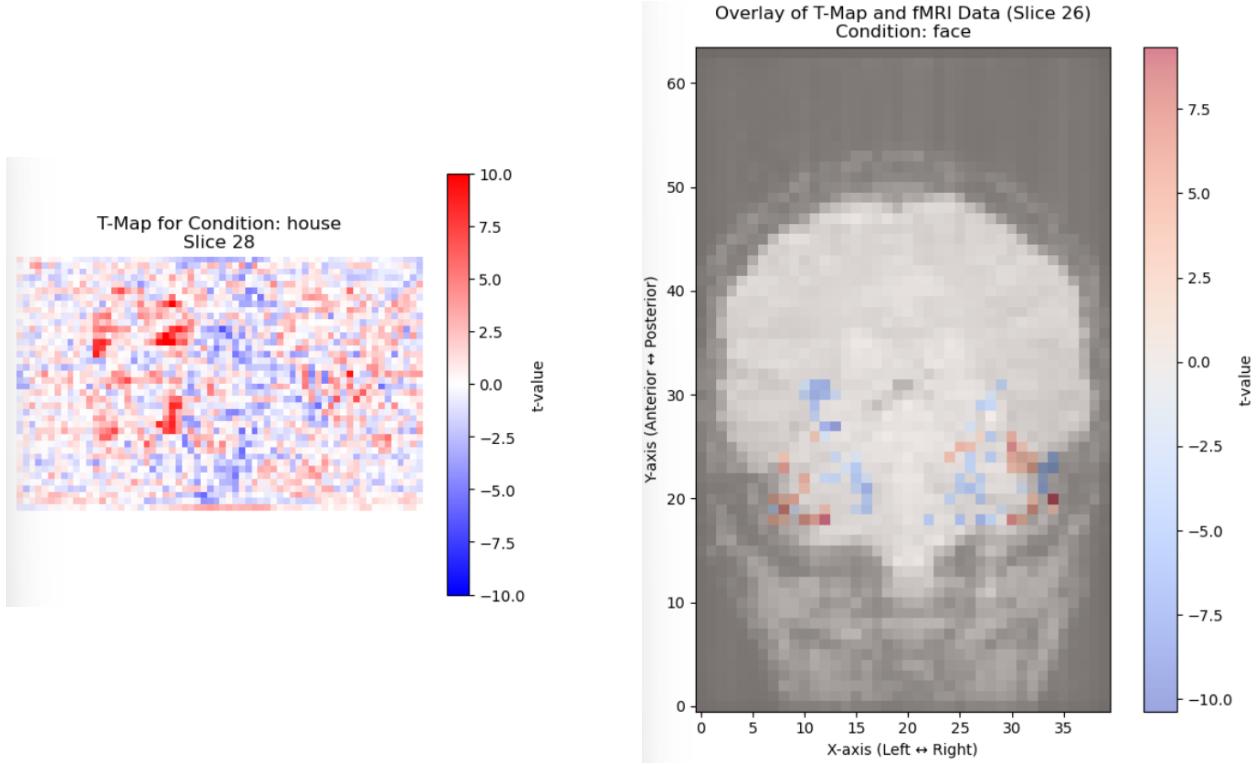


Figure 7: T-map visualization before and after overlaying on anatomical data. **Left:** T-map for the condition “house.” **Right:** Overlay of t-map on the fMRI data for the condition “face.”

The t-maps reveal regions with statistically significant activation, highlighting areas selectively engaged by the different conditions. The overlay visualization confirms the alignment between significant activations and anatomical structures.

2.2.8 Discussion

This project work focused on understanding the structure of the dataset and preparing the necessary pre-processing steps for later analyses. The design matrix construction, convolution with the HRF, and initial statistical analyses were performed to prepare the data for GLM fitting in the next project work.

2.3 Homework 2

(1) What is a cortical visual field map?

- A cortical visual field map is the systematic representation of the visual field across a region of the cortex. Each location on the retina is mapped to a particular place in the cortex such that nearby points in the visual field activate nearby cortical neurons. Multiple visual areas (e.g., V1, V2, V3) each contain their own visual field map, preserving the spatial layout of the external world in organized patterns on the cortical surface.

(2) How do you measure a visual field map in the human brain?

- Visual field maps in the human brain are measured using fMRI retinotopic mapping. Researchers present phase-encoded stimuli, such as expanding rings and rotating wedges to map eccentricity and polar angle, while recording BOLD signals. Each cortical voxel responds maximally when the stimulus passes through the part of the visual field it represents, and the timing of peak responses reveals the voxel's visual field selectivity.
- Data are analyzed using specialized software to compare stimulus sequences with BOLD signals and to model population receptive fields (pRFs), estimating receptive field location and size. Results are visualized on flattened cortical surfaces, highlighting retinotopic maps color-coded by eccentricity or angle.

(3) What is functional specialization?

- Functional specialization in the human visual cortex refers to the idea that distinct cortical regions are specialized for processing specific types of visual information, such as color, motion, or object recognition. While retinotopic mapping identifies where in the cortex the visual field is represented, functional specialization asks what each region does.

2.4 Project Work 2: ROI Analysis

2.4.1 Introduction

The goal of this project is to analyze functional MRI (fMRI) data using the general linear model (GLM) framework. Building on the previous assignment, I aim to:

- Finalize the design matrices and GLM fits.
- Identify voxels that exhibit significant contrast between conditions (e.g., faces vs. houses).
- Perform region-of-interest (ROI) analysis to investigate activity in predefined and random regions.

This report integrates the methods, results, and discussion into a unified structure for clarity. Each section describes the processing steps, presents the relevant findings, and interprets the outcomes.

2.4.2 Finalizing Design Matrices and GLM Fits

To prepare for the general linear model (GLM) analysis, I finalized the design matrices. This included defining a regressor for each stimulus category and a constant for each run, resulting in 12 constants for the 12 runs in the experiment.

The rationale behind this step is to ensure that the GLM model can account for variations across runs while modeling the neural response for each stimulus category separately. By including constants for each run, the model can isolate and control for run-specific baseline effects.

A custom Python function, ‘`modify_convolved_matrix`’ , was created to process the design matrix. The function performs the following tasks:

- Removes the ”rest” condition to focus on task-relevant activity.
- Adds a column for each run (e.g., `Run_1`, `Run_2`, etc.), where each column represents the presence of a specific run.

The resulting design matrix was visualized to verify correctness, as shown in Figure 8.

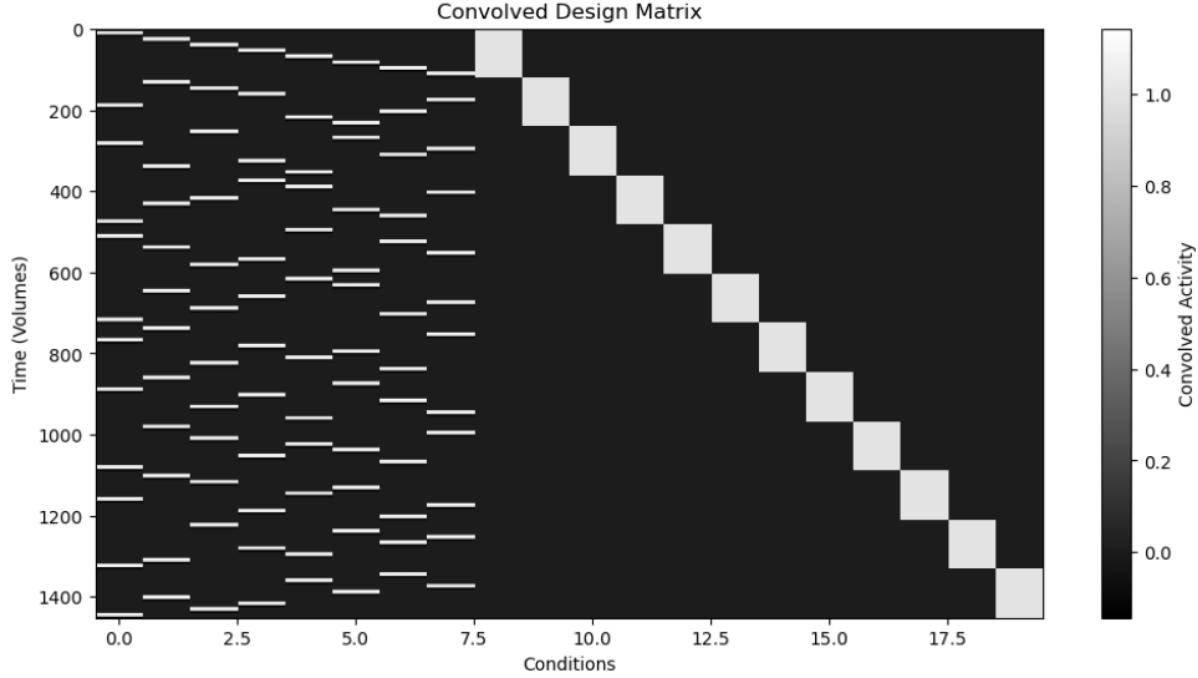


Figure 8: Convolved Design Matrix: Each column corresponds to a stimulus condition or run constant, while each row represents a time point (volume) in the experiment. The grayscale intensity represents the convolved activity.

This design matrix serves as the foundation for subsequent GLM fitting and statistical analysis. The structure ensures that the GLM captures condition-specific neural activity while accounting for run-level variability.

2.4.3 Contrasts: Faces vs. Houses and Other Comparisons

To investigate neural responses specific to different stimulus categories, I computed contrast maps using the general linear model (GLM). Specifically, I examined the following contrasts:

- **Faces vs. Houses:** To identify voxels with differential activation between faces and houses.
- **Scissors vs. Cats:** To explore activation differences between these two stimulus categories.

Why This Analysis? The goal of computing these contrasts was to examine whether specific regions of the brain showed category-selective responses. The contrasts allow for identifying areas with increased or decreased activation for one stimulus relative to another, providing insights into functional specialization in the brain.

Methodology The contrast maps were computed through the following steps:

- I defined a **contrast vector**, where the weights represented the conditions of interest (e.g., 1 for "faces" and -1 for "houses").
- I applied the contrast vector to the beta maps (parameter estimates from the GLM) to compute the contrast effect.
- I derived t-maps by dividing the contrast effect by its standard error, accounting for residual variance and the covariance of the design matrix.

- Bonferroni correction was applied to account for multiple comparisons across the brain, ensuring robust statistical results.

Results Figure 9 shows the uncorrected and Bonferroni-corrected t-maps for the contrast *Scissors vs. Cats*, while for the contrast *Houses vs. Faces*, it is visualized the complete t-map.

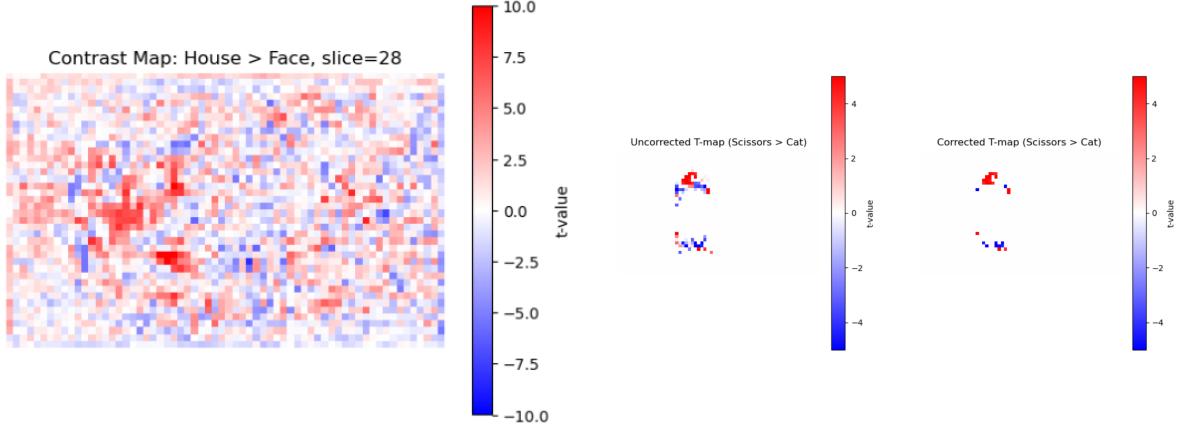


Figure 9: Visualization of T-Maps. (A) The full t-map for the *Houses vs. Faces* (B) The *Scissors vs. Cats* contrast shows mixed results.

Interpretation of Results For the **Houses vs Faces** contrast, I observed higher t-values (red regions) in ventral temporal areas for houses compared to faces, indicating relatively higher activation for houses in these regions. For the **Scissors vs. Cats** contrast, both regions of increased t-values (red) and decreased t-values (blue) were observed, highlighting mixed activation patterns for scissors relative to cats.

These results illustrate the value of contrast maps in revealing stimulus-specific activation differences across the brain.

2.4.4 Region-of-Interest (ROI) Analysis - Part 1

To investigate region-specific activity, I utilized predefined and random regions of interest (ROIs) from the Haxby dataset. Predefined masks included:

- **Ventral Temporal ROI:** A general mask covering ventral temporal regions.
- **Face ROI:** A face-selective region identified from GLM contrast.
- **House ROI:** A house-selective region identified from GLM contrast.

Additionally, I generated random ROIs for comparison:

- **Random Inside ROI:** Random voxels inside the brain mask.
- **Random Outside ROI:** Random voxels outside the brain mask.

Time-Course Analysis Average BOLD signal time courses were extracted for each ROI. This analysis helps identify stimulus-related activity and temporal dynamics within each ROI. Figure 10 shows the average time courses across all ROIs.

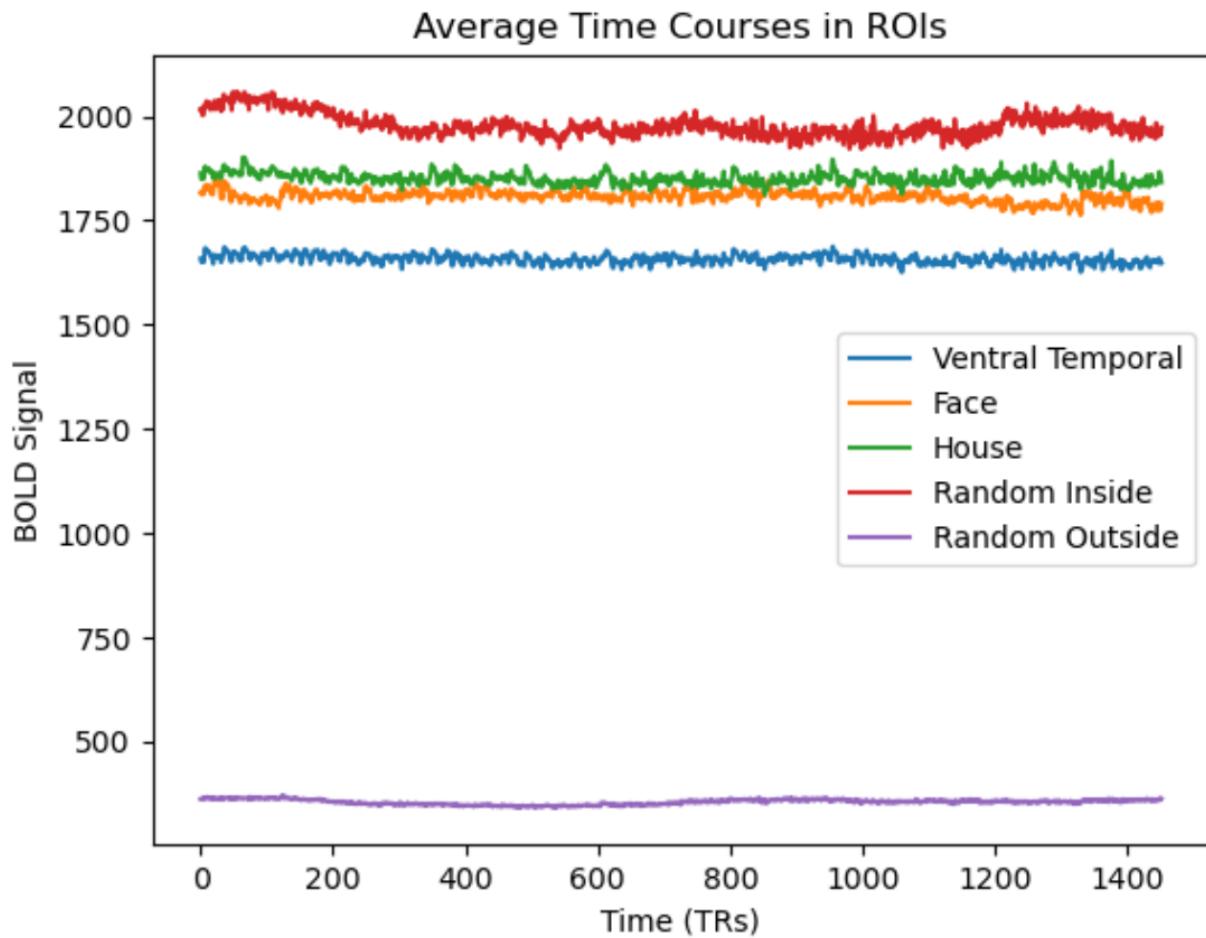


Figure 10: Average BOLD Signal Time Courses for ROIs. Time courses are averaged across all voxels within each ROI. Each curve represents a different ROI, allowing for comparisons of their temporal dynamics.

Face ROI Activation Highlighted To examine the relationship between the BOLD signal and the "face" condition, I plotted the average time course for the Face ROI with active face condition periods highlighted (Figure 11). This visualization helps identify the temporal correspondence between condition onsets and ROI activity.

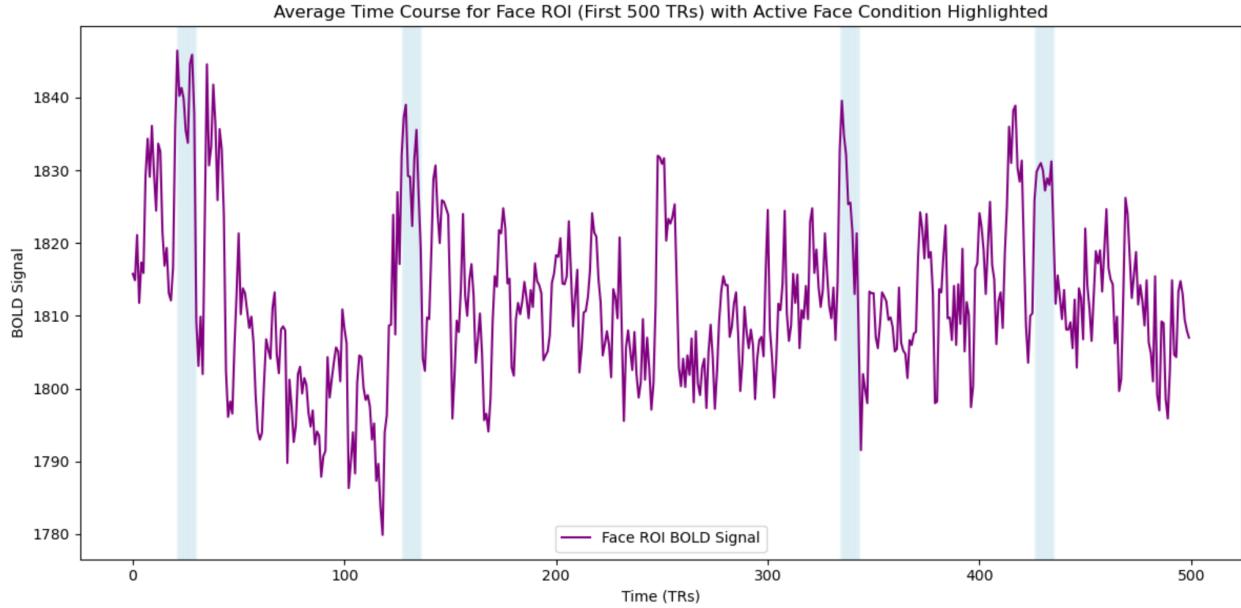


Figure 11: Average Time Course for Face ROI with Active "Face" Condition Highlighted. Shaded areas indicate time points when the "face" condition was active. A clear correspondence between activity peaks and condition onsets can be observed.

2.4.5 Region-of-Interest (ROI) Analysis - Part 2

Percent Signal Change Analysis To better understand the functional specialization of different brain regions, I calculated the percent signal change in BOLD activity for each condition and ROI. This analysis normalizes the beta values relative to baseline activity (constant terms), allowing for a more interpretable measure of neural activity as a percentage deviation from the baseline. The goal of this step is to:

- Quantify condition-specific activity within predefined ROIs (e.g., Face ROI, House ROI).
- Compare predefined ROIs to random ROIs to assess the reliability and specificity of the observed neural responses.

Figures 12 and 13 show the average percent signal change for select ROIs.

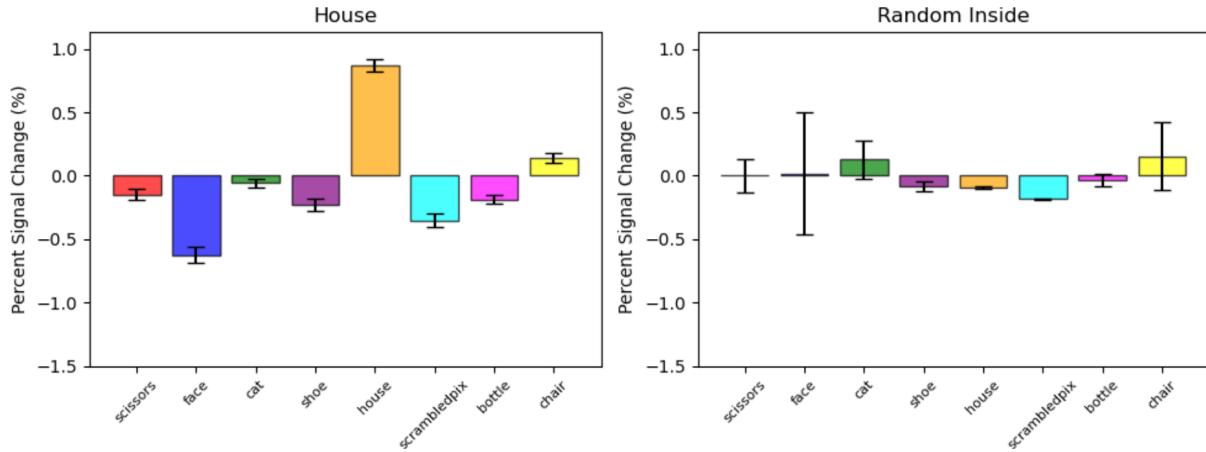


Figure 12: Percent Signal Change for "House" ROI and Random Inside ROI. Each bar represents the average percent signal change for a specific condition. Error bars indicate the standard error of the mean (SEM).

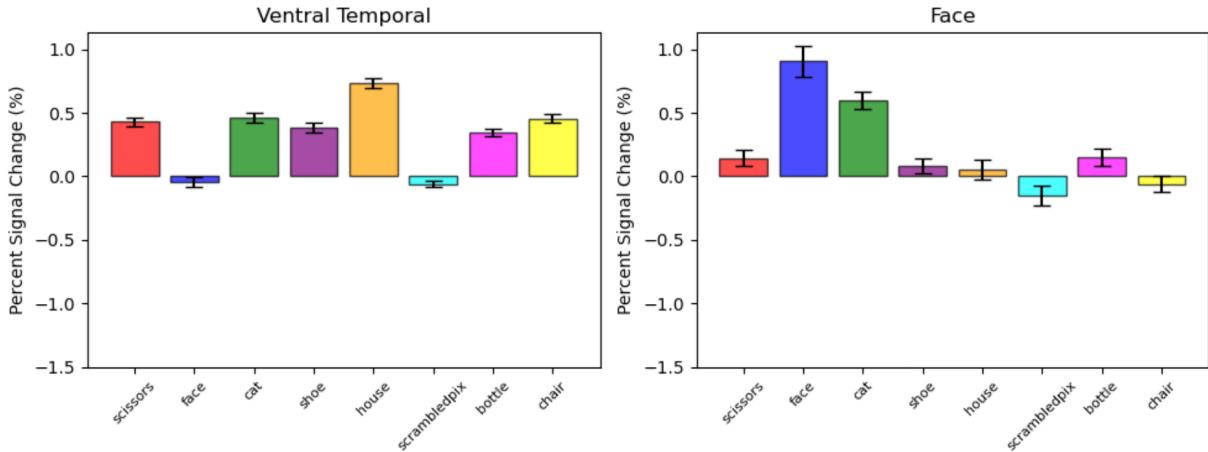


Figure 13: Percent Signal Change for "Ventral Temporal" and "Face" ROIs. Each bar represents the average percent signal change for a specific condition. Error bars indicate the standard error of the mean (SEM).

Discussion of Results The ROI analysis revealed:

- The **Face ROI** showed significant activation for the "face" condition, with clear correspondence between condition onsets and BOLD signal peaks.
- The **House ROI** showed significant activation for the "house" condition, reflecting its functional specificity.
- **Random ROIs** displayed negligible or inconsistent signal changes, demonstrating the robustness of the predefined ROIs.

The percent signal change analysis highlights the stimulus-specific responses within each ROI, providing insight into the functional specialization of ventral temporal regions.

2.4.6 Multi-Subject Analysis

To generalize the findings, I extended the ROI analysis to multiple subjects. The goal was to compute the average percent signal change across subjects for each ROI and condition. This analysis involved several steps, encapsulated in reusable functions for efficient processing:

Single-Subject Analysis The single-subject analysis pipeline includes:

- Loading subject-specific BOLD data and labels.
- Creating and modifying the design matrix.
- Fitting the GLM to generate residuals and beta maps.
- Extracting percent signal change for each ROI, normalized by baseline activity (constant terms).

Multi-Subject Analysis To aggregate results across subjects, I implemented a function to:

- Loop through all subjects and apply the single-subject analysis pipeline.
- Collect the percent signal change data for each ROI and condition.
- Compute the group-level mean percent signal change and standard error of the mean (SEM) for each ROI.

Results The group-level analysis was performed on data from four subjects. The averaged percent signal change across conditions is visualized in Figures 14 and 15.

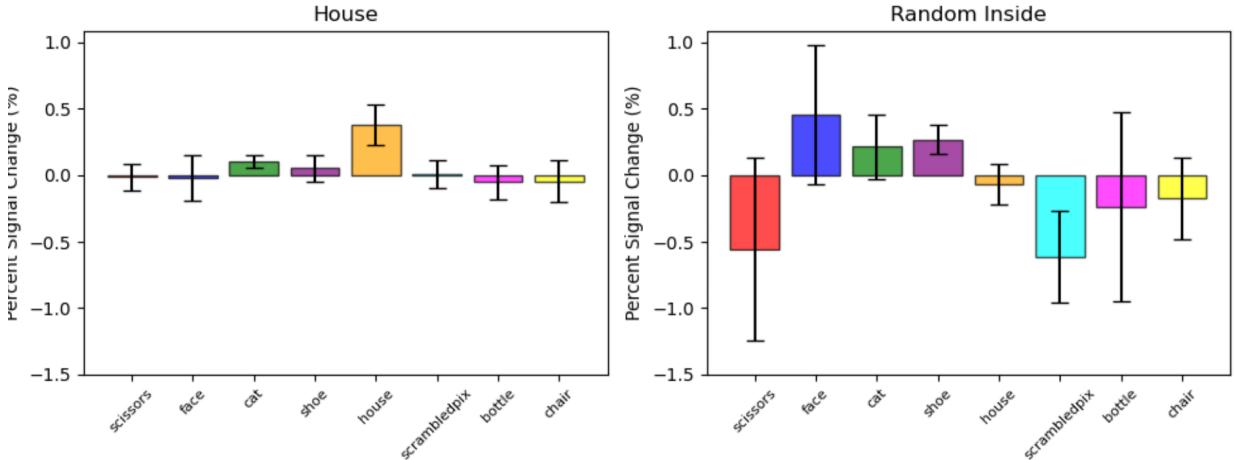


Figure 14: Group-Level Percent Signal Change for "House" and "Random Inside" ROIs. Each bar represents the average percent signal change across four subjects for a specific condition. Error bars indicate the standard error of the mean (SEM).

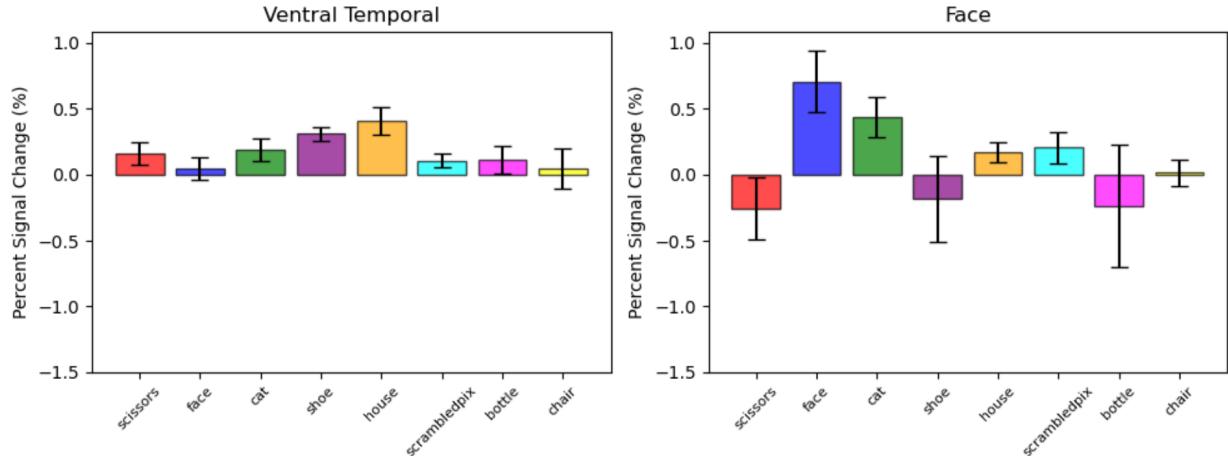


Figure 15: Group-Level Percent Signal Change for "Ventral Temporal" and "Face" ROIs. Each bar represents the average percent signal change across four subjects for a specific condition. Error bars indicate the standard error of the mean (SEM).

2.4.7 Discussion

The multi-subject analysis confirms the robustness of the findings:

- The **Face ROI** consistently shows higher percent signal change for the "face" condition across subjects, reaffirming its functional specialization.
- The **House ROI** demonstrates specificity for the "house" condition, with negligible activation for other stimuli.
- **Random ROIs** exhibit low and inconsistent signal changes, as expected.

By averaging across subjects, I account for individual variability and gain a clearer picture of condition-specific activation patterns in the predefined ROIs. This approach validates the functional relevance of the ventral temporal regions for category-specific processing.

2.5 Homework 3

(1) What is pattern-information analysis (also called multi-voxel pattern analysis, MVPA)?

- Pattern-information analysis (or MVPA) is a method used in fMRI research to examine spatial patterns of activity across multiple voxels. By analyzing these patterns, MVPA can decode the representational content, such as distinguishing between different stimuli or cognitive states.

(2) What is novel about pattern-information analysis compared to standard (univariate) fMRI analysis?

- The difference of pattern-information analysis lies in its ability to detect fine-grained spatial patterns of activity that are lost in standard univariate fMRI analysis. While univariate analysis averages activity across an entire region (e.g., focusing on whether a region is activated or not), MVPA examines the detailed spatial pattern of activation across voxels. This allows it to identify differences in representational content, even when the overall activation levels are similar.

(3) In practice, how would you perform pattern-information analysis on fMRI data?

- **Step 1:** Split data into training and test sets (use cross-validation for small datasets) and preprocess (correct slice timing, motion, trends; avoid smoothing).
- **Step 2:** Use models like GLM to estimate voxel-level activity patterns, producing beta values for each condition.
- **Step 3:** Select voxels using ROI-based approaches or searchlight mapping.
- **Step 4:** Train a classifier (e.g., linear SVM) using the training set to compute voxel weights.
- **Step 5:** Test classifier performance on the test set by calculating classification accuracy and verifying statistical significance (e.g., chi-square test).

2.6 Project Work 3: Classification Analysis

2.6.1 Introduction

The goal of this project is to analyze functional MRI (fMRI) data using classification analysis to investigate object representations in the brain. This process involves dividing the data into testing and training sets (even vs. odd runs), calculating correlations within and between categories using a pattern-correlation classifier, and applying these analyses to a specific region of interest (ROI). Furthermore, the results are compared to those of Haxby et al. (2001), which demonstrated how multi-voxel activity patterns can distinguish distributed and overlapping representations of stimuli. If the experimental conditions can be classified based on activity patterns significantly better than chance, it indicates that fMRI activity patterns encode meaningful information about the stimuli.

2.6.2 Data Splitting

The 20-condition design matrix (8 conditions and 12 run-specific intercepts) was split into even and odd runs, resulting in two separate design matrices. Each design matrix retained 14 conditions (8 conditions + 6 intercepts). Figure 16 illustrates the design matrices for even and odd runs after convolution.

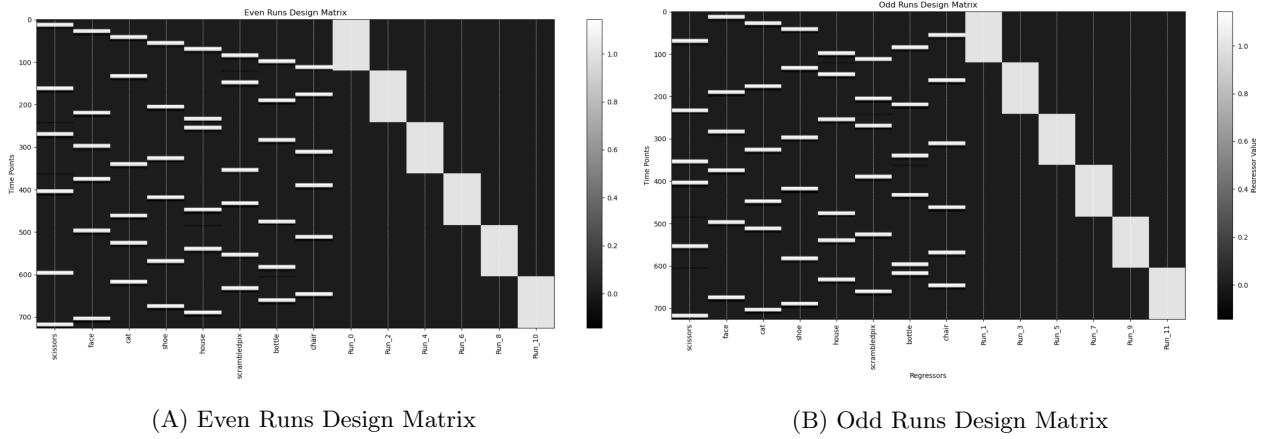


Figure 16: Convolved Design Matrices for Even and Odd Runs. Each column represents a condition or run-specific intercept.

2.6.3 GLM Fitting and T-Maps

For both even and odd runs, GLMs were fit to the data, and t-maps were computed for each condition. This process resulted in 14 t-maps per run type, but the primary focus was on the 8 stimulus conditions. These t-maps capture condition-specific neural activity and serve as inputs for the subsequent correlation analysis.

2.6.4 Pattern Correlation Analysis

To evaluate the object representations, a VT mask was applied to the t-maps, isolating voxels within the ventral temporal region. Pearson correlations were then computed:

- **Within-category correlations:** Between even and odd runs for the same condition.
- **Between-category correlations:** Between even and odd runs for different conditions.

The results were visualized as bar charts (Figures 17–20).

2.6.5 Correlation Results for Selected Conditions

Face Condition: For the face condition, the within-category correlation was higher than all between-category correlations (Figure 17).

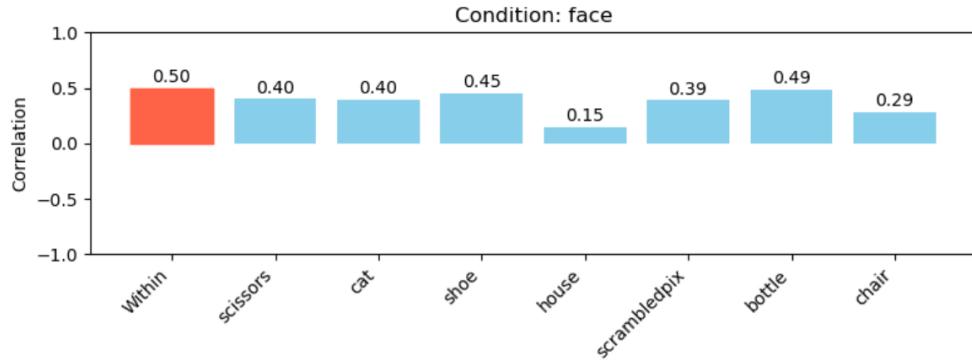


Figure 17: Within- and Between-Category Correlations for the Face Condition.

House Condition: The house condition also showed a strong within-category correlation, higher than most between-category correlations (Figure 18).

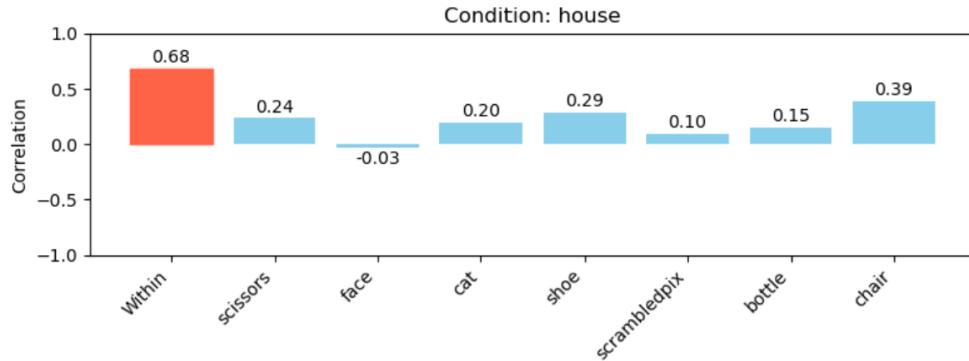


Figure 18: Within- and Between-Category Correlations for the House Condition.

Scissors Condition: Similar to the face and house conditions, the scissors condition displayed higher within-category correlation compared to between-category correlations (Figure 19).

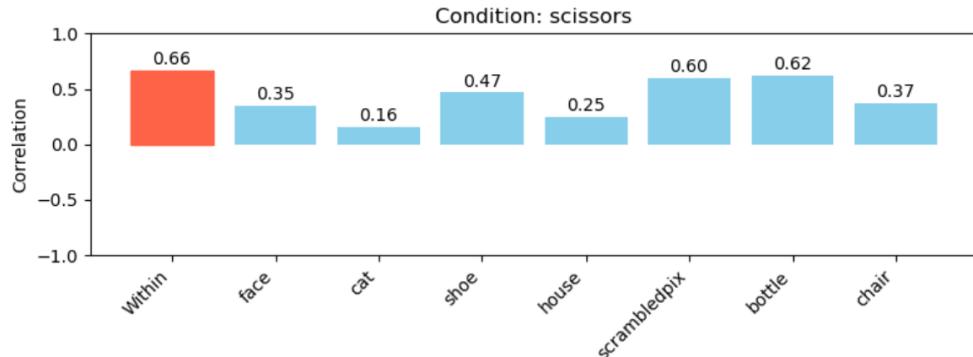


Figure 19: Within- and Between-Category Correlations for the Scissors Condition.

Bottle Condition: The within-category correlation for the bottle condition was lower than several between-category correlations, as shown in Figure 20. This suggests less distinct representations for the bottle category.

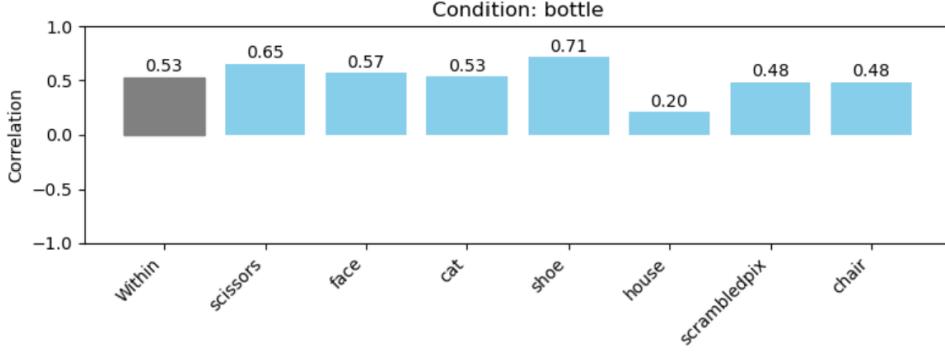


Figure 20: Within- and Between-Category Correlations for the Bottle Condition.

2.6.6 Correlation Results Across All Subjects

The within- and between-category correlations were computed across all six subjects, showing a consistent pattern: within-category correlations were always higher than between-category correlations. This strongly supports the hypothesis that object categories elicit distinguishable activity patterns in the ventral temporal cortex across participants.

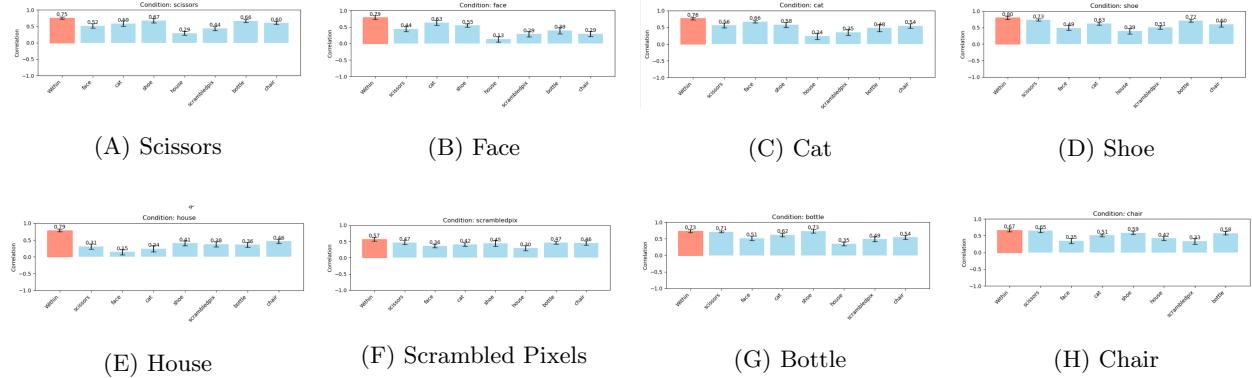


Figure 21: Within- and Between-Category Correlations Across All Subjects.

2.6.7 Discussion

The analysis demonstrates the utility of pattern-correlation classifiers in identifying object representations in fMRI data. Using the VT mask, within-category correlations were generally higher than between-category correlations, aligning with findings from previous work (Haxby et al., 2001). The results were replicated across all six subjects, showing consistent neural patterns distinguishing object categories.

A notable difference from Haxby et al. (2001) is the use of t-maps in this analysis, which resulted in positive correlation values across conditions.

2.7 Homework 4

(1) What is Representational Similarity Analysis (RSA)?

- Representational Similarity Analysis (RSA) compares how different stimuli are encoded by evaluating the similarity (or dissimilarity) of their neural representations. These relationships are summarized in a Representational Dissimilarity Matrix (RDM), which captures the pairwise dissimilarities between stimuli. RSA compares RDMs across datasets (e.g., brain activity, models, or behavior) to reveal how representational structures align and provide insights into neural organization.

(2) What is a Representational Dissimilarity Matrix (RDM)?

- A Representational Dissimilarity Matrix (RDM) is a symmetric matrix summarizing the pairwise dissimilarities between stimuli based on neural, computational, or behavioral data. Each row and column represents a stimulus, and cells contain dissimilarity values, with zeros on the diagonal. RDMs allow comparison of representational structures across different datasets.

(3) Example of a Research Question Addressed Using RSA

A research question mentioned in the paper and explored in a study used RSA is:

- *"How are sensory and motor representations of finger movements organized in the cerebellum compared to cortical areas M1 and S1?"*
- RSA revealed that both the cerebellum and cortical areas discriminated finger movements and sensations. Unlike M1 and S1, which showed consistent sensory-motor patterns for the same finger, the cerebellum's representations were inconsistent. This unique organization in the cerebellum may support flexible associations between movements and their sensory consequences, which is critical for learning new motor tasks.

2.8 Project Work 4: Representational Similarity Analysis (RSA)

2.8.1 Introduction

Representational Similarity Analysis (RSA) is a method for studying how information is encoded in the brain by quantifying neural activity patterns using Representational Dissimilarity Matrices (RDMs). These matrices allow us to investigate the representational structure of a brain region and identify which features are emphasized in its responses.

This project applied RSA to analyze brain responses to different stimulus categories. The analysis involved:

- Constructing RDMs for various regions-of-interest (ROIs),
- Comparing RDMs across ROIs and subjects,
- Evaluating replicability of RDMs using split-data analysis,
- Calculating the Exemplar Discriminability Index (EDI) to assess the separability of within- and between-condition patterns.

2.8.2 Extracting Response Patterns

Condition-specific beta maps were computed using General Linear Models (GLMs) applied to fMRI data from six subjects. These maps quantified neural responses for eight stimulus categories across five ROIs: Ventral Temporal, Face, House, Random Inside, and Random Outside regions.

2.8.3 Constructing RDMs

RDMs were computed for each ROI and subject by calculating pairwise dissimilarities between condition-specific patterns using 1 – Pearson correlation.

2.8.4 Visualizing RDMs

Heatmaps were used to visualize the RDMs and highlight the representational structure within each ROI (Figure 22). Multidimensional Scaling (MDS) was applied to project high-dimensional dissimilarity data into a 2D space, revealing possible clustering patterns for the stimulus categories (Figure 23).

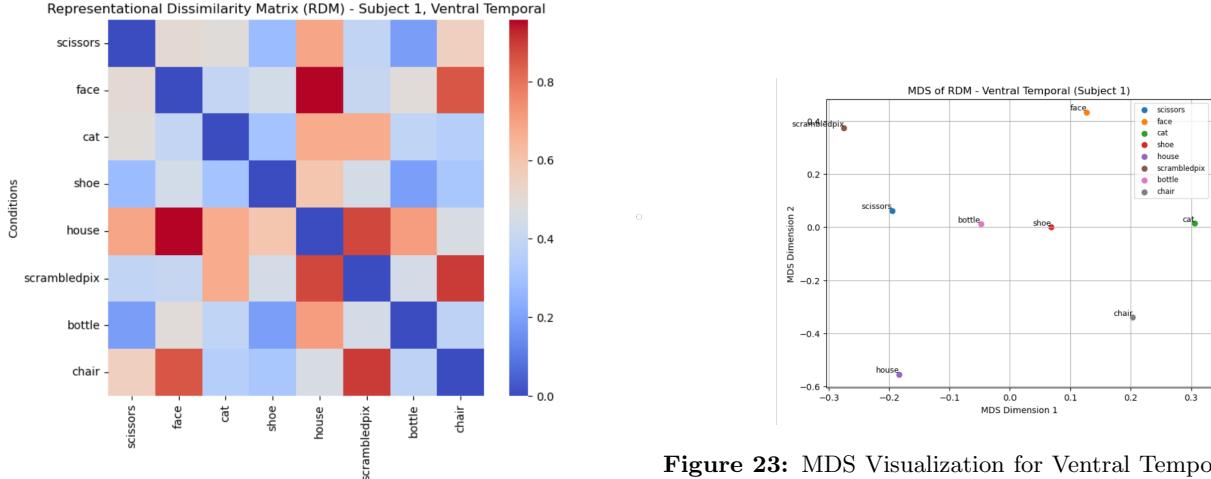


Figure 23: MDS Visualization for Ventral Temporal (Subject 1).

Figure 22: RDM for Subject 1, Ventral Temporal Region.

2.8.5 Comparing RDMs Across ROIs and Subjects

RDMs were directly compared across ROIs and subjects using Pearson correlation. Results are shown in Figure 24.

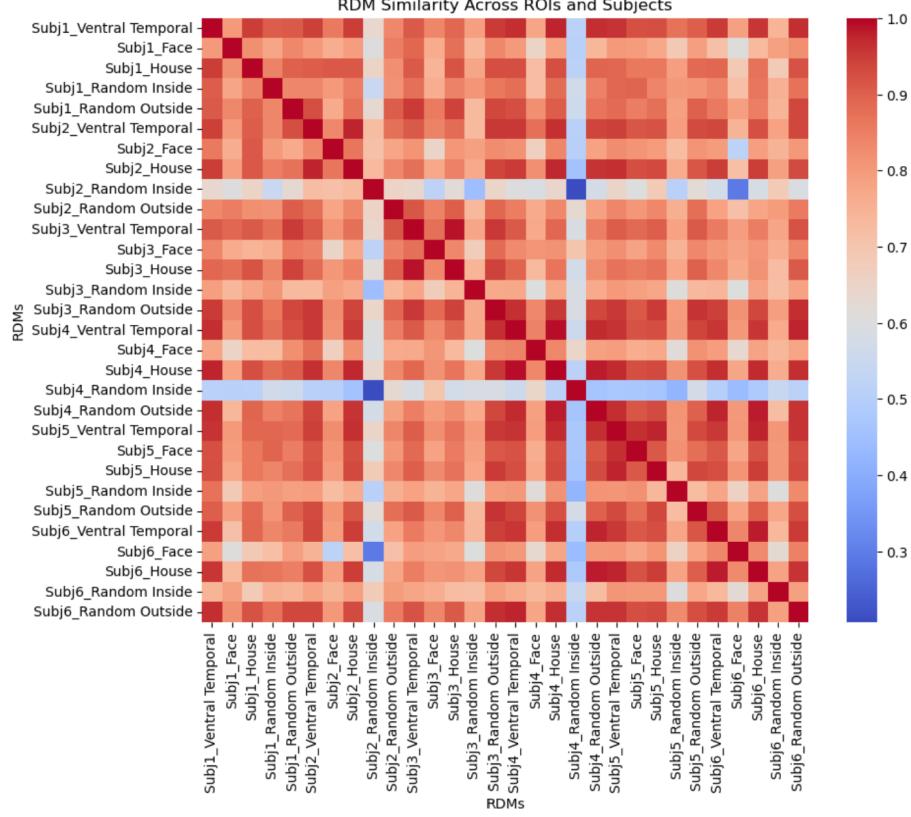


Figure 24: RDM Similarity Across ROIs and Subjects.

2.8.6 Split-Data RDMs and Exemplar Discriminability Index (EDI)

Split-data RDMs were computed for even and odd runs to study the replicability of RDMs. The EDI was calculated to evaluate how well response patterns for the same condition matched across splits compared to different conditions. Results are shown in Figures 25 and 26.

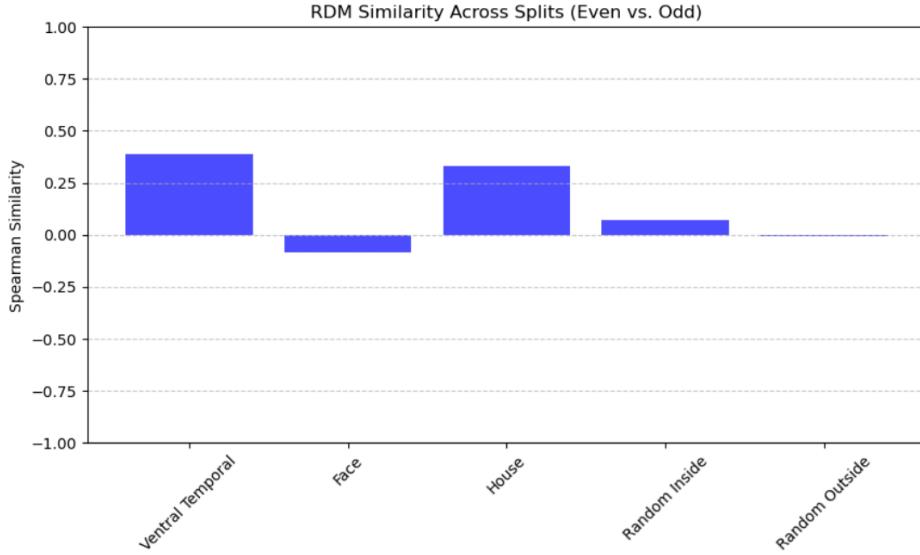


Figure 25: RDM Similarity Across Splits (Even vs. Odd).

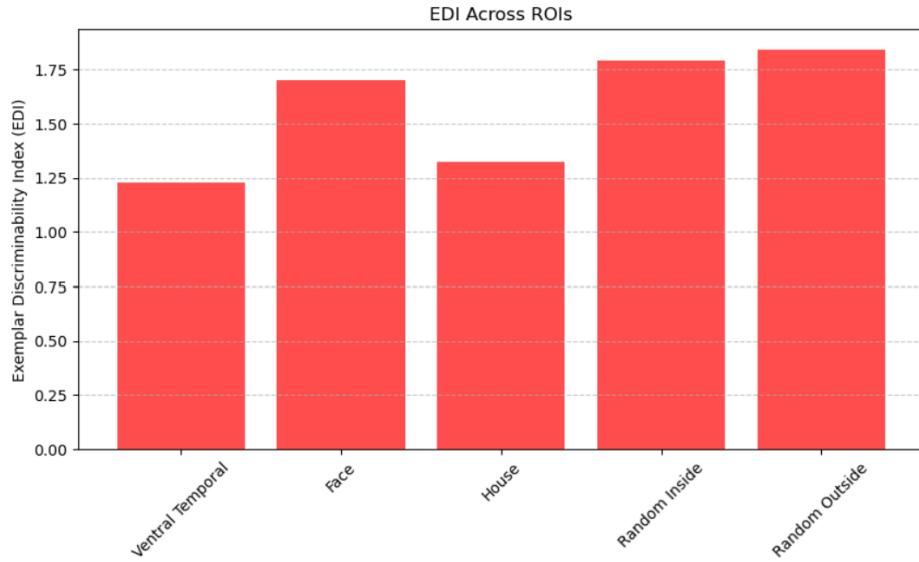


Figure 26: Exemplar Discriminability Index (EDI) Across ROIs.

2.8.7 MDS Visualization

The MDS plot for the Ventral Temporal region (for Subject 1) showed possible separability of stimulus categories (Figure 23).

2.8.8 RDM Similarity Across ROIs and Subjects

The similarity matrix (Figure 24) was challenging to interpret directly. However, diagonal correlations were evident for the same ROIs across subjects. Random ROIs exhibited consistently low correlation (horizontal and vertical lines), while 3x3 blocks for the Ventral, Face, and House ROIs (in the diagonal, for each subject) were generally higher, reflecting consistency.

2.8.9 Split-Data Analysis and EDI

RDM similarity between even and odd splits was moderate for Ventral Temporal and House ROIs (Figure 25), reflecting partial replicability. The EDI was highest for the Face ROI, indicating clear separability of conditions in this region (Figure 26).

2.8.10 Discussion

This analysis demonstrates that RSA can reveal how information is encoded in the brain by examining the representational geometry of specific ROIs. MDS showed some possible clustering for certain stimulus categories, while RDM comparisons highlighted high correlations for key ROIs (Ventral, Face, and House). The split-data analysis revealed moderate replicability, and the EDI showed that the Face ROI had the most separable response patterns.

2.9 Homework 5

(1) What are the differences between decoding and encoding models?

- Encoding and decoding models are mathematically related and can be derived from each other using Bayes' theorem. The key difference lies in the direction of mapping: encoding models predict brain activity (voxel responses) from stimulus features, while decoding models infer stimulus features from observed brain activity. In other words, an encoding model projects the feature space onto the activity space, whereas a decoding model projects the activity space onto the feature space (as shown in Figure 1 of the article).

(2) What are the main advantages of using an encoding model?

- Focusing on encoding models offers two key advantages over decoding models. First, an encoding model can, in principle, provide a complete functional description of a region of interest (ROI). Second, deriving an optimal decoding model from an encoding model is straightforward, but the reverse process is much more difficult. Additionally, encoding models provide an explicit, quantitative description of how information is represented in individual voxels, enabling direct comparison between multiple models.

(3) What might be the reasons why decoding models are much more common in fMRI than encoding models?

- Despite the advantages of encoding models, decoding models are widely used in fMRI for several reasons. First, decoding models allow for direct comparison with behavioral performance, making them useful for studying cognition and decision-making. Second, decoding plays a crucial role in "brain-reading" and neuroprosthetic applications, making it appealing for applied neuroscience research.

2.10 Project Work 5: vRF modeling

2.10.1 Introduction

This project explores the implementation of a **voxel receptive field (vRF) model** using the **Haxby dataset**, which contains fMRI data collected while participants viewed different categories of visual stimuli. The goal of vRF modeling is to characterize voxel responses to specific visual features such as edges, spatial frequency, and orientation.

When I attempted to fit the encoding model—mapping stimulus features to voxel responses—using Gabor or wavelet transforms optimized with least squares regression, I encountered an error related to **stimulus-to-fMRI alignment**. This prevented successful modeling, leading me to suspect a fundamental limitation in the dataset.

2.10.2 Loading the fMRI Data

The dataset consists of a 4D neuroimaging file (**bold.nii.gz**) with dimensions $(40 \times 64 \times 64 \times 1452)$, representing brain activity over 1452 time points. The experimental design matrix (**labels.txt**) provides condition labels for each time point. A **region-of-interest (ROI) mask** was applied to focus on the **ventral temporal region**.

2.10.3 Extracting Visual Features from Stimuli

To model voxel responses, **low-level visual features** were extracted from stimulus images using:

- **Gabor filters:** Captured orientation- and frequency-specific edges but were computationally **expensive**.
- **Wavelet transform:** A **faster alternative** preserving spatial frequency information.

However, a key challenge emerged: **the extracted features could not be reliably mapped to fMRI time points**, making further analysis infeasible.

2.10.4 Stimuli and Feature Alignment Challenges

The dataset follows a **block design**, where stimuli are presented in grouped time intervals. However, the dataset does not specify which **exact images** were shown in each block, preventing precise stimulus-response mapping.

2.10.5 Dataset Constraints and Dimensionality Mismatch

The first issue I encountered was the discrepancy between the number of unique stimulus images and the number of fMRI time points:

- The experiment included **108 repetitions per condition**, but only **48 unique images per category**, totaling **336 unique images**.
- The control set contained **328 scrambled images**, bringing the dataset to **664 images**.
- Despite these images being repeated over many trials, the extracted feature matrix had **only 335 rows**, while the fMRI data spanned **1452 time points**.
- This mismatch is not just a size issue but a **structural limitation**—features could not be assigned to the correct time points.

This misalignment caused a **matrix multiplication error** during vRF fitting, preventing receptive field estimation.

2.10.6 Limitations of the Haxby Dataset for vRF Modeling

- vRF models require a **one-to-one mapping** between stimulus features and fMRI responses. The Haxby dataset only provides **condition-level labels** (e.g., "faces" or "houses") instead of specifying **which exact image** was shown at each time point.
- Extracted features from **wavelets and Gabor filters** could not be aligned with specific time points due to the dataset's block design.

Finally, the Haxby dataset is inherently not well-suited for vRF modeling, as it contains only a few object categories. This makes it more appropriate for **classification and representational similarity analysis (RSA)**, where the goal is to discriminate between object categories rather than estimate voxel-specific receptive fields.

2.10.7 Discussion

This report highlights the challenges in applying vRF modeling to the Haxby dataset. The fundamental limitation is the lack of **precise stimulus-to-fMRI alignment**, which is essential for vRF modeling.

3 Conclusion

This portfolio illustrates the diverse analytical approaches used in fMRI research, spanning univariate activation mapping, multivariate pattern classification, and neural representational modeling. Across five project works, key insights emerged regarding the complementary strengths of these methods:

- **Utility of GLM-Based Approaches:** Univariate analyses using general linear models (GLMs) provided robust methods for detecting condition-specific activation patterns. Properly constructed design matrices and statistical contrasts revealed selective responses to different stimuli in functionally relevant brain regions.
- **Value of ROI Analysis:** Region-of-interest (ROI) analyses allowed for more targeted investigations into functionally selective regions such as the ventral temporal cortex. By comparing predefined ROIs (e.g., face- and house-selective areas) to random ROIs, the analysis demonstrated the importance of carefully selecting regions for statistical comparisons.
- **Power of Multivariate Decoding:** Classification-based techniques, including multi-voxel pattern analysis (MVPA), provided evidence that distributed voxel patterns encode meaningful stimulus information. The consistent finding that within-category correlations were higher than between-category correlations highlights the capacity of fMRI to detect representational structure beyond simple activation peaks.
- **Insights from RSA:** Representational Similarity Analysis (RSA) enabled a deeper examination of how different categories are encoded in the brain by comparing dissimilarity structures across conditions and subjects. The results reinforced the idea that fMRI activity captures complex representational geometry beyond what standard univariate analysis can reveal.
- **Challenges of vRF Modeling:** Attempts to apply voxel receptive field (vRF) modeling were hindered by dataset constraints, particularly the lack of precise stimulus-to-timepoint alignment. This highlighted an important limitation: while encoding models can provide detailed voxel-level tuning estimates, their applicability depends on datasets designed for fine-grained feature mapping.

Taken together, these analyses showcase the complementary nature of different fMRI methodologies.