

Exercise #3

Analysis of Visual Stimuli Correlation in fMRI Data

Introduction

This study analyzes fMRI data to investigate the brain's response to different visual stimuli: coherent motion, incoherent motion, and biological motion. Using a 4D DICOM dataset, we performed spatial and temporal analysis, generated stimulus-aligned brain activity maps, computed voxel-wise correlations, and evaluated the effect of convolving the stimuli with a Hemodynamic Response Function (HRF).

Methods

1. DICOM Data Exploration and Preprocessing

The DICOM files were loaded using the pydicom library, and the Repetition Time (TR) was extracted from the metadata. Each image in the dataset represents a time point and contains a grid of slices. These were reshaped into a 4D numpy array with dimensions (time, slice, height, width) by organizing the slices into rows and columns, cropping out extra lines, and adjusting for spatial layout. Axial, sagittal, and coronal views were extracted and visualized.

```
slices_4D_reshaped = images_cropped.reshape(num_samples, nSliceRows, slice_height, nSliceCols, slice_width)
slices_4D = slices_4D_reshaped.transpose(0, 1, 3, 2, 4).reshape(num_samples, slices_per_image, slice_height, slice_width)
```

2. Correlation with Stimuli

Binary stimulus vectors for coherent, incoherent, and biological motion were created, incorporating a 5-second hemodynamic delay to align with the expected brain response timing. The Pearson correlation coefficient was then calculated between the time series of each voxel and the stimulus vector for each condition. To highlight areas with significant activity related to the stimuli, the resulting correlation values were visualized as color-coded maps. These correlation maps were overlaid on anatomical slices, with a threshold applied to focus on voxels

showing strong positive associations with the stimulus time course (as was done in the instruction plot).

```
"correlation, p_value = pearsonr(voxel_timeseries, stim_vector)
corr_matrix[slice_idx, row, col] = correlation"
"start_idx = int(max(time_idx + delay_points, 0)), end_idx = int(min(time_idx + (stim_len // T
R) + delay_points, num_timepoints))"
```

3. Hemodynamic Response Modelling (HRF)

To model the delayed BOLD response, we implemented a gamma-based Hemodynamic Response Function (HRF), defined using specific parameters like tau and n (we used $n = 3$ as it fit the peak latency better). Binary stimulus vectors were then convolved with this calculated HRF to account for the temporal lag and smoothing of the hemodynamic response. Correlations between each voxel's time series and these convolved stimulus vectors were recalculated.

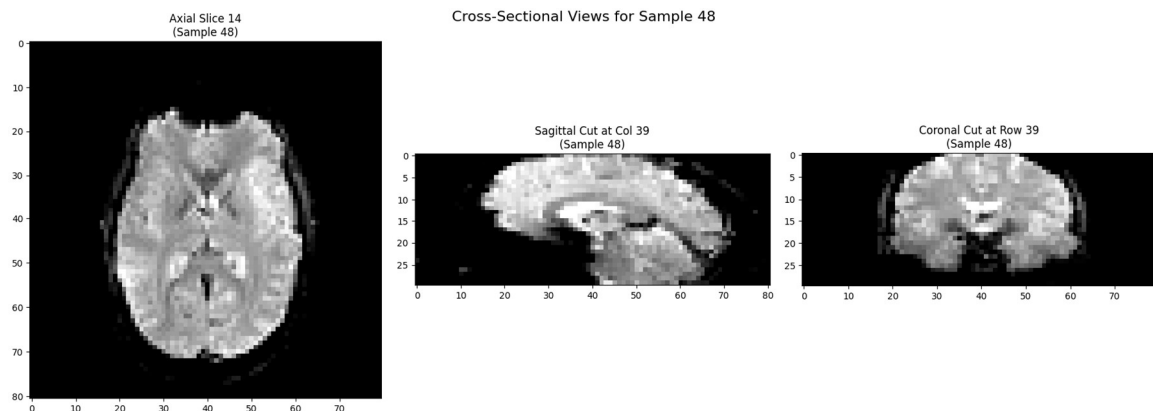
```
def hrf(t, tau=0.5, n=3):
    return ((t / tau) ** (n - 1)) * np.exp(-t / tau) / (tau * gamma(n))

stim_vector_convolved = np.convolve(stim_vector, hrf_values)[:num_timepoints]
```

Each part of the analysis—data organization, correlation, and modeling—was critical for understanding how brain responses vary by motion type and for identifying the most responsive voxels per condition.

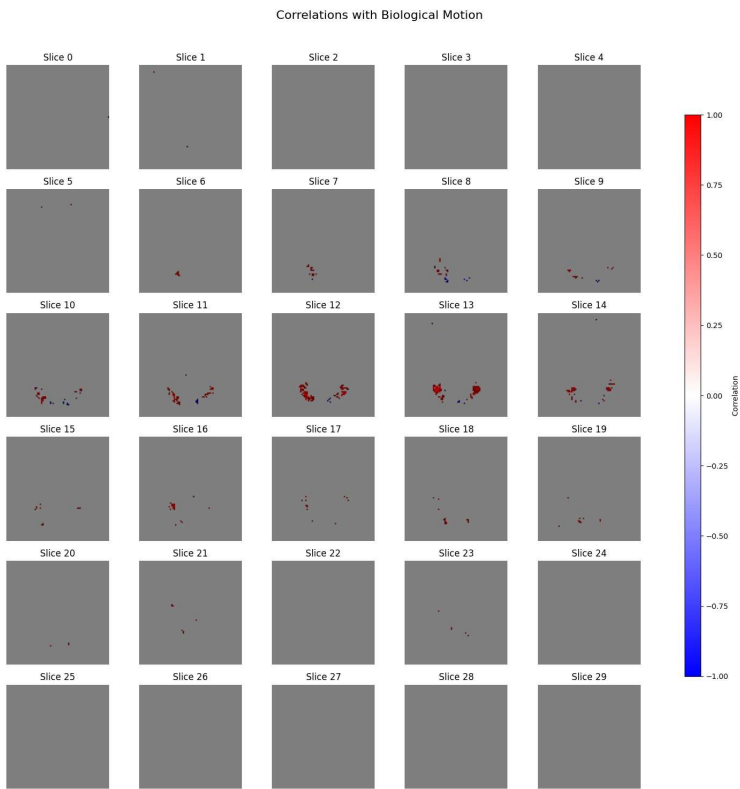
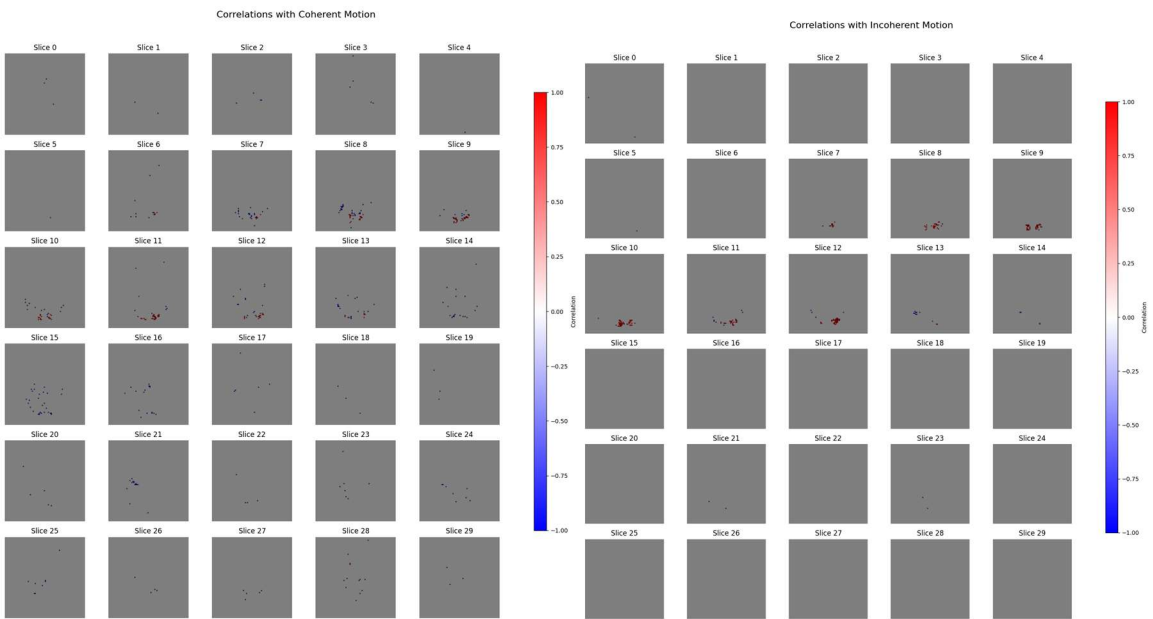
Results

Cross-Sectional Views

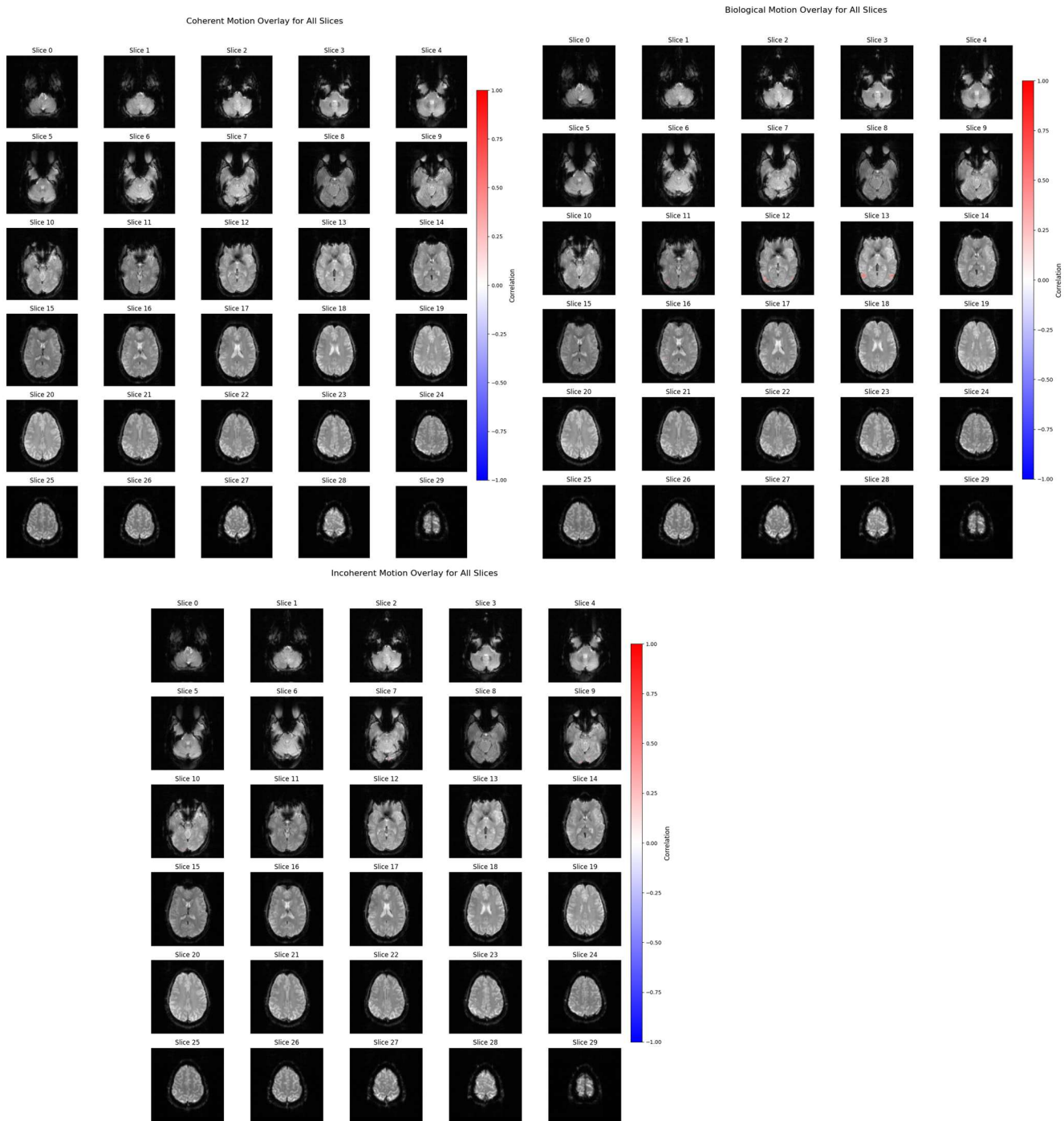


Axial, sagittal, and coronal cross sections for a selected timepoint.

Correlation Maps Without the images overlaid

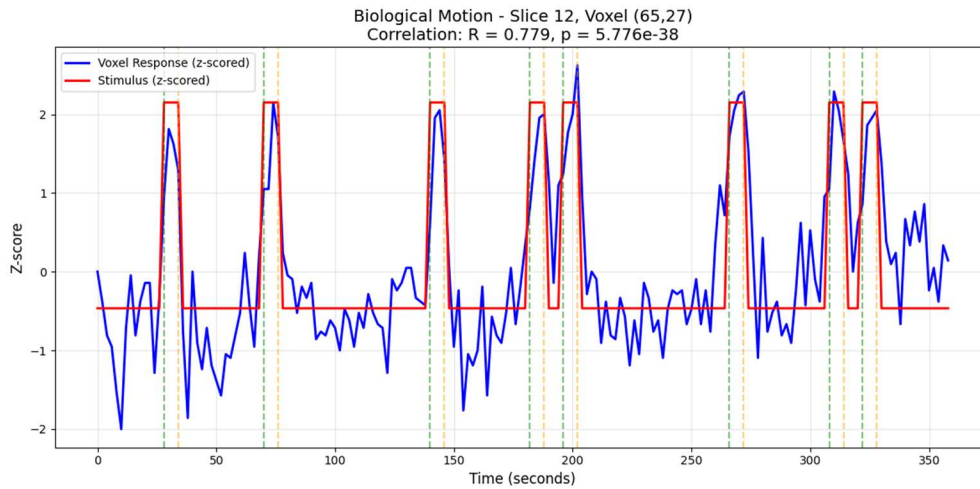


Correlations Overlay

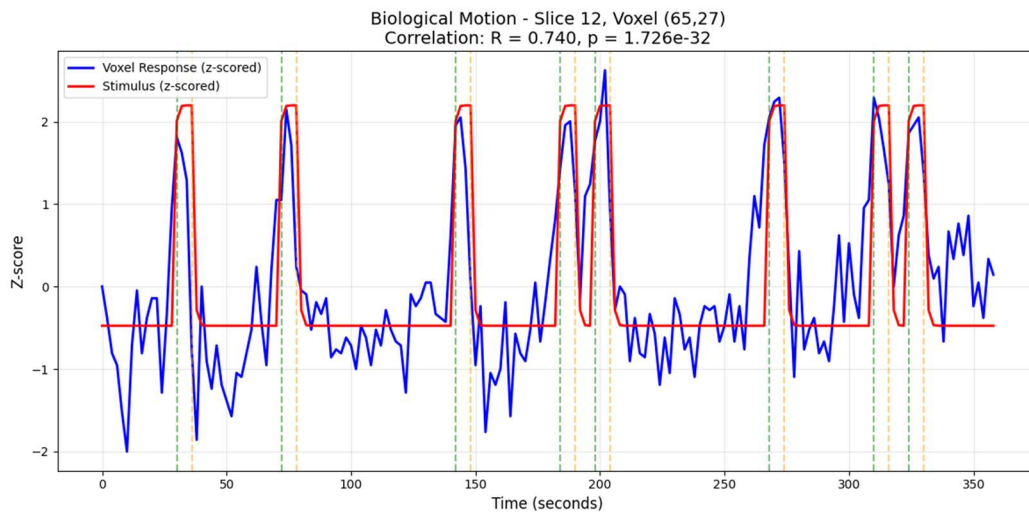


To further refine the visualization of functional activation, we overlaid the voxel-wise correlation results on top of anatomical grayscale images for each slice. This allows for better localization of activation within anatomical structures. As shown in the figures, the overlays highlight stimulus-specific activity patterns while preserving anatomical context.

Voxel Time Series For Biological Motion (Binary Signal Convolved)



Voxel Time Series For Biological Motion (HRF Convolved)



Voxel responses with HRF-convolved stimuli

Discussion

Key Correlation Findings:

We observed distinct correlation patterns for each stimulus type across brain slices. Some voxels strongly correlated specifically with coherent or biological motion.

Primary Visual Cortex (V1)

All three conditions show activation in the primary visual cortex (lowest areas in the axial slices). This is expected since V1 shows less selectivity in response to visual stimuli regardless of motion type (Tootell et al. (1995)), suggesting that basic visual processing occurs similarly for all motion types.

Superior Temporal Sulcus (STS) and Middle Temporal Gyrus (MTG)

In the biological motion condition, there are distinct clusters visible in slices 12-14 and slightly in slice 16, correlation in regions that likely correspond to the STS and MTG. These areas show notably stronger activation compared to the same regions in the Coherent and Incoherent motion conditions. This is consistent with Grossman and Blake's (2002) research demonstrating that the STS is specifically tuned to biological motion patterns.

From what we have learned in the class sessions, convolving the signal with the HRF function usually improves temporal alignment with expected neural activity, enhancing correlation detection. In our analysis, the R values for the correlation with the binary signal was slightly higher for all three motion types for the chosen voxel. We Assume that this is due to our choice of voxel, having chosen a voxel that is highly correlated with the binary signal.

Bibliography

Grossman, E. D., & Blake, R. (2002). Brain areas active during visual perception of biological motion. *Neuron*, 35(6), 1167-1175.

Tootell, R. B., Reppas, J. B., Kwong, K. K., Malach, R., Born, R. T., Brady, T. J., ... & Belliveau, J. W. (1995). Functional analysis of human MT and related visual cortical areas using magnetic resonance imaging. *Journal of Neuroscience*, 15(4), 3215-3230.