Neural Signals and Signal Processing Project 1

Jean Ciardo, Romain Frossard, Hugo Jeannin, Mathieu Verest
École Polytechnique Fédérale de Lausanne (EPFL), Switzerland

Abstract

This report presents our work on NX-421 Mini-Project 1, where we analyze neural responses to emotionally charged auditory stimuli using functional magnetic resonance imaging (fMRI) data. We investigate brain regions activated by positive and negative musical stimuli versus neutral tones. This work emphasizes the importance of rigorous data preprocessing, experimental design and image processing in developing a reliable statistical analysis.

1 Introduction

In this mini-project, we utilize relationship modeling and multivariate pattern analysis (MVPA) on fMRI data to map emotions to specific brain regions and functional brain networks, comparing the results from GLM analysis and PCA. The aim is to deepen our understanding of neural processing mechanisms in response to positive and negative auditory stimuli.

2 Dataset

2.1 Data description

The dataset used follows the BIDS structure. It consists of functional (EPI BOLD), anatomical (T1) MRI data and auditory paradigm from 20 control subjects and 19 subjects with depression. For the purpose of this work we focus exclusively on control subject 1 (sub_control01) and it's functional data obtained from the task-music runs.

The functional data consist of three 4 Dimensional (list of 3D volumes) nii.gz files. Each file represents a run following the auditory paradigm described in the corresponding `.tsv` file. Acquisition parameters such as `RepetitionTime` and `SliceTiming` are described in `task-music_bold.json`.

2.2 Data Preprocessing

The main preprocessing steps applied to the functional data are outlined below.These steps are crucial to ensure consistency between runs and enable comparative analysis.

- **Slice Timing Correction** Slice timing correction was applied to each run individually along the z-axis using the FLS SliceTimer. This adjusts the staggered acquisition of fMRI slices and ensures temporal alignment within the volume for more accurate comparison of volumes over time.
- **Z-Standardization** Z-standardization was applied to each run individually normalizing the signal intensity to a common scale, using the given formula:
  $z = \frac{x-\mu}{\sigma}$. Where z: standarized data, x: data, μ: data mean, σ: data standard deviation.
  This step ensure that the data from different runs is comparable in terms of intensity, allowing for consistent between runs analyses without intensity-based distortions.
- **Concatenation of Runs** The three fMRI 4D volumes have been concatenated into a single 4D volume (nii.gz file), making analysis easier since it can now be performed on a single file.
- **Motion Correction** Motion correction was applied to the concatenated run using McFlirt with 6 degrees of freedom, referencing the middle volume. This step ensure a consistent voxel alignment for accurate voxel-wise comparisons. We omitted Coregistration to an anatomical reference, as all data came from the same subject, and the runs were deemed sufficient reproducibility to ensure spatial consistency across them. We identified the Outliers using frame-wise displacement metric(FD), with frames showing excessive correction.
- **Smoothing** Spatial smoothing was applied using FSL's fslmath comand, for various Full Width at Half Maximum (FWHM) parameters with a Gaussian smoothing filter to enhance the signal-to-noise ratio: $\sigma = \frac{\text{FWHM}}{2.3548}$. Where, σ: standard deviation of the Gaussian smoothing function. Multiple FWHM values (2,3,6,10 mm) were tested to determine the optimal level of smoothing as larger FWHM values are better for detecting broader regional patterns, while smaller FWHM values preserve finer, localized activation points.

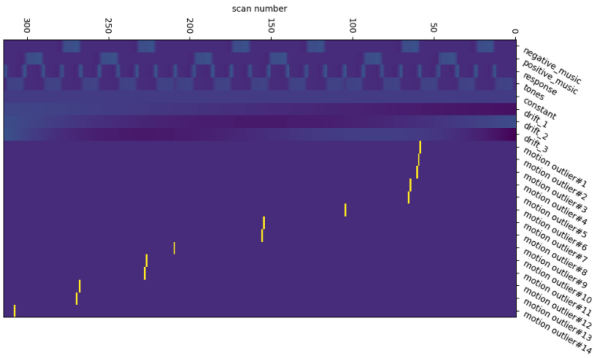

Figure 1: Experimental Design Matrix

3 Part 1 : GLM

In this section, we wanted to identify which brain regions are activated when subjects listen to emotionally positive versus negative musical stimuli, compared to non-emotional, non-musical stimuli (neutral tones), during fMRI scanning. For this purpose, we used a Generalized Linear Model (GLM).

3.1 Practicals

To analyze neuronal responses to emotional stimuli, we used an experimental design matrix that organized regressors representing experimental conditions and confounds, enabling us to estimate their effects on our BOLD signal. This allowed us to isolate neuronal responses specific to the stimuli of interest, while controlling for external factors likely to bias the results. The experimental design matrix we used for this subject incorporated regressors for each experimental condition (positive music, negative music, and neutral tones) as well as drifts modeled by a polynomial of degree 3. This degree of polynomial captured slow signal variations (such as fatigue or physiological fluctuations) without over-modeling noise or interfering with fast variations linked to the stimuli of interest. In addition, motion outlier regressors were added to correct for the impact of outliers in the signal, helping to obtain a more reliable estimate of stimulus-related effects. By using this matrix in a GLM, we could isolate condition-specific effects and obtain accurate individual activation maps for each regressor. We built a first-level GLM to model individual neuronal responses to emotional stimuli, targeting brain activations when subjects listened to positive music, negative music, and neutral tones. See figure 2.

These maps were then used to compare the activations associated with positive and negative emotions, providing a basis for the emotional analysis we targeted. The first-level GLM was appropriate here, as we analyzed data from a single subject. To compare the impact of positive versus negative music, we created contrast vectors using the GLM results for each condition, specifying a contrast vector for each stimulus type and for non-interest effects. See figure 3.

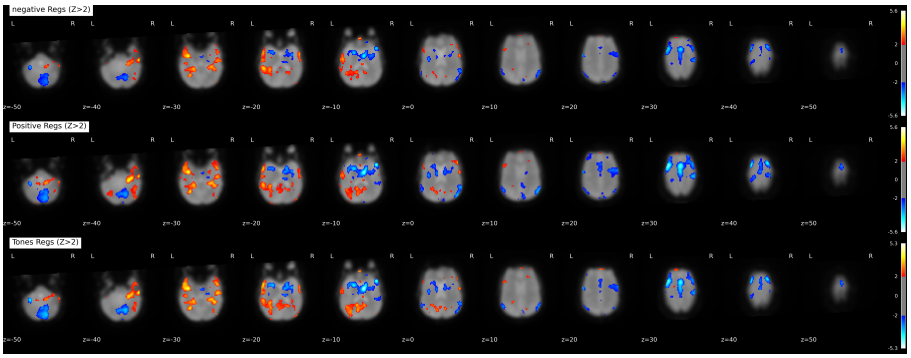

Figure 2: Z-map for positive, negative and pure tones regressors

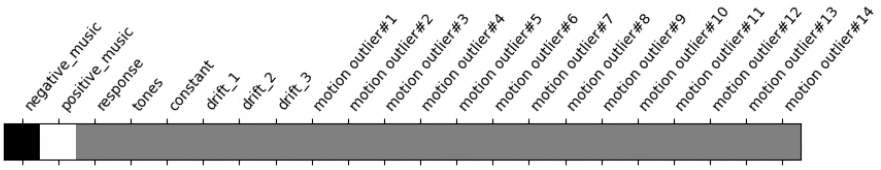

Figure 3: Contrast Vector

In this context, the difference between the positive and negative contrast vector provided a direct contrast between the two types of musical emotion (see Figure 3). The activation obtained by contrast thus revealed the difference in activation between the two conditions (positive vs. negative music), highlighting the brain regions that responded differently. As for identifying the high contrast regions ; we can see that the anterior insula, present high contrast (see sagittal view at x= -40 and -30) as well as Heschl's gyrus (see coronal view y = -20, -10) which is consistent with the litterature[1]. Looking at the axial view, near z=-10, z = -20, we also see the ACC (and the striatum near z = 0), which we can also be found in the litterature[2]. But we have a lot of other regions like the frontal gyrī. To take the analysis a step further, we performed a statistical map to obtain significant activation. We used a false discovery rate of 0.05. However, as the analysis was performed on a single subject, the statistical map does not provide any additional information.

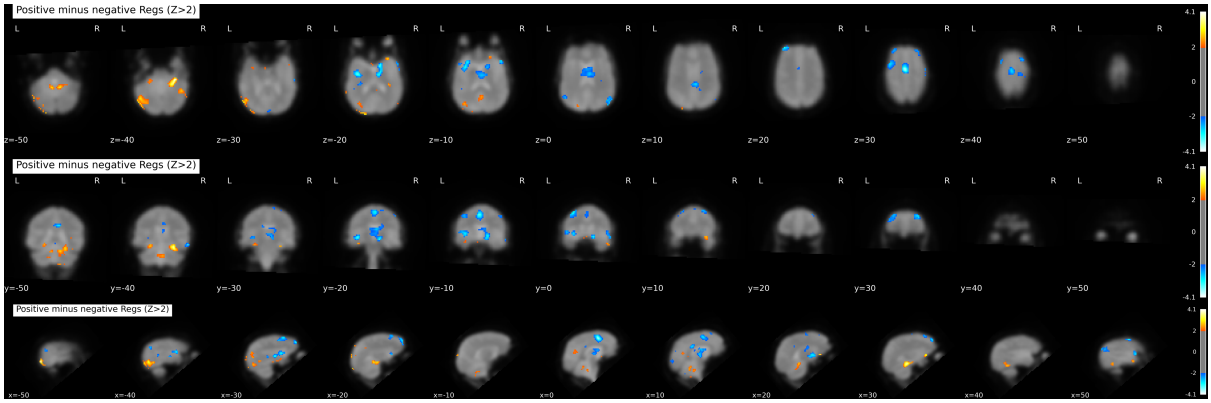

Figure 4: Z-map for positive minus negative tones

3.2 Theoreticals

- **1)** Yes because there are 20 control subjects and 19 depressed subjects. We would aggregate all our subjects and try to infer from the difference between groups.
- **2)** We could consider the contrast of being depressed against not being depressed, which would address the experimental question: "What is the difference in brain response to positive versus negative music between depressed and control subjects?"

4 Part 2 : PCA

As a confirmatory analysis we used PCA, effectively extracting the spatial patterns that would retain most of the variance from the brain activity data, and see if it would cover the same regions as the analysis performed with the GLM model.

4.1 Practicals

As with the GLM, we performed PCA on the subject fMRI runs with music. The preprocessing of the data was the same but since the outliers in the GLM were handled by specific regressors, in the case of the PCA we removed them from the dataset. We selected 6 components based on the elbow criterion that were able to explain approximately 75% of the data variance, since adding further

components would only add little variance explanation, each component explaining so little above the third one (<5%).

4.2 Theoreticals

- **1)** The results of our PCA are not exactly what we expected them to be. Indeed we can see on our first 3 PC that the eyes take up a lot of the data variance, but are not part of one of the seven big functional brain networks, making the relevant components harder to distinguish. We tried to mitigate that by applying different smoothing (2mm, 4mm, 6mm, 10mm), because the process could "spread" the artifact of the eyes, but less smoothing also means more isolated activation representations, which is not what we are looking for here. See figure 5 in Appendix.

- **2)** As stated previously, the eyeballs take up a lot of variance, the majority of the rest of the explained variance is then a blur. As for technique to systematically remove elements that are artifacts rather than task-relevant brain networks, we could think of analyze the frequency of some components ; the spectra of their time series (for things such as breathing-related artifacts). Or perform ICA which is more efficient than PCA at separating sources of signal (incl. noise) ; you can also inspect temporal patterns.

- **3)** Since we fail to identify relevant spatial patterns in the results of our PCA, comparing to the results of the GLM is quite hard, but we can see that the regions that appear in the PCA are more globally spread than the one of the GLM. In general, if we aim to identify specific regions of the brain activated in response to particular conditions (here positive against negative music) we would choose GLM. It enables us to model brain activity based on specific task conditions and produce statistical maps of activation using contrast vectors and therefore showcase regions with significant differences (e.g. no problems related to the eyes here). This is also making its output easier to interpret in this kind of tasks. On the other hand, we would use PCA when trying to reduce the dimensionality of the data (e.g. for further analysis) or looking for patterns across the whole brain (in an exploratory context for example) rather than testing an hypothesis based on a specific task.

5 Conclusion

In conclusion, this first project provided insights into neural signal processing methods and highlighted their potential application in neuroscience. The data processing and feature extraction methods we applied here are essential for analyzing neural data and understanding brain activity. The artifacts we encountered are probably due to insufficient preprocessing, data quality or error in the pipeline, highlighting once again the importance of rigor in these steps.

References

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6 Appendix

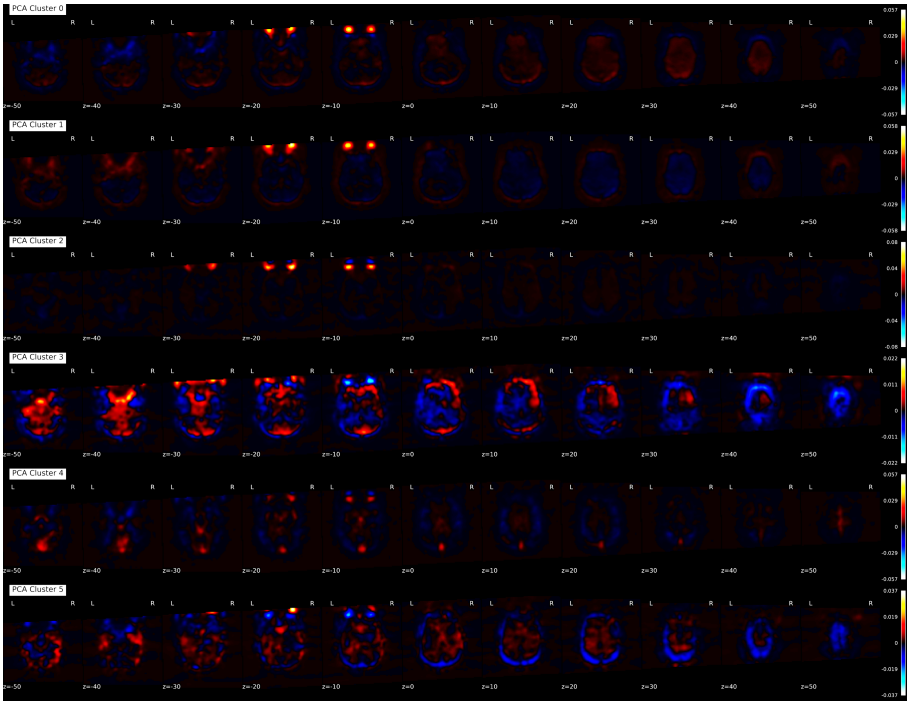

Figure 5: PCA Components