

# A Topology-based Approach Towards Subject-Specific Brain Activity Analysis in fMRI Data

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## Abstract

Functional MRI is a tool to indicate neural activity by measuring changes related to cerebral blood flow. However, factors other than cognitive stimuli can also influence the blood flow, adding noise to the pure neural signal. Thus, extracting underlying signals is a challenging process, typically approached by extensive preprocessing steps that require domain knowledge, e.g. registration with a standard brain atlas. In this work, we propose a topological analysis pipeline to extract activation patterns and a personalized brain atlas directly based on raw fMRI data. Specifically, a merge tree based feature vector is designed to identify and track activation regions of the brain over time. We demonstrate how such a feature vector can be used to investigate the temporal development of activation patterns, the connectivity between these activations, and their relation to cognitive tasks.

## CCS Concepts

• **Human-centered computing** → Scientific Visualization; Topological Data Analysis; • **Applied computing** → Medicine;

## 1. Introduction

Functional magnetic resonance imaging (fMRI) is a non-invasive tool to get insight into the human brain. It measures blood oxygenation level-dependent (BOLD) contrast, i.e., changes related to cerebral blood flow, which is assumed to couple with neural activity. In addition to the task or stimuli, the BOLD signal captures noise from many sources, including random brain activity, subject's head motion, physiological and psychological effects, scanner instability, etc. [Spe20]. Thus, the real-world measurement of BOLD signals is a complicated mixture of the true signal and noise, showing within and across subject variability [Bir12]. Therefore, extracting patterns with pure representations of a certain task is a challenging process. Current fMRI analysis approaches require extensive preprocessing steps attempting to model noise factors prior to analysis [DBCS\*20]. These methods further require information about regions of interest from standard atlas [SSGC\*18, GCHH\*15]. Instead, our method aims to explore the possibilities of recovering information from the fMRI signal using topological feature vectors computed directly from the raw signals without using any prior medical knowledge. The extracted topological feature vector significantly reduces the dimensionality while retaining salient information, and has a fixed size, making it possible to compare activity patterns over time. The main idea is to introduce a subject-specific reference brain combining all activation areas from the entire time

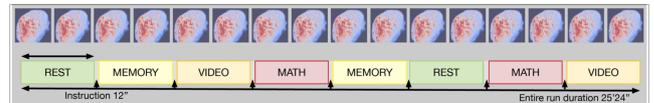


Figure 1: The order of cognitive tasks presented to participants.

series by utilizing merge trees, which provides a good means to define a distance metric between the individual time steps, thus supporting temporal analysis. The brain connectivity analysis is performed by computing the correlation between time-series of the subject-specific activation areas. The analysis results are presented in a set of visualizations in Figure 2(d). More details of the proposed method are described in our upcoming paper [RJN\*22].

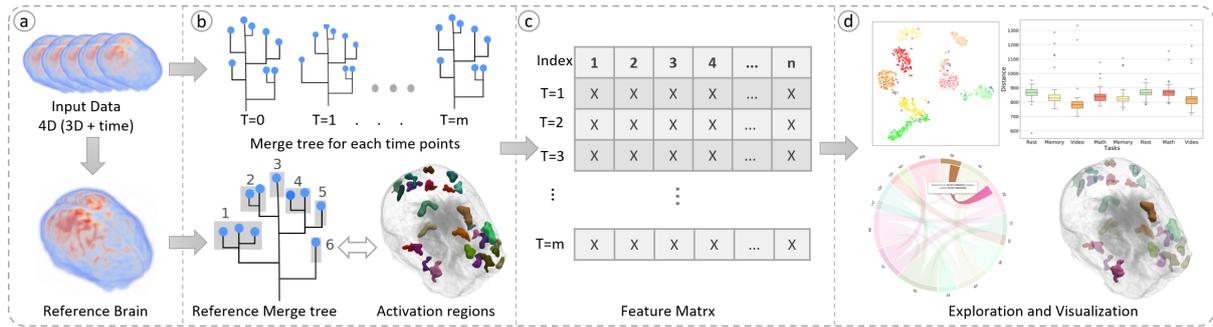
## 2. Data

The dataset used for this study was acquired and first analyzed by Gonzalez-Castillo *et al.* [GCHH\*15], which can be obtained from the XNAT Central database [central.xnat.org](http://central.xnat.org); ID: FCStateClassif. Participants were scanned continuously in a session of ca. 25 minutes while performing four different cognitive tasks: Rest, Memory, Math and Video. Each task was presented in two 3-minute blocks in a random order, starting with a 12-second instruction. The final order of tasks is shown in Figure 1.

## 3. Activation region extraction and correspondence

We present a pipeline to extract meaningful topological and geometrical features from fMRI data and propose a feature vector possessing the following key properties: 1) represents main characteristics of brain activity, 2) is acquired directly from the raw

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**Figure 2:** Pipeline overview: (a) First, a reference brain is constructed from raw temporal fMRI data, (b) followed by extracting merge trees for each time-point as well as for the reference brain. (c) Then correspondence across time is established by matching merge trees with reference merge tree, which results in a feature matrix. (d) Lastly, a set of visualization components are provided for visual understanding.

fMRI signal, i.e., without preprocessing, 3) is robust with respect to noise, and 4) is comparable over time, i.e., has a fixed size. In order to realize these properties, we use merge trees, a structure that encodes the topological level-sets in a scalar function, to extract highly active and stable features from raw fMRI data. Specifically, a personalized reference brain is generated by taking a voxel-wise maximum of volumes from all time points (see Figure 2(a)), followed by computing its merge tree which detects maxima points along with their persistence value. The maxima points with high persistent values defines the activation regions using local offset threshold (Figure 2(b)).

In the next step, a correspondence is established across time by matching all maxima from time points with the reference brain's maxima. We consider a match if the maxima points lie in each other's descending manifold. For each time step, the set of maxima points is then arranged into a 1D *feature vector* form with an index inherited from activation regions. Staking feature vectors from each time point results in a matrix of size  $m \times n$ , where  $m$  is the number of time points, and  $n$  is the number of extracted regions (see Figure 2(c)). This feature matrix is used for both temporal analysis and understanding connectivity between active regions.

**Spatio-temporal analysis and visualization.** We provide a distance plot comparing the reference feature vector with all time points, which enables us to find similar activation patterns in the temporal domain and observe their relation to the underlying task. A statistical summary of deviation from reference brain in the form of box plot is shown in Figure 2(d), we observe that the distance within the task block is stable to some extent, with a clear transition at the point when the subject changes the tasks. Moreover, we directly reduce the dimensionality of the feature matrix using t-distributed Stochastic Neighbor Embedding (tSNE) in order to observe the local similarity and overall feature development over time. The scatter plot resulting from tSNE is shown in Figure 2(d), which indicates clusters of time points within the same task blocks.

For connectivity analysis, we compute correlation between activation regions by utilizing the same feature matrix. The correlation between regions allows us to explore the behavior of the individual activation sites and their relationships to each other. Furthermore, to support the connectivity and temporal analysis, we provide a spatial rendering of the activation region linked with an interactive chord diagram (Figure 2(d)).

## 4. Conclusion

In this work, we present a topological analysis pipeline exploring task-based dynamic fMRI data. We introduce a subject-specific reference brain combining active regions from the entire time series, facilitating comparison across time. Furthermore, a series of feature vectors are generated from all time points using a topological merge tree representing the main characteristics of brain activity, capturing the most active regions in the brain while being robust to noise. The feature vector is extracted directly from raw data without the need for template registration, which is otherwise used to enable statistical analysis at the cost of signal loss. By utilizing the extracted feature vectors, we perform both temporal and connectivity analysis while providing a set of interactive, linked visualization components.

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