Classification of brain activity using synolitic networks

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Abstract. Because the brain is an extremely complex hypernet of interacting macroscopic subnetworks, full-scale analysis of brain activity is a daunting task. Nevertheless, this task can be greatly simplified by analysing the correspondence between various patterns of macroscopic brain activity, for example, through functional magnetic resonance imaging (fMRI) scans, and the performance of particular cognitive tasks or pathological states. The *purpose* of this work is to present and validate a methodology of representing fMRI data in the form of graphs that effectively convey valuable insights into the interconnectedness of brain region activity for subsequent classification purposes. *Methods.* This paper explores the application of synolitic networks in the analysis of brain activity. We propose a method for constructing a graph, the vertices of which reflect fMRI voxels' values, and the edges and edge weights reflect the relationships between fMRI voxels. *Results and Conclusion.* Based on the classification of fMRI data by graph properties, the effectiveness of the method in conveying important information for classification in the construction of graphs was shown.

Introduction

Functional magnetic resonance imaging (fMRI) is a type of magnetic resonance imaging that is performed to measure changes in blood flow caused by neural activity of the brain [1]. This method is based on the assumption that the cerebral blood flow and the activity of neurons are interconnected: with an increase in the activity of neurons, blood flow to the area containing

them increases, with a fall — decreases. Thus, fMRI allows you to determine the activation of macroscopic areas of the brain (with an approximate linear size of several millimeters) during its functioning under the influence of various factors and in various pathological conditions. Today it is one of the most used tools for the study of cognitive processes in the brain and actively developing and generally accepted methods of neuroimaging ([2]). During neuroimaging, the image is constructed as a grid of points (voxels) in a volume, which is then transformed into a collapsed two-dimensional manifold in three-dimensional space [3]. This allows you to reflect the activity of various parts of the brain.

The brain is an extremely complex hypernetwork of interacting macroscopic subnets. Conducting a full-scale analysis of its activity is a difficult task. However, this task can be significantly simplified by analyzing the correspondence of various patterns of macroscopic brain activity in fMRI images to the performance of various cognitive tasks or pathological conditions. One of the effective methods of studying the functional role of brain regions is based on building a classification model between two different modes of brain activity and assessing how much the classification accuracy changes when using available or unavailable data on the activity of a specific area of the brain for the [4] model.

Graph neural networks [4, 5] are the most effective in solving such problems. To build graphs of such networks, the vertices reflect the selected data features, and the edge weights show the relationships between the features. Currently, methods of representing fMRI data in the form of graphs are already used in brain activity classification tasks ([4,6,7]). But to reflect the relationships between brain regions in such graphs, fairly simple classical methods are used — linear Pearson correlation or partial correlation [4,7]. Despite the fact that these methods reveal the correlation of features, such a correlation does not carry useful information for classification.

In this article, we propose to eliminate this shortcoming and refine the methods of data representation. Thus, the purpose of this work is to present and validate a methodology of representing fMRI data in the form of graphs that effectively convey valuable insights into the interconnectedness of brain region activity for subsequent classification purposes. We called this method a synolytic one, as it was inspired by synolitic networks that allow graph analysis methods to be applied to multidimensional complex data [8].

Here we consider the simplest case in which we will distinguish only two brain modes, that is, when the task of binary classification is. Such a classification can be carried out based on the characteristics of [6] graphs and on the basis of their topology [4]. In this paper, we focus on classification based on graph characteristics.

1. Methods

1.1. Vectorization of fMRI data. The result of scanning the subject's brain after preliminary data processing is a three-dimensional three-dimensional image consisting of voxels and changing over time. Voxel is an element of a three-dimensional bitmap image, an analog of a pixel in a two-dimensional image. The value of the fMRI voxel at a specific time reflects the volume of blood (level of oxygenation) in a given area of the brain.

The set of fMRI data will be denoted by Ω. Multiple modes of brain activity will be denoted by $\Sigma = \{I, II\}$. Let $(\widetilde{\Omega}, \widetilde{\Sigma}) = \{(\omega_n, \sigma_n)\}_n$ is the final sample of (Ω, Σ) needed to build and train the method. Let's imagine an fMRI snapshot $\omega \in \Omega$ in computer memory as a four-dimensional array a of real non-negative numbers, where the first three indexes x, y, z fix the position of the fMRI voxel, and the fourth index t fixes the time. Thus, a_{xyz} denotes a voxel with indices x, y, z at time t, and through a_{xyz} — all values of a bill with indices x, y, z. If it is necessary to

index voxels by one number, we assume that all voxels in space are indexed in the order of their representation in the image.

1.2. The method of presenting fMRI data in the form of a graph. Each vertex in the graph reflects a voxel in the fMRI data, the edges between the vertices and the edge weights reflect the relationships between the voxels. Based on the array a, we construct a graph $g = (V, E, R, W)$, where $V = \{v_i\}_i$ is a set of vertices, $E = \{e_{ij}\}_{ij}$ is a set of undirected edges, $R = \{r_i\}_i$ is set of vertex values, $W = \{w_{ij}\}_{ij}$ is set of edge weights, v_i is vertex reflecting voxel i, e_{ij} is an edge reflecting the connection between the voxels i and j, r_i is the value of the vertex v_i, w_{ij} is the weight of the edge e_{ij}.

The vertex v_i corresponds to the voxel i, and it has the value r_i. That is, the voxel i is a time series with many values. To calculate r_i, the method uses T statistics, which converts all voxel values into a single number. Thus, we can introduce a new three-dimensional array $a^T = T(a)$. That is, for $\forall x, y, z\, a_{xyz}^T = T(a_{xyz})$. The values of the array are a^T and are used as the values of the vertices of R. The T statistic itself is selected based on the test results of the method. For example, it can be the average value of a time series or the difference of quantiles of different levels.

Since the edge weights reflect the relationships between voxels in different brain modes, one of the most important tasks is the method of calculating the value of the edge weights W. Let's define w_{ij} as

$$w_{ij} = P(\sigma = II | r_i, r_j) - P(\sigma = I | r_i, r_j). \tag{1}$$

The weight of the edge w_{ij} is equal to the difference in the probabilities of the modes of brain operation, provided the values of the incident edges of the vertices. In this case, the edge weights can only take values from -1 to 1. If the edge weight is negative ($w_{ij} < 0$), then the edge e_{ij} carries information that the most likely mode is the brain I. If the edge weight is positive ($w_{ij} > 0$), then this edge carries information that the most likely mode is II. The greater the absolute value of the edge weight $|w_{ij}|$, the more information the edge e_{ij} carries for classification. The closer to zero the absolute value of the edge weight $|w_{ij}|$, the less information it carries.

In practice, to calculate such probabilities, we will use the probability classifiers Cl_{ij} : $\{\sigma | (r_i, r_j), \{(r_i^n, r_j^n)\}_n, \{\sigma_n\}_n\} \to [0, 1]$, which are trained on the available sample $(\widetilde{\Omega}, \widetilde{\Sigma})$. Let's rewrite the formula (1) like this:

$$\begin{aligned} w_{ij} = Cl_{ij}(\sigma = II | (r_i, r_j), \{(r_i^n, r_j^n)\}_n, \{\sigma_n\}_n) - \\ - Cl_{ij}(\sigma = I | (r_i, r_j), \{(r_i^n, r_j^n)\}_n, \{\sigma_n\}_n). \end{aligned} \tag{2}$$

Thus, for each edge e_{ij}, you need to train your probabilistic classifier Cl_{ij} for the subsequent calculation of the weights of the edges W. The choice of the type of classifiers $\{Cl_{ij}\}_{ij}$ is discussed in section 2.2.

1.2.1. Graph topology. Having chosen the method for calculating the values of the vertices R and the values of the weights of the edges W, let's proceed to the description of the graph topology. When building synolitic networks, a complete graph is constructed. This allows you to take into account the interactions between all elements of the network. In the case of fMRI data, there are too many vertices in the graph. This leads to a large number of edges when constructing a complete graph. And the method requires huge computing power. For example, with an fMRI resolution of $100{\times}100{\times}100$voxels, the complete graph will have $1\,000\,000$ vertices and $499\,999\,500\,000$ of ribs. At the same time, for each edge e_{ij}, you need to train your own classifier Cl_{ij}.

Instead of a complete graph, we propose to construct a grid graph in which edges connect adjacent voxels. Two voxels are considered adjacent if they have a common side, edge, or angle. That is, the internal voxel is (xyz) is associated with voxels from the set $\{(\hat{x}\hat{y}\hat{z}) : \hat{x} \in \{x-1, x, x+1\}, \hat{y} \in \{y-1, y, y+1\}, \hat{z} \in \{z-1, z, z+1\}, (\hat{x}\hat{y}\hat{z}) \neq (xyz)\}$. With this graph topology, resource costs are reduced from $O(n^2)$ to $O(n)$, where n is the number of voxels.

fMRI shows not only the brain, but also the space around the subject's head. Therefore, edges that are incident to vertices whose values are below the threshold value of r should be removed from the graph. Such edges do not carry useful information for classification, as they are associated with vertices associated with voxels located outside the brain. Also, edges whose absolute weight value is below the threshold value of w should be removed from the graph. Edges in which $|w| \approx 0$, can only appear in two cases.

In the first case, they may be associated with vertices associated with voxels that are not active in either of the two modes of brain activity. In the second case, they can be connected to vertices associated with voxels, which are equally involved in the work of the brain in both modes, so the edges connecting them do not carry useful information for classification. Thus, edges from the set $\{e_{ij}g : r_i < r | r_j < r | |w_{ij}| < w\}_{ij}$ are removed from the graph. The r parameter is selected based on what value the fMRI machine assigns to voxels outside the brain. As a rule, this is a positive number close to zero. The parameter w affects the significance of the edges that remain in the graph g. The larger the w, the more edges will be removed.

As a result of these procedures, each internal voxel has no more than 26 neighbors. Accordingly, the degree of vertices in the graph is no more than 26.

1.3. Classification based on graph characteristics. After constructing the graph g, its characteristics $\{f_u\}_u = \{F_u(g)\}_u$ are calculated. What remains of the graph is a sequence of numbers $\{f_u\}_u$. The characteristics of the graph $\{F_u(g)\}_u$ can be the average of the edge weights, the variance of the edge weights, the number of connectivity components, and so on. Based on the characteristics of $\{f_u\}_u$, the final classification of fMRI data ω is performed using the classifier Cl, which was trained on a sample of $\{\{f_u^n\}_u\}_n$.

The characteristics of $\{F_u(g)\}_u$ are selected based on the results of the method on a training sample. The choice of the characteristics of $\{F_u(g)\}_u$ and the type of classifier Cl will be discussed in section 2.2.

2. Results

2.1. Data. The method was tested on the data of the [9] study. fMRI data were recorded while the subjects were viewing images of objects (an observation experiment) or imagining objects with their eyes closed (an imagination experiment). In the observation experiment, 1200 images from 150 categories of objects were used (8 images for each category). Each image was shown to the subject once. 24 cycles of fMRI scans were performed for each subject. All images were taken from ImageNet (http://www.image-net.org, Autumn 2011 issue) — a large-scale image database. During the observation experiment, the subjects performed a task to repeat the image in reverse order (5 attempts in each cycle), 55 images per cycle were shown. In the imagination experiment, the subjects had to visually represent a sequence of 25 objects. Each object belonged to one of the 50 categories. 20 fMRI scan cycles were performed for each subject.

In fact, within the framework of this experiment, two modes can be distinguished in which the brain of the subject functions. The first mode is observed when the subject is consistently shown 55 blocks, 50 of which are different images, 5 repeat the previous picture. If the subject sees a repeat image, he must press the button.

Table 1. Sample, division into training and test parts. The visual mode is
marked as "seen", the imagined mode is marked as "imagined"

	seen		imagined		
	training	test	training	test	
sub-01	17	7	14	6	44
sub-02	17	7	14	6	44
sub-03	17	7	14	6	44
sub-04	17	7	14	6	44
sub-05	16	8	14	6	44
	84	36	70	30	220
	120		100		

In the second mode, the subject's brain is located when he is asked to present 25 objects sequentially. After presenting each object, the subject is asked to evaluate on a five-point scale the degree of clarity of the presented image by pressing the appropriate buttons. In this work, we evaluate the effectiveness of our method by classifying two brain modes according to fMRI: in an experiment with observation and an experiment with imagination.

5 subjects participated in the data collection. Each of them had 44 fMRI scans on different days in two modes, of which 24 were in visual perception mode and 20 in presentation mode. The sequences of images and objects in the same subject were different from each other. The sample was divided in such a way that 30% of the sample of each mode for each individual falls into the test part and 70% into the training part. The Table 1 provides information about the fMRI sample and its division into test and training parts.

The peculiarity of the data is that they were obtained for 5 subjects. For each of them, they are divided into test and training parts. This approach does not allow us to assert that the effectiveness of the method has been tested on independent data. However, it allows you to check whether it is possible to predict the behavior of the person on whom the method was trained.

The original voxel size in the fMRI data was $3 \times 3 \times 3$ mm^3. To reduce the cost of computing resources and smooth out the individual features of the brain structure, the quality of fMRI data was lowered to $10 \times 10 \times 10$ mm^3.

2.2. Selecting and configuring parameters. As a T statistic, the following statistics were tested to calculate a^T: the average value of the time series, the median value of the time series, the minimum value of the time series, the maximum value of the time series, the difference between the maximum and minimum values of the time series, the quantile of the time series level 10%, the quantile of the time series level 90%, the difference between the quantiles of the time series of levels is 90% and 10%. The best result of the method was obtained when the median value was selected as the T statistic.

Probabilistic classifiers from the scikit-learn [10] library were used as classifiers $\{Cl_{ij}\}_{ij}$ to calculate the weights of the edges of W. They are based on the method of support vectors with a radial-basis core with standard parameters for this method. The Cl classifier for the final classification based on graph characteristics was also taken from the scikit-learn library. It is based on the method of support vectors with a radial-basis kernel with standard parameters for this method.

The characteristics of the graphs $\{F_u(g)\}_u$ are the average value of the edge weights, the quantile of the edge weights of the level 10%, the quantile of the edge weights of the level 90% and the standard deviation of the edge weights. Graphs of the distributions of these characteristics for the entire sample, when T is the median value of the voxel, $r = 1$, $w = 0$, are shown in Fig. 1. The distributions of characteristics in different modes of brain activity differ from each other by displacement. This should lead to a successful classification.
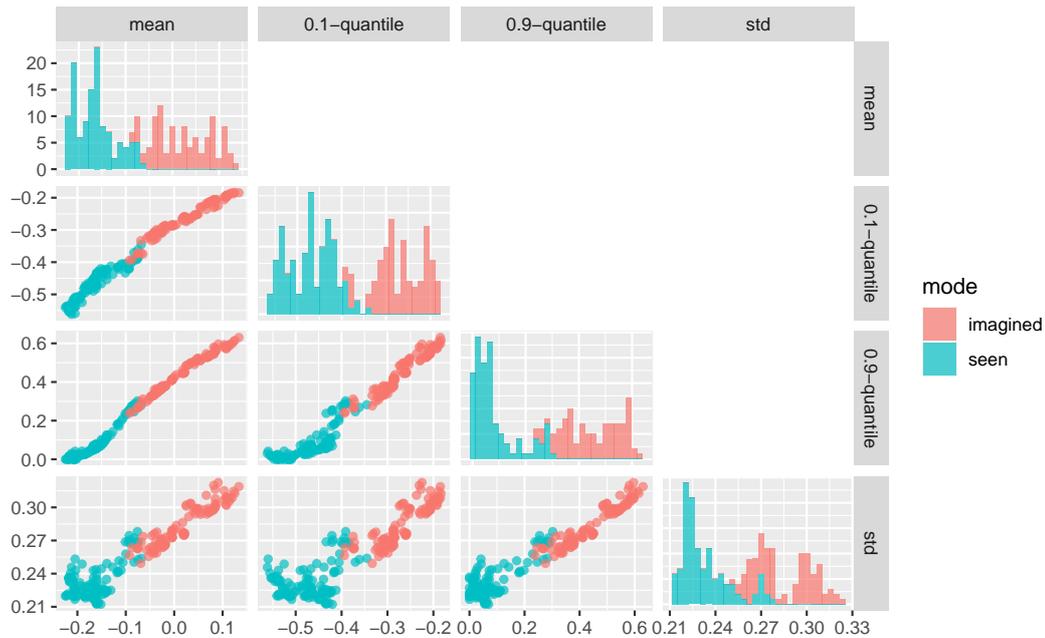
Fig 1. Distributions of the properties of graphs for the entire fMRI sample when T is the median value of voxel ($r = 1$, $w = 0$). The visual mode is marked as "seen", the imagined mode is marked as "imagined" (color online)

Table 2. The classification matrix for the case when the median voxel value was chosen as function T ($r = 1$, $w = 0.2$). The visual mode is marked as "seen", the imagined mode is marked as "imagined"

	seen	imagined
seen	36	0
imagined	1	29

2.3. Classification accuracy. The accuracy of the method for all the various methods of calculating a^T described above turned out to be very high: it did not fall below 90%. The best classification result was obtained when the T statistic was chosen as the median value of the time series ($r = 1$, $w = 0.2$, the classification matrix is presented in the Table 2). In this case, the accuracy was 98.5%. This allows us to recommend these statistics for use in subsequent studies.

Conclusion

In this paper, a method for representing fMRI data in the form of synolitic graphs is implemented and tested. Classification based on graph characteristics has shown high accuracy. It can be concluded that the method is effective in transmitting information important for classification when constructing graphs. The effectiveness of synolitic networks in analyzing brain data has been demonstrated. A new method for calculating the connectivity of brain regions has been proposed, which, unlike classical methods of calculating correlation, carries information useful for subsequent classification. In fact, we have shown that the classification can already be carried out on the basis of edge weights alone. The best results were achieved using the T statistic as the median value of a time series.

Further development of the method involves the clustering of voxels prior to classification and the binding of vertices not to voxels, but to sets of neighboring voxels. It is also possible to save more information, which is carried by the time series a_{xyz}. To do this, the method assumes

to use not one function T when calculating the values of vertices R, but a set of functions $\{T_k\}_k$. Then the vertex in the graph will contain several values. This should lead to an improvement in the results obtained.

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