

Classification of brain activity using Synolitic networks

Daniil Vlasenko

Centre for Bioelectric Interfaces
University Higher School of Economics
Moscow, Russia
dvlaskenko@hse.ru

Alexey Zaikin

Department of Mathematics
University College London
London, UK
alexey.zaikin@ucl.ac.uk

Denis Zakharov

Institute for Cognitive Neuroscience
University Higher School of Economics
Moscow, Russia
dzakh76@gmail.com

Abstract—The purpose of this work is to present and validate a methodology of representing functional magnetic resonance imaging (fMRI) data in the form of graphs that effectively convey valuable insights into the interconnectedness of brain region activity for subsequent classification purposes. 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. 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.

Index Terms—cognitive processes, functional magnetic resonance imaging, synolitic networks, graphs, classification, machine learning

I. INTRODUCTION

Functional magnetic resonance imaging or fMRI is a variation of magnetic resonance imaging that is performed to measure changes in blood flow caused by neuronal activity in the brain [1]. This method is based on the assumption that cerebral blood flow and neuronal activity are related: when the activity of neurons increases, blood flow to the containing them area increases; when neuronal activity decreases, blood flow decreases. Thus, fMRI makes it possible to determine the activation of macroscopic areas of the brain (with approximate linear size of several millimeters) during its functioning under the influence of various factors and under various pathological conditions. Today it is one of the most used tools for studying cognitive processes in the brain and is an actively developing and generally accepted method of neuroimaging (see, for example, [2]). Thus, an image is constructed as a grid of points (voxels) in a volume, which is then converted into a convolute two-dimensional manifold in three-dimensional space [3], which allows to reflect the activity of different parts of the brain.

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 analyzing the correspondence between various patterns of macroscopic brain activity, for example, through fMRI scans, and the performance of particular cognitive tasks or pathological states. In particular, one valid technique for investigating the functional role of brain regions

relies on constructing a classification model between two different modes of brain activity and assessing how much the classification accuracy changes when using available or unavailable data about the activity of a particular brain region to model [4]. Graph neural networks [4], [5] prove to be effective in such tasks. In graphs of such networks, the vertices reflect the selected data features, and the weights of the edges show the relationships between the features. At present, methods of representing fMRI data in the form of graphs are already used in the tasks of brain activity classification (see, for example, [4], [6], [7]). But rather simple classical methods, such as Pearson's linear correlation or partial correlation [4], [7], are used in such graphs to reflect the relationships between brain regions. Although these methods reveal the correlation of features, such correlation, by itself, does not provide useful information for classification. In this paper, we propose to eliminate this drawback and refine the methods of data representation. Thus, the goal of this paper is to propose and test a method of representing fMRI data in the form of graphs that would reflect information meaningful for subsequent classification about relationships between brain regions. We called this method synolitic because it was inspired by synolitic networks, which allow to apply graph analysis techniques to multidimensional complex data [8]. Here we will consider the simplest case in which we will distinguish between only two brain modes, or in other words, when the task is binary classification. Such classification can be done either on the basis of the properties [6] of graphs or on the basis of their topology [4]. In this paper, we will concentrate on classification based on the properties of graphs.

II. METHOD

A. Vectorization of fMRI data

The result of scanning the subject's brain after preprocessing the data is a three-dimensional, time-varying volumetric image composed of voxels. A voxel is an element of a volumetric raster image, it's analogous to a pixel in a two-dimensional image. A voxel's value of an fMRI at a particular point in time reflects the blood volume (oxygenation level) in a given region of the brain.

The fMRI data set will be denoted by Ω , and the set of brain activity modes by $\Sigma = \{1, 2\}$. Assume that $(\tilde{\Omega}, \tilde{\Sigma}) =$

$\{(\omega_n, \sigma_n)\}_n$ is the finite sample of (Ω, Σ) needed to construct and train the method. We can represent the fMRI scan $\omega \in \Omega$ in computer memory as a four-dimensional array a of real non-negative numbers, where the first three indexes x, y, z fix the voxel position of the fMRI, and the fourth index t fixes the time. Thus, voxel with indexes x, y, z at time t will be denoted by $a_{xyz,t}$, and all voxel values with indexes x, y, z will be denoted by a_{xyz} . Further, if it is necessary to index the voxels by a single number, we will assume that all voxels in the space are indexed in the order of their representation in the image.

B. Method of representing fMRI data as a graph

Each vertex in the graph reflects a voxel in the fMRI data, the edges between the vertices and the weights of the edges 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 a set of values of vertices, $W = \{w_{ij}\}_{ij}$ is a set of weights of edges, v_i is a vertex reflecting voxel i , e_{ij} is an edge reflecting the relationship between voxels i and j , r_i is a value of the vertex v_i , w_{ij} is an weight of the edge e_{ij} .

As stated above, vertex v_i corresponds to voxel i , and it has value r_i . In fact, in our case, voxel i is a time series with many values. To calculate r_i , the model uses the function T , 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 a^T are used as the values of the vertices R . The function T is chosen based on the results of method testing. For example, it can be the average value of time series or the difference of quantiles of different levels.

Since edges reflect the relationships between voxels in different modes of the brain, one of the most important tasks is the method for calculating the weights of edges W . We define w_{ij} as

$$w_{ij} = P(\sigma = 2|r_i, r_j) - P(\sigma = 1|r_i, r_j) \quad (1)$$

In other words, the weight of an edge w_{ij} is equal to the difference of the probabilities of brain modes given the values of the vertices incident to the edge. Thus, weights of edges can only take values from -1 to 1 . Accordingly, if the weight of an edge is negative ($w_{ij} < 0$), then edge e_{ij} carries information that the most probable brain mode is 1. If the weight of an edge is positive ($w_{ij} > 0$), then this edge carries information that the most likely mode is 2. The greater the absolute weight of the edge $|w_{ij}|$, the more information for classification the edge e_{ij} carries. Accordingly, the closer to zero the absolute weight of the edge $|w_{ij}|$ is, the less information it carries.

In practice, we will use the probability classifiers to compute such probabilities $Cl_{ij} : \{\sigma|r_i, r_j, \{(r_i^n, r_j^n)\}_n, \{\sigma_n\}_n\} \rightarrow [0, 1]$, which are trained on the available sample $(\tilde{\Omega}, \tilde{\Sigma})$. We can rewrite (1) as follows:

$$w_{ij} = Cl_{ij}(\sigma = 2|(r_i, r_j), \{(r_i^n, r_j^n)\}_n, \{\sigma_n\}_n) - Cl_{ij}(\sigma = 1|(r_i, r_j), \{(r_i^n, r_j^n)\}_n, \{\sigma_n\}_n) \quad (2)$$

Thus, each edge e_{ij} requires training its own probabilistic classifier Cl_{ij} for the subsequent computation of the weights of edges W . We will discuss the choice of the type of classifiers $\{Cl_{ij}\}_{ij}$ in section III-B.

C. Graph topology

Let us explain the method of calculating the values of vertices R , the weights of edges W , and the topology of the graph. As a rule, synolitic networks use the complete graph, which allows to take into account interactions between all elements of the network. But in case of fMRI data, there are too many vertices in the graph that leads to a large number of edges (when constructing a complete graph), and the method requires a huge amount of computing power. For example, if the fMRI resolution is $100 \times 100 \times 100$ voxels, the complete graph will have 1000000 vertices and 499999500000 edges. And for each edge e_{ij} a classifier Cl_{ij} must be trained.

Here, instead of a complete graph, we propose to construct a lattice graph, that is, a graph in which edges connect only adjacent voxels. Two voxels are called adjacent if they have a common side, edge, or corner. That is, the inner voxel (xyz) is connected to voxels from the set $\{(\hat{x}\hat{y}\hat{z}) : \hat{x} \in \{x-1, x, x+1\}, \hat{y} \in \{y-1, y, y+1\}, \hat{z} \in \{z-1, z, z+1\}, (\hat{x}\hat{y}\hat{z}) \neq (xyz)\}$. This graph topology reduces the resource cost from $O(n^2)$ to $O(n)$.

Since fMRI depicts not only the brain, but also the space around the subject's head, it is necessary to remove from the graph the edges that are incident to vertices whose values are below the threshold value r . Such edges do not provide useful information for classification, because they are incident with vertices associated with voxels that are outside the brain. Also, edges whose absolute weight is below the threshold value w should be removed from the graph. The edges where $|w| \approx 0$ can appear in only two cases. In the first case, they may be associated with vertices associated with voxels that are inactive in neither of the two modes of brain activity. In the second case, they can be connected with vertices associated with voxels that are equally involved in brain activity in both modes, so the edges connecting them do not carry useful information for classification. Thus, edges from the set $\{e_{ij} : r_i < r | r_j < r | |w_{ij}| < w\}_{ij}$ are removed from graph g . The parameter r is chosen based on what value the fMRI machine assigns to voxels outside the brain. As a rule, it is a positive number close to zero. The w parameter affects the significance of the edges that remain in graph g . The larger w is, the more edges will be removed.

As a result of these procedures, each inner voxel is left with no more than 26 neighbors. Accordingly degrees of vertices in the graph is no more than 26.

D. Classification based on graph properties

After constructing graph g its properties $\{f_u\}_u = \{F_u(g)\}_u$ are computed. Thus a sequence of numbers $\{f_u\}_u$ remains from the graph. The graph properties $\{F_u(g)\}_u$ can be the average of edge weights, variance of edge weights, number

of connectivity components, and so on. Based on the properties $\{f_u\}_u$, the final classification of the fMRI data ω is performed using the classifier Cl , which has been trained on the sample $\{\{f_u^n\}_u\}_n$. We will discuss the choice of the classifier type Cl in section III-B.

III. RESULTS

A. Data.

The method was tested on the data from study [9] in which fMRI data were recorded while subjects viewed images of objects (observation experiment) or imagined objects with their eyes closed (imagination experiment). In the observation experiment 1200 images from 150 object categories were used (8 images per 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>, Fall 2011 release), it's a large-scale image database. During the observation experiment, subjects performed the image repetition task in reverse order (5 attempts in each cycle), 55 images per cycle were shown. In the imagination experiment, subjects had to visually represent a sequence of 25 objects. Each object belonged to one of 50 categories. 20 cycles of fMRI scans were performed for each subject.

In fact, two modes in which the subject's brain functions can be distinguished in this experiment. The first mode is observed when the subject is shown 55 blocks in sequence, 50 of which are different images and 5 repeat the preceding picture. If the subject sees a repeat picture, he must press a button. The subject's brain is in the second mode when he or she is asked to sequentially visualize 25 objects. After presenting each object, the subject is asked to rate on a five-point scale the degree of clarity of the image he or she presented by pressing the corresponding buttons. For the purposes of this paper, we will evaluate the effectiveness of our method on the classification of two brain modes by fMRI: in the observation experiment and in the imagination experiment.

Five subjects participated in the data collection and each had 44 fMRI scans on different days in two modes, of which 24 in the observation mode and 20 in the imagination mode. Sequences of images and objects for the same subject varied with each other. The sample was divided so that 30% of sample for each mode for each subject fell into the test part and 70% into the training part. Table I presents information about the fMRI sample and its division into test and training parts. A peculiarity of the data is that it was obtained for 5 subjects, and for each of them it was divided into test and training parts. This approach does not allow us to claim that the effectiveness of the method has been tested on independent data. But it allows us to test whether it is possible to predict the behavior of the person on whom the method was trained.

The original voxel size in fMRI data was $3 \times 3 \times 3 \text{ mm}^3$; to reduce computational resource costs and to smooth out individual brain structure features, the quality of fMRI data was downgraded to $10 \times 10 \times 10 \text{ mm}^3$.

TABLE I
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		

B. Selecting and adjusting parameters

The following functions were tested as function T for calculation a^T : mean value of time series, median value of time series, minimum value of time series, maximum value of time series, difference of maximum and minimum values of time series, 0.1 quantile of time series, 0.9 quantile of time series, difference of 0.9 quantile and 0.1 quantile. The best model result was obtained when the median value was chosen as function T .

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

As properties of graphs $\{F_u(g)\}_u$ we chose the average value of edge weights, 0.1 quantile of edge weights, 0.9 quantile of edge weights and standard deviation of edge weights. Plots of distributions of these properties for the entire sample, when T is the median value of a voxel, $r = 1$, $w = 0$, are shown in Figure 1. As can be seen, the distributions of properties under different modes of brain activity differ from each other by bias, which should lead to a successful classification.

C. Classification accuracy.

The accuracy of the method for all different ways of calculation of a^T described above turned out to be very high: it did not fall below 90%. The best classification result was obtained when the statistic T was chosen as the median value of the time series ($r = 1$, $w = 0.2$), the classification matrix is presented in table II. In this case, the accuracy was 98.5%. This allows us to recommend this function for use in future studies.

IV. CONCLUSION

In this paper, a method for representing fMRI data in the form of synolitic graphs was implemented and tested. Classification based on the properties of graphs showed high accuracy, from which it can be concluded about the effectiveness of the method in the transfer of important information for classification in the construction of graphs. The



Fig. 1. Distributions of the properties of graphs for the entire fMRI sample when T is a median value of voxel ($r = 1$, $w = 0$). The visual mode is marked as “seen”, the imagined mode is marked as “imagined”.

TABLE II

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

effectiveness of synolytic networks in the analysis of brain data was also demonstrated, and a new method for computing the connectivity of brain regions was proposed, which, unlike the classical methods of correlation calculation, carries useful information for subsequent classification. In fact, we have shown that classification can already be performed on the basis of edge weights alone. The best results were achieved using the function T as the median value of time series.

Further development of the method implies voxel clustering prior to classification and linking vertices not with voxels, but with sets of neighboring voxels. It is also possible to store more information carried by the time series a_{xyz} . To do this, the method is supposed to use not one function T when calculating values of vertices R , but a set of functions $\{T_k\}_k$. Then a vertex in the graph will contain k values, which should lead to better results.

ACKNOWLEDGMENT

This article is an output of a research project implemented as part of the Basic Research Program at the National Research University Higher School of Economics (HSE University).

REFERENCES

- [1] S. Ogawa, T.M. Lee, A.R. Kay, and D.W. Tank. “Brain magnetic resonance imaging with contrast dependent on blood oxygenation”, *Proceedings of the National Academy of Sciences of the United States of America*, 1990; 87(24):9868–9872. DOI: 10.1073/pnas.87.24.9868.
- [2] M.J. Singleton. “Functional magnetic resonance imaging”, *Yale Journal of Biology and Medicine*. 2009;82(4):233.
- [3] J. Gao, A. Huth, M. Lescroart, J. Gallant. “Pycortex: an interactive surface visualizer for fMRI”, *Frontiers in Neuroinformatics*, 2015; 9. DOI: 10.3389/fninf.2015.00023.

- [4] X. Li, N.C. Dvornek, Y. Zhou, J. Zhuang, P. Ventola, J.S. Duncan. “Graph neural network for interpreting task-fMRI biomarkers”, *Medical Image Computing and Computer Assisted Intervention*, 2019; 11768:485–493. DOI: 10.1007/978-3-030-32254-0_54.
- [5] C. Saueressig, A. Berkley, R. Munbodh, R. Singh. “A joint graph and image convolution network for automatic brain tumor segmentation”, *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries*. 2021; 12962:356–365. DOI: 10.1007/978-3-031-08999-2_30.
- [6] A. Anderson and M.S. Cohen. “Decreased small-world functional network connectivity and clustering across resting state networks in schizophrenia: an fMRI classification tutorial”, *Frontiers in Human Neuroscience*, 2013; 7:520. DOI: 10.3389/fnhum.2013.00520.
- [7] B.-H. Kim and J.C. Ye. “Understanding graph isomorphism network for rs-fMRI functional connectivity analysis”, *Frontiers in Neuroscience*. 2020; 14:630. DOI: 10.3389/fnins.2020.00630.
- [8] T. Nazarenko, H.J. Whitwell, O. Blyuss, A. Zaikin. “Parenclitic and Synolytic networks revisited”, *Frontiers in Genetics*. 2021; 12. DOI: 10.3389/fgene.2021.733783.
- [9] T. Horikawa, Y. Kamitani. “Generic object decoding (fMRI on ImageNet)”, *OpenNeuro*. 2019. DOI: 10.18112/openneuro.ds001246.v1.2.1.
- [10] Pedregosa et al. “Scikit-learn: machine learning in Python”, *Journal of Machine Learning Research*. 2011; 12:2825–2830.