Environment. Technology. Resources. Rezekne, Latvia
Proceedings of the 12th International Scientific and Practical Conference. Volume II, 94-97

Brain Connections Analysis Using Graph Theory Measures

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***Abstract*—Brain is a part of the organism's complex structure that performs many functions, which are responsible for the main human abilities: to talk, to hear, to move, to see, etc. The brain consists of several areas that are not only directly connected with the different body systems, but also depend and may affect each other. Researchers and doctors are trying to summarize and visualize these relationships for an important purpose – to get the information about possible reactions of the body in case of various diseases, possibilities of recovery, risks, etc. important issues. Neurologists are looking for ways to "move" through the brain in virtual space for viewing the synapses between different areas. It might be useful to get a general idea of how brain regions are interrelated. The term "connectome", which is the complete structural description of the brain connections, or the map of connections, is used for the common perception of brain relationships. Connectome is a network of thousands of nerve fibres that transmits signals between the special regions responsible for functions such as vision, hearing, movement and memory, and combines these functions in a system that perceives, decides and acts as a whole. So, the relationships of brain neural regions can be represented as a graph with vertices corresponding to specific areas, but edges are links between these areas. This graph can be analysed using quantitative measures, like node degree, centrality, modularity etc. This article discusses the different network measures for the connections between brain's regions. The purpose is to determine the most important areas and the role of individual connections in the general functional brain model.**

Keywords— Brain network, connectome, functional connectivity, graph theory.

I. Introduction

Everyone has a unique combination of genetics, environmental impact and life experience. These factors affect the detailed "structure" of the brain, as even twins can have different levels of neural links. By arranging these connections, the researchers try to understand what could be the connectomes of different people.

Connectome is a full description of the structural connections of the brain. These connections can be between different elements of the nervous system - from neurons to whole areas of the brain [1].

Connectome is enough complex and poorly to be understood. So far, only one connectome was developed to the end. It was worm's *Caenorhabditis elegans* connectome. The problem is that this worm has only 300 neurons connected to each other by 7000 links, but the human has 100 billion times more neurons and a million times more links. [2].

There are currently several Connectivity Atlases, which, like maps, display different locations or regions of human brain. Several scientific projects are devoted to this problem. One of them is the *Brainnetome Atlas* [3]. The main goal is to explore the cerebral hierarchy by highlighting the two main elements - nodes and connections between them. The most important thing is not only to identify the structural architecture of these nodes, but to combine it with the functional consistency of the individual regions, i.e. how regions can affect each other and how the presence or interception of links can affect the functionality of the affected regions.

It turns out, that the structure of the brain can be visualized in the form of a graph. The graph structure consists of vertices or nodes and edges or connections. In different complex systems, they can display different elements and links between them, such as people and their social relationships, web sites and hyperlinks, etc. [1], [4]. In the case of the brain, regions will play the role of vertices, and the edges will implement links between these regions.

II. Materials and Methods

Graph theory offers a variety of tools for working with complex system models that also include brain structure. So, it is possible to calculate a number of mathematical values for the graph you created and then integrate them into the complex network.

The graph type must be determined before any calculations are made. This article analyses the graph obtained from the *Brainnetome Atlas* project, where information about the brain regions and the existence of connections is provided, and shows is this region connected with this. So here it's about the so-called *undirected graph* [5]. In order to get and visualize this graph, we need data about

Print ISSN 1691-5402
Online ISSN 2256-070X
http://dx.doi.org/10.17770/etr2019vol2.4141

Published by Rezekne Academy of Technologies.

the links that are gathered in one matrix, which is called *adjacency matrix*. This is a two-dimensional matrix consisting of rows and columns that reflect the names of regions (Fig. 1) [6] – [8].

Lobe	Gyrus	Left and Right Hemisphere
	SFG, Superior Frontal Gyrus	SFG_L(R)_7_1
		SFG_L(R)_7_2
		SFG_L(R)_7_3
		SFG_L(R)_7_4
		SFG_L(R)_7_5
		SFG_L(R)_7_6
		SFG_L(R)_7_7
	MFG, Middle Frontal Gyrus	MFG_L(R)_7_1
		MFG_L(R)_7_2
		MFG_L(R)_7_3
		MFG_L(R)_7_4
		MFG_L(R)_7_5
		MFG_L(R)_7_6
		MFG_L(R)_7_7
Frontal Lobe	IFG, Inferior Frontal Gyrus	IFG_L(R)_6_1
		IFG_L(R)_6_2
		IFG_L(R)_6_3
		IFG_L(R)_6_4

Names of brain regions from the adjacency matrix

Storage of information in the form of an adjacency matrix is usually associated with a term *density*. This parameter is equal to the ratio between the actual number of edges in the graph and the total number of possible edges [1], [5].

The names of 246 regions (SFG_L(R)_7_1, MFG_L(R)_7_7, IFG_L(R)_6_3 utt.) and two types of numbers – 0 and 1, are included in the adjacency matrix. If the edge between region *a* and region *b* exists then the corresponding matrix element is $A_{ab} = 1$, else $A_{ab} = 0$ [7]. The data is stored in *.csv* file format. A fragment of the adjacency matrix is shown in the Fig. 2. The number of edges connecting the vertex with others is called *node degree*. Thus, the number of "1" in the corresponding line of the adjacency matrix corresponds to the node degree of this row. Nodes with the highest degrees tend to be called *hubs* [1], [5]. On the basis of node degree we can calculate so-called *assortativity* [10], which describes the correlation between connected vertices. If this value is positive, it means that a high degree nodes prone to be connected to each other.

Another characteristic is an *average path length*. When we guess about the classic mathematical implementation, the path length is the number of edges to pass through to get from one vertex to the other. When it comes to brain topology, the path length can be used to assess the possibilities of transmitting information between the regions. Short path lengths make it quick to transfer information and reduce resource consumption during the transmitting process. This factor leads to the term „small world" [9].

```
,1 SFG_L_7_1,2 SFG_R_7_1,3 SFG_L_7_2,4 SFG_R_7_2,5 SFG_L_7_3,6 SFG_R_7_3,7 SFG_L
1 SFG_L_7_1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,0,1,1,1,0,1,1,1,1,1
2 SFG_R_7_1,1,0,1,1,1,1,1,1,1,1,1,1,1,0,1,1,1,1,0,1,0,1,1,1,1,1,1,0,0,0,0,1,1,0,0,1,1,1,1,
3 SFG_L_7_2,1,1,0,1,1,1,1,1,1,0,1,1,1,0,1,1,1,1,1,0,1,1,1,1,1,1,1,0,1,0,1,0,1,1,0,0,1,0,1,0,
4 SFG_R_7_2,1,1,1,0,0,1,1,1,1,1,1,1,0,0,0,1,0,1,0,1,1,1,1,1,1,1,0,1,0,1,0,0,1,1,0,0,0,0,1,1,
5 SFG_L_7_3,1,1,1,0,0,1,1,0,1,1,1,1,1,1,1,1,0,0,1,1,1,1,1,1,1,0,1,1,1,0,1,1,1,1,1,0,1,0,1,0,1
6 SFG_R_7_3,1,1,1,1,1,0,0,1,1,1,1,1,1,1,1,0,0,1,1,1,1,1,1,0,1,1,1,0,0,0,1,1,1,0,1,0,1,0,1,
7 SFG_L_7_4,1,1,1,1,1,0,0,1,1,1,1,0,0,0,1,0,1,1,1,0,1,0,1,1,1,1,1,0,1,0,1,0,1,0,0,0,0,0,1,1,
8 SFG_R_7_4,1,1,1,1,0,1,1,0,1,1,1,1,0,0,0,1,0,1,0,1,0,1,1,1,1,1,0,1,0,1,0,0,0,1,0,0,0,0,1,1,
9 SFG_L_7_5,1,1,1,1,1,1,1,1,0,1,1,1,1,1,0,0,0,1,1,0,0,0,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,1,1,1
10 SFG_R_7_5,1,1,0,1,1,1,1,1,1,0,1,1,1,1,0,0,0,1,0,0,0,0,0,0,1,1,0,1,0,0,0,0,0,0,0,0,0,0,1,1
11 SFG_L_7_6,1,1,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,0,0,1,1,1,1,0,1,0,0,1,1,0,0,1,1,1,1,1,1,0,1,1,1,0
12 SFG_R_7_6,1,1,1,1,1,1,1,0,1,1,1,1,1,0,1,1,1,1,0,0,1,1,1,1,1,1,1,0,0,1,1,0,0,0,1,1,1,0,1,1,1,1,1
13 SFG_L_7_7,1,1,1,0,1,1,0,0,1,1,1,1,0,1,1,0,0,0,1,1,1,1,0,0,0,0,1,1,0,0,0,0,1,1,1,1,1,0,1,0
14 SFG_R_7_7,1,1,0,0,1,1,0,0,1,1,1,1,1,0,0,0,0,0,1,1,0,1,0,0,0,0,1,1,0,0,0,0,0,1,0,1,0,0,0,0
15 MFG_L_7_1,1,0,1,0,1,1,1,0,0,0,1,1,1,0,0,1,1,0,1,1,1,1,1,1,1,0,1,0,1,0,1,1,1,0,1,0,1,0,1,
16 MFG_R_7_1,1,1,1,1,1,1,1,0,1,0,0,1,1,0,0,1,0,0,1,1,1,1,1,1,1,0,1,0,1,0,1,0,1,1,1,0,1,0,1,0,
17 MFG_L_7_2,1,1,1,0,0,0,1,0,0,0,0,0,0,0,1,0,0,1,1,0,1,0,1,1,1,1,1,0,1,0,1,0,1,0,1,0,1,0,1,
18 MFG_R_7_2,1,1,1,1,0,0,1,1,1,1,0,0,0,0,1,1,0,0,1,0,1,1,1,1,1,0,1,0,1,0,1,0,1,0,1,0,0,1,
19 MFG_L_7_3,1,1,1,0,1,1,1,0,1,0,1,1,1,1,1,1,1,1,0,0,1,1,1,1,1,1,1,0,1,1,1,0,1,0,1,0,1,0,1,0,1,
20 MFG_R_7_3,1,0,0,1,1,1,0,1,0,0,1,1,1,1,1,1,0,1,1,0,1,1,0,1,0,1,1,1,0,1,0,1,0,1,0,1,0,1,0,
21 MFG_L_7_4,1,1,1,1,1,1,1,1,0,0,0,1,1,1,0,1,1,1,0,1,1,0,1,1,1,1,0,1,1,1,0,1,1,1,1,1,0,1,0,1,
```

Fig. 1. A fragment of the adjacency matrix

This concept is associated with the networks where all elements are connected to others through a very short path. Society often meets the term with a similar meaning - „six degrees of separation" between any two people, which means, that they know each other through six acquaintances (connected with 6 or fewer edges). The brain connection graph is also considered „small world" system.

In terms of graph analysis, one of the most important issues is the definition of "the most important" vertexes. What does "importance" mean? There may be several interpretations here. One of them explains that "importance" refers to the flow of information in the network. The concept *centrality* is introduced [1], [11]. If *centrality* is high, it means that the node has an important place in the information exchange processes in a graph.

It should be noted that this attribute has some perceptions and different detection approaches. The simplest idea is related to the hypothesis that the node with a high degree is potentially active. This measure is called *degree centrality* and is equal to the count of vertexes, connected to a given one [12]. Another view of centrality is based on the shortest paths between the vertexes passing through the given. Such a node can affect others, maintain, suspend, or stop the information transfer process. This approach was named *betweenness centrality*. There are still a number of measures related to centrality, but in this article one another is described – *closeness centrality*. It follows from the name that this centrality describes proximity, thus, the greater this centrality is, the closer this node is to all others. This value is calculated as the inverted sum of the path lengths of a node [13].

The network has another local feature - clustering. It describes the interaction between the vertex neighbours. In other words, it is mathematically possible to calculate the probability that two nodes neighbours also are closer neighbours. The resulting value is called *clustering coefficient* [14]. This value can be used to determine how fragmented the network is. Thus, at a high clustering coefficient in the brain graph, we can expect that an event (for example., stroke) will affect only one cluster, i.e. a group of regions. On low clustering, the information is spread across the all network.

Of course, the described graph analysis parameters are only a small part of graph theory tools. But with regard to brain connections, they give a general idea of the interrelations and interactions between the regions. There is a wide range of software that can be used for mathematical and statistical processing of this graph and for calculating parameters of this graph. It can be divided into two groups: universal mathematical packages (MATHCAD, MATLAB, Wolfram Mathematica utt.), containing tool groups for working with graphs, and specialized computer programs (for example., Gephi), designed for purposeful processing and analysis of graphs.

This paper describes *NetworkX* software package. It is free software for creating and analysis of complex networks. The program for graph processing is created in *Python* programming language. Launching the created program, it represents parameters described above that gives the information about the links between brain regions.

III. Results and Discussion

NetworkX program allows you to import data from *.csv* file format. Such file is an adjacency matrix obtained from *Brainnetome Atlas*, where information about connections between 246 brain regions is stored. Program code for importing file:

```
#to import matrix from csv file
from numpy import genfromtxt
import numpy as np
mydata = genfromtxt("C:/Python/matrix.csv",
delimiter=',')
print(mydata)
```

Created program *mydata.py* is launches in the *cmd* window. Data is displayed on the screen (Fig. 3). As the matrix is large, only its part is visible on the screen. The names of the regions were imported as words *nan*.

```
[[nan nan nan ... nan nan nan]
 [nan  0.  1. ...  1.  1.  1.]
 [nan  1.  0. ...  1.  1.  1.]
 ...
 [nan  1.  1. ...  0.  1.  1.]
 [nan  1.  1. ...  1.  0.  1.]
 [nan  1.  1. ...  1.  1.  0.]]
```

Imported matrix from .csv file0

In order to "pull" the adjacency matrix from the imported data, some lines are added to the code:

```
#adjacency matrix from imported data
adjacency = mydata[1:,1:]
print(adjacency)
```

The adjacency matrix is output to the screen (Fig. 4).

```
[[0. 1. 1. ... 1. 1. 1.]
 [1. 0. 1. ... 1. 1. 1.]
 [1. 1. 0. ... 0. 1. 1.]
 ...
 [1. 1. 0. ... 0. 1. 1.]
 [1. 1. 1. ... 1. 0. 1.]
 [1. 1. 1. ... 1. 1. 0.]]
```

Fig. 2. Adjacency matrix

NetworkX programme is a console application, but there are additional extension packages that also allow visualization. Different types of graphical objects can be constructed in *NetworkX* by connecting the library *Matplotlib*. Connecting libraries, now we can create a graph from the adjacency matrix and display it:

```
#graph drowing
import networkx as nx
import matplotlib.pyplot as plt
G=nx.from_numpy_matrix(adjacency)
nx.draw(G)
plt.show()
```

When we run this code, a new pop-up window with a graph's image opens (Fig. 5). Since the number of vertexes and edges in the graph is large enough and the graph is wide, because the brain connections form a complex system, then the resulting drawing is complicated and non-informative. The vertexes and edges merge, so the graph cannot be used for further analysing.

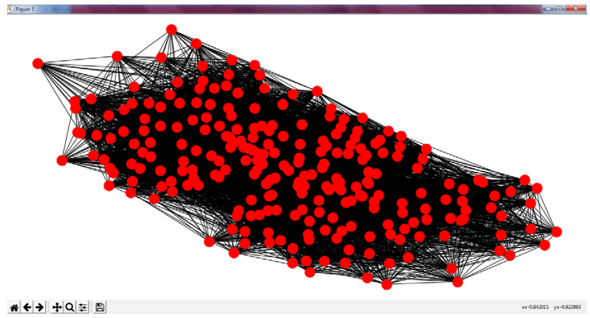

Fig. 3. Graph of brain connections

In turn, *NetworkX* has libraries with different graph parameters that can be calculated.

The first simplest parameter is node degree. It has a built-in function for calculating it - *Graph.degree*. Here are two options. If we analyse a particular vertex or some vertexes, which are similar to brain regions, then we can add a vertex number as a parameter to this function, for example:

```
G.degree[10]  # node's 10 degree
list(G.degree([0, 1, 2]))# degrees of 3 nodes
```

Alternatively, we can output a whole array of vertexes with the appropriate degrees to the screen (Fig. 6).

```
[(0, 115), (1, 107), (2, 46), (3, 38), (4, 91), (5, 83
02), (9, 96), (10, 110), (11, 113), (12, 113), (13, 10
6, 44), (17, 42), (18, 66), (19, 60), (20, 60), (21, 6
4, 49), (25, 49), (26, 104), (27, 114), (28, 42), (29,
(32, 69), (33, 70), (34, 77), (35, 76), (36, 84), (37,
(40, 88), (41, 88), (42, 79), (43, 76), (44, 53), (45,
(48, 126), (49, 107), (50, 90), (51, 93), (52, 63), (5
, (56, 59), (57, 47), (58, 70), (59, 72), (60, 55), (6
, (64, 105), (65, 98), (66, 83), (67, 80), (68, 114),
64), (72, 84), (73, 77), (74, 54), (75, 62), (76, 110)
 43), (80, 55), (81, 68), (82, 74), (83, 77), (84, 56)
 62), (88, 60), (89, 73), (90, 75), (91, 54), (92, 76)
 55), (96, 81), (97, 44), (98, 56), (99, 53), (100, 44
(103, 112), (104, 82), (105, 74), (106, 80), (107, 73)
10, 72), (111, 71), (112, 67), (113, 73), (114, 68), (
, 78), (118, 96), (119, 100), (120, 32), (121, 34), (1
76), (125, 83), (126, 87), (127, 94), (128, 21), (129,
, (132, 49), (133, 53), (134, 66), (135, 61), (136, 62
139, 40), (140, 63), (141, 56), (142, 54), (143, 38),
, 153), (147, 136), (148, 146), (149, 134), (150, 138)
(153, 138), (154, 61), (155, 64), (156, 53), (157, 57)
```

Fig. 4. Degrees of graph nodes

Other parameters were also calculated for graph analysis:

```
#Assortativity
r=nx.degree_assortativity_coefficient(G)
print("%3.1f"%r)
#Clustering coefficient
print(nx.average_clustering(G))
#Average path length in the graph
print(nx.average_shortest_path_length(G))
#Density
print(nx.density(G))
#Centrality
print(nx.degree_centrality(G))
print(nx.betweenness_centrality(G))
print(nx.closeness_centrality(G))
```

Launching such a program a number of numerical values is obtained and summarized in Table I.

TABLE I. Estimated Graph Parameters

Graph Parameters	Value
Assortativity	0
Clustering coefficients	0.69
Average path length	1.65
Density	0.37
Diameter	3

The first parameter – assortativity – equal to 0. This coefficient indicates whether high-level vertexes tend to interact with the same or similar vertexes. Since the calculated coefficient is equal to 0, this means that this graph can be called as *non-assortative graph*. In such graphs there is no correlation between vertexes that give the name of such complex systems - *uncorrelated networks*.

If you pay attention to the fragmentation of the graph, let's look at the value of the clustering coefficient obtained. Numerically it is equal to 0.69. It is difficult to assess whether this figure is considered to be low or too high. From a theoretical point of view „small – world" graphs have high clustering. The coefficients is between 0 and 1. This value reaches 0.69 for the given graph, that is noticeably larger than half, and means, that brain regions form separate groups or subgroups, in which almost all vertexes have connections to others. A more detailed view can be given by cluster analysis methods.

The characteristics of the information exchange in the graph should be analyzed separately. The obtained valu of density is 0.37. After this relationship, especially in the context of brain activity, it is impossible to say objectively and unambiguously whether the transmission of information between the regions is good or bad. Of course, this ratio is not approaching 1.0, where there are all the possible edges between nodes, but on the other hand it has gone far enough from 0. To create a full scene, let's look at how you can get from one node to the other. Average path length in the graph is 1.65. So you can transfer impulses from region *a* to region *b*, offending only a few regions on the road. Maximum path length directly from one node to other – diameter – is equal to 3. Therefore it also confirms the relatively efficient and fast flow of information in the graph.

IV. Conclusions

A method to describe brain connectivity using graph theory measurements is described in this article. There are a lot of parameters that can be calculated for the graph of connections between the brain regions. First of all, we can conclude that brain activity is a very complicated system and can be represented as a wide graph with a big number of vertexes and edges. So, it is difficult to analyse whole graph.

Brain connections graph can be called "small - world" system. The "small - world" graphs tend to contain subgraphs that have connections between almost all the nodes in them. This follows from the definition of such a property of the graph as a high coefficient of clustering. Secondly, most pairs of vertexes are connected at least in one short way. Thus, some of brain regions tend to make separate groups. It means that signals through connections will affect only one group of regions but not whole brain.

Mathematical analysis has been performed using *NetworkX* software. Calculated values have created a common presentation about the analysable graph. But for more accurate analysis, more mathematic software packages can be used to compare obtained results.

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