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Empirical survey on graph classification methods for Brain Networks

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Empirical survey on graph classification methods for Brain Networks
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Abstract

Our brain, as our entire body, is a perfect as complicated machine. For this reason is important to analyse it in an effective and efficient way. An important role in this purpose is given to machine learning and similar algorithmic methods. In fact, many papers have been written in this field on implemented methods of brain classification. In those papers the brain is represented as a graph or as a matrix and from that representation they want to recognize if a person is affected by a psychiatric disorder, such as Autism or Schizophrenia.

In this work, the aim is to study and compare some of those methods. First of all is important to have in mind which are the basic elements with which the papers work, such as graphs, classification and brain connectomes. Then, the algorithms taken in consideration can be classified according to the technique used, like Neural Networks or features embeddings, so, some methods of different techniques are described. For each method many experiments are made, to see how they work, in which case are more useful, and how good are the results. The experiments are made with different datasets, to see how the methods adapt and how general they are.

Future works can be implemented, studying more methods and maybe finding a method that could be easily used by neuroscientists.

Contents

Chapter 1

Introduction

Neuroscientists, to diagnose a psychiatric disorder, use symptom scores from clinical interviews. For a definitive validation, could be useful to study the interactions between brain regions, in order to see the different behaviours of these interactions in a brain of Typical Developed people and people with disorders. This could be seen through Magnetic Resonance Imaging (MRI), in particular functional MRI (fMRI). The neuroimaging data produced are then pre-processed and transformed in structures that an algorithm can study, in our cases graphs, matrices and time series. From the study of these interactions the important thing that we need to implement is the classification of the brain representation, meaning that each method taken in consideration in this work has the aim to implement a classification that says whether the brain that I give to it is affected by a disorder. This is called brain classification.

The studies taken in consideration, other than in techniques, differs also in the data that have in input. The inputs could be graphs, matrices, time series and even images. This work is focused on methods that take in input graphs, even in matrix representation. Many methods have been implemented for graph classification. They are important tools that can be applied in many fields and subjects. In our particular field, graph classification of brain networks, becomes important to take in account the structure of the graph, because there could be many brain regions that characterize a specific psychiatric disorder. We will see how in some methods are also studied those regions to identify the once that have different interactions in people with disorders, even if the described experiments of this works are concentrated on the simple classification of brain networks.

This thesis contains an explanation of the basics with which the study works, then a description of several methods on this subject and then experiments with some of these methods that more represent our field.

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1.1 Outline

The thesis is organized as follows:

- In the current chapter there is an explanation of some basics related to this work.
- Chapter 2 contains the classification of the several methods taken in account, so, an overview of the macro-classes of all the implemented techniques to do

graph and *brain classification*. Then, for each method, there is an explanation of the main characteristics.

- Chapter 3 contains the experimental part. Are described the set-up of the experiments, like the datasets and the kind of classification, the results of the experiments and a discussion of the results.
- Chapter 4 contains comments about the use of each method and possible future works.

1.2 Background

To understand better all the methods, we should do some explanation of what we will encounter during the lecture. The main arguments we should consider are **Graphs**, **Classification** and **Connectomes**.

Graphs
There are many subjects in which graphs are used, and consequently many definitions. In mathematics, a graph is a structured set of objects that, in pairs, could have a relation between themselves. Each object is called a *vertex*, and each relation between a pair of vertices is called an *edge*. So, a graph $G(V, E)$ is a pair where V are the vertices and E are the edges. Graphs are represented in diagram form, where vertices are in circle form and edges are lines that join pairs of vertices with a relation.

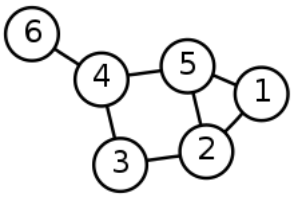

Figure 1.1

Graph could be *directed* or *undirected*. In a direct graph, edges have an orientation, the links between vertices can be represented by arrows going from one vertex to the other. In an edge (x, y) directed from x to y, the vertices are called respectively *tail* and *head* of the edge.

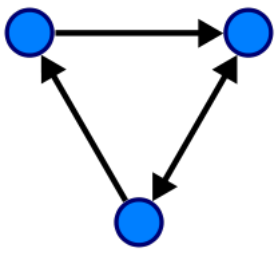

Figure 1.2

Graphs can be represented by matrices, the matrix representations in which we are interested for this thesis are **Adjacency matrix** and/or **Connectivity matrix**.

An **Adjacency matrix** is a square matrix that represents if there is an edge between two vertices. In particular in an unweighted graph with a vertex set $U = \{u_1, ..., u_n\}$ the Adjacency matrix A is an $n \times n$ matrix in which its element A_{ij} is 1 if there is an edge between the vertices u_i and u_j. If the graph is weighted the values in the matrix are not 1s and 0s, but depends on the weight of each edge. Also, if the graph is undirected the Adjacency matrix is symmetric.

The Adjacency matrix sometimes is called **Connectivity matrix**.

Classification

In machine learning, *Classification* is a supervised learning approach in which an algorithm is trained, with some given data, to classify new observations. It is a process.

First we have some data, of which we already know the belonging class, called *labelled* data. We could have two classes, in which case we will have a *binary classification*, or multiple classes, so *multi-class classification*. Our labelled data are given to the classification model, starting the **training** of the model.

Once trained the classificator, we can give to it new data that we want to classify. This is called the **prediction**. Finished the prediction we can evaluate our model through some scores, the main one in our case is the **accuracy**, that calculates the percentage of how many predictions of our classifier are right.

Connectomes

The **connectome** is the connection matrix of the human brain [**connectome**]. From the anatomic point of view, the connectome is defined by all the axonal origins, terminations and trajectories of all the brain neurons, through the brain regions. This means, the connectivity of neural pathways in the brain.

Being able to have a representation of the human brain allows us to understand fundamental cognitive operations, brain activities, conditional structure-function models of the brain, so, consequently, to understand and detect brain deceases. From this powerful tool, we can see how brain physiology is correlated to abilities and behaviours, underlying mental anomalies and pathology. This is fundamental to develop treatments ad hoc for each pathology and case.

Other fields, that we do not cover here, but that are very interesting, concern the memories (in fact neuroscientists believe that our memories are stored in the synapses between neurons) and the preservation of the brain (being able to recover the structure and connections of it). https://www.brainpreservation.org/content-2/connectome/

In the following image we can see an example of a connectome.

Figure 1.3

1.3 Related works

Here we concentrate the study of connectomes in graph form. This means that the fMRI of a brain, elaborated in a connectome, is then transformed in graph form, and the graph is studied in matrix form. The graph have as nodes the brain regions, and as edges the connections between them. It follows that the matrix is an *Adjacency matrix*, in which the values represent the degree of connections between the regions, and each row and each column is a node of the graph, a so called *Region of interest* (**ROI**).

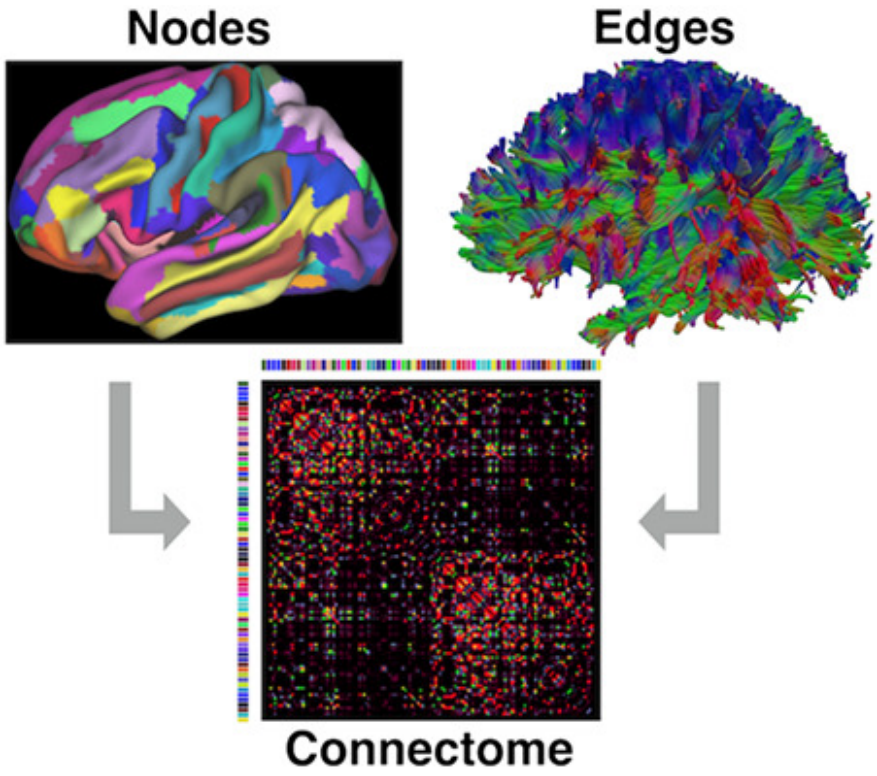

Figure 1.4

Graph Classification
The technique that studies the classification of graphs is called **Graph Classification**. The basic definition of graph classification is [**10.1145/3219819.3219980**]: given a set of graphs $\mathcal{B} = \{(\mathcal{G}_1, \ell_1), (\mathcal{G}_2, \ell_2), \cdots, (\mathcal{G}_n, \ell_n)\}$ the aim is to learn a function $f : \mathbf{G} \to \mathcal{L}$, where $\mathbf{G}$ is the input space of graphs, and $\mathcal{L}$ is the set of graph labels. Each graph $\mathcal{G}_i = (\mathbf{A}_{\mathcal{G}_i}, \mathbf{B}_{\mathcal{G}_i})$ has an adjacency matrix $\mathbf{A}_{\mathcal{G}_i} \in \{0,1\}^{N_i \times N_i}$ and an attribute matrix $\mathbf{B}_{\mathcal{G}_i} \in \mathbf{R}^{N_i \times N_i}$, where N_i is the number of nodes of the i-graph and B is the number of attributes. Each graph has also a corresponding label l_i.

The usual strategy to study graphs is to calculate graph statistics on the entire graph. A popular technique is to count the occurrences of various *subgraphs* on a graph, called graphlet kernel [**pmlr-v5-shervashidze09a**]. Then there is the *Morgan algorithm* [**Rogers2010ECFP**] that consists in an iterative process, that updates the attributes vector of each node by hashing a concatenation of all the attributes of in the node's local neighbourhood. Then from the final attributes of all

the nodes in the graph is computed the graph feature. Recently, learning data-driven graph features [**NIPS2015_f9be311e**] is becoming more important. This means that given a dataset, the task-relevant features are learned automatically from the graphs. Once we extract these features, independently of which method we would like to use, we use them for the classification. Another method that we can mention is all the literature that regards *Graph Neural Networks* (GNN), a deep learning technique. To build a GNN we need to find out the graph structure, the graph type and its scale, then we should define the loss function, depending on the task, and then we are ready to build a model using computational model [**ZHOU202057**].

These methods brings us to the field of our interest, **Brain Classification**. For Brain Classification have been used the previous graph classification techniques, adapted for a more suitable result. In the next chapter we will discuss various methods that inspired this work.

Chapter 2

Survey

2.1 All methods

In this chapter there will be a brief description of some papers that treated *brain classification*. We can divide the methods in the several techniques that the papers use to build the brain classification: Deep Learning, Statistical Fingerprints and Machine Learning. Also, to compare them, and find a possible good way to make brain classification, some have been tested. The results are in chapter 3.

2.1.1 Deep Learning

GroupINN: Grouping-based Interpretable Neural Network for Classification of Limited, Noisy Brain Data

This paper of Yan Y. et al [**groupinn**] proposes a grouping-based interpretable neural network model, GroupINN, that classifies cognitive performance with 85% fewer parameters than baseline deep models, while also identifying the most predictive brain subnetworks within several task-specific contexts. In the design of the neural network is included the idea of node grouping. In this way the model learns the node grouping and extracts the graph features jointly.

The problem statement of this paper is: given a set of subjects, each with corresponding fMRI data and a label associated with a certain phenotype, we seek to devise an efficient, interpretable, and parsimonious neural network model that can predict each phenotype with high accuracy.

To reduce the number of parameters used in the model, they adopted the idea of multi-graph clustering (where the goal is to find a common clustering across multiple graphs) to summarize the original graph into a supergraph with each cluster as a supernode.

The neural network is formed by three different types of layers: node grouping layer, graph convolutional layer and fully connected layer. The node grouping layer is designed to "hide" the non-indicative ('noisy') edges by grouping them into a cluster, thus highlighting the indicative edges: two nodes are assigned to different groups if their connection is identified as important. Graph convolutional layers are used to capture the structure of the supergraph.

The neural network is also divided in two branches, one processes the positive graphs and one the negative ones. All in all, the architecture consists of three kinds of layers and two branches. The input graph is the correlation matrix W. The first layer is a dimensionality reduction layer and the output is a matrix W^s representing the supergraph. Following the dimensionality reduction layer, three graph convolutional layers are used. At last, the positive and negative outputs of the previous layer are concatenated, flattened and sent to the fully connected layer (with softmax activation).

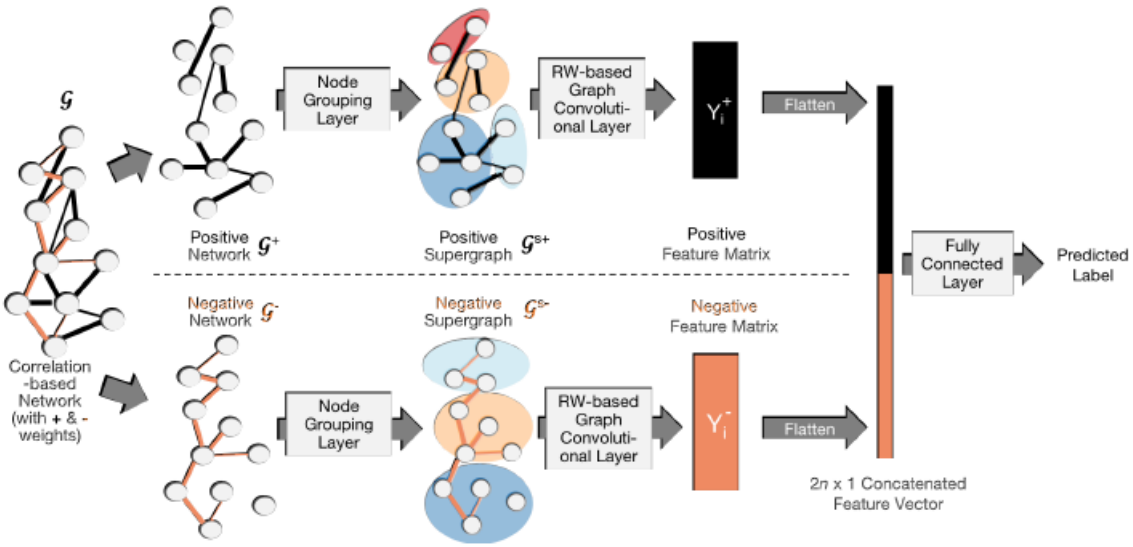

Figure 2.1

Regarding the experimentation part, they used a dataset taken from Human Connectome Project 1200 (HCPt) [**hcp**]. This dataset consists of 966 subjects to which has been measured brain activity, through fMRI, while they were performing specific tasks. The four task-based datasets used in this experiment are: *Emotion, Gambling, Social* and *Working Memory*. It is divided in 90% train/validation set and 10% testing set. For the evaluation they take in consideration *accuracy* and the *runtime*. Comparing their method, they found out that it is faster and with less parameters than other works, so it is more interpretable, as well as having good accuracy.

Deep Learning-based Pipeline to Recognize Alzheimer's Disease using fMRI Data

Functional Brain Network Classification for Alzheimer's Disease Detection with Deep Features and Extreme Learning Machine

2.1.2 Statistical Fingerprints

Explainable Classification of Brain Networks via Contrast Subgraphs

In this paper they introduce an approach for classifying brain networks based on extracting contrast subgraphs, i.e., a set of vertices whose induced subgraphs are dense in one class of graphs and sparse in the other. The model is extremely simple, with just one parameter, excellent interpretability and good classification accuracy. They exploited contrast subgraph TD-ASD (the subgraph that maximizes the difference between the number of edges in the class TD, typically developed brains, with respect to the same measure for class ASD, people with autism spectrum deseas). Vertex size represents the importance of the vertex in discriminating the two classes. In fact they ended up with some important rules: 1. If an individual exhibits more than 62 edges among the 15 vertices of the contrast subgraph ASD-TD, then there are high chances that the individual is affected by ASD; 2. If the number of edges induced by the contrast subgraph ASD-TD is smaller than half of the number of edges induced by the contrast subgraph TD-ASD, then there are high chances that the individual is not affected by ASD. 3. If the number of edges induced by the contrast subgraph ASD-TD is smaller than the number of edges induced by the contrast subgraph TD-ASD, then there are high chances that the individual is affected by ASD.
Each individual is represented by an undirected unweighted graph with $|V| = 116$ vertices.

Unsupervised Network Embedding for Graph Visualization, Clustering and Classification

Supervised classification of structural brain networks reveals gender differences

Sub-network Kernels for Measuring Similarity of Brain Connectivity Networks in Disease Diagnosis

Integration Of Network Topological Features And Graph Fourier Transform For Fmri Data Analysis

2.1.3 Machine Learning

Network Classification With Applications To Brain Connectomics

Stable Biomarker Identification For Predicting Schizophrenia in the Human Connectome

Multi-modality disease modelling via collective deep matrix factorization

Chapter 3

Experiments

3.1 Experimental setup

With datasets explanation

3.2 Results

(Data Science)

3.3 Discussion

Chapter 4

Conclusions

4.1 Future works

references