
Aiding Medical Diagnosis Through the Application of Graph Neural Networks to Functional MRI Scans

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Abstract

Graph Neural Networks (GNNs) have been shown to be a powerful tool for generating predictions from biological data. Their application to neuroimaging data such as functional magnetic resonance imaging (fMRI) scans has been limited. However, applying GNNs to fMRI scans may substantially improve predictive accuracy and could be used to inform clinical diagnosis in the future. In this paper, we present a novel approach to representing resting-state fMRI data as a graph containing nodes and edges without omitting any of the voxels and thus reducing information loss. We compare multiple GNN architectures and show that they can successfully predict the disease and sex of a person. We hope to provide a basis for future work to exploit the power of GNNs when applied to brain imaging data.

1 Introduction

The application of Graph Neural Networks to biological data has received great attention in recent years (Gilmer et al, 2017; Muzio et al, 2020). Their ability to predict characteristics of agents such as chemicals and other molecules has proven to be successful, as high predictive properties have been reported. However, thus far, success in this field has mainly been demonstrated on graph-structured biological data of relatively small size. Only few groups have tried to extrapolate these findings to brains, which due to their comparatively large size provide an additional layer of complexity (Li et al, 2020; Kim & Ye, 2020; Filip et al, 2020).

Functional magnetic resonance imaging (herein referred to as fMRI) is a widely used method to study brain activity, either when it is at rest (resting-state; rs-fMRI) or when performing a task (task-based fMRI). It is frequently used as a research tool in neuroscientific research and can aid medical diagnosis, and has contributed immensely to our understanding of the brain. However, fMRI is not yet being used as a diagnostic tool for immediate use in the clinic due to the time required to interpret the data and its complexity. Researchers have developed various algorithms for neuroimaging scans and applied these to fMRI data, with the goal of supporting medical diagnosis by generating quick predictions (Meszlényi et al., 2017; Patel et al., 2016). However, applying these to fMRI has proven to be more difficult than initially expected. Some reasons for this include the high dimensionality of the data and large inter-subject variability, as well as noise in the fMRI time series. Thus, there seems to be an unmet need for technologies that can successfully employ fMRI as a diagnostic tool.

In this paper, we propose a novel approach to learning from and predicting disease from fMRI data. Our method leverages the power of Graph Neural Networks, as well as the fact that they can be applied to graph-structured data, which the brain can be represented as. This ‘Brain Graph’ $\mathbf{G} = (\mathbf{X}, \mathbf{A})$ where $\mathbf{X} = \{\vec{\mathbf{X}}_1, \vec{\mathbf{X}}_2, \dots, \vec{\mathbf{X}}_n\}$, where n is the number of voxels in the fMRI image (representing brain activity in a given region) with time steps t and $\vec{\mathbf{X}}_i \in \mathbb{R}^t$, and $\mathbf{A} \in \mathbb{R}^{n \times n}$ is an

adjacency matrix generated by a bounded Pearson’s Correlation Coefficient function described in Eq. 1.

Previous approaches have combined voxels into so-called regions-of-interest by averaging them to produce a brain graph with fewer nodes. While this lossy approach results in a lower compute cost when calculating correlation coefficients, models constructed downstream from the application of this filter tend to suffer from poor predictive power. Instead, we use a lossless voxel-wise approach that removes this data-reduction step. We generate these graphs from two publicly available resting-state fMRI datasets and test various different GNN architectures to predict disease, in this particular example Autism or Attention Deficit Hyperactivity Disorder (ADHD). Our results reveal that GNNs are powerful tools for predicting disease from rs-fMRI data.

2 Methods

2.1 Datasets and preprocessing

971 and 794 preprocessed rs-fMRI scans from the publicly accessible Autism Brain Imaging Data Exchange (ABIDE) and ADHD-200 datasets were used (DiMartino, 2014; Bellec, 2017). These datasets contain preprocessed scans of control participants and subjects with either Autism or Attention Deficit Hyperactivity Disorder (ADHD), respectively. The signal from each voxel was normalised and voxels with no signal were filtered out. Each node contained the node features x_v , which were the coordinates and time series information from one voxel. The number of voxels per scan that were converted to a graph that would be fed into our network varied between 60,000-80,000. The Pearson’s Correlation Coefficient (PCC) was calculated between all of the voxels’ time series using the Fast-GPU-PCC algorithm (Eslami & Saeed, 2018). The edge features e_{vw} for the graph were represented by the PCC, which determines the linear association between two variables x and y:

$$p_{xy} = \frac{\sum_{i=1}^T (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{(x_i - \bar{x})^2} \sqrt{(y_i - \bar{y})^2}} \quad (1)$$

This was done on an instance with 16 vCPUs and 1 NVIDIA Tesla M60 GPU. The number of all the possible combinations equals $N(N-1)/2$, where N is the number of voxels. For a graph containing 60,000 voxels and thus the same number of nodes, this equals 1,799,970,000 correlation values. In order to limit the total number of edges in the graph and only keep the connections of high importance, only edges with correlation values of higher than 0.9 were included. In the final graphs, there were approximately 100 edges per node. The edges and nodes were loaded as a Pytorch Geometric object and used for subsequent experiments.

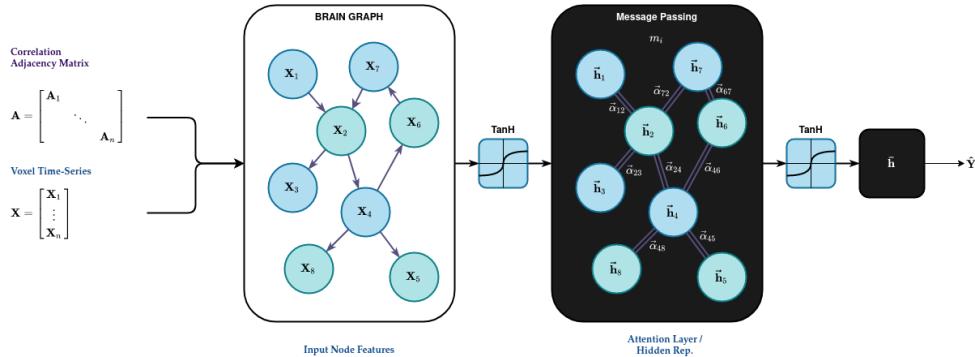


Figure 1: A high-level overview of our message-passing network (MPN) based model. Here m_i is one of three types of MPNs: a GCRN, GCN, or GAT. Node hidden states $\mathbf{H} = \{\vec{h}_1, \vec{h}_2, \dots, \vec{h}_n\}$ are averaged post-message-passing for down-stream binary classification.

2.2 Comparison of neural networks

For the purposes of this paper, we tested performance on graph-level, rather than node-level, predictions. Three different state-of-the-art GNN architectures were tested on these data, including Graph Convolutional Networks (GCN), Graph Attention Networks (GAT) and Graph Convolutional Recurrent Networks (GCRN) (Kipf & Welling, 2016; Velickovic et al, 2017; Seo et al, 2016). Performance of these algorithms was compared to a simple feedforward network that contained two linear layers. All network architectures were implemented in Pytorch Geometric and Pytorch Geometric Temporal (Fey & Lenssen, 2019; Rozemberczki et al, 2021). The optimal hyperparameters, which included the learning rate, batch size and number of units in a layer, were determined using a grid search. The data were separated into train, validation and test sets (80%, 10% and 10% of each dataset, respectively). The reported values are based on performance achieved on the test set. We tested performance on both a binary classification task of the medical condition (i.e. ADHD or Autism), as well as sex (female or male). Performance measures for comparison included the accuracy, F1 and AUROC scores.

3 Results

Table 1 summarises the performance of the different architectures tested on the two datasets and on two classification tasks, which were the medical condition and the sex of the subject. The network that included GAT layers performed the best out of all of the architectures tested, with the classification accuracy reaching 0.74 when classifying ADHD, and 0.87 when classifying sex on the ABIDE dataset. Interestingly, it could predict Autism better than ADHD. The network including GCN layers performed second best, with accuracies higher than the GCRN and FFN. The simple FFN had the lowest accuracy out of all the networks tested, which confirms the predictive abilities of GNNs on these data.

| Model | Autism | Sex (ABIDE) | ADHD | Sex (ADHD-200) |
|-------|--------|-------------|------|----------------|
| FFN | 0.51 | 0.61 | 0.58 | 0.51 |
| GCRN | 0.56 | 0.52 | 0.55 | 0.59 |
| GCN | 0.63 | 0.83 | 0.69 | 0.81 |
| GAT | 0.65 | 0.87 | 0.74 | 0.85 |

Table 1: Performance of the different neural network architectures tested using accuracy as a measure. The algorithms used in these experiments were: a Feedforward Network (FFN), a Graph Convolutional Recurrent Network (GCRN), a Graph Convolutional Network (GCN) and a Graph Attention Network (GAT). Performance was tested on two datasets, ABIDE and ADHD-200. They were trained to classify disease and sex.

4 Conclusion

In this paper, we demonstrate that resting-state fMRI data can be represented as a graph containing all voxels of an fMRI scan as well as their respective time series and does not require the removal or averaging of voxels, which can lead to loss of information and may not always provide a fully accurate representation of brain activity. Even though this brain graph contains thousands of nodes and edges, we prove that it is possible to analyse it using GNNs and make predictions. To our knowledge, this is a novel approach to analysing rs-fMRI scans. We find that compared to FFNs, GCRNs and GCNs, GATs had the highest performance on classification tasks. GATs classified scans from patients with ADHD versus controls with an accuracy of 74% compared to GCNs (65%), indicating that they are better suited for this particular task.

We anticipate that the dataset described here will be useful for the characterization of future novel graph methods. We also foresee that the reported accuracy can be further improved and has potential for clinical application. We showed that in both disease and sex classification tasks, GATs show state-of-the-art-performance compared to previously reported studies (Filip et al, 2020; Kim & Ye, 2020). Additionally, our results demonstrate that using a voxel-wise approach, rather than a

region-of-interest approach, is advantageous when interpreting fMRI data. We hope that our findings will encourage research groups to make use of the power of GNNs for analysing brain scans and will adopt a voxel-wise approach in their research.

Broader Impact

As discussed previously, this model has potential as an enabling technology for medical diagnosis and clinical decision making.

This dataset and its associated construction method are also useful as tools for benchmarking Graph-ML models because brains are a highly complex domain for which there is a lack of pre-constructed datasets.

It is important to ensure patient confidentiality and data protection if this tool were to be implemented clinically. It is also vital that the patient is aware of any findings that could arise, is prepared in case a diagnosis is made, and that the correct support and guidance is provided afterwards. As long as the mentioned points are controlled, we believe that such tools can be highly beneficial.

Acknowledgements

Authors of this project have been supported by the Institute for Neuroscience at the University of Cambridge, UK, The Alan Turing Institute, London, UK and Syntensor, Inc.

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