A novel deep learning framework on brain functional networks for diagnosis of psychiatric diseases

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Synopsis:

We developed a predicting algorithm based on brain connectivity to quantify the altered brain regions in schizophrenia, bipolar, and attention deficit hyperactivity disorders, to help diagnose them using neuroimaging biomarkers. Functional connectivity was utilized to construct brain graphs, on which the node2vec framework was applied to produce the node embeddings. The concatenation of embeddings was used to derive the region feature vectors to feed support vector machine (SVM) classifiers. Also, we build a model to assist the diagnosis of disorders using a weighted voting ensemble. The achieved accuracy proved to outperform to the state-of-the-art models.

Introduction:

Schizophrenia (SZ) is a severe psychiatric illness characterized by aberrant sensory perception cognition [1]. Bipolar Disorder (BP) is a serious mental disorder characterized by severe fluctuations in mood ranging from manic to depression [2]. Attention deficit hyperactivity disorder (ADHD) is, on the other hand, a mental disorder mainly characterized by attention deficits, excessive activity and behavioral impulses, most prevalent in young children [3]. Despite significant research focusing on mental disorders, the mechanisms underlying these disorders are still not completely understood, consequently, the diagnostic approaches may not be completely specific and reliable. With the recent advance in clinical neuroimaging and availability of medical imaging devices, promising results are obtained in reinforcement of specific diagnosis for SZ, BP, and ADHD patients, for which both medical and behavioral presentations may be confusing[4-6].

The diagnosis of these disease and also monitoring their progression or regression can be facilized by the means of neuroimaging modalities, such as functional magnetic resonance imaging (fMRI), by which, functional connectivity (FC) pattern of the brain can be reconstructed. FC has successfully identified fundamental differences between patients and healthy control subjects.

Methods and Materials:

Rs-fMRI datasets are accessed from the UCLA Consortium for Neuropsychiatric Phenomics (CNP) dataset [7], which is publicly available in the OpenfMRI database. Data from fifty healthy subjects, as well as fifty SZ and BP each, and forty ADHD patients were inspected during a quality control process. The fMRI data were preprocessed in MATLAB using SPM8 [8] and the package of data processing & analysis for brain imaging (DPARSF) [9].

Automated anatomical labeling (AAL) atlas was used to identify the brain regions of interest (ROI). As a result of Pearson's correlation (PC) between time series of brain region, a 116 × 116 correlation matrix was generated to define the relation amongst different regions of brain and match to the FC network. The FC can be modeled as a weighted graph using the graph theory, where the weak weights are eliminated by setting the values below a specified threshold to zero and retaining the rest.

Recent developments in deep learning, especially in natural language processing, have led several studies to extend language models to graph representation learning. The node2vec algorithm [10] aims to learn a vectorial representation of nodes in a graph by optimizing a neighborhood preserving objective. It has been inspired from the word embedding algorithm word2vec, expanding the prior node embedding algorithm "Deep Walk" [11]. The node2vec employs a second-order random walk algorithm to calculate the node' neighborhood network. It generally consists of three steps: sampling, training skip gram, and computing embedding

This random walk results in a bag of nodes of neighborhood from sampling by use of flexible biased random walks on the network. The bag of nodes is generated from the random walks and is fed into the skip-gram network. Each node is represented by a one-hot vector and maximizes the probability for predicting the neighbor nodes. The hidden layer output of the network is taken as the graph embedding. By concatenation of these embeddings, a feature vector of nodes for every group is generated.

By applying a grid search approach and obtaining the best parameters of SVM for classification of the groups of patients vs. HC in total regions, we achieved a unique accuracy in each region by calculating the feature discrimination rates. Consequently, features with an accuracy higher than 0.7 was chosen as experts of an ensemble learning model with utilizing majority voting for classification.

Conclusion:

We introduced a decision-making and classification framework takes deep learning-based feature extraction into account with connectivity graphs as the input and altered regions due to dysfunction as the output. Moreover, by utilizing an ensemble learning, we achieved the highest accuracy among the approached proposed in the previous literature. The promising results indicates that proposed method can be used for real-world systems.

Summary of main findings:

We introduce an algorithm to detect altered brain regions in schizophrenia, bipolar, and attention deficit hyperactivity disorders. The classifier achieved an accuracy of 88.33%, specificity of 93.33%, and sensitivity of 84.33% in distinguishing patient groups versus healthy controls.

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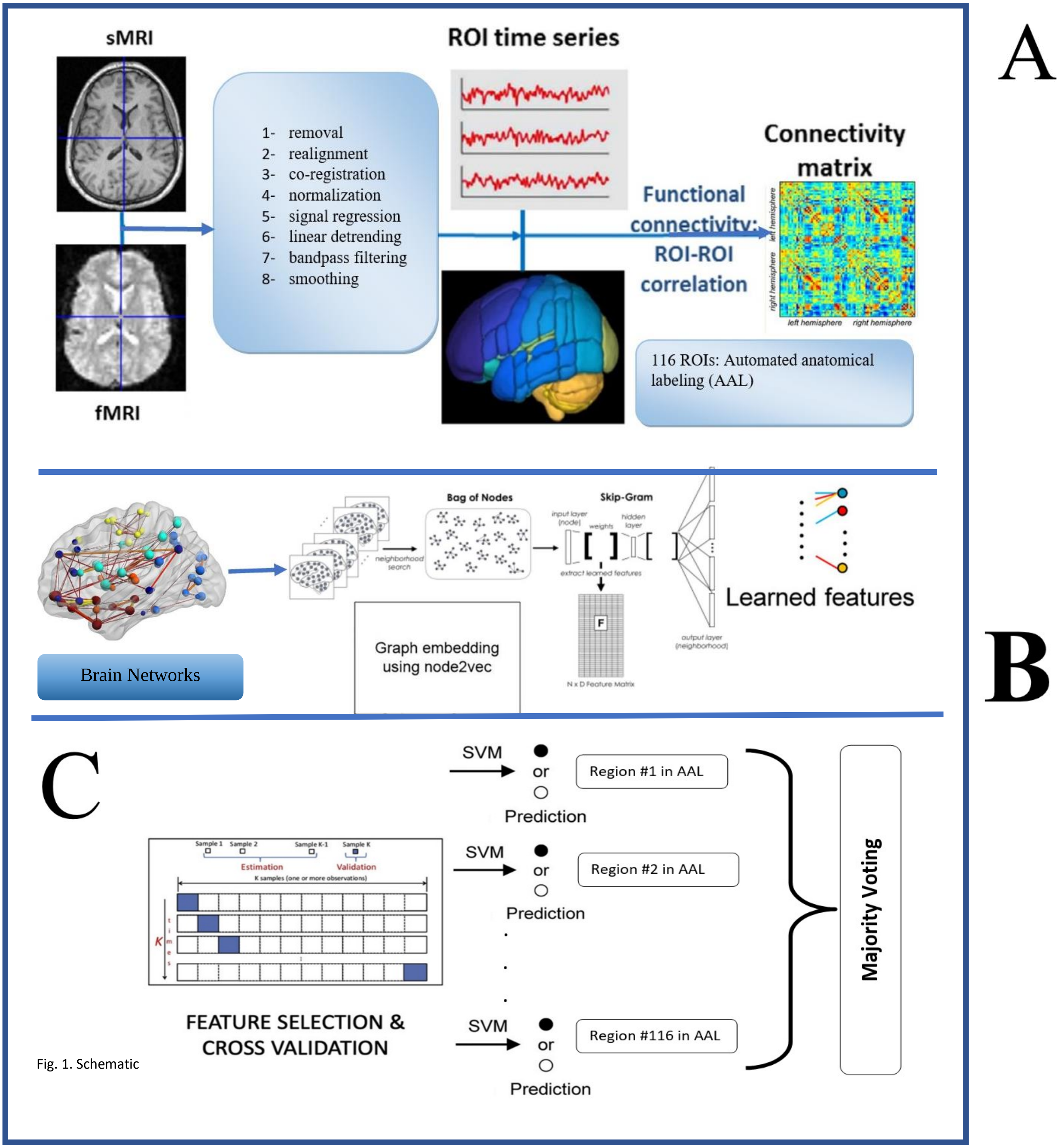

Fig. 1. Schematic

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