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Brain Age Classification from fMRI Data Using Graph Neural Networks and Evolutionary Algorithm

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Abstract— The brain is a complex organ that undergoes changes with age, and predicting brain age is crucial for monitoring brain health. It provides valuable insights into brain function and helps in the prevention of neurological diseases. This research predicts brain age through age classification based on fMRI data from the HCP dataset, consisting of individuals aged 22 to 36 years. After training a graph convolutional neural network, the model achieved an accuracy of 0.73 on the test data, demonstrating an improvement over previous studies on the same dataset. An evolutionary approach was then applied to optimize the selection of brain regions using a Genetic Algorithm to identify important and informative regions. This selection and optimization process maintained good predictive accuracy while reducing the number of brain regions. The results indicate that, despite using only half the original number of brain regions (8 regions), the model's accuracy remained at 0.65, showing only a slight decline. This highlights the significance of these regions in brain age classification. Identifying these key regions can contribute to the early diagnosis of brain and neurological diseases, enabling experts to better understand and manage the brain aging process.

Keywords— brain-age, GNN, EA, fMRI

I. Introduction

Brain age calculation is an essential topic in brain health. Brain age is a measure that enables a better understanding of the aging process [1], [2]. Brain age prediction is crucial for the assessment of individual cognitive and neurological health. This aids in understanding the aging process and also allows doctors to diagnose neurological disorders earlier and more effectively [3], [4]. A comparison of brain age and chronological age can reveal individuals with accelerated brain aging who are at high risk of disease and death. Research on the aging process is often performed using brain age prediction models. This technique trains machine learning models to monitor age-related structural changes in healthy brains and then applies these models to predict brain age in other individuals [5].

Over the years, alterations in the brain's structure and function can result in decreased cognitive abilities and an elevated risk of disease. An important challenge of this method is ensuring the model's prediction accuracy and enabling neuroscience experts to interpret their results. When specific brain regions of interest are known—in other words, those that have the greatest effect on age prediction—experts can conduct further research on these ROIs to detect brain aging in those specific regions and understand why this age gap has formed in these regions [6]. Brain age classification is also a very crucial task in addition to brain age prediction. For example, a specific age threshold could be used to classify individuals as either old or young, and then these two classes can be used to predict age and analyze results [3], [6].

Deep neural networks have achieved a wide range of successes in brain-related areas. A type of neural network has been designed for graph data, called a graph neural network. This variant is specifically designed to solve some challenges, such as node classification, whose goal is to predict node labels based on their connections and features [7]. Applying these networks to fMRI data has been successful in many domains, including studies on human subjects, where they have identified complex connectivity patterns to extract information such as brain age from the examined subjects [8].

II. Graph Convolutional Neural Networks

Compared to MRI, using fMRI data in Convolutional Neural Networks (CNNs) comes with some challenges. First, it is computationally intensive. Second, it mainly captures brain activity in cortical structures, and third, it is noisy at the single-voxel level. For these reasons, the focus has shifted firstly to ROIs instead of individual voxels, calculating correlation coefficients between them, and secondly to Graph Convolutional Neural Networks, which are more suitable because they preserve graph-structured data. GCNs are designed to handle graph-structured data, which makes them ideal for fMRI analysis, where the relationships and connections between brain regions (or nodes) are key to understanding the data [9].

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III. Genetic Algorithm

A genetic algorithm is a type of Evolutionary Algorithm inspired by natural selection. it starts with an initial population of possible solutions, then evaluates how fit each individual solution is. The best-performing individuals are selected, and through crossover and mutation, a new generation is created. By repeating this cycle, the algorithm steadily hones in on an optimal solution [10].

IV. Related work

The use of Convolutional Neural Network (CNN) models with convolutional layers has led to advancements in brain studies, as demonstrated in [11] and [12]. In [12], MRI data from healthy subjects were used to train a network that successfully simulated local and global visual features before integrating a self-attention module. Additionally, in [11], convolutional layers in a neural network were employed to predict age in infants, ranging from 1 to 811 days, using fMRI data. They utilized a three-layer GCN to achieve better results than previous non-graph methods.

CNN models with convolutional layers have contributed to progress in brain studies [11] and [12]. For example, in [12], a neural network was trained on MRI data from healthy subjects to predict brain age. This study introduced a GNN module called Multi-Hop Graph Attention within a CNN architecture. Integrating this module allowed the model to learn inter-node relationships, enabling it to extract local and global features critical for brain age prediction. In [11], convolutional layers were also used within a neural network to predict age in days from fMRI data for infants aged between 1 and 811 days. Using a three-layer convolutional GNN, they achieved state-of-the-art results compared to previously studied non-graph methods.

Machine learning methods for brain age prediction were applied to MRI data from the HCP dataset in [13]. Non-graph testing methods included linear regression-based approaches, such as Lasso and Multilayer Perceptron (MLP), for parametric-based approaches, while Kernel Ridge Regression (KRR), Support Vector Regression (SVR), Gaussian Process Regression (GPR), and k-Nearest Neighbors (k-NN) were evaluated as nonparametric models. Ensemble learning models, such as Decision Trees, Random Forests, and AdaBoost, were also tested. Study results showed that simpler regression models outperformed other tested machine learning methods in predicting brain age, achieving a mean absolute error (MAE) of 2.75 years on test data, which outperformed more complex models and was therefore considered superior. Another study on regression models in [14] trained on the PNC dataset yielded an estimated brain age correlation with chronological age, achieving an MAE of 2.43 years and a root mean square error (RMSE) of 2.93 years. The best predictors of brain age were located in sensorimotor, visual, and default mode brain regions, as they concluded.

For classification problems, age and gender classification using fMRI data from the HCP dataset was conducted in [6]. In their work, they claimed to be the first to adapt Graph Temporal Convolutional Networks (GTCNs) for age classification. The fMRI group dataset was divided into young (≤28 years) and old (>28 years). They achieved 63% accuracy in age prediction and 78% accuracy in gender classification. In 2024, [15] investigated changes in brain activity across different ages using fMRI data. Instead of looking only at connectivity between regions, they considered features from multiple regions and predicted participants' age and gender using an SVM. There were pairwise classifications across six different age decades, with prediction accuracies ranging from 49.5% to 84.8%. The highest accuracies were for the 21–30 years group and for participants aged 71 years and over. Moreover, it was shown that differences in neural signals in the brains of older individuals decrease over time, leading to lower accuracy in gender prediction.

V. Methodology

In this study, fMRI data from the Human Connectome Project (HCP) were used to predict brain age. The data included 1,108 samples of fMRI scans at high temporal resolution, comprising 593 healthy men and 498 healthy women, aged 22 to 36 years. The pre-processed data were available for download, these preprocessing steps included corrections for spatial distortions caused by susceptibility artifacts, adjustments for eddy currents and head motion, and the removal of physiological noise such as cardiac and respiratory fluctuations; however, some subjects' fMRI scans were missing, and after removing outliers, the final dataset used in this study consisted of 425 subjects. Their brain scans were divided into 17 regions using Yeo's brain atlas [16], which was performed in this research.

To categorize the data, a threshold of 28 years was used to create two age categories. In this research, due to the elimination of gender effects, only male subjects were considered. Next, time series and functional connectivity matrices were extracted and processed from the fMRI data, and the data were split into training and testing sets at an 80:20 ratio, as the frequency of each class in the training and test dataset is shown in Fig. 1. Subsequently, the model for age classification was trained using a GNN, and finally, evolutionary optimization techniques were applied to identify more effective regions, this workflow is illustrated in Fig. 2.

A. Apply GNN

In order to apply the GNN model, the data must first be represented as a graph. To do this, each region is considered a node, and the connection between any two regions is treated as an edge. Using time series data within 400-point time windows with 100-point time overlap, functional connectivity between any two regions is calculated, and a graph is generated from fMRI brain scans for each subject to obtain the edge values.

The GCN-based model used in this study is GCN-SE [11] for age prediction. This model was applied to fMRI data analysis and brain age prediction, as it utilizes a CNN that leverages edge and node permutation fusion processes to extract complex and important features. Fig. 3 illustrates the detailed structure of its layers. Also, the data are inputted as a 17 × 17 matrix, and key features are extracted through both direct and indirect pathways between brain regions.

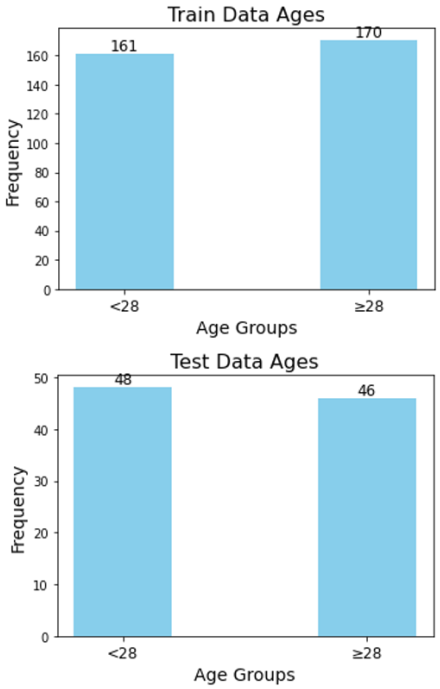

Fig. 1. Class distribution of training and test dataset for young and old age groups

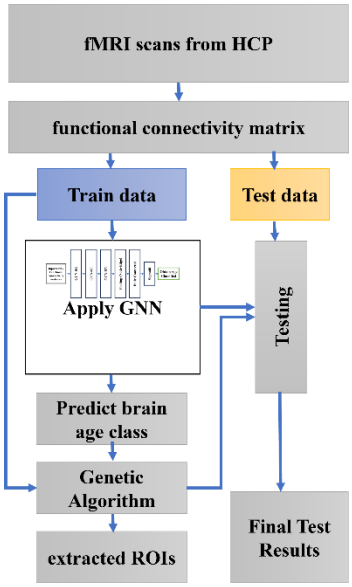

Fig. 2. Proposed workflow for brain age classification using GNN and genetic algorithm on fMRI data

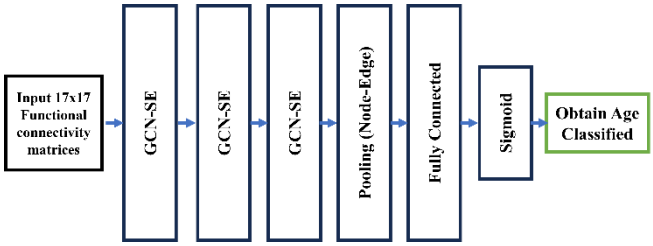

Fig. 3. The Architecture of the GCN-SE Model from [11] Used for Brain Age Classification

Additionally, each layer incorporates a squeeze-and-excitation block that helps focus on the most important features. Finally, pooling layers are applied to compress the data, enhancing the model's accuracy and efficiency in predicting brain age. Since the study aims to classify age, a sigmoid activation function is used in the final layer. The model is trained with a learning rate of 0.001, a batch size of 200, and over 20 epochs (10-fold cross-validation), with early stopping to prevent overfitting.

Fig. 4 and Fig. 5 show changes in accuracy and binary cross-entropy error during the training process, respectively. The model's training results are presented in Table 1, demonstrating that the data imbalance across real age groups has affected precision. However, as shown in Table 2, the model outperformed previous work on the same dataset.

VI. Apply Evolutionary Approach

An evolutionary approach can be helpful for selecting features and identifying a subset of important brain regions from a larger

set. In neuroimaging, specific brain regions, known as regions of interest, are used to reduce data dimensions and increase interpretability [17]. While graph neural networks are useful for understanding the interactions between various brain regions, they may lack focus on the most critical areas for age prediction. To address this issue, a genetic algorithm (GA) is employed to explore different combinations of brain regions, thereby reducing the search space [18]. The steps in a genetic algorithm include population generation, evaluation, crossover, mutation, and selection, with an additional check to prevent duplicate individuals in the population before stopping. These steps are illustrated in Fig. 6.

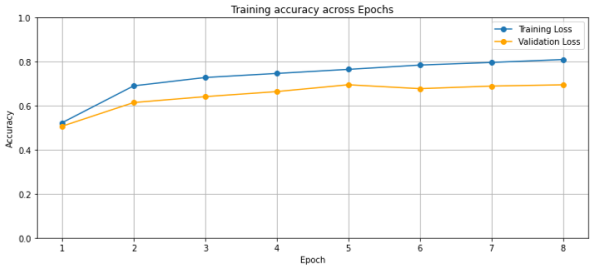

Fig. 4. Training and Validation Accuracy of the GNN Model Across Epochs

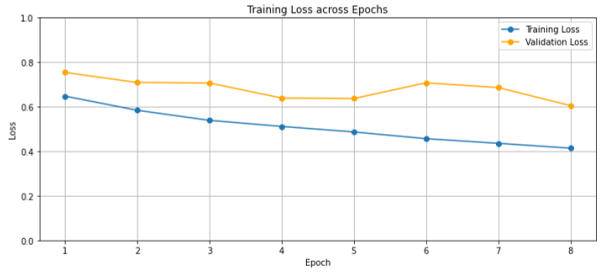

Fig. 5. Training and Validation Loss of the GNN Model Across Epochs

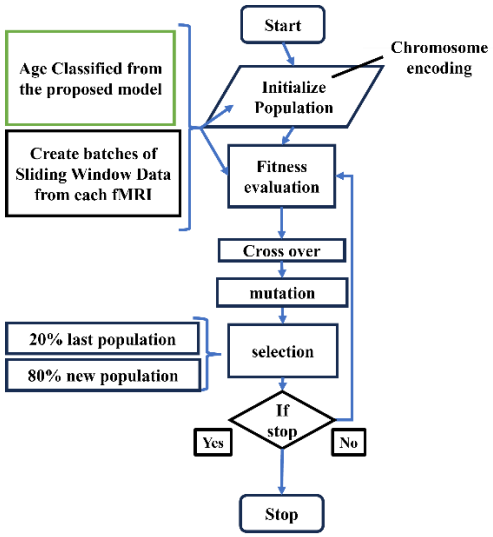

Fig. 6. Workflow of the Genetic Algorithm Used in This Study, Illustrating Key Steps in the Optimization Process

VII. Chromosome Encoding and Initial Population Generation

Each chromosome is represented as an array of binary values (0s and 1s), indicating the presence or absence of different brain regions. The chromosome length corresponds to the number of brain regions (17 in this study). Each row or column of the connectivity matrix can be considered a gene within a chromosome. The initial population is generated randomly, with each chromosome containing exactly a number of active regions (represented by ones), while the remaining genes are inactive (zeros). This study considers 15 brain regions in the initial population

VIII. Genetic Operators and Fitness

For crossover, three random points are selected, and genes are exchanged at these points. During mutation, two random points are chosen, and the genes between them are toggled between 0 and 1. Chromosomes are evaluated using a fitness function, as defined in Equation (1) [18], which favors chromosomes with fewer selected regions while maintaining high prediction accuracy. The generated connectivity matrix from these chromosomes is then fed into a pre-trained model, and fitness is assessed based on training data.

$$fitness_x = w_{acc} * acc + (1 - w_{acc}) * (\frac{1}{n_{regions}}) \quad \square\square\square$$

Equation (1) is fitness calculation, here w_{acc} represents the weight of accuracy for chromosome x, and $n_{regions}$ is the number of selected regions. The weight w_{acc} is set to 0.8. Fig. 7 shows the fitness value changes in the population over 100 generations on the training data. The chromosome length and population size are set to 17 and 200, respectively. This formulation aims to maximize accuracy while minimizing the number of regions, promoting a parsimonious model.

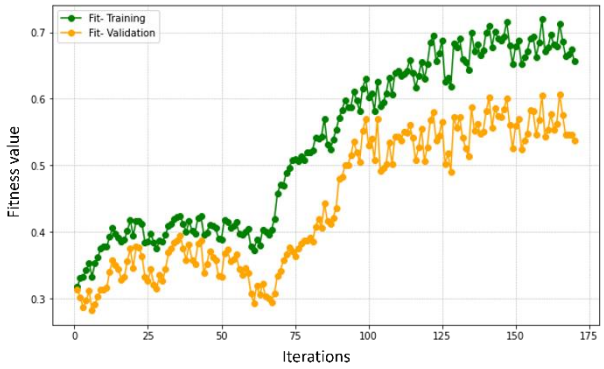

Fig. 7. Fitness Value of the Population Across Generations for Training and Validation

IX. Results and Discussion

The results of training the data on the GNN are summarized in Table 1, including the F1 score, recall, precision, and accuracy, which were 0.83, 0.89, 0.77, and 0.81, respectively. The genetic algorithm results demonstrated that selecting an optimal subset of brain regions led to only minimal degradation in evaluation metrics compared to using all regions. As shown in Table 1, training and testing on all 17 brain regions achieved F1 scores of 0.83 and 0.76, respectively, outperforming the scenario where only 8 regions were selected.

The selected regions, based on the Yeo atlas, include regions 3, 7, 8, 10, 13, 15, 16, and 17, corresponding to the Dorsal Somatomotor, Posterior Ventral Attention, Anterior Ventral Attention, Orbitofrontal-Limbic, Lateral Frontoparietal, Ventral DMN, Dorsal DMN, and Lateral DMN networks. These regions play a significant role in brain age prediction, making them valuable for studies on development and aging.

Table 2 presents a comparison between the proposed method and previous approaches, demonstrating that the proposed method, when using all brain regions, achieved an accuracy of 0.73. This performance is significantly higher than that of the graph neural network method proposed in [8], which achieved an accuracy of 0.502, and the graph convolutional network method in [6], which attained an accuracy of 0.63. The studies compared in Table 2 represent the latest advancements in brain age classification using the HCP dataset.

While reducing the number of brain regions from 17 to 8 leads to a slight decline in accuracy, it significantly reduces model complexity and computational cost. As seen in Table 1, using 8 selected regions resulted in a test accuracy of 0.65 compared to 0.73 when all 17 regions were included.

TABLE I. PERFORMANCE EVALUATION OF THE PROPOSED METHOD ACROSS DIFFERENT METRICS

Dataset	**Number of Regions**	**F1 Score**	**Recall**	**Precision**	**accuracy**
Train	17	0.83	0.89	0.77	0.81
	8	0.74	0.76	0.71	0.72
Test	17	0.76	0.85	0.68	0.73
	8	0.65	0.65	0.64	0.65

TABLE II. COMPARISON OF THE PROPOSED METHOD WITH PREVIOUS METHODS ON HCP DATASET

Method		**Accuracy**	**Categories**
Graph Neural Network [8]		0.50	3
Graph Convolutional Networks [6]		0.63	2
Proposed Model	Before GA	0.73	2
	After GA: 8 Regions	0.65	2

Reducing the number of regions affects model performance, particularly in accuracy. Fig. 7 and fig. 8 illustrate the best accuracy achieved for different numbers of selected regions on the training and test datasets using the genetic algorithm.

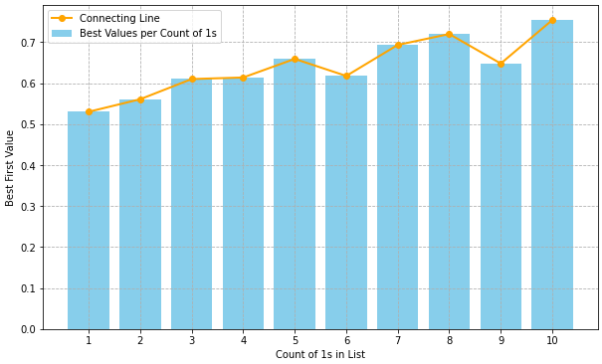

Fig. 8. Best Accuracy Achieved for Training Data Across Different Numbers of Selected Brain Regions

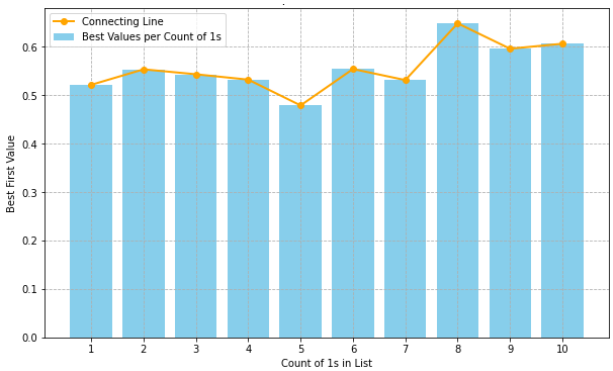

Fig. 9. Best Accuracy Achieved for Test Data Across Different Numbers of Selected Brain Regions

X. Conclusions

This study applied brain age classification using a graph neural network (GNN) on HCP data, focusing on ages 22 to 36. The method achieved an accuracy of 0.81 in the training phase and 0.72 in the testing phase, representing an improvement over previous results. Additionally, the model demonstrates high processing speed, reaching results in fewer epochs.

Moreover, an evolutionary approach was utilized to identify key regions for age classification. The genetic algorithm effectively used 8 regions from the Yeo atlas, achieving a comparable level of accuracy while reducing the total number of regions needed and that is 0.65 in test data. The identified regions helped narrow the search space, enabling neuroscientists to focus on fewer brain areas when predicting age-related diseases. In summary, the GA-based feature selection method effectively balances accuracy and complexity, achieving a streamlined model that retains substantial predictive power with fewer brain regions.

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