2026 Volume: 02 Issue: 02 www.ijrpa.com ISSN 2456-9995 Review Article

International Journal Research Publication Analysis

Page: 01-11

AN ASSESSMENT OF CONVOLUTIONAL AND GRAPH NEURAL NETWORKS IN BRAIN DEVELOPMENT ANALYSIS

***Parul Kashyap**

Assistant Professor, Department of Computer Science & Engineering, Meerut Institute of Engineering & Technology, Meerut, Uttar Pradesh.

Article Received: 27 December 2025
Article Revised: 16 January 2026
Published on: 05 February 2026

***Corresponding Author: Parul Kashyap**
Assistant Professor, Department of Computer Science & Engineering, Meerut Institute of Engineering & Technology, Meerut, Uttar Pradesh.

DOI: https://doi-doi.org/101555/ijrpa.1464

ABSTRACT

In this work, we present a novel analytical approach that does not rely on predetermined neuroanatomical references for analysing and comparing brain MRI data from non-standard animal models, like sheep. The created pipeline overcomes the drawbacks of conventional neuroimaging approaches by combining automated MRI segmentation techniques with graph neural networks (GNNs). Traditional methods typically rely on set anatomical atlases, which frequently don't adjust to rare species or developing brains. The suggested approach reduces template-related bias and enhances generalisation by directly identifying regions of interest from MRI scans and modelling the brain as a graph structure. In experiments, the GNN-based model performs better than a traditional convolutional neural network (CNN) model in age prediction tasks, with an accuracy of 63.22% versus 59.77%. Additionally, the application of GNNs facilitates efficient learning of intricate interregional brain interactions and improves model transparency. Additionally, improved biological understanding of developmental patterns and structural connectivity is supported by the suggested method. Overall, these findings show that the framework provides a reliable, flexible, and understandable alternative for brain MRI analysis in studies using non-traditional animal models and developmental research.

KEYWORDS: Neuroimaging Analysis, Brain Development, Graph Neural Networks (GNN), Convolutional Neural Networks (CNN), Brain MRI, Non-Standard Animal Models, Automated Segmentation

1. INTRODUCTION

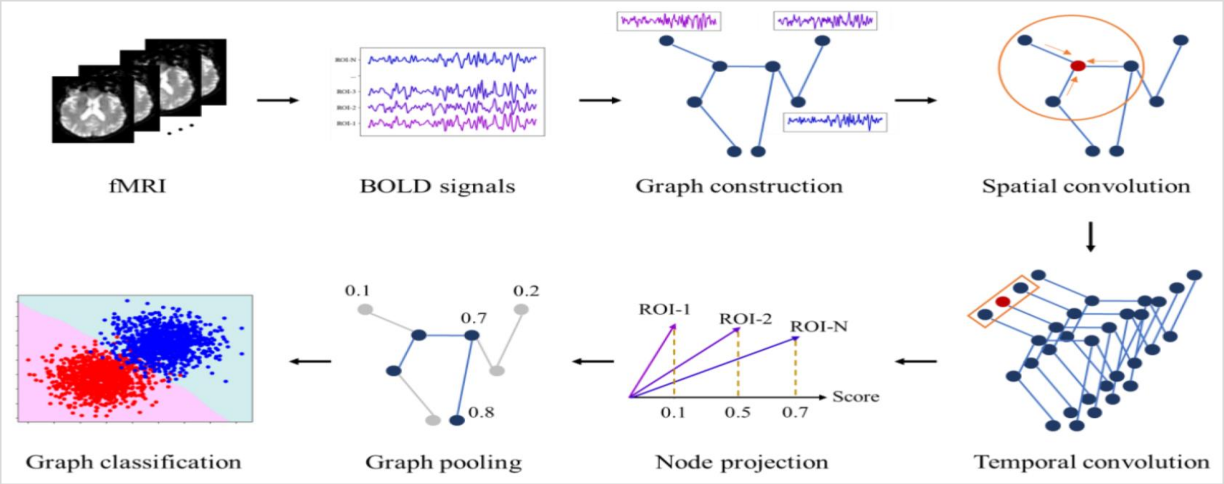

Figure 1:- pipeline for medical imaging based on graphs. An ROI network is created, fMRI volumes are transformed into BOLD time series for each ROI, relational dynamics are extracted by spatial graph operations and temporal modelling, node features are projected and combined, and a readout head produces subject-level predictions.

Brain MRI analysis has been greatly improved by automated methods, especially in research involving people and frequently used lab animals (Kaur and Gaba, 2021; Park and Friston, 2013). Comparable analytical methods are still scarce, though, for studies that concentrate on developing brains or less commonly used animal models, such sheep. Because of this, brain structure segmentation in these environments frequently relies on manual labelling or automatic techniques that are guided by existing anatomical templates and signal intensity, when such references are accessible (Nitzsche et al., 2015; Ella et al., 2017). These methods may miss individual variability, developmental changes, or pathological differences since they rely heavily on past anatomical knowledge and the calibre of current atlases. Accurate segmentation is made more difficult in developing brains due to low tissue contrast, uneven maturation rates, and insufficient structural construction (Li et al., 2019). Furthermore, exploratory research and the identification of new structural patterns associated with neurological illnesses may be constrained by the use of predetermined anatomical regions. In this study, we propose a unique processing framework to overcome the intrinsic limitations of traditional convolutional neural networks and reduce segmentation-related bias in Figure 1. The suggested approach does not use predetermined neuroanatomical information; instead, it creates regions of interest (ROIs) immediately from imaging data. In particular, two complementary segmentation algorithms are used to generate segmented images utilising voxel intensity-based features, guaranteeing resilience across different image qualities. Additionally, by representing the brain as a network of interconnected patches, graph neural networks (GNNs) are used to analyse anatomical patterns and effectively understand complicated inter-regional correlations (Cui et al., 2021; Li et al., 2021; Ravinder et al., 2023). The framework is able to capture both local and global structural features thanks to this graph-based representation. A more flexible, scalable, and data-driven investigation of brain organization is made possible by the suggested method, which eliminates reliance on set anatomical atlases. The framework's applicability in neuroscience research is further expanded by its support for cross-species analysis and its potential to be expanded to other developmental and pathological imaging studies.

2. LITERATURE REVIEW

Image segmentation and brain classification are the two main goals of previous research on brain MRI analysis (Coupeau et al., 2022; Srinivasan et al., 2024; Kaur and Gaba, 2021; Poriya, 2023). In both areas, machine learning techniques, particularly convolutional neural networks (CNNs) and graph convolutional networks (GCNs), have demonstrated strong capabilities in automatically extracting meaningful features and identifying complex patterns within neuroimaging data. To guarantee consistent voxel resolution, a number of crucial preprocessing techniques are regularly used, regardless of the learning architecture chosen. These include noise reduction, bias field correction, intensity normalisation, and spatial resampling. While skull-stripping and cropping techniques are used to exclude non-brain tissues and identify pertinent brain regions, spatial registration is frequently used to align individual scans within a shared anatomical space, frequently utilising standardised reference templates. In order to define regions of interest (ROIs), which are the foundation for creating graph-based representations, segmentation is essential. Traditionally, manual annotation or atlas-based techniques based on individual brain pictures or standardised templates have been used for this process (Van Essen and Drury, 1997; Yang et al., 2020; Fil et al., 2021). These methods rely mostly on prior anatomical knowledge and the quality of the atlas, which limits their capacity to account for developmental changes, inter-individual variability, and pathological abnormalities, even while they allow for consistent anatomical labelling and cross-subject comparisons. Advances in CNN architectures, including AlexNet, ResNet, VGG, and DenseNet, have significantly improved performance in MRI-based classification, clustering, and age estimation tasks (Krizhevsky et al., 2012; He et al., 2016; Cole et al., 2017; Jiang et al., 2020). More recent models incorporate attention mechanisms to enhance feature representation and further improve predictive accuracy (Lam et al., 2020; Cheng et al., 2021). Simultaneously, graph-based methods—in which nodes represent anatomical regions, voxels, or tissue types and edges encode structural, functional, or effective connections—have drawn more attention for modelling brain connectivity and regional interactions (Fedorov et al., 2012; Bullmore and Bassett, 2011; Sporns, 2018). While edge attributes might indicate distances, tract lengths, or connection strengths, node attributes frequently consist of spatial coordinates, morphological characteristics, and intensity-based measurements. However, defining meaningful edges and determining appropriate thresholding strategies remain challenging, as fully connected graphs are computationally expensive and difficult to interpret. In order to better simulate complicated inter-regional relationships and learn from these graph representations, graph neural networks (GNNs) have been created (Li et al., 2021; Ravinder et al., 2023; Srinivasan et al., 2024; Coupeau et al., 2022). By incorporating both local and global network features, GNN-based frameworks have shown increased performance in brain age estimation and developmental studies. However, a lot of current GNN techniques depend on clearly defined graph topologies that come from tractography or multi-modal data that are aligned to standard templates (Lim et al., 2024; Cai et al., 2023), which limits their use in non-traditional contexts. Additional difficulties include significant anatomical diversity, a lack of standardised atlases, a restricted supply of automated techniques, and tiny sample sizes for analysing developing brains and unconventional animal models. In these situations, segmentation is frequently still done by hand, requiring specialised knowledge and being vulnerable to operator-dependent bias and inter-observer variability (Fedorov et al., 2012). By creating representative templates using affine transformations and label propagation techniques, atlas-based registration methods provide partial solutions (De Vico Fallani et al., 2017). However, these methods often necessitate extensive post-processing to guarantee precise anatomical alignment. Recent efforts have introduced automatic and incremental segmentation methods incorporating biological priors as complementary strategies (Galisot et al., 2022); however, their generalizability remains limited. The need for more adaptable, data-driven, and atlas-independent analytical frameworks is thus highlighted by the fact that, despite notable advancements in deep learning and graph-based neuroimaging analysis, current approaches still have significant limitations in terms of adaptability, interpretability, and robustness, especially in developmental studies and research involving unconventional animal models.

3. THE PIPELINE THAT IS PROPOSED

3.1 From 3D MR Pictures to Graphs

In this work, we provide a general-purpose framework for creating graph-based representations from three-dimensional brain MRI data from developing brains and non-traditional animal models. This method's main goal is to maintain important structural and intensity-related information from the source images while facilitating effective and significant graph building. The suggested approach turns volumetric MRI data into graphs, which enables graph neural networks to automatically learn, recognise, and take advantage of the most instructive features while training. The modelling of both global anatomical links and local tissue qualities is made easier by this transition, which is frequently challenging to capture with traditional voxel-based or patch-based learning methods. Furthermore, the graph-based representation supports scalable analysis across varying brain sizes and developmental stages, enhancing the adaptability of the framework. By doing this, the suggested methodology seeks to eliminate the need for predetermined anatomical priors and offer a flexible, data-driven basis for upcoming learning and prediction tasks.

3.2 Preprocessing

To improve picture quality and guarantee consistency among MRI scans, the preprocessing step includes skull stripping and z-score intensity normalisation. In order to isolate brain areas for further examination, non-brain tissues like the scalp and skull are removed using a technique called skull stripping. This stage lessens background noise and keeps unrelated information from interfering with learning. Because Z-score intensity normalisation maintains the relative alignment of white matter, grey matter, and cerebrospinal fluid tissues while standardising voxel intensity distributions, it is frequently used in brain MRI investigations, especially in machine learning applications (Schmid, 2023). Robust feature learning is made possible by this normalisation procedure, which enhances comparability between people and imaging sessions. The two primary steps of the graph construction process are node definition and edge establishment, which come after preprocessing. The volumetric MRI data can be represented as structured graphs that are appropriate for graph-based learning and analysis by following these procedures.

3.3 Creation of Nodes and Edges

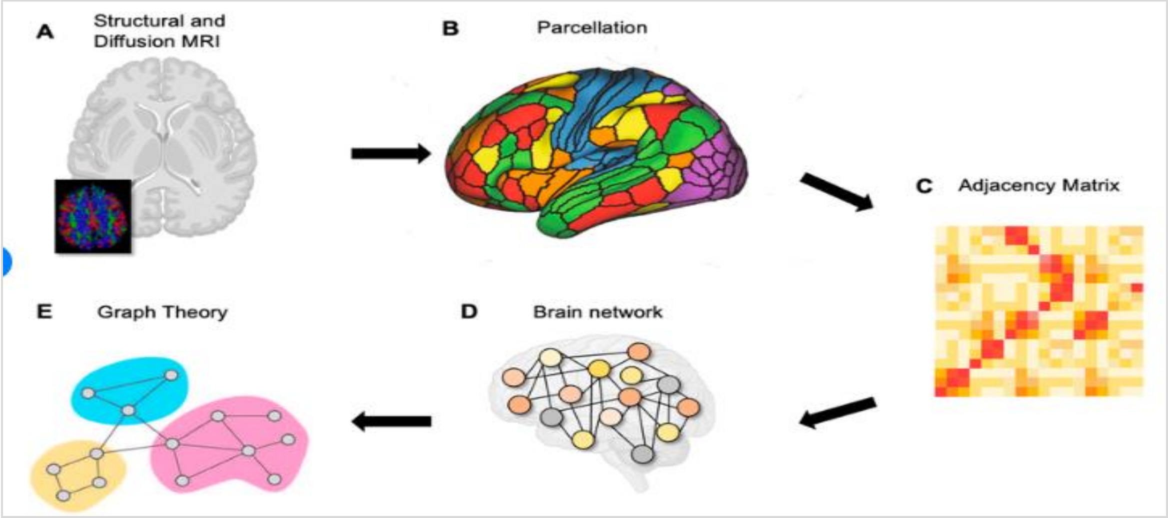

Figure 2:- Diagram showing the creation of a brain network using neuroimaging data.

As shown in Figure 2, node creation is carried out based on the segmentation of areas of interest (ROIs). The suggested framework uses a segmentation strategy that is independent of predetermined biological priors in order to analyse developing brains and unconventional animal models. A totally data-driven segmentation approach is made possible by treating MRI data as traditional intensity-based pictures rather than pre-labeled anatomical features. This approach enhances adaptability across different species and developmental stages. Two segmentation methods—a split-and-merge algorithm and a histogram-based clustering algorithm—are assessed in this study for ROI formation. Voxels with identical intensity levels are grouped into appropriate segments by the histogram-based technique, which divides the global intensity range into N equal intervals. A key challenge associated with this approach lies in selecting appropriate parameter values, as the optimal number of segments depends on the study objectives and the desired granularity of regional representation. Image 1 provides an illustration of this technique. The split-and-merge algorithm (Gonzalez and Woods, 2017), the second method, functions in two consecutive stages. In the split phase, a user-defined homogeneity criterion and a minimum region size are used to recursively divide the image into smaller, more homogeneous parts known as "cubes." The intensity range within each zone is usually used to evaluate homogeneity. In order to improve regional coherence and lessen over-segmentation, spatially nearby regions are merged in the succeeding merge phase if their union meets predetermined homogeneity criteria. Each ROI that is produced after segmentation is represented as a graph node with morphological, spatial, and intensity-based characteristics. The creation of organised brain graphs is therefore made possible by establishing edges between nodes based on spatial adjacency, similarity metrics, or distance requirements. This node-edge formulation offers a strong basis for further graph neural network analysis by making it easier to characterise both local tissue characteristics and distant anatomical relationships.

3.4 Classification and Analysis of Graphs

As was previously mentioned, because graph neural networks (GNNs) can capture intricate interactions between many areas of interest (ROIs), they are especially well suited for analysing brain MRI data. GNNs function at a higher structural level, with nodes representing different brain areas or subregions and edges encoding the interconnections between them, in contrast to convolutional neural networks, which are mainly concerned with extracting features from local voxel neighbourhoods. The network can learn both local and global dependencies within brain networks thanks to its relational modelling paradigm, producing predictions that are frequently more correct and biologically significant. The suggested framework formulates the task as a multi-class graph classification issue and uses a specialised GNN architecture to process the created brain graphs in order to accomplish age estimation. Each graph is associated with one of K distinct age groups and represents a unique brain scan. The model is able to capture developmental trends and changes in connectivity related to various age groups because node representations are updated through iterative message-passing procedures that aggregate data from nearby nodes. Furthermore, compact global representations are created using graph-level pooling techniques and then delivered to fully connected layers for final classification. By emphasising key areas and linkages involved in the prediction process, our design supports better interpretability while strengthening resistance to noise and anatomical variability.

3.4.1 Layers of Graph Convolution

The suggested approach uses a series of three graph convolutional layers to provide efficient information propagation throughout the graph structure. These layers allow the model to capture both local and global patterns in brain organization by iteratively aggregating and transforming features from nearby nodes. The available dataset in this study is relatively small, with just about 200 graph samples, despite the fact that many different graph convolutional designs have been described in the literature. Because such designs could result in overfitting and poor generalisation performance, the use of extremely deep or complicated networks with many parameters was avoided. The effect of feature dimensionality on learning performance was examined using two distinct parameter settings. In the first setup, the model starts by employing the first GCNConv layer to project the seven initial node features into an eight-dimensional feature space. The second layer then expands this representation to sixteen dimensions, while the third layer expands it even further to thirty-two dimensions. The network is able to gradually capture increasingly complicated structural and intensity-related patterns because each convolutional layer applies a learnt linear transformation followed by a non-linear activation function, namely the Rectified Linear Unit (ReLU). A more aggressive approach to feature extension is used in the second configuration. The dimensionality is extended from the initial seven input features to sixteen in the first layer, thirty-two in the second, and sixty-four in the third. The purpose of this exponential increase in feature dimensions is to assess the model's capacity to acquire more complex and expressive representations. The study examines the trade-off between model complexity and generalisation performance in the case of sparse training data by contrasting these two configurations.

3.4.2 Fully Connected Layers and Pooling

Following the graph convolutional layers, global pooling procedures are used to create a compact graph-level representation appropriate for classification. Both global mean pooling and global max pooling algorithms are assessed in this study to efficiently summarise node-level attributes while taking the dataset's small size into account. While global max pooling chooses the maximum feature values, highlighting the most noticeable and discriminative patterns, global mean pooling calculates the average feature values across all nodes, reflecting the overall structural properties of the neural graph. The framework seeks to determine the best approach for maintaining pertinent information in situations where data is scarce by contrasting these two pooling processes.

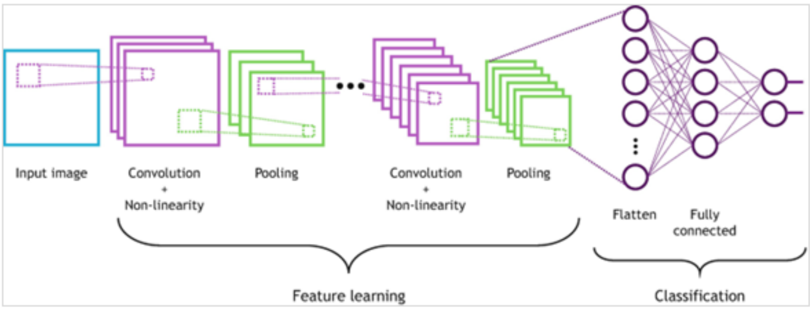

Figure 3: Fully Connected layers.

Graph-level classification is then carried out by passing the resulting pooled feature vectors through a series of three fully connected (FC) layers, fc1, fc2, and fc3 in Figure 3. In order to effectively discriminate between various age groups, these layers gradually convert the high-dimensional pooled representations into lower-dimensional feature spaces. The network may model complex decision boundaries by using a non-linear activation function after each fully connected layer applies a learnt linear transformation. Class probability scores for the predetermined age groups are generated by the last completely linked layer. Global pooling and fully linked layers work together to improve the overall predictive performance of the suggested GNN-based classification architecture and enable robust feature integration.

4. TESTS AND FINDINGS

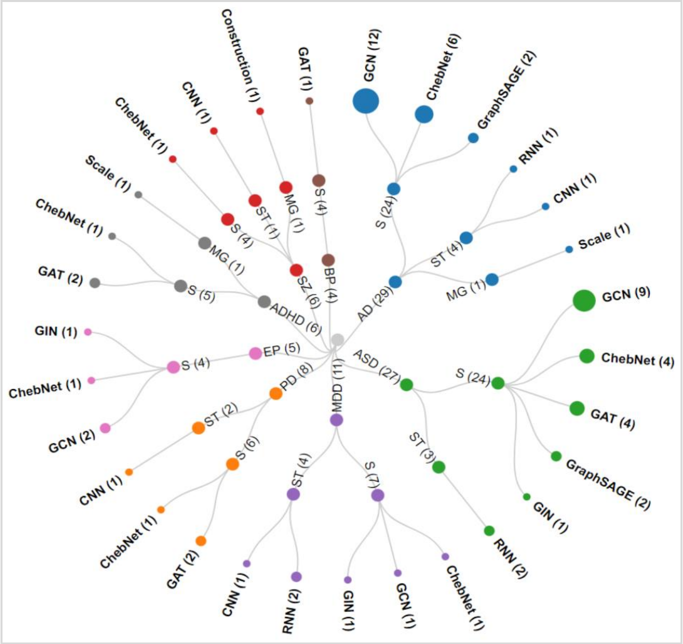

Figure 4: Feature extraction of ND diagnosis.

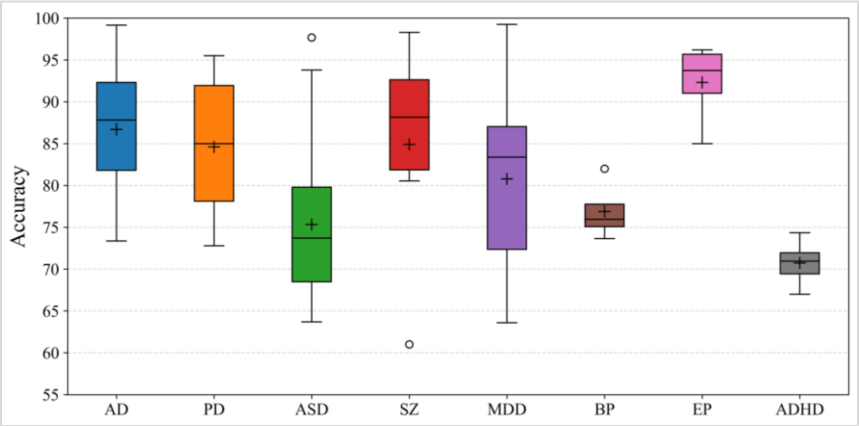

Figure 5: The accuracy of the ND diagnosis.

The effectiveness of several convolutional neural network (CNN) and graph neural network (GNN) designs in estimating brain age using unconventional animal models—specifically, sheep—was assessed through a series of tests in Figure 4. Finding the best modelling techniques to capture developmental trends in brain MRI data was the main goal of these experiments in Figure 5. A computing platform with an Intel Core i7-11850H processor running at 2.50 GHz, 32 GB of system memory, and an NVIDIA GeForce RTX A3000 laptop GPU was used for all experiments, guaranteeing adequate computational resources for training and assessment. The Python programming language and pertinent deep learning libraries were used to create the entire analysis pipeline, which included data preprocessing, model training, validation, and performance evaluation. This experimental design made it possible to evaluate the suggested framework consistently and reproducibly across various model configurations and parameter settings.

5. CONCLUSION

In order to minimise potential bias in the analysis, we introduced an innovative and adaptable pipeline in this study for predicting brain age in unconventional animal models without depending on predetermined neuroanatomical priors. A completely data-driven study of brain development is made possible by the suggested architecture, which combines automated MRI segmentation, graph creation, and learning based on graph neural networks (GNNs). According to experimental data, the suggested GNN-based pipeline continuously performs better in terms of age prediction accuracy than conventional convolutional neural network (CNN) techniques. Automatic MRI segmentation is the first step in the procedure. Segmented volumes are then transformed into graph representations and analysed using GNN models. Additionally, two segmentation methods with various GNN topologies and parameter configurations were thoroughly examined to determine how they affected robustness and performance. According to experimental data, the suggested GNN-based pipeline continuously performs better in terms of age prediction accuracy than conventional convolutional neural network (CNN) techniques. Automatic MRI segmentation is the first step in the procedure. Segmented volumes are then transformed into graph representations and analysed using GNN models. Additionally, two segmentation methods with various GNN topologies and parameter configurations were thoroughly examined to determine how they affected robustness and performance. The results demonstrate the benefits of using graph-based models to capture intricate interregional interactions and patterns of brain development. The suggested method improves interpretability and adaptability in addition to predicting accuracy, which makes it appropriate for a variety of cross-species and developmental neuroimaging investigations. In order to further enhance performance and generalisation, future work will concentrate on expanding the framework to larger and more varied datasets, including multimodal imaging data, and investigating sophisticated GNN structures. Further understanding of the biological processes behind brain development and ageing may also be possible with the incorporation of explainable artificial intelligence approaches.

REFERENCES

1. Bullmore, E. T. and Bassett, D. S. (2011). Brain graphs: Graphical models of the human brain connectome. 7:113–140.
2. Cai, H., Gao, Y., and Liu, M. (2023). Graph Trans- former Geometric Learning of Brain Networks Us- ing Multimodal MR Images for Brain Age Estimation. 42(2):456–466.
3. Cheng, J., Liu, Z., Guan, H., Wu, Z., Zhu, H., Jiang, J., Wen, W., Tao, D., and Liu, T.(2021). Brain Age Estimation From MRI Using Cascade Networks With Ranking Loss.40 (12):3400–3412.
4. W. A., Steves, C., Spector, T. D., and Montana, G. (2017). Predicting brain age with deep learning from raw imaging data results in a reliable and heritable biomarker. 163:115–124.
5. Krizhevsky, A., Sutskever, I., and Hinton, G. E. (2012). Im- ageNet Classification with Deep Convolutional Neu- ral Networks. In Advances in Neural Information Pro- cessing Systems, volume 25. Curran Associates, Inc.
6. Lam, P., Zhu, A. H., Gari, I. B., Jahanshad, N., and Thomp- son, P. M. (2020). 3D GridAttention Networks for Interpretable Age and Alzheimer's disease Prediction from Structural MRI.
7. Dong, P., Kim, J., Shi, F., Rekik, I., Lin, W., and Shen, D. (2019). Computational neuroanatomy of baby brains: A review. 185:906–925.
8. Li, X., Zhou, Y., Dvornek, N., Zhang, M., Gao, S., Zhuang, J., Scheinost, D., Staib, L. H., Ventola, P., and Duncan, J. S. (2021). BrainGNN: Interpretable Brain Graph Neural Network for fMRI Analysis. 74:102233.
9. Lim, H., Joo, Y., Ha, E., Song, Y., Yoon, S., and Shin, T. (2024). Brain Age Prediction Using Multi-Hop Graph Attention Combined with Convolutional Neural Net- work. 11(3):265.