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A Review of Brain Tumor Image Classification Using Graph Convolutional Neural Networks

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Abstract: Brain tumor refers to a cluster of abnormally proliferating cells in the brain, usually formed by uncontrolled division of malignant cancer cells, and belongs to high-risk neurological disorders. At present, the specific pathogenic mechanism of brain tumors has not been fully elucidated in the medical community. But research has shown that early screening can effectively prevent tumor malignancy and significantly improve clinical cure rates. In recent years, breakthroughs in deep learning technology have driven the development of intelligent assisted diagnostic systems, providing medical personnel with more efficient and accurate early detection methods. Among them, Graph Convolutional Neural Network (GCN) has become an important tool in the field of brain tumor image classification due to its powerful global feature extraction ability, especially in analyzing the correlation of medical images. This article systematically reviews the theoretical evolution of Graph Convolutional Neural Networks (GCN) and summarizes the current research progress on GCN based classification models for brain tumor datasets. At the end of the article, the challenges and future development directions faced by this technology were further discussed.

Keywords: Graph convolution network, Deep learning, Brain tumor.

1. Introduction

Patients with brain tumors often exhibit typical symptoms such as severe headaches, projectile vomiting, sudden vision loss, and epileptic seizures, which not only cause great pain to patients but also directly endanger their lives [1, 2]. Epidemiological data show that the global incidence rate of brain tumors continues to rise, which has become a major public health problem threatening human health. This disease is recognized by the medical community as one of the most malignant types of tumors and ranks among the top ten causes of death worldwide. It is worth noting that the incidence and mortality rates of brain tumors in China rank first in the world, and the disease burden is particularly severe [3].

The advancement of modern neuroimaging technology, such as non-invasive detection methods such as Magnetic Resonance Imaging (MRI), Computed Tomography (CT), Diffusion Tensor Imaging (DTI), and Positron Emission Tomography (PET), has greatly promoted the clinical detection of brain lesions [4]. However, diagnostic accuracy highly relies on image resolution and the experience judgment of radiologists, and subjective factors can easily lead to misdiagnosis risks. Therefore, computer-aided diagnosis (CAD) systems have emerged to provide objective and efficient diagnostic support for doctors.

In recent years, breakthroughs in deep learning technology have brought revolutionary progress to computer-aided diagnosis (CAD) systems. In the field of brain tumor MRI image classification, existing methods are mainly divided into two categories: traditional manual analysis methods and intelligent classification techniques based on deep learning. The traditional manual analysis methods depend entirely on the subjective judgment of the doctor, is susceptible to various interferences causes misdiagnosis, and has low efficiency. In contrast, Graph Convolutional Neural Networks (GCNs) have emerged as a transformative deep learning architecture in medical image analysis, particularly excelling in brain tumor characterization. These networks demonstrate unique capabilities in autonomously learning hierarchical feature representations while preserving and analyzing the complex spatial relationships inherent in neuroimaging data. Unlike conventional methods, GCNs overcome critical limitations by simultaneously processing local tumor characteristics and global contextual information through their graph-based processing framework. This dual capability enables more accurate modeling of tumor morphology and microenvironment interactions, while eliminating the subjectivity and information loss associated with manual feature extraction. The architecture's inherent ability to maintain structural integrity during feature transformation and aggregate multi-scale topological information has established new standards for computational analysis in neuro-oncology, offering clinicians more reliable decision support through its comprehensive pathological pattern recognition.

2. Theoretical Foundations and Evolution of Graph Convolutional Networks

Graph Convolutional Neural Networks (GCNs) represent a novel class of deep learning architectures specifically designed for processing non-Euclidean graph-structured data. Unlike conventional Convolutional Neural Networks (CNNs) that operate on regular grid-like data, GCNs employ specialized graph convolution operations to aggregate and propagate node information across graph structures, enabling effective learning of node-level and graph-level representations. The fundamental distinction between graph data and traditional image data necessitates the extension of standard convolution to graph convolution. Current GCN methodologies can be broadly categorized into two main approaches: Spectral-based GCN and Spatial-based GCN.

2.1. Graph Convolutional Neural Networks Based on Spectral

The Spectral-based GCN has rigorous mathematical theoretical support [5, 6] The core idea of this method originates from graph signal processing theory, which transforms the original graph structure data into frequency domain space for analysis by introducing Graph Fourier Transform. The specific implementation process includes three key steps: first, consider the node features in the graph as graph signals; Secondly, using the eigenvalue decomposition of Graph Laplacian matrix, the frequency domain basis of the graph is constructed; Finally, a learnable spectral filter is defined in the frequency domain space to perform convolution operations. This spectral domain based convolution method not only has clear mathematical interpretability, but also effectively captures the global topological characteristics of graph data. It is worth noting that this method provides theoretical support for processing non Euclidean data structures by converting complex graph convolution operations into multiplication operations in the frequency domain.

The convolution form on the graph is represented as follows:

$$f * g = U(U^T f \cdot U^T g) \tag{1}$$

Where f and g denote the input graph signals. By substituting $U^T g$ with a learnable spectral filter $g\theta$ parameterized by θ, the graph convolution operation as:

$$f * g = U g\theta U^T f \tag{2}$$

For this formula, it is decomposed into three key steps for analysis: firstly, $U^T f$ represents the Fourier transform process of transforming the graph signal f from the vertex domain to the frequency domain, which reveals the frequency domain characteristics of the graph signal; Secondly, $g\theta U^T f$ represents the convolution operation performed in the frequency domain, where the learnable parameterized filter $g\theta$ modulates the frequency domain signal to achieve selective enhancement of features; Finally, $U g\theta U^T f$ represents remapping the processed frequency domain signal back to the vertex domain through inverse Fourier transform to obtain the final graph convolution result.

Spectral Convolution Neural Network (SCNN) [7] is the first to generalize CNN to non Euclidean space, providing an innovative solution for processing irregular grid data. In order to update node features, the network defines the output of the k -th layer as:

$$x_{k+1,j} = h(U \textstyle\sum_{i=1}^{f_{k-1}} F_{k,i,j}\, U^T x_{k,i})(j = 1,2, \dots, f_k) \tag{3}$$

Where h is the activation function, $F_{k,i,j}$ is a convolutional kernel containing learnable parameters, and $x_{k,i}$ is the feature of the i -th node in the kth layer, f_k is the updated node feature of the f_{k-1} layer.

The dependency of SCNN on the Turalapras matrix requires time-consuming graph preprocessing, increasing implementation complexity. Secondly, when updating the features of the central node, SCNN finds it difficult to ensure that only the direct neighbor node information of that node is utilized, which may lead to inaccuracies in feature propagation.

In response to the limitations of SCNN, Defferrard et al. [8] proposed the Chebyshev Network (ChebNet), which approximates the eigenvectors of Turaplas through K iterations of the Chebyshev polynomial $T_k(x)$:

$$g\theta = h(U \textstyle\sum_{k=1}^{K-1} \theta_k\, T_k \widetilde{\Lambda})U^T \tag{4}$$

$$\widetilde{\Lambda} = \frac{2\Lambda}{\lambda_{max}} - I_n \tag{5}$$

where Λ is the eigenvector composed of the eigenvalues of the Laplacian matrix, λ_{max} is its maximum eigenvalue, and θ is the learnable Chebyshev coefficient.

Based on ChebNet, Kipf et al. [9] improved it using first-order Chebyshev polynomials to give the network better local connectivity.

$$x_{k+1,j} = h\left(\textstyle\sum_{i=1}^{f_{k-1}} \theta D^{-\frac{1}{2}} A D^{-\frac{1}{2}} x_{k,i}\right) \tag{6}$$

The core idea of frequency domain based GCN is to transform convolution operations on the graph into dot product operations in the Fourier domain. The advantage of this method is that it can effectively preserve the global information of the graph structure, thereby capturing the long-range dependencies between nodes in the graph. However, frequency domain based GCN also has significant limitations. Firstly, its high computational complexity is mainly due to frequent Fourier and inverse transforms, which limits its scalability on large-scale graph data; Secondly, as the number of model layers increases, the performance of frequency domain GCN does not significantly improve, and there may even be a phenomenon of performance degradation. This feature limits its ability to construct deeper networks, thereby affecting the model's ability to express complex graph structures. Therefore, although frequency-domain GCN has theoretical advantages, its computational efficiency and depth scalability remain the main challenges in practical applications.

2.2. Graph Convolutional Neural Networks Based on Spatial

Based on the spatial domain, GCN adopts a message passing mechanism and designs an efficient neighbor feature aggregation function to update the feature representation of the target node. The core concept of this method is to simulate the operation of traditional 2D convolution, as shown in Figure 1. 2D convolution is the use of convolution kernels to extract features of red and adjacent pixels; Graph convolution is a non-linear aggregation of red nodes and their neighboring nodes to update node features.

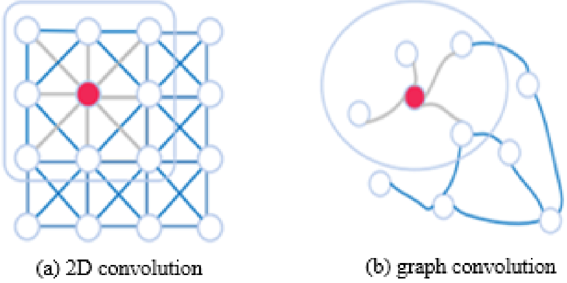

Figure 1. Comparison of 2D convolution and graph convolution

The mathematical definition of graph convolution operation based on spatial domain is:

$$h_i^{(l+1)} = \sigma\left(\textstyle\sum_{j \in N(i)} \frac{1}{c_{ij}} W^{(l)} h_j^{(l)}\right) \tag{7}$$

Where $h_i^{(l+1)}$ represents the feature output of node i at layer $l+1$, σ represents the activation function, $N(i)$ represents the set of neighbors of node i, C_{ij} represents the normalization factor, and $W^{(l)}$ is the learnable weight.

Micheli et al. [10] proposed the Neural Network for Graphs (NN4G), which is the first spatial domain based graph convolution model. This model uses simple neighbor feature addition as the convolution operation, while introducing residual connections and skip connections, effectively preserving the feature information of each layer.

$$h_v^{(k)} = f(W^{(k)^T} x_v + \sum_{i=1}^{k-1} \sum_{u\in N(v)} \theta^{(k)^T} h_u^{(k-1)}) \quad (8)$$

Where $f(\cdot)$ represents the activation function, $h_v^{(0)} = 0$.

Inspired by recurrent neural networks, Atwood et al. [11] proposed Diffusion Convolutional Neural Networks (DCNN). This network defines graph convolution operations as a diffusion process that iteratively propagates node features to achieve information flow in the graph structure. Node features propagate to their neighboring nodes according to predefined diffusion probabilities, and reach a global equilibrium state after multiple iterations. The diffusion operation can be expressed as:

$$H^{(t)} = \sigma(SH^{(t-1)}W^{(t-1)}) \quad (9)$$

Where $H^{(t-1)}$ is the feature representation of the $t-1$-th diffusion node, σ represents the activation function, and S represents the transition probability matrix between nodes.

Glimer et al. [12] proposed the Message Passing Neural Network (MPNN), which considers each graph convolution operation as a process of information transmission. This framework abstracts graph convolution operations as an iterative process of information transmission: in each iteration, nodes send messages to their neighboring nodes through edges, while receiving and aggregating messages from neighbors, and finally updating their own state. This design not only clearly describes the essence of graph convolution, but also provides a flexible foundation for designing new graph neural network architectures. The architecture defines graph convolution operations as:

$$h_v^{(k)} = U_k(h_v^{(k-1)}, \sum_{u\in N(v)} M_k\,(h_v^{(k-1)}, h_v^{(k-1)}, x_{vu}^e) \quad (10)$$

Where $h_v^{(k)} = x_v$, $U_k(\cdot)$ and $M_k(\cdot)$ are functions with learnable parameters.

Xu et al. [13] proposed Graph Isomorphism Network (GIN), which learns the representation of the entire graph by performing a series of graph isomorphism operations on node embeddings. This model updates the node features of each layer through multi-layer perceptrons and node neighbor information, and its operation is defined as:

$$h_v^{(k)} = MLP^{(k)}((1+\varepsilon^{(k)}) \cdot h_v^{(k-1)} + \sum_{u\in N(v)} h_u^{(k-1)}) \quad (11)$$

Where $MLP^{(k)}$ represents the multi-layer perceptron at the k-th layer, ε is an adjustable parameter representing the weight of the central node feature, and $N(v)$ represents the set of neighboring nodes of node v.

GCN based on spatial domain usually follows a three-stage feature update process. Firstly, in the feature propagation stage, each node transmits its feature information to neighboring nodes, achieving the diffusion of local information. Afterwards, in the feature aggregation stage, the target node integrates features from itself and its neighbors through a designed aggregation function to generate a comprehensive feature representation. Finally, in the feature update stage, the aggregated features are transformed using a nonlinear activation function to obtain the updated node features. The core of this process lies in how to efficiently and effectively aggregate the feature information of neighboring nodes. Therefore, designing a suitable aggregation function has become a key challenge to improve the performance of spatial domain based graph convolutional networks. Aggregation functions not only need to be able to capture local structural information between nodes, but also need to have strong expressive power to cope with different types of graph data and application scenarios.

2.3. The Architectures of Graph Convolutional Neural Networks

The architecture of GCN is shown in Figure 2. The model continuously updates the feature matrix and adjacency matrix of the input graph through multiple graph convolution layers. The core lies in the setting of graph convolution. Different graph convolutions aggregate information in different ways, resulting in different feature matrices generated after convolution.

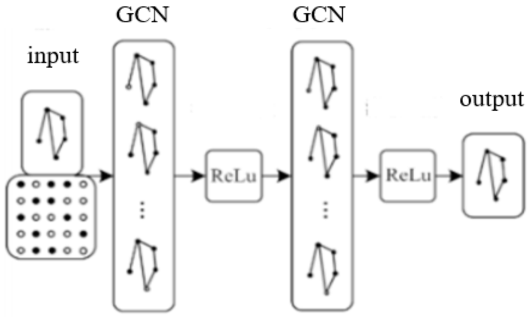

Figure 2. The Architectures of Graph Convolutional Neural Networks

Empirical studies have demonstrated that increasing the number of graph convolutional layers leads to node representations within the same connected component converging to nearly identical vectors, significantly degrading the model's classification performance. This critical limitation, known as the over-smoothing problem, arises from the intrinsic properties of graph convolution operations. Li et al. [14] used the eigendecomposition technique to prove that graph convolution is a special form of Laplace smoothing. Onno and Suzuke [15] also theoretically proved that graph convolution will converge to a subspace represented by the node degree basis using nonlinear functions and convolutional filters. Therefore, improving the classification performance of GCN requires urgently alleviating their inherent over-smoothing problem.

3. Application of Graph Convolutional Neural Networks

In recent years, GCN have shown excellent performance in medical image diagnosis tasks. In this section, we introduce the application of GCN on brain tumor images in detail.

3.1. Applying on Single Modality Images

MRI images have been widely used in brain tumor diagnosis due to their high-precision presentation of brain tissue and their ability to distinguish between gray matter and white matter. To address the challenges posed by the complex nonlinear relationships and high-dimensional nature of brain MRI data, Liu et al. [16] proposed a SASG-GCN network that combines deep belief networks with self-attention mechanisms to construct graph vertices and neighborhoods from 3D MRI data, employing a two-layer GCN for effective classification of infiltrating low-grade gliomas (LGGs) while addressing the challenges of high-dimensionality and complex nonlinear relationships in brain MRI images. To explain the correlation at the brain region level and the correlation at the subject level, Zhou et al. [17] developed a GIGCN framework that simultaneously models intra-brain regional connectivity and inter-subject population relationships through dual graph convolutional networks, where one GCN learns node representations of individual brain regions while another processes cross-subject correlations. Considering the propagation of relational and contextual information in spatial and channel dimensions, Ma et al. [18] proposed a dual-graph reasoning framework integrating both spatial and channel-wise relational modeling, where a GCN-based spatial module captures long-range regional dependencies while a GAT-powered channel module learns inter-channel semantic correlations, with their combined outputs fused through point-wise summation with original features for enhanced brain tumor classification. For the potential high-order associations between subjects, Yao et al. [19] developed a mutual multi-scale ternary GCN framework that captures high-order inter-subject relationships by constructing multi-scale brain connectivity networks through region-of-interest (ROI) parcellation, employing three parallel GCNs to learn hierarchical representations at different scales, and introducing a novel template mutual learning mechanism for joint optimization of the tri-network system to enhance neurological disorder classification performance.

Recent studies have demonstrated that hybrid architectures combining Graph Convolutional Networks (GCNs) with complementary deep learning models significantly outperform single-model approaches in brain tumor detection [20]. De et al. [21] developed a multimodal fusion framework that synergistically combines radiological and histopathological data through a hybrid CNN-GCN architecture, where CNNs initially detect glioblastoma from imaging data while whole slide images (WSI) enable the identification of astrocytoma and oligodendroglioma patterns, with a subsequent GCN employing normalized graph Laplacian operators to integrate these multimodal features for comprehensive tumor classification. To alleviate the impact of limited data and high-dimensional connectivity, Zhang et al. [22] proposed Deep Cross-Model Attention Network (DCMAT), an innovative framework that addresses data scarcity and high-dimensional connectivity challenges by synergistically combining RNNs and GCNs to model dynamic functional-structural brain relationships. Mishra et al. [23] achieved state-of-the-art performance (98.27% accuracy) on binary brain tumor classification by developing a hybrid GATE-CNN architecture that synergistically combines graph attention mechanisms with convolutional feature extraction, where the graph attention autoencoder first computes dynamic attention weights for pixel-level neighborhood relationships and then feeds these optimized graph representations into a CNN for final classification. Yang et al. [24] developed an innovative three-stage GAN-GCN hybrid framework that: (1) performs supervised multi-graph clustering to extract essential topological features and construct a condensed graph representation, (2) employs a generative adversarial network to synthesize biologically-plausible brain networks preserving the coarse-grained structural properties, and (3) integrates the synthesized and original graphs through a GCN-based fusion and classification module, effectively augmenting limited neuroimaging data while maintaining critical connectome characteristics for improved disease classification.

Table 1 summarizes some representative works of GCN on single-modality brain tumor images.

Table 1. Graph Convolutional Networks on Single-modality Images

Autor	Model	Method
Liu et al.	SASG-GCN	GCN
Zhou et al.	GIGCN	GCN
Yao et al.	MMTGCN	GCN
Ma et al.	DGRUnit	GCN + GAT
De et al.	-	CNN + GCN
Zhang et al.	DCMAT	RNN + GCN
Yang et al.	GraphCGC-Net	GAN + GCN
Mishra et al.	GATE-CNN	GATE + CNN

3.2. Applying on Multi-Modality Images

Multimodal medical imaging provides complementary diagnostic information by capturing diverse pathological signatures across different imaging modalities, enabling comprehensive disease characterization through the synergistic integration of structural, functional, and metabolic perspectives. Tian et al. [25] developed an EH-GCN framework that processes multimodal MRI data by jointly learning localized image features through ResNet [26] and global connectivity patterns via GCN, effectively fusing voxel-level intensity information with inter-regional structural/functional relationships. While demonstrating promising integration of multi-scale brain features, but the network uses all brain ROIs to analyze structural functional connections and does not discuss the impact of ROI selection on the final classification results. Meng et al. [27] proposed a Bilateral Adaptive GCN (BA-GCN) that synergistically integrates 2D and 3D image features through uncertainty-aware multi-instance learning for 2D feature extraction and adaptive bilateral graph convolution for cross-dimensional message passing, dynamically learning optimal graph structures to fuse multi-granularity features while resolving dimensional inconsistencies in medical imaging analysis. This framework uniquely bridges 2D slice-based and volumetric 3D representations through learnable feature projection and attention-weighted adjacency, demonstrating how adaptive graph architectures can overcome fundamental challenges in multi-planar medical image interpretation. Aiming at the spatiotemporal topological characteristics of brain networks, Xu et al. [28] proposed an adaptive multi-channel GCN framework (MSTGC) incorporating graph contrastive learning to model spatiotemporal brain network dynamics, where ROI-based signals are segmented into overlapping time windows to construct evolving connectivity graphs, processed through parallel GCN channels with contrastive constraints to extract multimodal spatial features, followed by stacked LSTM units to capture temporal dependencies, ultimately enabling multimodal brain network prediction through MLP classification. Zhang et al. [29] developed a unified graph-based framework that integrates neuroimaging data with clinical phenotypic information to construct personalized brain networks, enabling the joint representation of individual-level biomarkers and population-level associations through adaptive graph learning. This approach simultaneously models subject-specific neuroanatomical patterns and their statistical relationships within the broader cohort, effectively bridging the gap between individual patient characteristics and group-wise trends in neurological disorder analysis.

Table 2 summarizes some representative works of GCN on multi-modality brain tumor images.

Table 2. Graph Convolutional Networks on Multi-modal Images

Autor	Model	Method
Tian et al.	EH-GCN	CNNs + GCN
Zhang et al.	-	GCN
Meng et al.	BA-GCN	CNN + GCN
Xu et al.	MSTGC	LSTM + GCN

4. Challenges and Prospects

Brain tumors rank among the most lethal malignancies, making early detection critical for improving patient outcomes. This paper systematically reviews Graph Convolutional Networks (GCNs) as an emerging deep learning approach for neuro-oncology, detailing their theoretical foundations and recent applications in brain tumor analysis. However, there are still some problems to be solved:

Developing robust deep learning models with consistent cross-domain performance remains a critical challenge in medical AI research. While current graph convolutional networks demonstrate strong classification accuracy on standardized datasets, their performance significantly degrades when applied to heterogeneous clinical data due to: (1) inter-institutional variability in MRI scanners, (2) acquisition protocol variations, (3) population-specific imaging characteristics. This domain shift problem is particularly acute in brain tumor analysis where identical tumor types may exhibit markedly different imaging appearances across facilities. Key research priorities to address this include: developing scanner-agnostic feature learning methods, implementing self-supervised domain adaptation techniques, creating synthetic data augmentation frameworks that simulate multi-scanner effects, and designing modular architectures that can dynamically adjust to input data characteristics while maintaining diagnostic reliability across diverse clinical environments.

The interpretability gap in graph convolutional networks (GCN) presents a significant barrier to clinical adoption, as medical decision-making requires not just high accuracy but also transparent reasoning aligned with neuroanatomical principles. While visualization techniques like Grad-CAM [30] can highlight image regions influencing predictions, current methods fail to: (1) explain how node-level features propagate through graph structures, (2) reveal clinically meaningful connectivity patterns learned by the model, or (3) justify why specific brain regions are weighted differently in diagnoses. For GCNs in neuro-oncology, this opacity is compounded when processing multi-modal graphs combining imaging, genomic, and clinical data. Emerging solutions combining attention mechanisms with post-hoc explanation frameworks show promise, but must evolve to provide neurologically plausible explanations.

The clinical translation of graph convolutional neural networks faces significant implementation challenges that demand rigorous validation beyond conventional performance metrics. Three critical gaps must be addressed: (1) Technical reliability - GCNs require demonstrated stability across real-world clinical variability (e.g., imperfect imaging conditions, comorbid pathologies); (2) Decision safety - Need for fail-safe mechanisms when encountering novel tumor phenotypes or ambiguous cases, potentially through hybrid expert-system approaches; and (3) Clinical workflow integration - Developing interfaces that transform GCN outputs into actionable diagnostic reports aligned with neuroradiological reasoning paradigms. Therefore, graph convolutional neural networks require not only high accuracy but also reliability and safety in actual operation.

The scarcity of high-quality medical imaging data poses a fundamental constraint in training robust GCN models for brain tumor analysis. While GCNs offer unique advantages in processing non-Euclidean data and integrating multimodal patient information (including clinical, genomic, and radiomic features), their effectiveness heavily depends on two critical factors: (1) comprehensive data utilization strategies that effectively combine limited imaging data with available auxiliary patient information, and (2) advanced data augmentation techniques specifically designed for graph-structured medical data, such as topology-aware graph perturbation, conditional graph generation, and physiologically constrained synthetic network creation. Developing specialized augmentation pipelines that preserve the biological plausibility of brain connectivity patterns while expanding dataset diversity will be essential for improving model generalization and overcoming overfitting in clinical applications. Future work should focus on creating standardized frameworks for quality-controlled multimodal data integration and domain-informed augmentation tailored to neuro-oncological graph representations.

References

[1] Louis D N, Perry A, Wesseling P, et al. The 2021 WHO Classification of Tumors of the Central Nervous System: a summary [J]. Neuro-Oncology, 2021, 23(8): 1231-1251.

[2] Bénard F, Romsa J, Hustinx R. Imaging gliomas with positron emission tomography and single-photon emission computed tomography [J]. Seminars in Nuclear Medicine, 2003, 33(2): 148-162.

[3] Ali Khan H, Jue W, Mushtaq M, et al. Brain tumor classification in MRI image using convolutional neural network [J]. Mathematical Biosciences and Engineering, 2020, 17(5): 6203-6216.

[4] Villanueva-Meyer J E, Mabray M C, Cha S. Current Clinical Brain Tumor Imaging [J]. Neurosurgery, 2017, 81(3): 397-415.

[5] Sandryhaila A, Moura J M F. Discrete Signal Processing on Graphs [J]. IEEE Transactions on Signal Processing, 2013, 61(7): 1644-1656.

[6] Shuman D I, Narang S K, Frossard P, et al. The Emerging Field of Signal Processing on Graphs: Extending High-Dimensional Data Analysis to Networks and Other Irregular Domains [J]. IEEE Signal Processing Magazine, 2013, 30(3): 83-98.

[7] Bruna J, Zaremba W, Szlam A, et al. Spectral Networks and Locally Connected Networks on Graphs [M]. arXiv, 2014.

[8] Defferrard M, Bresson X, Vandergheynst P. Convolutional Neural Networks on Graphs with Fast Localized Spectral Filtering [M]. arXiv, 2017.

[9] Kipf T N, Welling M. Semi-Supervised Classification with Graph Convolutional Networks [M]. arXiv, 2017.

[10] Micheli A. Neural Network for Graphs: A Contextual Constructive Approach [J]. IEEE Transactions on Neural Networks, 2009, 20(3): 498-511.

[11] Atwood J, Towsley D. Diffusion-Convolutional Neural Networks [M]. arXiv, 2016.

[12] Gilmer J, Schoenholz S S, Riley P F, et al. Neural Message Passing for Quantum Chemistry [M]. arXiv, 2017.

[13] Xu K, Hu W, Leskovec J, et al. How Powerful are Graph Neural Networks? [M]. arXiv, 2019.

[14] Li Q, Han Z, Wu X ming. Deeper Insights Into Graph Convolutional Networks for Semi-Supervised Learning [J]. Proceedings of the AAAI Conference on Artificial Intelligence, 2018, 32(1).

[15] Oono K, Suzuki T. Graph Neural Networks Exponentially Lose Expressive Power for Node Classification [M]. arXiv, 2021.

[16] Liu L, Chang J, Zhang P, et al. SASG-GCN: Self-Attention Similarity Guided Graph Convolutional Network for Multi-Type Lower-Grade Glioma Classification [J]. IEEE Journal of Biomedical and Health Informatics, 2023, 27(7): 3384-3395.

[17] Zhou H, Zhang D. Graph-In-Graph Convolutional Networks For Brain Disease Diagnosis [C]//2021 IEEE International Conference on Image Processing (ICIP). 2021: 111-115.

[18] Ma Q, Zhou S, Li C, et al. Dual Graph Reasoning Unit for Brain Tumor Segmentation [C]//2021 IEEE 4th International Conference on Big Data and Artificial Intelligence (BDAI). 2021: 204-208.

[19] Yao D, Sui J, Wang M, et al. A Mutual Multi-Scale Triplet Graph Convolutional Network for Classification of Brain Disorders Using Functional or Structural Connectivity [J]. IEEE Transactions on Medical Imaging, 2021, 40(4): 1279-1289.

[20] Ravinder M, Saluja G, Allabun S, et al. Enhanced brain tumor classification using graph convolutional neural network architecture [J]. Scientific Reports, 2023, 13(1): 14938.

[21] De A, Mhatre R, Tiwari M, et al. Brain Tumor Classification from Radiology and Histopathology using Deep Features and Graph Convolutional Network [C]//2022 26th International Conference on Pattern Recognition (ICPR). 2022: 4420-4426.

[22] Zhang L, Wang L, Zhu D. Jointly Analyzing Alzheimer's Disease Related Structure-Function Using Deep Cross-Model Attention Network [C]//2020 IEEE 17th International Symposium on Biomedical Imaging (ISBI). Iowa City, IA, USA: IEEE, 2020: 563-567.

[23] Mishra L, Verma S. Graph attention autoencoder inspired CNN based brain tumor classification using MRI [J]. Neurocomputing, 2022, 503: 236-247.

[24] Yang W, Wen G, Cao P, et al. Collaborative learning of graph generation, clustering and classification for brain networks diagnosis [J]. Computer Methods and Programs in Biomedicine, 2022, 219: 106772.

[25] Tian X, Liu Y, Wang L, et al. An extensible hierarchical graph convolutional network for early Alzheimer's disease identification [J]. Computer Methods and Programs in Biomedicine, 2023, 238: 107597.

[26] He K, Zhang X, Ren S, et al. Deep Residual Learning for Image Recognition [C]//2016 IEEE Conference on Computer Vision and Pattern Recognition (CVPR). Las Vegas, NV, USA: IEEE, 2016: 770-778.

[27] Meng Y, Bridge J, Addison C, et al. Bilateral adaptive graph convolutional network on CT based Covid-19 diagnosis with uncertainty-aware consensus-assisted multiple instance learning [J]. Medical Image Analysis, 2023, 84: 102722.

[28] Xu R, Zhu Q, Li S, et al. MSTGC: Multi-Channel Spatio-Temporal Graph Convolution Network for Multi-Modal Brain Networks Fusion [J]. IEEE Transactions on Neural Systems and Rehabilitation Engineering, 2023, 31: 2359-2369.

[29] Zhang Y, He X, Chan Y H, et al. Multi-modal graph neural network for early diagnosis of Alzheimer's disease from sMRI and PET scans [J]. Computers in Biology and Medicine, 2023, 164: 107328.

[30] Selvaraju R R, Cogswell M, Das A, et al. Grad-CAM: Visual Explanations from Deep Networks via Gradient-based Localization [J]. International Journal of Computer Vision, 2020, 128(2): 336-359.