Hierarchical Brain Structure Modeling for Predicting Genotype of Glioma

Haotian Tang[1,*], Jianwei Chen[3,*], Xinrui Tang[2], Yunjia Wu[1], Zhengyang Miao[1], Chao Li[2,3,4] ✉

1 College of Medicine and Biological Information Engineering, Northeastern University, Liaoning, China
2 School of Science and Engineering, University of Dundee, Dundee, UK
3 School of Medicine, University of Dundee, Dundee, UK
4 Department of Applied Maths and Theoretical Physics, University of Cambridge, Cambridge, UK
✉ Corresponding author: cl647@cam.ac.uk

MICCAI2025 CMMCAWorkshop Daejeon REPUBLIC OF KOREA

I.Introduction

Background Issue

Glioma is a common primary brain tumor in adults. The mutation status of isocitrate dehydrogenase (IDH) is an important diagnostic biomarker, with mutant-type gliomas usually having a better prognosis than wild-type. However, current IDH detection relies on invasive biopsy, which carries surgical risks and is not feasible for inoperable patients. Recently, imaging-based deep learning methods have emerged as a promising non-invasive alternative to biopsy.

Research Motivation

The brain connectome, derived from MRI, depicts brain organization, with structural connectome(dMRI) showing white matter integrity and functional connectome(fMRI) indicating regional co-activation. Although many studies have coupled structural and functional connectomes for brain analysis, fMRI in glioma suffers from low signal quality and limited availability, reducing the reliability of multi-connectome analysis. Moreover, most existing methods overlook hierarchical interactions between connectomes, limiting brain representation.

Clinical Significance

This study introduces a non-invasive radiomics method for precise IDH mutation prediction, leveraging hierarchical modeling of multi-connectomes by coupling the dMRI with the morphological connectome (sMRI), instead of the conventional fMRI-based functional connectome, thereby advancing non-invasive diagnostic strategies in glioma.

II.Method

Overall Model Structure

The overall process of the proposed Hi-SMGNN framework is illustrated in Figure 1. It integrates structural connectome (SC) from diffusion MRI and morphological connectome (MC) from structural MRI. First, the brain network is adaptively partitioned into regional and modular subgraphs through a personalized modular partition. Then, a multimodal interaction module learns cross-modal embeddings that capture complementary information from SC and MC at both regional and modular levels. To reduce redundancy and highlight informative patterns, a multiscale feature fusion mechanism combines these representations into a compact global feature. Finally, this global representation is fed into a multilayer perceptron to predict IDH mutation status, optimized jointly with a modularity-based regularization.

Key Technical Details

- A shared GNN encoder extracts embeddings from SC and MC subgraphs in parallel, ensuring comparable representations. SC is treated as a stable backbone to guide MC through cross-modal attention, which filters noisy signals and integrates consistent, fine-grained features across modalities.
- Regional interaction representations are further organized into modules through a soft assignment matrix, allowing flexible grouping of brain regions. The modularity score, reflecting how well the network is divided into meaningful communities, is optimized to ensure biologically relevant partitions.
- To reduce redundancy in regional features, compact modular representations are used as filters via soft-thresholding. The purified regional features are then combined with modular features, yielding global representations that retain both fine-grained details and stable modular organization.

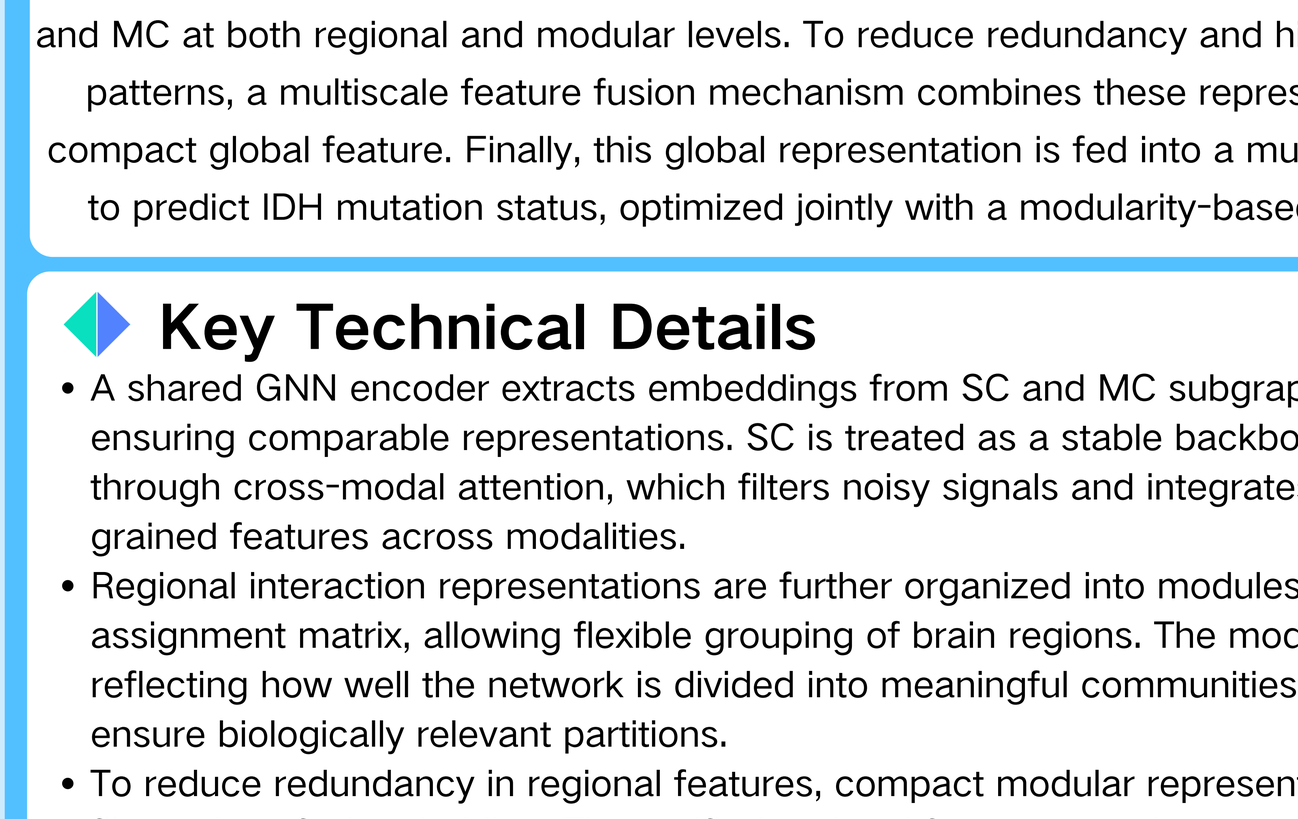

Figure 1

The SC and MC generate

- (a) regionalized and
- (b) modularized interaction representations through Personalized Module Partition.
- (c) These representations are combined to generate global interaction representations through multiscale features fusion.
- (d) The multimodal interaction is modelled by a Siamese network and cross-modal attention.
- (e) The Personalized Module Partition is achieved with a soft assignment matrix, optimized by the modularity score.

III.Results

UCSF-PDGM dataset is used, including 103 IDH-mutant and 392 IDH-wildtype glioma patients. MRI modalities include FA (for SC construction) and T1c (for MC construction), divided into training/validation/test sets in 7:1:2 ratio.

MIM	PMP	MFF	IDH	
			ACC ↑	F1 ↑
✓			71.72	50.00
	✓		78.79	66.67
		✓	84.58	69.39
✓	✓	✓	**84.85**	**72.73**

Table 1

Table1. Effectiveness of each module on UCSF-PDGM dataset for IDH prediction

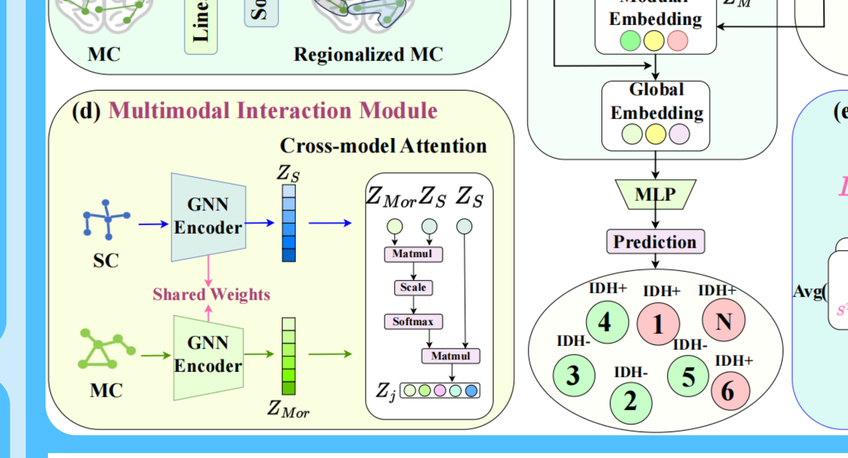

Table 2

Table2. Comparing IDH Prediction on the UCSF-PDGM Dataset with Other Multimodal Methods

IV.Conclusion

- Proposed a hierarchical framework fusing SC and MC to comprehensively model brain structure and improve IDH prediction performance.
- Designed MIM and PMP modules to realize fine-grained multimodal interaction capture and personalized modular partition,enhancing model interpretability.
- Proposed MFF mechanism to effectively filter redundant features and optimize multiscale feature fusion effect.