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MICCAI

Core-Periphery Principle Guided State Space Model for Functional Connectome Classification

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INTRODUCTION

- **Background**

Understanding the organization of human brain networks has become a central focus in neuroscience, particularly in the study of functional connectivity, which plays a crucial role in diagnosing neurological disorders. Advances in functional magnetic resonance imaging and machine learning techniques have significantly improved brain network analysis.

- **Purpose**

Existing works rely heavily on increasingly complex network architectures, which not only lead to overfitting problems due to inductive bias but also hinder their application on long sequences by computational complexity, such as the quadratic computational cost associated with the attention mechanism. And also, current methods often overlook the intrinsic characteristics of brain function during computational modeling, resulting in suboptimal performance in brain network analysis.

- **Contribution**

To address these limitations, we propose a Core-Periphery State-Space Model, an innovative framework for functional connectome classification. 1) We introduce Mamba, a selective state-space model with linear complexity, to effectively capture long-range dependencies in functional brain networks. 2) Inspired by the core-periphery organization, we design a CP-guided Mixture-of-Experts that improves the representation learning of brain connectivity patterns. 3) We evaluate CP-SSM on two benchmark fMRI datasets: ABIDE and ADNI. Experimental results demonstrate that CP-SSM surpasses Transformer-based models in classification performance while significantly reducing computational complexity.

METHODOLOGY

In this study, we evaluated the proposed method on two fMRI datasets, assessing its performance in diagnosing two neurological conditions: autism spectrum disorder (ASD) and mild cognitive impairment (MCI)—the prodromal stage of AD. (a) Autism Brain Imaging Data Exchange (ABIDE): This dataset collects resting-state fMRI data from 17 international sites. Based on the given quality control scores, 1009 subjects (516 with ASD and 493 with NC) from 1,112 subjects were selected. The dataset, preprocessed by the Configurable Pipeline for the Analysis of Connectomes tool, underwent band-pass filtering (0.01 - 0.1Hz) without global signal regression. The brain was parcellated using the Craddock 200 atlas. (b) Alzheimer's Disease Neuroimaging Initiative(ADNI): 440 subjects(215 MCI, 225 NC) were selected based on quality control. Each subject's data underwent the same standard preprocessing procedures as detailed in our previous works. The Destrieux Atlas was then applied for parcellation.

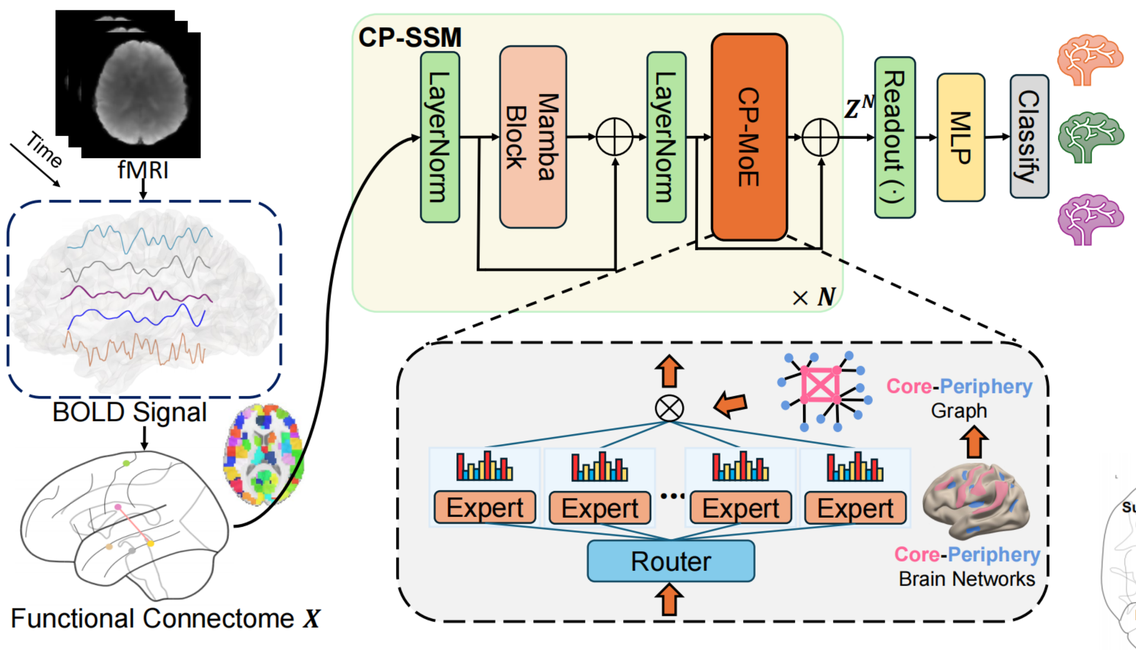


Fig. 1. Overall architecture of the proposed method. Our approach is founded on state-space model, with its key components comprising a Mamba block and a Core-Periphery principle guided MoE.

The overall pipeline of the proposed method is shown in Fig. 1. The FC matrix $X \in \mathbb{R}^{V\times V}$($V$ is the number of ROIs), derived by calculating the Pearson cross-correlation of the preprocessed BOLD signals across different brain regions, is first processed through N CP-SSM blocks to generate the node-level embedding representation $Z \in \mathbb{R}^{V\times V}$. Each CP-SSM block comprises two key components: an SSM module and a CP-MoE block. Subsequently, the output is passed through an Orthonormal Clustering Readout function to obtain the graph-level embedding. The embedding is then fed into a fully connected layer, with the final probability predictions generated through a softmax layer. The model is trained using cross-entropy loss.

RESULTS

Experimental setting. We partition each dataset into 70% for training, 10% for validation, and 20% for testing. For evaluation on the test set, we select the epoch that achieves the highest AUROC score on the validation set. We evaluate the performance of our proposed method against several baseline approaches, including 3 traditional machine learning methods: support vector machine (SVM), random forest (RF), and XGBoost; 2 CNN/GNN-based methods: FBNETGEN and BrainNetCNN; and 4 Transformer-based methods: VanillaTF, BrainNetTF, Com-BrainTF, and GBT.

Implementation details. Our method is configured with a state-space dimension of 16 in the Mamba block, an expansion factor of 2, two CP-SSM blocks, and a convolution kernel dimension of 4. The CP-MoE module consists of 8 experts, utilizing a Top-4 selection strategy. For dataset-specific settings, we set the core node rate to 0.2 for the ABIDE and 0.8 for ADNI. The CPSSM model is trained using the Adam optimizer with an initial learning rate of 10e-4 and a weight decay of 10e-4. A cosine annealing schedule is applied, gradually reducing the learning rate from 10e-4 to 10e-5 without a warm-up phase. Training is conducted over 200 epochs with a batch size of 64. All experiments were performed on a PC equipped with an NVIDIA RTX 6000 Ada GPU and a 3.6-GHz Intel Core i7 processor.

Table 1. Performance comparison with different baselines on ADNI and ABIDE.

Methods	Dataset: ABIDE				Dataset: ADNI			
	AUROC	ACC	SEN	SPE	AUROC	ACC	SEN	SPE
SVM	70.4±5.2	63.3±5.2	64.8±7.1	61.6±7.0	65.1±8.2	61.5±4.4	51.2±7.9	69.7±8.2
RF	69.2±4.3	63.8±3.4	71.0±5.2	56.1±5.2	67.9±3.8	63.9±1.2	55.9±4.7	71.4±4.5
XGBoost	71.2±4.4	63.4±5.1	68.6±4.9	57.8±9.1	65.4±5.0	62.7±1.1	61.5±6.0	63.8±6.2
FBNETGNN	72.9±5.1	65.7±5.6	64.3±10.6	66.6±8.2	69.1±7.9	66.3±3.9	66.7±8.1	65.7±8.4
BrainNetCNN	73.2±3.0	66.6±4.0	64.6±6.2	68.7±4.8	65.8±1.0	65.4±5.2	60.7±1.3	68.7±4.6
VanillaTF	79.6±4.6	69.8±6.0	64.1±8.1	**76.4±9.1**	73.1±6.4	69.3±3.8	68.7±8.1	70.3±8.8
BrainNetTF	79.1±4.8	70.1±4.9	67.9±5.0	72.2±6.6	73.0±7.4	70.3±4.7	69.7±7.6	69.9±7.7
Com-BrainTF	77.3±4.1	71.6±4.5	75.1±11.9	67.4±9.3	-	-	-	-
GBT	78.3±4.1	71.5±5.8	75.5±14.7	68.2±12.8	74.5±5.5	71.1±3.2	69.0±7.8	73.6±5.1
CP-SSM	**82.4±2.2**	**76.9±1.4**	**79.3±8.8**	74.5±8.4	**80.7±2.6**	**74.9±2.6**	**75.4±5.7**	**74.2±2.6**

Table 2. Ablation study of CP-SSM on ABIDE with the best and second-best values in **boldface** and underline, respectively.

	AUC	ACC	SEN	SPE
CP-SSM	**82.4±2.2**	**76.9±1.4**	79.3±8.8	**74.5±8.4**
w/o CP	79.9±3.3	75.9± 2.3	**81.9±7.3**	69.2±8.9
w/o MoE	81.1±3.1	74.1±1.6	75.7±5.7	72.5±8.0
w/o CP-MoE	80.1±2.3	73.0±1.3	72.4±4.5	73.0±1.3
w/o SSM	81.1±2.2	74.7±0.8	77.3±5.0	72.3±5.3
learnable mask	79.4±2.3	74.0±1.7	73.5±6.2	**74.5±4.9**

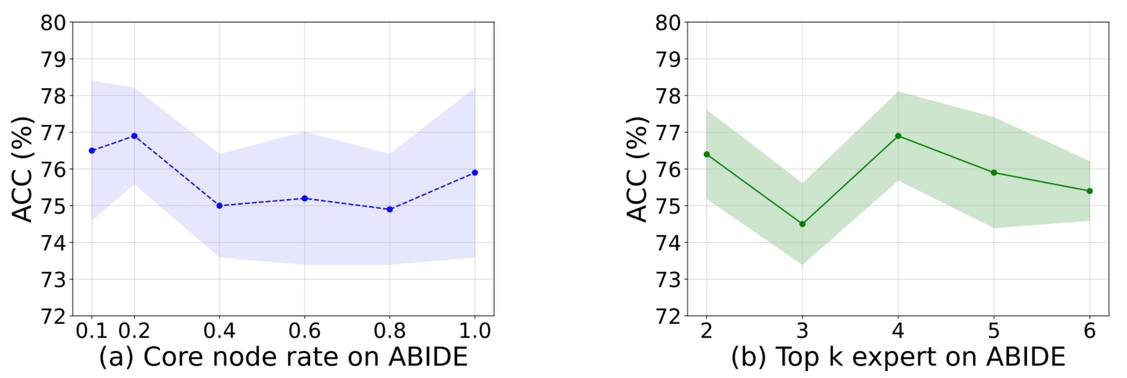
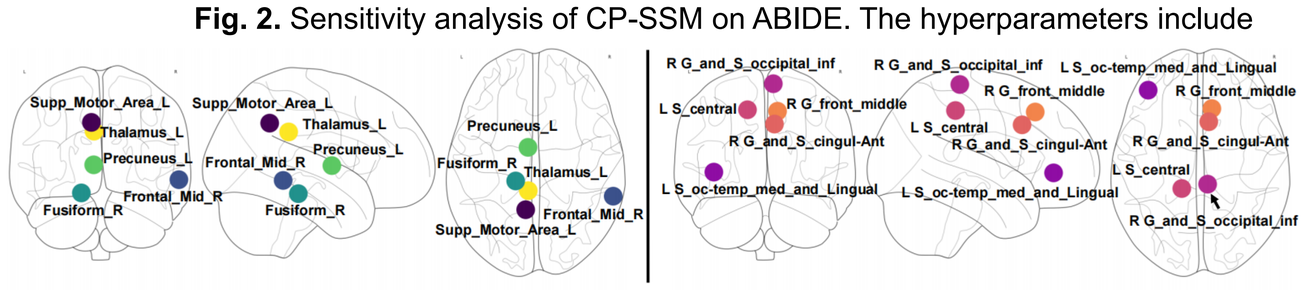


Fig. 2. Sensitivity analysis of CP-SSM on ABIDE. The hyperparameters include



(a) Top 5 discriminative brain regions on ABIDE in ASD diagnosis

(b) Top 5 discriminative brain regions on ADNI in MCI diagnosis

Fig. 3. Top 5 discriminative brain regions derived from the learnable weight in the last CP-SSM layer on ABIDE and ADNI, with different colormap intensities reflecting relative significance.

We visualize the learnable weights of the last layer of CP-SSM block to show the top 5 rated brain regions for ASD diagnosis and MCI diagnosis, respectively. In Fig.3(a), we present the brain region names from the AAL atlas that exhibit the highest overlap with each corresponding region. These findings corroborate existing research, highlighting the involvement of these brain regions in ASD and MCI.

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