

BRAINSTEAM: A PRACTICAL PIPELINE FOR CONNECTOME-BASED FMRI ANALYSIS TOWARDS SUBJECT CLASSIFICATION

Alexis Li, Yi Yang, Hejie Cui, Carl Yang

Hamilton High School, Duke University, Emory University, Emory University

Functional brain networks illustrate the dynamic connectivity patterns between anatomical regions of interest (ROIs) for different cognitive states and different responses to disease [1]. The study of functional brain networks provides insights into the underlying mechanisms of human consciousness and the neural bases of various neurological and psychiatric disorders such as autism, ADHD, and depression [2]. However, existing tools often extract a single static graph structure based on correlations among full BOLD signals, which ignores the dynamic changes of functional connectivity [3, 4].

1. ABSTRACT

Functional brain networks represent dynamic and complex interactions among anatomical regions of interest (ROIs), providing crucial clinical insights for neural pattern discovery and disorder diagnosis. In recent years, graph neural networks (GNNs) have proven immense success in analyzing structured network data. However, due to the high complexity of data acquisition, resulting in limited training resources of neuroimaging data, GNNs, like all deep learning models, suffer from overfitting. Moreover, their capability to capture useful neural patterns for downstream prediction is also adversely affected. To address such challenge, this study proposes BrainSTEAM, an integrated framework featuring a spatio-temporal module that consists of an EdgeConv GNN model, an autoencoder network, and a Mixup strategy. In particular, the spatio-temporal module aims to dynamically segment the time series signals of the ROI features for each subject into chunked sequences. We leverage each sequence to construct correlation networks, thereby increasing the training data. Additionally, we employ the EdgeConv GNN to capture ROI connectivity structures, an autoencoder for data denoising, and mixup for enhancing model training through linear data augmentation. We evaluate our framework on two real-world neuroimaging datasets, ABIDE for Autism prediction and HCP for gender prediction. Extensive experiments demonstrate the superiority and robustness of BrainSTEAM when compared to a variety of existing models, showcasing the strong potential of our proposed mechanisms in generalizing to other studies for connectome-based fMRI analysis.

Method	ABIDE				Method	HCP			
	Accuracy	AUC	Precision	Recall		Accuracy	AUC	Precision	Recall
MAGE	75.86	83.14	71.53	79.24	ST-GCN	83.7	-	-	-
SVM+MTFS	76.7 _{±2.7}	81 _{±0.31}	72.5 _{±2}	76.7 _{±2.7}	LTSM	81.7	-	-	-
MISO-DNN	77.73 _{±1.26}	-	76.73 _{±1.11}	77.16 _{±1.32}	GCN	83.98	-	84.59	87.78
e-STAGIN(Sch)	75.81 _{±1.70}	81.12 _{±0.39}	78.03 _{±1.34}	79.06 _{±0.89}	GC-LSTM	81.50	-	-	-
MAGIN	78.12 _{±0.91}	85.72 _{±0.2}	78.37 _{±1.31}	79.55 _{±1.12}	STAGIN-SERO	88.20 _{±1.33}	92.96 _{±1.17}	-	-
IMAGIN	79.25 _{±1.13}	86.44 _{±0.24}	81.03 _{±1.07}	79.06 _{±0.89}	DECENNT	86.00	93.6	87.2	88.6
BrainSTEAM	87.5 _{±0.99}	89.23 _{±0.18}	82.24 _{±1.06}	96.11 _{±1.17}	BrainSTEAM	91.41 _{±0.82}	93.67 _{±0.11}	100 _{±0.00}	78.78 _{±0.14}

Table 1. Overall performance (%) comparison on two datasets. Results with - were not provided in the original work.

Method	ABIDE				Method	HCP			
	Accuracy	AUC	Precision	Recall		Accuracy	AUC	Precision	Recall
BrainSTEAM	87.5 _{±0.99}	89.23 _{±0.18}	82.24 _{±1.06}	96.11 _{±1.17}	BrainSTEAM	91.41 _{±0.82}	93.67 _{±0.11}	100 _{±0.00}	78.78 _{±0.14}
BrainEAM	62.86 _{±0.17}	62.36 _{±0.17}	67.23 _{±0.09}	63.95 _{±0.10}	BrainEAM	77.20 _{±1.10}	80.15 _{±1.27}	87.43 _{±1.49}	66.59 _{±1.12}
BrainEM	63.66 _{±1.10}	62.50 _{±1.18}	68.09 _{±1.14}	71.24 _{±1.49}	BrainEM	74.42 _{±0.81}	74.48 _{±0.81}	77.11 _{±0.81}	73.79 _{±0.81}
BrainE	59.43 _{±1.08}	59.24 _{±1.08}	60.22 _{±0.61}	63.98 _{±1.14}	BrainE	67.85 _{±0.81}	68.01 _{±0.81}	68.97 _{±0.81}	70.46 _{±0.81}

Table 2. The ablation study with different model variants: BrainSTEAM is the full version with all components.

2. RESULTS

The overall prediction results presented in Table 1 show that BrainSTEAM outperformed the baseline model MAGE by 9.38% on the ABIDE dataset, and achieves 7.71% improvements over ST-GCN on the HCP dataset.

We further investigate the influence of each proposed component by removing each at a time. The results are shown in Table 2.

3. REFERENCES

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