



## Overview

- GNNs applied to fMRI data assume brain graphs are static over time and the graph adjacency matrix is known prior to model training.
- We propose **Dynamic Brain Graph Structure Learning (DBGSL)**, a method for learning the optimal time-varying dependency structure of fMRI data induced by a downstream prediction task.

## Problem formulation

- Let  $\mathbf{X}_{1:T'} = (\mathbf{x}_1, \dots, \mathbf{x}_{T'}) \in \mathbb{R}^{V \times T'}$  denote BOLD signal from  $V$  brain regions measured over  $T'$  timepoints and  $y \in [0, \dots, C - 1]$  a class label.
- Let the unknown BOLD dependency structure be represented by a dynamic brain graph  $G_{1:T} = (\mathbf{A}_{1:T}, \mathbf{F}_{1:T})$  consisting of a dynamic adjacency matrix  $\mathbf{A}_{1:T} \in \mathbb{R}_{\geq 0}^{V \times V \times T}$  and a dynamic node feature matrix  $\mathbf{F}_{1:T} \in \mathbb{R}^{V \times B \times T}$  over  $T \leq T'$  snapshots.
- With DBGSL we aim to predict class labels  $\hat{y}$  given input  $\mathbf{X}_{1:T'}$  using an intermediary learnt dynamic brain graph  $F_\theta(\mathbf{X}_{1:T'}) = F_{\theta_G}(F_{\theta_G}(\mathbf{X}_{1:T'})) = F_{\theta_G}(G_{1:T}) = \hat{y}$  where  $F_{\theta_G}(\cdot)$  is a dynamic graph learner and  $F_{\theta_C}(\cdot)$  is a dynamic graph classifier.

## Dynamic graph learner $F_{\theta_G}$

- Region-wise BOLD signals  $\mathbf{X}_{1:T'}$  extracted for fMRI data are first split into windows

$$f_{\theta_W}(\mathbf{X}_{1:T'}) = \tilde{\mathbf{X}}_{1:T} = (\tilde{\mathbf{X}}_1, \dots, \tilde{\mathbf{X}}_T), \quad \tilde{\mathbf{X}}_t = \mathbf{X}_{tS:tS+P}, \quad t = 1, \dots, T$$

where  $P$  and  $S$  are hyperparameters specifying window length and stride, respectively, and  $T$  is the number of windows.

- Windowed BOLD signals  $\tilde{\mathbf{X}}_{1:T}$  are next input to a 2D CNN to extract  $K_E$ -dimensional brain region embeddings  $f_{\theta_E}(\tilde{\mathbf{X}}_{1:T}) = \mathbf{H}_{1:T}^G \in \mathbb{R}^{K_E \times V \times T}$
- Each window embedding  $\mathbf{H}_t^G$  is used to learn the dependency structure between brain regions using scaled dot-product self-attention

$$\mathbf{A}_t = f_{\theta_S}(\mathbf{H}_t^G) = \text{Sigmoid}\left(\frac{\mathbf{Q}_t \mathbf{K}_t^\top}{\sqrt{K_S}}\right), \quad \mathbf{Q}_t = \mathbf{H}_t^G \mathbf{W}, \quad \mathbf{K}_t = \mathbf{H}_t^G \mathbf{W}$$

where  $\mathbf{Q}_t, \mathbf{K}_t \in \mathbb{R}^{V \times K_S}$  are query and key matrices, respectively, and  $\mathbf{W} \in \mathbb{R}^{K_E \times K_S}$ .

- To sparsify the learnt adjacency matrices, we propose a soft threshold operator

$$f_{\theta_P}(a_{i,j,t}) = \text{ReLU}(a_{i,j,t} - \text{Sigmoid}(\theta_P))$$

where  $\text{Sigmoid}(\theta_P) \in (0, 1)$  is a learnable edge weight threshold and  $a_{i,j,t} \in \mathbf{A}_{1:T}$ .

- Dynamic node features  $\mathbf{F}_{1:T}$  are created using the correlation matrix at each snapshot

$$\mathbf{F}_t = \tilde{\mathbf{D}}_t^{-1} \Sigma_t \tilde{\mathbf{D}}_t^{-1}, \quad \tilde{\mathbf{D}}_t = \sqrt{\text{diag}(\Sigma_t)}, \quad \Sigma_t = \frac{1}{P-1} \tilde{\mathbf{X}}_t^\top (\mathbf{I}_P - \frac{1}{P} \mathbf{1}_P^\top \mathbf{1}_P) \tilde{\mathbf{X}}_t$$

where  $\mathbf{I}_P$  and  $\mathbf{1}_P$  is a  $P \times P$  identity matrix and  $1 \times P$  matrix of all ones, respectively.

# DBGSL: Dynamic Brain Graph Structure Learning

## Dynamic graph classifier $F_{\theta_C}$

- We use a  $L_C$ -layered recurrent GNN to learn a  $K_C$ -dimensional brain graph representation

$$\mathbf{H}_{1:T}^C = \phi(\|_{l=1}^{L_C} \mathbf{H}_{1:T}^{(l)}) \in \mathbb{R}^{K_C L_C \times T}$$

where  $\phi = \frac{1}{V} \mathbf{1}_{1 \times V}$  is an average pooling matrix.

- Define a temporal attention score matrix to emphasize snapshots with the most important brain graph embeddings

$$\boldsymbol{\alpha} = \text{Sigmoid}(\text{ReLU}(\boldsymbol{\psi} \mathbf{H}_{1:T}^C \mathbf{W}_2) \mathbf{W}_3) \in (0, 1)^{1 \times T}$$

where  $\mathbf{W}_2 \in \mathbb{R}^{T \times \tau T}$ ,  $\mathbf{W}_3 \in \mathbb{R}^{\tau T \times T}$  encode temporal dependencies via a bottleneck controlled by the hyperparameter  $\tau \in (0, 1]$  and  $\boldsymbol{\psi} = \frac{1}{K_C L_C} \mathbf{1}_{1 \times K_C L_C}$ .

- The final graph-level representation  $\mathbf{h}_G \in \mathbb{R}^{L_C K_C}$  is obtained using the temporal attention score matrix to take the weighted sum over snapshots

$$\mathbf{h}_G = (\boldsymbol{\alpha} \odot \mathbf{H}_{1:T}^C) \boldsymbol{\xi}^\top$$

where  $\boldsymbol{\xi} = \mathbf{1}_{1 \times T}$ . The representation is then passed through a linear layer mapping onto class probabilities  $p(y|\mathbf{X}_{1:T'}) = \text{Softmax}(\mathbf{h}_G \mathbf{W}_4)$  where  $\mathbf{W}_4 \in \mathbb{R}^{L_C L_C \times C}$ .

## Loss

- DBGSL is trained by minimizing cross-entropy loss  $\mathcal{L}_{\text{CE}}(y, \hat{y})$  as well as a collection of prior constraints on the learnt graphs

$$\mathcal{L}(y, \{\hat{y}, G_{1:T}\}) = \mathcal{L}_{\text{CE}}(y, \hat{y}) + \lambda_{\text{FS}} \mathcal{L}_{\text{FS}}(\mathbf{F}_{1:T}, \mathbf{A}_{1:T}) + \lambda_{\text{TS}} \mathcal{L}_{\text{TS}}(\mathbf{A}_{1:T}) + \lambda_{\text{SP}} \mathcal{L}_{\text{SP}}(\mathbf{A}_{1:T})$$

where  $\lambda_{\text{FS}}, \lambda_{\text{TS}}, \lambda_{\text{SP}} \geq 0$  are hyperparameters weighting regularization contributions.

- Node feature smoothness (FS) and adjacency matrix temporal smoothness (TS) and sparsity regularization (SP) terms are defined

$$\mathcal{L}_{\text{FS}}(\mathbf{A}_{1:T}, \mathbf{F}_{1:T}) = \frac{1}{V^2} \sum_{t=1}^T \text{Tr}(\mathbf{F}_t^\top \hat{\mathbf{L}}_t \mathbf{F}_t), \quad \mathcal{L}_{\text{TS}}(\mathbf{A}_{1:T}) = \sum_{t=1}^{T-1} \|\mathbf{A}_t - \mathbf{A}_{t+1}\|_1$$

$$\mathcal{L}_{\text{SP}}(\mathbf{A}_{1:T}) = \sum_{t=1}^T \|\mathbf{A}_t\|_1$$

where  $\hat{\mathbf{L}}_t$  is the (symmetric) normalized Laplacian matrix.

## Experiments

- We evaluate the performance of DBGSL on the task of biological sex classification.
- Resting-state (HCP-Rest) as well as emotional task (HCP-Task) fMRI data is used the Human Connectome Project (HCP).
- All brain images are parcellated into  $V = 243$  mean region-wise BOLD signals using the Brainnetome atlas and transformed into a  $z$ -scores to remove amplitude effects.
- For baselines we include kernel ridge regression (KRR) [2], support vector machine (SVM), multilayer perceptron (MLP), bidirectional LSTM (BLSTM) [3], BrainnetCNN (BNCNN) [5], spatio-temporal GNN (STGCN) [1], STAGIN [6], FBNetGen (FBNG) [4] and Deep fMRI (DFMRI) [7].

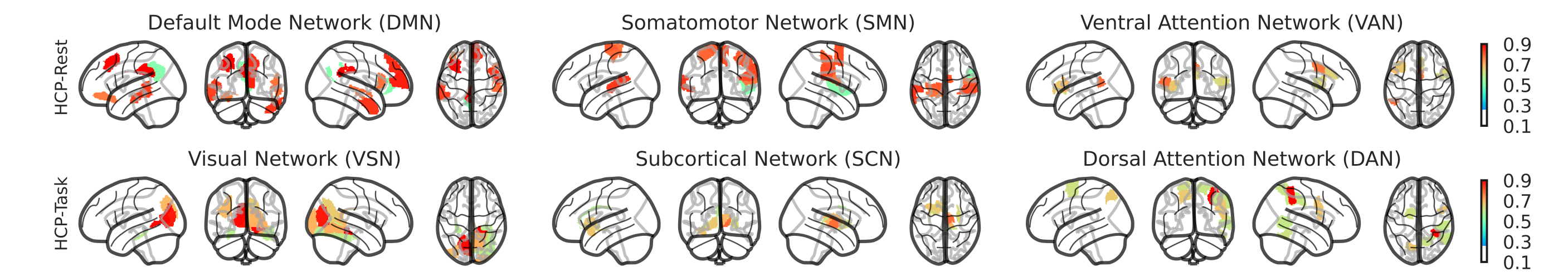
## Results

**Table:** Biological sex classification on HCP-Rest and HCP-Task. Results are mean plus/minus standard deviation across 5 runs. First and second-best results are **red** and **purple**, respectively. Statistically significant difference from DBGSL marked <sup>\*</sup>.

Model	HCP-Rest		HCP-Task	
	ACC (%), $\uparrow$	AUROC ( $\uparrow$ )	ACC (%), $\uparrow$	AUROC ( $\uparrow$ )
KRR	<b>83.50 <math>\pm</math> 1.94 <sup>*</sup></b>	<b>0.9187 <math>\pm</math> 0.0025 <sup>*</sup></b>	81.37 $\pm$ 2.17 <sup>*</sup>	0.9031 $\pm$ 0.0185 <sup>*</sup>
SVM	82.70 $\pm$ 2.68 <sup>*</sup>	0.9170 $\pm$ 0.0089 <sup>*</sup>	<b>83.16 <math>\pm</math> 1.91 <sup>*</sup></b>	<b>0.9097 <math>\pm</math> 0.0184 <sup>*</sup></b>
MLP	81.47 $\pm$ 3.29 <sup>*</sup>	0.9091 $\pm$ 0.0281 <sup>*</sup>	81.10 $\pm$ 3.44 <sup>*</sup>	0.8837 $\pm$ 0.0250 <sup>*</sup>
BLSTM	81.50 $\pm$ 1.26 <sup>*</sup>	0.9058 $\pm$ 0.0081 <sup>*</sup>	77.24 $\pm$ 4.05 <sup>*</sup>	0.8526 $\pm$ 0.0188 <sup>*</sup>
BNCNN	76.83 $\pm$ 7.46 <sup>*</sup>	0.6156 $\pm$ 0.0837 <sup>*</sup>	70.66 $\pm$ 8.23 <sup>*</sup>	0.5945 $\pm$ 0.0499 <sup>*</sup>
STGCN	62.63 $\pm$ 4.50 <sup>*</sup>	0.6991 $\pm$ 0.0264 <sup>*</sup>	54.87 $\pm$ 3.37 <sup>*</sup>	0.5629 $\pm$ 0.0355 <sup>*</sup>
DFMRI	82.65 $\pm$ 3.40 <sup>*</sup>	0.8941 $\pm$ 0.0342 <sup>*</sup>	81.34 $\pm$ 2.19 <sup>*</sup>	0.8024 $\pm$ 0.0317 <sup>*</sup>
FBNG	81.57 $\pm$ 2.90 <sup>*</sup>	0.8967 $\pm$ 0.0170 <sup>*</sup>	77.16 $\pm$ 3.90 <sup>*</sup>	0.8548 $\pm$ 0.0320 <sup>*</sup>
STAGIN	83.13 $\pm$ 2.11 <sup>*</sup>	0.8597 $\pm$ 0.0467 <sup>*</sup>	81.88 $\pm$ 2.73 <sup>*</sup>	0.8088 $\pm$ 0.0404 <sup>*</sup>
DBGSL	<b>92.32 <math>\pm</math> 2.22</b>	<b>0.9623 <math>\pm</math> 0.0433</b>	<b>89.54 <math>\pm</math> 3.48</b>	<b>0.9496 <math>\pm</math> 0.0423</b>

- DBGSL outperforms all baselines across both datasets by statistically significant margins.
- We attribute this to the brain graph being learnt rather than fixed as well as incorporating temporal dynamics.

## Interpretability



**Figure:** Sex-discriminative brain region scores for HCP-Rest (top) and HCP-Task (bottom). Score vectors are created using temporally weighted node degree  $\mathbf{z} = \frac{1}{T} \sum_{t=1}^T (\sum_{j=1}^V \mathbf{A}_{j,t}) \boldsymbol{\alpha}_t \in \mathbb{R}^V$ .

- HCP-Rest brain regions fall in the dorsal anterior cingulate cortex, middle frontal gyrus, and posterior superior temporal cortex within the default mode network (DMN).
- HCP-Task brain regions fall in the parahippocampal gyrus, medial occipital cortex, and superior parietal lobule within the posterior visual network (VSN).

## Conclusion

- DBGSL is an end-to-end trainable model capable of learning optimal time-varying dependency structure from fMRI data in the form of a dynamic brain graph.
- Learnt dynamic graph adjacency matrices reveal prediction-related brain regions that align with existing neuroscience literature.

## References

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