

Learning Similarity-Preserving Representations of Brain Structure-Function Coupling

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- Structural connectivity (SC) How is the brain wired?
 - \Rightarrow Anatomical tracts connecting brain regions
 - \Rightarrow Sparse with fewer connections between hemispheres



- ► Functional connectivity (FC) How the brain functions?
 - Statistical correlation between neural signals in different regions
 - Blood oxygen-level dependent (BOLD) signals from fMRI





- FC depends on anatomical connections
- Strong FC exists between regions with weak or none SC connections
 - FC correlates SC at an aggregate level
 - FC between brain regions related with indirect SC connections



Key problem: deciphering the relationship between SC and FC

- SC-FC correlation, graph feature comparisons [Hagmann et al'14]
- Simulations of nonlinear cortical activity models [Honey et al'09]
- Diffusion-based parametric inverse problem [Abdelnour et al'14]

Contributions: novel investigation of the SC-FC relationship

- Machine learning for network data
 - \Rightarrow Reconstruct FC from SC as a regression problem
 - \Rightarrow Learn lower-dimensional graph representations for classification
- Siamese network framework design
 - \Rightarrow Each input is a pair of graphs \rightarrow enlarge data size
 - \Rightarrow Increase robustness to integrate various prior information
 - ⇒ Similarity-preserving graph embeddings



- Learn a mapping from a discrete graph to a continuous domain
- Given G(V, E) with weighted adjacency matrix A ∈ ℝ^{N×N}
 ⇒ N brain regions, A_{ii} := anatomical connection strengths
- Goal: learn low dimensional vector representation, node embeddings
 ⇒ Capture information of the node and its neighbors
- ▶ Approach: Graph signal processing (GSP) and graph convolution
- Extensions to embed the whole graph, i.e. graph embeddings
 - \Rightarrow Graph clustering/classification
- Potential of GRL for neuroimaging data analysis rather unexplored
 - \Rightarrow Inductive GRL for brain network analysis among population



- Graph $G(\mathcal{V}, \mathcal{E})$ with $N = |\mathcal{V}|$ nodes \Rightarrow **A** and **L** = **D A**
 - \Rightarrow **D**: diagonal degree matrix
 - \Rightarrow Symmetric $\mathbf{L} = \mathbf{U} \mathbf{\Lambda} \mathbf{U}^{T}$
- Graph signals represented as vectors $\mathbf{x} \in \mathbb{R}^{N}$
- Graph Fourier Transform (GFT): $\hat{\mathbf{x}} = \mathbf{U}^T \mathbf{x}$
- Generalize machine learning models for network data
 - \Rightarrow GSP to define convolutions on graphs [Ortega et al'19]



• Graph convolution (filter) with frequency response $\hat{\mathbf{H}} = \operatorname{diag}(\hat{\mathbf{h}})$

 $\mathbf{y} = \mathbf{H}\mathbf{x} = \mathbf{U}\hat{\mathbf{H}}\mathbf{U}^{\mathsf{T}}\mathbf{x}$

- ChebNet: Chebyshev polynomials of Λ [Defferrard et al'16]
- First-order approximation of ChebNet [Kipf-Welling'17]

$$\mathbf{y} = \mathbf{H}\mathbf{x} = \mathbf{\theta}(\mathbf{I}_N + \mathbf{D}^{-1/2}\mathbf{A}\mathbf{D}^{-1/2})\mathbf{x}$$

Compact rule for per-layer filtering update

 $\tilde{\mathbf{X}} \leftarrow \tilde{\mathbf{A}} \mathbf{X} \mathbf{\Theta}$

- $\tilde{A} = I_N + D^{-1/2}AD^{-1/2}$
- X: set of multiple observations of the graph signal x
- \blacktriangleright \tilde{X} integrates nodal attributes in X and topology in \tilde{A}
- ▶ GCN: aggregate information from multiple hops within G
 - \Rightarrow Stack convolutional layers with pointwise non-linear activation
 - \Rightarrow Capture indirect interactions across the network



- Goal: summarize SC-FC relationship by simultaneously learning
 - Node embeddings X_C to reconstruct FC Σ from input SC networks
 - $\Rightarrow \mathbf{X}_{C}$ captures SC-FC relationship
 - Graph embeddings for graph classification
 - \Rightarrow Approximately preserve similarity input graphs



Data description and preprocessing

- 412 subjects from Human Connectome Project (HCP)
 - Two classes: 191 non-drinkers, 221 heavy drinkers
- Preprocessed SC network A from diffusion MRI
 - \Rightarrow Fiber counts between N = 68 cortical surface regions



- Preprocessed FC network from functional MRI
 - \Rightarrow Blood oxygen-level dependent (BOLD) signals
 - \Rightarrow Estimated FC \Leftrightarrow Pearson correlation between BOLD signals
 - \Rightarrow Discard negative correlation and keep only positive connections
 - One-hot encoding as the signal on each graph node $(X = I_N)$



- ▶ Input SC network $A \in \mathbb{R}^{N \times N}$, N = 68 regions from brain atlas
 - \Rightarrow Edge weights represent SC between brain regions

 \Rightarrow Preprocessing: $\mathbf{\tilde{A}} := \mathbf{\hat{D}}^{-1/2} \mathbf{\hat{A}} \mathbf{\hat{D}}^{-1/2}$, $\mathbf{\hat{A}} = \mathbf{I}_N + \mathbf{A}$

Learn vertex representations (i.e., embeddings) that capture

 Nodal attributes, e.g. intrinsic properties of brain regions
 Graph topology information, e.g. regional connection strengths

First GCN layer of the encoder to learn node embeddings

 $\mathsf{X}^{(1)} = \operatorname{ReLU}(\tilde{\mathsf{A}}\mathsf{X}^{(0)}\Theta^{(1)}) \in \mathbb{R}^{N \times F_1}$

- ▶ $X^{(0)} \in \mathbb{R}^{N \times d_0}$: input signal matrix
- $\Theta^{(1)} \in \mathbb{R}^{T \times F_1}$: learnable GCN filter coefficients
- $\operatorname{ReLU}(x) = \max(0, x)$ activation for training the network





- Multi-layer GCN with dimension $32 \times 16 \times 8$
- Node embeddings concatenation
- Global row-wise mean pooling





▶ Node embeddings X_C go through the outer-product decoder

 $\hat{\boldsymbol{\Sigma}} = \operatorname{ReLU}(\boldsymbol{X}_{C}\boldsymbol{X}_{C}^{T}) \in \mathbb{R}^{N \times N}$

- \blacktriangleright Generate estimate of empirical FC networks Σ
- Reconstruction loss $\mathcal{L}_{MSE}(\hat{\Sigma}, \Sigma)$





- Obtain whole graph embedding h_i via row-wise average of X_C
- For input graph pairs $\{A_i, A_j\}$ with label $\{I_i, I_j\}$, h_i, h_j shall be
 - \Rightarrow Highly (less) similar if $l_i = l_j$ ($l_i \neq l_j$)
 - \Rightarrow Measured by cosine similarity $s(\mathbf{h}_i, \mathbf{h}_j)$



- N_s (N_d) graph pairs with same (different) labels
 - Pairwise similarity global loss function [Ktena et al'18]

$$\mathcal{L}_{\mathsf{SIM}} = (\sigma^{2+} + \sigma^{2-}) + \mathbf{w} \times \max(0, \mathbf{m} - (\mu^+ - \mu^-))$$

• Minimize
$$\mu^- = \sum s(\mathbf{h}_i, \mathbf{h}_j) / N_d, I_i \neq I_j$$

 \Rightarrow Mean similarity between embeddings of different classes

• Maximize
$$\mu^+ = \sum s(\mathbf{h}_i, \mathbf{h}_j) / N_s, l_i = l_j$$

 \Rightarrow Mean similarity between embeddings of the same classes

Minimize the variance of similarities within and between classes

Overall loss function is

$$\mathcal{L} = \mathcal{L}_{\mathsf{SIM}} + \lambda imes (\mathcal{L}_{\mathsf{MSE}}(\hat{\mathbf{\Sigma}}_i, \mathbf{\Sigma}_i) + \mathcal{L}_{\mathsf{MSE}}(\hat{\mathbf{\Sigma}}_j, \mathbf{\Sigma}_j))$$



- ▶ Classify test sample (KNN= 5) by cosine similarity in vector space
- ▶ Baseline: supervised GRL model [Li et al'21]
 - $\Rightarrow \mathsf{Reconstruct}\ \mathsf{FC}\ \mathsf{from}\ \mathsf{SC}$
 - \Rightarrow Subject classification via a logistic regression classifier

Model	Accuracy	F score
Siamese model	$\textbf{0.6843} \pm \textbf{0.016}$	$\textbf{0.7391} \pm \textbf{0.016}$
Baseline	0.6610 ± 0.043	0.6962 ± 0.030





Summary

- Building the Siamese network and training it with graph pairs
 - Increase the amount of training data
 - Bring in the flexibility to incorporate additional prior information
- Graph reconstruction of FC from SC
 - Parsimonious representation of population-level SC-FC relationship
- Similarity estimation between input graphs
 - Use subject labels as additional inputs for supervised classification
- Prospect of using graph-level, similarity-preserving embeddings
 - Measure SC-FC coupling for brain network analysis

Future work

- Reflect more intrinsic differences between drinkers and non-drinkers
- Spatio-temporal analysis of dynamic brain networks