Learning Joint and Individual Structure in Network Data with Covariates

Modeling multiple heterogeneous networks

Motivation:

- We present the *common subspace independent-edge* (COSIE) model which describes a collection of networks with a shared latent structure on the vertices but potentially different connectivity patterns for each graph [1].
- COSIE encompasses many other popular network representations, including the stochastic blockmodel
- A joint spectral embedding - the *multiple adjacency spectral embedding*- leads to consistent estimation that is computationally efficient
- MASE estimates yield state-of-the-art performance on subsequent inference tasks, including dimensionality reduction, hypothesis testing and community detection

- Models for multiple network data are critical in statistical network theory and across multiple domains, including neuroscience, biology and the social sciences.
- Challenges in modeling graph differences while retaining sufficient model simplicity to render estimation feasible.
- Existing models require strong assumptions that limit their flexibility or scalability

Difussion MRI brain connectomes from the HNU1 data

Common subspace independent edge (COSIE) model

- Consider a sample of m graphs with n labeled nodes.
- Denote the graphs by their adjacency matrices $\mathbf{A}^{(1)}, \ldots, \mathbf{A}^{(m)} \in \{0,1\}^{n \times n}$
- Each graph $\mathbf{A}^{(i)}$ is modeled as independent-edge with parameter $\mathbf{P}^{(i)} \in \mathbb{R}^{n \times n}$

$$\mathbf{A}^{(i)}_{uv} \sim \text{Ber}(P^{(i)}_{uv}).$$

COSIE model

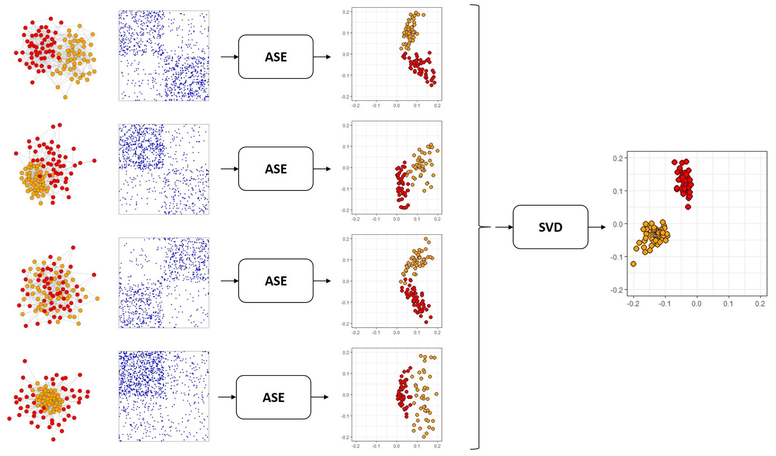
- The sample of graphs is jointly distributed according to the COSIE model if

$$\mathbf{P}^{(i)} := \mathbf{V}\mathbf{R}^{(i)}\mathbf{V}^T.$$

- $\mathbf{V} \in \mathbb{R}^{n \times d}$ is a matrix with orthogonal columns, with its rows representing vertex latent positions
- $\mathbf{R}^{(i)} \in \mathbb{R}^{d \times d}$ is a score matrix, potentially different for each graph
- The parameter d controls the complexity of the model

Multiple adjacency spectral embedding (MASE)

1. For each $i \in [m]$, obtain the d-dimensional unscaled *adjacency spectral embedding* of $\mathbf{A}^{(i)}$, denoted by $\hat{\mathbf{V}} \in \mathbb{R}^{n \times d}$ and corresponding to the d leading eigenvectors
2. Let $\hat{\mathbf{U}} = \left(\hat{\mathbf{V}}^{(1)} \cdots \hat{\mathbf{V}}^{(m)}\right)$ be the $n \times (md)$ matrix of concatenated ASEs.
3. Let $\hat{\mathbf{V}} \in \mathbb{R}^{n \times d}$ be the matrix containing the d leading left singular values of $\hat{\mathbf{U}}$.
4. For each $i \in [m]$, set $\hat{\mathbf{R}}^{(i)} = \hat{\mathbf{V}}^T \mathbf{A}^{(i)} \hat{\mathbf{V}}$.



Theoretical properties

Consistency of common invariant subspace estimator

- Under some assumptions on the smallest eigenvalue of the score matrices and on the sparsity of the graphs, the estimate of $\mathbf{V}$ obtained by MASE satisfies

$$\mathbb{E}\left[\min_{\mathbf{W} \in \mathcal{O}_d} \left\|\hat{\mathbf{V}} - \mathbf{V}\mathbf{W}\right\|\right] \lesssim \sqrt{\frac{d}{mn}} + \frac{\sqrt{d}}{n}.$$

- When $\mathbf{V}$ has only d different rows, COSIE is equivalent to the stochastic blockmodel, and k-means clustering expected error in community detection is $O\left(\sqrt{\frac{d}{m}} + \frac{1}{\sqrt{n}}\right)$.

Asymptotic normality of the score matrices

- The entries of the estimated score matrices $\hat{\mathbf{R}}^{(i)}$ are asymptotically normally distributed, in particular, as the size of the graphs n increases

$$\frac{1}{\sigma_{ijk}}\left(\hat{\mathbf{R}}^{(i)} - \mathbf{W}\mathbf{R}^{(i)}\mathbf{W}^T + \mathbf{H}\right)_{jk} \xrightarrow{d} \mathcal{N}(0,1)$$

where $\sigma_{ijk} = O(1)$, $\mathbb{E}[\|\mathbf{H}\|_F] = O(d/\sqrt{m})$ and $\|\mathbf{R}^{(i)}\|_F \to \infty$.

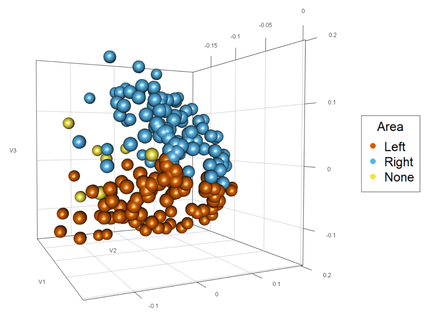
Brain network analysis

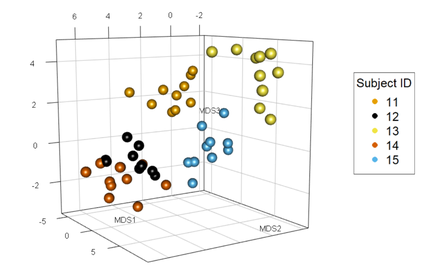
HNU1 data

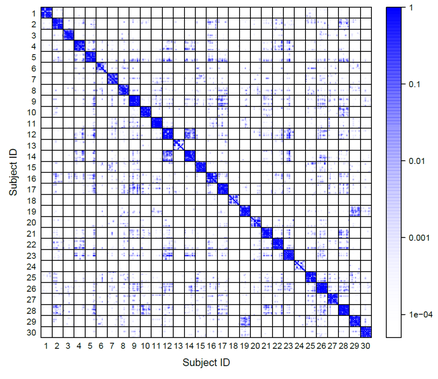
- 300 graphs constructed from diffusion magnetic resonance imaging (dMRI), with $n = 200$ nodes
- 30 different healthy subjects, and 10 graphs per subject
- **Goal:** identify differences and similarities between graphs

Dimensionality reduction

- The vertex embedding $\hat{\mathbf{V}}$ obtained by MASE (top figure) reflects the anatomical location of the vertices in the brain.
- A multidimensional scaling of the distance between the score matrices $\{\mathbf{R}^{(i)}\}_{i=1}^{300}$ (bottom figure) puts graphs from the same subject closer to each other







Matrix of p-values for the equal distribution test of every pair of graphs

Graph hypothesis testing

- For each pair of graphs i and j, we test the hypothesis that their distribution is the same, i.e., $H_0 : \mathbf{R}^{(i)} = \mathbf{R}^{(j)}$
- Test statistic $\|\hat{\mathbf{R}}^{(i)} - \hat{\mathbf{R}}^{(j)}\|_F$
- Semiparametric bootstrap: estimate the parameters with MASE to sample new graphs
- The p-values of the test (left figure) are generally high for pairs of graphs from the same subject (diagonal entries) and low for different subjects

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References

[1] Jesús Arroyo, Avanti Athreya, Joshua Cape, Guodong Chen, Carey E Priebe, and Joshua T Vogelstein, "Inference for multiple heterogeneous networks with a common invariant subspace," *arXiv preprint arXiv:1906.10026*, 2019.

Open R source code for MASE is available at `https://github.com/jesusdaniel/mase`, and in the Python GraSPy package at `https://neurodata.io/graspy`.