

Shira Yoffe<sup>1</sup>, Ziv Ben-Zion<sup>3</sup>, Guy Gurevitch<sup>6</sup>, Talma Hendler<sup>4,5,6,7</sup>, Malka Gorfine<sup>2</sup>, and Ariel Jaffe<sup>1</sup>

<sup>1</sup> Department of Statistics and Data Science, Hebrew University of Jerusalem <sup>2</sup> Department of Statistics and Operations Research, Tel Aviv University <sup>3</sup> School of Public Health, Faculty of Social Welfare and Health Sciences, University of Haifa <sup>4</sup> Sagol School of Neuroscience, Tel Aviv University <sup>5</sup> Sagol Brain Institute, Tel Aviv Sourasky Medical Center <sup>6</sup> Gray Faculty of Medical and Health Sciences, Tel Aviv University <sup>7</sup> School of Psychological Sciences, Faculty of Social Sciences, Tel Aviv University

## Problem and Motivation

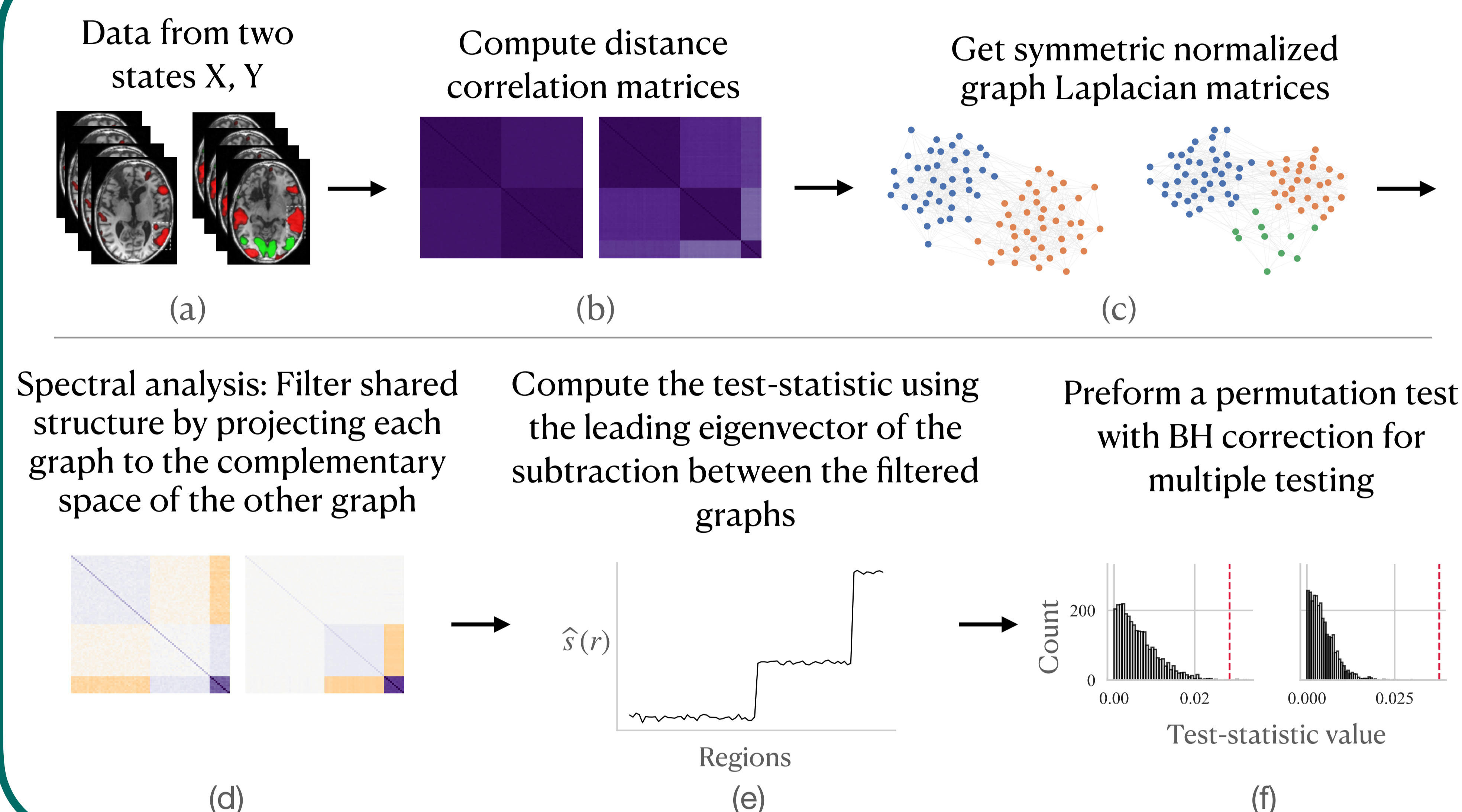
Functional connectivity (FC) networks quantify statistical dependence between brain regions using fMRI BOLD time series.

**Objective:** Given two experimental or clinical conditions, identify brain regions whose connectivity patterns differ between conditions.

**Challenges:** (i) noisy fMRI measurements, (ii) high-dimensional network structure, (iii) severe multiple-comparison burden, and (iv) potentially nonlinear dependencies. Existing approaches often have limited statistical power or fail to capture distributed connectivity changes [1].

We propose **SpARCD**, a spectral graph framework for identifying condition-specific brain regions.

## Methods



• The distance correlation (Fig. 1 (b)):

$$\widehat{W} = \widehat{\mathcal{D}}(X_r, X_{r'}) = \frac{\langle \tilde{D}_r, \tilde{D}_{r'} \rangle}{\sqrt{\langle \tilde{D}_r, \tilde{D}_r \rangle \langle \tilde{D}_{r'}, \tilde{D}_{r'} \rangle}}$$

• Filter shared spectral structure between graphs (Fig. 1 (d)):

$$\widehat{Q}_X = I_R - \sum_{k=1}^K \widehat{v}_X^{(k)} \widehat{v}_X^{(k)\top} \rightarrow \widehat{L}_Y^{\text{filt}} = \widehat{Q}_X (I_R - \widehat{L}_Y) \widehat{Q}_X$$

Main Novelty:

(i) SpARCD uses distance correlation (d-Corr) to build FC networks, capturing linear and nonlinear dependencies.

(ii) It applies spectral filtering to construct a differential connectivity operator that captures condition-specific changes.

(iii) A permutation-based testing framework provides interpretable region-level significance maps for robust detection of altered connectivity.

## Results

**Simulation Studies:** Evaluation across five connectivity scenarios demonstrated the robustness of SpARCD under diverse patterns of network change. Full results are reported in the paper.

**Real Data:** Data: We applied SpARCD to resting-state fMRI data comparing PTSD and control groups. Results: The method identified eight significant regions (Fig. 3), primarily within visual processing areas, suggesting altered connectivity organization in visual cortical systems in PTSD. Additional Real-Data Analyses: Consistent connectivity-alteration patterns were also observed across two EFMT datasets and in EFMT vs. resting-state comparisons, supporting the robustness of the proposed framework.

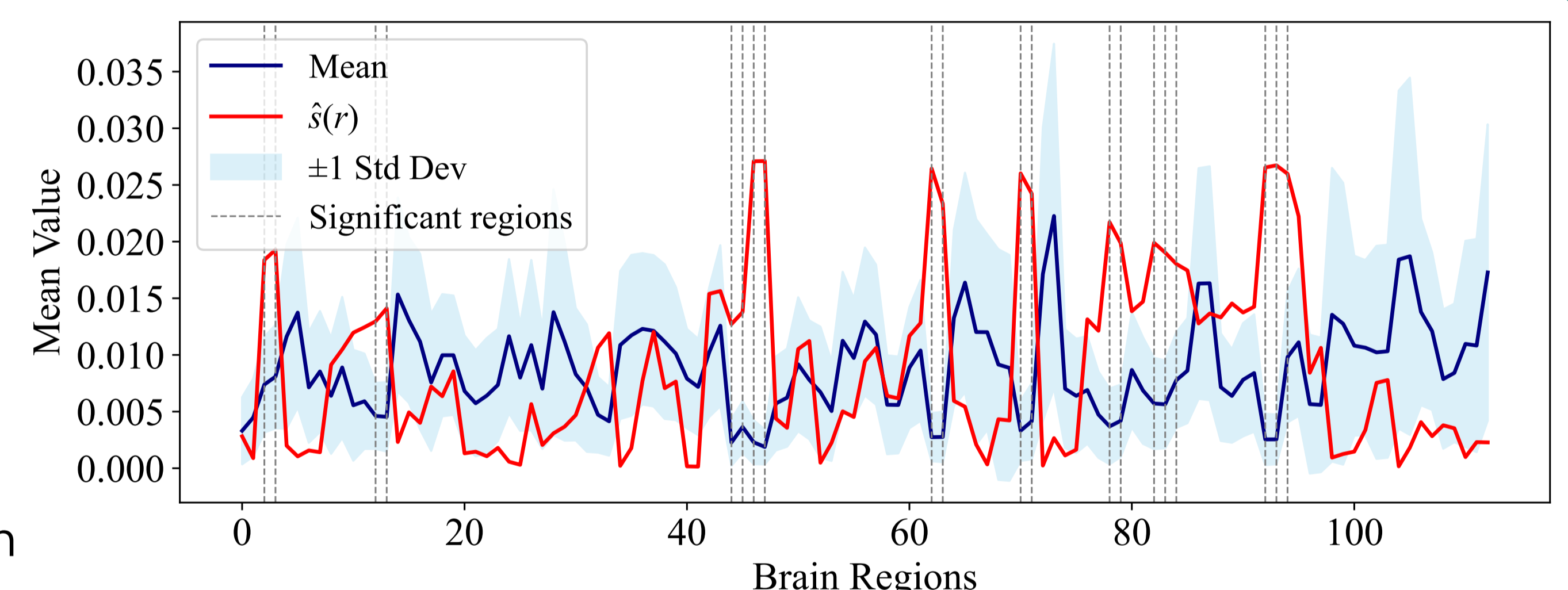


Figure 3: Results of SpARCD applied to the resting-state fMRI dataset. The observed test statistic  $s(r)$  (red) is shown together with the mean (blue) and standard deviation (light blue) of the permutation-based null distribution.

## Theoretical Guarantees

### Theorem 1 (Finite-sample validity of the block permutation test)

Fix a brain region  $r$ , and let  $\widehat{s}(r)$  denote the observed test statistic computed from block data  $\mathcal{B}$  and condition labels  $A$ . Let  $\mathcal{G}$  denote the set of allowable block permutations, and let  $\widehat{s}^{(\pi)}(r)$  denote the statistic computed from the permuted labels  $\pi A$ , for  $\pi \in \mathcal{G}$ . Assume that under the null hypothesis, the condition labels are exchangeable over  $\mathcal{G}$  conditional on the unlabeled block structure; that is,  $(\mathcal{B}, A) \mid \mathcal{O} \stackrel{d}{=} (\mathcal{B}, \pi A) \mid \mathcal{O}$ , for all  $\pi \in \mathcal{G}$ , where  $\mathcal{O} = \{(\mathcal{B}, \pi A) : \pi \in \mathcal{G}\}$  denotes the permutation orbit. If the statistic is computed using the same deterministic procedure for both observed and permuted data, and if all permutations in  $\mathcal{G}$  are enumerated, then the exact permutation  $p$ -value  $p_r^* = \frac{1}{|\mathcal{G}|} \sum_{\pi \in \mathcal{G}} \mathbb{1}\{\widehat{s}^{(\pi)}(r) \geq \widehat{s}(r)\}$  satisfies  $\Pr_{H_0}(p_r^* \leq \alpha \mid \mathcal{O}) \leq \alpha$  for every  $\alpha \in [0, 1]$ . Consequently,  $\Pr_{H_0}(p_r^* \leq \alpha) \leq \alpha$ .

**Theorem 2 (Stability of eigenvector-based region ranking)** Let  $R$  denote the number of brain regions, treated as fixed while  $n \rightarrow \infty$ . Let  $L_d$  be the population contrast matrix, and let  $\widehat{L}_d$  denote its empirical counterpart. Assume  $\Delta_n = \|\widehat{L}_d - L_d\|_2 = o_p(1)$ . Let  $\lambda_1, \dots, \lambda_R$  denote the eigenvalues of  $L_d$ , ordered so that  $|\lambda_1| > |\lambda_2| \geq \dots \geq |\lambda_R|$ , and assume that the leading absolute eigenvalue is separated from the rest of the spectrum. Specifically, define  $\rho = |\lambda_1| - \max_{j \geq 2} |\lambda_j| > 0$ , and the eigengap is defined by  $\varphi = \min_{j \geq 2} |\lambda_1 - \lambda_j| > 0$ . Let  $v_d$  be a unit-norm eigenvector associated with  $\lambda_1$ , and define  $s(r) = \frac{|v_d(r)|}{\|v_d\|_1}$ ,  $r = 1, \dots, R$ . Then, as  $n \rightarrow \infty$ , the following statements hold with probability tending to one:

- **Eigenvector stability:** There exists a sign  $\eta \in \{-1, 1\}$  such that  $\|\widehat{v}_d - \eta v_d\|_2 \leq C_{DK} \frac{\Delta_n}{\varphi}$ , where  $C_{DK}$  is a universal Davis-Kahan constant.
- **Score stability:**  $\sup_{1 \leq r \leq R} |\widehat{s}(r) - s(r)| = O_p\left(\frac{\Delta_n}{\varphi}\right)$ .
- **Ranking stability:** If  $s(r_1) - s(r_2) > 2 \sup_{1 \leq r \leq R} |\widehat{s}(r) - s(r)|$ , then  $\widehat{s}(r_1) > \widehat{s}(r_2)$ .
- **Top- $K$  stability:** Let  $S_K$  denote the set of the  $K$  regions with largest population scores, and define  $\Delta_K = s_{(K)} - s_{(K+1)}$ , where  $s_{(1)} \geq \dots \geq s_{(R)}$  are the ordered population scores. If  $\Delta_K > 2 \sup_{1 \leq r \leq R} |\widehat{s}(r) - s(r)|$ , then the estimated top- $K$  set equals  $S_K$ .