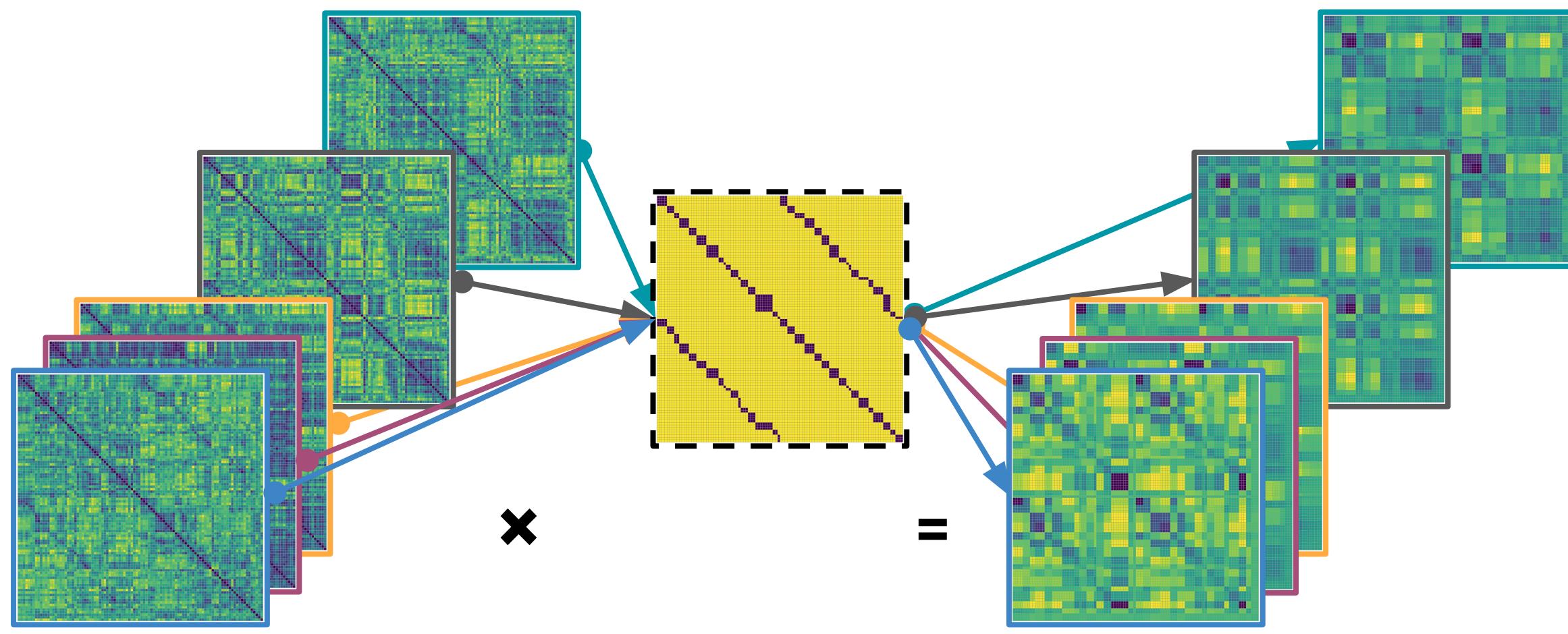


K+1 covSTATIS: a new method that integrates and analyzes multiple functional connectivity matrices with respect to an *a priori* reference connectivity structure

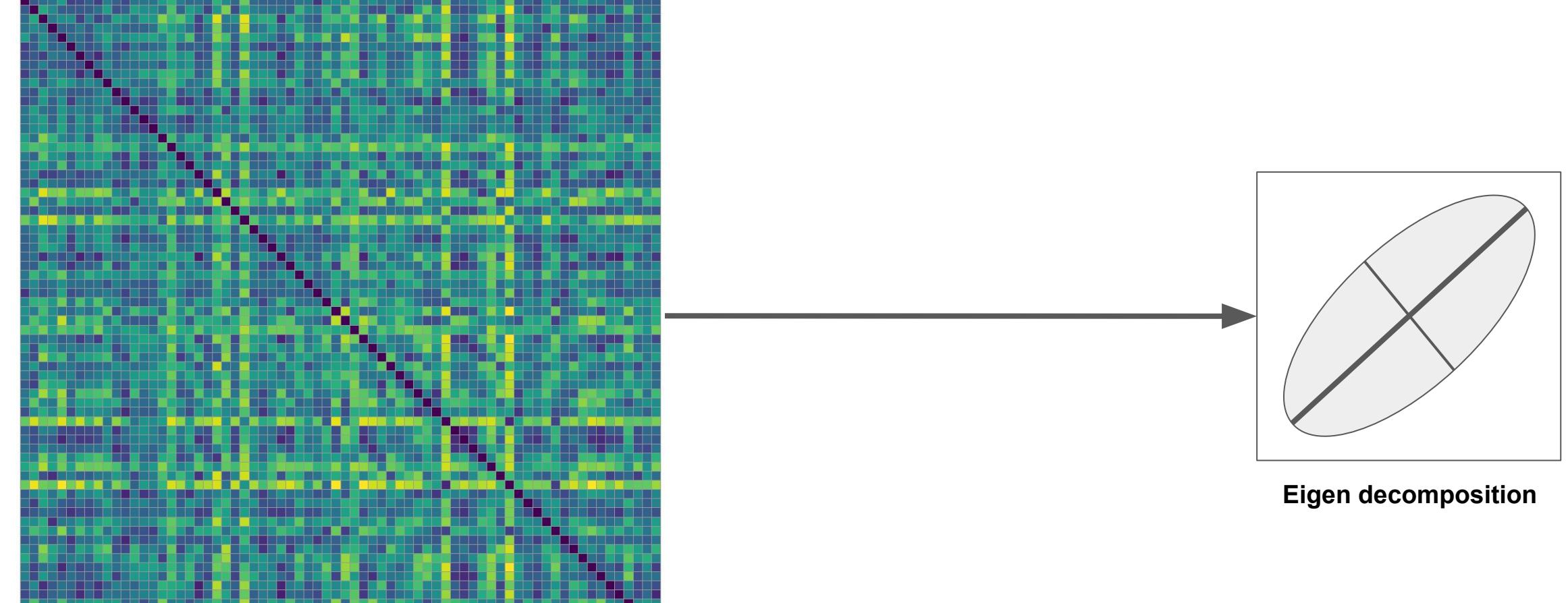
1

Akin to partial least squares, compute relationship between each matrix and the target. Performed on double centered and normalized (e.g., sums of squares equal to 1) square, symmetric, correlation or covariance matrices



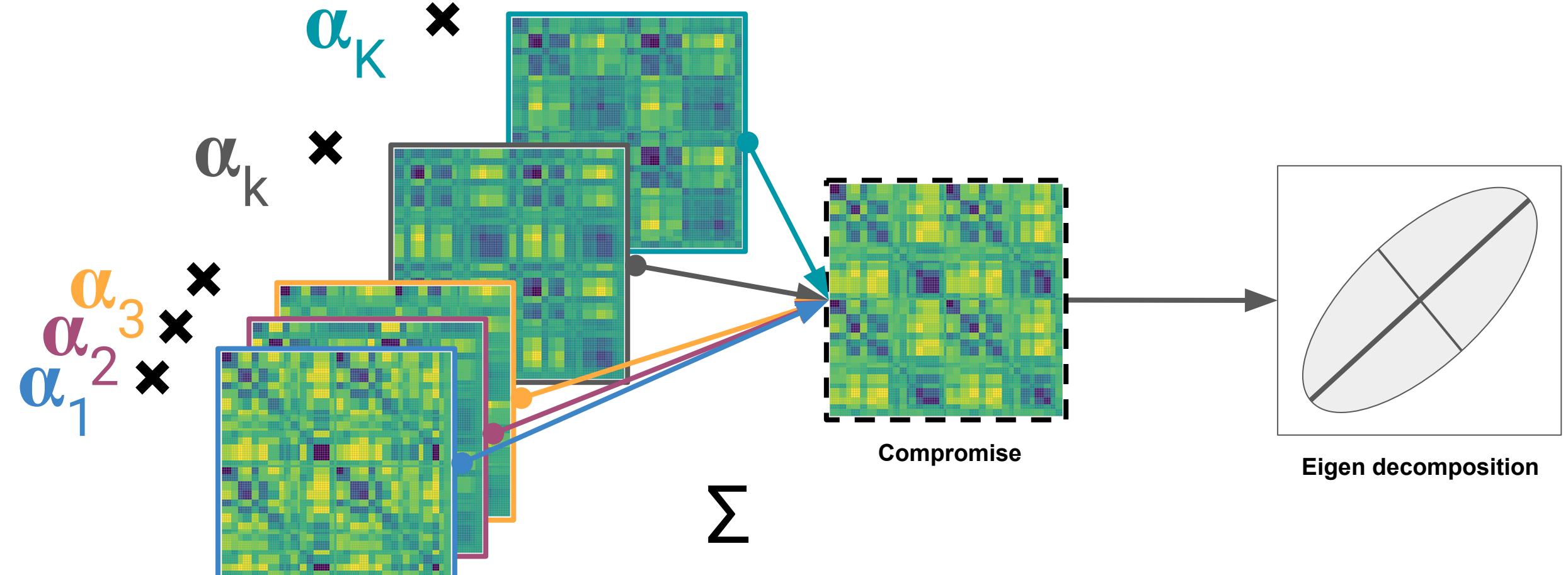
2

Compute similarity between all matrices via R^2 coefficient (akin to R^2), and decompose. Get weights (" α weights") from first eigenvector to compute weighted average correlation or covariance matrix ("compromise")



3

Compute compromise matrix and decompose through the eigenvalue decomposition. Each individual matrix is then projected onto ("predicted by") the compromise components



INTRODUCTION

- The Ontario neurodegenerative disease research initiative (ONDRI) is a multi-site study with wide-ranging data across five neurodegenerative diseases [1], including a battery of neuroimaging modalities such as resting state fMRI (rsfMRI).
- To identify potential biomarkers it is necessary to know how individuals or groups express differential resting state patterns with respect to a reference connectivity structure. We introduce K+1 covSTATIS (K+1CS) to do so.
- K+1CS is a hybrid multivariate technique that combines features of partial least squares [2] and STATIS (roughly translates to "structuring three way statistical tables") [3], in a multi-table principal components analysis framework. K+1CS computes all individual connectivity profiles with respect to a reference structure.

METHODS

- Participants included N=70 (F=27, M=43) vascular cognitive impairment without overt stroke (age range: 54.95-85.43, median=69.75; MoCA range: 18-30, median=26). Multisite rsfMRI was acquired for all subjects (TE=30ms, TR=2400ms, flip angle=70°, voxel size=3.5 x 3.5 x 3.5mm, scan time=10 minutes) and preprocessed with OPPNI [4]. Optimization was at the group level ("fixed") with respect to a seed voxel in the posterior cingulate cortex (PCC). A common (group) EPI template was created [5] and all individuals were warped to the group EPI template.
- We used the Yeo/Schaefer 17 network with 100 ROIs structure as our reference [6, 7]. We then computed 100 x 100 (Schaefer ROIs) correlation matrices for each individual, where we had K=70 correlation matrices and 1 reference structure ("K+1"), a network adjacency matrix.

DISCUSSION

- Generalizes similar methods [8] and allows us to identify a group structure (compromise) as well as individual differences with respect to a reference
- Provides the abilities to: (1) extract differential network expression for individuals and groups either per ROI or across all ROIs which may provide biomarkers of disease state or progression and (2) understand ONDRI rsfMRI data in the context of hypothesized networks but absent a control sample
- Use any square, symmetric, and positive semi-definite data and thus the K+1 table could be almost any reference such as a group average control set or meta analytic data, e.g., the Laird atlases [9] via BrainMap

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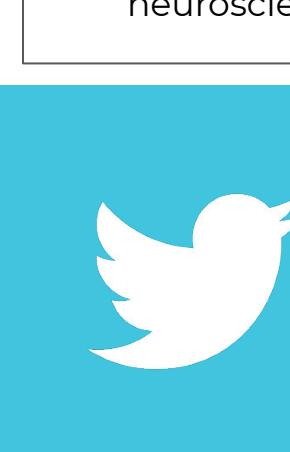
See the Github repo for software, updates, and examples:
github.com/jennyrieck/C-MARINeR



github.com/derekbeaton

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