# A multivariate approach to analyze connectivity matrices with individual-specific parcellation

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Abstract Submission

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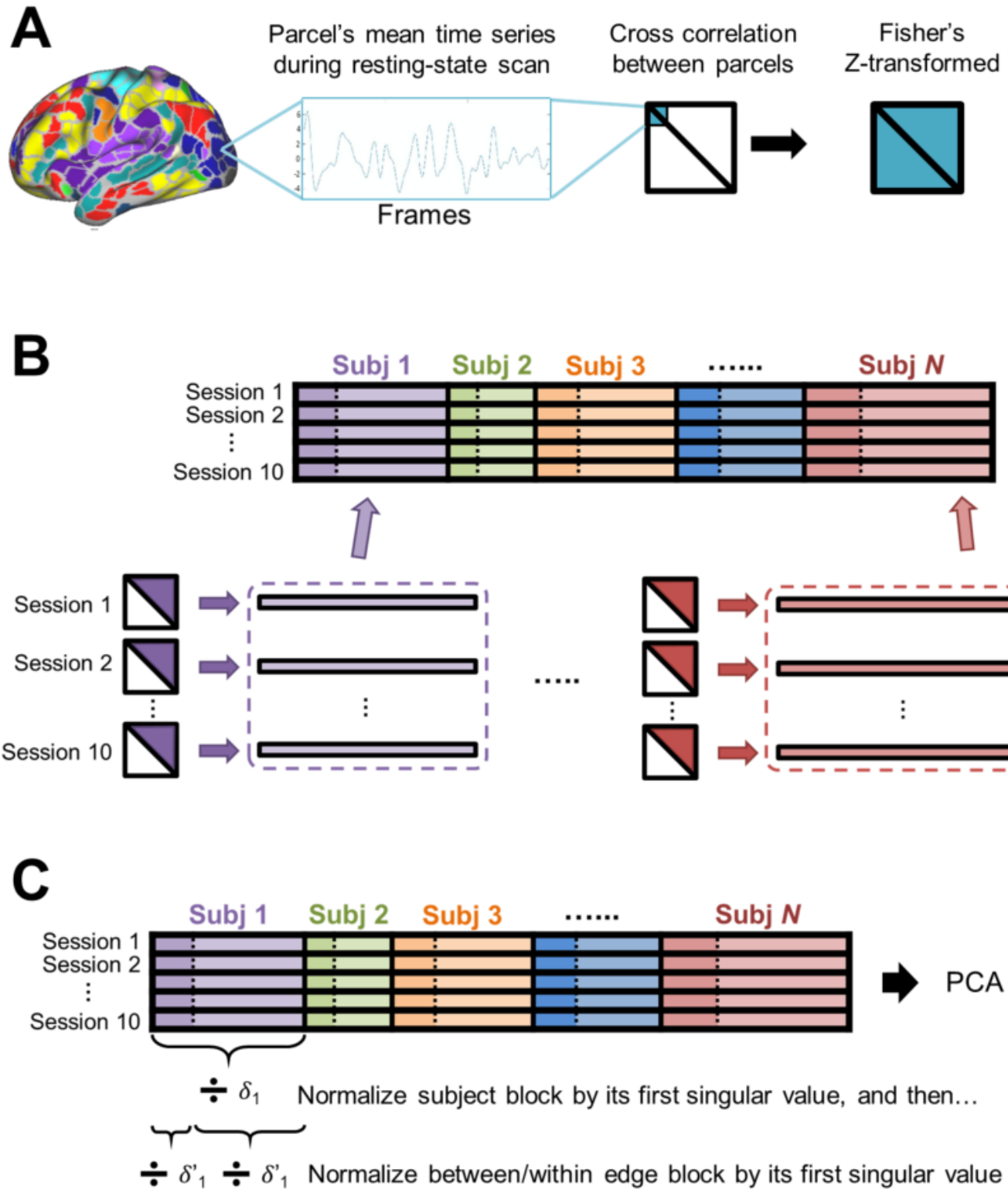
## Introduction:

DiSTATIS (Abdi, et al., 2012)-a three-way multidimensional scaling (MDS)-is used to analyze resting-state functional magnetic resonance imaging (rsfMRI) data and to visualize the pattern of dissimilarity between networks. These dissimilarities are obtained by analyzing multiple distance matrices that have matching rows and columns (i.e., distinct functional regions in rsfMRI analysis). These functional regions, referred to as parcels or networks, are usually derived from a shared template onto which all data are mapped. However, using a shared template could bias results against participants that vary greater from this template, and this issue is particularly problematic amongst participants with diverse brain structures and functions (e.g., elderly, lesion patients, children). For such participants, the optimal parcellation should maximize the homogeneity of the signal within each parcel region and of each participant. Therefore, recent work in rsfMRI analysis has developed techniques to derive individual-specific parcellations and sub-networks; the goal of this project is to propose a multivariate approach that accommodates such parcellation which allows differing parcel numbers and organization across participants.

## Methods:

The proposed multivariate approach first extracts the upper-triangle of the connectivity matrix of each participant session (Fig. 1A) and vectorizes it to form the rows of a data table. Sessions from the same participant are stacked to form a block of columns. Each participant's block is placed adjacent to one another to form the final data table, where the rows are sessions and the columns are network edges (Fig. 1B). Next, hierarchical multiple factor analysis (Fig. 1C) (Abdi, et al., 2013; Le Dien & Pagès, 2003) is used to preprocess the data table by normalizing each participant's column-block by its first singular value, then dividing the column-block of each edge-type (i.e., between- or within-network) within each participant's column block by its first singular value. Finally, a PCA is performed to visualize the edges, participants, and sessions.
To test this new technique, we obtained the Midnight Scan Club (MSC) dataset (Gordon, et al., 2017) from the OpenfMRI database (ds000224) of which the individual-specific functional parcellation for each participant was available. The functional network of each participant's session is represented by a symmetric, region-by-region

connectivity matrix, where connectivity (i.e., edge) is given by the Fisher's Z-transformed correlation of the BOLD signals between two regions. From the original MSC data, four sessions from each participant were selected for the analysis (sessions 1 – 4). For Sessions 2 and 4, the connectivity of three types of edges was manipulated to simulate commonly observed changes in functional brain networks: (1) decreases within the default mode network (DMN) and increases (2) between DMN and the fronto-parietal network (FPN) and (3) between the DMN and the dorsal attention network (DAN). Simulations of changes were restricted to specific networks to test whether our technique could detect where between-session changes are located.



## Results:

This new multivariate approach to analyzing the MSC data table showed the session effect (simulated vs. non-simulated sessions) on the first component (Fig. 2A). This separation is driven by the within DMN connectivity and several other between-network edges, including edges between DMN and FPN (Fig. 2B). A comparison analysis was conducted using DiSTATIS, where data were mapped to a shared template (Gordon, et al., 2016). Although DiSTATIS also revealed the session effect within DMN (Fig. 2C), between-network effects could not be detected.

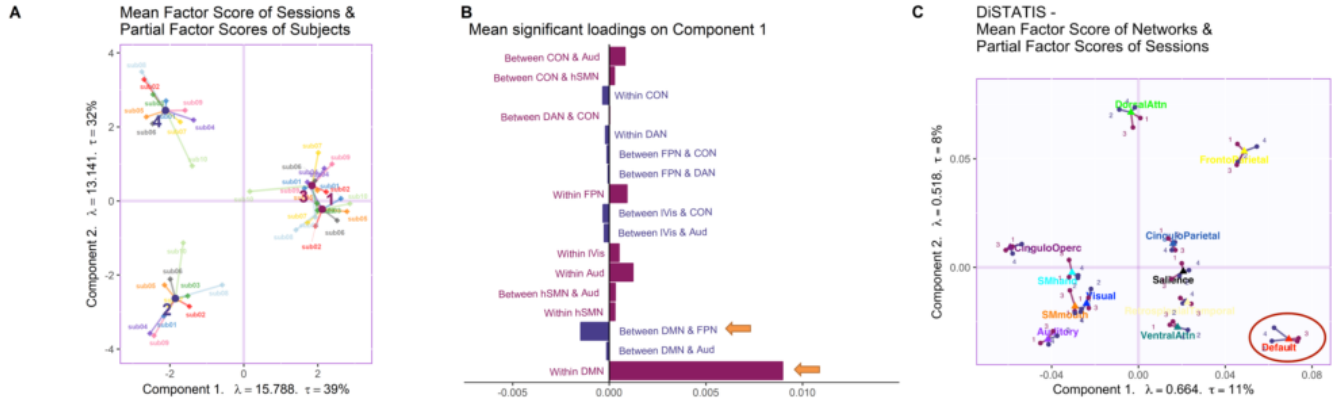



**Fig. 2 – HMFA detects the simulated session effect and identifies the types of edges simulated.** (A) The biplot shows the row factor scores from the hierarchical multiple factor analysis (HMFA). The first component distinguishes the simulated (blue dots; Sessions 2 and 4) and non-simulated (purple dots; Sessions 1 and 3) sessions. The small diamond dots that extend from each factor score are the partial factor scores which represent how each session is viewed from the perspectives of different tables (i.e., different participants). (B) The barplot indicates the mean loadings of all edges that significantly contribute to the first component and drive the session effect. The orange arrows point towards the simulated edges (i.e., the functional connectivity within the default mode network (DMN) as well as the functional connectivity between the DMN and the fronto-parietal network (FPN)). (C) A comparison analysis was conducted using DiSTATIS with the parcellation based on a shared template, and this biplot shows the mean factor scores of all networks from DiSTATIS (colored triangle dots). The four round dots that extend from each network factor score are the partial factor scores which represent how each network is viewed from the perspectives of different sessions. Only the partial factor scores of the DMN distinguish the simulated (blue dots) and the non-simulated (purple dots) sessions.

## Conclusions:

In conclusion, this technique provides a multivariate approach to analyze functional connectivity with individual-specific parcellation and is particularly useful for participant group of diverse brain sizes, functional parcellation or organization schemes.

## Modeling and Analysis Methods:

Connectivity (eg. functional, effective, structural)
Methods Development [1]
Multivariate Approaches [2]
Segmentation and Parcellation
Task-Independent and Resting-State Analysis

## Keywords:

Data analysis
FUNCTIONAL MRI
Multivariate
Statistical Methods

[1|2]Indicates the priority used for review

## My abstract is being submitted as a Software Demonstration.

No

**Please indicate below if your study was a "resting state" or "task-activation" study.**

Resting state

**Healthy subjects only or patients (note that patient studies may also involve healthy subjects):**

Healthy subjects

**Are you Internal Review Board (IRB) certified? Please note: Failure to have IRB, if applicable will lead to automatic rejection of abstract.**

Yes

**Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.**

Yes

**Was any animal research approved by the relevant IACUC or other animal research panel? NOTE: Any animal studies without IACUC approval will be automatically rejected.**

Not applicable

**Please indicate which methods were used in your research:**

Functional MRI

**For human MRI, what field strength scanner do you use?**

3.0T

**Which processing packages did you use for your study?**

FSL

**Provide references using author date format**

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