Independent Component Analysis on Functional MRI (fMRI) data

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Introduction

Functional Magnetic Resonance Imaging (fMRI) is an MRI method for looking at brain functional connectivity by detecting blood flow changes. Resting-state fMRI (RS-fMRI) is a widely used method for evaluating brain connectivity when a subject is at rest. Since it does not require any task, it has been applied to patients who are not able to do any task as well as health controls.

PURPOSE: To compare functional connectivity using different analysis methods (PCA/ICA and seed-based analysis) on fMRI data.

Theory

$$X X^T = \sum_{i=1}^{m} x^{(i)} x^{(i)T} = U \Sigma V^T V \Sigma U^T = U \Sigma^2 U^T$$

PCA

- PCA is a linear transformation that transforms the data to a new coordinate system such that variance becomes maximized.
- With fMRI data matrix X (each column has zero-mean), we can think that we project the data to the number of components axis.
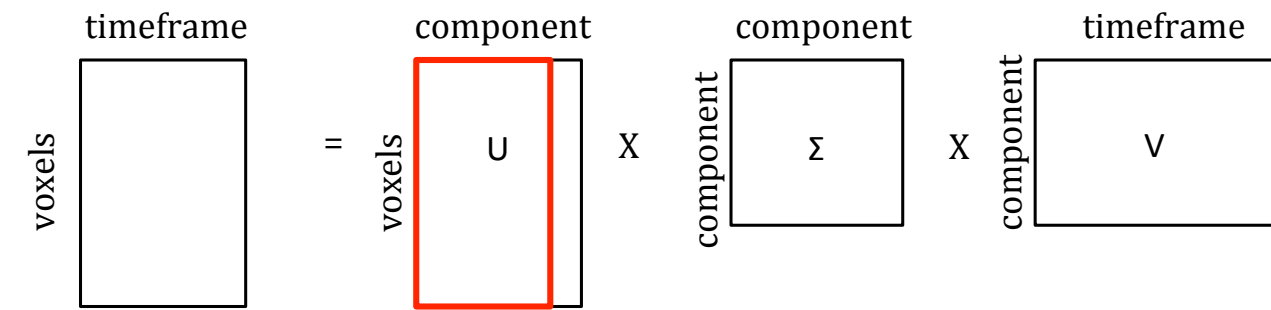
ICA

- ICA separates a signal into a set of spatially independent maps and corresponding time-courses.
- $x = As = W^{-1} s$ where W^{-1} is mixing matrix: W is initialized from random matrix

$$l(W) = \sum_{i=1}^{m} \left(\sum_{i=1}^{n} \log g'(w_i^T x^{(i)}) + \log|W| \right) , \text{ where } g(x) = \frac{1}{1 + e^{-x}}$$

$$W := W + \alpha \left(\begin{bmatrix} 1 - 2g(w_1^T x^{(i)}) \\ 2 - 2g(w_2^T x^{(i)}) \\ \vdots \\ 2 - 2g(w_m^T x^{(i)}) \end{bmatrix} x^{(i)T} + (W^T)^{-1} \right) \text{ , where } \alpha \text{ is a step size.}$$

Seed-based analysis

- Place an ROI in the regions and identify brain regions that are working in synchrony with this seed region by looking for correlations between the signal timeframes in the region and the signal timeframes from the rest of the brain.

Methods

Data acquisition

- 7T Siemens whole-body MRI scanner
- Single-shot gradient-echo EPI sequence
- TE/TR=25/3560ms, 1.5 mm isotropic
- FOV=19.2 cm×19.2 cm, 60 slices
- 180 time points, total scan time=11 min

Pre-processing

- Extract brain area/ Detrending
- Slice timing correction/Motion correction
- Regression of nuisance variables (WM, CSF and global signal)
- Temporal filtering (0.01 Hz)
- Smoothing (Gaussian kernel 3mm)

Results

PCA

- PCA is used to decide the number of components. Using SVD, eigenvalues and variance are calculated in terms of number of components and based on that, proper number of components for ICA is calculated.
- Eigenvalues and variance explained are shown in Figure 1 and 2, respectively.
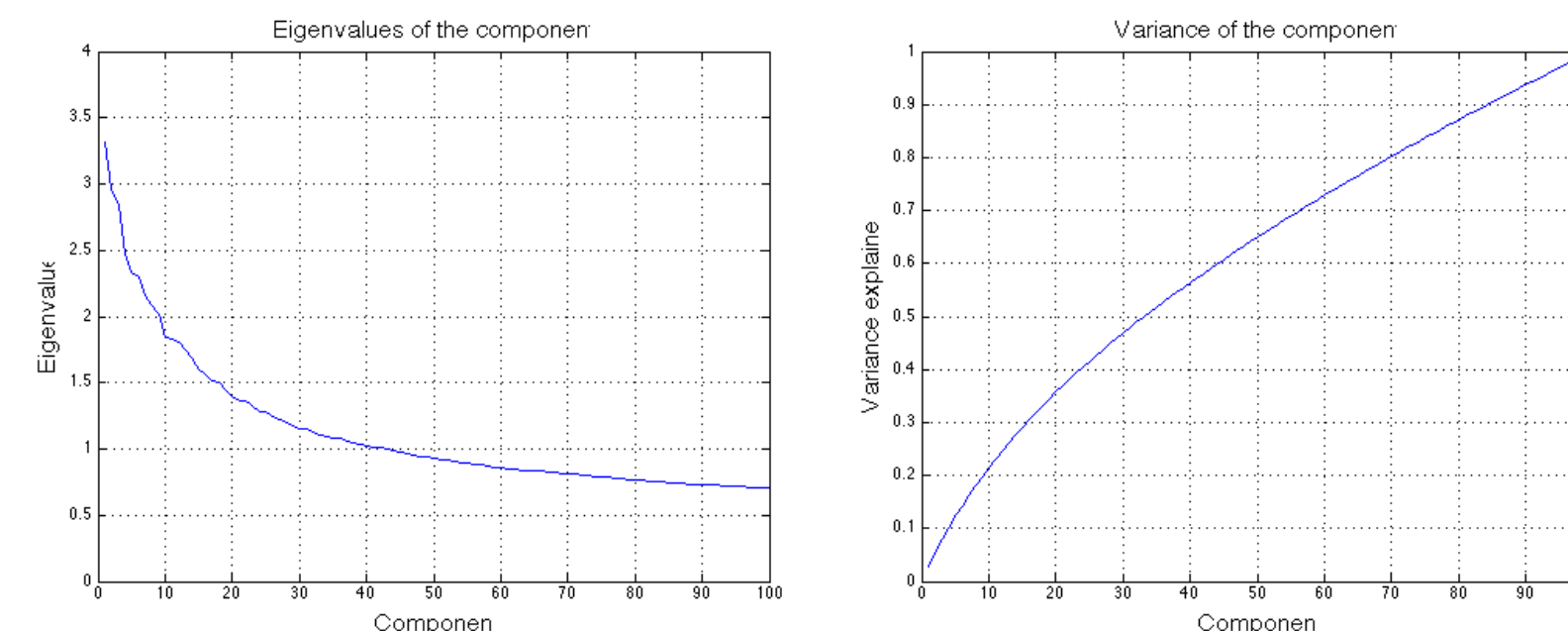
(Left) Figure 1. Eigenvalues in terms of component

(Right) Figure 2. Variance explained in terms of component

ICA vs. Seed-based analysis

- Connectivity maps of Default Mode Network (DMN), Right Executive Control Network (ECN), Primary visual network are shown in Figure 4.
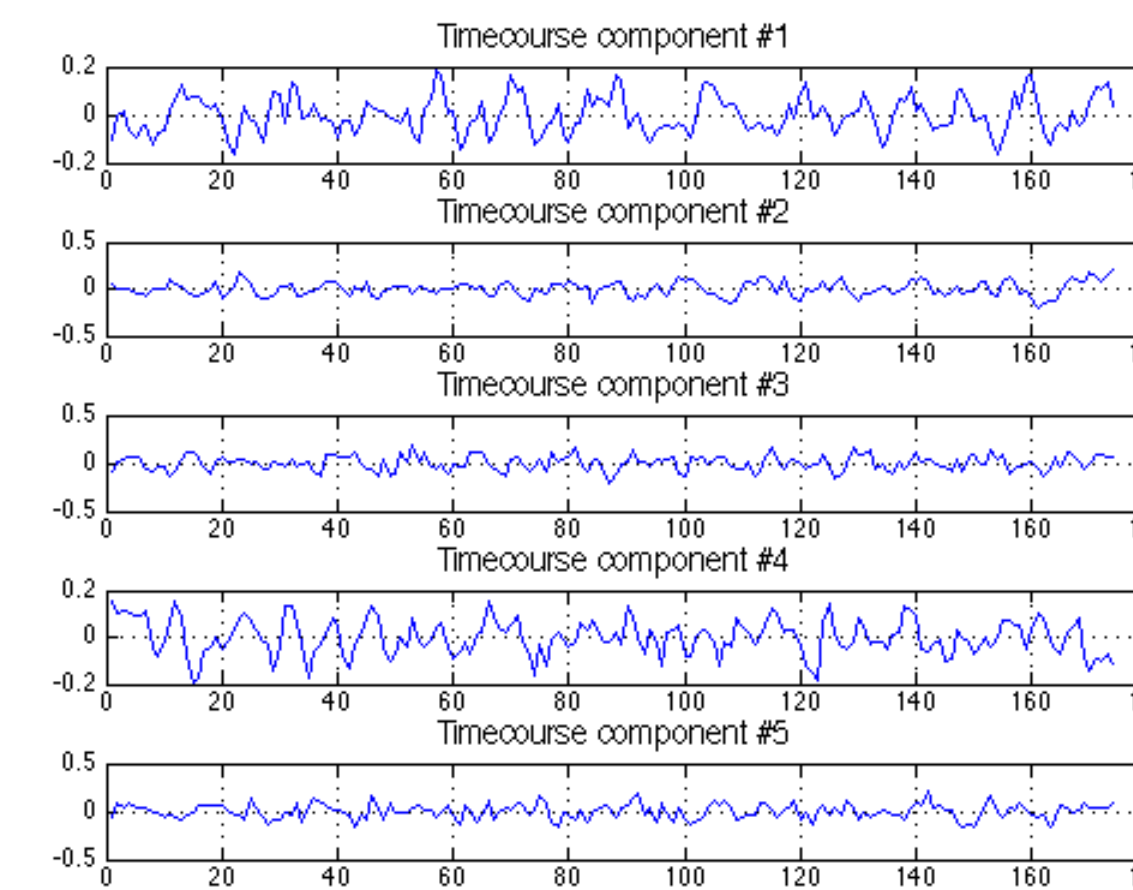- (significance threshold of P < 0.05)

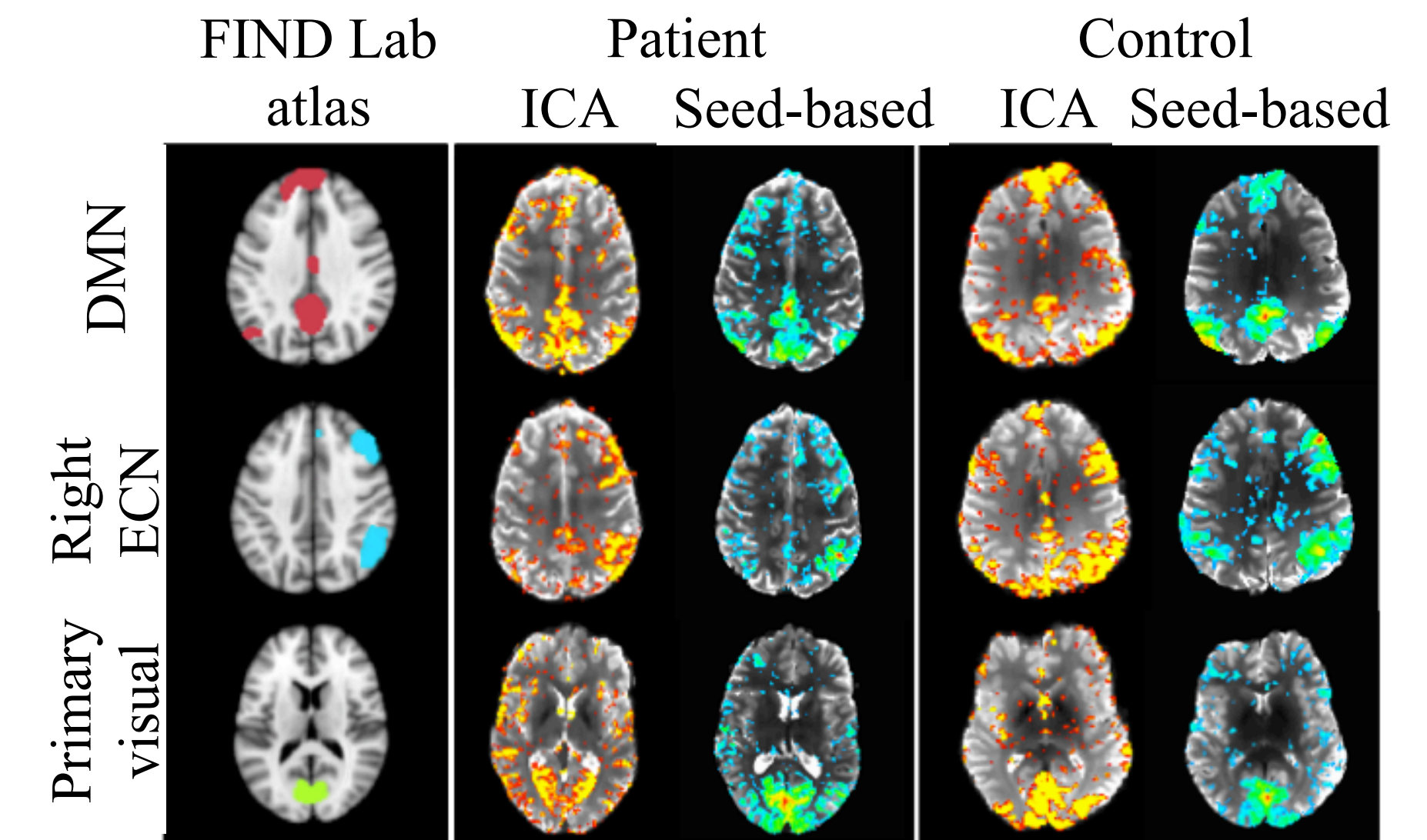Figure 3. Timecourses of first 5 components

Figure 4. Connectivity maps from ICA and seed-based analysis

Discussion

- PCA is used to decide the number of components for ICA.
- Both ICA and seed-based analysis can be used to recognize recognizable resting-state networks.
- In case that we are interested in whole brain networks, PCA can be used to reduce number of components and ICA can be applied to fMRI data.