The Dependence of ICA Decomposition on Dimensionality in Functional Connectivity

E. B. Beall[1], K. A. Koenig[1], and M. J. Lowe[1]

[1]Imaging Institute, Cleveland Clinic, Cleveland, OH, United States

Introduction

Resting state low frequency temporal fluctuations as measured using blood oxygenation level-dependent (BOLD) weighted imaging has been hypothesized to reflect a measure of functional connectivity for the reference region of interest (ROI) [1-3]. The study of endogenous low frequency BOLD fluctuations (LFBF) is promising and has been shown to correlate with white matter pathway integrity[4], but current hypothesis-driven methods restrict the function of interest to that delineated by separate task activation fMRI scans of the same subject. Traditional functional connectivity analyses proceed by acquiring an anatomic volume, one or more sets of BOLD-weighted functional activation data and then resting or continuous task performance BOLD-weighted data of the same subject and using the maximum activation in a known anatomic ROI to identify the location of a primary neuronal substrate of the underlying cognitive function. Independent Component Analysis (ICA) has been used to decompose resting connectivity data and identify what appear to be functionally relevant networks of LFBF[5]. The ICA hypothesis is that the specific patterns of coupling to each source are statistically independent in a chosen dimension and thus separable by higher order statistics (typically in fMRI the independence requirement is taken in the spatial domain, but also in temporal[6] or combined spatio-temporal[7] dimensions). The spatial patterns produced by the ICA decomposition can be compelling, and produce results which appear similar and in many cases superior to traditional analyses (commonly reported in connectivity data are a motor component, visual component, default mode network component, auditory component and so on). Despite promising results, the interpretation of ICA-derived analyses in resting connectivity studies is problematic due to a number of considerations: number of independent sources, preprocessing choices and effects, inability to assess completeness of separability due to lack of ground truth in real data (simulations fail to adequately capture the statistical characteristics of real data), algorithmic differences and convergence /initialization of algorithm[8]. Changes in algorithmic choice, initial conditions, number of components and preprocessing affect the decomposition results (e.g. a re-run of ICA with different initial conditions or a different number of components can result in large changes in a map, yet the map often may still appear to capture the foci of interest, though the component of interest's coupling map may be bifurcated/separated into sub-components or alternatively mixed with other components or noise). In this work, we compare traditional seeded connectivity analyses with ICA using four different algorithms and a range of components to investigate the level of dependence on number of components.

Methods: Data

The following four scans were performed on seven subjects using a bite-bar to reduce head movement. Scan1: anatomic whole-brain T1-weighted inversion recovery turboflash (MPRAGE), 120 axial slices, thickness 1.2mm, Field-of-view (FOV) 256mm×256mm, matrix=256×128. Scans 2-5: whole-brain functional EPI scans: 31-4mm thick axial slices TE/TR/flip = 29ms/2800ms/80°, matrix=128×128, 256mm ×256mm FOV, BW=250KHz, Scan 2-4=160 volumes during which time a block-paradigm complex finger tapping, spatial working memory, and covert word generation functional task was performed, Scan 5=132 volumes during which time the subject rested with eyes closed. Physiologic data was measured in parallel for the resting connectivity scan with a finger pulse plethysmograph and a respiratory bellows around the chest. The functional data was corrected for volumetric motion and spatially 2D hamming filtered. The connectivity data underwent slice-average covariate regression, physiologic noise identification with PESTICA[9] and regression with RETROICOR[10], volumetric motion correction, second-order motion regression and spatial 2D hamming filtering.

Methods: fMRI, Functional Connectivity and ICA

The functional datasets were analyzed using a least-squares fit method[11] to produce student's t-statistic maps. The max activation inside anatomic ROIs drawn on left and right primary motor, broca's area and dorso-lateral prefrontal cortex (DLPFC) were used to center a 9-voxel seed ROI for each of : 1. left motor, 2. right motor, 3. left broca's, and 4. right DLPFC. The 9-voxel ROIs centered on each of these was used with the individual subject's connectivity data to dump a reference timeseries for each, which were then detrended and least-squares fit to a low-pass filtered (<0.08Hz) timeseries of every voxel in the connectivity timeseries to produce a set of four connectivity maps[2]. Finally, the connectivity maps were zscore-normalized[2].

Four ICA algorithms (Infomax[12], JADE ,spatio-temporal SOBI, and Pearson's FastICA[13]) and a range of components from 20 to 30 in increments of 2 were used to decompose each individual dataset. The traditional connectivity maps were spatially correlated with every component and the greatest absolute correlation was taken as ICA connectivity maps related to each of the four functions.

The correlation of each map to the connectivity map was used as the "null" distribution of the random spatial correlations inherent in the data. The peak absolute correlation (since ICA produces arbitrary polarity, the polarity was normalized by the sign of the correlation with the connectivity map to be positive) for each decomposition was stored and compared with this "null" distribution to assess the specificity of the map. Specificity of the ICA decomposition is taken to be the overlap between the normalized Null and Alternate hypothesis distributions, or alpha. This is also examined versus number of components, and can be explored for algorithmic dependencies. The hypothesis is that if ICA decomposition is insensitive to number of components used, then the specificity will remain the same across a range of dimensionalities chosen.

Results

Figure 1 shows the "null" distributions of ICA decompositions in black for each activation-seeded connectivity map along with the test distribution in red. The overlap defines the power of the separation, in this case the specificity of the ICA maps. In Figure 2, the specificity as defined above is shown for a range of
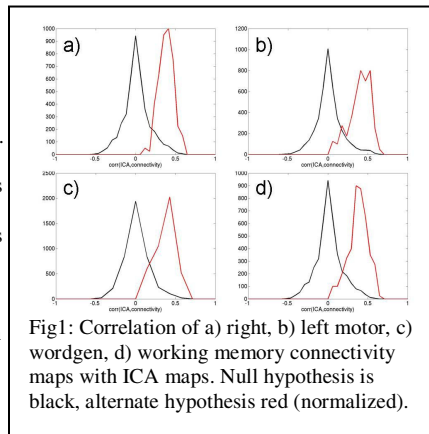

Fig1: Correlation of a) right, b) left motor, c) wordgen, d) working memory connectivity maps with ICA maps. Null hypothesis is black, alternate hypothesis red (normalized).
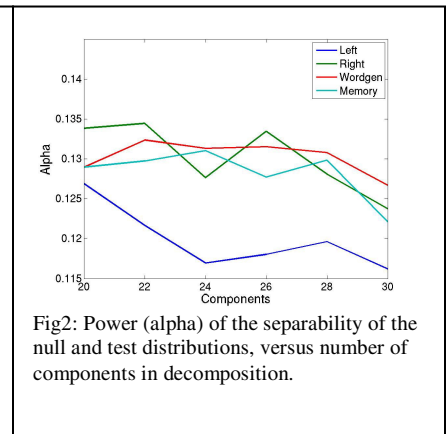

Fig2: Power (alpha) of the separability of the null and test distributions, versus number of components in decomposition.

dimensionalities for each of the four functionally-defined connectivity maps, averaged across the four algorithms. There were differences between the four algorithms, but on the whole, all achieved good specificity and so were averaged together to get a better picture of the dependence on dimensionality.

Discussion and Conclusion

Based on the moderate decline in separability as number of components increase, we conclude there is likely an effect on the decomposition, and that methods to optimize dimensionality should continue to be explored, such as in a manner similar to the consistency analysis of ICASSO[8]. Care should be taken in analyses being performed with ICA to ensure optimal dimensionality is used appropriately (i.e. subject specific dimensionality may be necessary) and in interpreting the results.

References

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