

Reproducible differentiation of individual subjects with minimal acquisition time via resting state fMRI

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TARGET AUDIENCE

Clinicians and researchers seeking subject-level analysis methodology for resting state fMRI data.

PURPOSE

Resting state fMRI (rs-fMRI) has received much recent attention for characterization of brain function as a complement to task-based fMRI¹⁻³. Although group level reproducibility of rs-fMRI has been well documented, reproducibility at the subject level is most desired for clinical applications and is less well characterized. We examined reproducibility of rs-fMRI at the subject level and define an analysis parameter set that allows maximal differentiation between individuals.

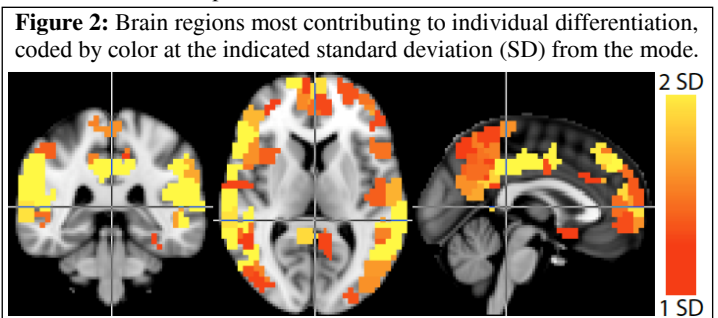
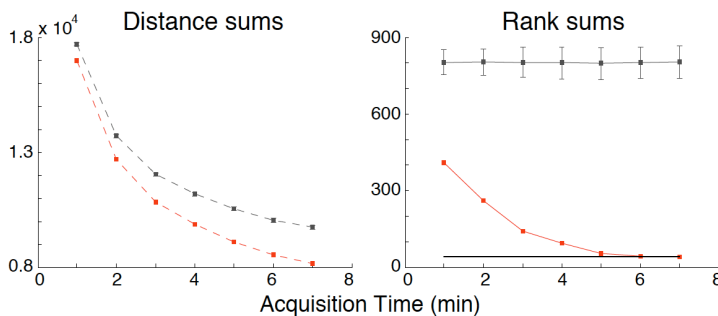
METHODS

A publicly available test-retest dataset¹ was analyzed that consists of 21 subjects who underwent two rs-fMRI scans, acquired at 3T, of 7 minutes each, separated by a break (one scan was excluded due to excessive high frequency motion). Analysis was completed in MATLAB (Mathworks, Natick, MA), using custom scripts and SPM8 (Wellcome Trust, UK). Preprocessing included slice-timing correction, rigid body motion correction, nuisance regression, and normalization to the MNI152 T1 anatomic template (2 mm resolution). Two recently published whole-brain parcellation schemes^{2,3} were used to extract region of interest (ROI) time-courses, either via taking the eigenvariate or the mean time-series from each ROI. The number of ROIs was varied from 126 to 1024 regions per brain. The amount of scan time analyzed was varied between 1 and 7 minutes. For each data set, an adjacency matrix of pair-wise correlations of ROI time series (i.e. edges) was constructed. For each pair of adjacency matrices a distance was calculated that was defined as the sum of the squared difference of corresponding correlation coefficients. To determine which pairs of test-retest scans were associated, for each adjacency matrix (one per scan) the distance between it and each other adjacency matrix was ranked, with lower ranks corresponding to more similar adjacency matrices. The sum of ranks across the group test-retest pairs was calculated and compared against a distribution of rank sums of 1000 random pairings of scans, yielding assessment of dissimilarity at the P=0.001 level relative to random label scrambling. Additionally, a similar rank sum was calculated for individual edges. To determine the brain regions most contributing to individual differentiation, the 5% of edges with the lowest rank sums was determined, and ROIs with the highest number of these edges were taken.

RESULTS

With only 1 minute of scan time, reliable partitioning of the data set into test-retest pairs could be completed (Figure 1), relative to a distribution of random pairings, using the rank sum calculation. By 6-7 minutes of acquisition time, the lowest possible rank sum was obtained for the data set, with best performance using the parcellation scheme of Craddock, et al.², with a maximal number of ROIs, and eigenvariate timecourse extraction. Brain regions contributing the most to individual differentiability (Figure 2) lie in cortical gray matter, particularly near the bilateral supramarginal gyri, prefrontal cortex, precuneus, and cingulate gyrus, but not in basal ganglia, cerebellum, V1, M1 or S1.

Figure 1: Sum of test-retest (red) adjacency matrix distances (left) and ranks (right) across the group versus total acquisition time compared to a distribution of 1000 random possible pairings of scans (grey), using the Craddock² parcellation with 875 nodes (1024 clustering target) and eigenvariate timecourse extraction. Black line at rank sum of 40 indicates the absolute minimum possible.



DISCUSSION

Minimal acquisition time (1 minute) was sufficient to pair individual subject test-retest data using the cross-correlation based adjacency matrix, suggesting individual subject rs-fMRI data is highly reproducible in this data set. While the distance between test-retest pairs continues to decrease with more acquisition time, the rank-sum metric saturates to its minimum by 6-7 minutes, suggesting that the information content of individual rs-fMRI scans is maximal by 7 minutes. The nodes most contributing to this individual characterization lie in brain regions typically identified with higher cortical processing, which makes neurobiological sense for the question of determinants of individual subject characteristics.

CONCLUSION

For individual subject rs-fMRI data, 6-7 minutes of acquisition time is sufficient to capture the maximal information content, given the strong reproducibility between test and retest of the single scan correlation-based whole-brain adjacency matrix.

REFERENCES

1. Landman, et al. (2011) Neuroimage. 54(4):2854. 2. Craddock, et al. (2012) Hum Brain Mapp. 33(8):1914. 3. Zalesky, et al. (2010) Neuroimage. 50(3):970.

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