Abstract

Resting-state functional MRI (fMRI) provides a crucial insight into brain organization, by offering a mean to measure the functional connectivity between brain regions. A popular measure, the effective functional connectivity, is derived from the precision matrix obtained by inverting the correlations between brain regions fMRI signals. This approach has been widely adopted to build brain connectomes for large populations. For small populations and single fMRI scans, however, the significant amount of noise in the fMRI scans reduces the quality of the precision matrices, and the non-invertibility of the correlation matrices calls for more sophisticated precision estimators. These issues are especially dramatic at full brain resolution. In this work, we investigate several approaches to improve full resolution precision matrices derived from single fMRI scans. First, we compare three approaches for the computation of the correlation matrix. Then, we investigate two regularized inversions, in combination with a correlation shrinkage and two spatial smoothing strategies. During these experiments, the quality of precision matrices obtained for random fMRI half scans was measured by their generalization: their fit to the unseen time points. Our experiments, using ten high resolutions scans of the Human Connectome Project, indicate that correlation shrinkage improves empirical correlation matrices. Several shrinkage methods exist. Linear shrinkage is parameter free, easy to implement, and doesn't require noise estimation [4].

Correlation Shrinkage

Shrinkage improves empirical correlation matrices. Several shrinkage methods exist. Linear shrinkage is parameter free, easy to implement, and doesn't require noise estimation [4].

Oracle Approximating Shrinkage (OAS) [4,5,6,7]

\[
\lambda = \frac{(1 - \lambda) \Sigma + \lambda}{(1 - \frac{1}{2} \text{Trace}(\Sigma^2) + \text{Trace}(\Sigma))} \quad (1)
\]

when the signal is a \( n \times t \) matrix

Tikhonov regularization [8]

\[
\max \left[ \log \det Q - \text{Trace}(Q \Sigma) - \rho \text{Trace}(Q) \right]
\]

Riccati regularization [1,8]

\[
\max \left[ \log \det Q - \text{Trace}(Q \Sigma) - \frac{\rho^2}{2} \text{Trace}(Q^2) \right]
\]

Spatial Smoothing

22 regions of the HCP parcellation [10] used to define a Laplacian matrix \( L \)

L used to smooth the signal before the regularized inversion

L included in the Riccati penalty [1]

Smooth Riccati Regularization

\[
\max \left[ \log \det Q - \text{Trace}(Q \Sigma) - \frac{\rho^2}{2} \text{Trace} \left( \left( L - f I \right) (L - I) \right) \right]
\]

Precision Generalizability

Generalizability measured by the average NLL for all the types of precisions. [1] without Oracle Approximating Shrinkage (OAS) of the signal [2] after OAS. Smooth Riccati precisions are obtained by solving (5), while “Riccati (smooth)” indicates the precision obtained by performing a Riccati regularized inversion of the signal smoothed by the Laplacian (spatial downsampling to 1188 nodes).


Future work

- test other precision smoothing strategies
- use the smooth Riccati precision matrices to define effective networks
- extract features from these effective networks, for clinical applications (diagnosis/prognosis)

References