ABSTRACT

Leveraging population information in brain connectivity studies via Bayesian ICA

Functional connectivity (FC)—the temporal synchrony between brain networks—is a widely popular measure of brain functional organization. Typically, FC is estimated using fixed, hard parcellations, which fail to capture the intrinsic overlapping and individualized nature of functional brain topography. Independent component analysis (ICA) offers a more flexible approach, modeling overlapping spatial topography while estimating FC. However, traditional FC estimation via ICA can be sub-optimal due to ad-hoc methods and the need for temporal dimension reduction. Bayesian ICA can address these limitations, avoiding dimension reduction, yielding more accurate estimates, and facilitating inference via posterior distributions. We have developed a computationally feasible single-subject Bayesian ICA model that leverages population information via priors on both the spatial component maps and their temporal correlation (i.e., their FC). A novel informative prior for correlation matrices integrates population information on FC into the model. Approximate Bayesian estimation and inference are performed via a computationally efficient variational Bayes algorithm. Realistic simulation studies and analyses of data from the Human Connectome Project demonstrate that this algorithm produces more accurate measures of brain function in individuals and facilitates inference on both spatial topography and FC. Because it is designed for single-subject analysis, this Bayesian ICA framework has potential clinical applicability. Finally, we discuss several scientific applications and areas of future work.