Evaluation of the possibility of using resting state functional brain networks as potential biomarker using LASSO

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Background: Recently, functional human brain networks have received an increasing attention as potential biomarkers for characterization of individuals and brain diseases. Since human brain networks contain a large number of variables, dimensional reduction and feature extraction are essential. For this purpose, we used least absolute shrinkage and selection operator (LASSO) approach to functional brain networks based on resting-state fMRI (rsfMRI). In previous study, Ingalhalikar et al. [1] revealed that male and female brain are known to show different structural network patterns. Such difference presumably leads to functional differences between genders. The purpose of this study is to examine the reliability of characterizing functional human brain networks as features and their availability as a method for gender classification.

Methods: We applied the proposed method to rsfMRI data from the Human Connectome Project (HCP) database [2], which was processed by group independent component analysis (ICA) to separate brain activity signals to 15, 25, 50, 100, 200 and 300 independent component nodes, respectively. We calculated six functional connectivity matrices among each group independent components (ICs) using Pearson correlation and converted them by Fisher r-to-z transformation. We used the functional connectivity matrices as input of LASSO, with optimized regularization coefficients “$\lambda$” for dimensional reduction to find the most relevant brain connection according to gender. We also compared classification accuracy among the IC numbers.

Results: The gender classification with functional connectivity of 50 independent components showed the highest classification accuracy of 99.88%. Most of the six gender classification with each functional ICs shows accuracy over 90% except that of 15 ICs. There was significant connection difference between genders in the cingulate-temporal-insula-occipital network, bilateral prefrontal-putamen, several cerebellar components and thalamo-cerebellar independent components.

Conclusions: All these results suggest the possibility of using human brain networks as potential biomarker for characterization of the human brain with rsfMRI. However, the accuracy was evaluated only in terms of optimized $\lambda$. The process of getting automatically optimized $\lambda$ values still needs further evaluation.

Reference: