Imaging genetic strategies for predicting the quality of sleep using depression-specific biomarkers

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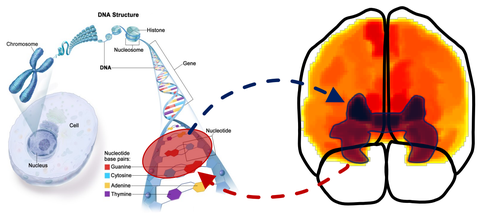
Overview

Background: Sleep is an essential phenomenon for maintaining good health and wellbeing [1]. Some studies reported that genetic and imaging biomarkers that depression is associated with sleep disorder [2]–[4].

Imaging genetics: Many studies adopted imaging genetics methodology to find associations between imaging and genetic biomarkers. In this study, we examine the imaging genetics association in depression and extract biomarkers for predicting the quality of sleep.



Material and methods

Data acquisition and pre-processing:

A total of 291 subjects of neuroimaging and genotyping data were obtained from the Human Connectome Project (HCP) database [5]. Functional and structural connectivity were used as edge measurements for functional and structural connectivity, respectively. We then computed the degree centrality of each node based on functional and structural connectivity. For the genotype data, we controlled the quality of genotype data, and then conducted a genome-wide association analysis to select candidate SNPs related to depression ($p < 0.0005$).

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Joint-connectivity-based sparse CCA

Imaging genetics model: The joint-connectivity-based sparse canonical correlation analysis (JCB-SCCA) was applied on preprocessed features (Figure 1). JCB-SCCA has an advantage for incorporating connectivity information and can handle multi-modal neuroimaging datasets.

Prior biological knowledge: The average connectivity matrix computed from the HCP dataset and linkage disequilibrium obtained from 1,000 genome project were used as the prior connectivity information of the algorithm. The parameters of the algorithm were tuned jointly by nested five-fold cross-validation.

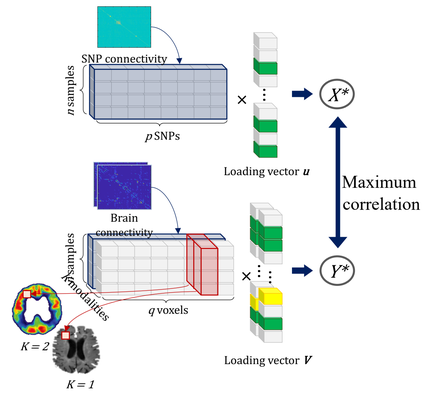

Figure 1. JCB-SCCA

Experiments and Results

Prediction task: We built a prediction model for the Pittsburgh sleep quality index (PSQI) using the identified biomarkers. We built the prediction models based on ridge regression. The algorithm was compared with five different models using different sets of the biomarkers: 1) those from SCCA, 2) fMRI biomarker alone, 3) dMRI biomarker alone, 4) SNPs alone, and 5) all fMRI, dMRI, and SNPs together. The performance of a linear regression model was assessed with root-mean-squared error (RMSE) and the correlation coefficient between predicted and actual PSQI scores

Result: The association between dMRI and SNPs was more robust than the association between fMRI and SNPs in both algorithms (Table 1, and Figure 2). Additionally, we found that our model showed improved prediction performance compared with the other models(Table 2).

Methods		Training results					Mean ± std
JCB-SCCA	Average	0.4460	0.4760	0.4637	0.4346	0.4339	0.4508 ± 0.0185
	fMRI-SNPs	0.1001	0.1972	0.1708	0.1216	0.1214	0.1422 ± 0.0402
	dMRI-SNPs	0.7919	0.7548	0.7567	0.7476	0.7464	0.7594 ± 0.0186
SCCA	Average	0.4144	0.4227	0.4277	0.4339	0.4017	0.4200 ± 0.0124
	fMRI-SNPs	0.1098	0.0944	0.0991	0.1164	0.1467	0.1132 ± 0.0206
	dMRI-SNPs	0.7190	0.7509	0.7562	0.7513	0.6568	0.7268 ± 0.0418
Methods		**Test results**					**Mean ± std**
JCB-SCCA	Average	0.3682	0.4182	0.4613	0.4022	0.5095	0.4318 ± 0.0548
	fMRI-SNPs	0.1437	0.0543	0.1671	0.0206	0.1515	0.1074 ± 0.0655
	dMRI-SNPs	0.5927	0.782	0.7555	0.7837	0.8676	0.7563 ± 0.1007
SCCA	Average	0.2702	0.4587	0.3692	0.3879	0.4209	0.3813 ± 0.0708
	fMRI-SNPs	0.0249	0.1696	0.0605	0.1237	0.0234	0.0804 ± 0.0643
	dMRI-SNPs	0.5154	0.7478	0.6778	0.6522	0.8183	0.6822 ± 0.1135

Table 1. Nested five-fold cross-validation results

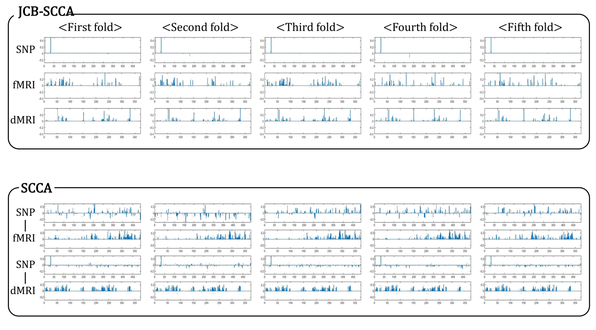

Figure 2. Estimated loading vectors

Methods	RMSE	r
JCB-SCCA	2.8921	0.2882
SCCA	3.0576	0.2231
fMRI alone	3.6410	-0.204
dMRI alone	3.4193	0.0335
SNPs alone	3.7330	0.0705
fMRI + dMRI + SNP	3.0724	0.1798

Table 2. Prediction performance

References

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Acknowledgements: This work was supported in part by the National Institutes of Health [R01 EB022574] and National Science Foundation [IIS 1837964].