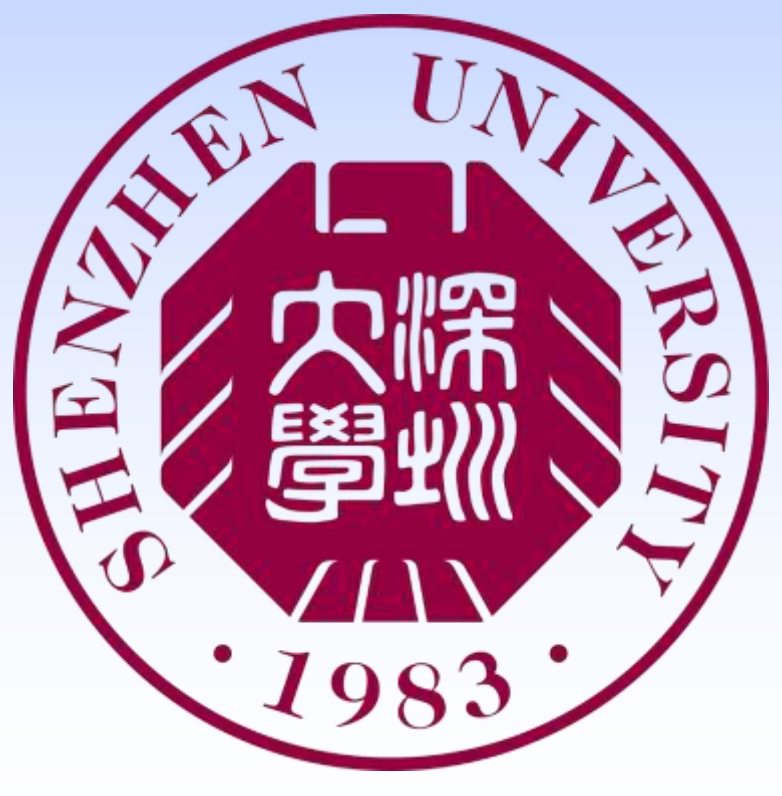


Connectome-based predictive modeling of individual anxiety



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Introduction

Anxiety and anxiety-related illnesses are highly prevalent in human society. Being able to identify neurobiological markers signaling high trait anxiety could aid the assessment of individuals with high risk for mental illness. Previous neuroimaging studies collapsed group data to decode anxiety in the brain (Dubois and Adolphs, 2016), but little is known with respect to predicting individual anxiety levels using neural models.

Methods

Here, we applied connectome-based predictive modeling (CPM; Finn et al., 2015; Fig. 1) to whole-brain resting-state functional connectivity (rsFC) data to predict the degree of anxiety in 76 healthy participants. Using a computational “lesion” method in CPM, we then examined the weights of the identified main brain areas as well as their connectivity. We also used a similar neural modeling to explore distinct brain networks between anxiety and depression (see *Preprint* for details).

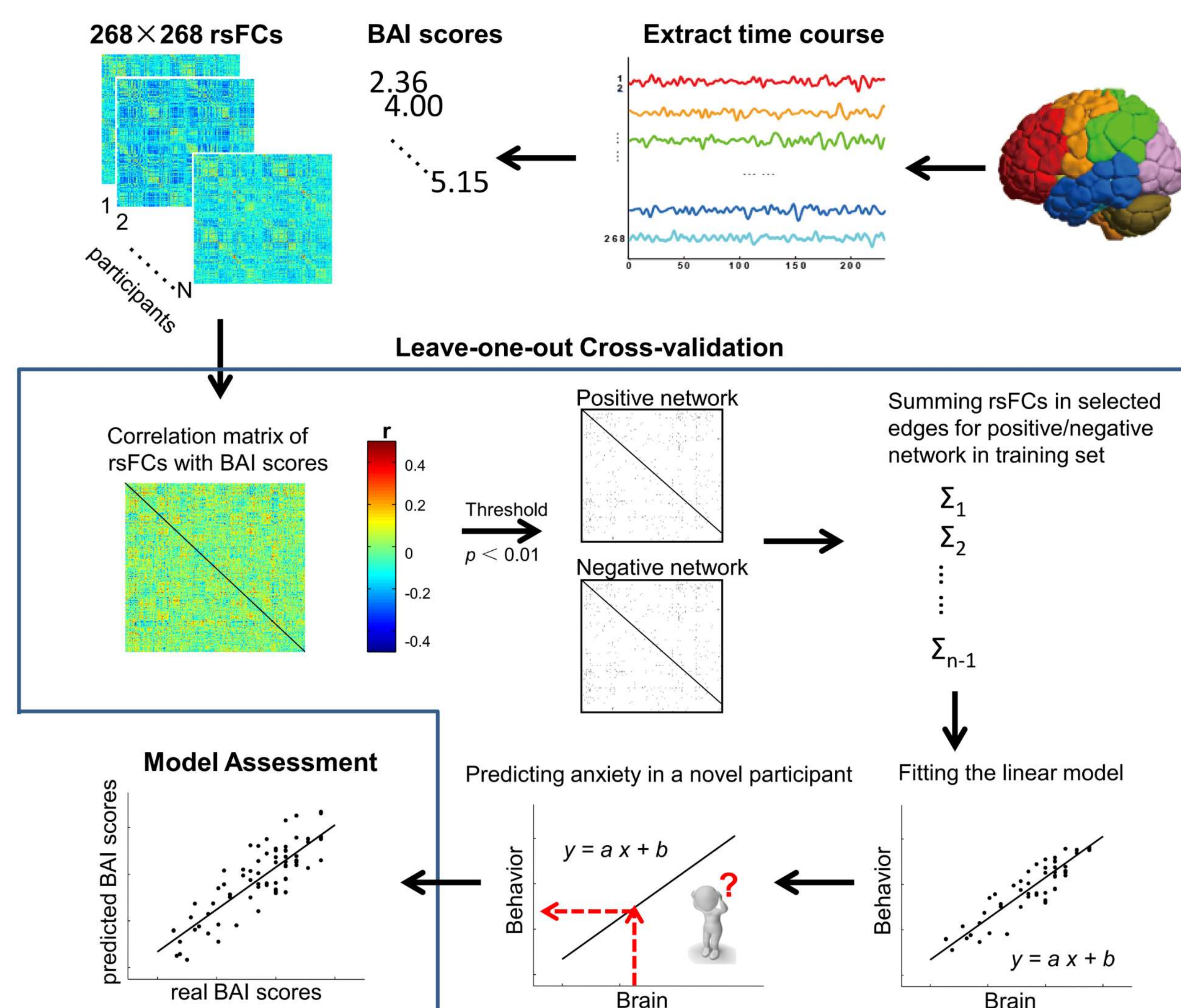


Fig. 1 The schematic flow of CPM

Results

Results showed that the CPM could predict individual anxiety from whole-brain rsFC (Fig. 2bc), especially from limbic areas-whole brain and prefrontal cortex-whole brain (Fig. 2efg). The top 10 highly connected brain nodes were shown in Fig. 3.

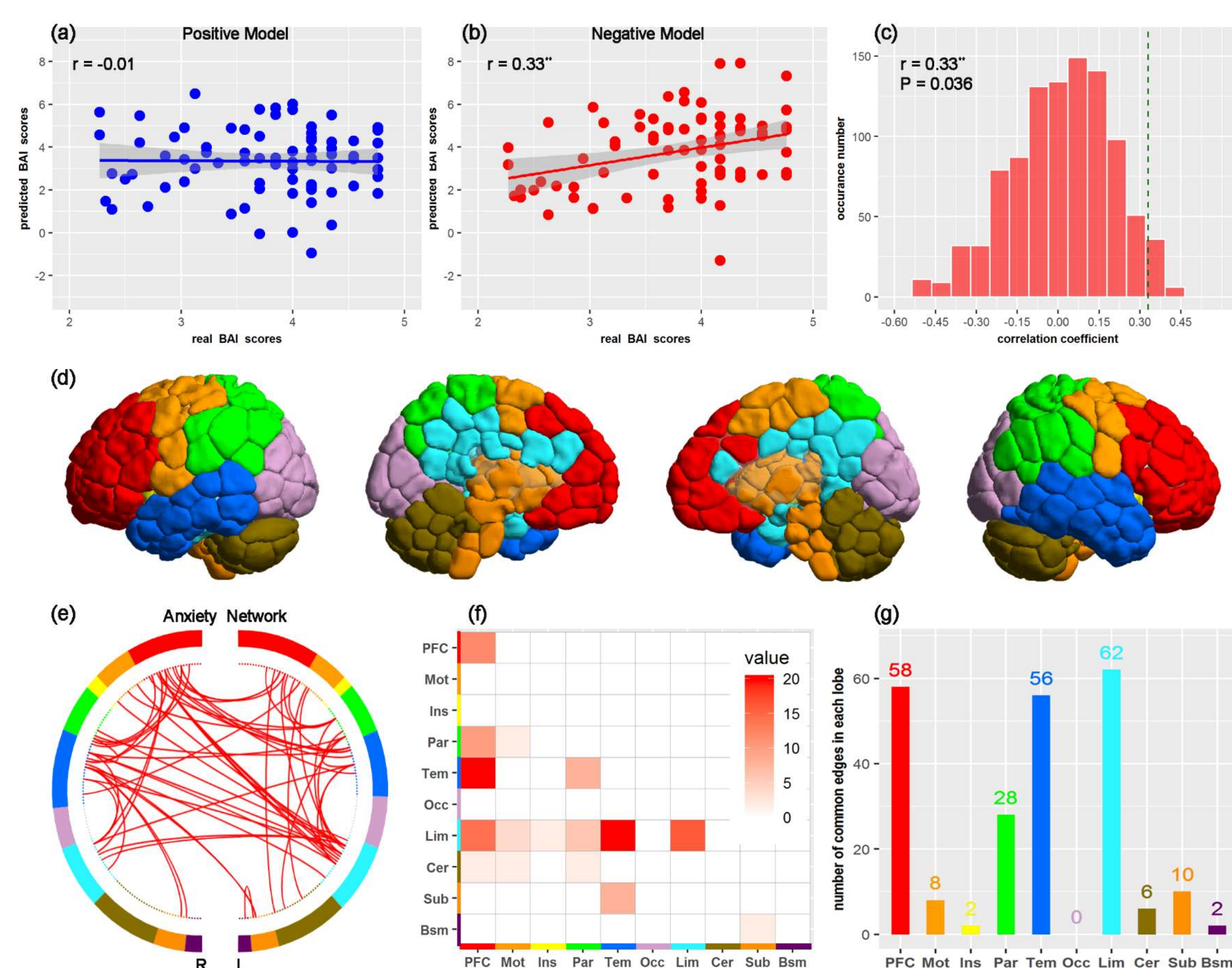


Fig. 2 CPM results

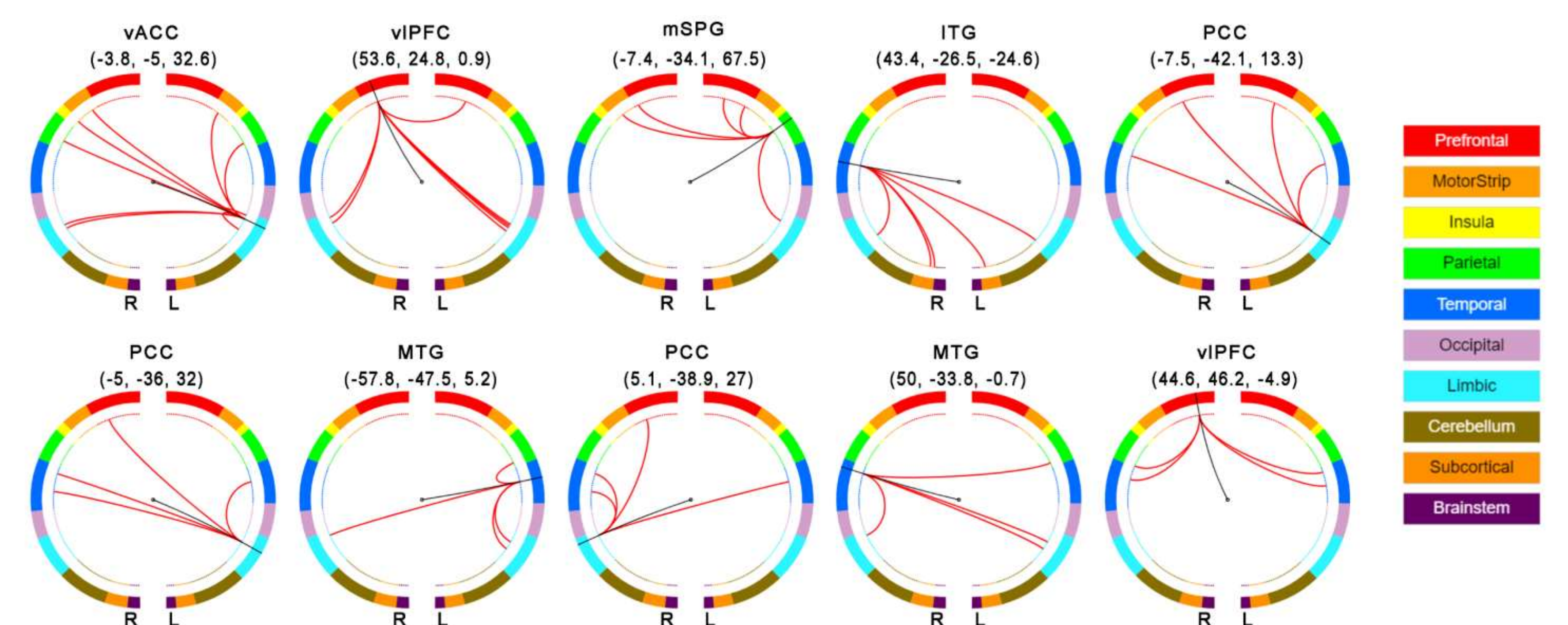


Fig. 3 Connectivity patterns of the top 10 most highly connected brain nodes

The prediction power of the model significantly decreased from (simulated) lesions of limbic areas, lesions of the connectivity within the limbic system, and lesions of the connectivity between limbic regions and the prefrontal cortex (Fig. 4).

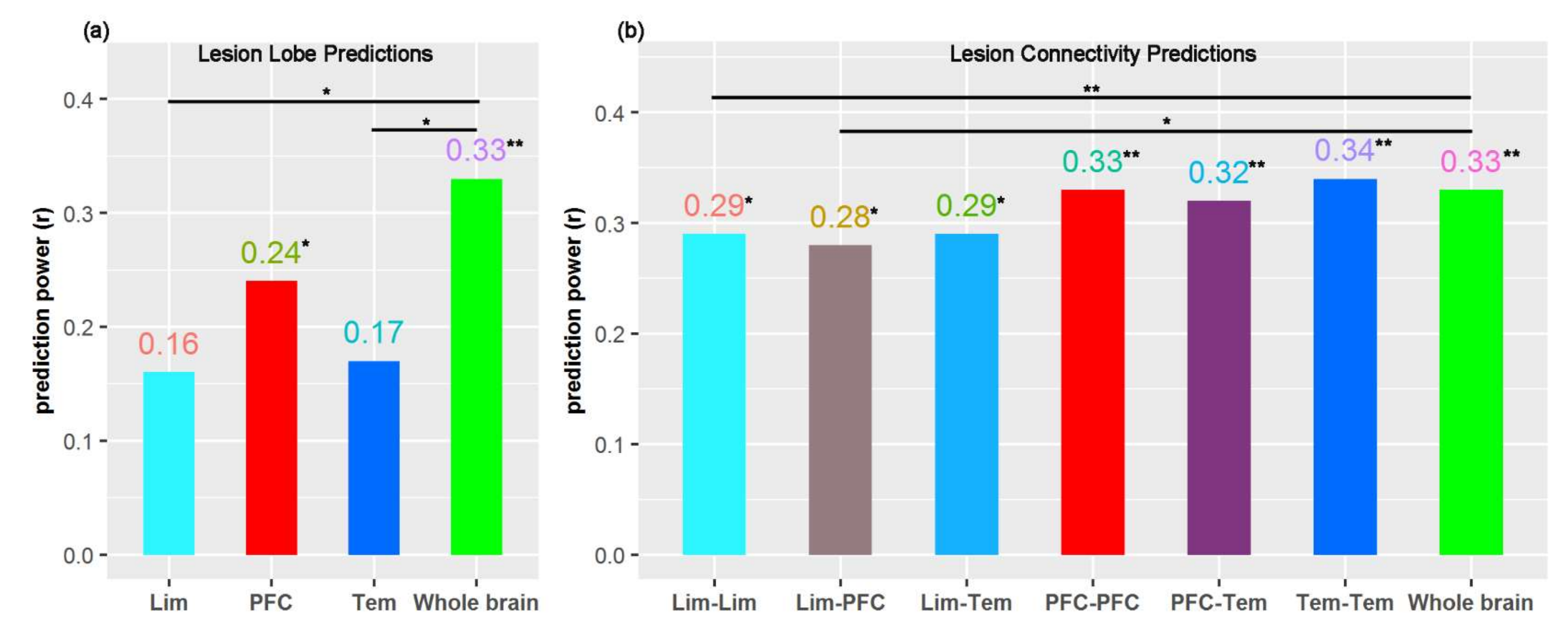


Fig. 4 Lesion predictions

After controlling for nuisance variables in edge selection and final correlation, and for scrubbing in preprocessing, the predictive models remained significant.

	Control at edge selection	Control at final correlation
Head motion	$r = 0.31, p = 0.006$	$r = 0.33, p = 0.004$
Age	$r = 0.24, p = 0.035$	$r = 0.30, p = 0.008$
Gender	$r = 0.22, p = 0.051$	$r = 0.32, p = 0.005$
Scrubbing	$r = 0.28, p = 0.015$	

Conclusions

These findings highlight the important role of the limbic system and the prefrontal cortex in the prediction of anxiety. Our work provides evidence for the usefulness of connectome-based modeling of rsFC in predicting individual personality differences and indicates its potential for identifying personality structures at risk of developing psychopathology.

Preprint: The preprint is available at

<https://www.biorxiv.org/content/10.1101/2020.01.30.926980v2>

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