Abnormal Salience Network Segregation in Adolescents and Young Adults with Prodromal Psychosis Symptoms

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Background
Coordination between the salience brain network and other networks is known to be altered in schizophrenia patients, but little is known for the psychosis prodrome (Bolton et al., 2020). Understanding neurobiological similarities between individuals who exhibit prodromal symptoms can help improve early identification and intervention strategies.

In this study, we aimed to:
1. Identify neurobiologically similar subject groups by integrating salience network functional connectivity (FC) and psychosis prodrome symptoms and different brain networks.
2. Identify subject segregation patterns in the subject groups.

Note: segregation is the extent to which different brain networks are responsible for distinct, non-overlapping cognitive processes. We measured it as the normalized difference in FC between two networks.

We used the Philadelphia Neurodevelopmental Cohort (PNC) to address our study aims.

Methods
Our sample (N=1158) included PNC subjects ages 12-21 with fMRI and self-reported psychopathology data (Satterthwaite et al., 2016). The middle proband (MP) group included subjects ages 12-17, and the adult proband (AP) group included subjects ages 18-21.

We preprocessed the neuroimaging data in the CONN toolbox using the fMR minimal preprocessing pipeline (Nieto-Castanon, 2020). After excluding subjects with a valid scan percentage of 80% or less, 792 subjects remained in the final analysis.

We first constructed a two-layer network (with a symptom layer and neuroimaging layer) for each subject group using distance measures between each pair of subjects. Distance measures were based on resting state FC within the salience network for the neuroimaging layer and responses to prodromal questions for the symptom layer.

We then fit a multiplex stochastic block model (SBM) for each network to identify subject clusters based on the computed similarity distances. Edge weights between vertices (subjects) were modeled by a gaussian probability density function (PDF) for each layer. We selected the number of blocks for each model via the stochastic block model (SBM) for each network to identify subject clustering.

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Findings
Across multiple age groups, the block with the highest mean response value to prodromal questions also had the greatest segregation between the salience network and each of the default mode, frontoparietal, and dorsal attention networks. This suggests a possible link between abnormal segregation involving the salience network and prodromal symptoms, although further investigation is required.

References

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