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
2. Identify **symptom profiles** and brain network **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.

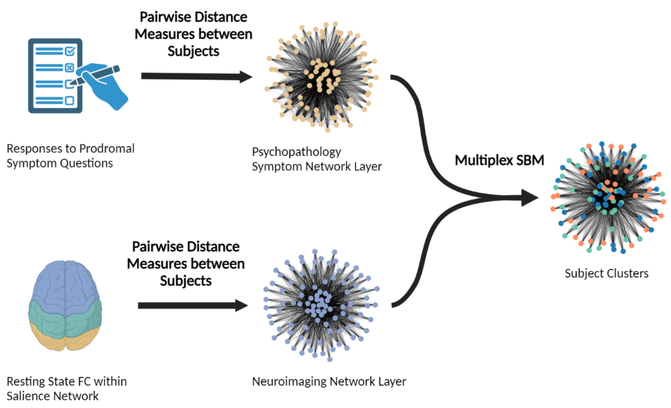
Methods

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 **fMRI 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.

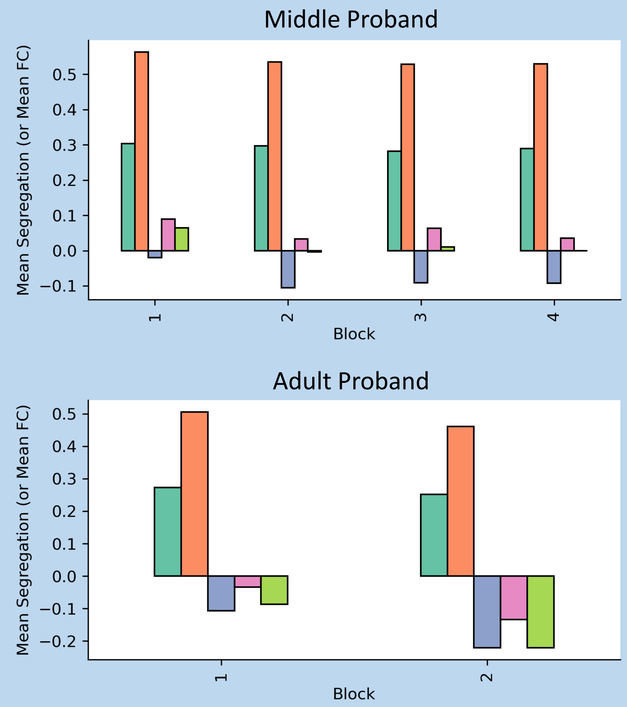
We first constructed a **two-layer network** (with a symptom layer and neuroimaging layer) for each subject group using **distance measures** between each **pair of subjects**. Distance measures were based on **resting state FC** within the salience network for the neuroimaging layer and **responses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



Note: networks in diagram are NOT fully representative of networks used in the analysis.

Mean Segregation Involving the Salience Network within Each Block



- Mean FC Within Network
- Segregation Between All Other Regions
- Segregation Between Default Network
- Segregation Between FrontoParietal Network
- Segregation Between DorsalAttn Network

Positive Segregation:
Within-Network FC > Out-of-Network FC

Negative Segregation:
Within-Network FC < Out-of-Network FC

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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PDF for Connections Between Subjects