Genomic connectivity networks based on the BrainSpan atlas of the developing human brain

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Summary
We studied the connectivity between brain regions across development based on the similarity of their gene expression profiles. Analyzing the development of connectivity networks based on the dynamics of gene expression provides a new insight on how the genetic signature of different brain regions instructs connections to other regions. We have used graph theoretic measurements to characterize the topological properties of the constructed Genomic Connectivity Networks (GCNs). These topological measures were compared between networks constructed based on the transcriptome-wide expression versus a set of autism-associated genes.

Genomic Connectivity Networks (GCNs)
Expression Matrix of Donor, Correlation Matrix of Donor, Network at Topological Cost 7%

Topological Properties of GCNs

Unique Brain Connectivity Based on Autism Genes

Conclusions
We presented the first analysis of the topological properties among brain regions based on their underlying gene expression profiles, genomic connectivity networks, across development.

Our work represents a new complimentary approach to integrate the functional genomics underlying brain regions with anatomical level brain networks.

References