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

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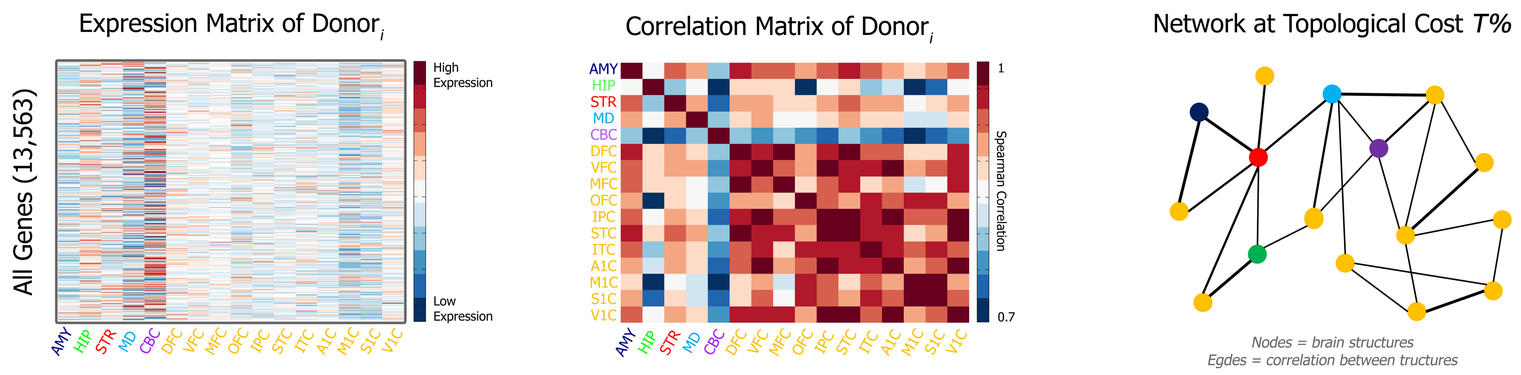
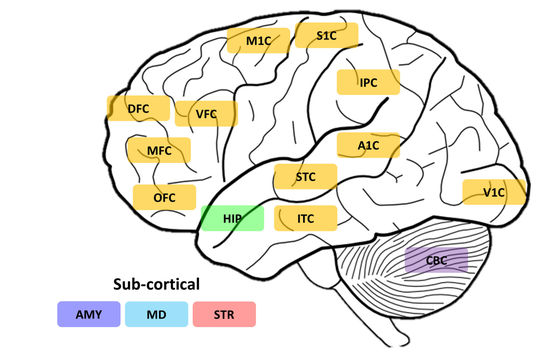
Summary

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.

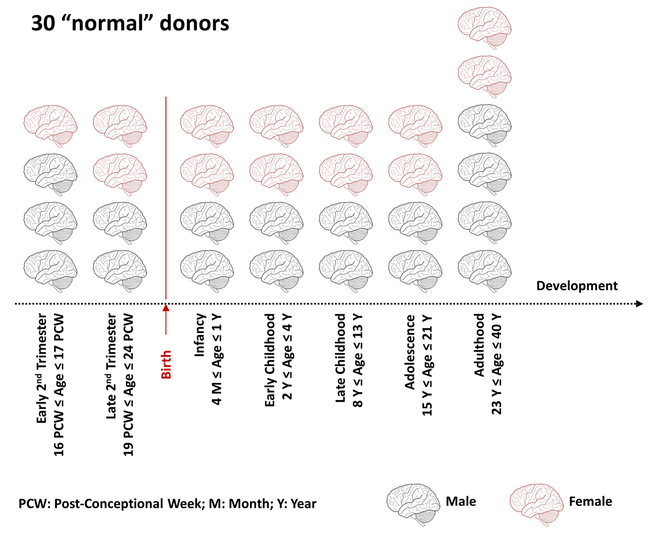
Genomic Connectivity Networks (GCNs)



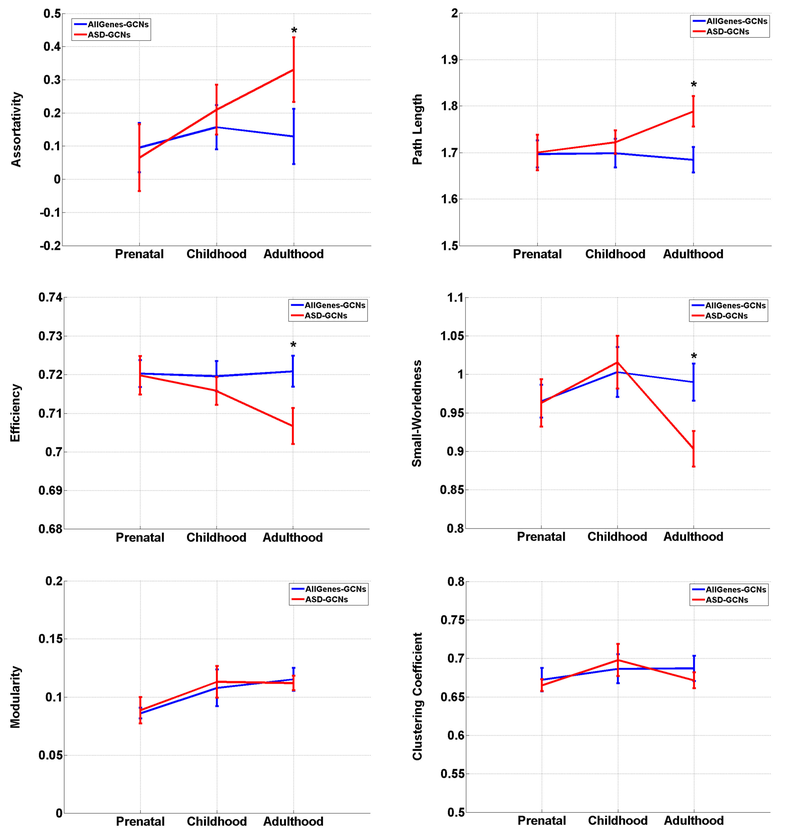
BrainSpan Transcriptional Atlas



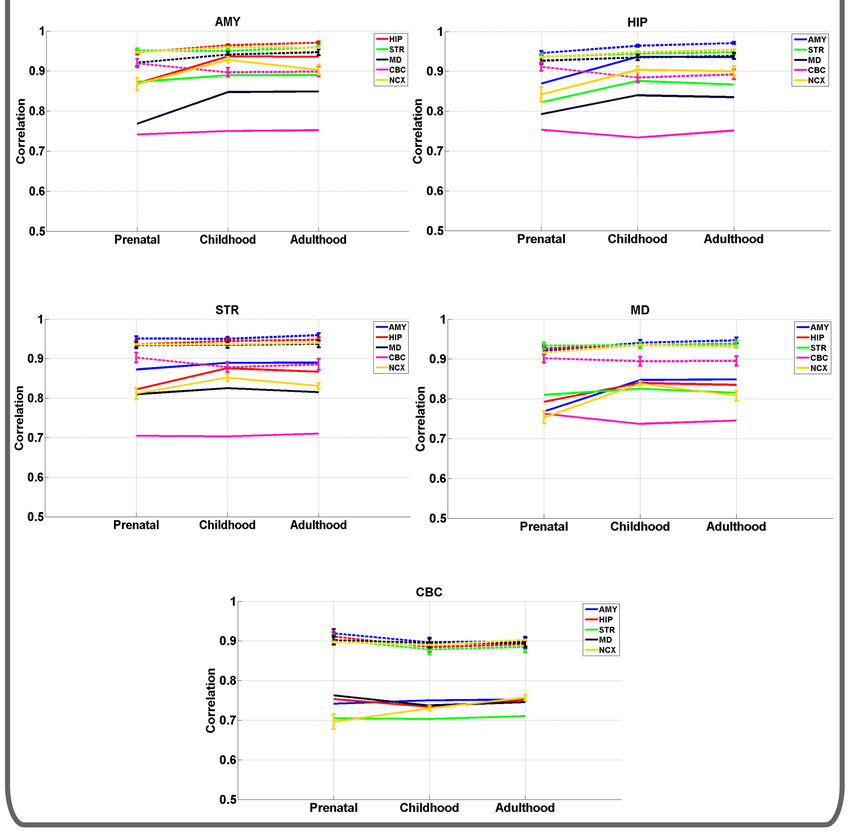
AMY	Amygdala	VFC	Ventrolateral prefrontal cortex
MD	Medial-dorsal nucleus of the thalamus	M1C	Primary motor cortex
HIP	Hippocampus	S1C	Primary somatosensory cortex
CBC	Cerebellar cortex	IPC	Inferior parietal cortex
STR	Striatum	A1C	Primary auditory cortex
OFC	Orbitofrontal cortex	STC	Superior temporal cortex
MFC	Medial frontal cortex	ITC	Inferior temporal cortex
DFC	Dorsolateral prefrontal cortex	V1C	Primary visual cortex



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

[1] BrainSpan: Atlas of the Developing Human Brain [Internet]. http://www.brainspan.org.

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[3] Rubinov, M. and Sporns, O., "Complex network measures of brain connectivity: uses and iinterpretations.," NeuroImage 52(3), 1059{1069 (2010).

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