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Molecular networks shared by Parkinson's disease and Alzheimer's disease

Parkinson's diseases (PD) and Alzheimer's (AD) have been shown to share extensive clinical and pathological features. For example, most PD patients with dementia have neurofibrillary tangles and senile plaques. At the molecular level, dysregulation of pathways such as immune response and autophagy have been observed in both PD and AD. The latest genetics studies of PD and AD further reveal that polymorphisms in *HLA*, *MAPT* and *PICALM* are associated with both PD and AD. To systematically investigate the commonality in molecular interactions between PD and AD, we performed multiscale embedded gene co-expression network analysis (MEGENA) on a large cohort of gene expression data from over 150 PD brain samples and two large cohorts of RNA-sequencing data from over 800 AD brain samples. Microglia/immune enriched modules in AD and PD are most conserved (P=1.26e-209, 15 fold enrichment). The other conserved gene modules, which are involved in synaptic transmission, transmission of nerve impulse, monovalent inorganic cation transport and cholesterol metabolism, are significantly enriched for the respective differentially expressed gene signatures between disease and control, indicating common molecular mechanisms underlying the two neurodegenerative diseases. We further evaluated the network rewiring of these conserved modules between PD and AD. The converged, disease-associated molecular networks identified here not only reinforce the findings from PD and AD specific studies, but also provide a general framework to study the two diseases simultaneously.

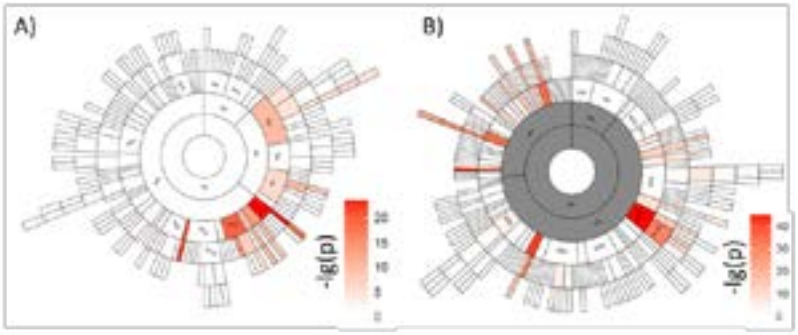

Figure 1. Multiscale Embedded Gene Coexpression Networks in Parkinson's Disease (A) and Alzheimer's Disease. Sunburst plots show the parent-child relationship among the modules in the networks. Color intensity is proportional to the significance level of association of a module with the corresponding disease.

Biography

Bin Zhang is a Professor (pending) of the Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York, USA. His expertise lies in Systems Biology, Machine Learning and Pattern Recognition. He has developed a series of influential gene network inference algorithms which have been extensively used for identification of novel pathways and gene targets, as well as development of drugs for several major human diseases. As a Prolific Researcher, he has published a number of high profile papers in Nature, Science, *Cell, Nature Genetics* and PNAS. As of January of 2017, his publications have been cited 11,386 times.

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