A Computational Approach inspired by Simulated Annealing to study the Stability of Protein Interaction Networks in Cancer and Neurological Disorders

Data Mining and Knowledge Discovery

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a
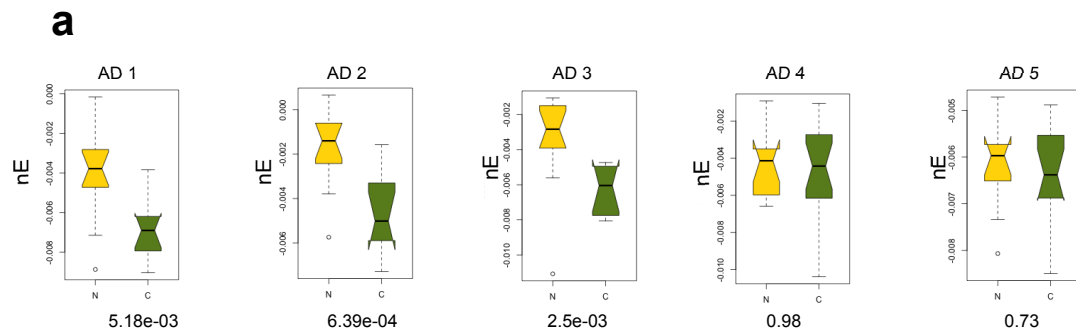
The *nE* distribution mapping all the genes in normal (N) and disease (C) states in AD into the sub-network created from proteins involved in the synaptic vesicle cycle. The Wilcoxon-rank p-value is presented below the x-axis

b
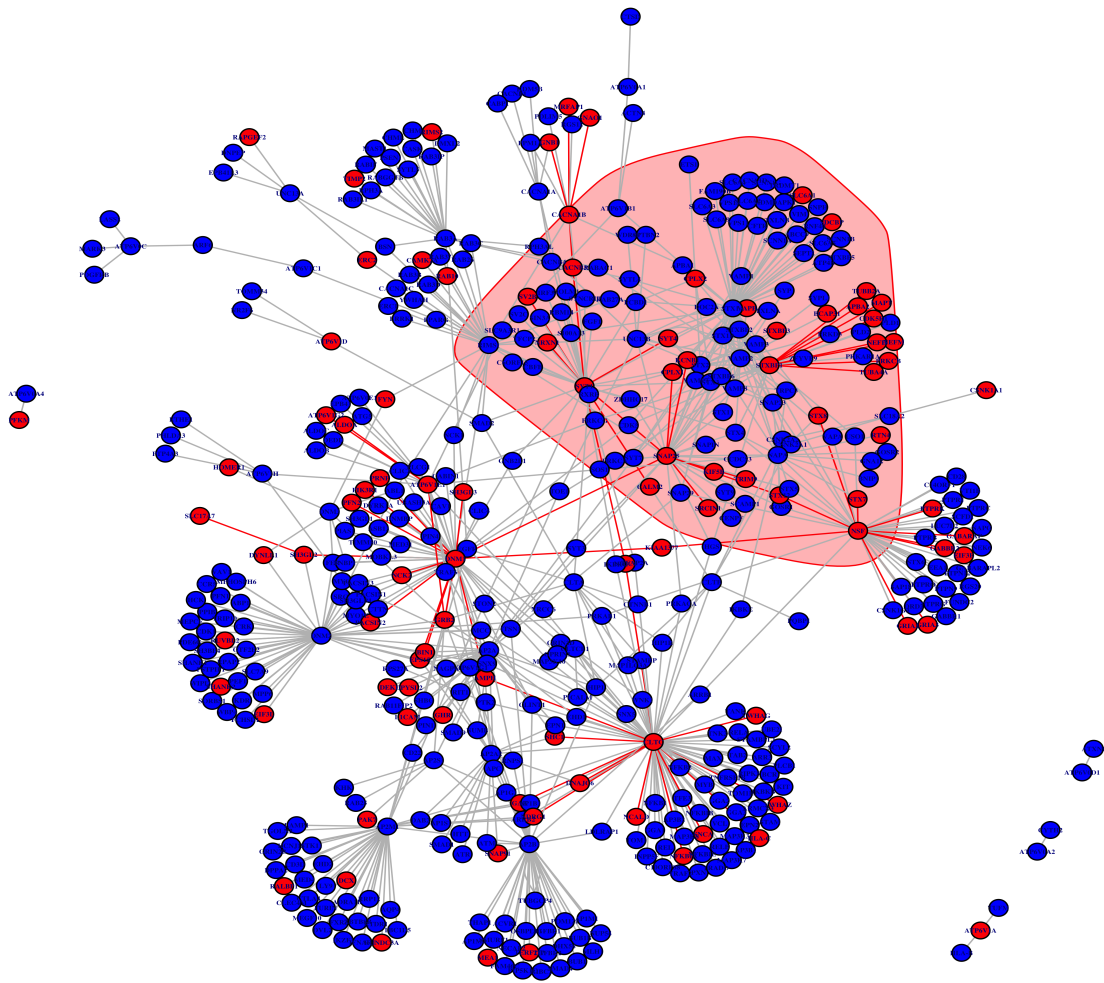
Protein-protein interaction sub-networks created from proteins involved in the synaptic vesicle cycle in AD. Blue nodes represent non-expressed gene products, red nodes expressed gene products, red edges represent interactions between proteins in which genes are both expressed and gray edges represent other combinations. The red clouds contain STX1A protein as well as all of its interacting partners

c
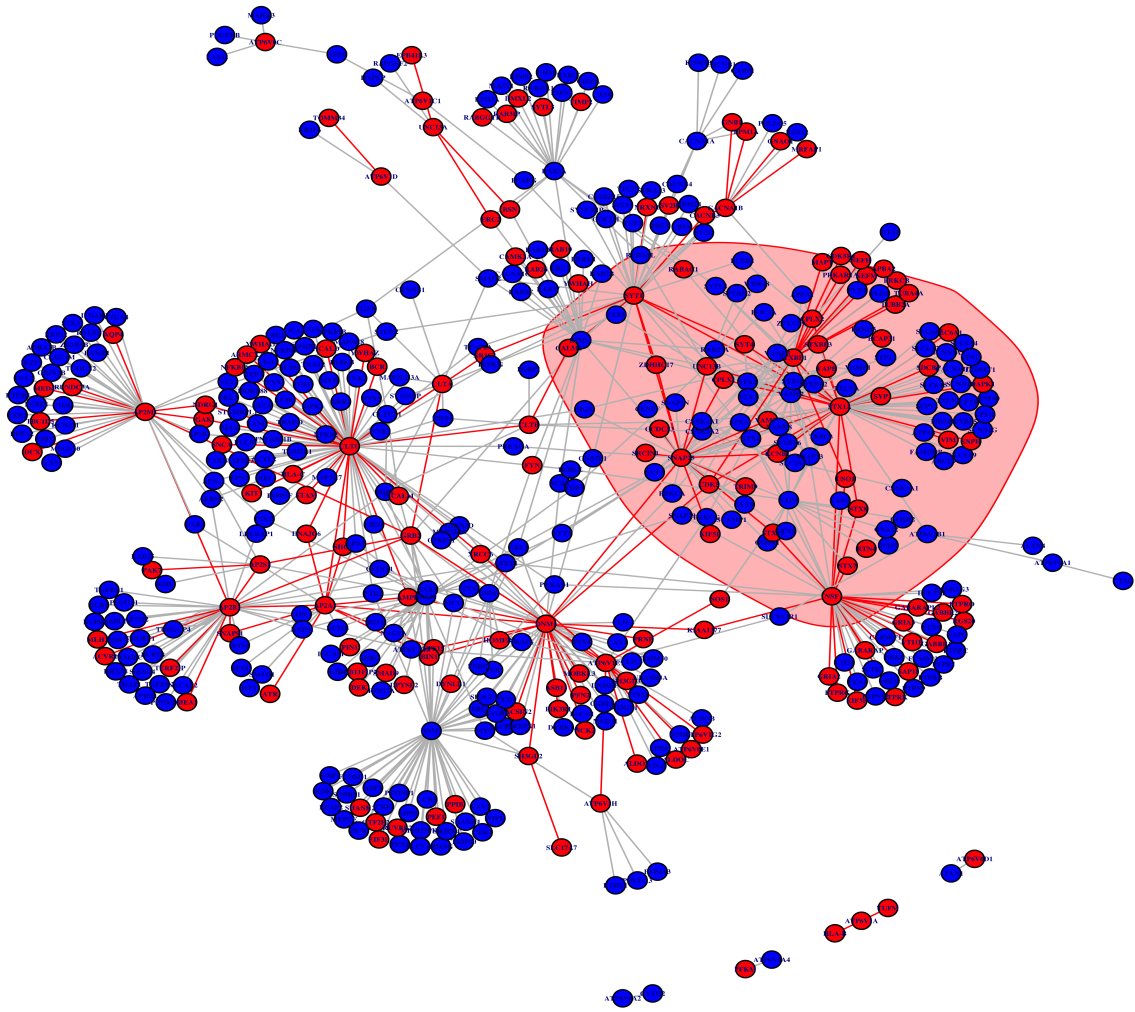
Protein-protein interaction sub-networks created from proteins involved in the synaptic vesicle cycle in normal states for AD. Blue nodes represent non-expressed gene products, red nodes expressed gene products, red edges represent interactions between proteins in which genes are both expressed and gray edges represent other combinations. The red clouds contain STX1A protein as well as all of its interacting partners