
Seminar

A computational algorithm for network alignment reveals common dysregulation network underlying two neurodegenerative diseases

Manikandan Narayanan

Systems Genomics and Bioinformatics Unit, NIH, USA

Interactions among proteins, regulatory DNA regions surrounding genes, and other biomolecules are central to cellular function and health. Constructing a network representation of these interactions makes it possible to dissect complex cellular behaviors using computational and statistical methods. I would like to talk about the design and application of a graph-theoretic algorithm that aligns gene networks derived from more than 600 human postmortem brain tissues to extract insights about dysregulation in two neurodegenerative diseases.

This work was supported by the Intramural Research Program of NIAID, NIH.

Friday, Jan 30th 2015

11:30 AM (Tea/Coffee at 11:15 AM)

Seminar Hall, TCIS