

ACMS Statistics Seminar

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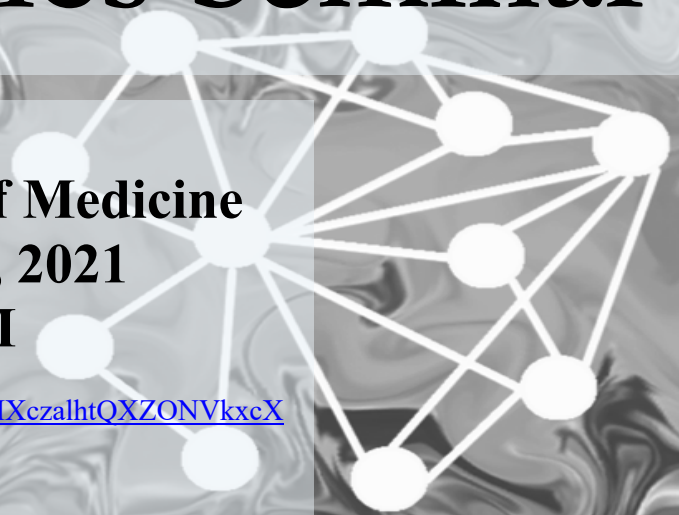
3:30 PM – 4:30 PM

Zoom Link:

<https://notredame.zoom.us/j/92712074286?pwd=ZzZGc1pzMXczalhtQXZONVkcXpXQT09>

Meeting ID: 927 1207 4286

Passcode: 952926



Modeling Single Cell Transcriptomics Data by Graph Structure Embedding

The development of single cell transcriptomics technology has provided gene expressions at the resolution of single cells, and are promising to deliver better understanding of the complexity within the disease microenvironment. Many pure data-driven models for single cell expression data have been developed, but models that incorporate known graph structures are much less abundant. Popular graph structures in biomedical knowledge database include the whole metabolic network and biological pathway networks, both of which are set of metabolic and biological processes that determine the physiological and biochemical properties of a cell. We here are presenting two models for single cell expression data: the first model, based on graph neural network, aims to incorporate the whole metabolic network to study the metabolic states of single cells, as well as the metabolic heterogeneity, and exchanges among different cell groups; the second model, based on covariance regression, aims to incorporate the biological pathway information to study the variations of gene-gene interactions, which allow rigorous statistical inferences for important covariates, such as disease status, sex, etc. Both models have been applied to important disease types, including cancer and Alzheimer's Disease.

The Department of Applied and Computational
Mathematics and Statistics

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