

MATHEMATICS COLLOQUIUM

Systems Learning of Single Cells

Cells make fate decisions in response to dynamic environments, and multicellular structures emerge from multiscale interplays among cells and genes in space and time. While single-cell omics data provides an unprecedented opportunity to profile cellular heterogeneity, the technology requires fixing the cells, often leading to a loss of spatiotemporal and cell interaction information. How to reconstruct temporal dynamics from single or multiple snapshots of single-cell omics data? How to recover interactions among cells, for example, cell-cell communication from single-cell gene expression data? I will present a suite of our recently developed computational methods that learn the single-cell omics data as a spatiotemporal and interactive system. Those methods are built on a strong interplay among systems biology modeling, dynamical systems approaches, machine-learning methods, and optimal transport techniques. The tools are applied to various complex biological systems in development, regeneration, and diseases to show their discovery power. Finally, I will discuss the methodology challenges in systems learning of single-cell data.

THURSDAY

MARCH

6

4:30 - 5:30PM
LECONTE COLLEGE
ROOM 444



Qing Nie

*Distinguished Professor of
Mathematics and
Developmental & Cell Biology,
University of California, Irvine*



UNIVERSITY OF
South Carolina

sc.edu/mathematics