Department of Applied and Computational Mathematics and Statistics Colloquium



Guo-Cheng Yuan

Department of Biostatistics & Computational Biology
Dana-Farber Cancer Institute & Harvard T.H. Chan
School of Public Health

Mapping Cell States from Single-Cell Gene Expression Data

Characterizing cellular hierarchy has profound implications in development and diseases. Single-cell technologies have great potential in discovering new cell types and lineage relationships, but there remain technical and conceptual challenges. In this talk, I will discuss our effort to overcome these challenges. In particular, I will present several computational methods we have recently developed. I will also discuss the perspective of using attractors and bifurcations to understand the dynamics of cell-fate transitions.

