CBDS Distinguished Speaker Seminar Series

"Spatiotemporal reconstruction of static single-cell genomics data"

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Zoom: https://yale.zoom.us/j/98021564798

Wednesday, December 1, 2021
4 p.m. to 5 p.m. Seminar

Cells make fate decisions in response to dynamic environment and multicellular structure emerges from interplays among cells in space and time. The recent single-cell genomics technology provides an unprecedented opportunity to profile cells. However, those measurements are taken as snapshots for groups of individual cells with only static information. Can one infer interactions among cells from such datasets? Is it possible to recover spatial information from non-spatial datasets? How to obtain temporal relationships of cells from the static measurements? In this talk I will present our newly developed computational tools that reconstruct interactions and spatiotemporal relationships for cells using single-cell RNA-seq, ATAC-seq, and spatial transcriptomics datasets. Through applications of those methods to systems in development and regeneration, we show the discovery power of such methods and identify areas for further development in spatiotemporal reconstruction.

Professor Qing Nie is a mathematician and systems biology researcher. He is a Chancellor's Professor of Mathematics, Developmental and Cell Biology, and Biomedical Engineering at University of California, Irvine. He is also the director of the Center for Mathematical and Computational Biology and the NSF-Simons Center for Multiscale Cell Fate Research at the University.

Professor Nie has published over 170 research papers in the areas of developmental biology, stem cells, computational single-cell genomics, multiscale modeling, deep learning, fluid mechanics & materials, and scientific computing. He has applied systems biology and data-driven methods to study complex biological systems, focusing on single-cell analysis, regeneration, development, and their applications to diseases.