

Sushmita Roy, Deciphering gene regulatory networks underlying cell-fate specification

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ZOOM ID: 997 8258 4700 (Biomedical Mathematics Online Colloquium), (pw: 1234) + Google Map https://www.ibs.re.kr/bimag/event/tbd-2/



SPEAKER

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Abstract: Cell fate specification is a dynamic process during which gene regulatory networks (GRNs) transition between different states and define cell type-specific patterns of gene expression. Identifying such cell type-specific gene regulatory networks is important for understanding how cells differentiate to diverse lineages from a progenitor state, how differentiated cells can be reprogrammed, and how these networks get disrupted in diseases such as cancer and developmental disorders. The advent of single cell omics has enabled us to perform high-throughput molecular phenotyping of individual cells at different omic levels. These technologies have revolutionized our understanding of cell type composition across diverse normal and disease conditions; however inferring cell type-specific networks and their dynamics from single cell omic datasets is an open challenge. I will present some of our recent efforts for inference and analysis of cell type-specific regulatory networks from single cell omic datasets. Application of our approach to hematopoietic differentiation and mouse cellular reprogramming predicted key regulatory nodes likely important for establishing different cell-type specific expression programs.

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