COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

DETECTION AND CHARACTERIZATION OF RARE TRANSCRIPTOMES

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TUESDAY, 15 SEPTEMBER 2020, 4 PM IST

Over the past decade, single-cell transcriptomics has transcended our understanding of complex biological systems. Single-cell expression readouts allow precise characterization of cellular heterogeneity in normal as well as diseased tissues. Further, single-cell RNA sequencing allows the detection of cells, present in a minority within a tissue. Examples of rare cell types include circulating tumor cells, cancer stem cells, circulating endothelial cells, endothelial progenitor cells, antigen-specific T cells, invariant natural killer T cells, etc. In practical scenarios, rare cell detection poses significant methodological challenges. In this talk, I will discuss our group's journey of raising a new breed of computational techniques for the efficient detection of rare transcriptomes.

GOOGLE MEET LINK:

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