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Single-cell transcriptome analysis

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Sequencing-based parallel analysis of large numbers of single cells is becoming a reality thanks to decades of technological progresses in molecular biology, imaging, and computing. This approach has started to bring new insights in neuroscience, immunology, cancer biology, diagnostics, genetics, biotechnology, and many other fields, where it contributed to the discovery of new cell types, to the reconstitution of cell lineages, to high-resolution profiling of differentiating cell populations, to the detection of rare cells such as circulating cancer stem cells, etc.

This lecture will focus on whole-transcriptome studies. In a first part I will review the existing methods and explain how they differ in terms on molecular biology and what consequences it has on data analysis. In a second part I will then introduce the current difficulties of large scale single-cell analysis, and discuss how these difficulties can be opportunities for computational biologists.

Keywords: single-cell, population, transcriptome, cell cycle, transcript counts