**Constructing atlas of human organ system to understand development and aging**

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Since the first single-cell transcriptome analysis in 2009, the throughput of single-cell transcriptomic techniques has grown exponentially, allowing for a single study to characterize millions of cells. Additionally, single-cell approaches are no longer limited to RNA analyses, but can also be used to characterize DNA and proteins. This powerful technique has been adopted in many fields of the life sciences and has rapidly expanded our understanding of biological systems. For example, a transcriptome and an open chromatin atlas of the embryonic development process of humans and mice are being created, thus providing new insights into the mechanisms by which gene expression modulates an individual’s developmental process. Moreover, the human immune system’s response to COVID-19 is being currently studied at various levels to gain insights into potential molecular mechanisms that could be targeted to control this disease. The Human Cell Atlas is an international collaborative initiative that has provided countless researchers with a platform to produce data cooperatively, as well as to compare and analyze their results and focus their efforts towards a single common goal. In this lecture, I will introduce the concepts and history of the Human Cell Atlas initiative, focusing on studying the development and aging of human immune system. I will also discuss the future directions for applying single-cell genomics in biomedical research at population level.