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Single–cell approaches to understand human development, aging and diseases

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Lecture : Since the first single–cell transcriptome analysis in 2009, the throughput of single–cell transcriptomics techniques has grown exponentially, allowing for a single study to characterize millions of cells. This technique is now being applied to various domains in biology, including human development, aging and pathologies. The human cell atlas initiative is a global network to bring all human single–cell data into a single map. As a part of this collaborative effort, we have built a map of human thymus across human lifetime, unraveling the process of birth and death of human organ. Meanwhile, to seamlessly integrate data with complex batch structure, we have developed a computational algorithm named BBKNN, which can be used to efficiently integrate large–scale dataset across multiple organs, timelines and diseases. With this pipeline, we have been building population–level single–cell atlas on multiple pathologies including inflammatory diseases and cancer tissues, which unveils new disease associated cell types and gene expression patterns.