Constructing single-cell maps of human organs.
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Detailed characterization of the cell types comprising the highly complex human organs is essential to understanding their functions. Such tasks require highly scalable experimental approaches to examine multiple aspects of the molecular state of individual cells, registering cells to 3D coordinates, as well as the computational integration to produce unified cell state annotations and interpretation. To this end, we have established experimental platforms and computational pipelines for constructing 3D single-cell maps for human adult organs. In this talk I will present our recent progress on single-cell method development, as well as the creation of an integrative single-cell transcriptome and chromatin accessibility maps of human brain and kidney.