Studying tissue heterogeneity by measuring single-cell gene expression

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A major challenge in biology and medicine is to develop experimental and statistical methods to survey body conditions. Current methods assess tissue functions by pulling thousands of cells and measuring their average gene expression but do not quantify tissue heterogeneity. In this talk I will present our recently developed automated single-cell RNA-seq method that simultaneously measures expression levels of thousands of genes in thousands of single-cells. After controlling for amplification biases and computationally filtering technical errors, clustering these sparse and discrete data allows ab-initio identification and characterization of functional sub-populations of highly correlated cells and studying their responses to different biological signals or diseases. Such approaches that sample, cluster, and classify single-cells with minimal biological prior assumptions may push forward our understanding of tissue development and disease progression.