Single Cell Gene Expression Analysis in Biomedical and Basic Research

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DNA sequencing technologies were the main driving forces behind the molecular biology revolution, which reached a milestone in 2001 with the first sequence analysis of the human genome. Almost 20 years later, a second revolution has started: the single cell revolution. The ability to sequence the RNA of individual cells (scRNA-seq) allows us to obtain a snapshot of the genes that are active at a given moment. The expression of these genes, which are translated into effector proteins, ultimately define what a cell does. The popularization of single cell sequencing technologies is completely changing our understanding of fundamental biological processes such as development, immunity or pathology. Current approaches enable us to define the gene expression profiles of thousands of single cells in parallel with high resolution, allowing us to characterize tumors, developing organs or even whole organisms. Moreover, we can label individual cells to reconstruct their relationships in space and time. Combined efforts involving different scientific disciplines have allowed us to jump from the first single cell ever sequenced in 2009 to a deep transcriptomic analysis of a whole embryo with single-cell resolution. In the Functional Genomics Center Zurich (FGCZ), we have implemented different pipelines to provide our users with access to state-of-the-art single cell technologies. We are applying our expertise to combine different single-cell sequencing strategies adapting them to the requirements of the researchers and the complexity of the analyzed samples. During the talk, following an introduction about current DNA sequencing platforms, the latest technological advances in single cell sequencing will be presented. Moreover, different examples about how the single cell revolution is helping to answer challenging biological questions will be highlighted.