

The Human Cell Atlas impact on life science and healthcare

The human genetic code is often portrayed as “The book of life” and in a way it is. Yet, each of the trillions of cells of an individual’s body carries the exact same genetic information however each cell type is defined by the genes it uses (and by the genes it doesn’t use). The set of genes that is used by a given cell type varies with age and changes in disease. We cannot—based on genomic sequences alone—compute predictive models for human health and disease and understand the principles of human development, aging or disease.

Crucial information can be uncovered by determining the cell’s transcriptome and epigenome, the layer of regulatory proteins including Transcription Factors and the histones/nucleosomes that facilitate or limits access and expression of the genes in a cell-type and cell-state specific manner. Hitherto, the analysis involved highly complex, heterogeneous mixtures of different cell types resulting in average profiles that vary significantly as a result of varying cell-type compositions. Single cell biological approaches have revolutionize life science permitting the simultaneous analysis of thousands and thousands of single cells that make of a given tissue. Dissociation of cells from tissues implies the loss of positional information of where the cell resides in the tissue and consequently hampering the modeling of cell-cell interaction and communication. Combining single cell assays with advanced microscopy and/or in situ sequencing provide the ‘lost’ positional information.

Using single cell biological approaches, the Human Cell Atlas initiative strives to provide a complete atlas of all genes that are expressed in all cell types of and their exact position within organs or tissues of the human body from birth to death, and in health and disease.

I will present our efforts in defining and understanding the epigenome and how it impinges on gene expression as well as our efforts on using single cell approaches to decipher and use (dys)regulatory pathways in health and disease to improve diagnosis and treatment.