*Single cell analysis*

*“The human body is a complex machine that heavily relies on the basic units of life - cells. Cells can be separated into different types, which even undergo transitions during development, under disease or when regenerating. This cellular heterogeneity is reflected in their morphology, function, and gene expression profiles. Strong disruptions causing deregulations of the cell types influence the entire system causing potentially even serious diseases like cancer[Macaulay et al., 2017]. It is therefore vital to understand how cells behave in a normal state and under perturbations to improve our understanding of the entire cellular systems.*

*This monumental task is approached in different ways of which the most promising one is to profile cells at the individual level. So far, each cells’ transcriptome was primarily examined in a process known as single-cell RNA sequencing. With recent advances in single-cell genomics, it is now possible to enrich the transcriptome information with spatial, chromatin accessibility or protein information. These advances generate not only insight into complex regulatory mechanisms, but also go along with additional complexity for data analysts.*

*Nowadays, data analysts are facing a vast analysis tool landscape with a collection of more than 1000 computational single-cell analysis methods. It is becoming increasingly challenging to navigate this large range of different tools to generate sound results which are at the forefront of science*.” ( https://www.sc-best-practices.org/preamble.html, accessed October 4, 2023)

Nowadays, there is a high number of single cell transcriptome data sets available in the scientific community, freely and easily accessible from the Gene expression omnibus (GEO) platform. We offer several possible topics studying the transcriptome of single cells.

- A large scale analysis of many similar transcriptomics studies that are comparable in terms of experimental setup, to provide a background for future studies. Example outcomes would be annotating known cell types in an automated way or finding differentially expressed genes in a systematic way.
- Investigating the sparsity in scRNA, or other datasets. A huge focus in the current practices is on the expressed and highly variable genes in a data set. We would like to explore different strategies, for example using constitutively expressed genes or finding groups of genes unique to certain putative cell groups.