

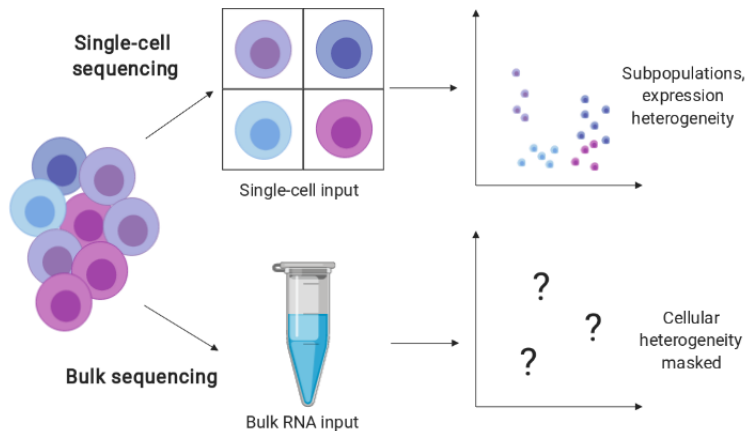
Introduction to single-cell sequencing and group project

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CSAMA 2019, 17th edition

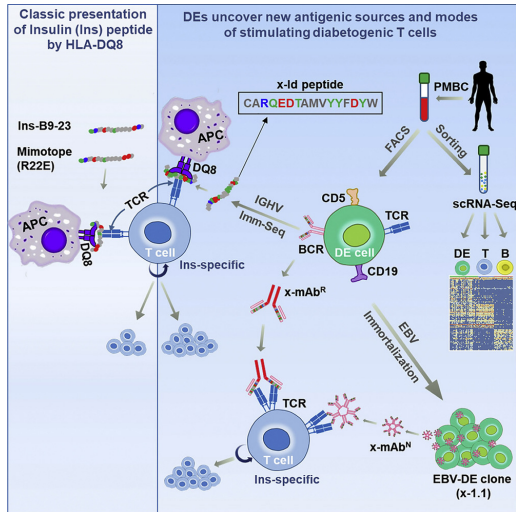
Why do we want to sequence single cells?



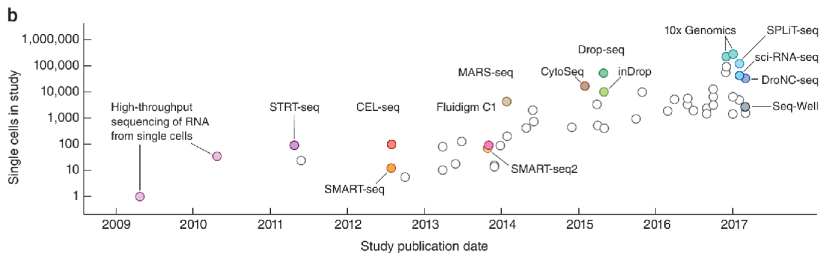
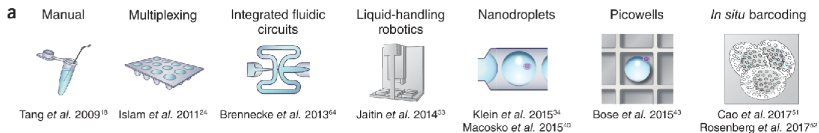
My favourite discovery by single-cell sequencing

A Public BCR Present in a Unique Dual-Receptor-Expressing Lymphocyte from Type 1 Diabetes Patients Encodes a Potent T Cell Autoantigen

Rizwan *et al.* *Cell* 2019



Isolation of single cells and sequencing protocols

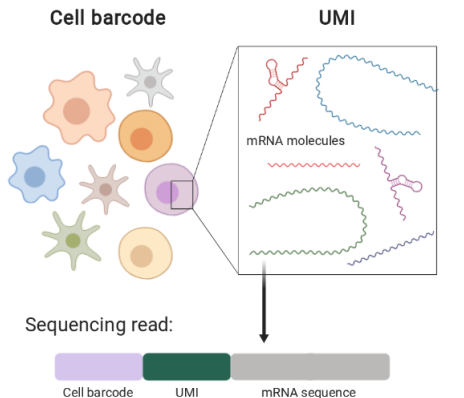


Svensson et al. 2018

Cell barcode and unique molecular identifier (UMI)

Sequencing data preserves information:

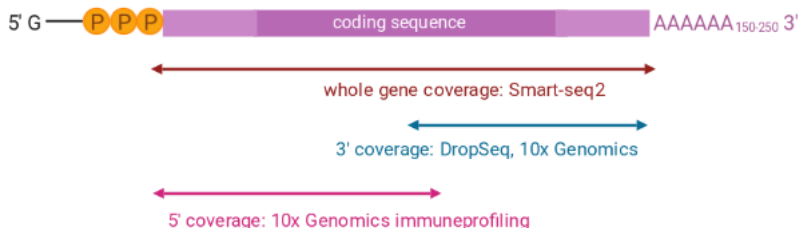
- ▶ Which cell did the sequenced transcript belong to? → **cell barcode**
- ▶ How many times did one transcript get sequenced? → **UMI**



Whole gene vs. 3' or 5' sequencing

Depending on the library preparation and sequencing protocols that you are using, you will get different coverage of mRNA molecules.

A typical mRNA molecule:



Overview of single-cell topics during CSAMA

- ▶ Wednesday morning: Lectures (Simon Anders, Davide Risso)
- ▶ Thursday afternoon: Group work on single-cell sequencing techniques (Katharina Imkeller)
- ▶ Friday afternoon: Lab on analysis of single-cell sequencing data (Simon Anders, Davide Risso)

Group project: Understanding the technical aspects of single-cell sequencing

Aims of the workshop

- ▶ Understand the molecular biotechnology behind single-cell sequencing.
 - ▶ How do we get from mRNA molecule to sequencing read?
 - ▶ Which method to choose for a specific question?
 - ▶ Why do we model the data differently for different sequencing approaches?
-
- ▶ 4 groups, 4-6 participants per group
 - ▶ Group work during **Thursday lab, 13h30-16h30**.
 - ▶ Presentation of results to the whole course on **Friday, 13h30**.
 - ▶ Please register on the list at front desk (limited space)!

The material for the group project is here...

https://github.com/Bioconductor/CSAMA/tree/2019/lab/group_project_scseq

GROUPS

- ▶ SMART-seq2
- ▶ Drop-seq and 10x Genomics 3'
- ▶ 10x Genomics 5' including VDJ sequencing
- ▶ SPLiT-seq