Master Thesis: Constructing Single Cell Immunerepertoire Analysis Pipeline

Background

The specificity of B and T cells towards antigens is determined by the receptor-forming protein complexes. To reflect the subgroups in the protein complex and their expression in its entirety, single-cell analyses must be applied.

Description

ScRNA sequencing allows characterization of cells, especially rare cells that are often overlooked in bulk approaches. In addition, scRNA sequencing opens up new possibilities to analyze the immune repertoire and its effects on immune cells. In order to investigate single cell analyses regarding the immune response to the CoVID-19 pathogen, an analysis pipeline for immune repertoires will be established using repositories.

Your Tasks

- Introduce single cell immune repertoire analysis
- Consideration of possible different processing pathways
- Research for usable, online available raw data
- Create a pre-processing & analysis workflow for scRNA immune repertoire data

Requirements

- Basic knowledge in computer science
- Interest in molecular biology & immunology

Bei Interesse melden Sie sich bei
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