Master Thesis: Generation and Analysis of SingleCell-RNA Data from CoVID Exposed PBMC's

Background

SARS-CoV-2 as a virus is still a big factor in our daily life. Besides obvious infections of the respiratory system, there are several other effects on health, from severe infections caused by cytokine storms to long-lasting problems after infection. Peripheral blood mononuclear cells 'PBMC' are a promising object for scientific questions regarding immune responses.

Description

To gain insight into the immune response to the virus, it is possible to study the transcriptome of immune cells, specifically the monocytes and lymphocytes of peripheral blood. In order not to miss small effects on the different cell types from these heterogeneous samples, the best possible method is a single cell transcriptome and immune repertoire analysis. Bioinformatic analysis of these data will allow for better interpretation of the immune response to viral infections.

Your Tasks

- Preparing single cell solution from isolated human pbmc's
- Constructing single cell RNA sequencing libraries
- Using and improving analysis workflow for scRNA sequencing data
- Interpreting results for biological relevant connections

Requirements

- Interest or knowledge in bioinformatic science
- Interest or knowledge in molecular biology & immunology

Bei Interesse melden Sie sich bei
Dr. rer.nat Anke Fähnrich
anke.faehnrich@uksh.de