

HIWI Position in Bioinformatics

Single cell genomics is revolutionizing biology and medicine. Rapid technological advances now allow the profiling of genomes, transcriptomes and epigenomes at an unprecedented level of resolution. To harness the full potential of these developments, new computational methods specifically tailored towards the analysis of single cell omics data are essential. This has now also been appreciated with the nomination “technology of the year 2019 and 2020” by the journal *Nature Methods*.

Our research group employs state-of-the-art single cell sequencing technologies (10x Genomics, BD Rhapsody) to unravel the dynamics of the human immune system.

We currently look for a motivated HiWi-student in the area of bioinformatics/computational biology who contributes in a team effort to **unravel the regulation of the human immune system in inflammatory diseases and COVID-19** and to discover novel immune cell subsets that could be exploited for successful **vaccination strategies**. We have scRNAseq data sets from 10x Genomics available and need you for data analysis using already implemented bioinformatic pipelines under the guidance of a postdoc. You will be part of a group of other HiWi-students and an experienced postdoc.

Job: HIWI-Position, 5-12h/week (more or less hours also possible, flexible, home office possible)

Qualifications: Applicants should be students of bioinformatics/computational biology and be highly motivated to contribute to single-cell RNA-seq data analyses and preparation of manuscripts for publication.

When: The HiWi position is available immediately.

Contact: Prof. Christina Zielinski (christina.zielinski@tum.de)