

## Computational Postoc Position in Multimodal Spatial Single-Cell Analysis

The chair of "Computational Biology of Spatial Biomedical Systems" (<u>https://www.med.uni-wuerzburg.de/en/systemimmunologie/research/quantitative-single-cell-biology-of-the-immune-system-gruen-lab/</u>) at the Würzburg Institute of Systems Immunology, Julius-Maximilians-University Würzburg, is looking for a computational postdoc in multimodal spatial single-cell analysis. The research group of Prof. Dr. Dominic Grün studies intrinsic and extrinsic driving forces of cell fate decision, and utilizes single-cell sequencing and high-resolution imaging- as well as sequencing-based spatial transcriptomics methods for investigating cell fate choice in a given tissue environment.

The project will focus on the analysis of large-scale in-house datasets generated by multimodal single-cell sequencing and spatial transcriptomics of corresponding tissue samples. Data will be generated from human bone marrow biopsies of leukemia patients undergoing different kinds of therapies (e.g., CAR-T cell therapy), and from human liver biopsies, e.g., from hepatocellular carcinoma patients. The overaching goal is a better understanding of diease ontogeny and therapy response on the tissue level to enable the identification of novel therapeutic targets. This will be complemented by data generated from corresponding mouse models.

You will join an international vibrant hybrid group of experimental and computational biologists within the recently founded Institute of Systems Immunology with excellent computational and experimental infrastructure. The group is affiliated with the newly founded CAIDAS institute of artificial intelligence (<u>https://www.uni-wuerzburg.de/caidas/home/</u>) providing a direct interface to state-of-the art data science. You will interact with AI/ML experts at CAIDAS to enable transfer of cutting-edge data science to single-cell analysis.

This position will initially be given for two years with the option to be extended.

Salary and benefits are based on the public service positions in Germany (TV-L).

Job duties:

- Development of machine lerning tools for the integration of single-cell sequencing data with highresolution spatial transcriptomics (e.g. Stereo-Seq or Seq-Scope) and multiplexed imaging data (seqFISH)
- Integrated computational analysis of spatial transcriptomics data and corresponding multimodal single-cell sequencing data across patient cohorts and disease mouse models
- Support of experimental scientists in experimental design and data analysis
- Data visualization using online interfaces (e.g., Shiny app)

Expected qualifications:

- PhD in natural sciences, life sciences, informatics, mathematics (or similar)
- Programming proficiency in Python (PyTorch), R, and ideally C/C++
- Proficiency of deep learning and other machine learning techniques
- Experience with single-cell sequencing data analysis
- Experience with image analysis, ideally single-molecule FISH
- Experience with data visualization and programming of web interfaces
- At least one first author paper in an international peer-reviewed journal
- Fluency in English

The University of Würzburg strives to increase the proportion of women in research and teaching and therefore expressly requests applications from suitably qualified female scientists. Severely handicapped applicants will be employed preferentially if their aptitude is otherwise essentially the same.

Please submit your application documents by December 15th to systemimmunologie@uni-wuerzburg.de