

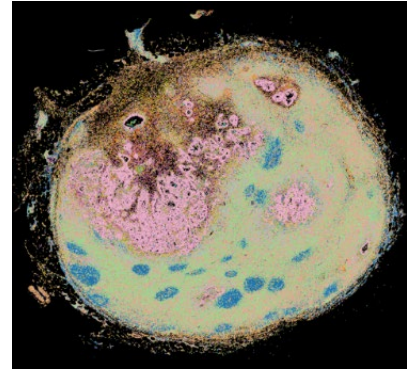
**Job Offer: Master Thesis**

**Title:** Development and Benchmarking of an Open-Source Python Toolbox to Analyze Single-Cell Spatial Transcriptomics.

**Duration:** 6 months

**Start Date:** As soon as possible.

**Supervisors:** Johannes Wirth, M.Sc., PD Dr. Katja Steiger, Prof. Dr. Peter Schüffler



**Institution Information:** Institute of Pathology, Technical University Munich.

**Keywords:** Spatial Transcriptomics, In Situ Sequencing, Xenium In Situ, Python, Cell segmentation, Benchmarking, Data Analysis, Single-Cell Transcriptomics

**Background:** Intra-tumoral heterogeneity (ITH) is one of the major causes for unsuccessful treatments in human cancers. The development of spatially-resolved transcriptomic (ST) methods facilitates the exploration of heterogeneity in tumor samples and gives the opportunity to better understand cancer biology and treatment responses. In situ sequencing (ISS) uses an imaging-based approach to map single transcripts at subcellular resolution and characterize the transcriptional state of nearly all cells of a tissue section. Currently, spatially-resolved transcriptomics represents one of the most promising biological methodologies and is expected to shape biological research in the coming decades.

**Problem:** The enormous amount of data generated in ISS experiments needs to be processed and interpreted. Especially in the context of clinical research and routine diagnostics, this data analysis has to be done quickly. Currently, the lack of standardized pipelines to analyze the data and benchmarking experiments to ensure optimal quality of the results hinder its general application in clinical research. In particular, the segmentation of single cells, efficient analysis of the large datasets and the integration of pathological workflows into the analysis present a challenge.

**Goals:**

1. Writing an open-source, Python-based toolbox to efficiently analyze large in situ sequencing spatial transcriptomic data using a high performance cluster.
2. Benchmarking different segmentation methods to ensure optimal cell segmentation.
3. Packaging the code and making it publishable.

**What We Offer:**

- The opportunity to work in an interdisciplinary research team at the intersection of pathological, clinical, and molecular biological research.
- Access to the high-performance computing cluster of the Leibniz-Rechenzentrum (LRZ).
- Access to unique datasets of the state-of-the-art in situ sequencing system 'Xenium in situ.'

**Requirements:**

- B.Sc. in bioinformatics, computational biology, biology, or a related field.
- Sound knowledge of Python or a comparable programming language.

**Preferred Qualifications:**

- Familiarity with tools for the analysis of single-cell or spatial transcriptomics methods (Scanpy, spatialdata), Image analysis (Napari, QuPath, ImageJ), Bash scripting, Python packaging

**Contact Information:** Interested candidates are invited to submit their applications, including a CV and a brief statement of interest, to [j.wirth@tum.de](mailto:j.wirth@tum.de).

We look forward to receiving your applications and welcoming you to our research team!