Master Thesis Project:

Development of analytical pipeline for robust phenotyping of highly multiplexed imaging data across different spatial omics modalities

Background

Are you interested in pushing the boundaries of imaging techniques in the field of molecular neuroscience and neurochemistry? We have an exciting opportunity for a master's thesis project that focuses on integrating mass spectrometry imaging with spatial transcriptomics.

Improvements in multiplexed (omics) imaging technologies, such as spatial mass spectrometry imaging and spatial transcriptomics, can provide an unprecedented understanding of tissue spatial organization and single-cell-level phenotypes, as well as their importance in both healthy and disease conditions. However, no single multiplexed technology currently delivers robust and comprehensive phenotyping of the biological microenvironments, including genes, proteins, and metabolites/lipids. There are several challenges associated with combined omics analysis, including computational pipelines for data integration, segmentation, analysis, and interpretation. These challenges arise from factors such as different pixel sizes and difficulties in assigning pixels to single cells that vary in size.

Spatial omics approaches have the potential to generate information not only about individual cells but also about the surrounding environments, such as extracellular markers that provide insight into cell-to-cell communication. In this project, the student will adopt and further develop existing analytical pipelines to integrate, extract, and annotate single-cell and cell microenvironment information. This information can only be obtained through the analysis of different modalities. The project primarily focuses on the preprocessing and postprocessing of available multimodal datasets but also offers opportunities for "wet lab" when time permits. The resulting analytical tools and data will directly contribute to our understanding of disease-relevant phenotypes and lay the foundation for a multimodal screening platform.

Master-thesis project description and aims

In this thesis project you will develop an analytical pipeline for integration of highly multi-dimensional datasets obtained from two cutting-edge imaging modalities (spatial mass spectrometry imaging and spatial transcriptomics). Your task will involve (i) dataset conversion, adaptation, and improvement of (ii) dataset alignment, (iii) segmentation and annotation of single-cells and local microenvironments across multiple-platforms.

Methods

- Adapt and improve image format conversion, alignment, and segmentation strategies
- Address challenges linked to image resolution differences and multiplexed datasets
- If time permits: adapt for high-throughput automated single cell phenotyping

Requirements

Master-level student with a strong background in programming (bioinformatics). Project requires proficiency in programming languages such R, Python or Julia

Strongly recommended/Advantageous

Knowledge in machine learning algorithms

Interested? Please contact Wojciech Michno, wojciech.michno@scilifelab.uu.se

The scope of the project is a 30-45 hp master thesis.