Automated cell type calling for high-resolution spatial omics

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Spatial omics techniques[1] allow spatially resolved quantification of protein or RNA species abundance in tissue. Spatial omics techniques can roughly be divided into two categories:

- Low-resolution, high-coverage techniques (LR-SO) allow measuring the entire transcriptome at super-cellular resolution (several cells per spot):
- High-resolution, low-coverage techniques (HR-SO) such as MIBI[2], MERFISH[3], or MELC[4] allow targeted measurement of fewer proteins or RNA species at single-cell resolution.

This project focuses on a specific pre-processing task for HR-SO data, the automated assignment of cell type labels (e.g., T cells, B cells, melanocytes, etc.) to individual cells. This is a challenging problem, because in HR-SO data, conventionally used cell type markers may not have been measured, complicating straightforward application of automated cell type assignment algorithms designed for whole transcriptome single-cell RNA-sequencing data. Specifically, the project will proceed in the following steps:

1. Individuate state-of-the-art methods that allow automated cell type assignment for HR-SO data.
2. Individuate HR-SO datasets with high-confidence expert-provided cell type annotations.
3. Based on these datasets, design and implement a validation pipeline to benchmark the methods individuated in step 1.
4. Include a prototype method (https://github.com/bionetslab/THEORETIC) for cell type assignment in HR-SO data developed at the BIONETS lab into the validation pipeline and compare its performance against the state of the art.

Requirements

- Python programming.
- Highly independent and rigorous workstyle.
- Willingness to independently dive into cellular biology (reading textbooks, etc).

Depending on the results, continuation of the project in the context of a MSc thesis is possible.

References

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