

Biologia Systemów 2024/25

Spatial Proteomics, zadanie 3

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CellCharter - Neighborhood Representation (10 pts)

As your homework, you will use **CellCharter** to compute the cellular neighborhood representations and analyze them. The task is inspired by a tutorial:

https://cellcharter.readthedocs.io/en/stable/notebooks/cosmx_human_nsc1c.html and we highly recommend going through it before starting the assignment.

Your task consists of the following steps:

1. Warm-up (1 pt):

- Perform a PCA on cells' marker expressions.
- Your PCA should explain at least 95% of the variance in markers.
- Store the PCA-transformed marker expressions in the field `train_anndata.obsm["X_PCA"]` (note: this corresponds to the "X_SCVI" field from the tutorial).

2. Neighbor Aggregation (2 pts):

- Perform a CellCharter neighbor aggregation using the provided function.
- Hint: for our data, the `sample_key` parameter corresponds to `sample_id`.
- Choose the `n_layers` parameter on your own and shortly explain your choice.

3. Cluster Selection (2 pts):

- Perform cluster selection in the same manner as done previously for the mean marker and cell type histogram representations.

4. Cluster Analysis (3 pts):

- Perform PCA, cell type abundance, and mean marker analyses — following the same approach as for the mean marker and cell type histogram representations.

5. Cross-count Matrices (2 pts):

- For each pair of clustering results (mean marker vs. cell type histogram, mean marker vs. CellCharter, and cell type histogram vs. CellCharter):
 - Compute a cross-count matrix (it stores how many cells are assigned to a predefined pair of clusters across two modalities).
 - Visualize these matrices.
 - Briefly explain your results.

Important notes:

- You do **not** need to prepare a formal report.
- Inline comments in your notebook are sufficient.
- Make sure to comment on any important steps, decisions, or results to ensure the work is understandable.

Deadline: 12th May 2025, 12:00 (noon)

Have fun!