Passaggio d'anno II -> III

tentative title of the thesis…

1. Spatial transcriptomics: what is it? [01:30]

2. Imaging-based Spatial Transcriptomics and its challenges [02:30]

3. Exploiting prior knowledge to perform feature selection [01:30]

4. Cell-Cell communication [01:00]

5. Complex networks and multilayer networks [02:00]

6. Appendix [01:00]

7. Publications, teaching and courses [00:15]

- History of how single cell measurements went from bulk to capture the state of individual cells in space.
- Reference to the Nature methods awards.
- Analogy and definition of biological terms that will be used in the talk:
    - **Cell**: a biological unit that can be measured.
    - **Feature**: a biological measurement of a cell, such as a gene expression level.
    - **Cell type**: a group of cells that share similar features.
    - **Cell state**: the condition of a cell at a given time, which can change over time.

The definitions aims to avoid using excessive biological terms but stick to `observations`, `state`, `features`.

- Thee different technologies to measure spatial transcriptomics (without details).
- im-scRNAseq from ISH data can be collected with MERFISH, seqFISH, and other technologies. (without details)
- Comparison with scRNAseq and challenges of being limited to hypothesis testing.

- Integration between im-scRNAseq and scRNAseq aims to estimate the location of the signal of cells based on the ones that are measured in space.

- TANGRAM solves an optimization problem estimating the probability of optimal location of the scRNA-seq cells in space.

- TANGRAM is the suggested method for MERFISH data from a benchmark, but requires careful handling.

- Reference to a thesis student working on it and argue that some refinement is needed.

Biologically informed feature selection

- Cells are measured in space, but may differ in their state even if of the same type.

- Something must be regulating the state of the cells. Their regulatory mechanism.

- THeir regulatory mechanism is stored in Gene Regulatory Networks (GRNs).

- We estimate the activity of each regulatory element in space using DecoupleR.

- Results of spatially emergent patterns of colocalized features with biological relevance.
- Results of ISMBECCB 2025 poster IJCNN2025 paper.

Now i phrase it in a way that uses biological terms but will eventually be the ones i state at the beginning of the talk.

- Cell-Cell communication is the process by which cells exchange information.
- Analogy with antennas that send and receive at different frequencies.
- Analogy with users that subscribe to different social networks, where they can only communicate with those that subscribe to the same network.

- Cell-Cell communication is a system of systems, and multilayer networks can model them.

- Each layer of the multilayer network represents a different type of communication.

- Each node represents a cell, and each edge represents a communication between two cells.

- The multilayer network can be used to analyze the structure of the communication system.

- Structural analysis of the multilayer network can reveal patterns of communication.
- Tensor decomposition can be used to extract features from the multilayer network.
- Questions to be answered:
  - How do different layers of the multilayer network interact?
  - What are the most important nodes in the network?
  - How can we use the multilayer network to predict cell-Cell communication?

Appendix: Vignette of N2SIMBA

- N2SIMBA is a simulator of bacteria communities driven by a bacteria interaction networks.
- bacteria interacts with each other using the cross feeding mechanism.
- Interaction networks are unknown and this tool aims to produce realistic synthetic data that reconstruction methods can use to assess their performance.

- Analysis of the diversity of piglets in a farm that was suspected to present C. Difficile infection.
- Results show that the safety guidelines of the farm allowed to avoid the infection.

- List of publications
- Which courses I took
- Which courses I assisted

Thank you!

- Questions?
- Contact me at …