INSTITUT DES MALADIES GÉNÉTIQUES

M2 internship: Machine learning for spatial perturbations of transcriptomic data

Ricci Lab @ Institut Imagine
Contact: `matthew.ricci@institutimagine.org`

Summary: Our lab is looking for a six-month M2 intern to develop computational methods for predicting the geometric effects of genetic perturbations on biological tissues. Candidates should have backgrounds in machine learning, physics and/or applied math. Transitioning to PhD role is possible. Please apply by **January 15, 2026**.

When and where: February-August 2026 (flexible). Institut Imagine. 24 Boulevard du Montparnasse, 75015 Paris.

To apply: Send an email to `matthew.ricci@institutimagine.org` with `M2` in the subject line by **January 15, 2026**. Please include a **CV** and **one-page statement describing relevant research/coursework.**

Background: How does the shape of your brain change during development when a given gene is mutated? Can knocking out a gene allow the immune system to invade and kill a tumor? Our lab is taking steps to understand these deep biological questions using tools from machine learning, physics and computational biology.

This project will make use of recent developments in high-throughput omics technologies [1, 2, 3], which have revealed the molecular underpinnings of biological systems in exceptional detail. In particular, *spatial transcriptomic* (ST) methods link molecular profiles to single cells at specific spatial locations, and *perturbation* methods reveal the effect of many genetic changes on the molecular state of a biological system. The goal of this project is to build a machine learning framework that combines these data types to predict how the geometrical and mechanical properties [4] of biological tissue changes in response to genetic perturbations.

Your role: You will extend existing non-spatial models to the spatial case and train them on cutting-edge, open-source perturbation data. You will also work with our team to develop computational methods for characterizing the geometrical and mechanical properties of the data before and after perturbation. Concretely you will

- Conduct a literature review to survey open biological questions in spatial perturbation studies.
- Augment spatial prediction [5] and perturbation [6] models with perturbation inputs and spatial decoders, respectively. You will then train and evaluate these models on open-source brain and tumor ST data.
- Analyze the geometry (e.g. boundary positions and sharpness, cell density) of predicted perturbations.
- Work with our team to incorporate direct mechanical prediction (e.g. tensions, pressures, stresses) into this framework.

Required skills:

- Training in applied/pure math, physics, computer science or computational biology.
- Experience with modern deep learning methods, e.g. diffusion modeling, flow matching, neural ODEs, dynamical optimal transport, etc.

Desirable background:

- Coursework or research in continuum mechanics, numerical PDEs, inverse problems.
- Experience with biological data, especially omics (e.g. scRNA-seq, spatial transcriptomics).

Scientific environment

Institut Imagine is Europe's top research institute on genetic disease. It commands significant biological and computational resources, including

- **Compute:** 12PB PureStorage (Flash) cluster, 8x NVIDIA DGX H200, 150TB PureStorage FlashBlade S scratch space, and 16–20 CPU nodes.
- **Data:** Large, growing in-house omics datasets (scRNA-seq, spatial transcriptomics, proteomics, ATAC-seq, PACBio long-read sequencing, etc.).
- **Collaboration:** Close integration with top institutions like Institut Pasteur, PR[AI]RIE, Institut Necker, and others.
- **Housing and quality-of-life:** Reserved apartments near the Institut, subsidized travel.

Employment Details

- **Monthly salary:** $\sim$ €1160 gross.
- **Work time:** $\sim$ 40 hours/week.
- **Leave:** 2 paid vacation days per month.
- **Benefits:** 100€ of restaurant tickets; public transport reimbursement at 75%.

References

[1] Maxime Dhainaut, Samuel A. Rose, Guray Akturk, Aleksandra Wroblewska, Sebastian R. Nielsen, Eun Sook Park, Mark Buckup, Vladimir Roudko, Luisanna Pia, Robert Sweeney, Jessica Le Berichel, C. Matthias Wilk, Anela Bektesevic, Brian H. Lee, Nina Bhardwaj, Adeeb H. Rahman, Alessia Baccarini, Sacha Gnjatic, Dana Pe'er, Miriam Merad, and Brian D. Brown. Spatial crispr genomics identifies regulators of the tumor microenvironment. *Cell*, 185(7):1223–1239.e20, 2022.

[2] Kimberle Shen, Wan Yi Seow, Choong Tat Keng, Daryl Lim Shern, Ke Guo, Amine Meliani, Irfan Muhammad Bin Hajis, Kok Hao Chen, and Wei Leong Chew. Spatial perturb-seq: Single-cell functional genomics within intact tissue architecture. *bioRxiv*, 2024.

[3] L. Binan et al. Simultaneous crispr screening and spatial transcriptomics reveal intracellular, intercellular, and functional transcriptional circuits. *Cell*, 2025. S0092-8674(25)00197-7.

[4] Adrien Hallou, Ruiyang He, Benjamin D. Simons, and Bianca Dumitrascu. A computational pipeline for spatial mechano-transcriptomics. *Nature Methods*, 22(4):737–750, 2025.

[5] Tingyang Yu, Chanakya Ekbote, Nikita Morozov, Jiashuo Fan, Pascal Frossard, Stephane D'Ascoli, and Maria Brbic. Tissue reassembly with generative ai. *biorxiv*, 2025.

[6] Mohammad Lotfollahi, Anna Klimovskaia Susmelj, Carlo De Donno, Leon Hetzel, Yuge Ji, Ignacio L Ibarra, Sanjay R Srivatsan, Mohsen Naghipourfar, Riza M Daza, Beth Martin, Jay Shendure, Jose L McFaline−Figueroa, Pierre Boyeau, F Alexander Wolf, Nafissa Yakubova, Stephan Günnemann, Cole Trapnell, David Lopez−Paz, and Fabian J Theis. Predicting cellular responses to complex perturbations in high−throughput screens. *Molecular Systems Biology*, 19(6):e11517, 2023.