Ph.D. thesis offer

Statistical methods for the assessment of the departure from equilibrium of biological systems

Cell differentiation is crucial for proper development and therapeutical targeting. Yet, how and when cells acquire distinct fates and what dynamical laws govern the process of cell fate specification remains largely unknown. Thanks to recent developments in high-throughput cell screening, we have nowadays access to large datasets quantifying cell molecular properties over time, i.e., snapshots of cell trajectories over time. Although statistical methods, such as UMAP (Uniform Manifold Approximation), have been proven to be powerful instrument to reconstruct trajectories via dataset correlations over time, little is known about the underlying dynamical properties of these systems and, in particular, to what extent the observed fluctuations depart from an equilibrium state. The aim of this Ph.D. project is that of developing a statistical method combining statistical physics, machine learning and the theory of stochastic processes with large biological datasets to quantitatively assess how far from equilibrium are biological systems and infer the underlying dynamical laws.

The ideal Ph.D. candidate will have a background in theoretical physics, mathematics or computer science. No prior knowledge of biology/bioinformatics is needed but strongly appreciated.

The candidate will be supervised by Silvia Grigolon (Laboratoire Jean Perrin, Sorbonne Université, Paris), Thierry Mora and Aleksandra Walczak (LPENS Paris) and they will thus benefit of the strong interdisciplinary environment of the two institutions and the surrounding community.

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Starting date: October 2024, flexible.

To apply, please send an email with a full CV, motivation letter and one contact for a recommendation letter.