



Loop extrusion as a writer of chromatin memory

Location:	Institut Curie, Paris. 'Nuclear Dynamics' and 'Physical Chemistry' units.
Position type:	Master 1, Master 2 or Engineering school internships. Possibilities to stay as a PhD student or as an engineer can be considered.
Team:	http://www.coulonlab.org/
Supervisor:	Vittore Scolari and Antoine Coulon
Duration:	Ideally, 3 to 6 months.

We are interested in the way chromatin organizes inside the nucleus, and in particular how cellular activities define chromatin conformation and how this can affect the transcriptional regulation. In this project the focus is loop extrusion, a process that has been proposed to control transcription, and consists in the activity of a molecular motor (cohesin) that extrudes loops in the chromosomes of mammalian cells. We want to discover how activities define chromosome shapes, and how shapes can encode for memory and affect cell behavior.

In this context, we are developing two **simulation Python packages**, *polyFlux* and *simLoop*, to perform theoretical studies and make predictions for experiments. The two packages play complementary roles in our simulation framework: simLoop is a flexible implementation of the Gillespie algorithm that can realize different dynamics of the cohesin proteins on DNA, while polyFlux is a powerful innovative numerical



approach that performs polymer simulations using the Rouse model and predicts full probability distribution functions by solving the Einstein-Smoluchovsky equation for this stochastic process. A problem that has a solution in **linear algebra calculations of large matrices**. This tool is currently implemented to run on **CPUs** and **GPUs**, and has the ambition of outperform molecular simulations.

We propose an **internship in Computational** or **Theoretical Physics** to develop, test and utilize polyFlux in order to optimize it to its full potential. The student will choose and work towards *one or more* of the following objectives:

- Work on the eigenvalue problem for a real symmetric positive matrix. Study the general problem and devise optimisations to exploat additional information available.*
- Replace the implementation of the algorithm to use banded or sparse matrices instead of dense matrices. Possibly devising perturbation approaches.^{*†}
- Expand the Rouse model by more general linear models. Currently the beta model is working and implemented, to introduce viscoelastic effects of the nucleoplasm and hydrodynamic interactions.[†]
- Introduce spherical confinement.⁺

We are looking for an enthusiast intern driven by the curiosity for modelling biology, with theoretical/computational physics or applied mathematics backgrounds. Experience of Python and the Numpy package programming is required.

^{*} Objective that requires mostly computational skills

⁺ Objective that requires mostly theoretical skills

Context

Our team studies the physical organization of the genome –in space and in time– in the mammalian nucleus and its relationship with transcriptional regulation or other functional genomic processes. We take a quantitative and interdisciplinary approach at the physics-biology interface, combining advanced microscopy, mechanical micro-manipulation and physical modeling. – More info: http://www.coulonlab.org/

Our team is part of the '**Physical Chemistry**' unit (UMR168), with physicists working on diverse biological topics and the '**Nuclear Dynamics**' unit (UMR3664), with biologists studying different aspects of the cell nucleus.

Institut Curie is a major player in cancer research. It consists of a Research Center for basic research and Hospital group for translational and clinical research. It has more than 1000 employees and is strongly international. It is an inclusive, equal opportunity employer and is dedicated to the highest standards of research integrity.

Application

Contact us at <u>recruitment@coulonlab.org</u> with your CV and a letter explaining your interest in joining our lab.