Université Paris Cité

LPENS
LABORATOIRE DE PHYSIQUE DE L'ÉCOLE NORMALE SUPÉRIEURE

Postdoc Offer

Optimizing a physical RNA force-field via Machine Learning

The importance of the study of RNA molecules has been highlighted by the recent pandemic, with the SARS-CoV-2 virus featuring an RNA-based genome and a replication mechanism controlled by non-coding RNA. The ncRNAs of viral genomes are often more conserved because they perform fundamental functions related to the ability of the genome to be translated, making them interesting targets for drug design. However, the flexible and dynamic nature of RNAs, where multiple structures can be adopted by the same sequence, represents one of the main challenges associated with targeting them with small molecules. Computational modeling using dedicated force-fields can provide a coherent view of the molecule, which can follow this dynamical behavior and include the effect of the environment.
Physical modeling consists in describing a system as a set of particles interacting via some energetic potentials that are responsible for the forces acting among the particles. The set of interactions and the equations describing them in mathematical terms are commonly referred to as a "force field" which can in turn be used to carry out simulations such as molecular dynamics or Monte Carlo. In our group, we develop a coarse-grained RNA model and force-field (HiRE-RNA). Among the currently existing models it is the one retaining the highest resolution and it has been designed with energy potentials chosen empirically to reproduce the main structural behavior of RNAs. The model force-field was originally optimized using standard techniques (genetic algorithm maximizing the energy difference between a native structure and decoys) and limited experimental data. The recent advent of machine learning (ML) provides an array of tools with the potential to dramatically improve both the functional form and parameter optimization.

The main goal of this project is the optimization of our RNA model through ML to obtain a cutting-edge RNA force field to facilitate building functional three-dimensional structures for RNA molecules. We will employ machine learning to optimize the model exploiting extensively the structural data available in databanks and the sparse thermodynamic and dynamic data available from experiments. This approach will allow our model to give much more accurate and reliable structural predictions and to be deployed on systems of more complex architectures than currently possible.
Our aim here is to anchor our force field model deep into the corresponding physics by adapting recent and promising Symbolic Regression algorithms to our data format and selecting the possible improvements in the functional form of the force field uncovered by this technique, based on sound physical principles.

The postdoc will first optimize the current force field using Machine Learning on data generated by atomistic MD trajectories using force-matching and using structural data from Energy Landscape enhanced sampling to obtain a solid starting point for the second, more challenging part of the project, which is the optimization of the functional forms of the energy potentials themselves using a perturbative approach and the symbolic regression.

He/She will test the performance of the new force field by running enhanced sampling simulations such as Replica Exchange Molecular Dynamics and Basin Hopping Monte Carlo to generate the view of the energy landscape and of the thermodynamic behavior of molecules with which we have extensive experience simulating with both the coarse-grained model in its previous version and with atomistic simulations, and for which there is abundant experimental evidence to compare our results, as directly studied by our experimental team.
The postdoc will interact with three other teams (two computational and one experimental) involved in a larger project devoted to developing modeling techniques for drug design targeting RNA molecules.

Duration of the postdoc is of two years, with the possibility of extending it to up to 3 years depending on the candidate's experience level.
The postdoc should start before December 2023.
Starting salary ~2500 €/month.
Research will be conducted in the LPENS laboratory in Paris.

The ideal candidate should have a degree in statistical physics, theoretical chemistry, or structural bioinformatics, with extensive experience in computational methods and molecular modeling. Programming skills are required (Python and possibly a compiled language such as Fortran or C) as well as some previous experience with machine learning techniques. Application of ML method to molecular modeling is a plus.
Previous knowledge of French is not required as all scientific communication can be done in English.

The work will be co-supervised by Pr. Samuela Pasquali, main developer of the HiRE-RNA model, and by Dr. Frederic Lechenault, professor of Machine Learning at Ecole Normal Supérieure in Paris.

If interested, please send a motivation letter, a CV and at least one reference letter to:
samuela.pasquali@u-paris.fr and to frederic.lechenault@phys.ens.fr
We will consider application util a suitable applicant is found.

Samuela Pasquali
Physics professor

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