PhD Project

A new specific knowledge base for modeling and design of RNA-binding protein

Domain: Structural bioinformatics, computational biology, methods development

Key words: KDD; molecular dynamics; RNA-protein binding energy; protein design

Promotor/Supervisor:	Dave Ritchie / Isaure Chauvot de Beauchene
Location:	LORIA (CNRS – INRIA – Lorraine University) at Nancy, France
Starting date:	Between March and December 2019
Duration:	36 months
Funding:	H2020-MSC-ITN project RNAct
Salary:	~2100 euro/month net (+ family allowance if relevant)

Project: The aim of the RNAct project is to integrate experiment and computation to design novel proteins with RNA recognition motifs (RRMs), for exploitation in synthetic biology and bio-analytics. RNAct will create and characterize novel functional RRMs with customized recognition of specific single-stranded RNA (ssRNA). Our approach requires novel computational methodology that can handle the dynamic nature of ssRNA and RRM.

In this global project, our PhD project focuses on two main axis:

1/ **The creation of a complete and comprehensive database** of available RRM information from the many available RRM data covering a broad range of behaviours (with initial help of the other PhD students in the project). This includes their sequence, structure, dynamics, RNA specificity and other data (binding affinity, biological function...). This database will be regularly extended with internal and external data as it becomes available, will be released at the end of the project, and is key to the development of computational approaches in the RNAct project. The PhD student will analyse these different RRM data, and will liaise with the other PhD students to enrich the data with results from in silico methodologies.

2/ **The computation of protein-RNA binding energies** by molecular dynamics simulations of RRM-RNA models obtained by his/her fellow- PhD students. For example, he/she will investigate why the Drosophilia Sex-lethal (Sxl) protein, and its putative human homologue HuR, bind more specific Py-tracts than the U2AF65 protein and cannot accommodate cytosine.

The PhD student will spend 3 month of secondments at the VUB (Brussel, Belgium) to learn about sequence-based methods for protein design and analysis.

Eligibility: European funding require an international mobility: The candidates must not have resided or carried out their main activity in France for more than 12 months in the 3 years prior to the recruitment.

Candidates must have a masters degree in any of the relevant disciplines: (bio-)physics, structural biology, bio-informatics or computer science.

The project is highly interdisciplinary: the day-to-day work involves a lot of programming on atomic representations of proteins and nucleic acids. Good programming skills (preferentially Python and/or C++) are essential. Knowledge of structural biology is very desirable, skills in discrete mathematics and statistics would be appreciated. Most importantly, candidates must be motivated to learn about all disciplines relevant to the project.

Candidates must be fluent either in French or in English.

Applications should be sent on the RNAct centralized application web site. On https://wvranken.wufoo.com/forms/zjepab507unqzd/, select project ESR4