A propos du centre ou de la direction fonctionnelle

Grenoble Rhône-Alpes Research Center groups together a few less than 800 people in 35 research teams and 9 research support departments.

Staff is localized on 5 campuses in Grenoble and Lyon, in close collaboration with labs, research and higher education institutions in Grenoble and Lyon, but also with the economic players in these areas.

Present in the fields of software, high-performance computing, Internet of things, image and data, but also simulation in oceanography and biology, it participates at the best level of international scientific achievements and collaborations in both Europe and the rest of the world.

Contexte et atouts du poste

The PhD will be co-supervised by Marie-France Sagot (DR Inria) and Christine Gaspin (DR Inra). It will take place mainly in the Inria Erable team, which is institutionally associated to and physically located inside the Laboratoire de Biométrie et Biologie Évolutive (LBBE – UMR 5558) of the University of Lyon, with regular visits to Christine Gaspin at the Inra - Toulouse - BIA Unit.

Mission confiée

The idea that sncRNAs are able to regulate gene expression inside a given organism is well accepted. A cell is able to auto-regulate itself by means of sncRNAs (intracellular regulation) or even target other cells and different cell types in such a way as to coordinate a wider response to different stimuli (inter-tissue regulation). These stimuli can be environmental changes in substrate, temperature or salt concentrations, or they can be related to the infection of a pathogen, the competition for food with another organism or the mere existence of a new species in the environment. In this way, organisms are constantly changing their gene expression to accommodate these changes and better survive in the new ecosystem. The study of such changes of gene expression by sncRNAs has relied on the development of a plethora of mathematical models and of computational tools for identifying targets of the sncRNAs (for some more recent surveys of these, see [2,3,6,8,9,10,11]). These use a number of features for such identification, that include (i) seed complementarity between sncRNAs and mRNAs; (ii) evolutionary conservation of the target sites among species; (iii) free energy of the mRNA:sncRNA mixed duplex; (iv) target site accessibility; and in some cases (v) the contribution of multiple binding sites. Which features are reliable and used may vary depending on the kingdom or sncRNA family, with currently more reliable models existing for eukaryotes than for prokaryotes, and mRNA:sncRNA mixed duplexes (seed conservation, accessibility, etc.) and expression profiles from dual sRNAseq data; (ii) evolutionary conservation of the target sites among species; (iii) free energy of the mRNA:sncRNA mixed duplex; (iv) target site accessibility; and in some cases (v) the contribution of multiple binding sites. Which features are reliable and used may vary depending on the kingdom or sncRNA family, with currently more reliable models existing for eukaryotes than for prokaryotes, and mRNA:sncRNA mixed duplexes (seed conservation, accessibility, etc.) and expression profiles from dual sRNAseq data.

Surprisingly however there is growing evidence [4,5,7,12] that supports the idea that these RNA molecules are also able to target another organism and regulate their gene expression, but a whole world remains to be explored in this case, that furthermore contains many open issues [1].

The main objective of this PhD will be divided into (i) developing new algorithmic methods that allow to identify more accurately intra and inter-cellular targets of sncRNAs using both general features (seed conservation, accessibility, etc.) and expression profiles from dual sRNAseq data; (ii) establishing new models for cross-species targets of sncRNAs; and (iii) developing the methods for given such models, inferring the said targets.

Expected results: Better characterisation of sncRNA targets intra and inter-cell/tissues and first time attempts to characterise cross-species targets, new methods for target inference in both cases.

References


Principales activités

As usual for a PhD, we expect that work on the above will lead to publications in international journals or conferences with a selection committee. The algorithms developed should also lead to software that will then be made publicly available.

Compétences

Technical skills and level required: The recruited PhD student should have a background in computer science, with an important experience already in or taste for mathematical modelling. A previous experience with biological problems and with discussing with biologists would be a plus but is not
Languages: A good knowledge of English is required.

Relational skills: Good relational skills, in particular to facilitate a fruitfully interaction with researchers from other disciplines, will be much appreciated.

Avantages
- Subsidized meals
- Partial reimbursement of public transport costs
- Leave: 7 weeks of annual leave + 10 extra days off due to RTT (statutory reduction in working hours) + possibility of exceptional leave (sick children, moving home, etc.)
- Possibility of teleworking (after 6 months of employment) and flexible organization of working hours
- Professional equipment available (videoconferencing, loan of computer equipment, etc.)
- Social, cultural and sports events and activities
- Access to vocational training
- Social security coverage

Rémunération