

Inserm Unit 1011: Nuclear receptors, cardiovascular diseases and diabetes

Research Engineer Bioinformatics

Duration : 1 year renewable

Deadline for application : April 1st 2021

Location : Lille, France

Laboratory: INSERM U1011 Nuclear receptors, cardiometabolic diseases and diabetes

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Key words: Bioinformatics, transcriptomic, high-dimensional data, omics, Biostatistics, R, Galaxy

Host laboratory :

Our laboratory is located in Lille (Northern France), a very active and attractive city at the intersection of Brussels, Paris, and London. The unit is part of the University of Lille, Lille University Hospital, Institut Pasteur de Lille and the European Genomic Institute for Diabetes (EGID, <http://www.egid.fr>).

Our laboratory has a long standing interest in mechanisms involved in the development of metabolic diseases (<https://u1011.pasteur-lille.fr/5/home/>). Our unit comprises over 100 people with a broad range of expertise and interests ranging from molecular biology to clinical research. Bioinformatics is used for data mining in projects involving omics data within the different teams of the laboratory. The successful candidate will be hosted in team “Molecular analysis of gene regulation in cardiometabolic diseases” (<https://u1011.pasteur-lille.fr/5/the-unit/theme-4-integrated-molecular-analysis-of-gene-expression-in-liver-diseases/>).

Job description :

The successful candidate will contribute/support the bioinformatics team in its effort to develop bioinformatic tools and procedures allowing to provide manageable information to biologists. Indeed, our laboratory has set up a local instance of Galaxy for omics data mining. In addition to public tools, this instance comprises in-house developed pipelines such as GIANT (Galaxy-based Interactive tools for ANalysis of Transcriptomic data) (Vandel et al. *Sci Rep.* 2020). The successful candidate will work to maintain this local instance of Galaxy and extend available tools and functions. In particular, he/she will provide a standardized, comprehensive and user friendly transcriptomic analysis pipeline for bulk and single-cell RNA-seq data. In parallel, he/she will teach and provide help/guidance to biologists with regards to their transcriptomic data analyses.

In addition, the successful applicant will also participate in high-dimensional data projects to help biologists mining heterogeneous omics data (e.g. transcriptomics, metabolomics, epigenomics...). Multi-omics data integration will make use of statistical inference and machine learning methods which will need to be identified and developed/adapted by the successful candidate.

Candidate profile : PhD in bioinformatics

- Experience in statistical analyses of transcriptomic data and knowledge in omics data
- Knowledge in Galaxy tools developpement/installation and in R/Bioconductor
- A previous experience in integration of omics data and/or single-cell RNA-seq would be an asset
- Organizational skills, ability to provide synthetic and didactic presentation of scientific results are also required
- Ability to efficiently work and interact with biologist in a pluridisciplinary environment
- Autonomy and team spirit