Inserm U1011: Nuclear receptors, cardiovascular diseases and diabetes. Lille, France

Lead Bioinformatics Engineer – scRNA-seq Data Strategy & Pipeline Development

Duration: 1 year renewable
Deadline for application: June 1st 2025
Location: Lille, France
Laboratory: INSERM U1011 Nuclear receptors, cardiometabolic diseases and diabetes
Contact: Pr Bart Staels, bart.staels@pasteur-lille.fr

Key words: Single-cell RNA sequencing (scRNA-seq); Machine Learning; Computational Pipeline Optimization; Data Strategy; Reproducible Research; Training & Mentorship

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.univ-lille.fr/; https://www.linkedin.com/company/umr1011-pr-bart-staels/). Our unit comprises over 100 people with a broad range of expertise and interests ranging from molecular biology to clinical research. Bioinformatics is used in projects involving (multi-)omics data and the unit comprises skilled bioinformaticians with strong experience in transcriptomic data analyses including single-cell/nuclei RNA-seq.

Available position:

We are seeking a highly motivated Bioinformatics Engineer to lead and define the laboratory's strategy for single-cell RNA sequencing (scRNA-seq) data analysis. The selected candidate will work under the supervision of internal experts and will build-up upon already existing internal pipelines and tools (including tools dedicated to non-programmers). The selected candidate's role will be crucial in further establishing and evolving a centralized analytical framework, ensuring that research teams within the laboratory can effectively develop and refine their scRNA-seq projects.

With this aim, he/she will be responsible for:

- Providing guidance and training to research teams with varying levels of bioinformatics expertise, empowering them to independently advance their projects.
- Evaluating and implementing existing academic and commercial bioinformatics tools, ensuring the most appropriate methodologies are applied.

- Designing, develop, and maintain in-house analysis pipeline(s) to facilitate efficient and reproducible data processing.
- Conducting advanced analyses of selected scRNA-seq datasets and support research teams in their data processing needs.
- Staying updated on cutting-edge scRNA-seq machine learning approaches, ensuring the laboratory adopts state-of-the-art practices.
- Coordinate collaborations with internal and external partners to optimize data analysis workflows.

Candidate profile:

√ Ph.D. or Master's degree in Bioinformatics, Computational Biology, or a related field.
√ Proven expertise in scRNA-seq data analysis, including quality control, preprocessing and clustering.
√ Strong proficiency in at least one programming language and relevant single cell workflows (R: Seurat, Bioconductor; Python: scanpy; Bash).
√ Strong knowledge in machine learning approaches applied to omics data.
√ Familiarity with biostatistics.
√ Ability to develop scalable and maintainable bioinformatics pipelines.
√ Proven strong communication and leadership skills, with the ability to work collaboratively across multidisciplinary teams. The candidate should be comfortable working autonomously with support from supervisors.

Application Process

Interested candidates should submit a CV, a cover letter detailing their experience with scRNA-seq analysis, and contact information for at least two references to Pr Bart Staels (bart.staels@pasteur-lille.fr).