Job opportunity: Postdoctoral fellow in RNA-seq analysis

Duration : 36 months

Location : Cancer Research Centre of Lyon (CRCL, Inserm U1052), FRANCE

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Job description:

A full time post-doctoral fellow position is available at the Cancer Research Centre of Lyon, in the team « Transcriptome diversity in stem cells » headed by Dr. Gabut (http://www.crcl.fr/501-Transcriptome-diversity-in-stem-cells.crcl.aspx?language=en-GB).

Scientific context :

The Gabut team studies rare populations of cancer stem cells (CSC) which are responsible for glioblastomas (GBM), the most prevalent primary brain tumors in adults. These tumors are extremely aggressive and invasive. As a consequence, GBM patients have a median survival of about 18 months and tumor relapse is observed in virtually 100% of cases despite stringent treatments combining surgery, chemo- and radio-therapy. Since CSCs play a key role in both tumor development and relapse, targeting their activity is therefore a priority in order to define innovative and efficient therapeutic approaches to treat GBM patients.

The research Centre :

The Centre Léon Bérard is a national leading cancer research and treatment centre located in Lyon, France. It is composed of a hospital treating adult patients, of a pediatric hospital (IHOP) and of the Cancer Research Centre of Lyon (CRCL).

The CRCL hosts 20 laboratories, including more than 450 staffs, students, clinicians and researchers, developing both cancer fundamental research programs as well as applied research programs to improve cancer diagnostic, prognostic and treatment.

Missions :

The Gabut team combines multi-disciplinary approaches (clinical, cellular, molecular and transcriptomics) in order to :
-   characterize CSCs responsible for glioblastomas ;
-   Identify new markers of CSCs ;
-   Identify novel therapeutic targets to counteract CSC's activities.

The objective of the project is to perform a comparative transcriptome analysis of cancer stem cells, normal stem cells and GBM tumors using next-generation sequencing (RNA-seq). We will integrate the quantitative (gene expression) and qualitative dimensions (alternative splicing, poly-adenylation, binding sites for regulatory factors) of transcriptome regulation. This project will be performed in close collaboration with the bioinformatics plateform Synergie Lyon Cancer of the CRCL (http://www.synergielyoncancer.com/our-projects/bioinformatics-center).

Job objectives:

-   Perform the analysis of NGS data and support the development of the project with biologists, clinicians and bio-informaticians. The candidate will also have the opportunity to develop her/his own research project in the laboratory.
-   Setup analysis pipelines for transcriptomic data (RNA-seq, CLIP-seq).
-   Integrate RNA-seq data with other « omic » data (e.g. : CLIP-seq).
-   Setup bio-informatic tools to develop collaborative projects with clinicians.

- Provide a specific expertise to foster the resolution of scientific questions in the cancer field in coordination with biologists and bio-informaticians.

Required expertise:
- Demonstrated experience in sequence and NGS data analysis.
- Solid knowledge of Unix/Linux and script languages (bash, R, perl/python)
- Prior experience in using a calculation cluster and managing large amounts of data workflows.
- Knowledge in statistics applied to genomics.

Qualifications:
- Ph.D. in computational biology and/or biological science
- Capacity to work at the interface with biologists, clinicians and bio-informaticians
- Real interest for biological questions and medical research.
- Demonstrated ability to take initiatives.
- Demonstrated ability to work independently and as part of a team
- Interest and drive to create their own novel research direction
- Attention to detail and strong organizational skills
- Good verbal and written communication skills.