

Research engineer in data analysis with background in biology

Background

The recent developments of technologies based on high-throughput sequencing (scRNA-Seq, scATAC-Seq, CITE-Seq, Tapestry, spatial transcriptomics...) now allow the analysis of the transcriptome and epigenome in single cells. Combined with imaging, spatial transcriptomics allows to determine the subcellular location of mRNA molecules in cells from histological sections. Finally, the CITE-Seq technology which uses specific antibodies allows to combine transcriptomic and proteomic analysis. All of these technologies have recently revolutionized oncology research to analyse heterogeneity of tumors and to better understand the fundamental mechanisms involved in oncogenesis, such as the processes leading to genetic instability and escape from checkpoints. The research centres (CRCT, IPBS and CBI) involved in this program are at the forefront of research in developing new single cell sequencing modalities.

Missions

This position is to respond collectively to an urgent need for expertise, to support the analysis effort and to boost the development of original tools, and to bring together expert research centres with complementary skills. The person recruited will be responsible for the statistical analysis and processing of data produced by high-throughput sequencing techniques (NGS) and generated by the partner centres. The candidate will be responsible for:

- 1- processing NGS data using existing software,
- 2- training users in the use of this software and associated statistical methodologies,
- 3- implementing and developing new analysis methods and algorithms.

In greater details:

Collect data and control their quality (implementation of procedures for importing data series, cleaning and formatting, detection of outliers ...)

Propose analysis strategies and carry out the required statistical processing sequences

Propose and carry out more specific analyses using existing software or dedicated R packages and scripts

Ensure the implementation and development of R scripts for new analysis methods

Ensure scientific and technical watches in this field

Integrate all analysis and data processing procedures into a quality approach

Provide training and advice to users

Important: this position will be part time @CRCT and part time @CBI

Expected skills

Strong background in biology, molecular biology techniques, genomics, transcriptomics,...

Strong background in bioinformatics (software and statistical methods commonly used for the analysis of NGS data)

Knowledge of R software, analysis software using programming languages commonly used in bioinformatics (Python, Perl, Java etc,...

Knowledge of the main biomedical databases used in oncology (NCBI, TCGA, EBI, KEGG, BROAD, etc.)

Educational level

Master or PhD.

Position details

Starting May 2022, 2 years-contract, starting gross salary: 2400 euros.

Contact: send CV, motivation and recommendation letters to Pierre Cordelier
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