POSTDOC / IR in bioinformatics

Identification du poste :

Fonctions	Postdoc / IR
Emploi type (referens III)	Postdoc / IR
Catégorie	A
Corps	Postdoc / IGR
Quotité	Temps plein / Full time

Affectation : Laboratoire TIMC-IMAG Grenoble, Université Grenoble Alpes, France

Context

The postdoctoral position is funded by the MIAI Grenoble Alpes (Multidisciplinary Institute in Artificial Intelligence), which promotes applications of data science and artificial intelligence in several scientific domains. The MIAI seeks to leverage methodological advances in machine learning, signal processing, statistics, and computational sciences to provide actionable tools for addressing concrete scientific challenges.
The candidate will be hosted in the Computational Biology and Mathematics (BCM) team in the TIMC-IMAG laboratory in Grenoble, made of researchers, engineers and students with skills in bioinformatics, genetics, statistics and physics.
The project will be supervised by Magali Richard, a CNRS researcher. The project involved close collaborations with Yuna Blum (a bioinformatics researcher at the French League against Cancer, Paris) and Jérôme Cros (a cancer pathologist at the hospital Beaujon, APHP, Paris).

Missions

High throughput multiomic cancer studies have described the inter-tumor heterogeneity and led to well defined molecular classifications. Nevertheless, these classifications are neglecting intra-tumor heterogeneity and only reflect the most abundant tumor subtype in the examined sample. The research project aims to develop integrative models of tumor heterogeneity and to infer biological behavior and associated clinical indicators using new computational methods based on Artificial Intelligence.

The successful candidate is expected to develop original methods applied to the study of heterogeneous tumor samples using benchmark datasets. These methods will rely on bio-informatic analysis and integration of transcriptomes, methylomes and chromatin accessibility data coming from original tumor surgical samples. The successful candidate will address the problem of biological confounding factors detection while deconvoluting complex signals. He/She will also assess the impact of multiomic data integration and feature selection in tumor heterogeneity quantification. Finally, He/She will apply the developed algorithms to large tumor cohorts and decipher resistance to standard chemotherapies.

Profil

- PhD degree in bioinformatics (experience in sequencing data analysis and -omic data integration would be considered as an advantage)
- Good communication skills that allow productive interactions with an interdisciplinary team (including computer scientists, biologists and cancer pathologists)
- Programming skills (R, Python, bash), prior experience with relevant analytical software and related packages, knowledge of biostatistics would be appreciated
- Experience in artificial intelligence and machine learning would be appreciated
- Ability to communicate in both spoken and written English
- Autonomous and rigorous with a critical mind, ability to handle and analyze large and various data sets with biological and clinical information
- Prior experience with cancer is not mandatory

Mission d'encadrements : ☐ oui ☒ Non

Expérience professionnelle souhaitée : ☒ débutant ☒ de 2 à 5 ans

General information

TYPE of CONTRACT: temporary, up to 24 months
CONTRACT STARTING DATE: from 01/11/2020 to 01/01/2021
APPLICATION DEADLINE: 01/10/2020

If interested, send a CV, a cover letter and 3 references at

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