Comprehensive analysis of cell type heterogeneity in cancer. Post-doctoral position.

Post-doc (24 months/2 years), starting 01/01/2020

Localisation :

Laboratoire TIMC-IMAG – BCM team. Grenoble, France Contact : Magali Richard. magali.richard@univ-grenoble-alpes.fr

Context.

Successful treatment of cancer is still a challenge and this is partly due to a wide heterogeneity of cancer composition across patient population. Quantification and comprehensive characterization of tumor heterogeneity is of the utmost interest as it is now clear that the multiple components of a tumor are key factors in tumor progression and response to therapy. Advanced microdissection techniques, to isolate a population of interest from heterogeneous clinical tissue samples, are not feasible in daily practice. Bioinformatic tools to estimate and functionally characterize tumor heterogeneity are therefore urgently needed.

Job description.

The research project aims to understand the molecular causes of cellular heterogeneity in gastric cancers, before and after therapeutic treatment. It will rely on bio-informatic analysis and integration of transcriptome and methylome data coming from tumor surgical samples. One approach will specifically reside in heterogeneity quantification by single cell RNA sequencing. This project will be developed in close collaboration with the CIT program of the French league against cancer (Yuna Blum).

Moreover, the successful candidate will be part of the collaborative program COMETH, aiming to develop a benchmarking platform to evaluate deconvolution methods to quantify cell-type heterogeneity within tumors. We expect the successful candidate to be involved in the benchmarking dataset generation and processing, as well as in the elaboration of benchmarking guidelines to evaluate the performance of existing methods.

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.

Profile.

- PhD degree in bioinformatics (experience in -omic data integration and/or sc-RNAseq analysis 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

- 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

Candidates interested in this position should send a cover letter, CV/resume, start date availability, a scientific abstract (one page) of their research project, and three reference letters (recent supervisor/advisor required) to magali.richard@univ-grenoble-alpes.fr.

For the subject line please use "COMETH post-doctoral position 2020".

Candidates can also direct any pertinent questions regarding this position to this e-mail address. Salary is fixed based on Grenoble University internal guidelines