Revenir à la liste des offres d'emplois

Single cell transcriptomics profiling of human and mouse rhabdoid tumours.

Stage · Stage M2 · 6 mois Bac+5 / Master Institut Curie · Paris (France)

Date de prise de poste : 1 février 2023

Mots-Clés

rhabdoid tumours, mouse models, single cell RNA-seq, data integration, SMARCB1

Description

Bioinformatics Internship (Master 2)

“Single cell transcriptomics profiling of human and mouse rhabdoid tumours.”

Description

Rhabdoid tumours are rare and aggressive cancers of young children, occurring at a median age of 20 months. They preferentially affect intracranial tissues, but also various organs such as kidney or liver, and miscellaneous soft parts outside the central nervous system. At molecular level, rhabdoid tumours are characterized by bi-allellic inactivation of SMARCB1, a tumor suppressor gene encoding for a major component of the SWI/SNF chromatin remodeling complex. With an extremely simple genome, these tumours show no other recurrent rearrangement or mutations. However, the cells of origin of these tumours remain to be identified.

In our team, we developed numerous mouse model of rhabdoid tumours in order to address this question but also to provide interesting model for pre-clinical study. In addition, single cell data were generated from human and mouse rhabdoid samples to tackle this question of cells of origin along with the intra-tumoral heterogeneity of the rhabdoid tumours.

Main objectives of the study

Using single cell RNA sequencing (scRNA-seq) data, the trainee will:

- characterize the intra-tumoral heterogeneity of human and mouse rhabdoid tumours,
- integrate human and mouse samples and identify consistent cell populations between the two species
- Identify putative cells of origin for different rhabdoid tumour subgroups

Main missions

- scRNA-seq data pre-processing (from raw data FASTQ files)
- scRNA-seq data analysis including cell filtering, dimensionality reduction and unsupervised clustering to find optimum clustering
- Cell population characterization based on marker genes and reference atlases (in close interaction with biologists)
- Cross-species single cell data integration

Pre-requisites

- Familiar with UNIX command line tools for bioinformatics analyses
- Familiar with R programming language (python is a plus)
- Basic knowledge in statistics and machine learning
- Great interest in the biology of cancer

The internship will take place in the well-known worldwide Institut Curie – Centre de Recherche, in Inserm U830 - RTOP team (Dr. Franck Bourdeaut's Lab) and in Inserm U900 – Bioinformatics Core Facility (Dr. Nicolas Servant's Lab) under the supervision of Dr. Mamy

Andrianteranagna and Dr. Zhi-Yan Han.

Keywords: rhabdoid tumours, mouse models, single cell RNA-seq, data integration, SMARCB1

Candidature

Procédure : Envoyer votre candidature par e-mail à mamy-jean-de-dieu.andrianteranagna@curie.fr contenant votre CV et une lettre de motivation.

Date limite : 31 octobre 2022

Contacts

Mamy ANDRIANTERANAGNA

mamy-jean-de-dieu.andrianteranagna@curie.fr

Offre publiée le 14 octobre 2022, affichage jusqu'au 31 octobre 2022
