



Flora Mikaeloff

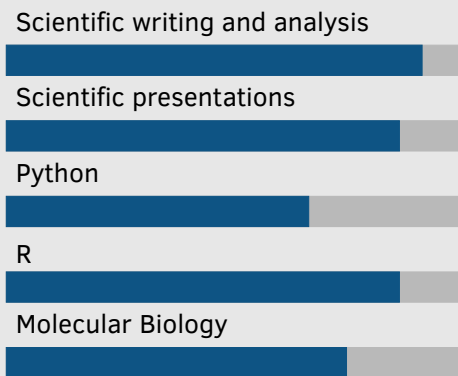
PhD Application

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About me

Currently intern at Karolinska institute. I have a master's degree in genetics from the Paris Diderot University (Paris VII) in France obtained in 2018. I am currently finishing an additional Master 2 in Bioinformatics also at Paris VII. The aim of my project is to develop bioinformatics pipelines towards the proteo-transcriptomics analysis of blood cell population with specific to HIV-infection. I am developing pipelines for proteomics on isolated immune cell populations (CD4 and CD14) using machine learning algorithms.

Skills



Communication*5 Organization*5.5
Flexibility*6

(*)[The skill scale is from 0 (Fundamental Awareness) to 6 (Expert).]

Education

since 2018	MSc in Bioinformatics Specializing in Structure and Genomics	Paris Diderot University
2016-2018	European Magisterium of Genetics 3rd year of bachelor degree and M.Sc. in Genetics	Paris Diderot University
2014-2015	BSc (1st-2nd year) in Biology-Chemistry Majoring in Statistical Tests for Biology	Paris Saclay University
2013	High school Degree with honors Specializing in Biology	High School Claude Monet

Computer skills

Python	Modeller - Biopython - Tkinter - Protein structure prediction project : Meet-U 2019 competition (https://github.com/meetU-MasterStudents/Fold_U)
R	Bioconductor - Statistics - Graphics (PCA, heatmaps, ROC curves, gg-plots) - Differential expression Analysis (limma, DESeq2) - Transcriptomics - Machine Learning (caret, Botura)
Java	Basics
ImageJ	Built-in Macro Functions

Experience

- 01/2019 - ... Development of bioinformatics pipelines towards the proteo-transcriptomics analysis of blood cell population with specific to HIV-infection
Karolinska Institutet, Sweden
Proteomics, Transcriptomics, R, Human Disease, Singleomics, Pathways Analysis
- 01 - 06/2018 Continuation of characterization of SRPK1, a new gene of Renal Hypodysplasia
Imagine Institute, France
Human disease, Western Blot, Cell culture, Whole exome sequencing and RNA sequencing data analysis, Zebrafish modeling
- 04 - 08/2017 Modeling cis-complementation of disease-causing mutations in zebrafish
Duke Center for Human Disease Modeling, United States
Epistasis, Human diseases, Zebrafish modeling, Molecular Biology, Neurology, Sequencing, Immunostaining, Imaging
- 05 - 07/2016 Investigation of tat-2, tat-4 and tat-6 gene expression in Caenorhabditis Elegans
Umeå Center for Molecular Medicine, Sweden
C.elegans genetics, Confocal microscopy, PCR, Behavioural analysis of C.elegans mutants, Phenotypic analysis by light microscopy

Other information

Other experiences Pedagogy (Youth Leadership Certificate in Holiday Camp)
Interests and activities Scandinavian literature, playing celtic harp, handball

Review

Elite controllers (EC) are a small subset of people living with HIV who are resistant to the virus for years without treatment. The aim of my project is to develop transcriptomics (analysis of RNA-seq) and proteomics (analysis of protein quantification by mass-spectrometry) pipelines. I am trying to define biomarkers differing between elite controllers, HIV-infected patients and healthy controls in peripheral blood mono-nuclear cells and isolated cell populations : CD4+ and CD14+. For this purpose, I am comparing differential expression detection tools and supervised machine learning algorithms. I am also working on the proteomics and transcriptomics data integration.