Universitat Pompeu Fabra Barcelona | Master in Bioinformatics for Health Sciences

Master project 2021-2022

Personal Information

Supervisor	Marta Melé
Email	marta.mele.messeguer@gmail.com
Institution	Barcelona Supercomputing Center
Website	https://www.bsc.es/discover-bsc/organisation/scientific-structure/transcriptomics-and-functional-genomics-lab-tfgl
Group	Transcriptomics and Functional Genomics Lab

Project

Computational systems biology

Project Title:

Single-cell transcriptomic analysis across individuals

Keywords:

Cell type deconvolution, single-cell transcriptomics, disease, aging, smoking, meta-analysis.

Summary:

Summary: The candidate will join Marta Melé's Transcriptomics and Functional Genomics lab in the Life Sciences Department at the Barcelona Supercomputing Center. The lab is interested in understanding how individual variation in gene expression and splicing profiles can explain phenotypic differences between individuals both in the context of health and disease. To address this question, we use large-scale transcriptomic analysis and the latest single-cell sequencing technologies combined with methods development to study gene expression, splicing and cell type composition variation across human tissues and phenotypes. In this project, we will perform a large-scale analysis of single-cell RNA-sequencing datasets across tissues to address how individual variation in gene expression can explain phenotypic differences between individuals. First, we will explore human single-cell RNA-sequencing datasets to explore the impact of phenotypes such as aging, smoking and gender on gene expression and cell type composition in blood. Second, we will use cell type deconvolution methods to map single-cell signatures to bulk expression data from individuals affected by a wide array of different conditions from diabetes to cardiovascular diseases, to get a deeper understanding of the disease aetiologies and discriminate between gene expression changes due to differences in cell type proportions, differences in gene expression levels or combinations of both.. Overall, in this project we will explore in depth the role of gene expression and cell type composition in determining why human individuals differ from one another in the context of health and disease. What you will learn: Development of computational pipelines to analyse and interpret large datasets, especially from single-cell RNA-seq, and bulk RNA-sequencing. Working in a High Performance Computing environment. Interpretation of multi-omics data. Scientific collaboration in the context of international consortia, effective communication of research findings in internal and external meetings, scientific writing, and critical thinking. Also, the master student will join the Melé lab journal clubs, lab meetings and lab lunches to talk about science but also have fun and discuss non-science related topics with the group.

References:

Melé, M. et al. The human transcriptome across tissues and individuals. Science (80-.). 348, 660–665 (2015).

Expected skills::

Strong programming skills in bash, python, R, perl, or similar. Excellent communication skills in spoken and written English. Capacity to contribute to research projects with novel research ideas and analysis. Capacity to work as a team in a highly collaborative and diverse environment. Experience working in HPC clusters will be appreciated. Experience with Next Generation Sequencing data analysis will be appreciated. Availability to start in July 2020 is preferred.

Possibility of funding::

Yes

Possible continuity with PhD: :

To be discussed