upf. 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 genomics

Project Title:

Understanding human individual variation in splicing

Keywords:

Transcriptomics, differential gene expression, human populations, splicing, ribosome profiling, posttranscriptional processing, RNA binding proteins.

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 the development of novel methods 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 splicing variation between individuals with different phenotypes and from different ethnic groups. In previous studies, we observed that in certain contexts splicing varies more between individuals than between tissues. Also, we have found that ancestry contributes more to explain splicing differences between individuals than other traits such as age. Remarkably, we observe that ribosomal proteins have strikingly large splicing variation between individuals of different ancestries. This pattern could have functional consequences for the translation machinery that we will explore further. Ultimately, the question that we want to tackle in this project is what is the role of splicing in determining why human individuals are different from one another. What you will learn: Development of computational pipelines to analyse and interpret large omics datasets such as RNA-Seq, single-cell RNA-seq, ribosome profiling, and CLiP-seq. Working in a High Performance Computing environment. 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