

Master project 2020-2021

Personal Information

Supervisor Marta Melé

Email marta.mele@bsc.es

Institution Barcelona Supercomputing Center

Website <https://www.bsc.es/discover-bsc/organisation/scientific-structure/transcriptomics-and-functional-genomics-lab-tfgl>

Group Transcritomics and functional Genomics

Project

Computational genomics

Project Title:

Understanding individual variation in splicing in human populations

Keywords:

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

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 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 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 splicing variation between individuals with different phenotypes and from different ethnic groups. In previous studies, we observed that variation in splicing may play in contrast a comparatively greater role in defining individual phenotypes than variation in gene expression. contributes more to individual variation than to changes in gene expression (Melé et al. Science 2015). Moreover, we observed an enrichment of specific genes showing large splicing variation between individuals that was especially strong for ribosomal proteins and that will be explored further. Ultimately, in this project we will explore in depth what is the role of splicing in defining why human individuals are different from one another. What you will learn: Development of computational pipelines to analyze and interpret large omics datasets such as RNA-Seq, single-cell RNA-seq, ribosome profiling, and CLIP-seq). Working in a high performance computing (HPC) environment. Effective communication of research findings, scientific writing, critical thinking.

References:

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

Expected skills::

Availability to start in July 2020 is preferred Strong programming skills in bash, python, R, perl, or similar, Some experience working in HPC clusters Some experience with Next Generation Sequencing data analysis 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

Possibility of funding::

Yes

Possible continuity with PhD: :

To be discussed
