Master project 2020-2021

Personal Information

Supervisor   Marta Melé

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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 meta-analysis of human disease across tissues

Keywords:

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

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 single-cell RNA-sequencing datasets across tissues to address how individual variation in gene expression can explain phenotypic differences between individuals. First, we will analyze hundreds of single-cell RNA-sequencing datasets to explore the impact of aging, smoking, gender and certain disease conditions to changes in gene expression and cell type composition in blood. Second, we will use cell type deconvolution methods to map single-cell signatures in expression data across many tissues from individuals with different conditions including diabetes and cardiovascular diseases. Overall, this project will explore in depth what is the role of gene expression and cell type composition in defining why human individuals are different from one another and how this impacts disease progression. What you will learn: Development of computational pipelines to analyze and interpret large datasets specially from single-cell RNA-seq, and bulk RNA-sequencing. Working in a high performance computing (HPC) environment. Interpret multi-omics data, working through scientific collaboration, effective communicating research, writing scientific articles and 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 encouraged 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