Transcriptomics and Functional Genomics Lab (TFGL)
The Transcriptomics and Functional Genomics Lab is interested in understanding how the information encoded in our genome determines gene expression variation across individuals and tissues. To address this, we use a combination of cutting-edge computational analyses, next generation sequencing, and high-throughput functional assays. Our goal is to perform integrative analyses of "-omics" data to ultimately understand how expression changes in both coding and non-coding genes are associated with disease.

Objectives

Personalized transcriptomics

Transcriptional regulation plays a central role in cellular identity and tissue organization. Thus, the study of the transcriptome at the organism level is critical to understanding disease. Most disease studies are performed on specific tissues, which can fail to account for differences in cell-type composition, either on a gene-by-gene basis or using a networks approach. Related publication: Melé M, et al. Science. 2015.

GTEx project and thus, we have unique access to human transcriptomics data across hundreds of human individuals and tissues simultaneously. Rather than focusing on specific tissues, we try to understand how the transcriptome at the organism level varies under different environmental conditions, such as smoking or diet, or as a result of differences in cell-type composition, either on a gene-by-gene basis or using a networks approach. Related publication: Melé M, et al. Science. 2015.

Additionally, through collaborations we have access to unique transcriptomics datasets, related to specific diseases such as Ebola, through a collaboration with Pardis Sabeti (Broad Institute of Harvard and MIT), and cancer, through Sandra Peiró's group (VHIO, Barcelona).

Characterization of non-coding regulatory elements

Genome wide association studies have identified hundreds of genomic loci harboring common genetic variants associated with disease. These loci are likely to contain causal non-coding variants, which are able to mediate disease susceptibility. Related publication: Mattioli KM et al. Genome Research. 2018.

We plan on performing MPRA experiments in house very soon but we are also collaborating with the Maass lab (University of Toronto, Canada) to perform MPRA to answer questions related with specific diseases such as breast cancer and hypertension.

Group News

Marta Melé is awarded the L'Oréal-Unesco for Women in Science Award.

Kaia Mattioli is awarded Severo Ochoa mobility grant to visit our lab at BSC Barcelona Supercomputing Center - Centro Nacional de Supercomputación.

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