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 is a key step in understanding the link between gene expression and disease states across many individuals simultaneously. For example, we are involved in the 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 conditions, such as age, sex, or environmental stimuli, and how these differences in cell-type composition, either on a gene-by-gene basis or using a networks approach.


Characterization of non-coding regulatory elements

Genome wide association studies have identified hundreds of genomic loci harboring common genetic variants associated with disease. We hypothesize that differences in disease susceptibility between individuals arise from the effect of specific genetic variants that mediate these differences in 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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