Universitat Pompeu Fabra Barcelona | Master in Bioinformatics for Health Sciences

Master project 2020-2021

Personal Information

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Project

Computational genomics

Project Title:

Decoding transcriptional heterogeneity one cell at a time (Deletome-seq)

Keywords:

single-cell RNA-seq, transcriptional heterogeneity, stress-responses, SAPK

Summary:

Single cell RNA-seq (scRNA-seq) has become the method of choice to dissect complex samples. These studies have provided striking insights such as the identification of novel cell types, but they also unveiled an unexpectedly high degree of transcriptional heterogeneity. The molecular mechanisms underlying this variability are not understood. Yet, cell-to-cell heterogeneity provides a mechanism to alter cell fate and cell identity. Currently, it remains a challenge to understand which mechanisms regulate transcriptional heterogeneity and their consequences. Here we propose to combine single cell transcriptomics with functional genome-wide genetic screen to identify the principles underlying transcriptional heterogeneity.

References:

- Nadal-Ribelles M&, Islam S&, Wei W&, Latorre P&, Nguyen M, de Nadal E, Posas F, Steinmetz LM. Sensitive high-throughput single-cell RNA-seq reveals within-clonal transcript correlations in yeast populations. Nat Microbiol. 4:683-692 (2019). - Nadal-Ribelles M, Islam S, Wei W, Latorre P, Nguyen M, de Nadal E*, Posas F*, Steinmetz LM*. Yeast Single-cell RNA-seq, Cell by Cell and Step by Step. Bio-Protocol Bio-protocol 9: e3359 (2019). - de Nadal E*, Posas F*. Osmostress-induced gene expression - a model to understand how stress-activated protein kinases (SAPKs) regulate transcription. FEBS J. 282: 3275-85 (2015). - de Nadal E, Ammerer G, Posas F. Controlling gene expression in response to stress. Nat Rev Genet. 12: 833-45. (2011).

Expected skills::

Biology, biochemistry or related fields

Possibility of funding::

To be discussed

Possible continuity with PhD: :

To be discussed