Universitat Pompeu Fabra Barcelona

Master in Bioinformatics for Health Sciences

Master project 2024-2025

Personal Information

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Project

Computational genomics

Project Title:

Exploring evolutionary novel genes in the mammalian germline

Keywords:

Chromatin, Transcriptomics, Translatomics, Evolution, Novel genes

Summary:

This project will innovatively combine the fields of genome architecture, transcriptomics and translatomics to detect new genes in the mouse germline. The hypothesis behind this is that chromatin organisation is defined by both the transcriptional state and the evolutionary age of genes. Thus, conserved genes would present a finely tuned system of transcription, with very precise chromatin contacts enhanced by chromatin epigenetic remodelers. while more evolutionary recent genes (e.g., species-specific genes), would not have that tight regulation yet. These more evolutionary recent genes are mostly detected in the brain and the testes, and their appearance and relevance in the germline remains largely unexplored. While most novel genes appear throughout evolution by gene duplication, some new genes arise by de novo mechanisms that entail new transcription in previously inactive regions, and this could be considered an additional local chromatin remodelling event that could directly impact the function of close-by regions. To develop this project, it will be necessary to: i) Define mouse-specific genes using data from Wang et al 2020 and characterise newly evolved proteins, ii) investigate chromatin interaction patterns in regions in which new genes are being born by using Hi-C data available from Vara et al 2019 and references therein.

References:

1. Ruiz-Orera, J., Verdaguer-Grau, P., Villanueva-Cañas, J. L., Messeguer, X. & Albà, M. M. Translation of neutrally evolving peptides provides a basis for de novo gene evolution. Nat. Ecol. Evol. 2, 890–896 (2018). 2. Wang, ZY., Leushkin, E., Liechti, A. et al. Transcriptome and translatome co-evolution in mammals. Nature 588, 642–647 (2020). https://doi.org/10.1038/s41586-020-2899-z 3. Vara, C. et al. Three-dimensional genomic structure and cohesin occupancy correlate with transcriptional activity during spermatogenesis. Cell Rep. 28, 352-367.e9 (2019). 4. Vara, C. & Ruiz-Herrera, A. Unpacking chromatin remodelling in germ cells: implications for development and evolution. Trends Genet. (2021) doi:10.1016/j.tig.2021.10.007.

Expected skills:

R, Linux/Unix, Python

Possibility of funding:

No

Possible continuity with PhD:

To be discussed

Comments:

Group located in the 4th floor of PRBB, at GRIB. Possibility of a hybrid work model.