Universitat Pompeu Fabra Barcelona | Master in Bioinformatics for Health Sciences

Master project 2020-2021

Personal Information

Supervisor	Mar Albà
Email	mar.alba@upf.edu
Institution	IMIM-UPF
Website	evolutionarygenomics.imim.es
Group	Evolutionary Genomics, Research Programme on Biomedical Informatics

Project

Computational genomics

Project Title:

Gene expression dysregulation in cancer and neoantigen formation

Keywords:

Transcriptomics; cancer; small ORFs; neoantigens; immunotherapy.

Summary:

In cancer, genomic structural rearrangements and mutations result in the expression of many novel transcripts that are not expressed in normal conditions. Recent studies suggest some of these transcripts translate peptides that can be presented by MHC molecules and be an important source of neoantigens. Such neoantigens are non-self proteins and could thus trigger a potent immune response and be very relevant for immunotherapy approaches to fight against cancer. However, the lack of studies measuring novel transcriptional events in cancer prevents us from fully understanding the contribution of these neoantigens. The aim of the project will be to perform transcriptome assembly directly from RNA-Seq data using large publicly available cancer cell datasets. In the group we have previously employed massive transcriptomics data to identify recently originated transcripts in human and mouse and predict any encoded protein products (Ruiz-Orera et al., 2015; Ruiz-Orera et al., 2018). Here we will use similar techniques to identify novel, non-annotated, transcripts in cancer cell RNA-Seq data and to characterize putative neoantigens.

References:

Ruiz-Orera, J., Hernández-Rodríguez, J., Chiva, C., Sabidó, E., Kondova, I., Bontrop, R., Marqués-Bonet, T., Albà, M.M. (2015). Origins of de novo genes in human and chimpanzee. Plos Genetics, 11(12): e1005721. Ruiz-Orera, J., Grau-Verdaguer, P., Villanueva-Cañas, J-L., Messeguer, X., Albà, M.M. (2018). Translation of neutrally evolving peptides provides a basis for de novo gene evolution. Nature Ecology and Evolution, 2:890–896.

Expected skills::

Interest in computational genomics and transcriptomics; knowledge of a programming language; knowledge of R; good command of English.

Possibility of funding::

Yes

Possible continuity with PhD: :

To be discussed