Universitat Pompeu Fabra Barcelona | Master in Bioinformatics for Health Sciences

Master project 2020-2021

Personal Information

Supervisor	João Curado
Email	joao.curado@flomics.com
Institution	Flomics Biotech
Website	www.flomics.com
Group	Liquid biopsies group

Project

Web development & bioinformatic tools

Project Title:

Deconvolution of cell-free RNA transcriptome using RNA-seq

Keywords:

Plasma RNA; deconvolution model; sample heterogeneity; diagnosis;

Summary:

Years of literature demonstrate the existence of cell-free RNA, both messenger RNAs (mRNAs) and long noncoding RNAs (lncRNAs) originating from a wide variety of organs, from heart to the brain, and which change in response to external stimuli, namely diseases. Cell-free RNA molecules, circulating in human fluids such as plasma, saliva or urine, are potential windows into the health, phenotype or development stage of a variety of human organs, in a minimally invasive way. Despite this huge promise, the use of RNA sequencing (RNAseq) methods for global profiling of cell-free RNAs is in its infancy. In this project we propose to take advantage of the public available databases of RNA-seq such as Genotype-tissue expression (GTEx) consortium and tissue-specific gene expression databases, to determine the relative RNA contributions of each tissue in a sample using different methods (quadratic programming, least-squares regression, etc.). From a standard plasma RNA-seq experiment, the resulting tool will be used to calculate the relative contributions of the tissues and to monitor unexpected abnormalities that can be used as warning signs for complex disease detection.

References:

Koh, W. et al. Noninvasive in vivo monitoring of tissue-specific global gene expression in humans. Proc. Natl. Acad. Sci. 111, 7361–7366 (2014). Newman, A. M. et al. Robust enumeration of cell subsets from tissue expression profiles. Nat. Methods 12, 453–457 (2015). Everaert, C. et al. Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. Sci. Rep. 9, 17574 (2019).

Expected skills::

Transcriptomics; statistics; programming; autonomy

Possibility of funding::

Yes

Possible continuity with PhD: :

To be discussed
