Universitat Pompeu Fabra Barcelona

Master in Bioinformatics for Health Sciences

Master project 2021-2022

Personal Information

Supervisor	Antonio Julià
Email	toni.julia@vhir.org
Institution	Vall Hebron Institut de Recerca
Website	www.vhir.org
Group	Grup de Recerca en Reumatologia

Project

Computational genomics

Project Title:

Single-cell RNA-seq study of Juvenile Idiopathic Arthritis

Keywords:

single-cell; RNA-seq; autoimmune; TCR; juvenile arthritis

Summary:

Background: single-cell analysis technologies are revolutionizing our understanding of chronic autoimmune diseases. Juvenile Idiopathic Arthritis (JIA) is the most frequent chronic rheumatic disease during childhood, and is a leading cause of disability in the short and long term. JIA encompasses different clinical entities, where oligoarticular JIA (oJIA) is the most prevalent. However, despite involving more than 50% of the juvenile patients, the pathology of oJIA is much poorly understood. Objective: to identify the pathogenic cell subtypes associated with oJIA. Methods: samples of inflammatory synovial fluid and blood from patients with oJIA will be obtained, as well as from healthy control infants. Using single cell RNA-seq technology (10xGenomics), the different cell subpopulations will be identified in both tissues and associated to disease and clinical phenotypes. This project will using cutting-edge technology in a fast evolving and exciting research area.

References:

“Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry.”. Nature Immunology 2019. Massoni-Badosa, Ramon, et al. "Sampling time-dependent artifacts in single-cell genomics studies." Genome biology 21 (2020): 1-16. Prakken, Berent, Salvatore Albani, and Alberto Martini. "Juvenile idiopathic arthritis." The Lancet 377.9783 (2011): 2138-2149.

Expected skills::

Fluency in R and/or Python. Desire to learn

Possibility of funding::

To be discussed

Possible continuity with PhD: :

Yes