Systems biology and network analysis of autoimmune and inflammatory disorders

The i3 laboratory launched in 2015 an observational clinical trial, **Trans*i*mmunom** (NCT02466217) which aims at studying nineteen autoimmune and inflammatory disorders. The final goal is to guide the development of novel and redefine the nosography of autoimmune and autoinflammatory diseases. Our current strategy is **to integrate clinical and "omics" data** to identify and understand the complexity of the immune responses underlying these immunopathologies by applying a systems biology approach. In particular, we focused our investigations on processing, analyzing and creating solutions to integrate transcriptome (RNA-seq), TCR repertoire (Rep-seq), deep immunophenotyping (flow cytometry), microbiome (metagenomics), cytokines (luminex) and clinical (eCFR) data.

Currently, we processed samples from 200 patients (affected by one of the nineteen pathologies) and 50 healthy donors. **Data have been generated and stored in dedicated servers**.

The project proposal for a Master 2 internship aims at developing, under the supervision of a bioinformatician and an immunologist, tools and methods for transcriptome data modelling. We already implemented an automated pipeline that addresses all the conventional steps of RNA-seq data processing and first level analysis (quality control of sequences till quantification of gene expression, as well as differential gene expression analysis). We previously developed an algorithm for gene signature detection [1] based on Independent Component Analysis and Gene Set Enrichment Analysis (ICA-GSEA) for microarray data currently adapted for RNA-Seq data. The candidate will build on this experience to apply this strategy to answer specific biological question regarding the clustering of patients with regard to disease diagnosis, disease severity, treatment…

The laboratory is offering an interdisciplinary environment, including biologists, immunologists, clinicians, computer scientist and bioinformaticians. The current IT infrastructure core services rely on Hyper-V and Windows Servers 2012, Active Directory, SharePoint Foundation 2013 & SQL Server 2012 hosted in the i^3 laboratory, in addition to a new OpenStack-based framework. The candidate will be based in the i^3 laboratory located on the Pitié-Salpêtrière hospital campus in Paris (13ème).

Candidate profile:

MSc students in either bioinformatics, biostatistics, statistics, mathematics or computer science. Significant experience with R tools and coding languages (Python, C++) as well as with linux OS are required.

Application:

Application (motivation letter, CV and references) must be sent in English by email only at encarnita.mariotti-ferrandiz@upmc.fr and felipe.leal_valentim@upmc.fr.

[1] Int J Data Min Bioinform. 2014;9(3):277-304. A novel strategy for molecular signature discovery based on independent component analysis. Pham HP, Dérian N, Chaara W, Bellier B, Klatzmann D, Six A.

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