Opened positions: Bioinformatics engineer
Date posted: October 8th, 2014
Application deadline: December 31st, 2014

Institut Curie is seeking a highly motivated engineer in bioinformatics or computational biologist to work in Vassili Soumelis' research group, in the Immunity and Cancer Unit (U932). The successful candidate will work in close collaboration with the "Bioinformatics and Computational Systems Biology of Cancer" Unit (U900) led by Emmanuel Barillot.

Context

Institut Curie is one of the largest European institutions for cancer research with strong interdisciplinary traditions. It also comprises a hospital specialized in cancer treatment, and therefore disposes of a continuum of expertise from basic research to patient care. It is located in the center of Paris in France, in a both cultural and scientific rich environment.

Projects will be developped under the supervision of Vassili Soumelis, in the Immunology Department headed by S. Amigorena. Our Immunology Department includes 8 independent research teams in the fields of basic and applied immunology, working in a very collaborative and international environment. Importantly, the Immunology Department and the "Bioinformatics and Computational Systems Biology of Cancer" Unit have established a tight and productive collaboration, which has been successful over the past few years to improve our understanding of complex inflammatory and immune reactions, as well as basic mechanisms of signal integration and cell behavior [Touzot et al (Nat. Commun. 2014), Segura et al (Immunity 2013),Volpe et al (Blood 2009),Volpe et al (Nat. Immunol 2008)].

The open position is in line with recent developments at the interface between Immunology, Bioinformatics and Systems Biology.

More information: www.curie.fr and http://u932.curie.fr/.

Mission

Interactions between cancer cells and the tumor micro-environment (TME) play a critical role in tumor development and progression. Among the many components of the TME, dendritic cells (DC), which consist of 4 different subsets, participate in both tumor progression and prevention. Fully characterize breast tumor-associated DC and investigate how the TME contributes to their phenotypic diversity is crucial in our understanding of mechanisms related to the development of breast cancer.

In this context, the candidate's role will be to apply and develop methods to analyze RNA-seq data from breast cancer patients in order to bring new insights into DC immune functions and the mechanisms of tumor-stroma cross-talk by which they are modulated. It includes approaches dedicated to subset-specific signature identification (differential analysis, classification), multivariate analysis strategies (multivariate regression, ACP, ICA, clustering...) and reverse engineering approaches.

Profile

Ideal candidate will have a background in Bioinformatics, Biology or Biostatistics, and good publication records. Extensive experience in bioinformatics and statistical analysis of high-throughput data (quality control, normalisation, differential analysis, pathways enrichment, network reconstruction...), R/bioconductor and unix environment is required. Prior experience with the analysis of RNA-seq datasets as well as some knowledge of cancer biology, cell biology and/or immunology is not mandatory but would be appreciated. The candidate should be able to work independently, on different projects in parallel, be proactive and have excellent communication skills. A working knowledge of English is essential.

Starting date : as soon as possible
Salary : Precise salary will depend on the past experience of the candidate.

Duration : position is open for 1 and up to 3 years.