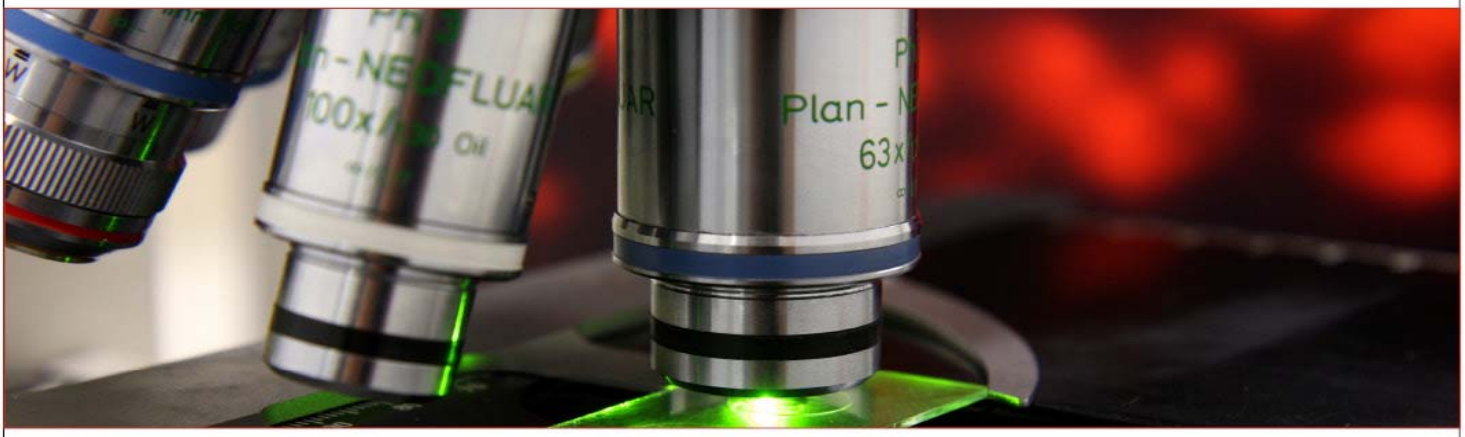
# SÉMINAIRES ET CONFÉRENCES



**Note: Candidate for IVADO Principal Investigator position in computational biology and its applications in biology and medicine (Ste-Justine & Biochemistry)**

## Sajjad Ghaemi

Stanford University

## « Multiomics and Multicohort Integrative Analysis of Full Term, Preterm, and Preeclampsia in Human Pregnancy»

Understanding the biological mechanisms of pregnancy through high-throughput technological advances can provide novel opportunities to analyze pregnancy and its pertinent dysregulations to unravel unrecognized crosstalks. Such crosstalks can shed lights on several lines of investigation. From a biological perspective, it can point to important disease mechanisms such as immune programming by the microbiome, or specific interactions between proteins and cellular elements. From a diagnostic perspective, it can reveal biomarkers from several biological domains with higher predictive power if combined. Most clinical assays ( *e.g.* , those based on ultrasound) can only capture abnormalities at a late pregnancy stage that lack predictive power. Complete profiling of the human pregnancy can only be achieved with a coordinated set of omics assays targeting various levels of biology. The maintenance of pregnancy hugely relies on a finely-tuned immune balance between tolerance to the fetal allograft and protective mechanisms against invading pathogens. Demonstrating the chronology of immune adaptations to a term pregnancy provides the framework for future studies examining deviations implicated in pregnancy-related pathologies including preterm birth and preeclampsia.

In this talk, I will present a machine learning approach for combining data from immunome (measured using mass cytometry), transcriptome, proteome, metabolome, inflammasome, and microbiome. The central tenet of this work is that holistic analyses of pregnancy and its symbiotic interactions with other biological modalities can provide a detailed and actionable understanding of the mechanisms underlying the human pregnancy. In this regard, an Elastic-Net model, with prior distributions extracted from literature-based knowledge will be introduced to develop a predictive model of inter-related biological systems that is accurately able to capture the chronology of pregnancy. Our model components have highlighted existing knowledge, such as enhanced innate immune responses during pregnancy. Next, I will demonstrate how integrative analysis with other assays of the same cohort, including data from the transcriptome, microbiome, proteome, and metabolome can identify a holistic understanding of immunity during pregnancy. This predictive perspective not only significantly increases the predictive power by combining all available datasets, but also is able to reveal unique interactions between different aspects of pregnancy and its dysregulations such as preterm and preeclampsia.



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