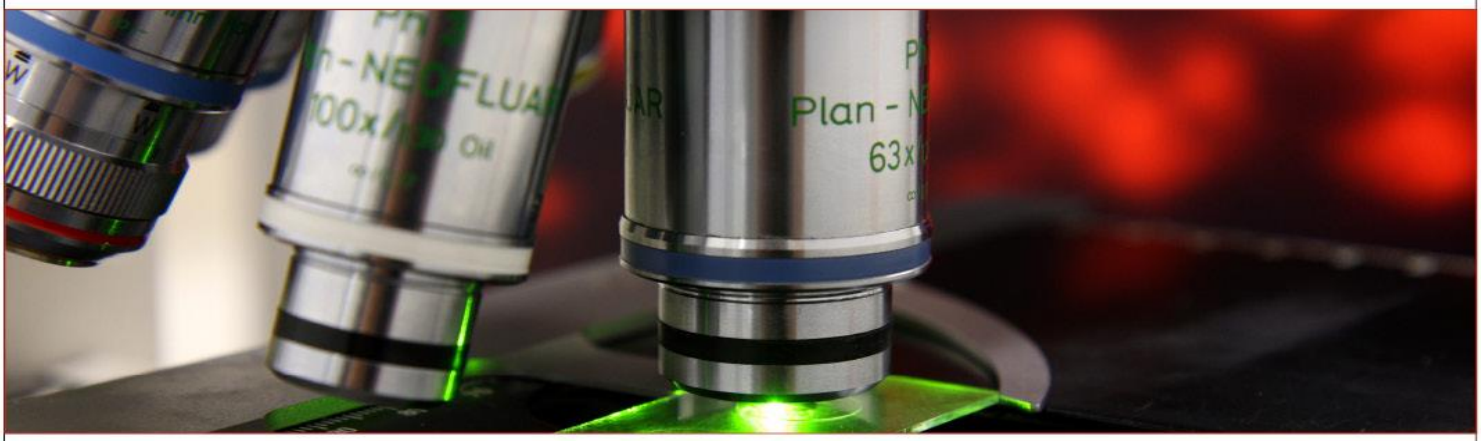
SÉMINAIRES ET CONFÉRENCES



Selin Jessa, Ph.D.

Standford University

'' Deep learning approaches to dissect the regulatory logic underlying transcription factor binding''

Transcription factors (TFs) bind DNA in a sequence-specific manner to activate the right genes at the right time, place, and quantity. Consequently, TF binding mechanisms can be disrupted in disease, or engineered for gene therapies. However, we lack a systematic understanding of how a limited repertoire of TFs regulates thousands of genes in a cell context-specific manner. My research employs interpretable deep learning approaches that map DNA sequence to the physical accessibility of DNA to infer TF binding landscapes. Using these trained models, I design massive *in silico* experiments to systematically interrogate TF binding.

I will discuss two applications of this framework. First, I will present a new multi-omic atlas of human fetal development, where I discovered syntax rules for TF binding sites in the genome, revealing mechanisms of TF cooperativity. Second, by training models in therapeutically relevant blood cell types, I demonstrated that deep learning models can accurately predict the regulatory impact of CRISPR base editors. I show how this approach can prioritize off-target edits based on their predicted disruption to gene regulation, a vital step for improving clinical safety. This work establishes a platform for decoding gene regulatory logic to advance fundamental biology and precision medicine.

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Le lundi 19 janvier, 13h00

Pavillon Joseph-Armand-Bombardier, Salle : 1035

et

Zoom

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