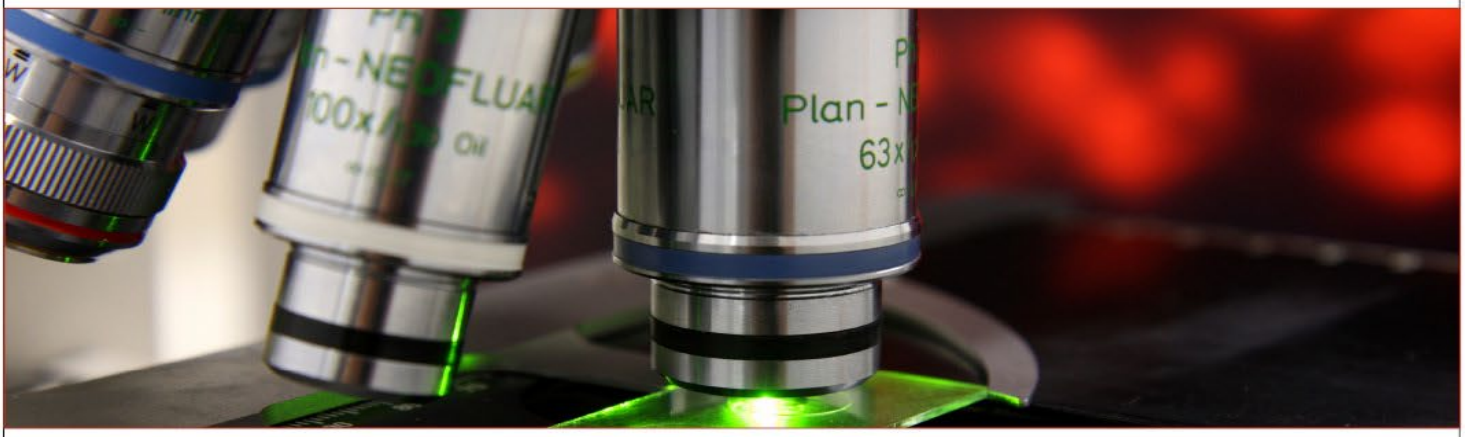
SÉMINAIRES ET CONFÉRENCES



Jean-Benoît Lalanne

Department of Genome Sciences

University of Washington

" High-throughput & quantitative phenotyping of the transcriptional cis-regulatory code "

Complex multicellular development relies on tight spatiotemporal control of gene expression. Yet, in part as a result of the limited throughput of existing experimental approaches, we still only have an fragmentary understanding of the non-coding sequence features that dictate when, where, and at what level genes are expressed along differentiation trajectories in metazoans.

I will introduce a method combining multiplexed reporter assays and single-cell RNA-sequencing to map the activity of cis-regulatory elements in multicellular systems at scale and with high sensitivity. Applied in a stem cell model of early development (mouse embryoid bodies), we screened hundreds of putative cis-regulatory elements for function and discovered numerous lineage-specific enhancers, some of which near critical endoderm-defining transcription factors (e.g., *Gata4* and *Foxa2*). I will further present ongoing experiments leveraging the throughput of the technique to test hypotheses about the regulatory code (e.g., additivity, sub-optimization).

I will conclude by describing the complementary approaches, both experimental (e.g., multiplexed non-coding CRISPRi screen, genome-scale screen of developmental enhancers, porting the technology to combinatorial indexing) and computational (modeling, phylogenetic), I am taking to delineate sequence-to-function maps within regulatory landscapes, and how these fit within the long-term goal of a predictive, quantitative, and multi-scale understanding of the non-coding genome.

MERCK Vivre mieux · VWR · Boehringer Ingelheim · AstraZeneca

Le lundi 1er mai, 11h30

Pavillon Joseph-Armand-Bombardier, Salle : 1035

ET

Lien Zoom

invité de Pascale Legault
pascale.legault@umontreal.ca

Faculté de médecine
Département de biochimie et médecine moléculaire
Université de Montréal