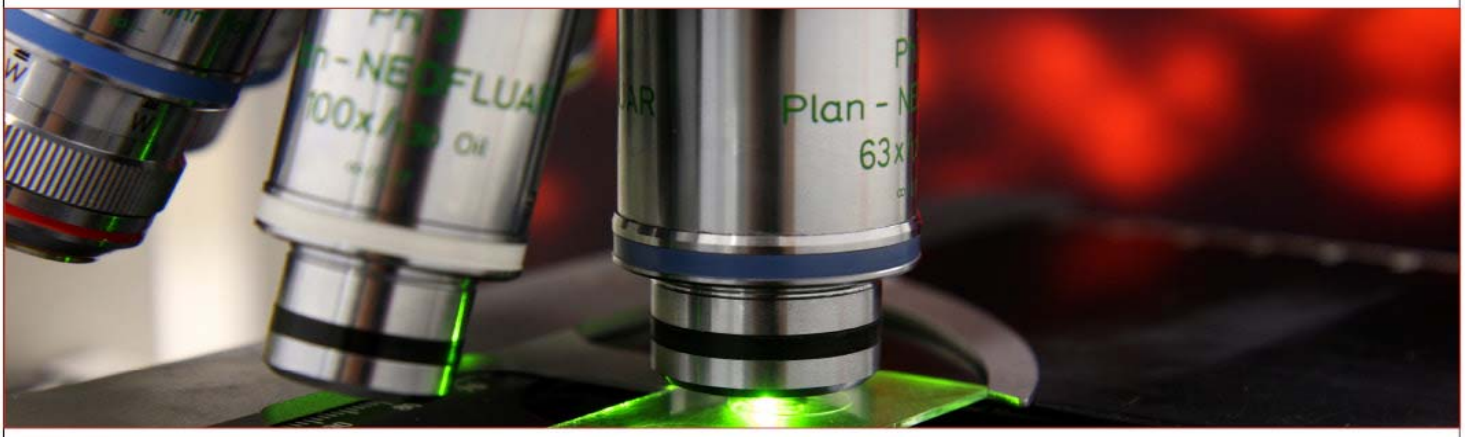
SÉMINAIRES ET CONFÉRENCES



Sébastien Lemieux

IRIC

« Novel tools for cohort-scale transcriptomics »

As a mature technology, RNA-Seq is now routinely applied to characterize abundance changes in mRNAs. The majority of software tools available to identify and exploit these changes were specifically developed for experiments comparing defined groups at relatively low replication levels (N = 3). Thus, we currently have few options to fully take advantage of broad RNA-Seq campaigns, often offering several hundred to several thousand samples for analysis. I will present three approaches developed in my lab over the last few years: i) MiSTIC to visually explore and compare gene correlation clusters across cohorts, ii) km to rapidly and accurately identify sequence variants from raw RNA-Seq reads, and iii) Factorized Embeddings, a deep learning framework, allowing for flexible, RNA-Seq-driven integration of heterogeneous data. These approaches will be demonstrated on three datasets: Leucegene (437 AML samples), TCGA (10,407 samples from 33 cancer types) and GTEx v6 (8,910 samples from 30 tissue types).

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