SÉMINAIRES ET CONFÉRENCES

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"Decoding cancer through transcriptomics"

Complex and heterogeneous disorders such as cancers remain hard to treat in the clinic. Factors complicating the development of new cancer treatments include how driver mutations differ between and within cancer types, how the number of mutations is high in certain cancer types but low in others, and how the cellular pathways underlying oncogenesis vary between cases. These observations raise two critical questions: 1) Are there common molecular signatures of cancer? and 2) Can we target cancer-specific molecular variations to develop new therapies?

I will present how we identified patterns of transcriptomic variations that are common across a large array of tumor types using machine learning modeling on a dataset comprising 13,461 RNA-Seq samples from normal and tumor tissues. These signatures exist in the form of protein-coding gene expression, long non-coding RNA expression and splice junction usage variations, and point to a central role of RNA processing in cancer. I will also introduce a novel computational pipeline that leverages transcriptomic variations to identify tumor-specific antigens that could be targeted with immunotherapy. This pipeline uncovered splice junctions that modify extracellular regions of cell surface proteins and that are used by B-cell acute lymphoblastic leukemia cells but not by any of 48 normal tissue types surveyed. Together, these projects highlight how the analysis of the transcriptome can provide new insight into complex disorders, in particular cancer.

Lien zoom:
https://umontreal.zoom.us/j/89560119712?pwd=ZWVMOXpXWC9JNS95YjJOamQ1d3lYdz09

Le lundi 4 avril 2022, 11h30

Invité de Pascale Legault

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