TCAG New Technologies Seminar

Illuminating the "Dark Matter": Mapping of the Structural Variation of the Genome, and *de novo* Assembly

Date: **Monday May 2nd**
Time: **3 PM**
Location: **Event Room 3a/b, PGCRL**
Peter Gilgan Centre for Research and Learning
686 Bay Street, Toronto, ON M5G 0A4
Speaker: **Nancy Groot**
BioNano Genomics

The majority of complex genomes is made up of repetitive and regulatory elements, yet our current analysis of the genome focuses on single nucleotide changes and exome sequencing. The "Dark Matter" that controls most of our genome is largely ignored, because short read sequencing is unable to map these highly repetitive sequences.

BioNano Genomics' Irys instruments use nanochannels to linearize and image megabase size single DNA molecules. This extremely long read data can elucidate genome-wide complex structural variation, like balanced/unbalanced translocations, inversions, and large indels. Our *de novo* genome maps can identify Copy Number Variations, resolve complex repetitive regions, and scaffold NGS contigs to create better-than-reference assemblies.

Coffee and Snack

Hosted by The Centre for Applied Genomics and the Ontario Genomics Institute

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