Rapid SV Detection and *De Novo* Assembly in Complex Genomes Using Extremely Long Single Molecule Level Imaging

January 29, 2014
10:00 AM
Q&A to follow

Hosted by:
Princess Margaret Genomics Centre
TMDT 4-204
Light refreshments provided.

Despite continued cost reduction in raw base generation, improvement in base-calling accuracy, and recent advances in read length, complete *de novo* assembly and genome wide structural variant analysis of individual large complex genomes remain expensive and challenging.

We present here a rapid genome wide analysis method based on a new NanoChannel Array technology (Irys) that dynamically streams and linearizes extremely long DNA molecules for direct image analysis at tens of gigabases per run. This high-throughput platform automates the imaging of genomic DNA hundreds to thousands of kilobases in length at the single molecule level, for unambiguous assembly of complex genomes. High-resolution genome maps assembled *de novo* via unique sequence motif labeling, preserving long-range structural variation information that is intractable by current short read NGS platforms. This information is independent of current sequencing biochemistry

BIONANO GENOMICS