BIONANO GENOMICS SEMINAR

You're Invited!

Bionano Genome Mapping Builds the Most Contiguous and Correct Genome Assemblies

High throughput sequencing technologies have made the generation of genomic sequences increasingly affordable, but organizing these reads of hundreds to thousands of basepairs into entire genomes remains challenging.

The Bionano Genomics solution for whole genome optical mapping offers an extremely long-read technology, providing the ability to assemble chromosome-arm length maps used to scaffold sequence contigs and correct assembly errors. Additionally, Bionano has unmatched sensitivity to identify all major types of structural variation.

Examples will be presented of how the Bionano Saphyr platform is helping to build the most complete and accurate genome assemblies, and how it compares to other scaffolding methods like Hi-C.

Next-Generation Cytogenomics: High-throughput Mapping of Structural Variation in Cancer and Genetic Disease

The diagnostic yield in genetic disease has seen very little improvement over the last few decades, despite the introduction of whole genome sequencing. The promise of personalized medicine in cancer remains elusive, because no single technology can comprehensively detect all the rearrangements in the cancer genome.

Bionano Genomics' platform for whole genome mapping offers an extremely long-read technology, providing unmatched sensitivity to detect structural variation, genome wide, at low cost. Our de novo maps can resolve complex repetitive regions, identify Copy Number Variations, and elucidate genome-wide structural variation like balanced/unbalanced translocations, inversions, and indels with much higher sensitivity and precision than sequencing-based methods.

For heterogeneous cancer samples or mosaic patient cases, Bionano's extremely high coverage depth allows for the detection of any type of structural variant with more than 90% sensitivity, present in as little as 5% of the cells, genome wide, and completely unbiased.

Examples will be presented of how Bionano's platform is helping provide a molecular diagnosis for patients with undiagnosed genetic disorders, and how it elucidates genomic rearrangements in cancer that are missed by NGS and cytogenetic methods.

Event Info

DATE:

Monday, 10th February, 2020

TIME:

10:30 – 11:30AM

LOCATION:

University of Queensland

AIBN SEMINAR ROOM

Building 75

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THANKS TO:

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For more information about the Saphyr® System, please visit www.bionanogenomics.com