You’re Invited!

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 80% sensitivity, present in as little as 10% 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.

Coffee and pastries will be provided

Event Info

DATE: Thursday, May 2nd, 2019

TIME: 10:00 AM to 11:30 AM – Seminar/Q&A

LOCATION: BSRB, ABC seminar rooms 109 Zina Pitcher Place Univ of Michigan Ann Arbor, MI 48109

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