Bionano Genomics Announces Immediate Availability of New Suite of Genomic Analysis Tools

SAN DIEGO, CA – April 4, 2017 – Bionano Genomics®, Inc., a company focused on genome structure analysis, today announced the immediate availability of its entirely new suite of tools for genome assembly, structural variation (SV) detection, and visualization of the genome's true structure. The Bionano Access™ 1.0 and Bionano Solve 3.0 software tools are released as a free download, and will be introduced during two live webinars on Wednesday, April 5.

Mark Borodkin, Bionano's Vice President, Systems Development, commented, "With Bionano Access and our updated Bionano Solve analysis pipeline, we are making it easier than ever for scientists to get more value from Bionano genome maps related to their genome research. Following feedback from our customers, we have designed Bionano Access to be feature-rich, fast and intuitive. Bionano Access is also a browser-based application, allowing it to be run on an enterprise server or a lightweight laptop; Linux, Windows, macOS supported. Coupled with Bionano Solve, Bionano Access provides a powerful set of new tools for identifying structural variants or performing hybrid scaffolding, and this will benefit any scientist studying the true structure of the genome."

Bionano Access centralizes all software tools required to generate, edit, analyze and visualize Bionano maps. For Irys® users, it replaces the IrysView software. It enables visualization of Bionano results in a web browser, providing instantaneous interaction with Bionano maps used for the scaffolding and SV applications.

Bionano Access also comes with a powerful variant annotation pipeline that can filter out common variants based on a database of controls, analyze trios or two samples to identify inherited and de novo SVs, and visualize and export in a dbVar-compliant VCF file for downstream analysis.

Hybrid scaffolding is enhanced with map editing, improved two-enzyme scaffolding and NCBI-compliant data exporting.

When connected with the Saphyr™ System it allows users to set-up experiments, start runs, monitor data quality metrics in real-time and automatically start de novo assemblies and SV discovery analysis when enough data is collected.

The Bionano Solve 3.0 assembly pipeline within Bionano Access allows users to run SV analysis or hybrid scaffolding. Bionano Solve 3.0 automatically calls SVs with unprecedented sensitivity. Insertions and deletions larger than 1 kilobasepair (kbp) are detected with more than 90% sensitivity and translocations with 98% sensitivity. Significant improvements to translocation calling and masking of common variants significantly reduces the false positive translocation calls.

The pipeline also significantly improves the hybrid scaffolding application by integrating two genome maps created separately with different nicking enzymes. Compared to the prior version, the new two-enzyme hybrid scaffolding incorporates up to 50% more NGS contigs in the assembly, improves contiguity significantly and allows for improved resolving of conflicts and correction of chimeric sequence contigs. This application continues to support any NGS data of suitable quality.

Bionano has validated these tools across a variety of patient samples, including those with undiagnosed disorders and leukemia.

"We have applied Bionano genome mapping technology to a variety of cancer cell lines and primary patient leukemia samples and compared our results to those obtained by other genome mapping techniques, such as cytological karyotyping and whole genome sequencing," said James Broach, chair of Biochemistry and Molecular Biology, Pennsylvania State College of Medicine. "In all cases, using the Bionano technology, we were able to detect all the translocations identified by these other techniques but were also able to detect many more translocations that had not been identified by those techniques. Moreover, we also detected hundreds of deletions and insertions that could not be seen by these other methodologies and therefore whose role in cancer onset and progression have not been evaluated. Given increased speed, lower cost, higher sensitivity and greater reliability of the Bionano technology, we surmise that it may supplant classical cytology as the primary method for clinical detection of genomic structural variation."

Bionano is introducing key new features in Bionano Access and Bionano Solve during two webinars on Wednesday April 5th, at 9 am and at 6 pm PDT / 12 pm and 9 pm EDT. They can be found online here Webinar 1: April 5th, 9am PDT and Webinar 2: April 5th, 6pm PDT and will be available shortly thereafter for replay on the Bionano website on new support pages dedicated to Bionano Access and Bionano Solve.

About Bionano Genomics®

Bionano Genomics, Inc. provides the Irys and Saphyr systems for next-generation mapping (NGM), which is the leading solution in physical genome mapping. NGM offers customers whole genome analysis tools that reveal true genome structure and enabling researchers to capture what's missing in their data to advance human, plant and animal genomic research. NGM uses NanoChannel arrays to image DNA at the single-molecule level with average single-molecule lengths of about 350,000 base pairs, which leads the genomics industry. The long-range genomic information obtained with NGM detects and deciphers structural variations (SVs), which are large, complex DNA segments involving repeats that are often missed by sequencing technologies and which are a leading cause of inaccurate and incomplete genome assembly.

As a stand-alone tool, NGM enables the accurate detection of SVs, many of which have been shown to be associated with human disease as well as complex traits in plants and animals. As a complementary tool to next-generation sequencing (NGS), NGM integrates with sequence assemblies to create contiguous hybrid scaffolds for reference-quality genome assemblies that reveal the highly informative native structure of the chromosome. NGM also provides the additional ability to verify, correct and improve a NGS-generated genome assembly.

Only Bionano provides long-range genomic information with the cost-efficiency and high throughput to keep up with advances in NGS.

NGM has been adopted by a growing number of leading institutions around the world, including: National Cancer Institute (NCI), National Institutes of Health (NIH), Wellcome Trust Sanger Institute, BGI, Garvan Institute, Salk Institute, Mount Sinai and Washington University. Investors in the Company include Domain Associates, Legend Capital, Novartis Venture Fund and Monashee Investment Management.

For more information, please visit www.BionanoGenomics.com.

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