

For Immediate Release

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GenomeQuest and INRIA Announce Collaboration in Genome Mapping Technology for Multi-Genome Analysis

Westborough, MASS., January 18, 2011—[GenomeQuest](#) and [INRIA](#) today announced the integration of the GASSST technology into the GenomeQuest sequence data management (SDM) platform. Licensed by GenomeQuest from INRIA, GASSST is an advanced, open-source genome read mapper designed to maintain accuracy and high-performance as datasets scale to billions of reads with lengths beyond 100 nucleotides.

Jean-Jacques Codani, GenomeQuest CSO, comments, “Our priority is to enable multi-genome analysis at NGS resolution for our users. In this demanding environment, mappers must maintain high accuracy as projects scale to large and widely heterogeneous collections of datasets. After an exhaustive evaluation, GASSST not only met this top requirement but its elegant design proved a strong structural and performance fit into our platform. We're very excited about the integration and feel that the combination will accelerate the advance of GenomeQuest users and their organizations to multi-genome analysis.”

Dominique Lavenier, GASSST scientific leader, notes, “The integration of GASSST into a broad industry platform like GenomeQuest is a very gratifying and important step for our team and organization. It allows us to directly contribute to and participate in the larger world of comparative genomics, multi-genome analysis, and personalized medicine research. And the expansive feedback will be fundamental to keeping GASSST as a technology leader in mapping accuracy and performance.”

The GASSST technology and algorithm was recently published and detailed in *Bioinformatics*. GenomeQuest and the mapping team collaborated closely on this six-



month integration project. Specifically, GASSST was built into the [GQ-Engine](#) -- the sequence database engine at the heart of GenomeQuest.

As a result, the GASSST mapper inside the GQ-Engine provides the following features:

- Supports reads from all sequencing technologies
- Handles all read lengths from ultra-short to very-long reads, with a variable number of errors, and no restrictions on the number of indels
- Maps to any kind of reference, from mRNAs to complete genomes, including contigs, without the need of pre-built, static indexes
- High-performance and scalable to NGS and multi-genome analysis in commercial data centers

These capabilities are available as a deployed solution or using the GenomeQuest hosted service. The hosted service, based on a joint GQ-SGI architecture, is now processing hundreds of deep coverage genomes per month. The GASSST mapping choice is now available in the GenomeQuest whole/multi-genome analysis, ChIP-Seq, RNA-Seq, and additional workflows.

Immediately, researchers can apply the accuracy and performance advantages of GASSST in multiple phases of their multi-genome analysis work: in prepping raw sample data for analysis, in prepping large datasets for inclusion in downstream comparisons, and/or for re-prepping retained evidence in future analysis.

GenomeQuest and INRIA have agreed to continue their collaboration with efforts focused on GASSST performance optimization inside GenomeQuest.

Codani adds, “The relationship with INRIA on GASSST has been both a technical and commercial success and we look forward to further collaboration and progress. More broadly, we’ll continue to avidly support and engage the open source community – their work is critical to the progress of genomics and continued leadership of GenomeQuest.”

Philippe Gesnouin, Technology Transfer Associate for the Life Science market at INRIA, comments, “We are delighted with the collaboration with GenomeQuest. The relationship



has been a clear win-win – our open source, enabling technology has advanced the GenomeQuest product while their platform and commercial support will clearly expand the application and rewards of our work.”

GASSST was developed by the Symbiose group of CNRS, the French National Center for Scientific Research, in concert with INRIA and the University of Rennes. CNRS is a government-funded research organization, under the administrative authority of France's Ministry of Research. The University of Rennes is the leading higher education and research center in western France with a strong emphasis on genomic and bioinformatics research activities.

This announcement follows this month's announcement by GenomeQuest and Ingenuity that the two companies are partnering to support next-generation sequencing workflows specifically targeted for personalized medicine research. Specifically, the companies will integrate GenomeQuest's Sequence Data Management (SDM) platform with Ingenuity's IPA software. As a result, researchers can seamlessly exchange gene information, perform interactive analysis, and create and test hypothesis across the domains of genome sequencing and biological pathways.

About INRIA

INRIA, the French national institute for research in computer science and control, operating under the dual authority of the Ministry of Research and the Ministry of Industry, is dedicated to fundamental and applied research in information and communication science and technology (ICST). The Institute also plays a major role in technology transfer by fostering training through research, diffusion of scientific and technical information, development, as well as providing expert advice and participating in international programs.

About GenomeQuest

GenomeQuest, the global leader in sequence data management, helps life science organizations realize the full promise of genomics. Over 160 leading health and agriculture companies use GenomeQuest for mission-critical work, including nine of the top ten pharmaceuticals. The core technology of the company is the GQ-Engine -- a



sequence database engine that is purpose-built for storing, managing, and analyzing sequence data at whole- and multi-genome scale.

Learn more at <http://www.genomequest.com>.