



For Immediate Release

Convey Computer's Implementation of PacBioToCA Algorithm Speeds DNA Sequence Assembly, Delivering Up to Fifteen Times Acceleration

--PacBioToCA Is the Newest Addition to Convey's Expanding Bioinformatics Suite, Helping to Speed Genomic Research--

Richardson, Texas—December 11, 2013—Convey Computer™

Corporation announced today the newest addition to Convey's expanding bioinformatics suite, PacBioToCA, an application that facilitates the assembly of genomes sequenced with Pacific Biosciences® long-read technology. Optimized to take advantage of the highly parallel processing architecture of the Convey hybrid-core (HC) server, PacBioToCA delivers six to fifteen times acceleration.

Researchers running PacBioToCA on Convey HC systems for sequencing and assembly are seeing exceptional results. "The speed up is significant; but even more importantly, researchers are now able to test more parameters," commented Dr. George Vacek, Director of Convey Computer's Life Sciences business unit. "Achieving results in a matter of days instead of weeks allows them to refine their approach and get better answers."

The PacBio® RS II DNA Sequencing System, from Pacific Biosciences (Nasdaq:PACB), helps scientists solve genetically complex problems. Their single-molecule sequencing instruments can generate industry-leading sequence read lengths that dramatically improve genome and transcriptome assembly.

Researchers are attracted to the exceptionally long PacBio reads because they can deliver higher quality assemblies. Prior to the development of algorithms optimized for PacBio read data (such as PacBioToCA), single-pass error rates had been perceived to limit their utility in *de novo* assembly.

Last year, Dr. Sergey Koren, Bioinformatics Scientist at the National Biodefense Analysis and Countermeasures Center, and his colleagues

developed an assembly strategy that uses short sequences (either from PacBio circular consensus sequencing or short read technologies) typical of high-throughput sequencers to correct the errors in PacBio reads. This strategy was subsequently extended to use shorter single-molecule reads to correct the longest ones. These techniques deliver high-accuracy long reads, resulting in gold standard genome assemblies.

For larger genomes, the PacBioToCA algorithm can be time-consuming; therefore, Koren collaborated with Convey to optimize the PacBioToCA algorithm for Convey's highly parallel HC systems. The optimized version of PacBioToCA runs much faster on the Convey HC servers because the alignment algorithm it uses is significantly faster on a Convey HC-2^{ex} server than the best implementation on a standard server.

"It has been shown that long PacBio reads processed with PacBioToCA lead to such high-quality assemblies, researchers are saved the significant subsequent cost of manual finishing," explained Kevin Corcoran, Senior Vice President of Market Development at Pacific Biosciences. "The combination of the PacBioToCA algorithm and a Convey HC system allows our customers to dramatically speed up research for projects in areas such as functional genomics, comparative genomics, and beyond."

Convey's groundbreaking hybrid-core computing architecture tightly integrates advanced computer architecture and compiler technology with commercial, off-the-shelf hardware—namely Intel® Xeon® processors and Xilinx® Field Programmable Gate Arrays (FPGAs). Particular algorithms are optimized and translated into code that's loaded onto the FPGAs at runtime to accelerate applications that use these algorithms. The systems help customers dramatically increase performance over industry standard servers while reducing energy costs associated with high-performance computing.

"Adding PacBioToCA to the Convey Bioinformatics Suite reflects our ongoing commitment to the bioinformatics and life sciences community," concluded Vacek. "We enjoy working with innovators to bring solutions to the industry that will help solve the challenges of the rapidly changing area of sequencing. We look forward to continuing to collaborate with Pacific Biosciences and others on optimization of bioinformatics workflows."

Convey's expanding bioinformatics suite is made up of a number of personalities including the Convey GraphConstructor™ for *de novo* short read assembly, Smith-Waterman for local sequence alignment, and Burrows-Wheeler Aligner for fast reference mapping.

About Convey Computer Corporation

Based in Richardson, Texas, Convey Computer breaks power, performance and programmability barriers with the world's first hybrid-core computer—a system that marries the low cost and simple programming model of a commodity system with the performance of a customized hardware architecture. Using the Convey hybrid-core systems, customers worldwide in industries such as life sciences, research, big data, and the government/military enjoy order of magnitude performance increases while reducing acquisition and operating costs.

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