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Convey Computer Announces Record-Breaking Smith-Waterman Acceleration of 172x

***Innovative Hybrid-Core Computing Ideal Match for 'Data Deluge'
at University of South Carolina and
Virginia Bioinformatics Institute***

RICHARDSON, Texas (May 24, 2010) – Convey Computer™ Corporation announced today that its implementation of the Smith-Waterman algorithm, widely used in life sciences applications for aligning DNA and protein sequences, is 172x faster than conventional methods and represents the fastest Smith-Waterman implementation¹ to date.

Convey is focused on increasing the computer processing productivity required by life sciences applications – applications where analyzing 340 terabytes of data is the norm and developing complete phylogenetic trees is just another day at the research lab. With such hefty performance increases in Smith-Waterman and other algorithms, bioinformatics and computational biology researchers are able to discover more information about genes and, in turn, find new ways to cure and manage diseases.

Convey's revolutionary hybrid-core computing architecture tightly integrates advanced computer architecture and compiler technology with commercial, off-the-shelf hardware – namely an Intel® Xeon® processor and Xilinx® Field Programmable Gate Arrays (FPGAs). The systems help customers

¹According to Convey's internal benchmarking, the Smith-Waterman implementation is 172x faster than SSEARCH in FASTA on an Intel Nehalem core using the SIMD SSE2 instruction set. The company's hybrid-core computer can process 688 billion cell updates per second (GCUPS) as compared to four GCUPS for SSEARCH in FASTA.

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reduce energy costs associated with high-performance computing, while dramatically increasing performance over industry standard servers. Additionally, Convey systems are easy for programmers to use because they provide full support of an ANSI standard C, C++ and FORTRAN development environment.

The FPGA-based architecture is a blank slate for application innovation, meaning it is especially well suited for the life sciences research underway at the University of South Carolina and Virginia Bioinformatics Institute (VBI) at Virginia Tech. Both institutions are recent Convey customers.

According to Dr. Jason D. Bakos, assistant professor at the University of South Carolina with the Department of Computer Science and Engineering, the mission of his Heterogeneous and Reconfigurable Computing Group is to “use reconfigurable coprocessor technology to accelerate applications that have never been accelerated before.” Such applications range from computational phylogenetics and sparse linear algebra to data mining and logic minimization. Additionally, the research group focuses on uncovering new design methodologies for high-performance computing ranging from developing new automatic partitioning tools to improving system architecture with multi-FPGA interconnects.

Beyond working with new computer systems, Dr. Bakos and his team develop “non-traditional applications” such as computationally intensive phylogenetics inference methods. Computational phylogenetics, which studies the evolutionary development of a species or group of organisms, involves the search for the most accurate “evolutionary tree” from a space of possible trees. The search space grows exponentially with the number of inputs, going from 2 million possible trees for 10 species to 25 *trillion quadrillion* (2.5×10^{28}) possible trees for just 25 species.

Aside from the size of the search space, assessing the accuracy of each candidate tree itself involves complex methods in order to match a specific tree to its evolutionary model – a computationally expensive operation. By studying the past and building accurate phylogenetic trees, scientists are able to more

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quickly identify treatments to combat everything from an emerging virus to pesky weeds growing in a front yard.

“Convey’s FPGA-based coprocessors are much more flexible and amenable to the optimization algorithms used in computational biology,” said Dr. Bakos. “Convey offers a complete system and full support, which allows us to focus on using the machine for our research as opposed to wasting time on getting the machine to work.”

By using bioinformatics, which combines transdisciplinary approaches to information technology, medicine and biology, researchers at VBI generate, interpret and apply vast amounts of data from basic research to some of today’s key challenges in the biomedical, environmental and agricultural sciences.

Dr. Harold “Skip” Garner, executive director of VBI and a professor in the Department of Biological Sciences at Virginia Tech, explains that VBI will use Convey’s hybrid-core platform for its data analysis work for the 1000 Genomes project (an international effort to sequence the genomes of approximately 2,500 people from about 20 populations around the world). The team has looked at 340 terabytes of data so far and much more is anticipated. The Convey systems will also be used to support text data mining as well as decision and policy informatics work at the Institute.

VBI is a leader in the new field of “decision and policy informatics” where researchers use mathematical models and computer simulations to investigate, for example, how infectious diseases like influenza emerge and spread through populations of millions of people. These simulations allow experts to test the impact of different public health interventions on the spread of infectious agents like viruses through large populations.

Dr. Garner adds that VBI is concentrating on “the often under-appreciated and difficult computational area of repetitive DNA or microsatellite analysis. Microsatellites play very important roles in cancers as well as neurological diseases such as schizophrenia and autism. We are trying to

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cure cancer by developing diagnostics, identifying therapeutic targets, and working out how best to combine these approaches with drug treatments.”

Already a computational power house, VBI is working with Virginia Tech to develop a new high-performance computing hub for the university. “Bioinformatics is making huge advances but, with the advent of modern technologies such as the ultra high-throughput next-generation sequencers, the volume of generated data is out-stripping our ability to reduce that data to knowledge. As a consequence, we will need more and more processing power and data storage power.”

For Dr. Garner’s research teams, Convey’s hybrid-core computing is a novel computing approach with great promise. “We are intrigued by the concept of putting together traditional processors and FPGAs such that it would reduce the ‘threshold of pain’ for using these very high-throughput, very efficient processors. Also, there is the promise of having certain codes that will run on this architecture unlike anything else and anywhere else.”

Both Drs. Garner and Bakos agree they have confidence in the “very talented people” on the Convey team. Convey is managed by a seasoned team of technology executives including CEO Bruce Toal, CTO Tony Brewer, and chief scientist Steve Wallach. The co-founders first worked together at Convex Computer Corporation, which was purchased by Hewlett-Packard in 1995. The trio assembled the Convey team, which includes many former colleagues from Convex Computer Corporation.

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. Convey brings decades of experience and intellectual assets to performance problem solving. Its executive and design teams all come from successful backgrounds of building computer companies, most notably Convex Computer Corporation and Hewlett-Packard. Convey Computer investors include Braemar Energy Ventures, CenterPoint Ventures, Intel Capital, InterWest Partners, Rho Ventures, and

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Xilinx. More information can be found at: www.conveycomputer.com.

About the Heterogeneous and Reconfigurable Computing Group at the University of South Carolina

The Heterogeneous and Reconfigurable Computing Group at the University of South Carolina (herc.cse.sc.edu) was founded in 2000 by Dr. Duncan Buell, a pioneer in the field of high-performance reconfigurable computing. Dr. Jason Bakos succeeded Dr. Buell as the group's leader in 2005 and, under Bakos's leadership, the group was one of the first in the world to accelerate computational biology applications with FPGAs and was the first to accelerate non-distance based phylogeny reconstruction. The group actively publishes in several IEEE Computer Society transactions and participates in the world's largest FPGA conferences. The group is funded by the National Science Foundation and is part of the Department of Computer Science and Engineering in the College of Engineering and Computing at the University of South Carolina.

About Virginia Bioinformatics Institute

The Virginia Bioinformatics Institute (<http://www.vbi.vt.edu>) at Virginia Tech is a premier bioinformatics, computational biology, and systems biology research facility that uses transdisciplinary approaches to science combining information technology, biology, and medicine. These approaches are used to interpret and apply vast amounts of biological data generated from basic research to some of today's key challenges in the biomedical, environmental, and agricultural sciences. With more than 240 highly trained multidisciplinary, international personnel, research at the institute involves collaboration in diverse disciplines such as mathematics, computer science, biology, plant pathology, biochemistry, systems biology, statistics, economics, synthetic biology, and medicine. The large amounts of data generated by this approach are analyzed and interpreted to create new knowledge that is disseminated to the world's scientific, governmental, and wider communities.

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For More Information:

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