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The Jackson Laboratory Chooses Convey's HC-2 Hybrid-core Computer to Speed BWA and Expand Genomic Research

Boston—April 24, 2012—Convey Computer today announced The Jackson Laboratory (JAX), Bar Harbor, Maine, has deployed Convey's new HC-2 hybrid-core computer to expand JAX's genomic analysis capability. In early benchmarks, the HC-2 accelerates BWA-based alignmentⁱ—a critical step in identifying disease-causing mutations in the mouse genome—roughly ten-fold compared with the original workflow on their 32-core servers. The new capabilities enable JAX researchers to undertake whole genome studies that were previously impractical on JAX's compute cluster.

Long at the forefront of mammalian genetics research and an NCI-designated Cancer Center, The Jackson Laboratory has rapidly increased its use of next generation sequencing (NGS). "Once we could afford whole genome sequencing, we found a significant bottleneck in the time required to process the data," said Laura Reinholdt, Ph.D. a research scientist at JAX. "That's when biologists here began to seek tools and infrastructure to more expediently manage and process the expanding volumes of NGS data."

JAX settled on heterogeneous computing. "It comes down to power consumption, space, and performance for a fixed amount of dollars," said Glen Beane, senior software engineer, JAX. "We looked at various options for hybrid systems. We found GPUs weren't a good fit for alignment—there are packages that do alignment but the performance isn't that compelling. We looked at other FPGA system vendors, but they didn't have the number of tools Convey does or the system wasn't as easy to use. Also a developer community is evolving around the Convey systems where we could share third-party tools."

The HC-2 deployed at JAX is one of Convey's recently introduced advanced HC-2 Series. Convey's innovative hybrid-core architecture pairs classic Intel® processors with a coprocessor comprised of FPGAs. Particular

algorithms—DNA sequence assembly, for example—are optimized and translated into code that's loadable onto the FPGAs at runtime, greatly accelerating performance-critical applications. The new Convey HC-2 systems increase application performance 2-3 times over previous generations of Convey servers and orders of magnitude over commodity servers.

“We're pleased to see leading research organizations, such as JAX, accelerate their research by complementing their traditional servers with heterogeneous systems,” said Bruce Toal, CEO of Convey. “Hybrid-core computing allows our customers to dramatically increase capacity while decreasing power consumption and floor space.”

The Jackson Laboratory conducts a wide range of basic and applied research on topics such as cancer, aging, cardiovascular disease, immunology, reproductive biology, and neurobiology. A pioneer in the use of mouse models in biomedical research, JAX has roughly 5,000 strains of mice. JAX uses high throughput sequencing for a variety of purposes; including discovery of spontaneous mutations, strain specific variation, and genome wide analysis of gene expression. JAX uses the Illumina® HiSeq platform.

The combination of Convey's high performance hardware and the Convey bioinformatics suite (CBS), which includes optimized versions of BWA (alignment) and Velvetⁱⁱ (short read assembly) greatly speeds throughput. For example, it's common for researchers to want to tweak BWA alignment parameters to improve the results. If researchers must wait a few days between each alignment run, optimizing parameters isn't as practical. “You can end up spending weeks just trying to find the right parameters. If you can do two or three alignment runs in parallel, optimization of the alignment becomes much less time consuming,” noted Reinholdt. Most recently, her group has used high throughput sequencing to improve mouse models of ALS (Lou Gehrig's), Down syndrome and Alzheimer's disease. Performing alignment on JAX's existing 32-core servers is a slow process. The HC-2's higher throughput will give researchers more flexibility to adjust parameters, quickly perform multiple runs, and achieve better results.

Besides doing more refined alignment and whole genome sequencing analysis, JAX researchers also plan to wade carefully into *de novo* assembly where it can help their research. The HC-2, with its high performance memory subsystem, and the CBS' optimized version of Velvet, will make tackling *de novo* assembly practical. Currently, JAX scientists access the computer resources using the popular GALAXY sequencing analysis suite which they have installed onsite.

The new HC-2 will complement JAX's existing 32-core servers. "Rather than add five more nodes to our cluster this system will essentially allow us to add one optimized alignment node that we can use instead. There are two ways to look at the Convey addition," says Beane. "One is we are scaling up because we need to add more alignment capacity. There was no question about that. The other aspect is we looked at how scaling up could help do things that we weren't able to do before. The Convey system also helps achieve that goal."

The Jackson Laboratory

The Jackson Laboratory is an independent, nonprofit biomedical research institution based in Bar Harbor, Maine, with a facility in Sacramento, Calif., an institute for genomic medicine planned in Farmington, Conn., and a total staff of about 1,400. Its mission is to discover the genetic basis for preventing, treating and curing human disease, and to enable research and education for the global biomedical community.

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 are enjoying increased application performance and lower costs of ownership.

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*The Jackson Laboratory Chooses Convey's HC-2 Hybrid-core Computer
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ⁱ The Burrows-Wheeler Aligner is one of the most popular and most efficient algorithms for performing sequence alignment; <http://bio-bwa.sourceforge.net/>

ⁱⁱ Velvet is the most widely used algorithm for assembling short reads typical of NGS technology;
<http://www.ebi.ac.uk/~zerbino/velvet/>