**Scalable Informatics, University at Buffalo, SUNY and NVIDIA Announce GPU-HMMER to Speed Up Analysis with MPI-HMMER**

*Canton, MI –February 3, 2009* - Scalable Informatics (www.scalableinformatics.com), provider of high performance computing and storage solutions, in cooperation with researchers at the University at Buffalo, announced the introduction of GPU-HMMER, an NVIDIA CUDA implementation and extension of MPI-HMMER. GPU-HMMER and MPI-HMMER are open-source implementations of the HMMER protein sequence analysis suite that profoundly reduce computation times.

The MPI-HMMER implementation capitalizes on the computational power of multiple processors on large clusters, whereas GPU-HMMER is designed to leverage NVIDIA GPUs (graphics processing units) to accelerate processing on computing systems.

"MPI-HMMER provides a highly scalable platform upon which to perform protein homology analysis. Runs which had taken weeks to complete previously now require only hours of computational time on a cluster system. Moreover, with the inclusion of GPU support, MPI-HMMER can now provide significant performance on your NVIDIA CUDA-enabled desktop supercomputer," said Dr. Joseph Landman, CEO and Founder of Scalable Informatics and contributor to MPI-HMMER development.

In support of this software, Scalable Informatics offers NVIDIA Tesla-based Pegasus many-core workstations and JackRabbit servers pre-configured to run mpiHMMER, allowing end users to leverage the hardware's high-end performance.

"Scalable Informatics provides high performance, tightly-coupled computing and storage platforms, perfect for use with MPI-HMMER and GPU-HMMER. The Pegasus many-core desktop system can contain from 4 to 16 processor cores, from 4 to 128 GB ram, and from 1 to 3 NVIDIA CUDA-enabled Tesla C1060 GPU Computing processors," Dr. Landman said, commenting on available workstation systems.

In regard to available servers, he referenced Scalable Informatics' successful JackRabbit line. "JackRabbit provides capability similar to Pegasus, coupled with a 750 to 1500 MB/s disk I/O channel. Both products have bundled MPI-HMMER and GPU-HMMER options, pre-configured and supported." Support for all versions of MPI-HMMER is available through Scalable Informatics.

"The phenomenal speedups achieved by GPU-HMMER represents a fundamental shift in productivity for bio-informatics researchers," said Sumit Gupta, Sr. Product Manager, Tesla GPU Computing at NVIDIA. "We are excited about the acceleration in the pace of research this will enable. Compute-intensive applications such as HMMER are perfectly suited to the NVIDIA Tesla GPU's massively parallel, many-core CUDA architecture. GPU-HMMER is an excellent example of how to leverage the GPU to get supercomputer-class performance at the desktop."

Many researchers have identified the benefits of desk-side supercomputing over large, shared systems as increased flexibility and availability of compute cycles. The Pegasus many-core workstation is a strong example of this type of high-end performance.

The efficiency of a workstation such as the Pegasus extends beyond its computational performance according to Dr. John Paul Walters, Lead Developer of MPI-HMMER; such a machine offers energy savings for the user as well. "One Pegasus workstation consumes far less power than a rack of general purpose machines, and will outperform them on this application," he stated.

Dr. Walters and Dr. Vipin Chaudhary led the development of MPI-HMMER and GPU-HMMER at the University of Buffalo. As part of Scalable Informatics, Dr. Chaudhary has worked closely with Dr. Landman on several projects and is pleased with the reception MPI-HMMER and GPU-HMMER have received.

Demonstrated at the SC08 supercomputing conference in August, MPI-HMMER has generated significant attention in both the high performance computing as well as scientific research arenas. This comes as no surprise to Dr. Landman: “Both MPI-HMMER and GPU-HMMER represent a significant upward step-function in performance, and can enable researchers to investigate larger databases in reasonable time. Research workflows that are rate-limited by their analytical performance on HMMER would see immediate and profound benefit in using these programs.”

MPI-HMMER and GPU-HMMER are immediately available under the GNU General Public License from http://mpihmmer.org.

Both desk-side and rack-mounted hardware systems, as well as support for MPI-HMMER and GPU-HMMER, are available from Scalable Informatics.

**ABOUT SCALABLE INFORMATICS**

Scalable Informatics is a privately-owned high performance computing solutions company focusing on delivering pragmatic solutions to computational problems. They design, build, and support high performance clusters, storage and workstation hardware, scalable and accelerated software, and offer support, consulting and development services.

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**ABOUT UNIVERSITY AT BUFFALO, SUNY**

The University at Buffalo is a premier research-intensive public university, a flagship institution in the State University of New York system and its largest and most comprehensive campus. UB’s more than 28,000 students pursue their academic interests through more than 300 undergraduate, graduate and professional degree programs. Founded in 1846, the University at Buffalo is a member of the Association of American Universities. mpiHMMER and GPUHMMER were developed within UB's Accelerated Computing Lab (http://cadi.buffalo.edu), which includes research in computer-assisted surgery and high performance computing.