

Contributing to Human Welfare

Japan's HGC Developing Novel Methods of Diagnosis, Prevention and Cure of Diseases

Key Facts

Organization:

Human Genome Center,
Institute of Medical Science,
The University of Tokyo

Location:

Tokyo, Japan

Application:

Life Sciences



Research on the human genome is aimed at greatly contributing to human welfare through developing novel methods of diagnosis, prevention and cure of human diseases. The Human Genome Center (HGC) within the Institute of Medical Science at The University of Tokyo focuses on this area of study.

Upgrading the SGI Altix® 4700

In January 2009, HGC purchased an SGI Altix 4700 shared memory system with 64 Intel® Itanium® 2, 1.66GHz, two-core processors and 2TB of RAM as part of its Shirokane supercomputer network. The Center used this installation until its decommissioning in December of 2011.

As part of the new Shirokane2 network, HGC unveiled its newest 2TB shared memory supercomputer on January 1, 2012. Its performance is higher than the former SGI Altix 4700 system on various application workloads. The system, a SGI UV 100, is powered by Intel® Xeon® E7-8837 processors and features the SGI NUMAlink® 5 interconnect. Together with the full 2TB of memory access support, users can explore a brand new set of approaches to compute-intensive problems.

System Specifications of New SGI UV 100

- SGI UV 100
- 16 Intel® Xeon® E7-8837, 2.66GHz, eight-core processors
- 2TB of RAM
- 80TB of SGI InfiniteStorage™ 4000 SATA drives

According to Professor Satoru Miyano, Ph.D., “We use the SGI system primarily for genome assembly based on the data coming from our Next Generation Sequencer.

Assembling the Human Genome

Miyano explains, “We decided to include shared memory in our system specifications, aiming toward features and architecture that are advantageous to life science research projects. Our prime contractor on the project selected the SGI systems because they best fit our requirements.”

“Besides genome assembly, I run genome network simulation, a Bayesian Network application,” states Miyano. “The simulation requires a large amount of memory. A job like this would be completed smoothly if the system provides a large amount of coherent shared memory. I previously ran this simulation on a PC cluster, but encountered an issue, as internode communication limits the parallel performance scaling. This is why we needed a large shared memory system.”

“The SGI shared memory systems — Altix, then UV — have accelerated life science research projects without much of a hassle. The systems allow researchers to run large memory jobs without taking memory constraints into consideration,” Miyano says.

Applications Used for Next Generation Sequencer Data Analysis and Genome Assembly

- Velvet
- AbySS
- SOAPdenovo
- Newbler
- InterProScan
- HMMER
- BLAST+
- Bowtie
- BWA
- Maq
- Trinity
- MACS

Deliberate Decision Process Led to the UV Purchase

At the time of the initial procurement decision five years ago, HGC leadership had debated if they needed a large shared memory system at all. They only narrowly favored the purchase of shared memory as an important part of the entire life science research infrastructure, so decided to purchase it in the later phase of the system procurement. They subsequently discovered their timing to be correct, because they report that only more recently have they seen significant advancements in capabilities of Next Generation Sequencers.

“At the time of procurement, we had considered a system from Sun Microsystems, but ultimately chose SGI. For a programmer, SGI UV frees us from memory constraints. This helps a lot as we constantly update and rewrite programs to keep up with the latest data and methodology,” Miyano explains. “Most programs have a five-year or less life cycle, and programmers are constantly under pressure to update, rewrite and tune programs to perform ever better. The SGI UV frees us from time consuming coding and tuning work that requires close attention to per-node-memory-constraints. This decrease of required administrative time has been, and will continue to be, a main contributor of the acceleration of our Life Science research projects,” Miyano concludes.

About the Human Genome Center

After the sequence analysis of the human genome, analyzing the function of the genes that could be related to diseases is thought to be next in importance. The Human Genome Center is predominantly conducting the research of such intractable diseases as cancer using the cDNA microarray system and supercomputer. Their final aim is to develop personalized medicine by identifying the novel molecular marker of the disease and developing individualized genetic diagnoses and molecular targeted therapy. The Ministry of Education, Science, Sports and Culture in Japan started the Human Genome Project, and the Human Genome Center was established as its standard-bearer, in 1991. Please visit www.hgc.jp for more information.

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