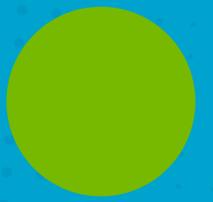


CSIRO Advances in GPU Computing

What could you do with 256 GPUs?



Luke Domanski¹⁾, Tim Gureyev²⁾, Yakov Nesterets²⁾, Lawrence Murray⁴⁾, Emlyn Jones⁵⁾, John Taylor⁷⁾

The Commonwealth Scientific and Industrial Research Organisation (CSIRO) is Australia's national science agency. CSIRO is currently applying GPU Computing on a scale ranging from single GPU workstations through to their **256 GPU cluster**.

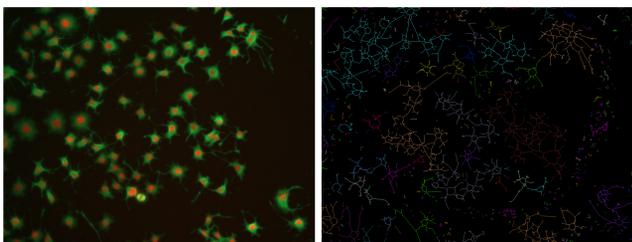
Biotech Image Analysis

L. Domanski¹⁾, W. Dadong¹⁾, P. Vallotton¹⁾, Changming Sun¹⁾, R. Hassan¹⁾

The Biotech Imaging group of CSIRO MIS uses GPUs to accelerate high-throughput imaging applications for the biotech industry.

High-Content Analysis

HCA is a technology used by pharmaceutical companies & research organisations in automated drug discovery. It involves analysing 100s to 1000s of biological images generating during large automated experiments, which can take hours. Biotech Imaging is using GPUs to reduce the processing time of the Neurite Outgrowth assay found in their HCA-Vision software. Early tests for detecting neurites, long thin tree structures mediating neuron communication in the brain, show speed-ups of up to 13x for accelerated algorithm components on a GeForce GTX260 over a 2.3GHz Intel Xeon CPU. CSIRO's Neurite Outgrowth module can be used to study the effects of inhibitors on degenerative brain diseases, such as Parkinson's disease, and the regenerative capabilities of brain cells after trauma.



Neurons (left), courtesy of Dr. Xiaokui Zhang, Helicon Therapeutics, Inc., USA, and output of HCA-Vision neurite tracing (right)

3D Deconvolution

Deconvolution is important in many areas of science, including astronomy, microscopy, and medical imaging. It reduces the effects of blurring introduced during image capture, revealing objects and structures not clearly visible in the raw image. Accurately deconvolving 3D images is a computationally challenging task. Biotech Imaging has developed a spatially-variant heterogeneous implementation of the Richardson-Lucy algorithm on CSIRO's 200 GPU cluster. The algorithm can utilize GPUs and CPUs to cooperatively perform processing. For a 512x512x16 image, 64 GPUs outperform an optimized single thread CPU implementation by 100x and completes in under 0.5secs. This application is a first step towards interactive deconvolution at the microscope, allowing biologist to see fine details while exploring a sample live.

X-ray Science & CT reconstruction

T.E. Gureyev²⁾, Ya.I. Nesterets²⁾, S.C. Mayo²⁾, D. Ternovski³⁾

The X-ray Science and Instrumentation (XRSI) group of CSIRO MSE has developed multi-GPU implementations of the filtered back-projection and Feldkamp-Davis-Kress CT reconstruction algorithms that run on Windows clusters. Reconstruction of large 3D CT images is important in biomedical and materials science applications, but is a computationally intensive problem. High-end X-ray imaging facilities, such as the Australian Synchrotron, can now readily capture data volumes with 4096³-8192³ voxels in a single scan, which may take days to reconstruct on a single-CPU system. Using a small cluster of Windows servers and NVIDIA GeForce GTX280 GPUs, XRSI has shown speed-ups of between 90-230x over a single-thread CPU implementation (Figure 1).

This work will help increase the job throughput at large X-ray imaging facilities, allow diagnosis of imaging problems during a single experimental session, and make the reconstruction of very large CT datasets feasible. The algorithms have been incorporated in a remote reconstruction service implemented in the XRSI's XLI software. XRSI is currently extending their software to run on a large CPU/GPU computing cluster to be installed at the Australian Synchrotron in 2010.



Leg of a common fly. CT data collected and rendered by Sherry Mayo, CSIRO MSE

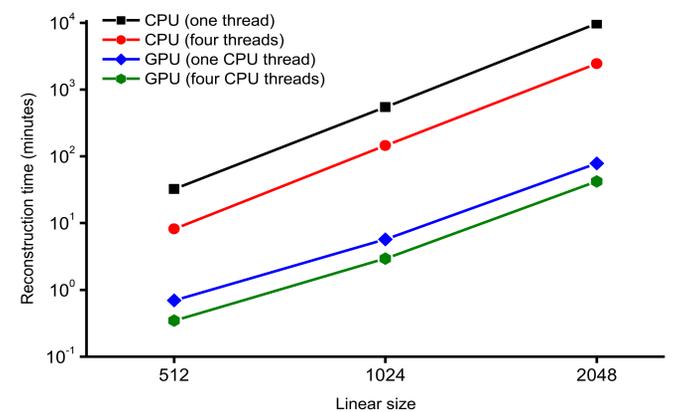


Figure 1: CT reconstruction times for CPU and GPU implementations of FDK algorithm.

Project Partners: National e-Research Architecture Taskforce (NeAT), Australian Synchrotron, Victorian eResearch Strategic Initiative (VeRSI), Victorian Partnership for Advanced Computing (VPAC), X-ray Technologies Pty Ltd (XRT)

Quantifying uncertainty in complex environmental models

E. Campbell⁴⁾, J. Parslow⁵⁾, N. Cressie⁶⁾, N. Margvelashvili⁵⁾, E. Jones⁵⁾, L. Murray⁴⁾

Marine biogeochemical models characterise the interaction between phytoplankton, zooplankton and environmental factors such as nutrient (e.g. nitrogen) and light availability. CSIRO are developing methods for statistical inference in these and other complex environmental models, suitable for deployment on its GPU cluster. Such methods will provide environmental managers with a quantitative assessment of model uncertainty, which is presently not available in the current generation of deterministic marine biogeochemical models.

This work has already seen speed ups of up to 100 fold by using NVIDIA GPUs for model simulation and sequential Monte Carlo inference (Figure 2). This speedup has facilitated the use of more sophisticated ensemble algorithms (e.g. particle filters), which may otherwise have been considered too computationally expensive.

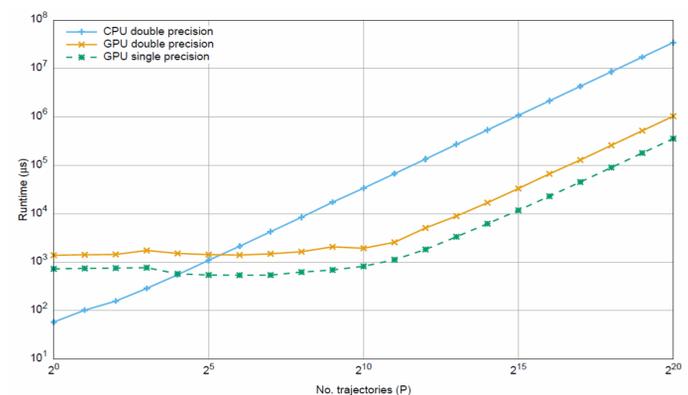
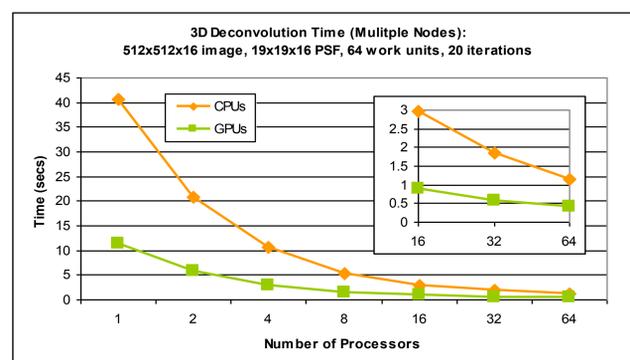


Figure 2: Environmental simulation using GPUs



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