

Computational Chemistry Applications at NCSA/UIUC

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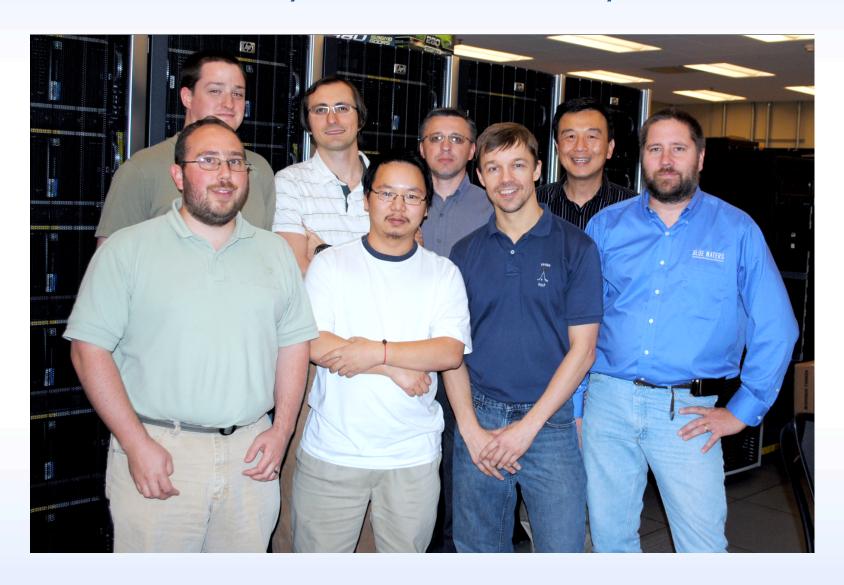


Blue Waters





Innovative Systems Laboratory at NCSA





ISL Research

- Evaluation of emerging computing architectures
 - Reconfigurable computing
 - Many-core (GPU) architecture
 - Heterogeneous clusters
- Systems software research and development
 - Run-time systems
 - GPU accelerator cluster management
 - Tools and utilities: GPU memory test, power profiling, etc.
- Application development on emerging computing applications
 - Computational chemistry (electronic structure, MD)
 - Computational physics (QCD)
 - Cosmology
 - Data mining



Computational Chemistry Applications at NCSA/UIUC

NAMD

- Theoretical and Computational Biophysics Group at Beckman Institute
- Key researchers
 - Prof. Klaus Schulten, Director
 - Dr. James Phillips, NAMD developer
 - John Stone, VMD developer
- http://www.ks.uiuc.edu/Research/namd/

Electronic structure

- Innovative Systems Laboratory at NCSA
- Key researchers
 - Prof. Thom Dunning, project PI
 - Prof. Todd Martinez, project co-PI, now at Stanford
 - Dr. Volodymyr Kindratenko, project co-PI
 - Dr. Alexey Titov, quantum chemistry on GPU research/development
 - Guochun Shi, GPU/Cell development/implementation
- http://cyberchem.ncsa.illinois.edu/



NAMD Acceleration Efforts: FPGAs

- Work done at ISL (V. Kindratenko)
- SRC-6 Reconfigurable Computer platform
- Observations/Conclusions
 - FPGA technology (Xilinx Virtex II) enabled some acceleration
 - ~3x speedup for the non-bonded force-field kernel
 - But it quickly started to loose its ground to the emerging multi-core architectures
 - We have not revisited this with the latest (e.g., Virtex 6) FPGAs
 - Programming efforts are substantial
 - Hardware is expensive and is not widely used

Ref: V. Kindratenko, and D. Pointer, A case study in porting a production scientific supercomputing application to a reconfigurable computer, in Proc. IEEE Symposium on Field-Programmable Custom Computing Machines - FCCM'06, 2006, pp. 13-22.

NAMD Acceleration Efforts: Cell

- Work done at ISL (G. Shi)
- IBM Cell blade platform
- Observations/Conclusions
 - Cell enabled a very substantial acceleration
 - ~45x speedup for the non-bonded force-field kernel
 - A very high percentage of device utilization is achievable
 - Programming efforts are substantial
 - Explicit code vectorization, explicit memory management, ...
 - Hardware is expensive and is not widely used

Ref: G. Shi, V. Kindratenko, Implementation of NAMD molecular dynamics non-bonded force-field on the Cell Broadband Engine processor, In Proc. 9th IEEE International Workshop on Parallel and Distributed Scientific and Engineering Computing - PDSEC'08, 2008.



NAMD Acceleration Efforts: GPU

- Work done at TCBG (J. Phillips)
- NVIDIA CUDA GPU platform
- Observations/Conclusions
 - Moderate acceleration is achievable
 - ~5-7x speedup for the non-bonded force-field kernel on GT100 architecture
 - Note that the original CPU code is already highly optimized
 - The GPU version of NAMD is now available for download from the developers' website
 - Programming efforts are substantial
 - Memory management, overlapping data transfers with computations, ...
 - Commodity nature of GPUs makes it practical for NAMD



Electronic structure calculations: FPGAs

- Work done at ISL (V. Kindratenko)
- SRC-6/7 Reconfigurable Computer platform
- Observations/Conclusions
 - Available hardware resources were only sufficient to implement a highly restructured and simplified kernel for computing (ss|ss) integrals over contracted s-orbitals, with marginal speedup
 - We have not revisited this with the latest (e.g., Virtex 6) FPGAs
 - Programming efforts are substantial

Ref: V. Kindratenko, I. Ufimtsev, T. Martínez, Evaluation of two-electron repulsion integrals over Gaussian basis functions on SRC-6 reconfigurable computer, In Proc. 4th Annual Reconfigurable Systems Summer Institute - RSSI'08, 2008.



Electronic structure calculations: Cell

- Work done at ISL (G. Shi)
- IBM Cell blade platform
- Observations/Conclusions
 - Cell enabled a very substantial acceleration
 - ~7x speedup on relatively uncontracted basis set
 - ~65x speedup on a highly contracted basis set
 - (kernels for computing (ss|ss) integrals over contracted s-orbitals)
 - Programming efforts are substantial
 - Explicit code vectorization, explicit memory management, ...
 - Hardware is expensive and is not widely used

Ref: G. Shi, V. Kindratenko, I. Ufimtsev, T. Martinez, J. Phillips, S. Gottlieb, Implementation of scientific computing applications on the Cell Broadband Engine, Scientific Programming, vol. 17, no. 1-2, pp. 135-152, 2009.



Electronic structure calculations: GPU

- Work done at ISL (A. Titov)
- NVIDIA CUDA GPU platform
- Observations/Conclusions
 - Substantial all-application speedup (SCF including *s*-, *p*-, and *d*-orbitals)
 - Up to 50x compared to GAMESS performing the same calculations
 - Programming efforts are huge
 - ~300,000 lines of autogenerated GPU code
 - Symbolic computations are used to manipulate the contraction equations needed for GPU implementation
 - This work is now integrated into a commercial code TeraChem from Stanford

Ref: A. Titov, V. Kindratenko, I. Ufimtsev, T. Martinez, Generation of Kernels to Calculate Electron Repulsion Integrals of High Angular Momentum Functions on GPUs – Preliminary Results, In Proc. Symposium on Application Accelerators in High-Performance Computing - SAAHPC'10, 2010.



Summary

- NVIDIA CUDA GPU efforts have been most fruitful so far
 - Commodity nature of the hardware
 - Widely available, inexpensive
 - Relative maturity of the software development tools
- But application acceleration continues to be very labor-intensive
 - New/different algorithms
 - Extensive code transformations
- When there are challenges, there are opportunities to do some interesting work and to collaborate

