

Porting LAMMPS to the Titan System

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LAMMPS

- Large-scale Atomic/Molecular Massively Parallel Simulator
 - <http://lammps.sandia.gov>
- General Purpose Classical Molecular Dynamics Software
 - Simulations for biology, materials science, granular, mesoscale, etc.
- Open source (GPL), with a user community
 - 1700 Citations
 - 100K downloads, 25K mail list messages
 - 100 contributors to code base
- Flexible and extensible:
 - 80% of code-base is add-ons by developers and users
 - styles: atom, pair, fix, compute, etc

Force Fields

- Biomolecules: CHARMM, AMBER, OPLS, COMPASS (class 2), Gromacs, long-range Coulombics via PPPM, point dipoles, ...
- Polymers: all-atom, united-atom, coarse-grain (bead-spring FENE), bond-breaking, bond-forming, ...
- Materials: EAM/MEAM for metals, Buckingham, Morse, Yukawa, Tersoff, COMB, AI-REBO, ReaxFF, **GAP**, ...
- Mesoscale: granular, DPD, SPH, PD, colloidal, aspherical, triangulated, ...

Porting Strategy

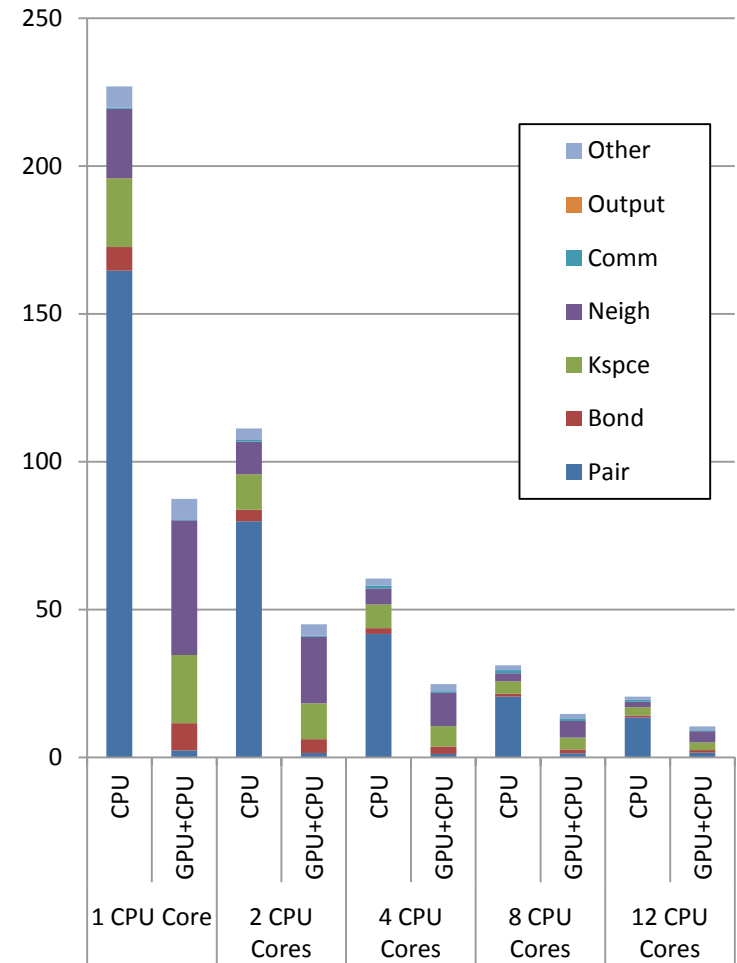
- LAMMPS is a large legacy code with many routines and is constantly growing with new features and algorithms
 - Impractical to port the entire code base
 - Use a “modular” acceleration strategy that targets computationally intensive routines while allowing full compatibility with LAMMPS many features/options
 - In order to get efficient acceleration with this strategy, we must
 - Parallelize routines that are not ported on the CPU cores
 - Exploit as much CPU/accelerator computation and data transfer concurrency as possible

LAMMPS with Accelerators

- Acceleration for neighbor-list builds, short-range force calculation, and long-range electrostatics
- CPU/Accelerator/Data-transfer concurrency to achieve efficient simulation on hybrid nodes
- Use existing spatial decomposition for MPI processes
- Variety of parallel decompositions for the accelerator depending on the routine
 - Atom, Force, Spatial, Mesh, Sorts, Etc.
- Deterministic Algorithms
 - Same result with same number of procs/random seed
- Portability to future CPUs, GPUs, APUs, and other accelerators
 - Geryon library

1. Minimize Porting Effort - Need to parallelize code not ported for the accelerator on the CPU cores

- Example: Rhodopsin Benchmark on a box with 12 CPU cores and 1 GPU
 - Here, only the non-bonded “pair” force calculation is accelerated for an example
 - Speedup on 1 CPU core with a GPU is only 2.6x with this approach
 - Speedup vs 12 CPU cores is still > 2x because we use all 12 cores in addition to the GPU
 - MPI Processes Share the Accelerator
 - Trivial parallelization of host code
 - Allows for trivial (from a programmer view) overlap of host-device comm and computation (but not optimal)
 - Improves data locality for random access with multiple kernel executions on smaller subdomains
 - Expands options for CPU/accelerator concurrency...

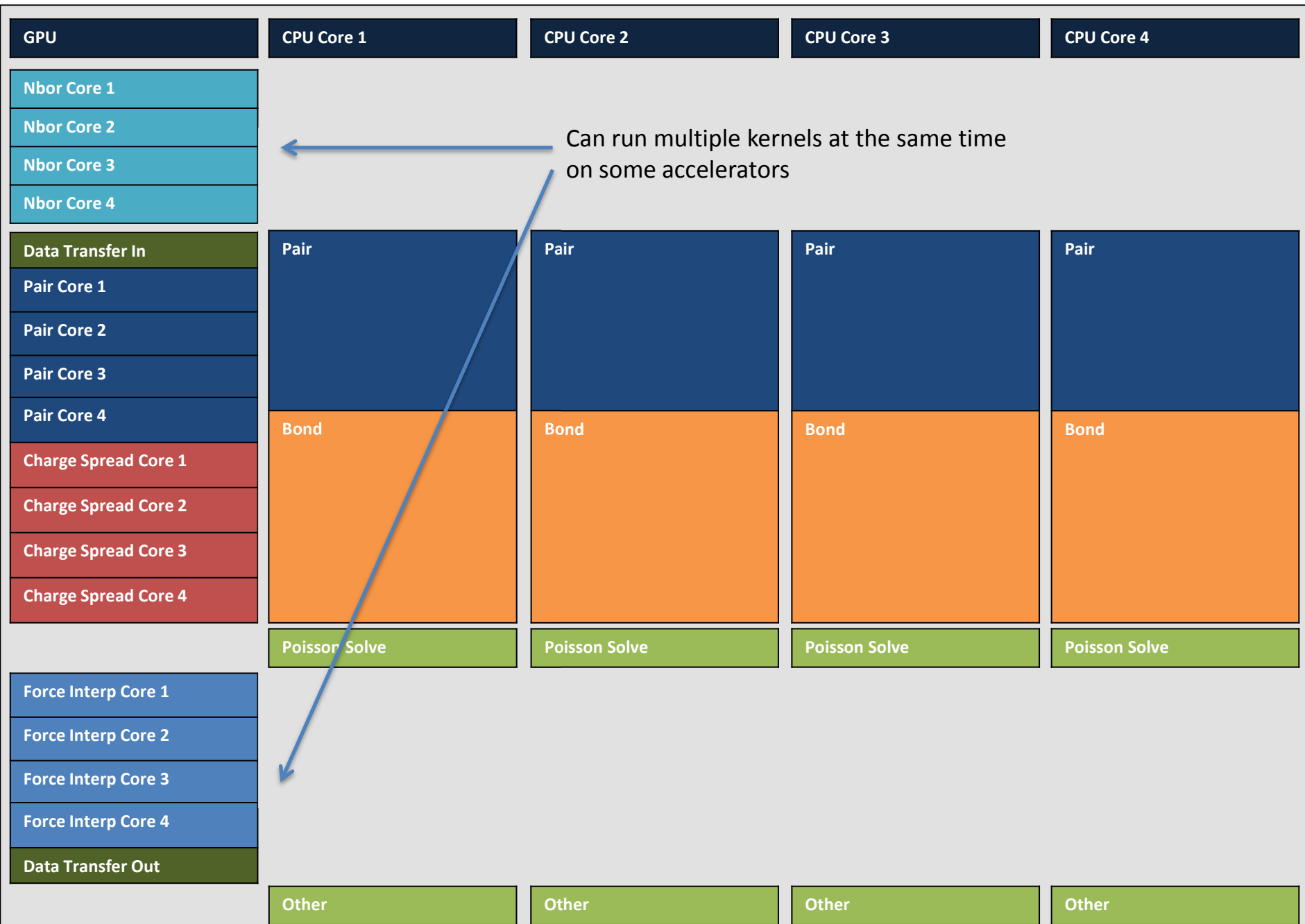


2. Host-Device Load Balancing

(- PPPM Acceleration) *Not to scale*

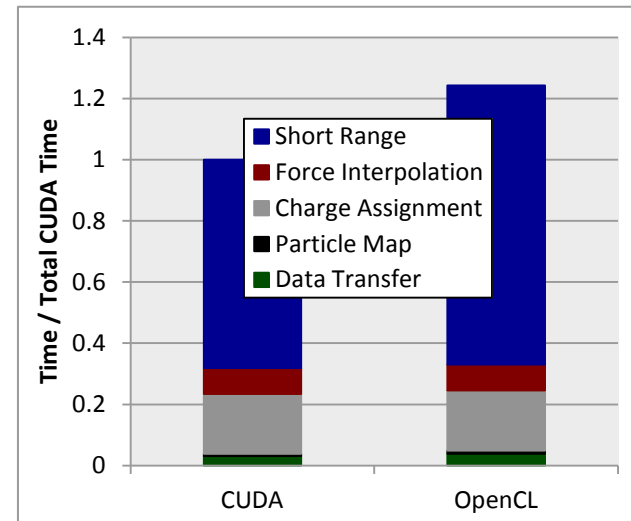


Host-Device Load Balancing (+PPPM Acceleration)



Geryon Library

- Allows same code to compile with CUDA Runtime, CUDA Driver, and OpenCL APIs
- Allows portability to accelerators, CPUs, and any future chips with OpenCL support
- Simple classes allow for more succinct code than CUDA-Runtime
 - Change from one API to another by simply changing the namespace
 - Use multiple APIs in the same code
 - Lightweight (only include files – no build required)
 - Manage device query and selection
 - Simple vector and matrix containers
 - Simple routines for data copy and type casting
 - Simple routines for data I/O
 - Simple classes for managing device timing
 - Simple classes for managing kernel compilation and execution



<http://users.nccs.gov/~wb8/geryon/index.htm>

Early Optimizations for the XK6

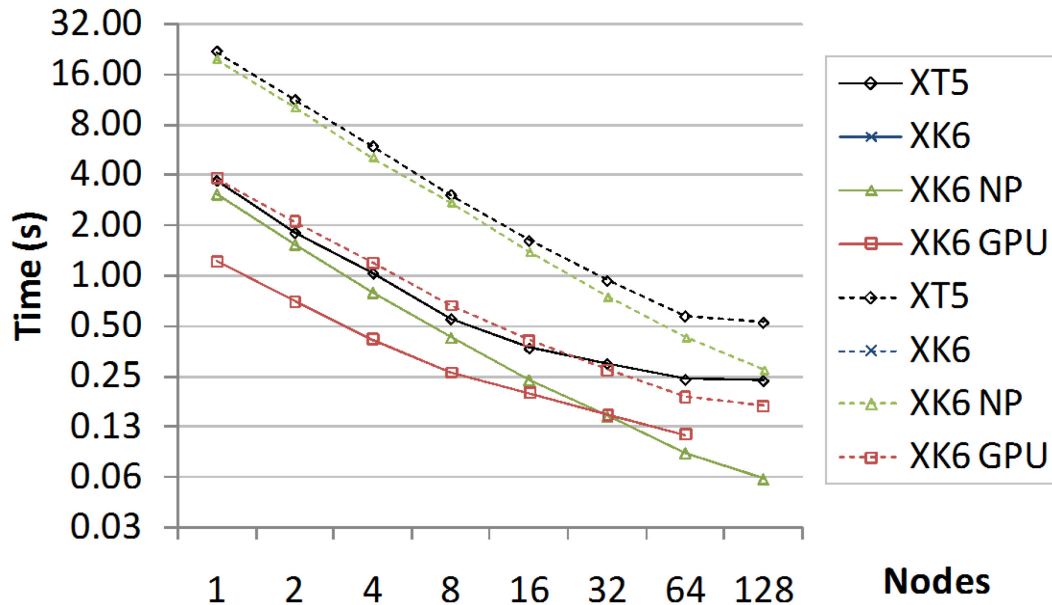
- Using MPI-only on multicore nodes can impact performance at scale
 - Increased MPI communication times
 - MPI Cartesian topologies (e.g. `MPI_Cart_create`) are designed to allow vendors to optimize process mapping for grids
 - Typically do nothing to optimize for multicore nodes
 - Implemented a two-level domain decomposition algorithm to minimize off-node communications
 - Increased K-space times for P^3M calculations
 - Many processes involved in effectively all-to-all communications for 3D FFTs
 - Use separate process partitions for the K-space calculation
 - Implemented by Yuxing Peng and Chris Knight from the Voth Group at the University of Chicago
- Improved data layout for neighbor list builds with an arbitrary number of threads assigned to each atom
 - Can efficiently use 4X the number of threads for some simulations
- Implementation of the embedded atom method (and other new models)
 - Many-body potential for simulation of metals

X2090 Benchmark Results

- Run on the Titan development partition with Fermi+ GPUs
- Benchmarks with acceleration used mixed-precision as compared to double precision
- Left: Strong Scaling for fixed-size simulations of approximately 256K particles
- Right: Weak Scaling with $\sim 32\text{K}$ particles/node
- XK6 NP results use a new MPI process to grid mapping and a separate partition for long-range electrostatics (as do the GPU results)
- The next 4 plots are speedups versus the XT5 on a node per node basis
 - XK6 only comparisons later

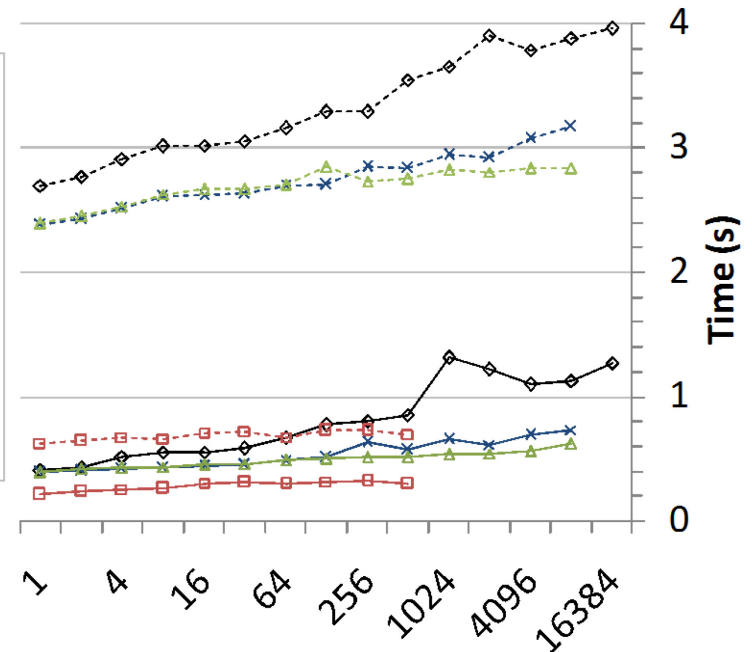
Atomic Fluid

- Atomic fluid - microcanonical ensemble, Lennard- Jones potential, reduced density 0.8442, neighbor skin 0.3σ , cutoffs of 2.5σ and 5.0σ



XK6 Single Node: 1.17X

XK6 GPU Single Node: 3.03X, 5.68X



XK6 Single Node: 1.04X

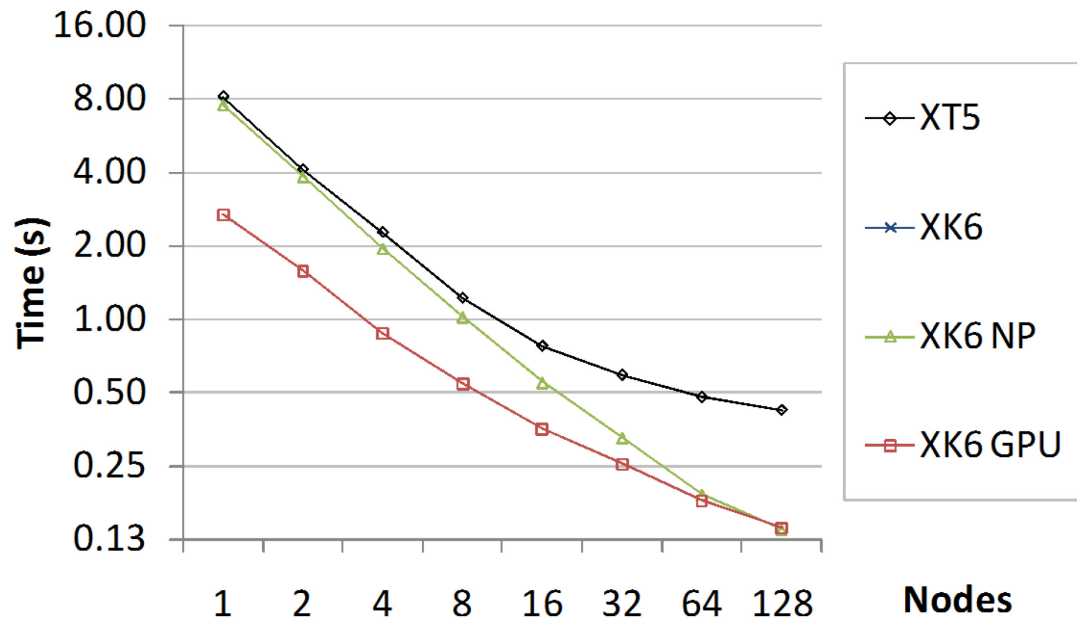
XK6 GPU Single Node: 1.92X, 4.33X

XK6 GPU 512 Nodes: 2.92X, 5.11X

NP gives up to 20% improvement

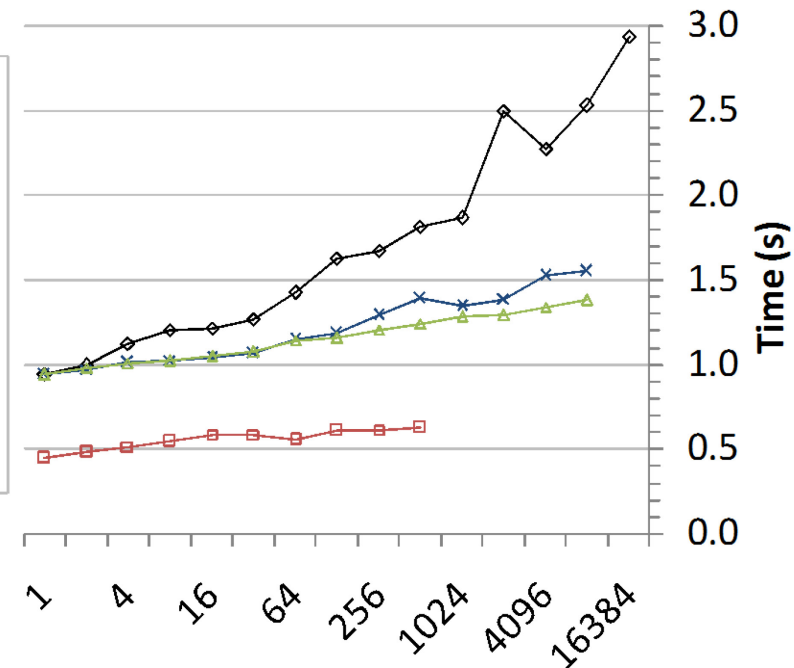
Bulk Copper

- Copper metallic solid in the microcanonical ensemble. The force cutoff is 4.95\AA with a neighbor skin of 1.0\AA .
 - Requires additional ghost exchange during force calculation for electron densities



XK6 Single Node: 1.07X

XK6 GPU Single Node: 3.05X



XK6 Single Node: 1.0X

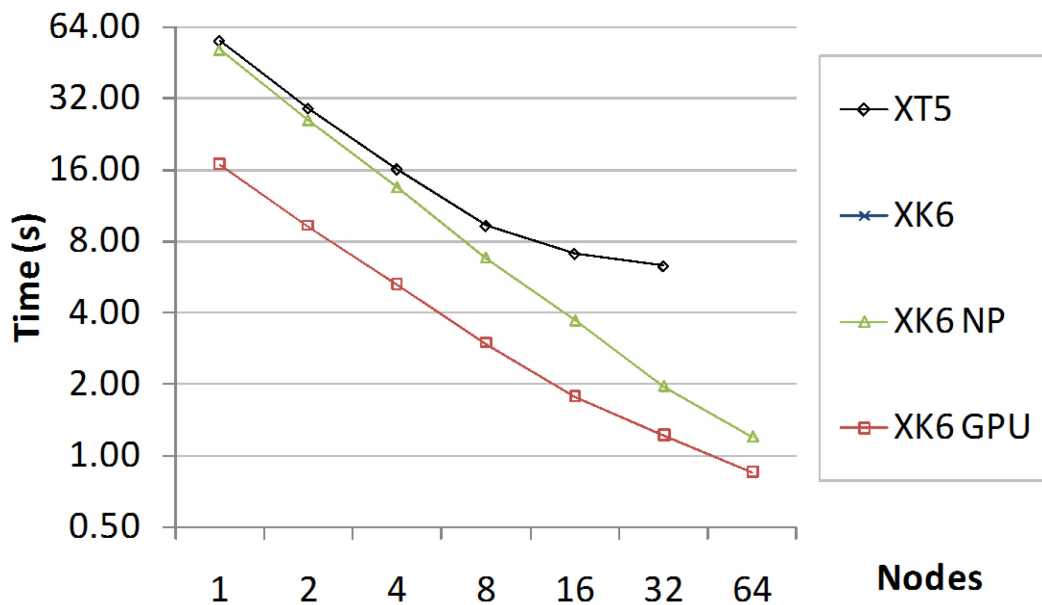
XK6 GPU Single Node: 2.12X

XK6 GPU 512 Nodes: 2.90X

NP gives up to 12% improvement

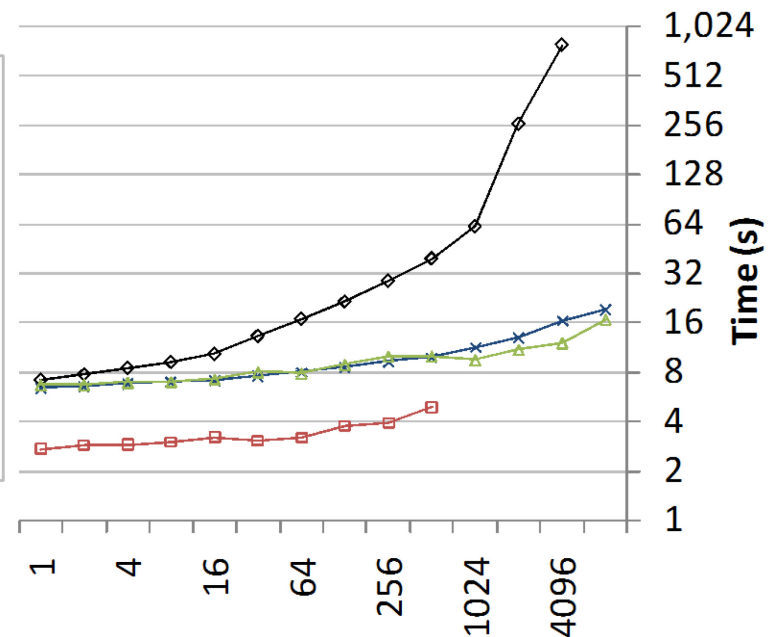
Protein

- All-atom rhodopsin protein in a solvated lipid bilayer with the CHARMM force field. Isothermal-isobaric ensemble, SHAKE constraints, 2.0fs timestep. Counter-ions, water, 8Å/ 10Å cutoff
 - Long range electrostatics are calculated with P3M.



XK6 Single Node: 1.1X

XK6 GPU Single Node: 3.3X



XK6 Single Node: 1.1X

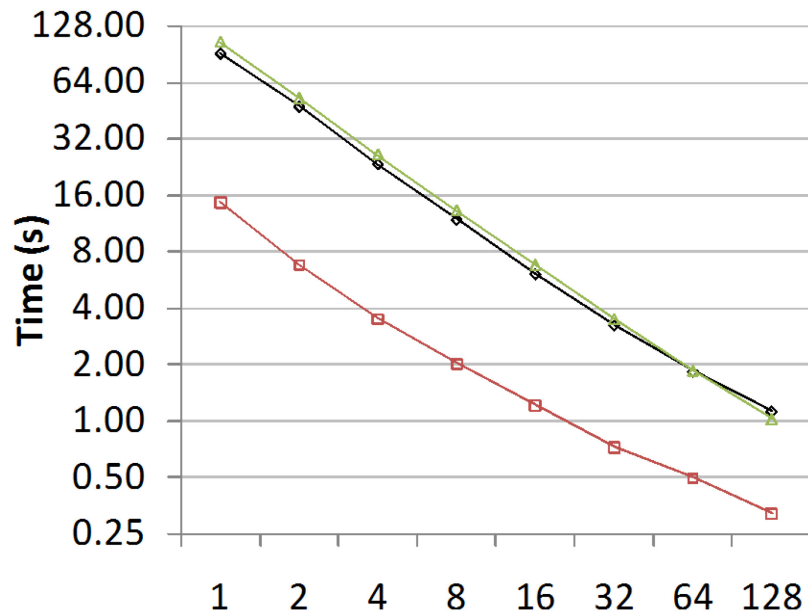
XK6 GPU Single Node: 2.6X

XK6 GPU 512 Nodes: 8X

NP gives up to 27% improvement

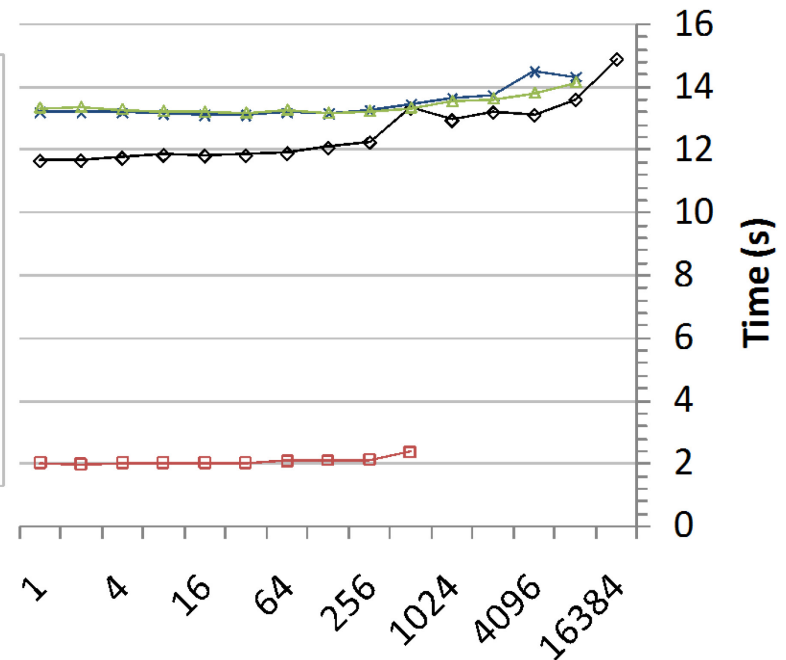
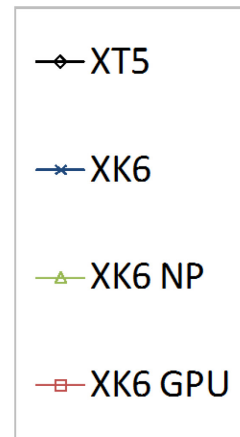
Liquid Crystal

- Liquid crystal mesogens are represented with biaxial ellipsoid particles, Gay-Berne potential, isotropic phase, isothermal-isobaric ensemble, 4σ cutoff with a 0.8σ neighbor skin
 - High arithmetic intensity



XK6 Single Node: .9X

XK6 GPU Single Node: 6.23X



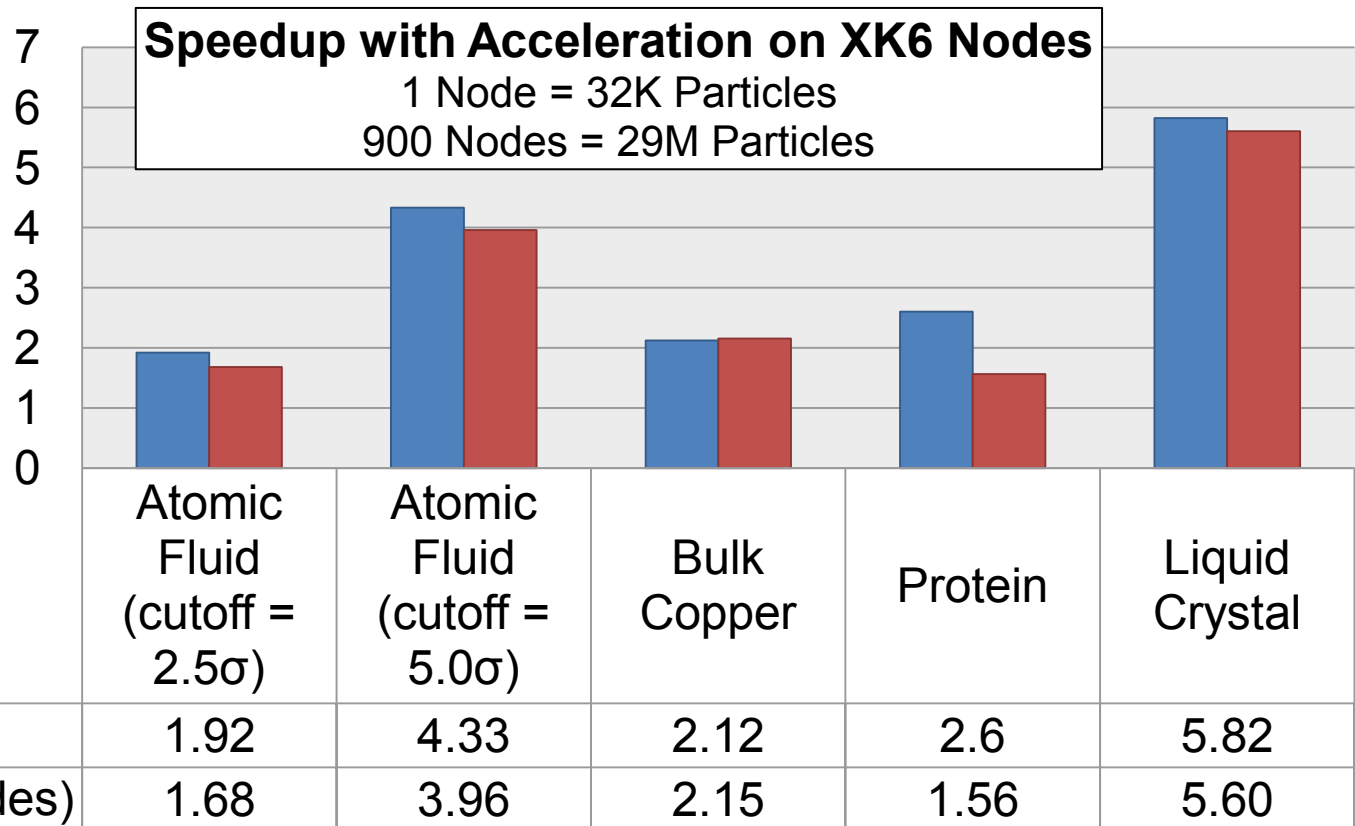
XK6 Single Node: .9X

XK6 GPU Single Node: 5.82X

XK6 GPU 512 Nodes: 5.65X

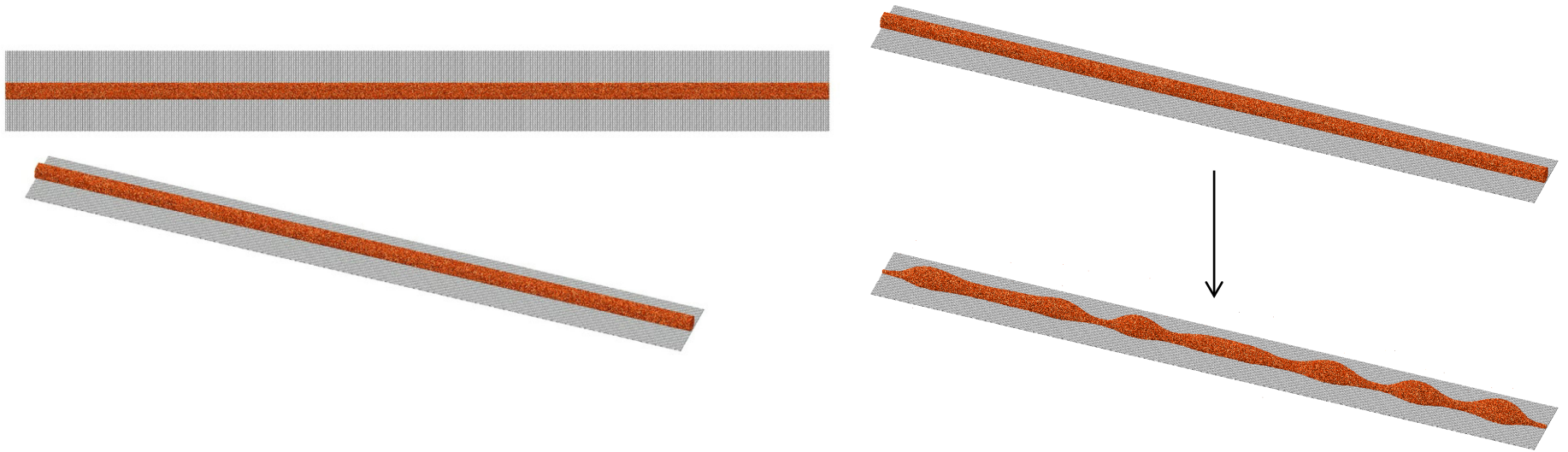
XK6 vs XK6+GPU Benchmarks

- 32K per node



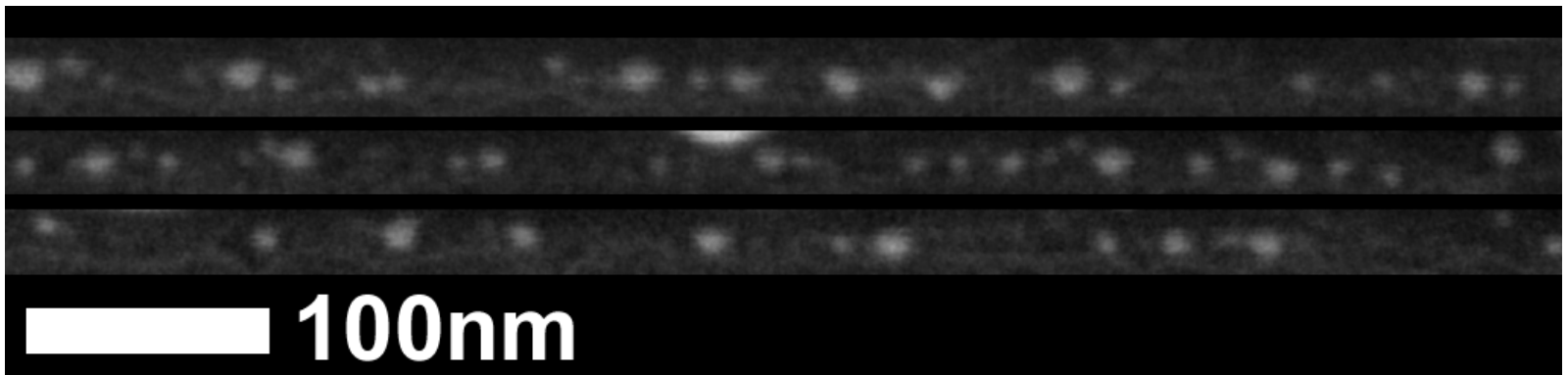
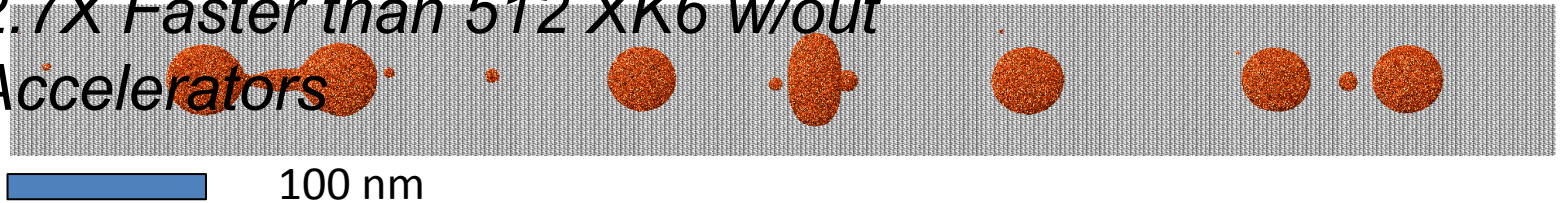
Example Science Problems 1.

- Controlling the movement of nanoscale objects is a significant goal of nanotechnology.
- Pulsed laser melting offers a unique opportunity to dictate materials assembly where rapid heating and cooling rates and ns melt lifetimes are achievable
- Using both experiment and theory we have investigated ways of controlling how the breakage occurs so as to control the assembly of metallic nanoparticles
- Here, we illustrate MD simulation to investigate the evolution of the Rayleigh-Plateau liquid instability for copper lines deposited on a graphite substrate
- Simulations are performed with GPU acceleration on Jaguar at the same scales as experiment



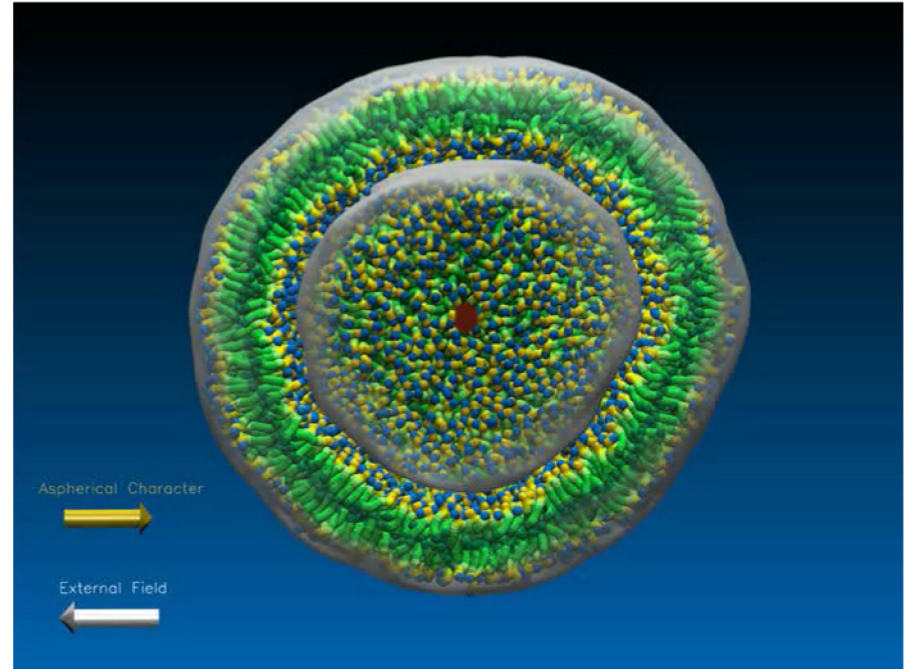
11.4M Cu Atom Simulations on Graphitic Substrate

- 2.7X Faster than 512 XK6 w/out Accelerators



Example Science Problems 2.

- Membrane fusion, which involves the merging of two biological membranes in a controlled manner, is an integral part of the normal life cycle of all living organisms.
- Viruses responsible for human disease employ membrane fusion as an essential part of their reproduction cycle.
- Membrane fusion is a critical step in the function of the nervous system
 - Correct fusion dynamics requires realistic system sizes
- Kohlmeyer / Klein INCITE Award



*39M Particle Liposome System
Simulated at 115 ns/day on 900 XK6
Nodes*

- *2.7X Faster than 900 XK6 w/out
Accelerators*

Kepler II vs Fermi +

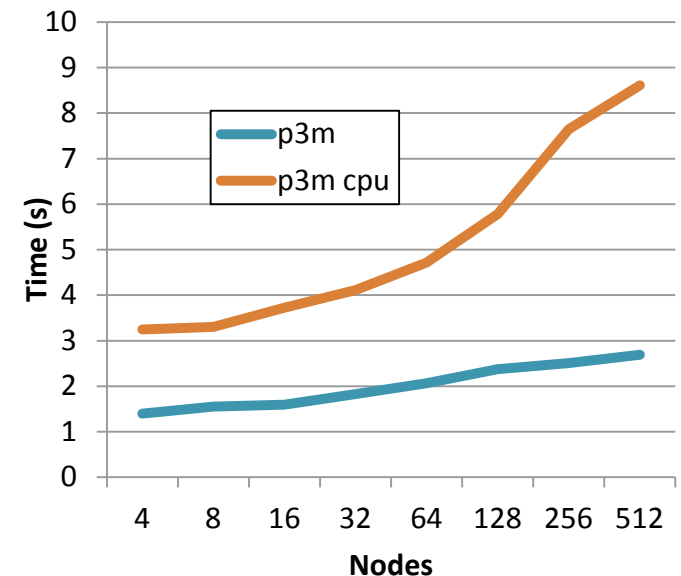
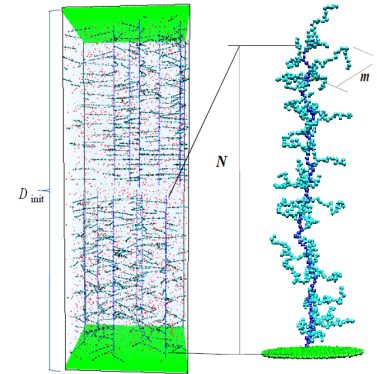
- More cores
 - Efficiently handle larger problems, better performance for complex models
- Improved thread performance
 - Faster time to solution for same problem (increased clock, etc.)
- Larger register file
 - Better performance for complex models such as the liquid crystal case
- Warp shuffle
 - Reduced shared memory usage for reductions across threads
- Hyper-Q
 - MPI processes sharing the GPU can share a context
 - Reduced memory overhead per process
 - Concurrent kernel execution from multiple processes
 - Better strong-scaling performance (performance with smaller number of particles per GPU)

The “Porting Wall”

- Although you can get performance improvements by porting existing models/algorithms and running simulations using traditional parameterizations...
 - There is a limit to the amount of parallelism that can be exposed to decrease the time-to-solution
 - Increasingly desirable to re-evaluate computational physics methods and models with an eye towards approaches that allow for increased concurrency and data locality
 - Parameterize simulations to shift work towards routines well-suited for the accelerator
 - Methods/models with increased computational requirements can perform better if they can increase concurrency, allow for larger time-steps, etc.
- Computational scientists will play a critical role in exploiting the performance of current and next-generation architectures
- Some very basic examples...

Electrostatics Example with Polyelectrolyte Brushes

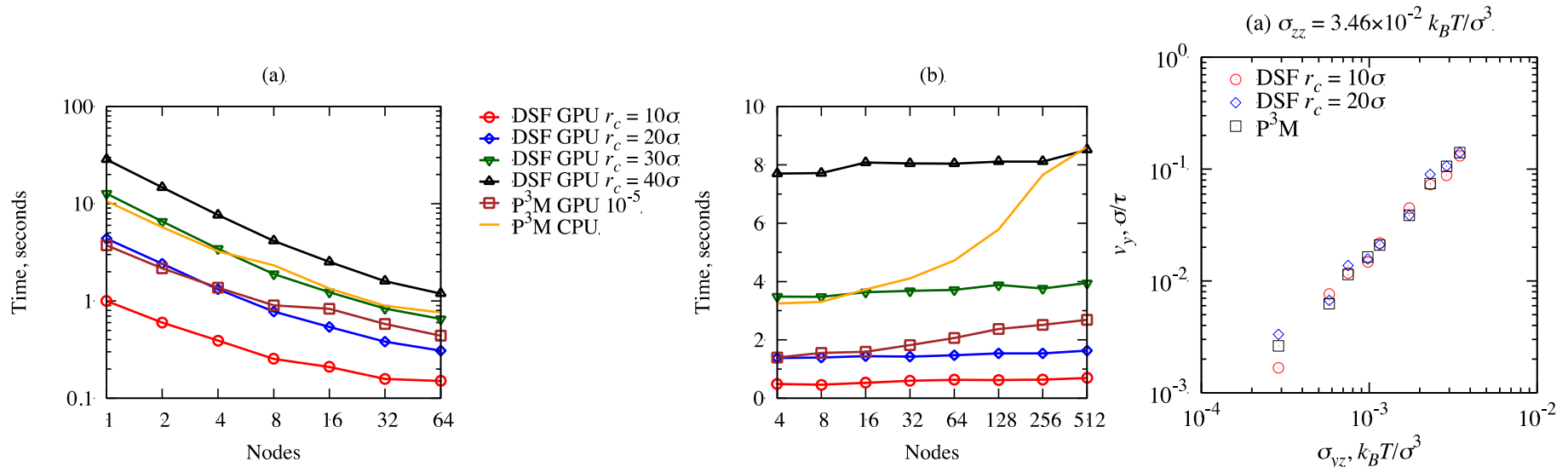
- Electrostatics are typically solved by splitting the Coulomb potential into a short-range potential that decays to zero at the cutoff and a long-range potential that converges rapidly in k-space
 - Long-range component is typically solved with discretization on a mesh
 - Poisson solve with 3D FFTs
 - Communications bottleneck
 - The traditional parameterizations that work well on older high-performance computers are not necessarily optimal for many simulations
 - Shift the work towards the short-range component
 - Disproportionate performance improvements on accelerator with larger short-range cutoffs
 - Benefits from acceleration **improve** at larger node counts!



Nguyen, T.D., Carrillo, J.-M., Dobrynin, A.V., Brown, W.M. **A Case Study of Truncated Electrostatics for Simulation of Polyelectrolyte Brushes on GPU Accelerators.** *To Appear.*

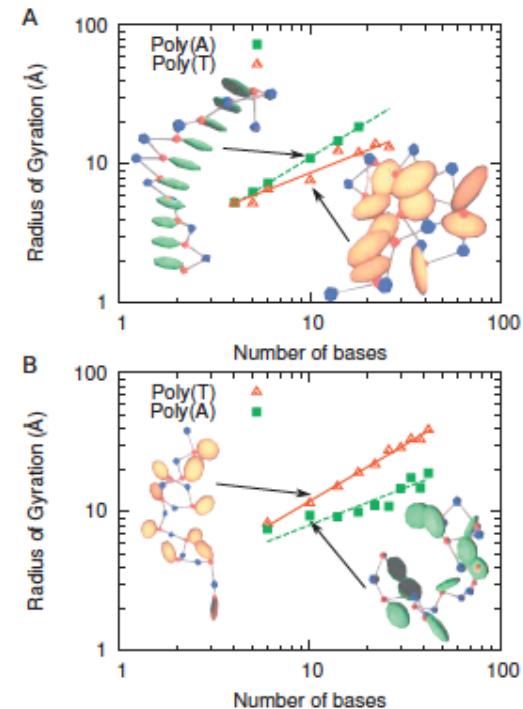
Electrostatics Example with Polyelectrolyte Brushes

- Eliminate the long-range component?
 - In condensed phase systems, charges can be effectively short-range due to screening from other charged particles in the system
 - Use a large short range cutoff, correct for issues due to non-neutral spherical cutoff regions, and modify cell list calculation to be efficient for large cutoffs in parallel simulations
 - Accurate results with faster time-to-solution for some simulations

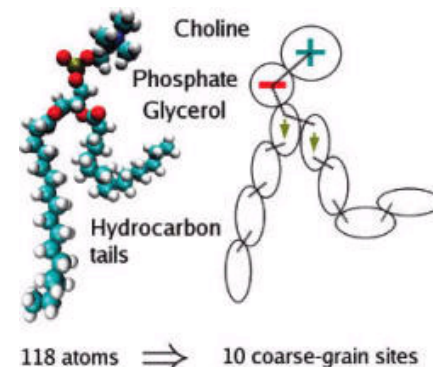
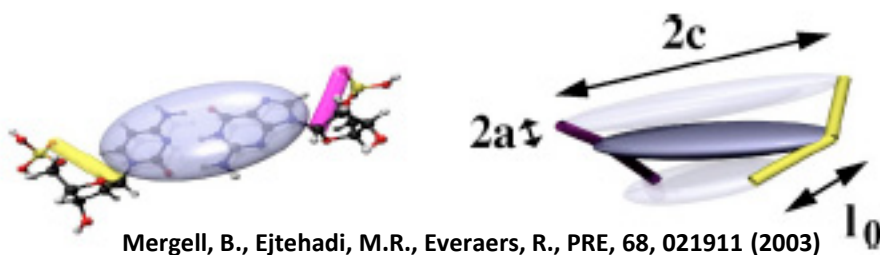


Alternative Potential Energy Models?

- Implementation of new models that can exploit high peak accelerator performance to improve accuracy and sampling
 - Computational cost of a single ellipsoid-ellipsoid interaction can be 15x that for Lennard-Jones on the CPU
 - With GPU acceleration, it is more competitive
 - Higher arithmetic intensity, so better speedup when compared to LJ acceleration
 - Better parallel efficiency *relative* to the CPU
 - Still get performance with fewer threads

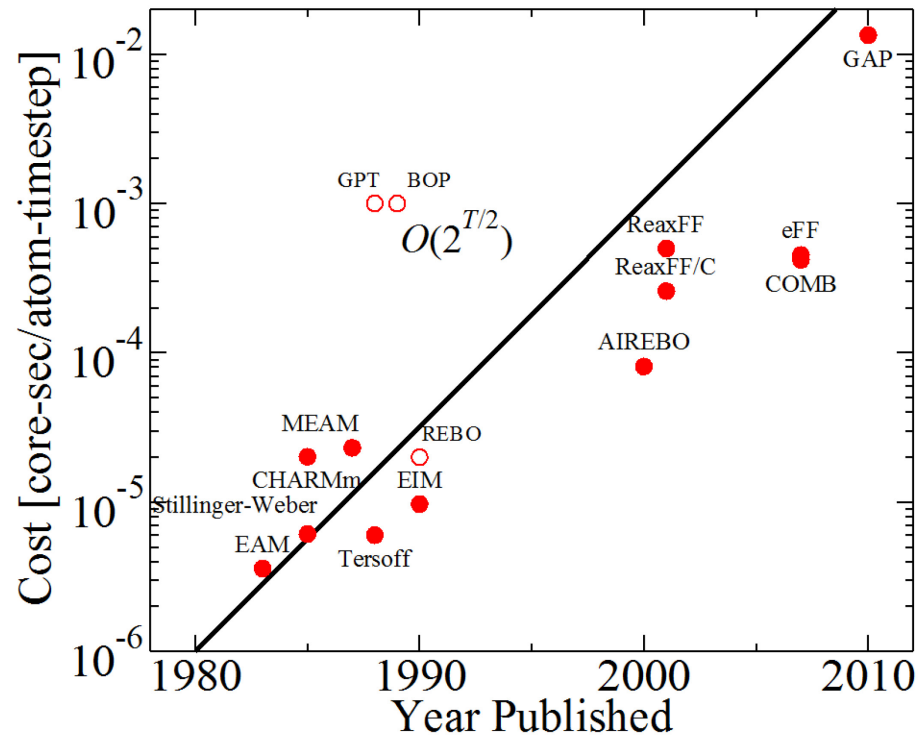


Morriss-Andrews, A., Rottler J., Plotkin S. S., JCP 132, 035105, 2010.



Orsi, M. et al, J. Phys. Chem. B, Vol. 112, No. 3, 2008

Moore's Law for Potentials



More creative examples...

- Advanced time integrators, time parallelism, etc...

Ongoing Work

- Implementation and evaluation of alternative algorithms for long-range electrostatics.
 - Multigrid(-like) Methods for Poisson Solve
 - $O(N)$, no FFTs
- Implementation of complex models well suited for accelerators
- Improvements driven by specific science problems

Publications

- Brown, W.M., Wang, P. Plimpton, S.J., Tharrington, A.N. **Implementing Molecular Dynamics on Hybrid High Performance Computers – Short Range Forces.** *Computer Physics Communications*. 2011. 182: p. 898-911.
- Brown, W.M., Kohlmeyer, A., Plimpton, S.J., Tharrington, A.N. **Implementing Molecular Dynamics on Hybrid High Performance Computers – Particle-Particle Particle-Mesh.** *Computer Physics Communications*. 2012. 183: p. 449-459.
- Brown, W. M., Nguyen, T.D., Fuentes-Cabrera, M., Fowlkes, J. D., Rack, P. D., Berger, M., Bland, A. S. **An Evaluation of Molecular Dynamics Performance on the Hybrid Cray XK6 Supercomputer.** *Proceedings of the ICCS Workshop on Large Scale Computational Physics*. 2012. Published in *Procedia Computer Science*, 2012. 9 p. 186-195.
- Nguyen, T.D., Carrillo, J.-M., Dobrynin, A.V., Brown, W.M. **A Case Study of Truncated Electrostatics for Simulation of Polyelectrolyte Brushes on GPU Accelerators.** *To Appear*.

Science Applications

- Carrillo, J.-M., Brown, W.M., Dobrynin, A.V. **Explicit Solvent Simulations of Friction between Brush Layers of Charged and Neutral Bottle-Brush Macromolecules.** *Submitted*.
- Nguyen TD, Fuentes-Cabrera M, Fowlkes JD, Diez JA, Gonzalez AG, Kondic L, Rack PD, **Competition between collapse and breakup in nanometer-sized thin rings using molecular dynamics and continuum modeling,** *Langmuir* 28, 13960-13967, 2012.

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- Geryon Library
 - W. Michael Brown (ORNL), Manuel Rodriguez Rodriguez (ORNL), Axel Kohlmeyer (Temple)
- K-Space Partitions
 - Yuxing Peng and Chris Knight (University of Chicago)
- Metallic Nanoparticle Dewetting
 - Miguel Fuentes-Cabrera (ORNL), Trung Dac Nguyen (ORNL), W. Michael Brown (ORNL), Jason Fowlkes (ORNL), Philip Rack (UT, ORNL)
- Lipid Vesicle Science and Simulations
 - Vincenzo Carnevale (Temple), Axel Kohlmeyer (Temple), Michael Klein (Temple), et. al.
- Enhanced Truncation/Bottlebrush Simulations
 - Trung Dac Nguyen (ORNL), Jan-Michael Carrillo (UC), Andrew Dobrynin (UC), W. Michael Brown (ORNL)
- Multilevel Summation
 - Arnold Tharrington (ORNL)