Refactoring EXAALT MD for Emerging Architecture

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Connections between CoPA & EXAALT & LAMMPS

- ECP EXAALT project seeks to extend accuracy, length, and time scales of material science simulations for fission/fusion reactors using LAMMPS MD
- EXAALT wants to run millions of small MD replicas (1K to 1M atoms) via ParSplice as fast as possible (not one large simulation with billions of atoms)
- Primary KPP target is MD of nuclear fusion materials that uses the SNAP interatomic potential in LAMMPS
- Performance directly depends on single-node performance for SNAP
- ECP CoPA codesign project targeting MD as one of its "sub-motifs"





Summary of EXAALT KPP Improvements

LAMMPS/Kokkos SNAP GPU FOM Improvements (Summit Full-Machine)



http://exascaleproject.org

"Episode 44: ECP Team Reengineers Materials Simulation Code, Achieves Atypical Performance Increase"

EXAALT Performance Improvements

- Joint effort by Aidan Thompson (EXAALT), Stan Moore (CoPA), Rahul Gayatri (NESAP), Sarah Anderson (Cray), Evan Weinberg (NVIDIA)
- Created stripped-down proxy code (TestSNAP)
- Completely rewrote TestSNAP to reduce flops and memory
- Explored many different GPU strategies, using OpenACC and CUDA
- Ported best implementation back to production code with Kokkos
- Other kernels required for ParSplice (time stepping, minimization) also implemented on accelerators
- These kernels account for essentially all of the flops in base challenge

SNAP: Spectral Neighbor Analysis Potential

- ML interatomic potential (IAP) have three critical parts:
 - Descriptors of the local environment
 - Energy and force functions expressed in the descriptors
 - Training(regression method) on large amount of 'ground truth' energies and forces
- Demonstrated *ab initio* accuracy in classical MD!





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SNAP: Spectral Neighbor Analysis Potential



- GAP (Gaussian Approximation Potential): Bartok, Csanyi et al., *Phys. Rev. Lett, 2010.* Uses 3D neighbor density bispectrum and Gaussian process regression
- **SNAP (Spectral Neighbor Analysis Potential):** Our SNAP approach uses GAP's neighbor bispectrum, but replaces Gaussian process with **linear regression**.
 - More robust
 - Lower computational cost (training and predicting)
 - Decouples MD speed from training set size
 - Enables large training data sets, more bispectrum coefficients
 - Straightforward sensitivity analysis
 - Fast

SNAP Bispectrum Components

Neighbors of each atom are mapped onto unit sphere in 4D

3D Ball: $(r, \theta, \phi), r < R_{cut} \implies 4D$ Sphere: $(\theta_0, \theta, \phi), \theta_0 = \frac{r}{R_{cut}}\pi$

Expand density around each atom in a basis of 4D hyperspherical *harmonics*,

$$\rho_i(\mathbf{r}) = \delta(\mathbf{0}) + \sum_{r_{i'} < R_{cut}} f_c(r_{i'}) w_{i'} \delta(\mathbf{r}_{i'})$$

- Bispectrum components of the 4D hyperspherical harmonic expansion are used as the geometric descriptors of the local environment
 - Preserves universal physical symmetries
 - Rotation, translation, permutation
 - Size-consistent (extensible)

$$u_{m,m'}^{j} = U_{m,m'}^{j}(0,0,0) + \sum_{\substack{r_{ii'} < R_{cut}}} f_c(r_{ii'}) w_i U_{m,m'}^{j}(\theta_0,\theta,\phi)$$
$$B_{j_1,j_2,j} = \sum_{m_1,m_1'=-j_1}^{j_1} \sum_{m_2,m_2'=-j_2}^{j_2} \sum_{m,m'=-j}^{j} (u_{m,m'}^{j})^* H_{\substack{j_1m_1m_1'\\j_2m_2m_2'}}^{jmm'} u_{m_1,m_1'}^{j_1} u_{m_2,m_2'}^{j_2}$$



SNAP Force Calculation

Function Calc_dBdR(i, j): for (η, η_1, η_2) in GetBispectrumIndices() { $\nabla_j B_{\eta_1,\eta_2,\eta} = 0$ for $(\mu = 0; \mu \le \eta; \mu + +)$ { for $(\mu' = 0; \mu' \le \eta; \mu' + +)$ { $\nabla_j B_{\eta_1,\eta_2,\eta} += Z^{\mu,\mu'}_{\eta_1,\eta_2,\eta} (
abla_j u^\eta_{\mu,\mu'})^*$ for $(\mu_1 = 0; \mu_1 \le \eta_1; \mu_1 + +)$ { for $(\mu'_1 = 0; \mu'_1 \le \eta_1; \mu'_1 + +)$ { $abla_j B_{\eta_1,\eta_2,\eta} \mathrel{+}= rac{\eta+1}{m_1+1} Z^{\mu_1,\mu_1'}_{\eta,\eta_2,\eta_1} (
abla_j u^{\eta_1}_{\mu_1,\mu_1'})^*$ for $(\mu_2 = 0; \mu_2 \le \eta_2; \mu_2 + +)$ { for $(\mu'_2 = 0; \mu'_2 \le \eta_2; \mu'_2 + +)$ { $abla_j B_{\eta_1,\eta_2,\eta} \mathrel{+}= rac{\eta+1}{\eta_2+1} Z^{\mu_2,\mu_2'}_{\eta_1,\eta,\eta_2} (
abla_{\mu_2,\mu_2'}^{\eta_2})^*$

- Deeply nested loops
- Loop structure not regular
- Loop sizes <= 14

Original Kokkos Version of SNAP

- Christian Trott (SNL) created the original Kokkos version in the ExaMiniMD proxy app
- Used advanced Kokkos features: three levels of hierarchical parallelism and shared scratchpad memory (global)
- Very memory compact
- Stan Moore (SNL) ported this version to the LAMMPS KOKKOS package
- Not clear of the possible improvements, if any...

parallel_for(num_atoms) { // Use TeamPolicy (level 1) here
 // Count Neighbors in Cutoff

parallel_reduce(num_neighs) // Use TeamThreadRange (level 2) here // Build reduced NeighborList

if (team_rank==<mark>0</mark>)

team barrier

// Compute U i

compute_ui ()

team barrier

// Compute Z i

compute_zi () team_barrier

parallel_scan(num_neighs) // Use ThreadVectorRange (level 3) here

compute_zi() {

parallel_for(num_idx) { // Use TeamThreadRange (level 2) here
parallel_for(jxj) { // Use ThreadVectorRange (level 3) here
for(ma1<ma1_max)
for(mb1<mb1_max) ...</pre>

parallel_for(num_neighs_reduced) { // Use TeamThreadRange (level 2) here
// Compute derivative of U_i
compute_duidrj() // Use ThreadVectorRange (level 3) inside
// Compute derivative of B_i
compute_dbidrj() // Use ThreadVectorRange (level 3) inside
// Update force on i and j
for(k<ncoeff)
fij += dbvec(k)
f(i) += fij;
f(j) += fij;
} ... // Compute energy</pre>

SNAP Performance before Jan2019 Hackathon

SNAP Potential, 256 atoms, single node or GPU 45 40 35 thousand atom-steps/s 0 1 0 0 0 0 0 0 0 0 10 5 0 P100 GPU Haswell CPU KNL Titan CPU Titan GPU Kokkos Lammps CPU Lammps ExaMiniMD

SNAP Benchmarking on Summit

- EXAALT FOM benchmark uses 205 bispectrum coefficients, tungsten crystal
- Mira (IBM BG/Q) FOM baseline: 0.182 Katoms-steps/s/node * 49152 Mira nodes
- On Summit, run 6 GPU + 1 CPU (36 cores) replicates per node
- 2018 LAMMPS performance on Summit: 33.7 Katom-steps/s/node * 4608 Summit nodes: projected 17.4x faster than Mira baseline



KPP: Challenges

- SNAP fraction-of-peak performance has been steadily declining on most hardware
- Recommendation from 2018 EXAALT review was to focus on SNAP GPU performance
- Developed a collaboration between EXAALT, CoPA, and NERSC/NESAP in order to address this risk

Architecture	Year	Normalized fraction of peak
Intel SandyBridge/Chama	2012	1.0
IBM PowerPC/Mira	2012	0.23
AMD CPU/Titan	2013	0.71
NVIDIA K20X/Titan	2013	0.037
Intel Haswell/Trinity	2016	0.47
Intel KNL/Trinity	2016	0.080
NVIDIA P100/SNL testbed	2016	0.077
Intel Broadwell/Serrano	2017	0.39
NVIDIA V100/SNL testbed	2018	0.093

Benchmarks for 2000 SNAP atoms

TestSNAP - standalone independent SNAP module

- Standalone SNAP kernel mini app derived from CPU version (90% similar)
- Proxy in memory and computation
- Included correctness check
- Blank slate to try something new without biases
- Initial OpenACC port very slow



During Jan~2019 hackathon



- Break up the compute kernels
- Store atom specific information across kernels
- Increases memory footprint
- Distribute the atom specific work in each kernel over the threadblocks and threads of a threadblock

(Results for V100 GPU)

Parallelize over atoms and neighbors



Post Jan-2019 hackathon

- Nick Lubbers (EXAALT, LANL) suggested re-arranging the order of summation (Y-array trick)
- Memory footprint was reduced by 20x by compacting multi-dimensional arrays in to simple lists
- Y-array trick was first applied to the sequential memory and merged into Kokkos-LAMMPS in June 2019
- Allowed the FOM 2J14 benchmark into the memory

Y-array Trick

• Old Algorithm: Dominated by neighbor loop

$$\begin{aligned} \mathbf{Z}_{j_{1}j_{2}}^{j} &= \mathbf{U}^{j_{1}} \cdot \mathbf{H}_{j_{1}j_{2}}^{j} \cdot \mathbf{U}^{j_{2}}, \\ \nabla_{j} E_{SNAP}^{i} &= \sum_{j_{1}j_{2}j} \beta_{j_{1}j_{2}}^{j} \mathbf{Z}_{j_{1}j_{2}}^{j} \colon \nabla \mathbf{U}^{j} \\ \mathbf{O}(\mathbf{J}^{5}) \times \mathbf{N} \text{eighs} \end{aligned}$$

New algorithm: Pre-compute Y factors
 outside neighbor loop

$$\mathbf{Y}^{j} = \sum_{j_{1}j_{2}} eta^{j}_{j_{1}j_{2}} \mathbf{Z}^{j}_{j_{1}j_{2}},$$
 $abla_{j} E^{i}_{SNAP} = \sum_{j} \mathbf{Y}^{j} \colon
abla \mathbf{U}^{j} \quad \mathbf{O}(\mathbf{J^{3}}) \times \mathbf{Neighs}$

- Cost of neighbor loop is now negligible
- Dominated by Y pre-compute O(J^7)
- 2x reduction in Flops/atom
- 5.5x speedup on Mira/BGQ!!



Y-array trick in TestSNAP

- New version can now fit in the memory for large problem size
- Exposed parallelism initially via
 - 1. OpenACC
 - 2. Cuda (to expose higher degree of parallelism with multi dimensional grid generation)
 - 3. Kokkos (Moved to a kokkos implementation to be consistent with the LAMMPS implementation)

Apply smaller problem optimizations on bigger problem size



- With the Y-array trick, 2J14 could now be fit in the GPU memory
- We applied the 2J8 tricks to the FOM (2J14) benchmark
- Initially parallelized over atom loops

Collapse atom and neighbor loops



- Distribute the works across atom and neighbor loops
 - The memory-footprint was now reduced to 12GB

Row major vs Column Major

Row major

Avoid false sharing in cache && improve cache utilization



Column major

Promote memory coalescing



- Memory access patterns
 - Row major C style access, optimal for CPUs
 - Column Major FORTRAN style access, optimal for GPUs
 - Gave a 2X performance improvement

Column major data access pattern



 Accessing the data in a column major fashion gave us a ~2X performance boost

Reverse the loop order

for neighbor j { for atom i {

. . .



- Reverse the loops to make atom index as the fastest moving index
 - Gave a 2x performance boost

Row major access for one of the data structures



- Increased runtime of kernel with atomics by 10%
- Improved runtime of another kernel by 25%
- Overall gave a 15% improvement

TestSNAP was ~7.5x faster than Baseline LAMMPS implementation of SNAP



Status at the end of the July 2019 hackathon

July2019 Hackathon

- Integrated several optimizations from TestSNAP into the Kokkos module in LAMMPS
 - Broke up kernels: actually made the code significantly slower at first (could be due to suboptimal memory layout)
 - Requires storing intermediate results between kernels for atom/neighbor pairs (extreme memory overhead that requires chunking up the loops)
 - Column major
 - Loop reorder: led to significant speedup, but not possible without breaking up the kernels
 - Removed advanced Kokkos features: used flat parallelism instead of hierarchical and no shared scratchpad memory
- New performance on Summit: 175.1 Katom-steps/s/node * 4608 Summit nodes: projected 90x faster than Mira baseline (5.2x speedup)

post July2019 Hackathon

- Integrated more optimizations from TestSNAP into the Kokkos module in LAMMPS
 - Refactored loop indices data structures to use complex numbers and be mutidimensional arrays instead of arrays of structs
 - Replaced more hierarchal parallelism with flat parallelism and exposed additional parallelism by collapsing loops
 - Changed data layout between kernels via transpose
- Current master LAMMPS on Summit: 262.0 Katom-steps/s/node * 4608 Summit nodes: projected 134x faster than Mira baseline (7.7x speedup)

post July2019 Hackathon (TestSNAP)

- Implemented a transpose routine for U-array to take advantage of column major updates for kernels with atomics and row major updates for other kernels
- Used double2 vector type from CUDA to optimize on 128 bit load/stores
- Improved the algorithm and reduced the memory footprint to 3.5GBs
- > 2x speedup in TestSNAP since July 2019 hackathon

Looking Forward

- Evan Weinberg (NVIDIA) has added additional optimizations to Kokkos SNAP in LAMMPS:
 - refactoring algorithms to avoid thread atomics
 - use of Kokkos hierarchal parallelism and scratch memory
- New version being tested by CoPA and EXAALT project members
- Not yet released, but should be merged into master LAMMPS soon
- Unreleased LAMMPS on Summit: 407.7 Katom-steps/s/node * 4608 Summit nodes: projected 210x faster than Mira baseline (12x speedup)
- And we are not done yet!

Lessons Learned

- Performance gains came from both algorithmic improvements (i.e. changes to the serial code) and implementation improvements targeting specific hardware (i.e. changes to the CUDA/Kokkos code)
- Small proxy app with correctness check is invaluable, allows rapid prototyping
- Profiling helps to know where to focus next
- Pay attention to memory access on GPUs

Supplementary Material

Source Code

TestSNAP: <u>https://gitlab.com/NESAP/EXAALT/q1-2019-hack-a-thon</u>

LAMMPS: https://github.com/lammps/lammps/tree/master/src/SNAP

FitSNAP: https://github.com/FitSNAP/FitSNAP

Papers

C.R. Trott, S.D. Hammond, A. P. Thompson, "SNAP: Strong scaling high fidelity molecular dynamics simulations on leadership-class computing platforms," *Supercomputing*, *(Lecture Notes in Computer Science)*, **8488** 19 (2014).

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Reports

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ECP CoPA Milestone Report, "Deploy ExaMiniMD optimizations into LAMMPS, Stan Moore, Christian Trott, Steve Plimpton, June (2018)