CP2K PERFORMANCE ON ARCHER

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Overview

- ARCHER / HECToR architecture comparison
- Benchmarks and results
- Performance hints and tips
- Conclusions



Architecture comparison

Feature	HECToR	ARCHER
Processors	AMD Interlagos 2.3GHz	Intel Ivy Bridge 2.7GHz
Cores per node	32 (4× 8-core NUMA)	24 (2× 12-core NUMA)
Memory per node	32 GB (1 GB/core)	64GB (2.66 GB/core) 128GB (5.33 GB/core)
Nodes	2816 (90,112 cores)	3008 (72,192 cores)
Interconnect	Cray Gemini	Cray Aries
Topology	3D Torus	Dragonfly
Post-processing Nodes	(None)	2 Nodes: 48 core SandyBridge 1TB Memory



Benchmarks

- The performance of the code has been evaluated using five benchmarks which are indicative of the different types of calculations that can be run with CP2K.
- As both HECToR and ARCHER charge per node, our tests utilise full nodes.
- The PSMP (i.e. MPI/OpenMP) version of CP2K has been used with appropriate combinations of MPI processes and threads tested.



H2O-64

- Short molecular dynamics simulation (10 steps) in NVE ensemble at 300K
- 64 water molecules (192 atoms, 512 electrons) in 12.4 Å³ cell
- Quickstep DFT, LDA functional, TZV2P basis set and 280 Ry cut-off









- Short molecular dynamics simulation (1000 steps) in NPT ensemble at 300K
- 28000 atoms (10³ supercell, 28 atoms per unit cell)
- Fe₂SiO₄ (Iron silicate a.k.a. fayalite)
- Classical potential (Morse with hard-core repulsive term, cutoff 5.5 Å), plus long-range electrostatics with SPME summation (Smoothed Particle Mesh Ewald)







LiH-HFX

- Single-point energy calculation using Quickstep GAPW (Gaussian and augmented plane-waves) with hybrid Hartree-Fock Exchange
- 216-atom lithium Hydride crystal (432 electrons) in 12.3
 Å³ cell
- ~10x computational cost of standard DFT
- This benchmark was used as part of the ARCHER procurement process







H2O-DFT-LS

- Single-point energy calculation using linear-scaling DFT
- 6144 atoms in 39 Å³ cell (32 water molecules in 4x4x4 supercell)
- LDA functional, DZVP MOLOPT (molecular optimised) basis set, 300 Ry cutoff
- Uses 5-level multigrid (finest grid is 420³)
- Similar computational cost per atom to standard DFT (and scales to 100,000s+)







H2O-64-ri-mp2

- H2O-64-ri-mp2 = resolution-of-the-identity MP2
- Single-point energy calculation using 2nd order Moller-Plesset Perturbation Theory (MP2) to calculate the exchange-correlation energy
- 64 water molecules in 12.4 Å³ cell (same as H2O-64)
- ~100x computational cost to standard DFT







Performance hints and tips

- Several additional tweaks to improve performance suggested by Cray
- MPICH variables may improve the MPI performance export MPICH_GNI_MAX_EAGER_MSG_SIZE=131072 export MPICH_GNI_NDREG_MAXSIZE=16777216 export MPICH_GNI_RDMA_THRESHOLD=128
- Adding -r 1 to aprun options, e.g. aprun -r 1 -n 128 -N 4 -d 6 -S 2 cp2k.psmp



Performance hints and tips

- May get some benefit by using a specific rank reordering
- e.g. if you want to use 169 nodes with 4 MPI processes per node, you can run:

module load perftools
grid_order -R -H -m 676 -n 4 -g 26x26 -c 1x1 > MPICH_RANK_ORDER

- In your batch script add: export MPICH_RANK_REORDER_METHOD=3
- Square grids are likely to give the best performance
- None of these gave any notable improvement for H2O-DFT-LS on ARCHER
 - But benchmark for your specific system!



Conclusion

- ARCHER is $\sim 2 3$ times faster (runtime) than HECToR
- ARCHER costs (kAU) more than HECToR but the improvements in runtime you'll get more than offset this
- To obtain good performance you should:
 - Use the package account version of CP2K
 - Benchmark your problem before starting any large runs
 - When benchmarking reduce the problem to a small number of time steps and run over a range of node counts
 - If you use a large number of MPI processes (> 1000) then using threads may well help you

