Multicore Applications in Physics and Biochemical Research

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The culmination of our HPC efforts so far:



Joint project between Sofia University and Technical University Assembled by PERSY Ltd Proudly hosted in the department of Theoretical Physics Faculty of Physics, Sofia University "St. Kliment Ohridski" http://physon.phys.uni-sofia.bg/ (in Bulgarian only)

Physon – the pink cluster



- 4 compute nodes:
 - dual Intel Xeon E5335 (4 cores @ 2 GHz)
 - I2 GB (I6 GB @ node001) ECC DDR2-667 RAM
 - 250 GB SATA2 HDD
 - 2 x I Gbps Fast Ethernet
 - I x 20 Gbps 4x DDR InfiniBand
 - Scientific Linux 4.4 64-bit
 - Sun NI Grid Engine executives
- NFS/NIS server:
 - Intel Core2 Duo E6600 (2 cores @ 2,4 GHz)
 - 2 GB ECC DDR2-667 RAM
 - 4 x 500 GB SATA2 HDD (total of 1,75 TB in ZFS RAIDZ1 array)
 - 2 x I Gbps Fast Ethernet
 - Sun Solaris
 - Sun NI Grid Engine master

Sun NI Grid Engine queues

- Interactive queue
 - For GUI and interactive programs
 - Up to 8 cores (I node)
- Batch queues
 - For long running non-interactive tasks
 - Up to 24 cores (3 nodes)
 - Interactive node available for serial batch tasks at night
- Fair share scheduler (to be enabled soon)

Parallel environments

- ompi for MPI tasks
 - OpenMPI both GNU and Sun Studio compiled
 - Up to 24 cores per task
 - Uses SysV IPC on single node and InfiniBand transport between nodes
- threads for threaded tasks
 - OpenMP Sun Studio only
 - POSIX Threads
 - Intel TBB
 - Up to 8 cores per task (single node only)
 - Intel Cluster OpenMP considered

Ganglia monitoring system



And here they come:

Multicore applications on Physon

- Hybrid architecture it is both shared and distributed memory machine
- Public domain codes:
 - GROMACS molecular biology research
 - Quantum ESPRESSO electronic structure and nanoscale simulations
- Custom codes
- Development tools and libraries:
 - Sun Studio I2 C/C++/Fortran compilers and IDE, Sun Performance Library
 - GNU Compiler Collection C, C++, FORTRAN77
 - OpenMPI

Molecular Dynamics

Solves in discrete time steps equations of motion:

$$m_i \ddot{\mathbf{r}}_i = -\nabla_i U \langle \mathbf{f}_1, \dots, \mathbf{r}_N \rangle$$

 Force computation is the single time consuming operation – done in parallel using space decomposition techniques



Molecular Dynamics (2)

- Requires only local communication between neighboring CPUs for short ranged forces
- Asynchronous communication leads to good parallel scaling
- Long ranged forces require global (synchronous) communication – bad scaling ⁽³⁾

Density Functional Theory

- A tool to compute/predict electronic structure and properties of molecules and crystals
- Minimizes $\langle \Psi | H | \Psi \rangle$ given a set of basis functions $\langle E \rangle$, usually planar waves or gaussians
- Essentially solves a large number of linear equations
- Requires vast amount of memory

Density Functional Theory (2)

- Can be combined with Molecular Dynamics – Car-Parrinello MD
- DFT parallelization:
 - Use parallel versions of basic linear algebra packages like BLAS and LAPACK
 - Distribute memory requirements between nodes
 - Global communication leads to bad parallel scaling



Buckling of carbon nanotube under rotational load – MD simulation using Brenner-Tersoff potential and custom code (BOZA).

Application: nanotechnology

BOZA

- Molecular Dynamics tool for simulations of carbon nanostructures
- Written in FORTRAN 77
- Parallelized using OpenMP
- Runs on shared memory computers
- Compiles as pure serial application on uniprocessors or with compilers that do not understand OpenMP



Electron density for cis-[Co(en)₂Cl₂]

Application: nanotechnology

Quantum ESPRESSO

- Swiss army knife for quantum simulations
 - Electronic structure
 - Geometry optimization
 - Car-Parrinello molecular dynamics
- Written in Fortran 90/95
- Parallelized using MPI library calls
- Runs on both distributed memory (clusters) and shared memory machines

QE: performance

# of cores	Speedup	Parallel efficiency (speedup per core)
2	1,98	99,2%
4	3,64	91,1%
8	5,55	69,3%
12	5,77	48,1%
16	5,87	36,7%



cores



Interferon-gamma alpha-receptor complex studied with MD simulation using GROMACS

Application: drug design



GROMACS

- Molecular Dynamics tool for simulations in molecular biology and biochemistry
- Written in C
- Parallelized using MPI library calls
- Many built-in force fields
- Runs on both distributed memory (clusters) and shared memory machines

GROMACS: performance

# of cores	Computation speed	Comp. speed per core
8	12,30 GFLOP/s	I,54 GFLOP/s
16	21,65 GFLOP/s	I,35 GFLOP/s
24	24,91 GFLOP/s	I,04 GFLOP/s



cores

Propaganda:

Challenges

- Parallel programming still not popular at Sofia University
- Most people still using moderate PCs to do research
- Masters course "Parallel programming and applications":
 - Already taught for two years (MPI only)
 - MPI and OpenMP basics
 - Performance measurement and optimization
 - Using batch processing engines and HPC
- Demands for computational power are growing!

And thus it ends.

* THANKYOU FORYOUR ATTENTION!

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