# Application performance on the UK's new HECToR service

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#### Overview



- Synthetic Benchmark Results
- Application Benchmark Results
- Conclusions

#### Systems for comparison

- HPCx (Phase 3): 160 IBM e-Server p575 nodes
  - SMP cluster, 16 Power5 1.5 GHz cores per node
  - 32 GB of RAM per node (2 GB per core)
  - IBM HPS interconnect (aka Federation)
  - 12.9 TFLOP/s Linpack, No 101 on top500
- HECToR (Phase 1): Cray XT4
  - MPP, 5664 nodes, 2 Opteron 2.8 GHz cores per node
  - 6 GB of RAM per node (3 GB per core)
  - Cray Seastar2 torus network
  - 54.6 TFLOP/s Linpack, No 17 on top500
- Also included in some plots:
  - HECToR Test and Development system (TDS)
    - Cray XT4, 64 nodes: 2.6 GHz dual core, 4 GB RAM/node





## System Comparison (cont)

	НРСх	HECToR
Chip	IBM Power5 (dual core)	AMD Opteron (dual core)
Clock	1.5 GHz	2.8 GHz
FPUs	2 FMA	1 M, 1 A
Peak	6.0 GFlop/s	5.6 GFlop/s
Perf/core		
cores	2560	11328
Peak Perf	15.4 TFLOP/s	63.4 TFLOP/s
Linpack	12.9 TFLOP/s	54.6 TFLOP/s

#### Synthetic Benchmarks

- Memory Bandwidth
  - Streams
- MPI Bandwidth
  - Intel MPI Benchmarks
    - PingPing

#### Memory bandwidth - Streams



#### Memory bandwidth - Streams

- Can clearly see caches
- HECToR better at L1, slightly better on main memory
   HPCx has advantage for intermediate array sizes.
- Underpopulating nodes (1 core per chip) gives improvements on both systems
  - memory bandwidth cannot sustain 2 cores per chip
  - HECToR worse than HPCx, especially on main memory
  - Of course, 1 core/chip means double the resource for same no. tasks
- TDS has lower clock rate than HECToR, but has higher bandwidth from main memory!
  - 4=2+2 GB RAM on TDS is symmetric, interleaving possible
  - 6=4+2 GB RAM on HECToR only allows partial interleaving

#### MPI bandwidth - PingPing



HPCx reaches saturation point earlier – HECToR may scale better

On both systems the latency (via IMB PingPong) ~5.5µs

AlltoAll - HPCx has the advantage for small (<100 bytes) messages, HECToR outperforms HPCx for larger messages

#### Applications

- Fluid Dynamics
  - PDNS3D
  - Ludwig
- Fusion
  - Centori
  - GS2
- Ocean Modelling
  - POLCOMS
- Molecular Dynamics
  - DL\_POLY
  - LAMMPS
  - GROMACS (see paper)
  - NAMD
  - AMBER (see paper)

### Fluid Dynamics: PDNS3D (PCHAN)

- Finite difference code for Turbulent Flow
  - shock/boundary layer interaction (SBLI)
- Simulates the flow of fluids to study turbulence
- T3 benchmark Involves a 360x360x360 grid
- Developed by Neil Sandham, University of Southampton

#### PDNS3D – compilation optimization



#### PDNS3D – system comparison



## PDNS3D Memory Bandwidth sensitivity



- Underpopulating nodes gives huge improvement (in terms of performance/core) on HECToR, slight improvement on HPCx
- TDS outperforms HECToR
- c.f. streams

#### PDNS3D – Optimised version

#### • New optimised version less sensitive to memory bandwidth



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#### PDNS3D – Optimised version

#### • PathScale gives a further 10-15% improvement



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#### Fluid dynamics - Ludwig



- Ludwig
  - Lattice Boltzmann code for solving the incompressible Navier-Stokes equations
  - Used to study complex fluids
  - Code uses a regular domain decomposition with local boundary exchanges between the subdomains
  - Two problems considered, one with a binary fluid mixture, the other with shear flow

#### Ludwig 256x512x256 lattice



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#### **Fusion**



ITER tokamak reactor (www.iter.org)

#### • Centori

- simulates the fluid flow inside a tokamak reactor developed by UKAEA Fusion in collaboration with EPCC
- GS2
  - Gyrokinetic simulations of lowfrequency turbulence in tokamak developed by Bill Dorland et al.

CENTORI



GS2



## **Ocean Modelling: POLCOMS**



- Proudman Oceanographic Laboratory Coastal Ocean Modelling System (POLCOMS)
  - Simulation of the marine environment
  - Applications include coastal engineering, offshore industries, fisheries management, marine pollution monitoring, weather forecasting and climate research
  - Uses 3-dimensional hydrodynamic model

#### **Ocean Modelling: POLCOMS**



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#### Molecular dynamics



Protein Dihydrofolate Reductase

• DL\_POLY

- general purpose molecular dynamics package which can be used to simulate systems with very large numbers of atoms
- LAMMPS
  - Classical Molecular Dynamics can simulate wide range of materials
- NAMD
  - classical molecular dynamics code designed for high-performance simulation of large biomolecular systems
- AMBER
  - General purpose biomolecular simulation package
- GROMACS
  - General purpose MD package specialises in biochemical systems, e.g. protiens, lipids etc

DL\_POLY - system comparison



DL\_POLY – system comparison



LAMMPS



LAMMPS



## LAMMPS

LAMMPS performance (Rhodopsin) against problem size for HECToR and HPCx







#### Conclusions

- On a core by core basis, not much difference between HECToR and HPCx in terms of application performance
  - But HECToR has many more cores and a more scalable interconnect
- Scaling better at high core counts on HECToR
  HECToR can also run much bigger problems, e.g. LAMMPS
- Memory bandwidth cannot sustain fully populated nodes for both systems
  - general problem for HPC systems these days
  - This is seen in performance of memory bandwidth sensitive applications
  - Problem is worse for HECToR, especially with current nonsymmetric memory setup.