



PHYSICS & ASTRONOMY
TEXAS A&M UNIVERSITY

High Performance Computing: Concepts and Best Practices

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August 12, 2016

Slides available at <http://www.github.com/jgerity/talks>

What is HPC?

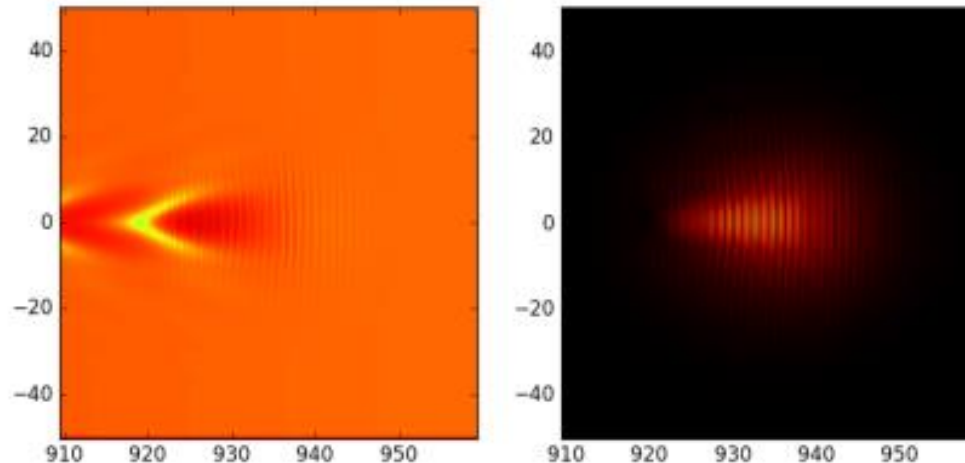
- **High performance computing (HPC)** is a catch-all term for computing at greater scales than what is realized by a typical workstation.
- Some problems would require tens of thousands of hours (or years!) on a single machine
 - With more computing power and memory, perhaps we can do better.

Example problem: Particle-in-cell

- Simulating the time evolution of a plasma is a demanding challenge:
 - N^2 interactions to calculate in the worst case
 - Number density of 10^{25} m^{-3} not at all uncommon
 - Small timestep, mesh is necessary
- Linearity of Maxwell's equations lets us apply the “divide and conquer” strategy

Why use parallel architecture?

- **Recent example:** Laser-wakefield simulation to interpret experiments at LBNL.



3D grid with 2500 x 200 x 200 grid points
0.2 billion macroparticles
140,000 timesteps (Courant limit!)

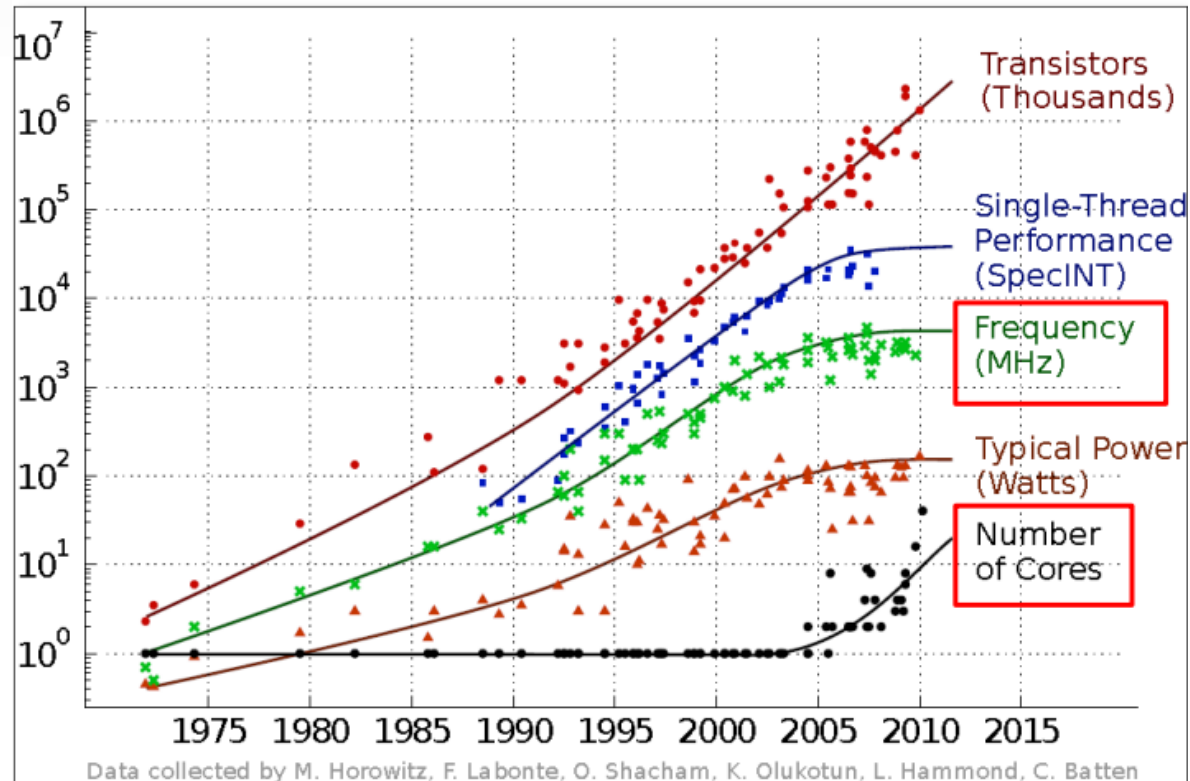
~60,000 hours on 1 core = 7 years!

=> Need either faster cores or more cores in parallel



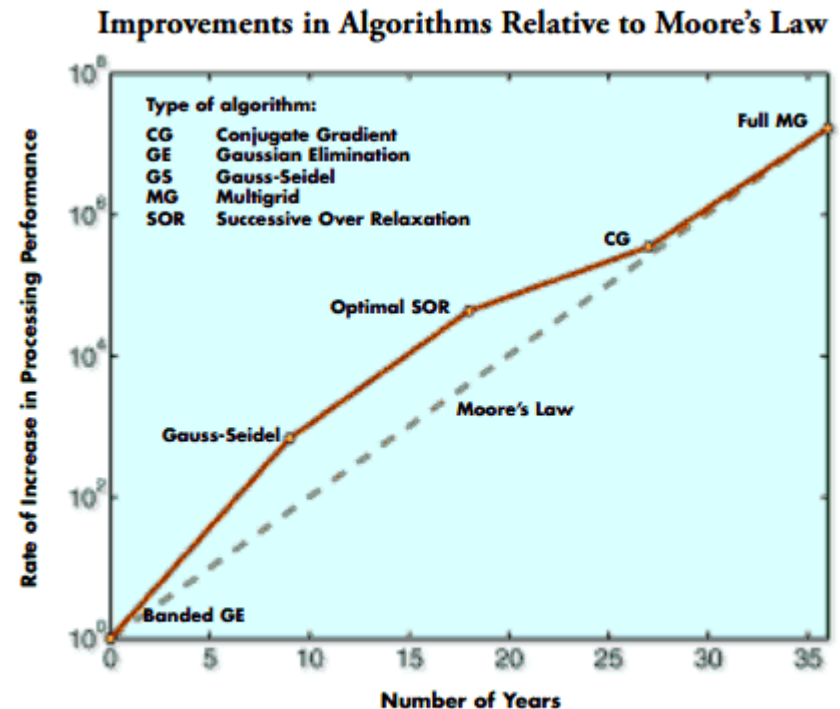
Can we just wait on faster processors?

History of CPU performance



What problems does HPC *not* solve?

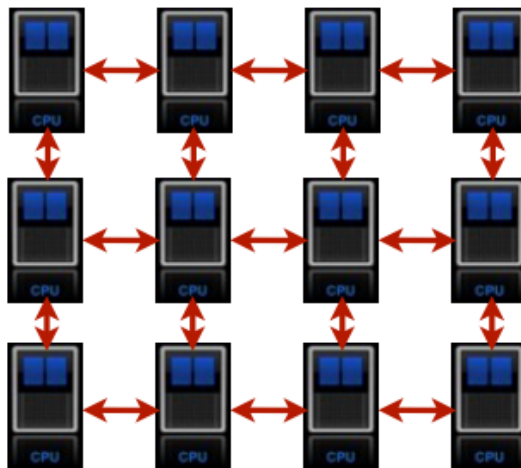
- If the problem requires sharing information between CPUs, we have to communicate, which is slow!
- Better algorithms yield more gain than Moore's Law does



The relative gains in some algorithms for the solution of an electrostatic potential equation on a uniform cubic grid compared to improvements in the hardware (Moore's Law).

From 2005 report "Computational Science: Ensuring America's Competitiveness"

What is a cluster?



Individual nodes have several cores (i.e. computing units):

- “Traditional” CPUs: ~10 cores
- Xeon Phi: 68 cores
- GPUs: ~1000 (slow) cores

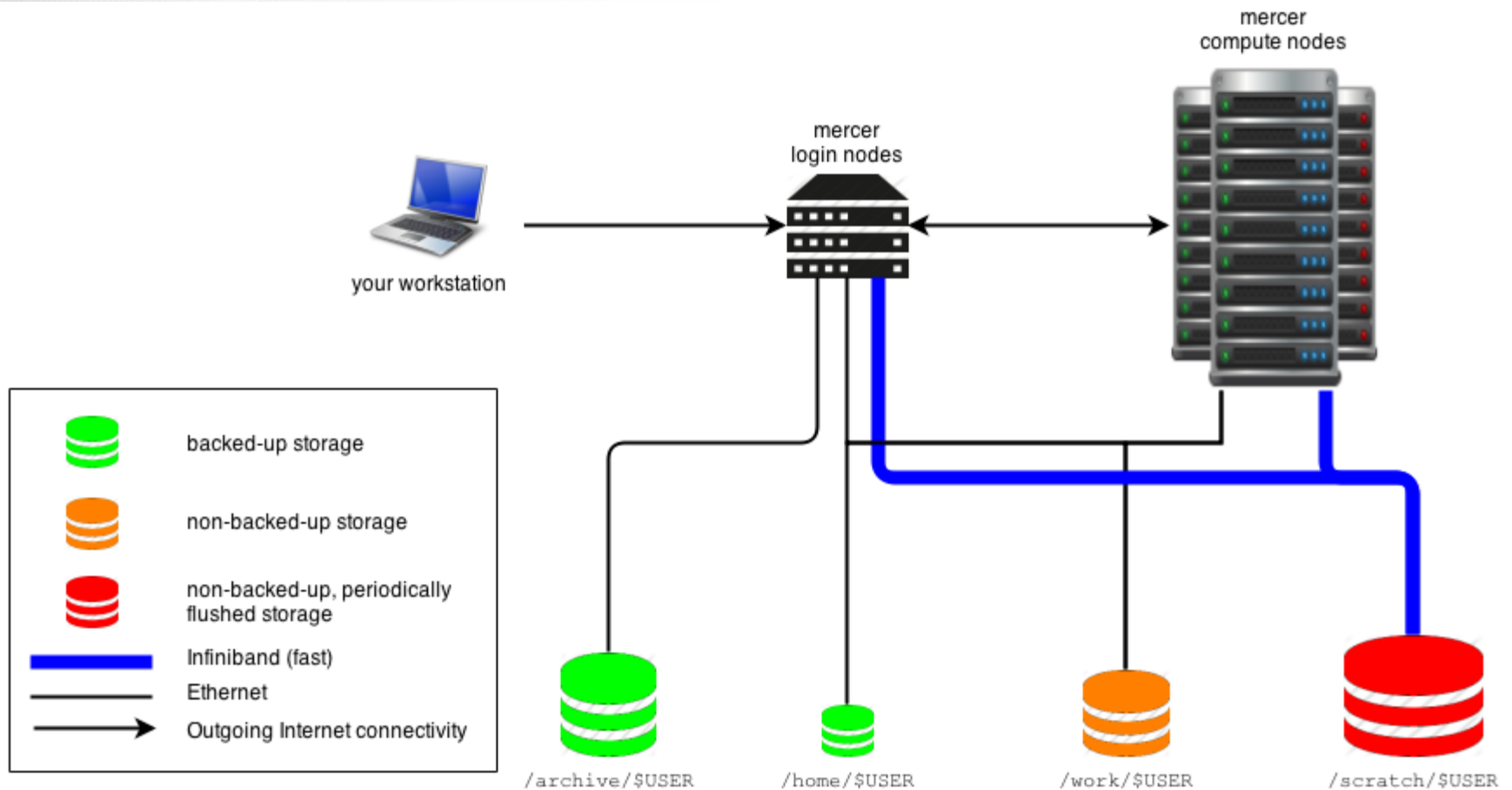
Cores within one node share memory

- How to use this architecture to make a PIC code faster?
- How to use the two levels of parallelism?
(within one node and between nodes)



Slide courtesy of Remi Lehe

What is a cluster?



Cluster layout

- Login nodes
 - Main form of user interaction with the system
 - Allows some development, as well as submitting jobs
- Compute/worker nodes
 - Computational work done here, generally less aware of the broad view of how a job is split up.

Cluster layout

- Storage
 - At large machines, usually have separate facilities that can be accessed from many places
 - Networked file systems like AFS, NFS
 - Important to understand what is available to compute nodes and how fast it is
 - If you bottleneck at filesystem I/O, potentially several orders of magnitude slower!

Schedulers

- From the login node, jobs are submitted to a **scheduler**, software that handles the logistics of balancing many jobs from different users across nodes.
 - Knowing the ins and outs of the scheduler you're using is an absolute must!
- Examples of schedulers: SLURM, TORQUE, HTCondor

How not to be “that jerk” on a shared system

- It is *your* responsibility to know the local machine’s policy. Read the MOTD and the documentation!
- Make sensible resource requests – does your job actually benefit from tying up several nodes? Benchmark it first!

How not to be “that jerk” on a shared system

- Don't use the login node for heavy computational work!
 - Best case scenario, you waste your own time
 - Worst case scenario, you crash the login node and waste *everybody's* time
- Ideally, develop locally and understand how things scale, so there aren't surprises when you go to bigger jobs.

How not to be “that jerk” on a shared system

- Some remarks c/o Alexx Perloff:
- World-wide LHC Computing Grid (WLCG): This is a complicated beast, but we make use of it through a system called CRAB (CMS Remote Analysis Builder).
- There is an assumption that you will be submitting a certain type of job (I.e. Single core not requiring memory over 1.9 GB, and a job that won't last more than 48 hours). Beyond that there is a priority that takes things into account similar to the LPC computing cluster, but it also takes into account where your requested data is, where the stage-in and stage-out are coming from, how many jobs are running on a particular cluster and how many open slots it has.
- Basically it is a world-wide balancing act across >100 computing clusters of various locations, sizes, throughput, and architecture.
 - The value of understanding the “right” way to submit jobs on a system like this cannot be overstated!

MPI

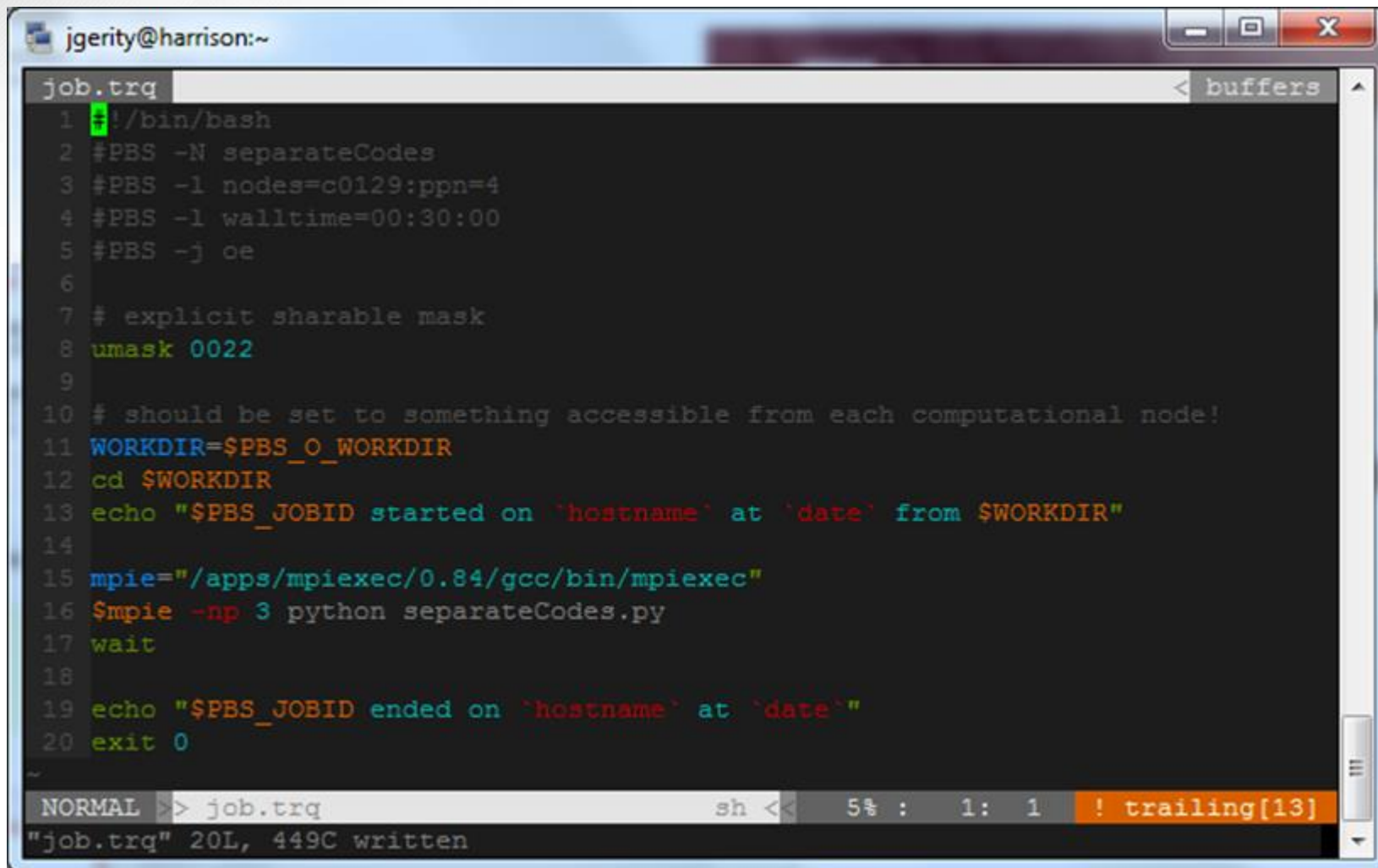
- **Message Passing Interface (MPI)** is a standardized and portable **message-passing** system
- Run MPI-aware program with “`mpiexec`” command and `-np` flag for number of processes to use
 - Tasks can be divided among processes of different “rank,” with a communication framework for exchanging information.

A simple MPI example in Python

```
#seperateCodes.py
from mpi4py import MPI
rank = MPI.COMM_WORLD.Get_rank()

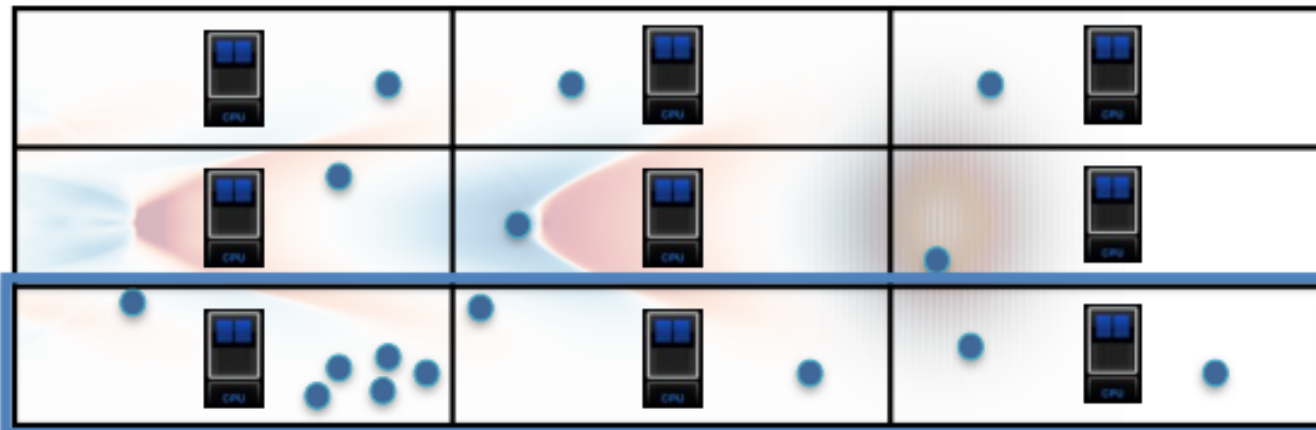
a = 6.0
b = 3.0
if rank == 0:
    print a + b
if rank == 1:
    print a * b
if rank == 2:
    print max(a,b)
```

A simple MPI example in Python



```
jgerity@harrison:~  
job.trq buffers  
1 #!/bin/bash  
2 #PBS -N separateCodes  
3 #PBS -l nodes=c0129:ppn=4  
4 #PBS -l walltime=00:30:00  
5 #PBS -j oe  
6  
7 # explicit sharable mask  
8 umask 0022  
9  
10 # should be set to something accessible from each computational node!  
11 WORKDIR=$PBS_O_WORKDIR  
12 cd $WORKDIR  
13 echo "$PBS_JOBID started on `hostname` at `date` from $WORKDIR"  
14  
15 mpie="/apps/mpiexec/0.84/gcc/bin/mpiexec"  
16 $mpie -np 3 python separateCodes.py  
17 wait  
18  
19 echo "$PBS_JOBID ended on `hostname` at `date`"  
20 exit 0  
~  
NORMAL >> job.trq sh << 5% : 1: 1 ! trailing[13]  
"job.trq" 20L, 449C written
```

Problem: load balancing



Example:
particle pusher,
schematic view

Push particle 1	Push particle 1	Push particle 1
Push particle 2	Push particle 2	Push particle 2
Push particle 3	Exchange particles ↔	Exchange particles
Push particle 4	Wait	...
Push particle 5	Wait	
Push particle 6	Wait	
Exchange particles ↔	Exchange particles	

The simulation will always progress at the pace of the slowest node (the one doing the most work)

=> Problematic when the particle distribution is very non-uniform

Slide courtesy of Remi Lehe

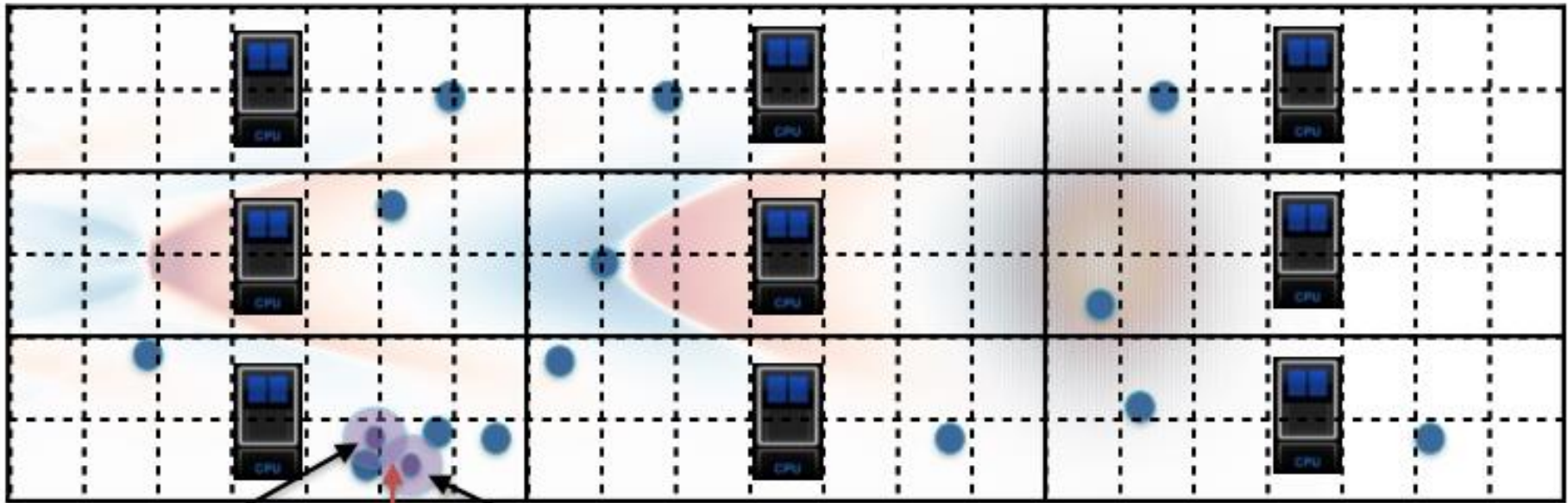
OpenMP

- “OpenMP Application Program Interface (API) is a portable, scalable model that gives parallel programmers a simple and flexible interface for developing portable parallel applications. OpenMP supports multi-platform **shared-memory** parallel programming in C/C++ and Fortran on all architectures”

OpenMP

- OpenMP allows separate threads to operate as fast as they can...
- ...BUT introduces the possibility of a *race condition* in some cases

OpenMP's dangers: race condition



Core 2 performs current deposition Race condition! Core 3 performs current deposition

- The cores do not exchange information via MPI send/receive. Instead they **directly** modify the value of the current in shared memory, without notifying the other cores.
- Potentially, two cores could simultaneously try to modify the value of the current in a given cell (leads to inconsistencies). This can be avoided with proper care (e.g. “atomic operations”).

GPGPU

- A video card, more generally known as a graphics processing unit (GPU), is a collection of *many* processors that share memory.
- Designed with computer graphics in mind, but there is substantial overlap with non-graphics computation!
- Increasingly common to utilize this hardware for computation (future topic, maybe...)

We have a small computational cluster!

- The 20 iMac workstations in MPHY 330 are networked in an HTCondor cluster, giving you access to 20 i5 quad-cores and 80 GB of RAM!
- Some more information available from <https://csg.physics.tamu.edu/docs/condor/>

Interactive Condor computing session

- Let's log into the Condor cluster.
- Use your ssh client to log into metis.physics.tamu.edu with your department credentials
 - On Mac/Linux:
 - ssh [username@metis.physics.tamu.edu](https://metis.physics.tamu.edu)
 - On Windows:
 - Use a terminal emulator like PuTTY

Interactive Condor computing session

```
jgerity@metis: ~  
login as: jgerity  
Using keyboard-interactive authentication.  
Password:  
  
*****IMPORTANT*****  
**  
** This machine is the submit node for the Condor Computing Cluster and **  
** should not be used to run individual jobs. If you must run an individual **  
** job, please use one of the other Mac computers; they all have SSH access. **  
** Any job running for more than 4 hours on this machine is subject to **  
** termination with no further warning. More information on Condor can be **  
** found here https://csg.physics.tamu.edu/docs/condor/ **  
**  
** Any executable run under condor need to begin with "condor_" in order to **  
** be recognized as a condor job and not killed after exceeding our run **  
** time limitations. Any processes running for more than 2 hours with out **  
** the condor_ prefix will be suspended. **  
**  
** Thank you, **  
** Computer Support Group **  
**  
*****  
jgerity@metis:~$
```


Submitting Condor jobs

- To run a job on metis, follow the CSG instructions:
 1. Create a working directory called **Condor** in your home directory
 2. Create a job file describing your task. See **fourier.job** for an example
 3. Submit the job using the **condor_submit** command



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Thank you!