



# Institute for Cyber-Enabled Research

Dr. Dirk Colbry  
Director, High Performance  
Computing Center

# Agenda

- What is iCER / HPCC
- Common classes problems
- Overview of Hardware
- Getting started, Seven Steps to High Performance
- Running in parallel
- Tips and tricks

# Institute for Cyber Enabled Research

The Institute for Cyber-Enabled Research (iCER) at Michigan State University (MSU) was established to coordinate and support multidisciplinary resource for computation and computational sciences. The Center's goal is to enhance Michigan's national and international presence and competitive edge in disciplines and research thrusts that rely on advanced computing.

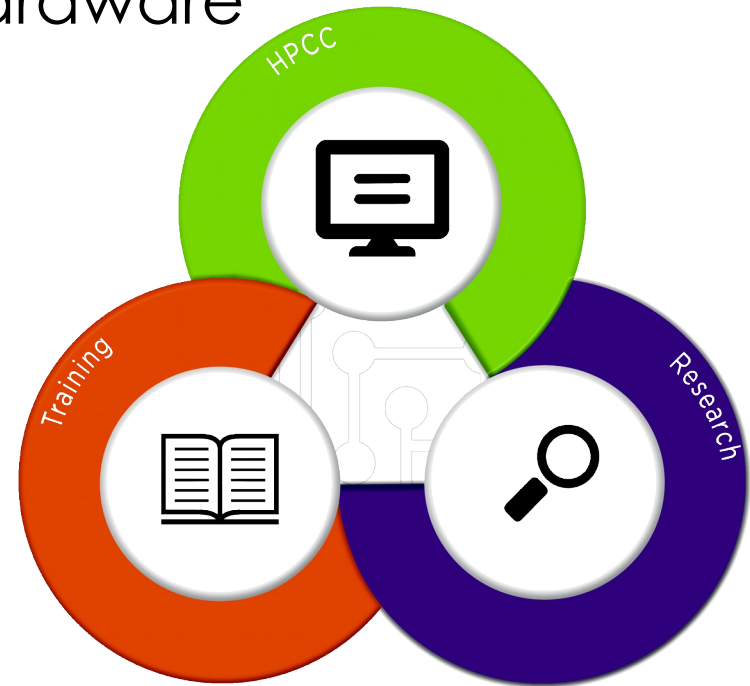
# WMU/ MSU Partnership

- WMU researchers are HPCC Buy-in User  
[wmichhelp@hpcc.msu.edu](mailto:wmichhelp@hpcc.msu.edu)
- Please make sure you send us your login name
  - Emailing us from your wmich account should be more than sufficient.

# Research Resource

iCER is a research unit at MSU. We provide:

- Advanced computing hardware
- Software-as-a-service
- Training
- Consulting
- Proposal writing support



# Advanced Architectures

- Anything more advanced than your desktop
- Local resources
  - Lab, Department, Regional (iCER)
- National resources
  - NSF (XSEDE), DOE (Titan) , Others
- Commercial Resources (cloud computing)
  - Amazon, Azure, Liquid Web, Others

# Why use Advanced Computing Hardware?

- Science takes too long
- Computation runs out of memory
- Needs licensed software
- Needs advanced interface (visualization/database)
- Lots of file i/o

# Bigger & Better ?

- The goal of iCER is NOT:
  - Kflops / second
- Instead, the goal of iCER IS:
  - KSciences / second
- Doing More Science, Faster
  - Reducing the “Mean time to Science”
- iCER is designed to help researchers do their science and when appropriate scale them up to national resources





# Hardware Highlights

- > 600 nodes, 7600 computing cores, 50 TB RAM
  - Large Memory Nodes (up to 6TB!)
  - GPU clusters (K20, M1060)
  - Xeon PHI cluster (5110p)
  - + 8000-core condor cluster
- High-speed file servers
  - 360TB parallel scratch file space
  - 1PB replicated home/research file servers
- High-speed network (FDR,QDR,SDR,10g)
- Evaluation nodes

# Shared System

- Development Nodes
  - Interactive computers for testing software and compiling code
- Evaluation Nodes
  - Interactive computers for evaluating older and cutting edge systems
- Queuing system
  - Submit jobs to the queue
  - Jobs will run as resources become available
  - Up to one-week walltime
  - Up to 520 processing cores per user at any time
  - The larger the job, the longer/harder it is to schedule

# Software Stack

- Compiled open-source software stack
  - Close to 2000 titles!
- Optimized Math/Communications libraries
- Some commercial software available
  - Due to licensing limitations we can not provide all of our software to WMU users
  - We can help install software for you

Full list: <http://wiki.hpcc.msu.edu>

# Miscellaneous Musings

iCER provides many other services:

- Data sharing (Globus Online Subscriptions)
- Visualization Servers
- Virtual Computing Lab
- Specialized bioinformatics support (BICEP)
- Support for scaling to XSEDE resources
- + ... ?

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# What problems are we solving?

- Simulations
- Data Analysis
- Search

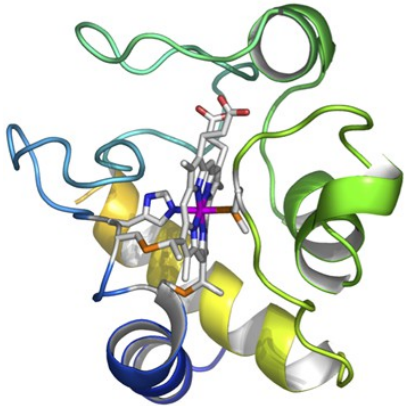
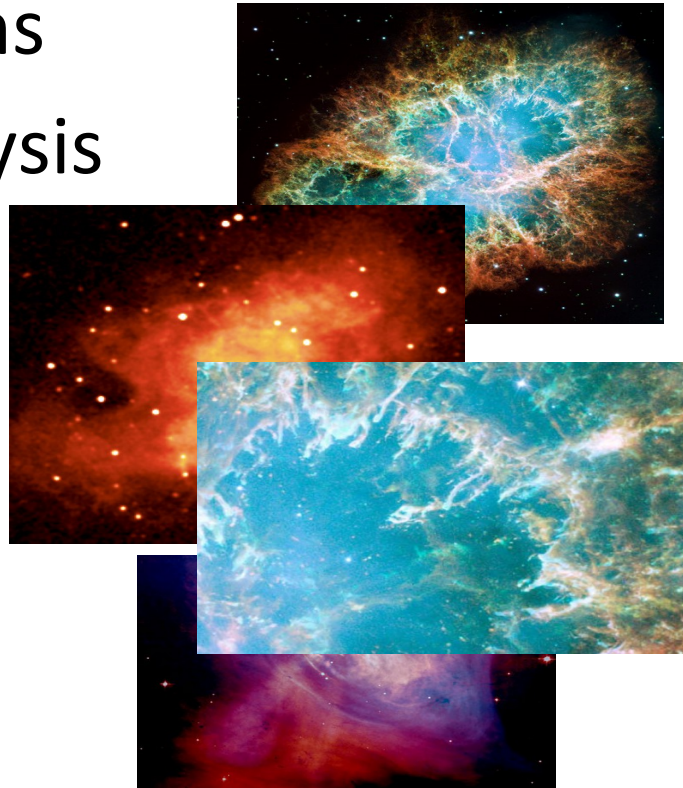


Image Provided by Dr.  
Warren F. Beck, MSU



Images from, "Understanding the H<sub>2</sub> Emission from the Crab Nebula", C.T. Richardson, J.A. Baldwin, G.J. Ferland, E.D. Loh, Charles A. Huehn, A.C. Fabian, P.Salomé

<https://wiki.hpcc.msu.edu/x/6QFiAQ>

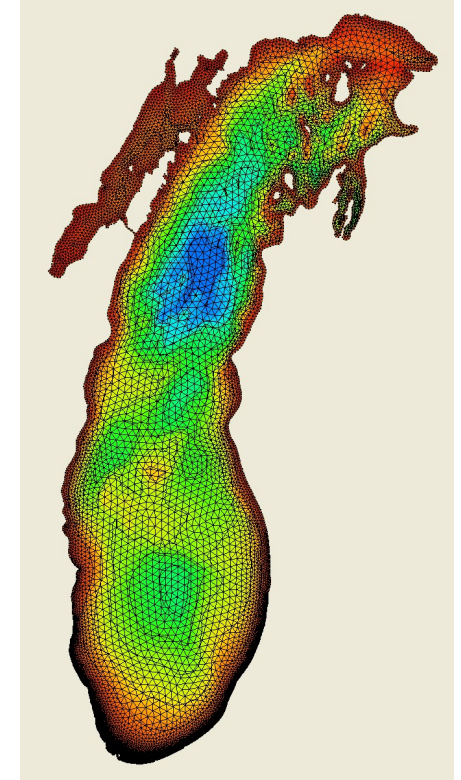
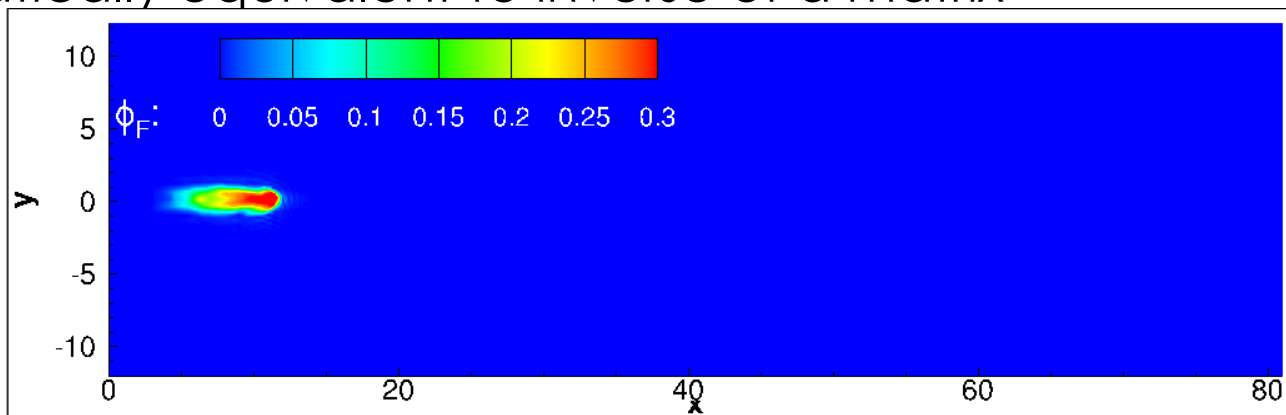


Image Provided by Dr. Mantha  
Phanikumar, MSU

# Simulations

- Typically System of PDE (Partial Differential equations)
  - Fluid dynamics
  - Finite element analysis
  - Molecular dynamics
  - Weather
  - Etc.
- Mathematically equivalent to inverse of a matrix

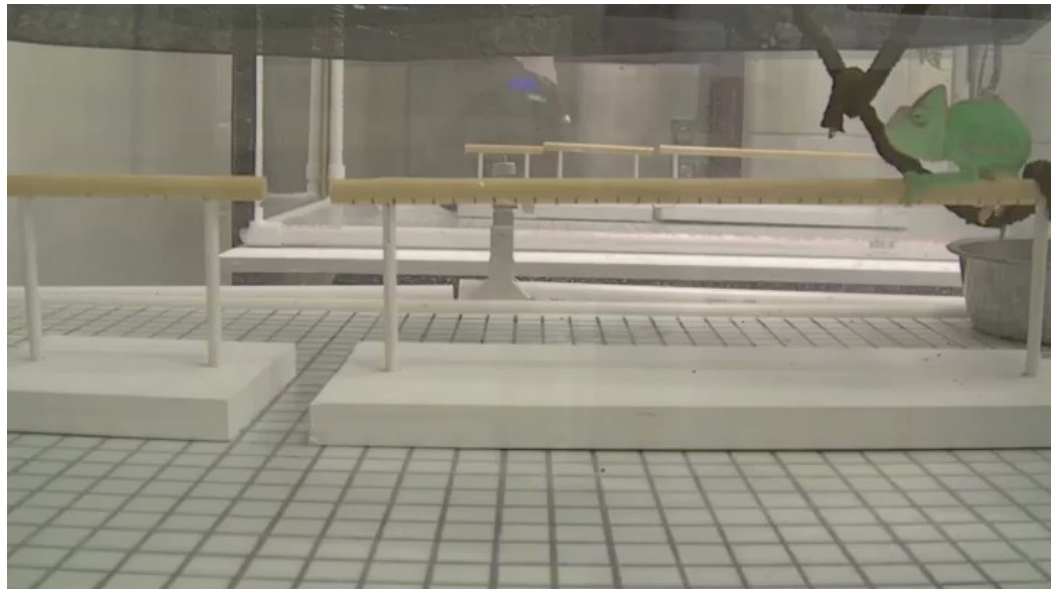
Premixed mixture of  
H<sub>2</sub>-air auto igniting  
and flame  
propagation at  
supersonic flow  
Provided by Dr Jabari  
and Mani (Abolfazl)  
Irannejad



# Data Analysis

- Computer vision tasks
- Some Bioinformatics
- Astrophysics
- Etc.

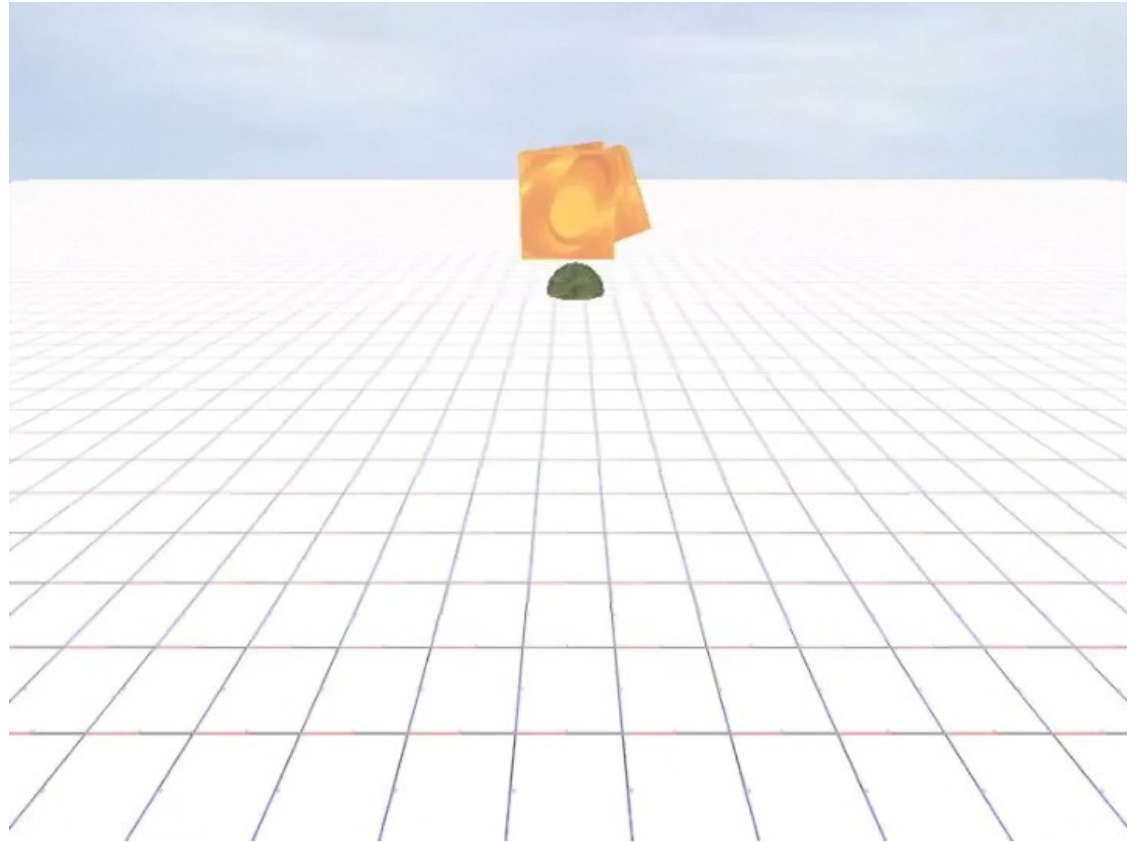
Video Provided by Dr. Fred Dyer





# Search

- Genome sequencing
- Analytics
- Optimization
- Etc.



Evolution of an artificial organism that can move and forage for food, Dr. Nicolas Chaumont

# Agenda

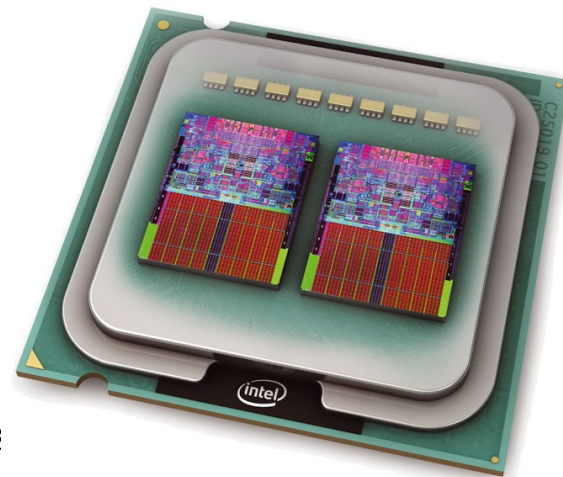
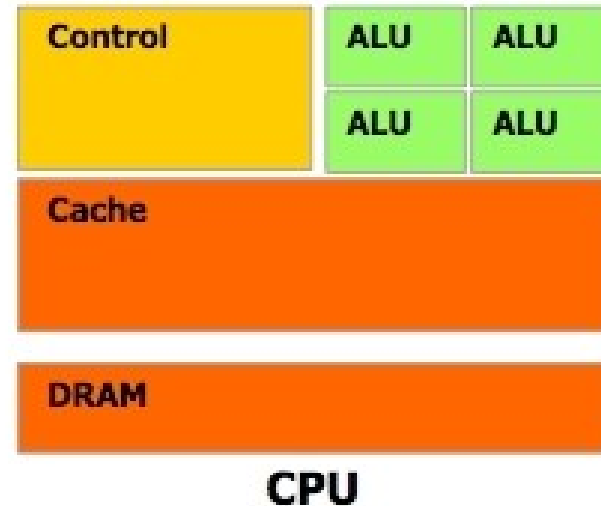
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# Large Shared Memory Systems (Fat Nodes)



# Shared Memory Communication

- Fast!
- Cores on a system share the same memory
- OpenMP
- Fat nodes
  - 96 cores
  - 6TB of memory



# Accelerated Systems

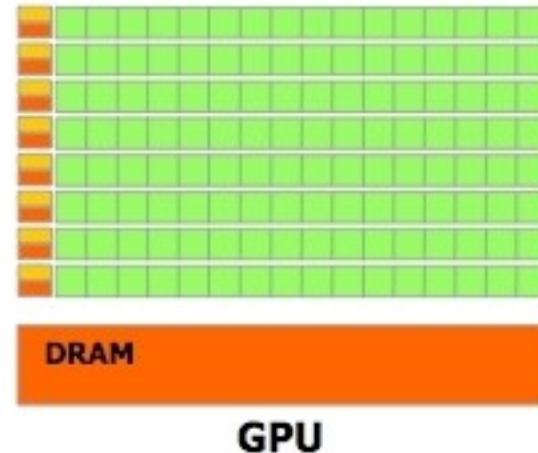




# GPU

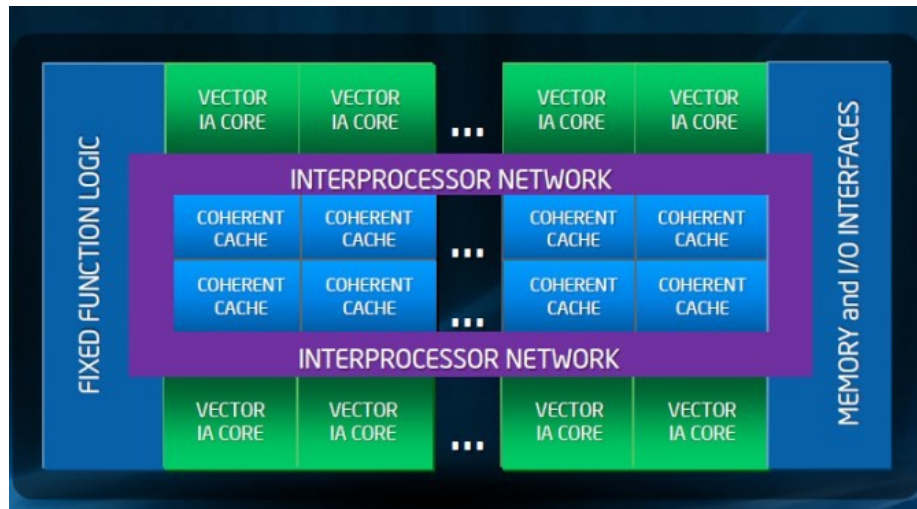
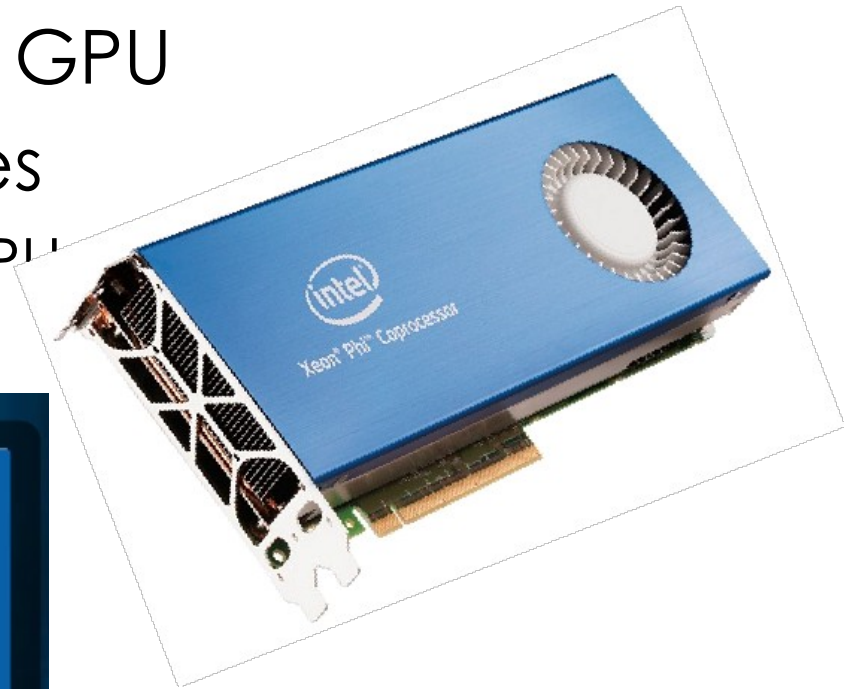


- Cards used to render graphics on a computer
- Hundreds of cores
- Not very smart cores
- But, if you can make your research look like graphics rendering you may be able to run really fast!



# Intel Xeon Phi

- Cross between CPU and GPU
- About 61 Pentium III cores
  - Less cores/slower than GPU
  - Easier to use than GP



# High Throughput HTCondor Cluster





# MSU HTCondor Cluster

- Runs like a screen saver and Scavenges CPU cycles:
  - Approximately 400+ nodes
  - Approximately 7000 cores
  - Windows 7



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# Steps in Using the HPCC

1. **Get an account**
2. Install needed software (SSH, SCP, X11)
3. Transfer input files and source code
4. Compile/Test programs on a developer node
5. Write a submission script
6. Submit the job
7. Get your results and write a paper!!

# Accounts

- Pis can request accounts through Don Weber:  
[donald.weber@wmich.edu](mailto:donald.weber@wmich.edu)
- Each account has access to:
  - 50 GB of replicated file spaces
  - 520 processing cores
  - 360 TB of high-speed scratch space
- Also available: shared group folders
- We have temporary accounts for today.

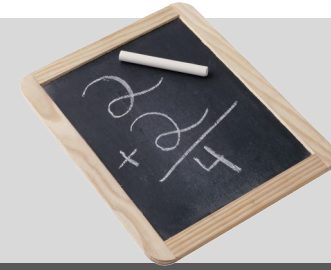
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# Required Software

- Secure Shell (ssh)
- File transfer
  - Secure Copy (scp)
  - Mapping home directories
- Graphical User Interface (x11)
  - Optional

# Apple



- Run Terminal program
  - ssh – already installed  
ssh -X [userid@hpcc.msu.edu](mailto:user@hpcc.msu.edu)
    - scp – already installed  
scp ./mylocalfile [userid@hpcc.msu.edu:~/mylocalfile](mailto:user@hpcc.msu.edu)
- May need to install Xquartz (mac X11 Server)
  - Installer should be on USB drive



# Windows Software

- PuTTY:
  - <http://www.chiark.greenend.org.uk/~sgtatham/putty/>
- Xming:
  - <http://www.straightrunning.com/XmingNotes/>
- Xming install:
  - <https://wiki.hpcc.msu.edu/x/swAk>
- WinSCP:
  - <http://winscp.net>



# MobaXterm (windows)

- Complete toolbox for remote computing:
  - Multi-tab terminal
  - X11 server
  - SSH
  - File transfer
  - More
- Opensource
- <http://mobaxterm.mobatek.net/>



# Exercise: Portable HPCC



- If you have Windows
- Plug in your USB thumb drive
- Open the thumb drive folder and select
  - PortableApps
- You should see a new menu in your system tray for navigating



# Exercise: Connect to HPCC



- Step 1: Log into gateway.hpcc.msu.edu
- Step 2: ssh into a dev node (developer node)
  - `ssh dev-intel10`
- Step 3: execute a command
  - `echo "Hello world"`

```
HPCC: dev-intel10

Welcome to Michigan State's High Performance Computing Center
** Unauthorized access is prohibited **

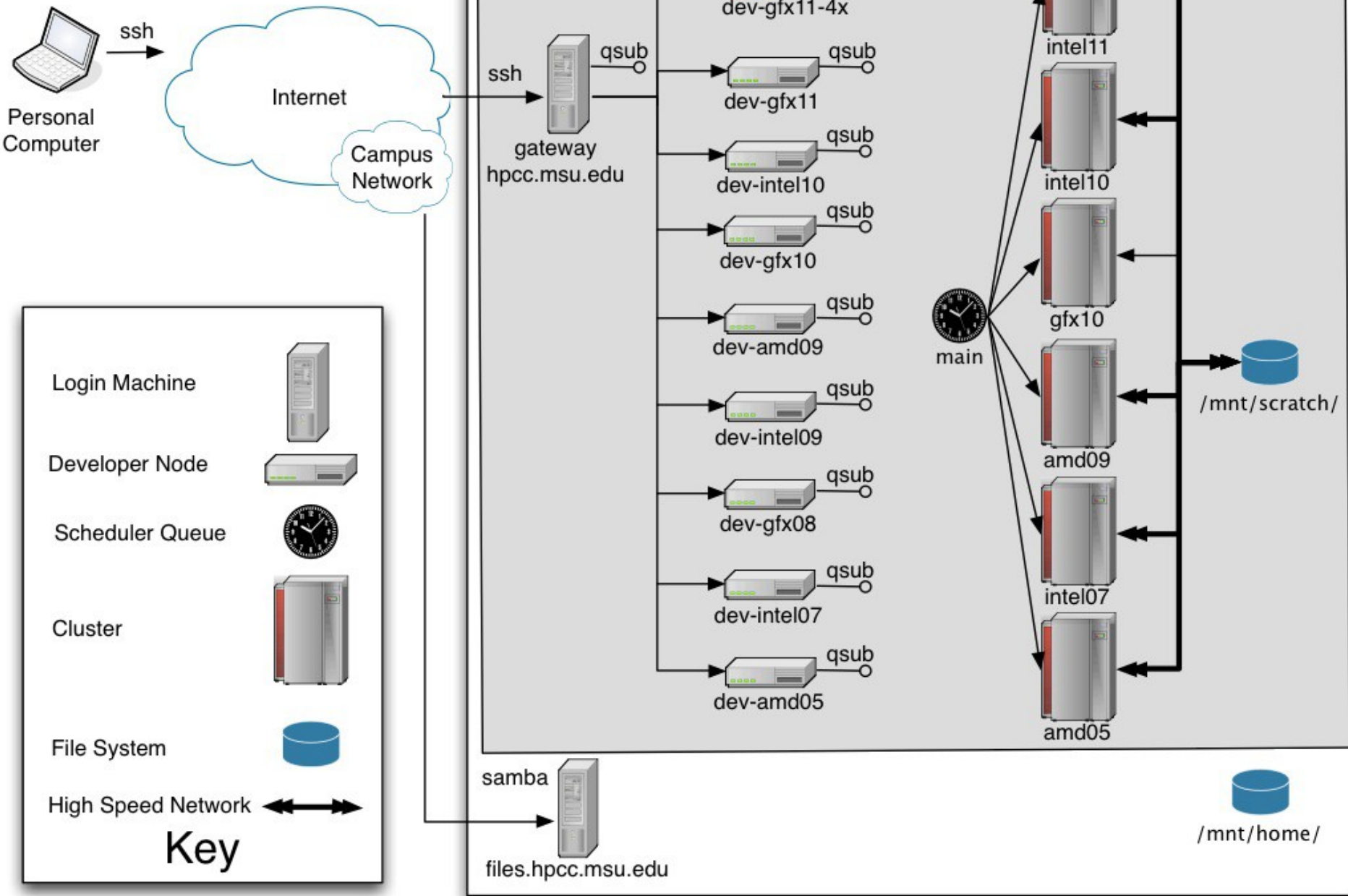
We recommend using dev-amd09 (or nodes with low usage).
For GPU development please use green nodes.
For MIC development please use underlined nodes

Development Nodes (usage)
-----
dev-intel07 (low)    dev-amd09 (low)
dev-intel10 (high)  dev-gfx10 (low)
dev-gfx13 (low)     dev-phi13 (low)

Filesystem Information
-----
${HOME} at 95% usage
(used ~48G of 50G)

**WARNING - REACHING QUOTA**
Request at: www.hpcc.msu.edu/quota

Cluster Load (utilization)
-----
short jobs (< 4 hrs) (85%)    general jobs (73%)
large memory jobs    (100%)   gpu jobs    (9%)
```



# Command Line Interface

- Command Line Interface (CLI)

- Shell

- Program to run Programs

More information, I recommend:

<http://www.softwarecarpentry.org/>

- Bash (Bourne Again Shell)

- Use it because:

- many tools only have command-line interfaces
  - allows you to combine tools in powerful new ways

# Module System

- To maximize the different types of software and system configurations that are available to the users, HPCC uses a Module system
- Key Commands
  - **module avail** – show available modules
  - **module list** – list currently loaded modules
  - **module load** modulename – load a module
  - **module unload** modulename – unload a module
  - **module spider keyword** – Search modules for a keyword

# Exercise – Module



- List loaded modules
  - `module list`
- Show available modules:
  - `module avail`
- Try an example (Shouldn't work):
  - `powertools`

# Exercise: getexample



- Load a module:
  - `module load powertools`
- Show powertools (should work now):
  - `powertools`
- Run the “getexample” powertool
  - `getexample`
- Download the helloworld example
  - `getexample helloworld`



# Steps in Using the HPCC

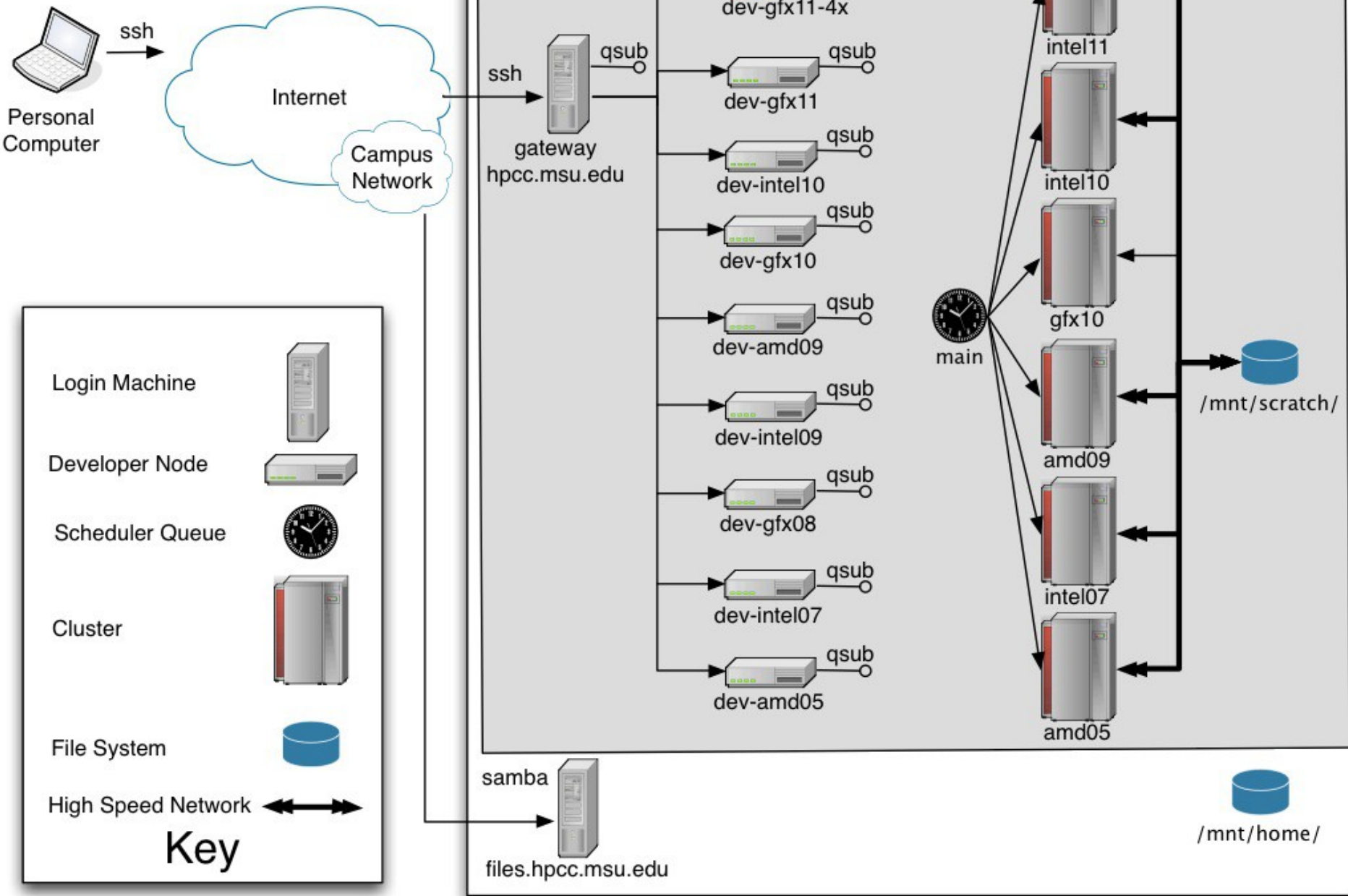
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# SCP/SFTP – Secure File transfer

- WinSCP for Windows
  - <https://wiki.hpcc.msu.edu/x/Y4nh>
- Command-line “scp” and “sftp” on Apple/Linux
- Many other scp and sftp clients out there as well
- Functions over SSHv2 protocol, very secure

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# Advantages of running Interactively

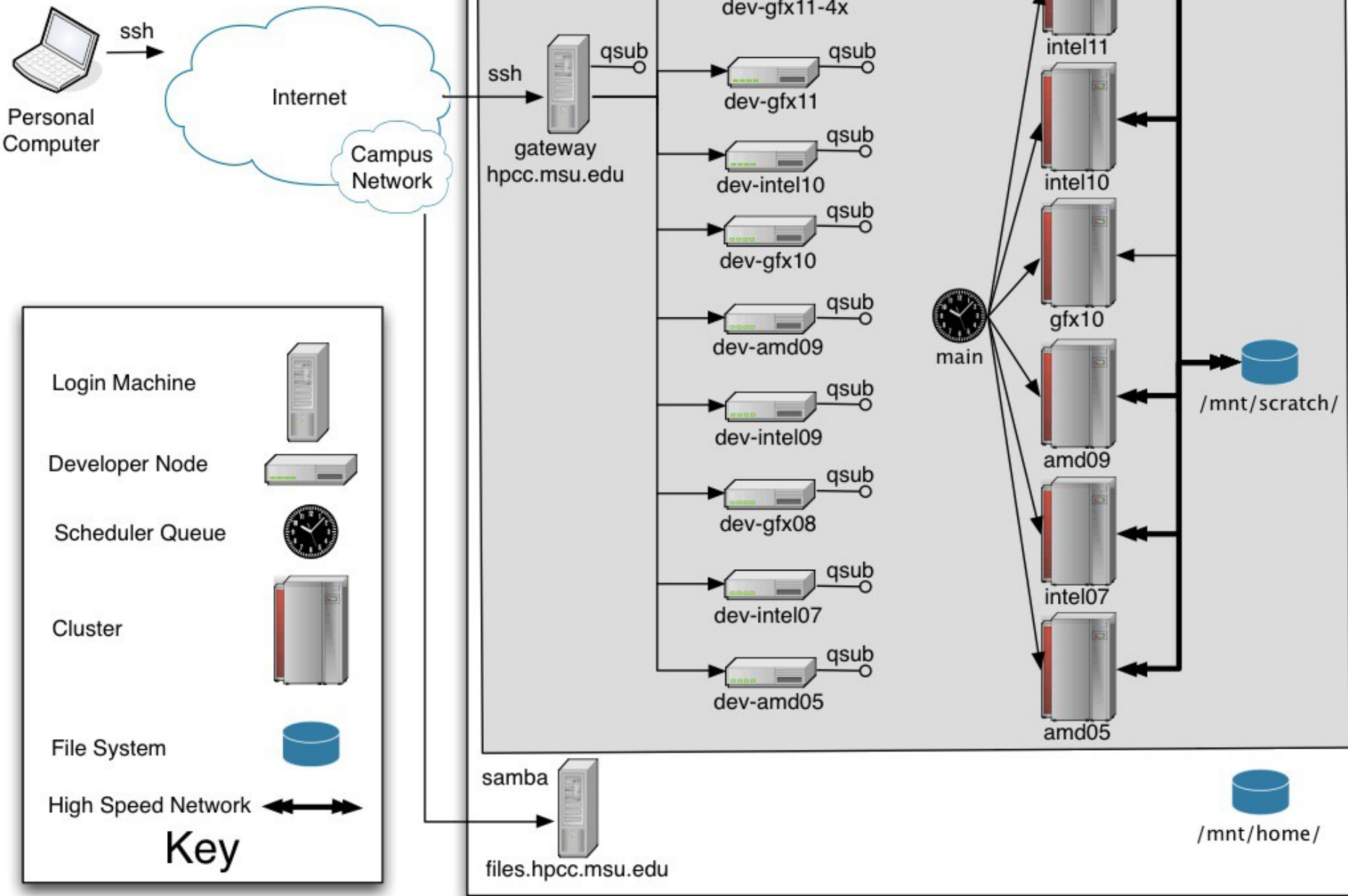
- You do not need to write a submission script
- You do not need to wait in the queue
- You can provide input to and get feedback from your programs as they are running

# Disadvantages of running Interactively

- All the resources on Interactive nodes are shared between all users.
- Any single process is limited to 2 hours of cpu time. If a process runs longer than 2 hours it will be killed.
- Programs that overutilize the resources on an integrative node (preventing other to use the system) can be killed without warning.

# Steps in Using the HPCC

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# Submission Script

1. List of required resources
2. All command line instructions needed to run the computation

# Typical Submission Script

Shell Comment

Define Shell

```
#!/bin/bash -login
#PBS -l walltime=10:00:00,mem=3Gb,nodes=10:ppn=1
#PBS -j oe

cd ${PBS_O_WORKDIR}

./myprogram -my input arguments

qstat -f ${PBS_JOBID}
```

Resource Requests

Shell Commands

Special Environment Variables

# Example: Submit a job



- Go to the top helloworld directory
  - `cd ~/helloworld`
- Look at the simple submission script
  - `nano hello.qsub`
- Nano is a simple program you can use to edit text files on the HPCC
- See bottom line of nano for commands the “^” character indicates the “control” key

# hello.qsub

```
#!/bin/bash -login
#PBS -l walltime=00:10:00
#PBS -l nodes=1:ppn=1,feature=gbe

cd ${PBS_O_WORKDIR}

./hello

qstat -f ${PBS_JOBID}
```

# Steps in Using the HPCC

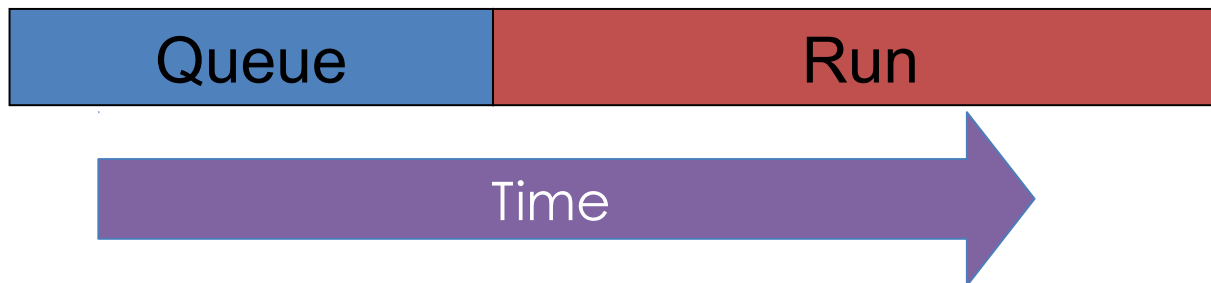
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# Common Queue Commands

- **qsub** <Submission script>
  - Submit a job to the queue
- **qdel** <JOB ID>
  - Delete a job from the queue
- **showq** -u <USERNAME>
  - Show the current job queue
- **checkjob** <JOB ID>
  - Check the status of the current job
- **showstart** -e all <JOB ID>
  - Show the estimated start time of the job.

# Submitting a job

- `qsub –arguments <Submission Script>`
  - Returns the job ID. Typically looks like the following:
    - 5945571.cmgr01
- Time to job completion



# Example: Submit a job, cont.



- Submit the file to the queue
  - **qsub hello.qsub**
- Record jobid number (#####) and wait at most 30 seconds
- Check the status of the queue
  - **showq -u \${USER}**



# Example: Monitor a job



- Get the status of the job:
  - `qstat -f #####`
- When will a job start:
  - `showstart -e all #####`

# Scheduling Priorities

- Jobs that use more resources get higher priority (because these are hard to schedule)
- Smaller jobs are backfilled to fit in the holes created by the bigger jobs
- Eligible jobs acquire more priority as they sit in the queue
- Jobs can be in three basic states:
  - Blocked, eligible or running

# Current Cluster Resources

Year	Name	Description	ppn	Memory	Nodes	Total Cores
2007	intel07	Quad-core 2.3GHz Intel Xeon E5345	8	8GB	126	1008
2010	gfx10	NVIDIA CUDA Node (no IB)	8	18GB	32	256
2010	intel10	Intel Xeon E5620 (2.40 GHz)	8	24GB	191	1528
2011	intel11	Intel Xeon 2.66 GHz E7-8837	32	512GB	2	64
			32	1TB	1	32
			64	2TB	2	128
2014	intel14	Intel Xeon E5-2670 v2 (2.6 GHz)	20	64GB	128	2560
			20	256GB	24	480
		2 NVIDIA K20 GPUs	20	128GB	40	800
		2 Xeon Phi 5110P	20	128GB	28	560
2014	Intel14-XL	Intel Xeon E7-8857 v2 (3 GHz)	48	1-3TB	5	240
			96	6 TB	1	96
Total					580	7752

# Job completion

- By default the job will automatically generate two files when it completes:
  - Standard Output:
    - Ex: jobname.o5945571
  - Standard Error:
    - Ex: jobname.e5945571
- You can combine these files if you add the join option in your submission script:
  - “#PBS -j oe”
- You can change the output file name
  - #PBS -o /mnt/home/netid/myoutputfile.txt

# Other Job Properties

- resources (-l)
    - Walltime, memory, nodes, processor, network, etc.
  - #PBS -l feature=gpgpu,gbe
  - #PBS -l nodes=2:ppn=8:gpu=2
  - #PBS -l mem=16gb
  - Email address (-M)
    - Ex: #PBS -M [colbrydi@msu.edu](mailto:colbrydi@msu.edu)
  - Email Options (-m)
    - Ex: #PBS -m abe
- Many others, see the wiki:  
<http://wiki.hpcc.msu.edu/>

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# What is the Bottleneck

- Not enough Memory
  - Solution: use a bigger node (6tb 96 cores)
- Slow File I/O
  - Solution: use scratch
  - Solution: use a ram disk
- Too many calculations
  - Solution: run your code in parallel



# Steps to parallel code

Note: Every application is different

1. Analyze your code

- Profilers (gprof, vtune, map, perfreport, tau)
- Debuggers / memory trackers (gdb, ddt, totalview)

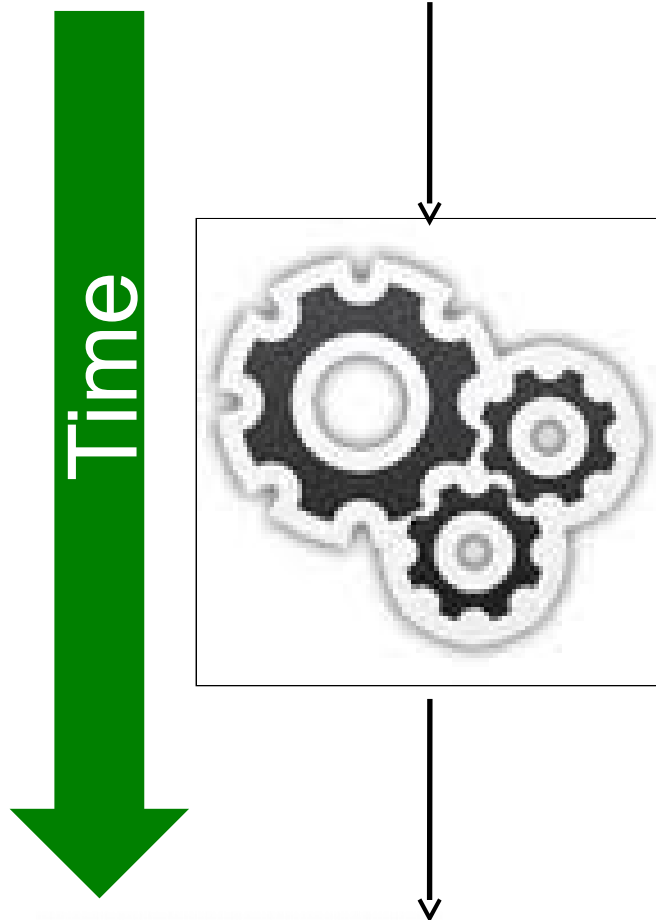
2. Optimize calculations

- Trade memory for time (i.e., never do the same calculation twice)

3. Find ways to parallelize

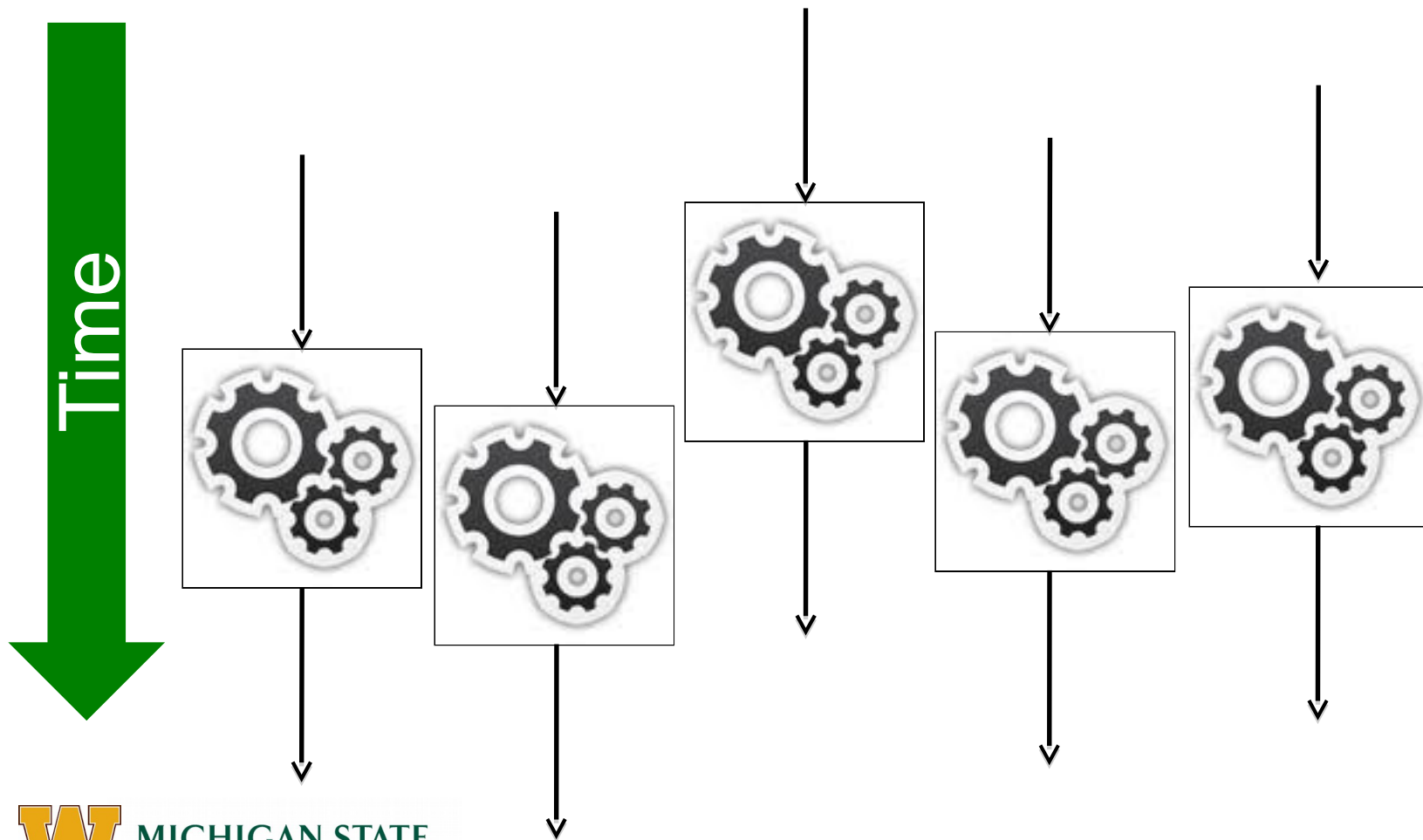
- Look for loops
- Find iterations independent from each other
- Determine how much information needs to be transferred

# Single Thread Jobs

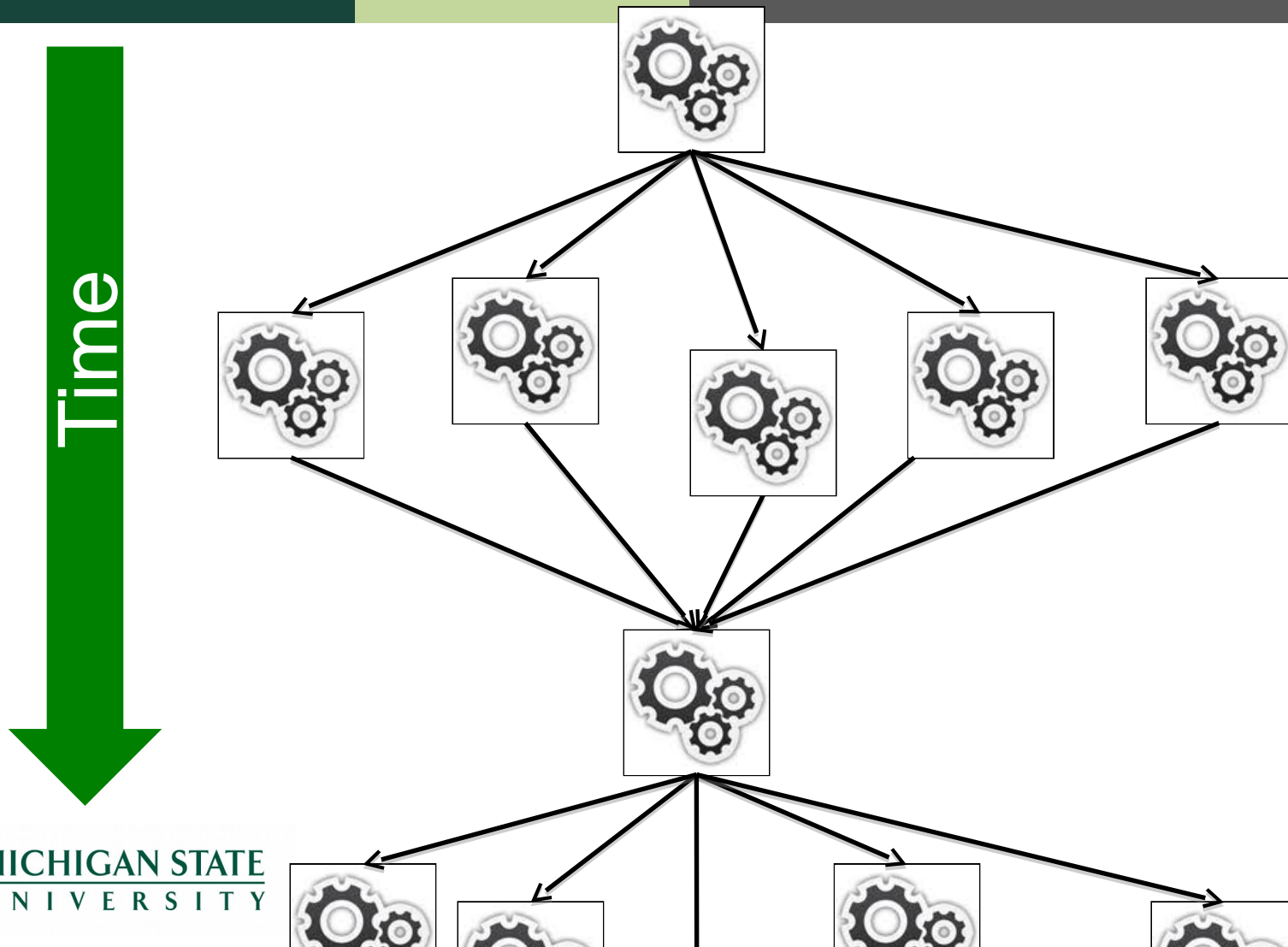


One CPU can only run one thing at a time. (sort of)

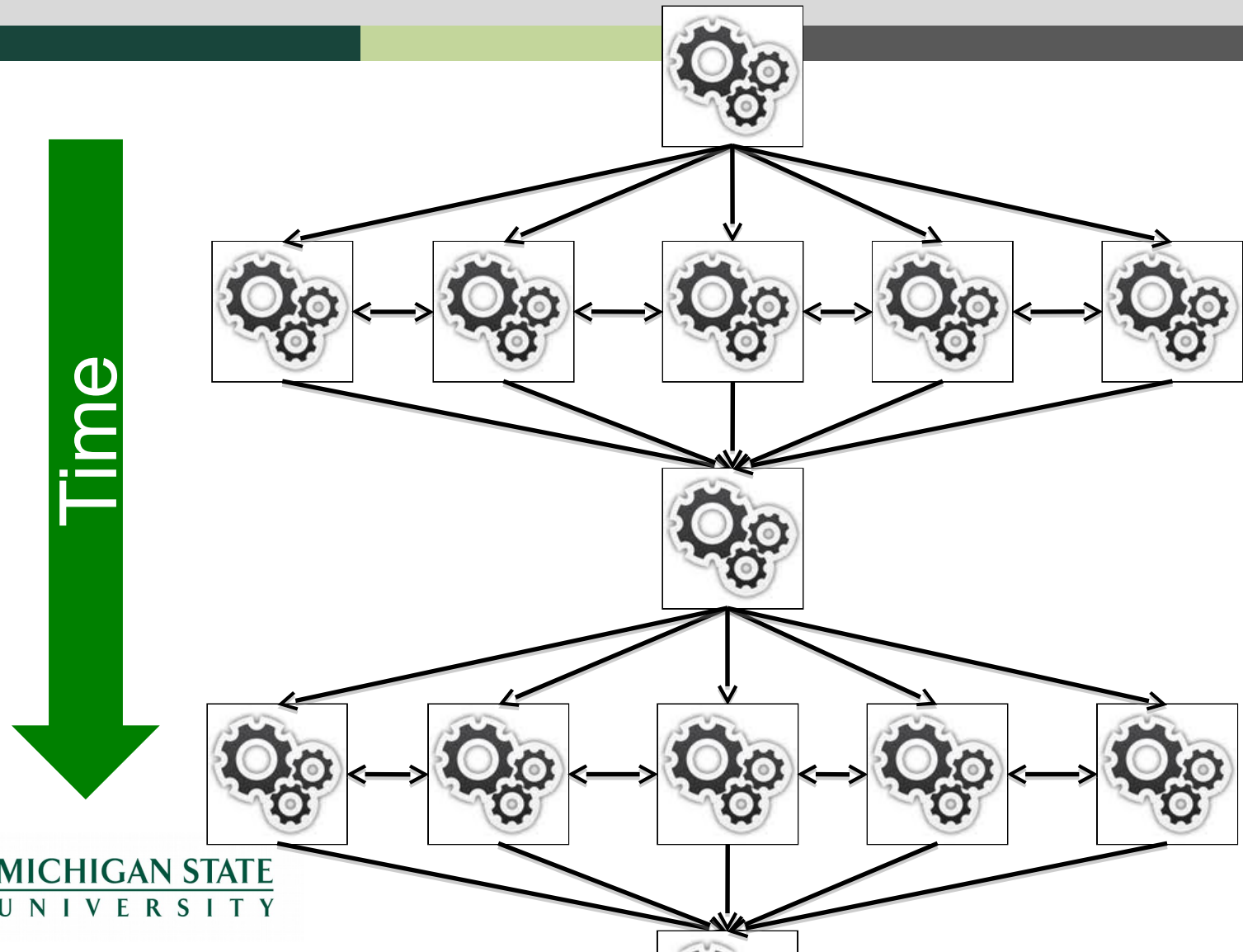
# Pleasantly Parallel



# Loosely Coupled



# Tightly Coupled



# Communication

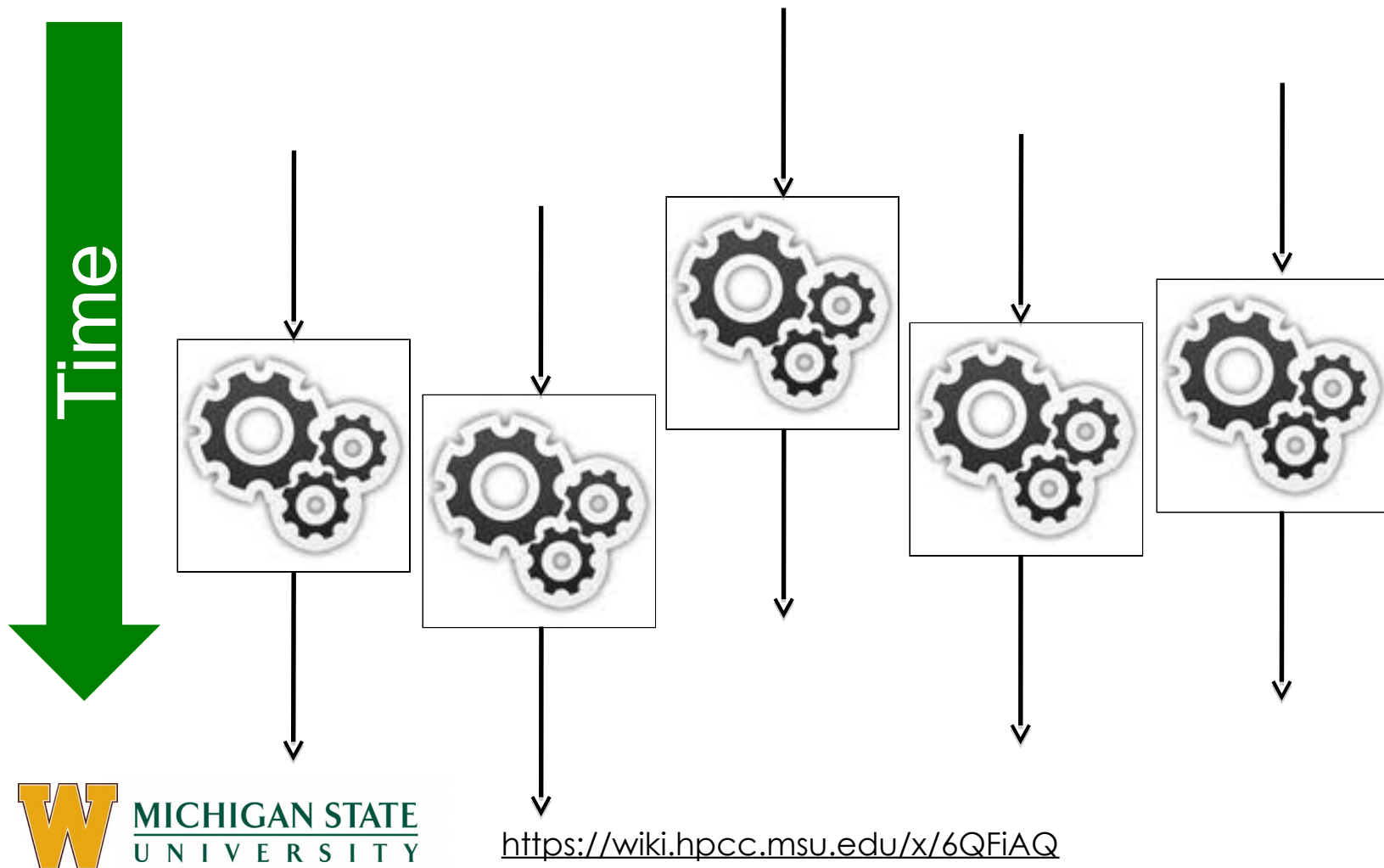
- Shared Memory
- Shared Network
- Distributed Network
- Dedicated Accelerator
- Hybrid Systems





# Pleasantly Parallel

# Pleasantly Parallel

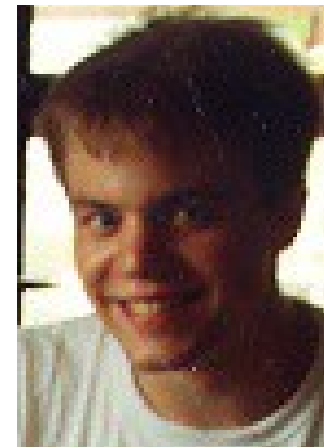
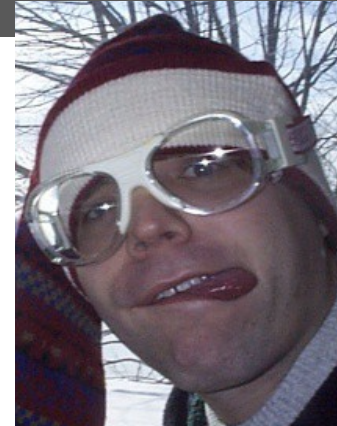




# How fast can we go?

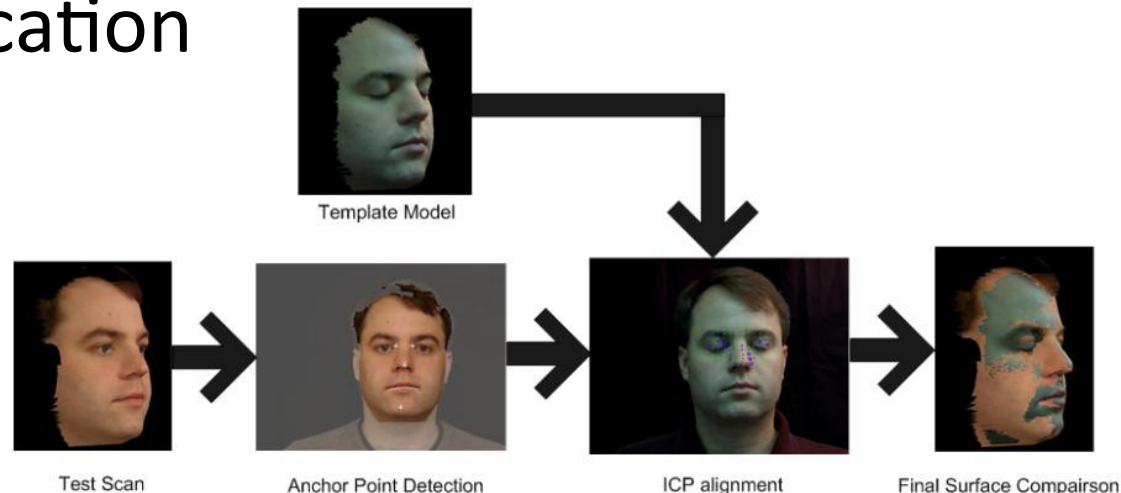
- T - How long does each operation take?
- N - How many operations do you need to run?
- CPUs – Number of Cores job will run on.
- Single CPU time estimate:
  - $T \times N$
- Best possible Pleasantly parallel time:
  - $(T \times N) * \text{overhead} / \text{CPUs}$

# Who are you? -- Biometrics

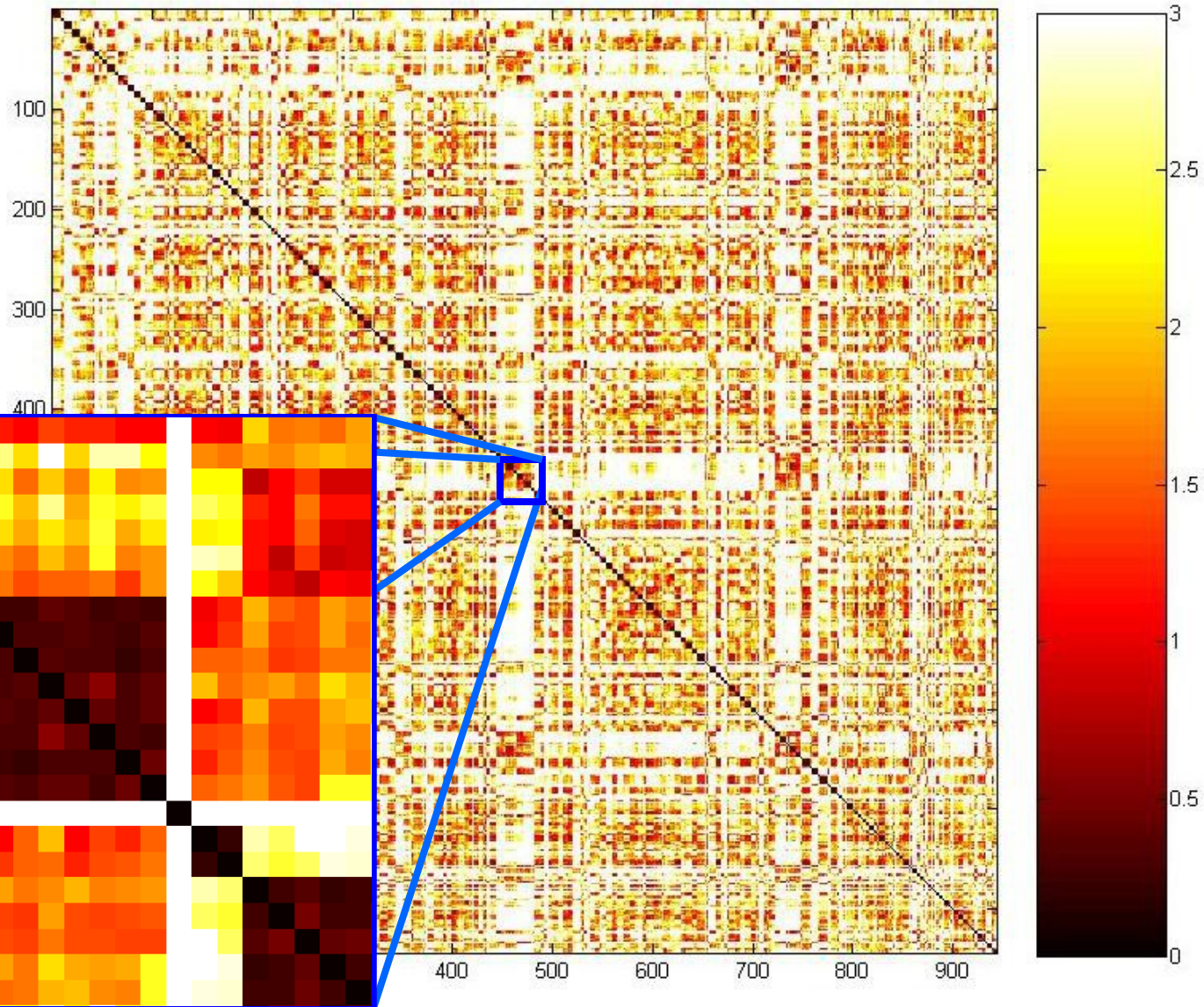


# Pairwise-All Problem

- Database of faces
- Compare everything to everything else
- Calculate a Matching score to use for identification



# 943 x 943 Similarity Matrix

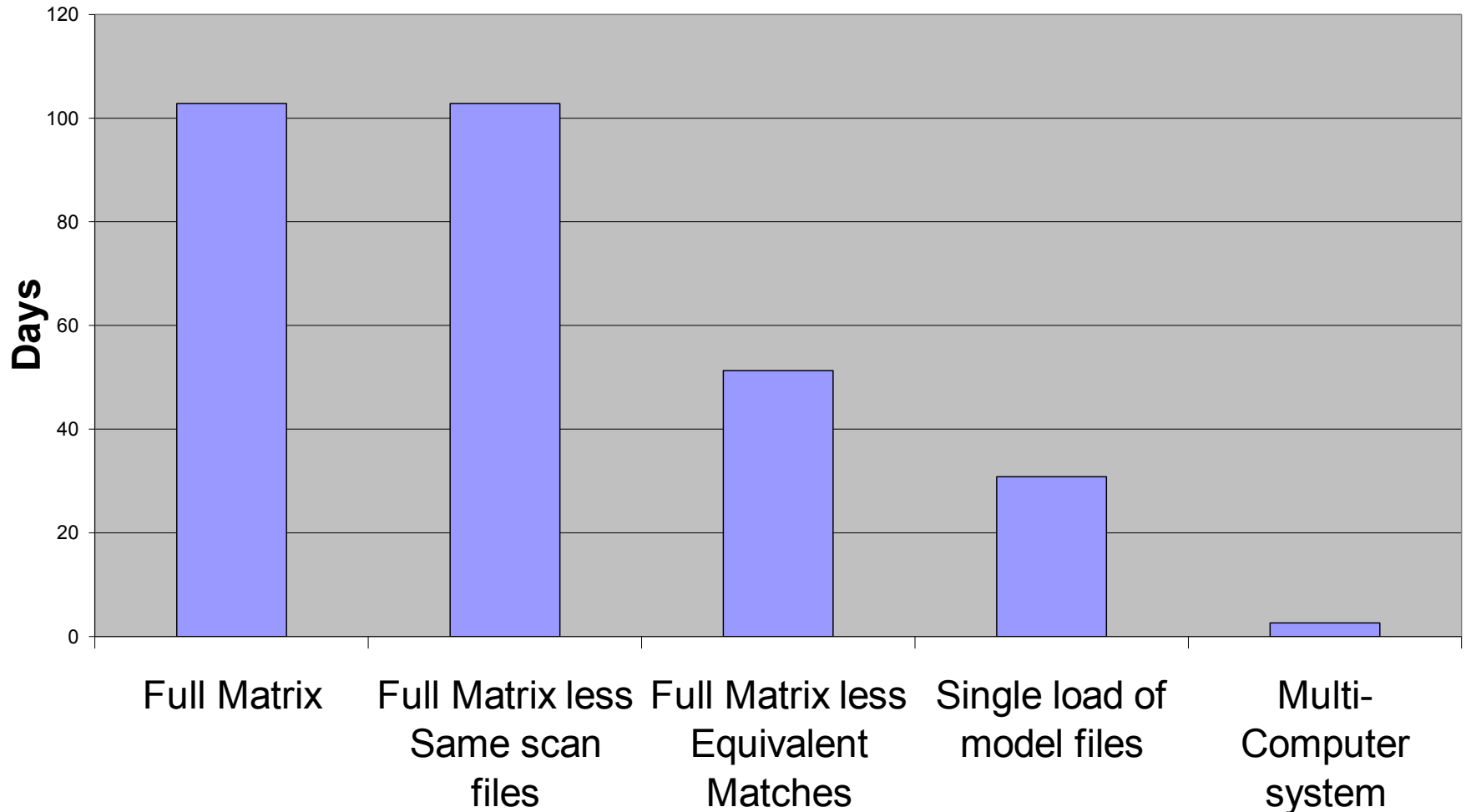




# Estimated Calculation Times

- Preprocessing
  - $943 * 12$  (seconds)  $\approx$  189 Minutes
- Matching
  - $943 * 943 * 5$  (seconds)  $\approx$  103 Days
- Scans matched to themselves always result in 0 mm
  - $(943 * 943 - 943) * 5$  (seconds)  $\approx$  103 Days
- The Proposed Alignment Algorithm is symmetric.
  - $(943 * 943 - 943)/2 * 5$  (seconds)  $\approx$  51.5 Days
- We also load models once per row instead of every time
  - $(943*943-943)/2 * 3$  (seconds) +  $943 * 2$  (seconds)  $\approx$  31 Days

# Calculation Time for Full Similarity Matrix



# How do we go even bigger?

- 5000 scans.
  - 1.5 years on a single processor computer
  - 13 days on our ad-hoc cluster.
  - 1.5 days a commodity cluster at MSU

# Steps to Pleasantly Parallel

- Figure out command line
- Estimate single job time:
  - Should be  $> 5$  minutes
  - Should be  $< 1$  week
  - Best if  $< 4$  hours
- Make a submissions script
- Submit Job



# Pleasantly Parallel Example

- Folder full of input files:

1.in	5.in	9.in	13.in	17.in
2.in	6.in	10.in	14.in	18.in
3.in	7.in	11.in	15.in	19.in
4.in	8.in	12.in	16.in	

- Want folder full of output files:

1.out	5.out	9.out	13.out	17.out
2.out	6.out	10.out	14.out	18.out
3.out	7.out	11.out	15.out	19.out
4.out	8.out	12.out	16.out	

- Command Syntax:

```
./myprogram inputfile > outputfile
```

<https://wiki.hpcc.msu.edu/x/6QFiAQ>

# PBS Job Arrays

- One submission script copied many times
- Uses the PBS -t option
  - Ranges: 1-10
  - Lists: 2,4,100,3
  - Combination: 1-10,20,50,100
- Distinguish between jobs by using the PBS\_ARRAYID environment variable

# Simple Job Array



```
#!/bin/bash -login
#PBS -l walltime=00:05:00,mem=2gb
#PBS -l nodes=1:ppn=1,feature=gbe
#PBS -t 1-19

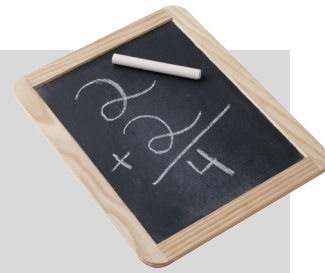
cd ${PBS_O_WORKDIR}

mkdir ${PBS_ARRAYID}
Cd ${PBS_ARRAYID}

../myprogram ../${PBS_ARRAYID}.in > ${PBS_ARRAYID}.out

qstat -f ${PBS_JOBID}
```

# Example: Job Arrays



- Get the blender\_farm example:
  - `getexample`
  - `getexample blender_farm`
  - `cd ./blender_farm`
- Look at the qsub file, using “less” command
  - `less blender_farm.qsub`
- Submit the job
  - `qsub blender_farm.qsub`

# HPCC Job array limitations

- Can not have more than 520 cores running at once
- Can not submit more than 1000 jobs at once
- Each job can not run longer than one week
- Lots of ways to work around these limitations

# Job array numbers

- All numbers in a job array have the same base number
  - 7478210
- Each PBS\_ARRAYID is show in square brackets
  - 7478210[1]
  - 7478210[2]
- Delete all jobs using one command
  - `qdel 7478210[]`

# Files as Semaphores (FAS)

- Use a list of input files as your task list
- Use a list of output files (or flag files) as your in-progress/complete list
- Rely on the file system to ensure that no two jobs are selected at the same time (not a great assumption but it works)

# Simple FAS

```
#!/bin/bash -login
#PBS -l walltime=00:05:00
#PBS -l nodes=1:ppn=1,feature=gbe
#PBS -t 1-100
cd ${PBS_O_WORKID}
sleep $(( ${RANDOM} % 100 ))

for file in *.in; do
    output="./${file%.*}.out"
    if [ ! -f ${output} ]; then
        touch ${output}
        ./myprogram ${file} > ${output}
        qsub -t 0 -N ${PBS_JOBNAME} ${0}
    fi
done
exit 0
```





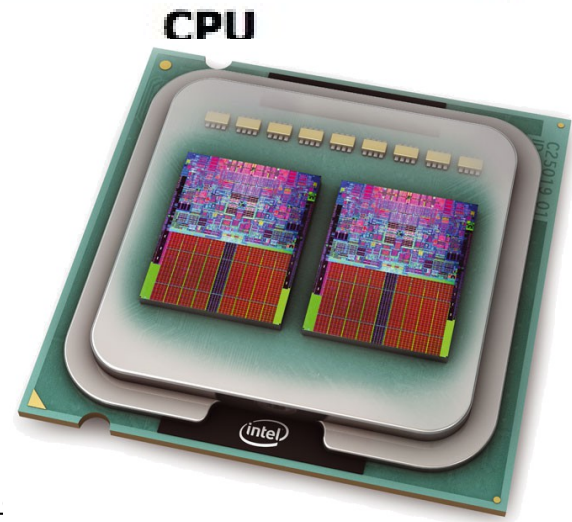
# Shared Memory Parallelization

# Shared Memory

- Different threads (cores, processes) communicate through pointers to the same memory location
- Problems can occur if different threads write the same memory at the same time
- Flags (also called locks and/or semaphores) are used to allow only one thread to access memory at the same time

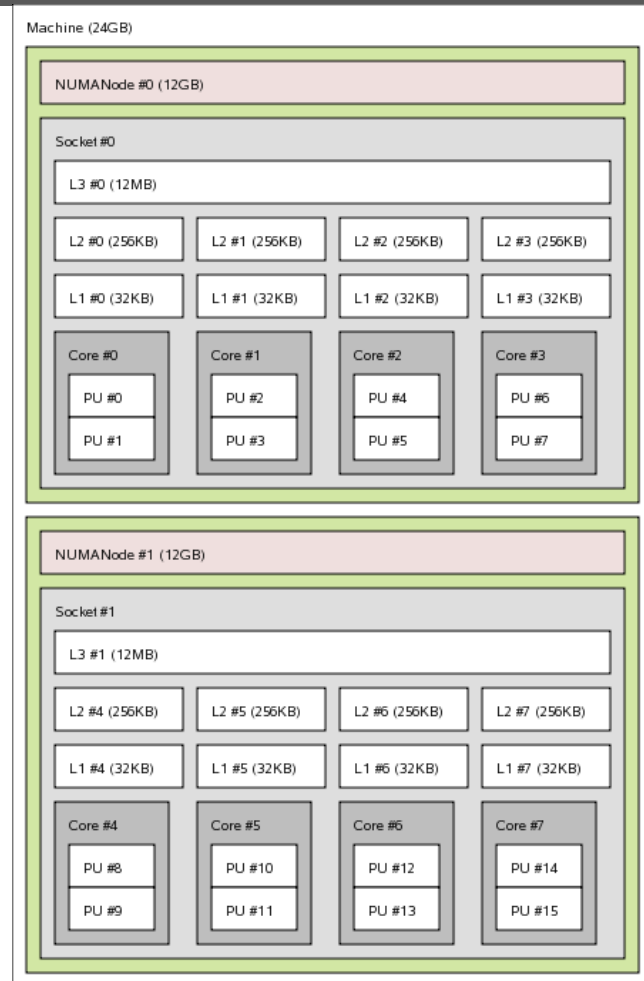
# Shared Memory Communication

- Cores on a processor share the same memory
- OpenMP
- Fat nodes
  - 96 cores
  - 6TB of memory



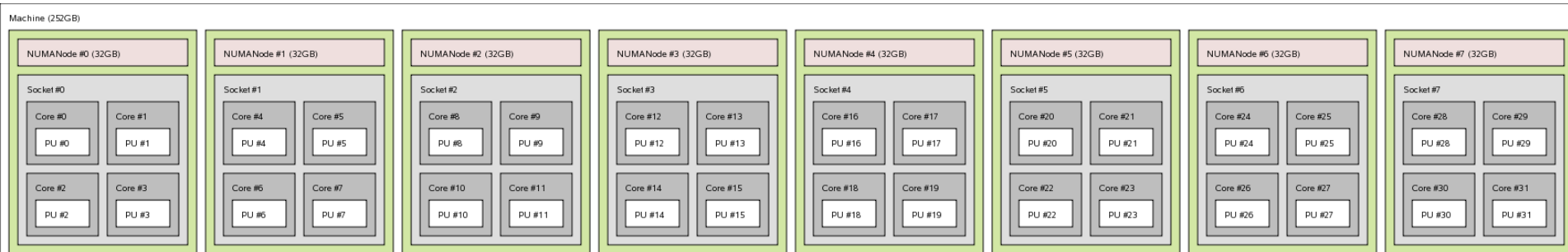
# Intel10

- 8 cores
- 24 GB memory



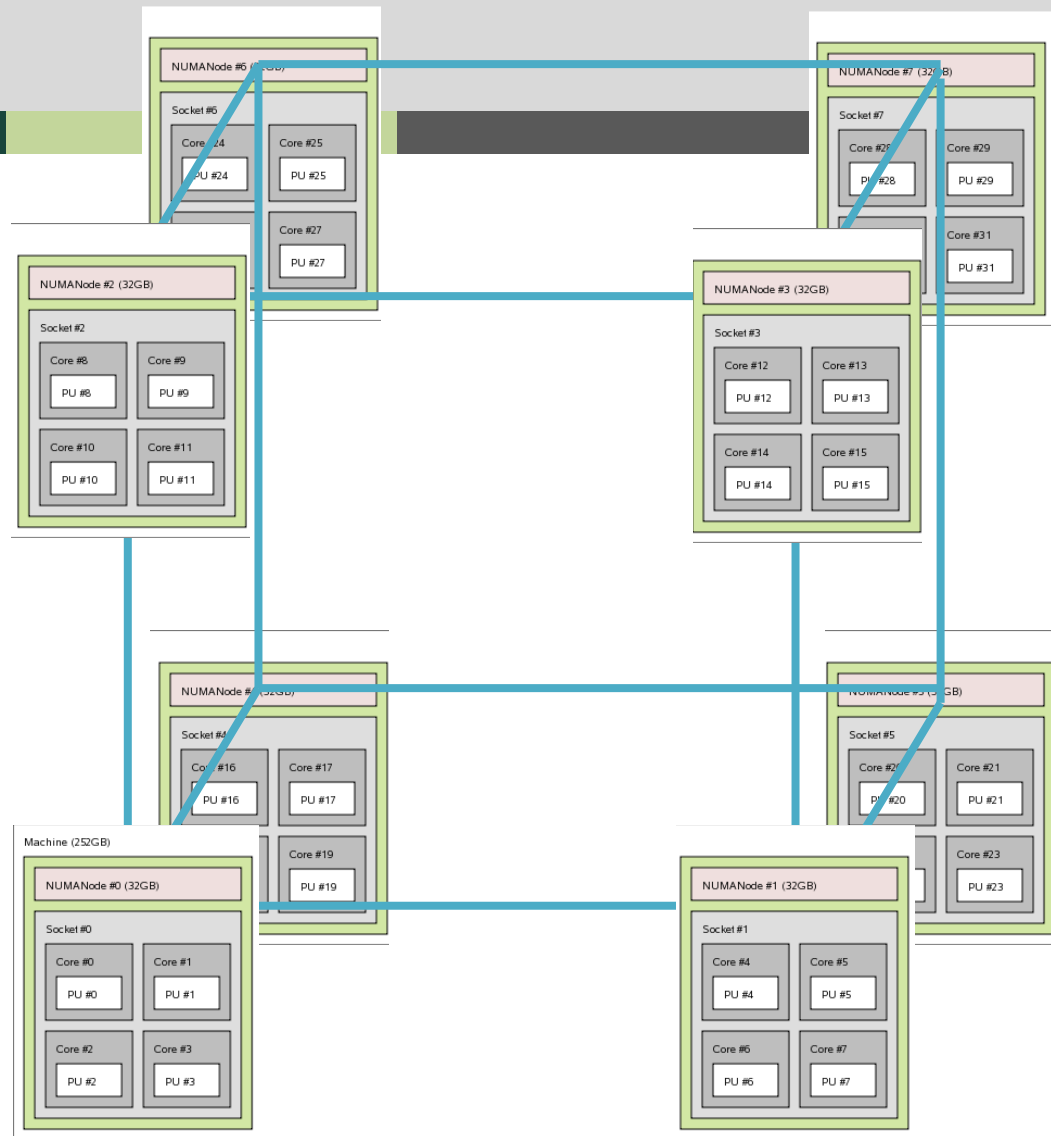
# Large Memory Example

- 32 cores
- 256 GB memory



- We also have nodes with up to 64 cores and 2TB of memory

# NUMA



# Shared memory submission scripts

- Typically one node with multiple processors per node (ppn)
  - #PBS -l nodes=1:ppn=8
- Different programs use different methods to tell them how many processors to use
  - Command line arguments
  - Environment variables

# Example: shared memory Script

- Bowtie uses shared memory parallelization
- Get the bowtie example
  - `getexample bowtie`
- Change to the bowtie directory
  - `cd ./bowtie`
- Look at the submission script
  - `less ./bowtie.qsub`
- Run the job
  - `qsub bowtie.qsub`





# OpenMP

- Common Shared Memory parallelization
- Single program runs in many threads
- Really easy to pick loops that are parallel and split them into multi threads
- Minor modifications to code that can be written not to affect single

# OpenMP is easy

```
#include <omp.h>
```

```
...
```

```
#pragma omp parallel for
```

```
for (i=0;i<100;++i) {
```

```
    A(i) = A(i) + B
```

```
}
```

```
...
```

# Compile OpenMP Jobs

- Use compiler option `fopenmp`.
  - `fopenmp`
- Example:

```
gcc -fopenmp mycode.cc -o mycode
```

# simpleOMP.qsub example

```
#!/bin/bash -login
#PBS -l walltime=00:01:00
#PBS -l nodes=1:ppn=5,feature=gbe

cd ${PBS_O_WORKDIR}
export OMP_NUM_THREADS=${PBS_NUM_PPN}

./simpleOMP

qstat -f ${PBS_JOBID}
```

# Try another getexample

getexample helloOpenMP

getexample OpenMP\_profiling



# Shared Network Parallelization

# MPI program (1 of 4)

```
/* Needed for printf'ing */
#include <stdio.h>
#include <stdlib.h>

/* Get the MPI header file */
#include <mpi.h>

/* Max number of nodes to test */
#define max_nodes 264

/* Largest hostname string hostnames */
#define str_length 50
```

# MPI program (2 of 4)

```
int main(int argc, char **argv)
{
    /* Declare variables */
    int    proc, rank, size, namelen;
    int    ids[max_nodes];
    char    hostname[str_length][max_nodes];
    char    p_name[str_length];

    MPI_Status status;
    MPI_Init(&argc, &argv);
    MPI_Comm_rank(MPI_COMM_WORLD, &rank);
    MPI_Comm_size(MPI_COMM_WORLD, &size);
    MPI_Get_processor_name(p_name, &namelen);
```



# MPI program (3 of 4)

```
if (rank==0) {  
    printf("Hello From: %s I am the receiving processor  
%d of %d\n", p_name, rank+1, size);  
    for (proc=1; proc<size; proc++) {  
        MPI_Recv(&hostname[0][proc], \\  
                str_length, MPI_INT, proc, \\  
                1, MPI_COMM_WORLD, &status);  
        MPI_Recv(&ids[proc], \\  
                str_length, MPI_INT, proc, \\  
                2, MPI_COMM_WORLD, &status);  
        printf("Hello From: %-20s I am processor %d of  
%d\n", &hostname[0][proc], ids[proc]+1, size);  
    }  
}
```

# MPI program (4 of 4)

```
} else { // NOT Rank 0
    srand(rank);
    int t = rand()%10+1;
    sleep(t);
    MPI_Send(&p_name, str_length, \
             MPI_INT, 0, 1, MPI_COMM_WORLD);
    MPI_Send(&rank, str_length, \
             MPI_INT, 0, 2, MPI_COMM_WORLD);
}
MPI_Finalize();

return(0);
}
```

# Trying out an example



1. Log on to one of the developer nodes
2. Load the powertools module:
  - `module load powertools`
3. Run the getexample program. This will create a folder called helloMPI:
  - `getexample helloMPI`
4. Change to the helloMPI directory and read the readme files
5. Or just type the following on the command line:
  - `./README`

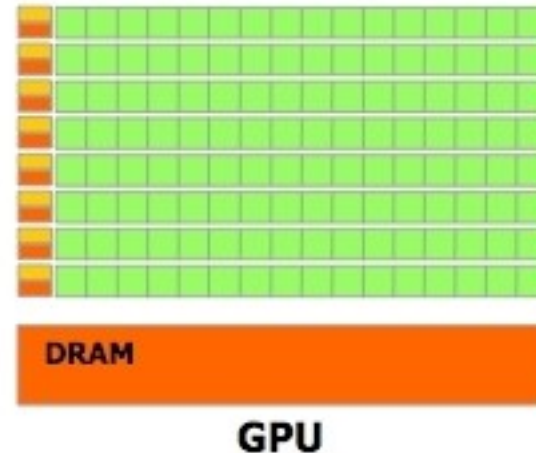


# Accelerator Cards

# GPU



- Cards used to render graphics on a computer
- Hundreds of cores
- Not very smart cores
- But, if you can make your research look like graphics rendering you may be able to run really fast!



# Running on the GPU

- Program Starts on the CPU
  - Copy data to GPU (slow-ish)
  - Run kernel threads on GPU (very fast)
  - Copy results back to CPU (slow-ish)
- There are a lot of clever ways to fully utilize both the GPU and CPU.

# Pros and Cons

- Benefits

- Lots of processing cores.
- Works with the CPU as a co-processor
- Very fast local memory bandwidth
- Large online community of developers

## Drawbacks

- Can be difficult to program.
- Memory Transfers between GPU and CPU are costly (time).
- Cores typically run the same code.
- Errors are not detected (on older cards)
- Double precision calculations are slow (On older cards)

# CUDA program (1 of 5)

```
#include "cuda.h"
#include <iostream>

using namespace std;

void printGrid(float an_array[16][16]) {
    for (int i = 0; i < 16; i++){
        for (int j = 0; j < 16; j++) {
            cout << an_array[i][j];
        }
        cout << endl;
    }
}
```



# CUDA program (2 of 5)

```
__global__ void theKernel(float * our_array)
{
    // This is array flattening,
    //(Array Width * Y Index + X Index)
    our_array[(gridDim.x * blockDim.x) * \
              (blockIdx.y * blockDim.y + threadIdx.y) + \
              (blockIdx.x * blockDim.x + threadIdx.x)] = \
              = 5;
}
```

# CUDA program (3 of 5)

```
int main()
{
    float our_array[16][16];

    for (int i = 0; i < 16; i++) {
        for (int j = 0; j < 16; j++) {
            our_array[i][j] = 0;
        }
    }
}
```

# CUDA program (4 of 5)

**//STEP 1: ALLOCATE**

```
float * our_array_d;  
int size = sizeof(float)*256;  
cudaMalloc((void **) &our_array_d, size);
```

**//STEP 2: TRANSFER**

```
cudaMemcpy(our_array_d, our_array, size, \\  
           cudaMemcpyHostToDevice);
```

# CUDA program (5 of 5)

```
//STEP 3: SET UP
```

```
dim3 blockSize(8,8,1);
```

```
dim3 gridSize(2,2,1);
```

```
//STEP 4: RUN
```

```
theKernel<<<gridSize, blockSize>>>(our_array_d);
```

```
//STEP 5: TRANSFER
```

```
printGrid(our_array);
```

```
cudaMemcpy(our_array, our_array_d, size, \\  
           cudaMemcpyDeviceToHost);
```

```
cout << "-----" << endl;
```

```
printGrid(our_array);
```

```
}
```

# Compile CUDA Jobs

- Just like MPI, to compile an cuda program you need to use the cuda compiler wrappers:
  - `nvcc simple.cu -o simple_cuda`

# Try a cuda getexample

getexample cuda

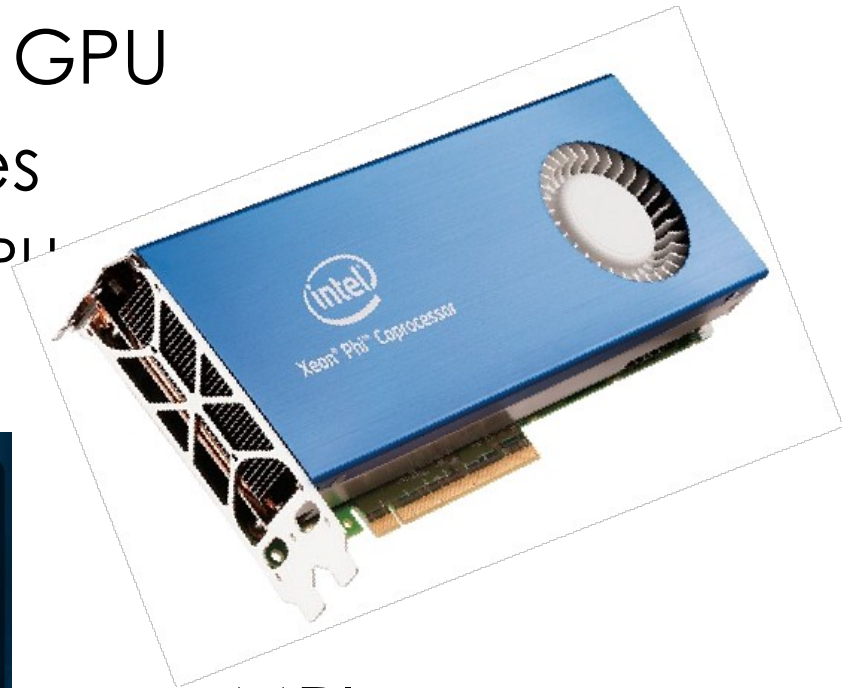
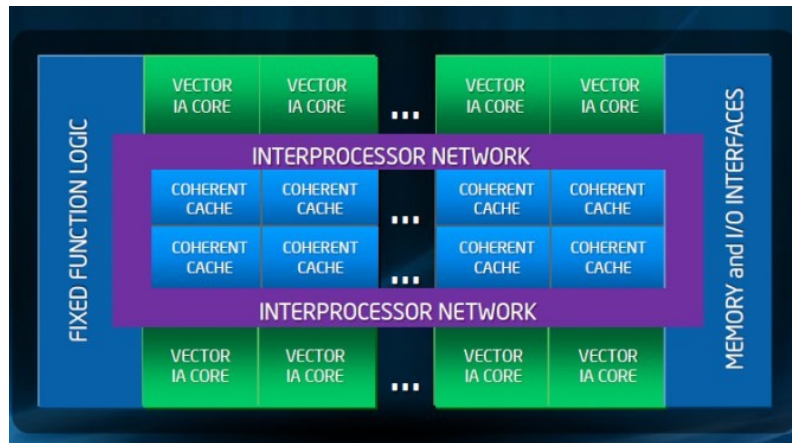
getexample cuda\_clock

getexample cuda\_hybrid

getexample NAMD\_CUDA\_example

# Intel Xeon Phi

- Cross between CPU and GPU
- About 61 Pentium III cores
  - Less cores/slower than GPU
  - Easier to use than GP



- MPI
- OpenMP

# Try a Phi Card example

```
getexample MIC_examples  
getexample MKL_mic
```





# Standard Libraries

# Standard Libraries

- When possible take advantage of parallel libraries
  - Easy to use
  - Saves time
  - Takes care of the parallel coding for you
  - Tested and vetted by the community

# Math Kernel Library

- `getexample MKL_benchmark`
- `getexample MKL_c_eigenvalues`
- `getexample MKL_Example`
- `getexample MKL_mic`
- `getexample MKL_parallel`

# Other Libraries

- fftw
- BLAS
- ACML
- BLAS (Basic Linear Algebra)
- Lapack
- trilinos
- petsc
- Magma
- Cudatools
- Mumps

# Which approach is the best?

- Depends on what you are doing?
- Depends on how much communication you need.
- Depends on what hardware you have.
- Depends on how much time you have.

# My Recommendations


- Pleasantly Parallel
- Standard Libraries
- OpenMP
- OpenACC
- OpenMP on Phi
- MPI
- MPI on Phi?
- GPGPU

EASY

Hard

# Agenda


- What is iCER / HPCC
- Common classes problems
- Overview of Hardware
- Getting started, Seven Steps to High Performance
- Running in parallel
- Tips and tricks



# Tips and Tricks

## Going beyond system Limits



- 
- Going beyond system Limits
    - More than 520 jobs
    - Jobs longer than 1 week
    - Taking advantage of more nodes

# Finding more Nodes

- Owners are guaranteed access to their buy-in node within 4 hours. If they are not using the node, others can use it:
  - #PBS -l walltime=04:00:00
- Some of the nodes do not have Infiniband. If you are not using scratch and do not need between node communication you can access these nodes:
  - #PBS feature=gbe

# Checkpoint / Restart

- What?
  - Save the state of your program
  - Restart your program from the saved point
- How?
  - Design into your program
  - BLCR (Berkley Lab Checkpoint Restart)
  - Condor Checkpoint Restart
  - Others
- Why?
  - Robust jobs
    - As HPC scales ... hardware failures are guaranteed
  - Longer jobs
  - Better science

# Questions?

- Software Carpentry (the basics):
  - <http://www.softwarecarpentry.org/>
- Announcements:
  - <https://wiki.hpcc.msu.edu/>
- Documentation and User Manual:
  - <https://wiki.hpcc.msu.edu/x/A4AN>
- Training Videos:
  - <https://www.youtube.com/user/icermisu>
- Western Michigan University contact:
  - [donald.weber@wmich.edu](mailto:donald.weber@wmich.edu)
- Online Chat:
  - <http://www.hipchat.com/gYlrQfgah>
- Contact us:



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