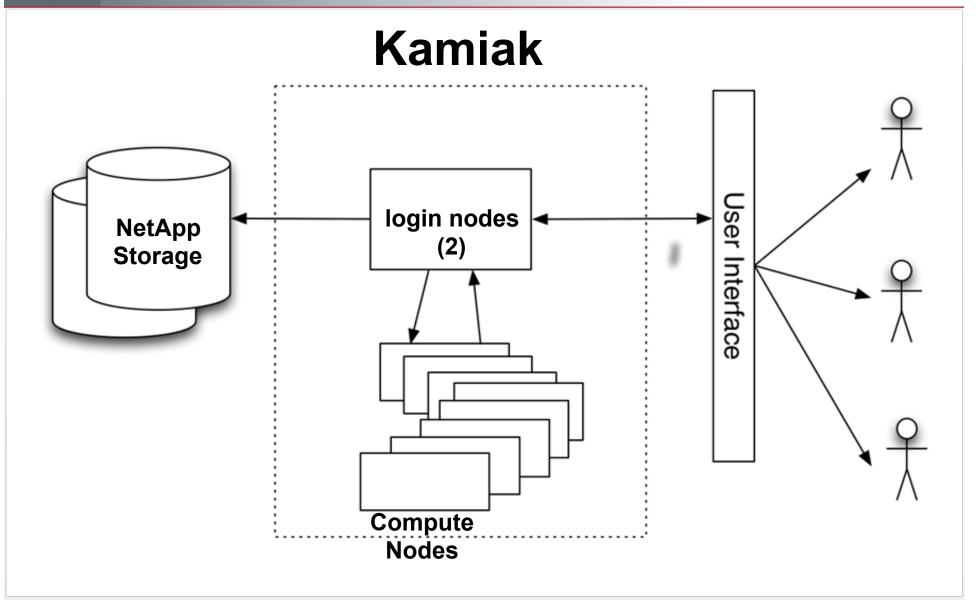


Welcome to Kamiak

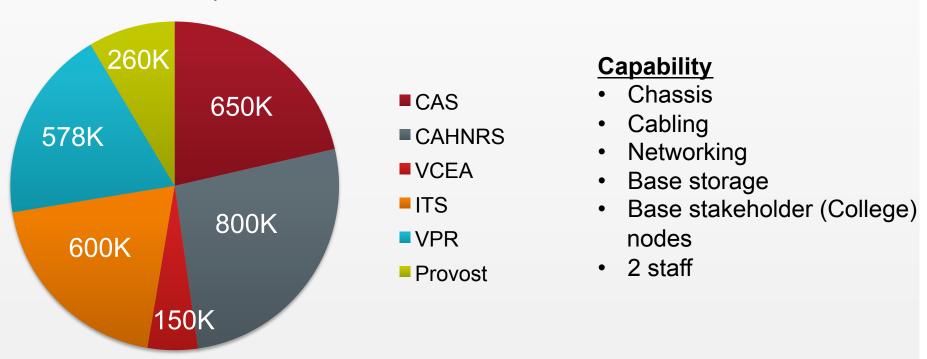
1/20/2017 Training Session
Aurora Clark, CIRC Director
Jeff White, Kamiak Linux Admin
Shenting Cui, Computational Scientist





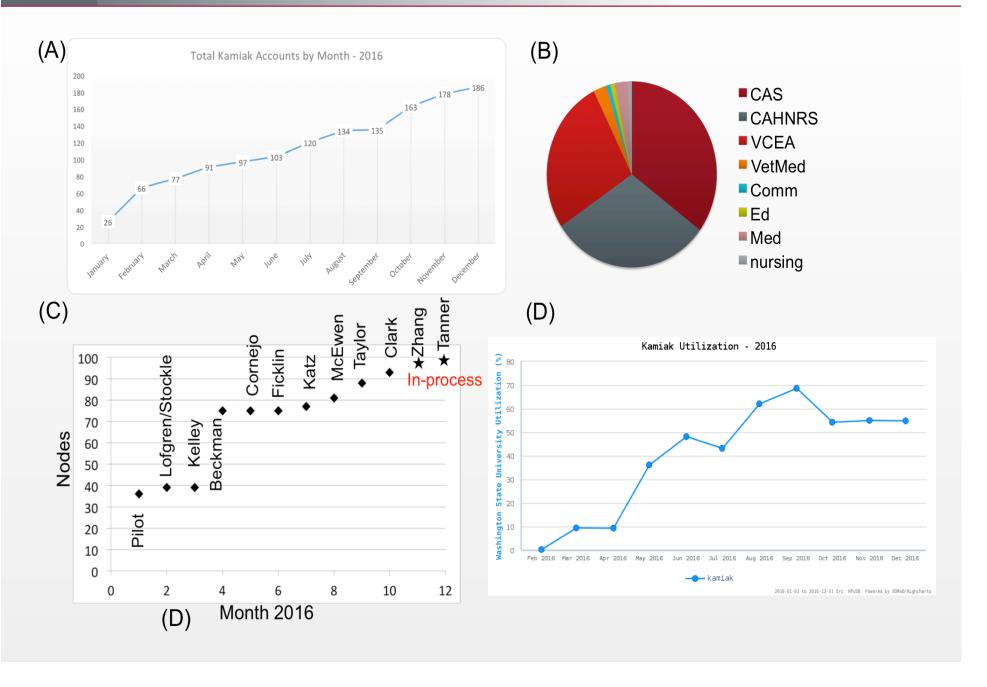
Where did this infrastructure come from?

- \$3 Mil
 - Founding investing units (CAHNRS, CAS, VCEA)
 - Office of Research
 - Information Technology Services
 - Provost/President

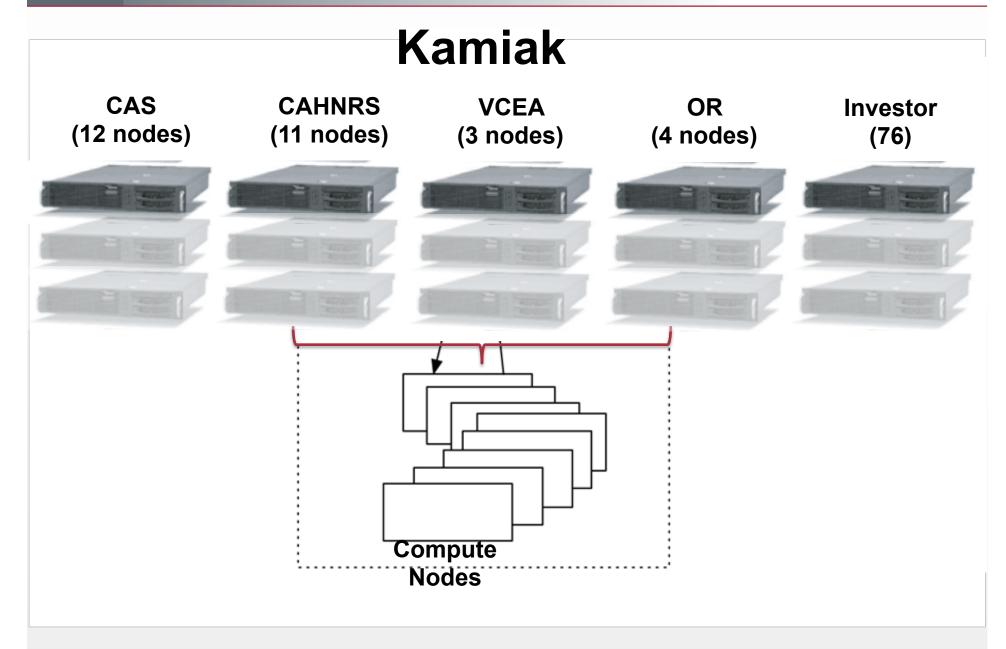


 Sustainable ongoing support is being provided as Kamiak grows through faculty investment



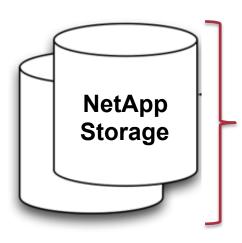








Kamiak



-every user /home directory has 10Gb (*quota -s -f /home*)

-extra storage goes into /data

Extra storage:

1) CIRC/ITS Service Center for Storage

144 Tb total, with 63 Tb purchased by faculty investors (df -h /data/investor name)

2) 5-year storage purchased by Colleges:

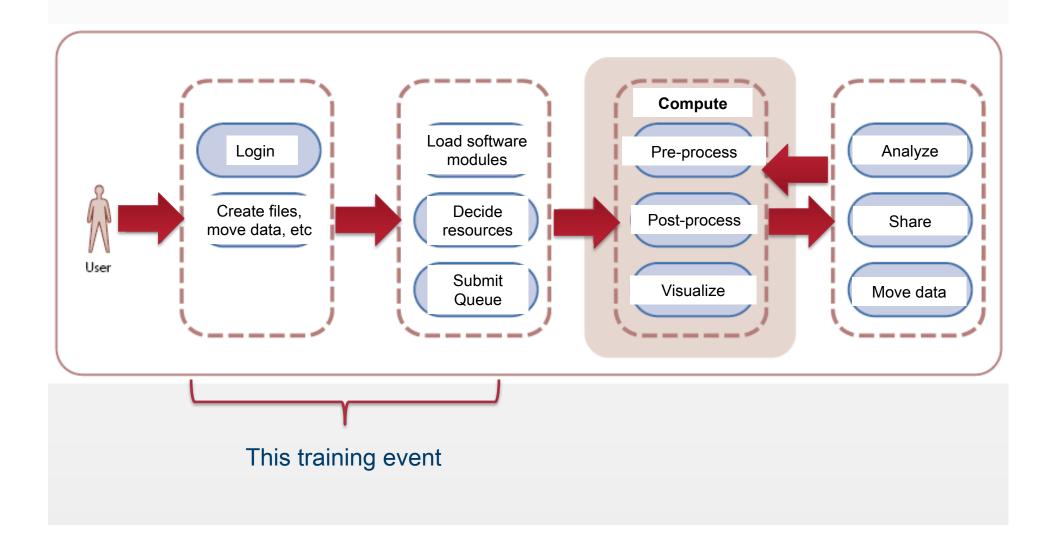
CAHNRS: ~200 Tb

CAS: ~100 Tb VCEA: ~25 Tb OR: ~13 Tb



Introduction

Example Workflow:



What you will learn today

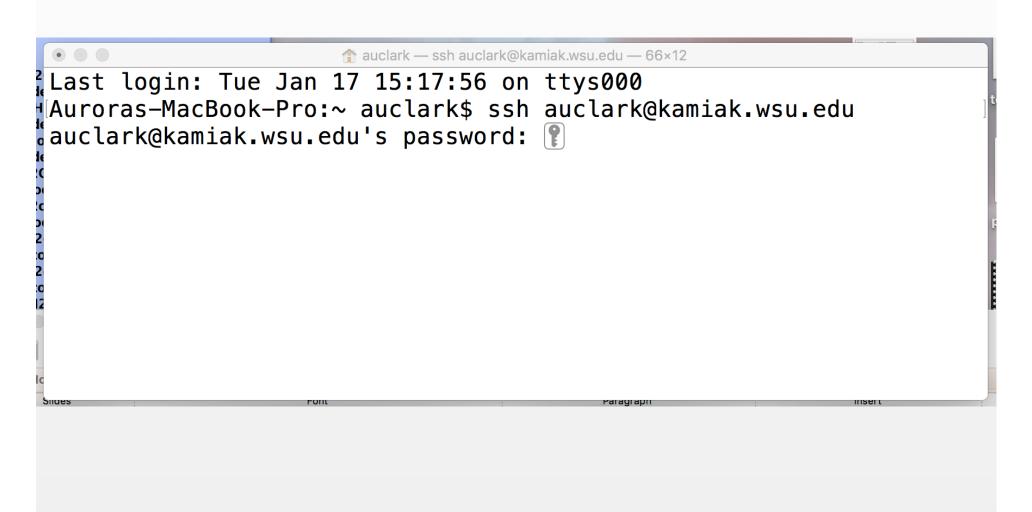
- Navigating Kamiak using essential linux commands
- How to transfer files on and off Kamiak
- How to find and load software modules
- How to submit jobs and optimize your computational efficiency using the queue
- Best practices to being a good user
- Tips and tricks to installing your own software
- How to get help
- How to invest (nodes or storage)



- If you are on a PC/Mac you will utilize an Xterminal, which mimics the "non-graphical" command-line prompt of a Linux/Unix OS
 - Free software: putty (for windows), terminal (for mac preinstalled)



 Secure shell protocol (ssh) typically used to login to Kamiak





 Once logged in – there are many basic linux commands you must master (see Ch2 of tutorial sent in email)

FILE COMMANDS =>Display all information about files/ directories ls –al =>Show the path of current directory bwa mkdir directory-name =>Create a directory rm file-name =>Delete file rm -r directory-nam =>Delete directory recursively =>Forcefully remove file rm -f file-name =>Forcefully remove directory recursively rm -rf directory-name =>Copy file1 to file2 cp file1 file2 =>Copy dir1 to dir2, create dir2 if it doesn't exist cp -r dir1 dir2 =>Rename source to dest / move source to directory mv file1 file2 In -s /path/to/file-name link-name #Create symbolic link to file-name touch file =>Create or update file =>Place standard input into file cat > file =>Output contents of file more file head file =>Output first 10 lines of file tail file =>Output last 10 lines of file =>Output contents of file as it grows starting with the tail -f file last 10 lines gpg -c file =>Encrypt file gpg file.gpg =>Decrypt file =>print the number of bytes, words, and lines in files WC =>Execute command lines from standard input xargs



 Once logged in – there are many basic linux commands you must master (see Ch2 of tutorial sent in email)

DIRECTORY TRAVERSE

```
cd .. =>To go up one level of the directory tree
```

cd =>Go to \$HOME directory

cd /test =>Change to /test directory



 Once logged in – there are many basic linux commands you must master (see Ch2 of tutorial sent in email)

DIRECTORY TRAVERSE

```
cd .. =>To go up one level of the directory tree
cd =>Go to $HOME directory
cd /test =>Change to /test directory
```

 There are many, many tutorials online that can help you solidify your linux command expertise



 Once logged in – there are many basic linux commands you must master (see Ch2 of tutorial sent in email)

DIRECTORY TRAVERSE

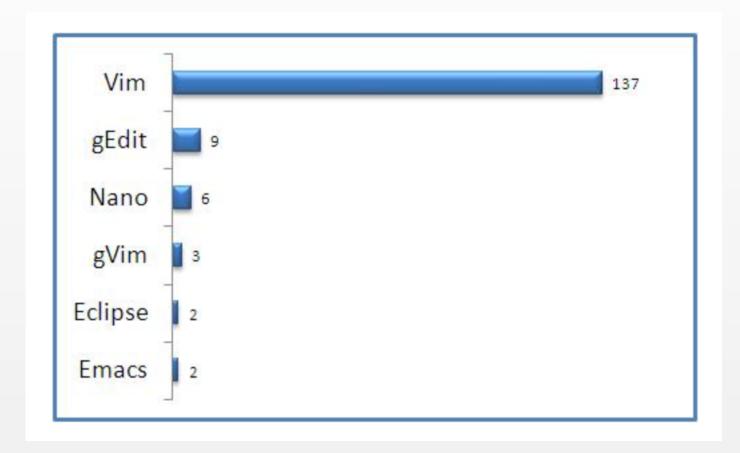
```
cd .. =>To go up one level of the directory tree
```

cd =>Go to \$HOME directory

cd /test =>Change to /test directory



 If you want to open and edit files, you need to also choose a text editor to use:



 There are many, many tutorials on different text editors as well

File Transfers

- There are several ways to transfer and synchronize files across different computers
- Transfer only
 - scp (secure copy), sftp (secure file transfer protocol)
- Synchronize
 - rsync (once two copies are established on 2 computers, you can only copy the most recent updates to files – this decreases network traffic, good for large amounts of data)
 - Versatile for data backups and mirroring

Some common options used with rsync commands

- -v : verbose
- -r: copies data recursively (but don't preserve timestamps and permission while transferring data
- -a: archive mode, archive mode allows copying files recursively and it also preserves symbolic links, file permissions, user & group ownerships and timestamps
- -z : compress file data
- -h: human-readable, output numbers in a human-readable format



File Transfers

- Example uses of rsync
 - Copying data **from your local computer to your home directory** on Kamiak
 - A file:

```
🚾 Auroras-MacBook-Pro:Desktop auclark$ rsync -avz test.xyz auclark@kamiak.wsu.edu:~/
 [auclark@kamiak.wsu.edu's password:
 building file list ... done
 test.xyz
 sent 1551 bytes received 42 bytes 167.68 bytes/sec
 total size is 3987 speedup is 2.50
             - A directory Trailing slash vs. none → contents only vs. dir+contents
Auroras-MacBook-Pro:Desktop auclark$ rsync -avz codes-n-scriots/ auclark@kamiak.wsu.edu:~/
auclark@kamiak.wsu.edu's password:
                                        Current file and location
```

Destination location



File Transfers

- Example uses of rsync
 - Copying files/synching files from Kamiak to your local machine

```
Auroras-MacBook-Pro:Desktop auclark$ rsync -avz auclark@kamiak.wsu.edu:~/test.xyz .auclark@kamiak.wsu.edu's password: receiving file list ... done

sent 20 bytes received 102 bytes 11.62 bytes/sec total size is 3987 speedup is 32.68

Current file and location
```

Present working directory

Need more than 10Gb for a short period of time?
-Use Scratch!



Creating a Workspace and Using Scratch

Scratch Space

All users have access to **temporary**, fast, scratch storage. Scratch storage is allocated using the mkworkspace function which can be found in the workspace_maker module. **All data written to scratch will be deleted one week after the workspace is created.**

Let's look at an example of how to create a scratch space allocation.

Creating a Scratch Space

To create a scratch space run the *mkworkspace* command.

[myWSU.NID@login-p1n01 ~]\$ mkworkspace
Successfully created workspace. Details:
Workspace: /scratch/myWSU.NID_509834

User: myWSU.NID

Group: its_p_sto_qa_hpc_kamiak-my_group Expiration: 2016-06-13 10:34:14.583285

[myWSU.NID@login-p1n01 data]\$ cd /scratch/myWSU.NID_509834/

[myWSU.NID@login-p1n01 myWSU.NID_509834]\$

Notice that our new scratch space was given an expiration date of 2016-06-13, one week after the creation of /scratch/myWSU.NID_509834/. On this date, the directory /scratch/myWSU.NID_509834/ and it's contents will be deleted.

*By default, this creates space on the shared 10K disks in the NetApps storage device (runs over 10Gb network)

Creating a Workspace and Using Scratch

Using the Local SSD

The program mkworkspace will allow you to select from different backends using the -b flag. To use the local disk, select the /local backend.

```
[myWSU.NID@login-p1n02 ~]$ idev --partition=cas --account=cas
Requesting 1 node(s) from cas partition
1 task(s)/node, 20 cpu(s)/task
Time: 0 (hr) 60 (min).
Submitted batch job 75937
Job is pending. Please wait. 0(s)
JOBID=75937 begin on cn14
--> Creating interactive terminal session (login) on node cn14.
--> You have 0 (hr) 60 (min).
--> Assigned Host List: /tmp/idev nodes file myWSU.NID
[myWSU.NID@cn14 ~] $ mkworkspace -b /local -t 0-2:00
Successfully created workspace. Details:
    Workspace: /local/myWSU.NID_600982
    User: myWSU.NID
    Group: its p sto ga hpc kamiak-my group
    Expiration: 2016-06-06 13:12:29.834586
[myWSU.NID@cn14 ~]$
```

Notice that we create the allocation with a 2hr life span (matching the lifespan of our idev session). This ensures that the 600GB local disk remains available to all users.

Creating a Workspace and Using Scratch

Listing Scratch Allocations

A list of your scratch allocations and their expiration dates can be obtained using the command *Isworkspace*

```
[myWSU.NID@login-p1n02 ~]$ lsworkspace
Workspace: /scratch/myWSU.NID_509834
```

Creation host: login-p1n02.kamiak.wsu.edu Creation time: 2016-06-06 10:34:14.583205

User owner: myWSU.NID

Group owner: its_p_sto_qa_hpc_kamiak-my_group Expiration time: 2016-06-13 10:34:14.583285

[myWSU.NID@login-p1n02 ~]\$



- Now you should be able to (and practice):
 - Logging into kamiak
 - Decide and learn what text editor you want to use
 - Basic linux commands to navigate directories, move files, etc.
 - Moving files onto and off of kamiak
- What's next → exploring the available software

Software Modules on Kamiak

```
How to use environment modules (not kernel modules)
$ module -help
                         # lots of options and sub_commands
$ module avail # all modules available on the system
$ module whatis libint/1.1.4 # what the module does
$ module spider module_name # more info about a module
$ module swap m_old m_new # unload m_old, load m_new
$ module purge # unload all modules
$ module unload module_name # unload a module
$ module load netcdf/4 # demonstrate module dependency
Lmod has detected the following error: Cannot load module
"netcdf/4" without these module(s) loaded:
hdf5/1.8.16 # You have to module load hdf5/1.8.16 first
Check the module you loaded:
$ module load octave; module list
$ which octave # check whether octave is in your path
$ env | $LD_LIBRARY_PATH # check whether the library you
loaded is in your path
$ icc -v # tell you what icc version is in your path
```



Software Modules on Kamiak

```
------/opt/apps/modulefiles/Compiler ------
StdEnv (L) gcc/4.9.3 gcc/5.2.0 gcc/6.1.0 (D) intel/xe_2016_update2
intel/xe_2016_update3 (L,D)
 ------/opt/apps/modulefiles/intel/xe_2016_update3 ----------
corset/1.06 espresso/5.3.0 lammps/16feb16
                                                    nwchem/6.6
siesta/4.0_mpi elpa/2016.05.003 hdf5/1.8.16
                                                   netcdf/4
octave/4.0.1
  ------/opt/apps/modulefiles/Other ------/opt/apps/modulefiles
                           google_sparsehash/4cb9240 python3/3.4.3
anaconda2/2.4.0
anaconda2/4.2.0 (D)
                                                      python3/3.5.0 (D)
                           qsI/2.1
anaconda3/2.4.0
                           java/oracle_1.8.0_92
                                                      r/3.2.2
anaconda3/4.2.0 (D)
                           jemalloc/4.4.0
                                                      r/3.3.0 (D)
bamtools/2.4.1
                            libint/1.1.4
                                                      samtools/1.3.1
blast/2.2.26
                            libxc/2.2.2
                                                      settarg/6.0.1
                            libxsmm/1.4.4
bonnie++/1.03e
                                                      sratoolkit/2.8.0
boost/1.59.0
                            Imod/6.0.1
                                                      stata/14
bowtie/1.1.2
                            lobster/2.1.0
                                                      superlu_dist/4.3
                                                      svn/2.7.10
canu/1.3
                            mercurial/3.7.3-1
cast/dbf2ec2
                            music/4.0
                                                      tophat/2.1.1
clc_genomics_workbench/6.0.1 netapp/5.4p1
                                                      towhee/7.2.0
```



Software Modules on Kamiak Cont'd

```
clc_genomics_workbench/8.5.1 (D) netapp/5.5 (D)
                                                   trinity/2.2.0
cp2k/4.1
                  openblas/0.2.18_barcelona valgrind/3.11.0
cuda/7.5
                  openblas/0.2.18_haswell
                                             workspace_maker/master (L,D)
gaussian/09.d.01
                  openblas/0.2.18 (D)
                                             workspace_maker/1.1b
gdal/2.1.0
                  parmetis/4.0.3
                                             workspace_maker/1.1
gdb/7.10.1
                  pexsi/0.9.2
                                             workspace_maker/1.2
geos/3.5.0
                  proj/4.9.2
git/2.6.3
                  python/2.7.10
Where:
```

L: Module is loaded

D: Default Module in cases there are several versions are available

```
For example, try:

$ module load python3; module list # note: not necessary to # include version number
```

You can see that python3/3.5.0 is loaded

You can also do module load in job script



 How to get this software to work for you → submitting to the queue

Running Jobs on Kamiak - Batch Processing

- Kamiak is primarily a batch processing system intended to run non-interactive compute jobs on the individual compute nodes of a queue/partition
- Slurm is the batch scheduler and resource manager used to control compute nodes and run jobs on them
- A node is a computer which has resources available for jobs:
 - CPU cores
 - Memory
 - Accelerators (GPU, Xeon Phi)
- A queue/partition is a set of nodes
- Slurm does not automatically parallelize or otherwise improve your program, it just runs your program on the node(s) it assigns your job to.



Running Jobs on Kamiak – Login

See also:

https://hpc.wsu.edu/users-guide/terminal-ssh

- Follow along (optional):
 - Log into Kamiak
 - · Linux or Mac: ssh -Y kamiak.wsu.edu
 - Windows: PuTTY, MobaXterm, etc.



Running Jobs on Kamiak - Slurm

- sinfo: Information about the cluster
 - sinfo --all
 - What partitions are available?
 - What/how many nodes are in each of them?
- squeue: View running and queued jobs
 - squeue --all
 - Are my jobs running, pending, or held?
- scontrol: View information about aspects of the cluster
 - scontrol show node sn11
 - scontrol show job \$job_id
 - How many GPUs does node sn11 have?
 - How much time is left in my job before its time limit?
- scancel: Cancel one or more jobs
- sbatch: Submit a new job
 - sbatch my code.sh
- srun: Run a parallel job (usually within a batch job)
 - srun my mpi program



Running Jobs on Kamiak - Slurm

```
kamiak$ squeue
JOBID PARTITION NAME
                       USER ST
                                 TIME NODES NODELIST (REASON)
                                           0:00 2 (Resources)
474239
                    tp4 craig.te PD
            cas
                     tp5 craig.te PD
474240
            cas
                                           0:00 2 (Priority)
474241
                     tp6 craig.te PD
                                           0:00 2 (Priority)
            cas
468054
         kamiak q09test e.martin PD
                                           0:00 2 (launch
failed requeued held)
471077 popgenom BFS.3L.i joel.t.n R 9-03:34:38 1 cn77
       popgenom BFS.2R.i joel.t.n R 9-03:34:03 1 cn29
471078
471079 popgenom BFS.2L.i joel.t.n R 9-03:33:14 1 cn29
473678
         kamiak cle 6cma tung.ngu
                                  R 6-05:07:11 1 cn7
473722
        beckman hydr-vra hong.zho R 6-04:28:26 2 cn[43-44]
473726
        beckman occ-1na3 hong.zho
                                   R 5-23:37:54 2 cn[52-53]
        kamiak dbl Pt21 mareike. R 2-23:09:49 2 cn[3-4]
473727
```



Running Jobs on Kamiak - Slurm

See also:

https://hpc.wsu.edu/

kamiak\$ sinfo

queue-list					
PARTITION	AVAIL	TIMELIMIT	NODES	STATE	NODELIST
cahnrs	up	7-00:00:00	1	mix	cn9
cahnrs	up	7-00:00:00	10	alloc	cn[1-8,10-11]
cahnrs_bigmem	up	7-00:00:00	1	mix	sn4
cahnrs gpu	up	7-00:00:00	1	mix	sn2
cas	up	7-00:00:00	2	mix	cn[23-24]
cas	up	7-00:00:00	9	alloc	cn[14-15,17-2
cas	up	7-00:00:00	1	down	cn16
clark	up	7-00:00:00	5	idle	cn[80-84]
test	up	4:00:00	1	mix	cn32
test	up	4:00:00	1	alloc	cn33
free_gpu	up	7-00:00:00	1	mix	sn3
free_phi	up	7-00:00:00	1	resv	sn1
kamiak*	up	7-00:00:00	1	maint*	cn72
kamiak*	up	7-00:00:00	1	resv	sn1
kamiak*	up	7-00:00:00	27	mix	cn[9,12-13,23-
kamiak*	up	7-00:00:00	34	alloc	cn[1-8,10-11,
kamiak*	up	7-00:00:00	30	idle	cn[53-71,80,
kamiak*	up	7-00:00:00	1	down	cn16



Running Jobs on Kamiak - Slurm Backfill

- Backfill vs. investor and sponsor partitions
- Backfill includes all nodes of the cluster
- Preemption
 - Slurm will cancel and resubmit backfill jobs if an investor's job requires use of the node
 - Example:
 - 1. You submit a job to the backfill partition, it gets assigned to cn83
 - 2. cn83 is also in the "clark" partition
 - 3. A user of the Clark lab submits a job to the clark partition
 - 4. Slurm attempts to find idle resource in the clark partition to assign
 - 5. Failing that, Slurm cancels the backfill job and runs the investor job
 - 6. The backfill job is resubmitted to the backfill partition
- Investors have on-demand access to the nodes they own
- Resource limits
 - Currently: 6 standard compute nodes (120 CPU cores)



Running Jobs on Kamiak - Slurm Serial Jobs

So that's how I view the cluster, how do I use it?

- To use Kamiak, write submission script to submit a batch job to Slurm defining:
 - What resources your job needs (CPU cores, memory, GPU, ...)
 - Various constraints and other settings (see man sbatch)
 - Your program and how to run it

```
kamiak$ cat test_gpu_job.sh
#!/bin/bash
#SBATCH --ntasks=1  # Number of tasks
#SBATCH --cpus-per-task=1  # Number of CPU cores per task
#SBATCH --nodes=1-1  # Number of nodes (min-max)
#SBATCH --gres=gpu:tesla:1  # Generic RESources
#SBATCH --partition=kamiak  # Partition/Queue to use

echo "Starting test GPU job on host $HOSTNAME"

module load cuda
deviceQuery
echo "Completed test GPU job on host $HOSTNAME"

kamiak$ sbatch test_gpu_job.sh
Submitted batch job 296129
```

Note: Do not run your script, pass it to sbatch

You can use myworkspace with Slurm

Using mkworkspace in a SLURM script

The program mkworkspace was written to work well within a SLURM submission script. By adding the -q flag, one can suppress the all the output except the name of the directory that was created for the allocation. This can then be stored in a local variable and invoked within the script.

```
#!/bin/bash
#SBATCH --job-name=WSM ### Job Name
#SBATCH --partition=free
#SBATCH --time=0-00:010:00 ### Wall clock time limit in Days-HH:MM:SS
#SBATCH --nodes=1 ### Node count required for the job
#SBATCH --ntasks-per-node=1 ### Nuber of tasks to be launched per Node

SCRATCHDIR="$(mkworkspace -q)"

my_executable $SCRATCHDIR

rmworkspace -a -f --name=$SCRATCHDIR
```

Running Jobs on Kamiak - Slurm Serial Jobs

```
kamiak$ scontrol show job 296129
JobId= 296129 JobName=test gpu job.sh
   UserId=my.NID(8003) GroupId=its p sys ur kam-its staff(7000)
   Priority=4294898447 Nice=0 Account=its staff QOS=normal
   JobState=COMPLETED Reason=None Dependency=(null)
   Requeue=1 Restarts=0 BatchFlag=1 Reboot=0 ExitCode=0:0
   RunTime=00:00:02 TimeLimit=7-00:00:00 TimeMin=N/A
   SubmitTime=2017-01-10T11:34:32 EliqibleTime=2017-01-10T11:34:32
   StartTime=2017-01-10T11:34:33 EndTime=2017-01-10T11:34:35
   PreemptTime=None SuspendTime=None SecsPreSuspend=0
   Partition=kamiak AllocNode:Sid=login-p1n02:28486
   NodeList=sn2
   NumNodes=1 NumCPUs=1 NumTasks=1 CPUs/Task=1 ReqB:S:C:T=0:0:*:*
   TRES=cpu=1, mem=6400M, node=1
   Socks/Node=* NtasksPerN:B:S:C=1:0:*:* CoreSpec=*
   MinCPUsNode=1 MinMemoryCPU=6400M MinTmpDiskNode=0
   Features=(null) Gres=gpu:tesla:1 Reservation=(null)
   Command=/home/my.NID/job scripts/test gpu job.sh
   WorkDir=/home/my.NID
   StdErr=/home/my.NID/slurm-296129.out
   StdIn=/dev/null
   StdOut=/home/my.NID/slurm-296129.out
```

Running Jobs on Kamiak - Slurm Serial Jobs

```
kamiak$ cat slurm-296129.out
Starting test GPU job on host sn2
deviceQuery Starting...
 CUDA Device Query (Runtime API) version (CUDART static linking)
Detected 1 CUDA Capable device(s)
Device 0: "Tesla K80"
  CUDA Driver Version / Runtime Version
                                          8.0 / 7.5
  CUDA Capability Major/Minor version number: 3.7
  Total amount of global memory:
                                                11440 MBytes
(11995578368 bytes)
  (13) Multiprocessors, (192) CUDA Cores/MP: 2496 CUDA Cores
 GPU Max Clock rate:
                                                824 MHz (0.82 GHz)
** output snipped for brevity **
deviceQuery, CUDA Driver = CUDART, CUDA Driver Version = 8.0, CUDA
Runtime Version = 7.5, NumDevs = 1, Device0 = Tesla K80
Result = PASS
Completed test GPU job on host sn2
```



Running Jobs on Kamiak - Slurm MPI Jobs

A serial job? That's fine, but how can I use Kamiak for some parallel work, with MPI?

```
kamiak$ cat test mpi job.sh
#!/bin/bash
#SBATCH --cpus-per-task=1  # Number of CPU cores per task
#SBATCH --ntasks-per-node=5  # Number of tasks per node
#SBATCH --nodes=2-2
                             # Number of nodes (min-max)
#SBATCH --constraint=ivybridge # Restrict to Ivybridge nodes (optional)
#SBATCH --partition=kamiak # Partition/Queue to use
#SBATCH --output=%j.out # Output (STDOUT)
#SBATCH --error=%j.err # Error (STDERR)
echo "Starting test MPI job on host $HOSTNAME"
echo "I am job $SLURM JOBID running on nodes $SLURM JOB NODELIST"
# Intel module includes MPI
# gcc with openmpi, mpich, or mvapich2 are also available
module load intel/xe 2016 update3
# My program I compiled on Kamiak
cd $HOME/mpiicc test
srun ./hello mpiicc
echo "Completed test MPI job on host $HOSTNAME"
kamiak$ sbatch test mpi job.sh
Submitted batch job 613498
```



Running Jobs on Kamiak - Slurm MPI

```
kamiak$ squeue -u my.NID
JOBID PARTITION
                                          TIME NODES NODELIST (REASON)
                   NAME
                            USER ST
613498 kamiak test mpi
                          my.NID R
                                          0:02
                                                    2 cn[3-4]
kamiak$ squeue -u my.NID
JOBID PARTITION
                   NAME
                            USER ST
                                          TIME NODES NODELIST (REASON)
kamiak$ cat 613498.out
Starting test MPI job on host cn3
I am job 613498 running on nodes cn[3-4]
Hello world from processor cn3, rank 0 out of 10 processors
Hello world from processor cn4, rank 5 out of 10 processors
Hello world from processor cn3, rank 1 out of 10 processors
Hello world from processor cn3, rank 2 out of 10 processors
Hello world from processor cn3, rank 3 out of 10 processors
Hello world from processor cn3, rank 4 out of 10 processors
Hello world from processor cn4, rank 6 out of 10 processors
Hello world from processor cn4, rank 7 out of 10 processors
Hello world from processor cn4, rank 8 out of 10 processors
Hello world from processor cn4, rank 9 out of 10 processors
Completed test MPI job on host cn3
```



Running Jobs on Kamiak - Slurm Arrays

 Job arrays offer a mechanism for submitting and managing collections of similar jobs quickly

```
kamiak$ $ cat job scripts/test array job.sh
#!/bin/bash
#SBATCH --ntasks=5
                   # Number of tasks
#SBATCH --reask=1 # Number of CPU cores per task
#SBATCH --partition=kamiak # Partition/Queue to use
#SBATCH --array=0-4
echo "Starting test array job on host $HOSTNAME"
echo "I am Slurm job ${SLURM JOB ID}, array job ${SLURM ARRAY JOB ID},
and array task ${SLURM ARRAY TASK ID}"
export my files=("data0.txt", "data1.txt", "data2.txt", "data3.txt",
"data4.txt")
#/path/to/some/app --input=${my files[$SLURM ARRAY TASK ID]}
echo "Completed test array job on host $HOSTNAME"
kamiak$ sbatch test array job.sh
Submitted batch job 471096
```



Running Jobs on Kamiak - Slurm Arrays

```
kamiak$ squeue -u my.NID
JOBID PARTITION NAME
                           USER ST TIME NODES NODELIST (REASON)
471096 0 kamiak test arr my.NID R 0:01 1
                                                  sn2
471096 1 kamiak test arr my.NID R 0:01 1
                                                  sn2
471096 2 kamiak test arr my.NID R 0:01 1
                                                 sn5
471096 3 kamiak test arr my.NID R 0:01 1
                                                 sn5
471096 4 kamiak
                  test arr my.NID R 0:01 1
                                                 sn5
kamiak$ cat slurm-471096 0.out
Starting test array job on host sn2
I am Slurm job 471097, array job 471096, and array task 0
Completed test array job on host sn2
kamiak$ cat slurm-471096 1.out
Starting test array job on host sn2
I am Slurm job 471098, array job 471096, and array task 1
Completed test array job on host sn2
kamiak$ cat slurm-471096 2.out
Starting test array job on host sn5
I am Slurm job 471099, array job 471096, and array task 2
Completed test array job on host sn5
```



Running Jobs on Kamiak - Interactive Jobs

- idev is a tool used to create an interactive job
- idev supports a limited set of Slurm options (see -- help)
- SSH to a compute node is also possible if you have a job running on it

```
kamiak$ idev
Requesting 1 node(s) from kamiak partition
1 task(s)/node, 1 cpu(s)/task
Time: 0 (hr) 60 (min).
Submitted batch job 470692
Job is pending. Please wait. 0(s)
JOBID=470692 begin on cn13
--> Creating interactive terminal session (login) on node cn13.
--> You have 0 (hr) 60 (min).
--> Assigned Host List : /tmp/idev_nodes_file_my.NID

cn13$ echo "Hello"
Hello
cn13$ exit
Connection to cn13 closed.
Removing job 470692
```

Running Jobs on Kamiak - Other Slurm Options

See also:

man sbatch

- Time limit
 - #SBATCH --time=1-00:00 # D-HH:MM
- Delayed start
 - #SBATCH --begin=now+1hour
 - #SBATCH --begin=16:00
- Require a specific hardware constraint
 - #SBATCH --constraint=haswell
- Depend on another job
 - #SBATCH --dependency=after:\$job_id
- Job name
 - #SBATCH --job-name=test

Running Jobs on Kamiak - Troubleshooting

Kamiak's User Guide

hpc.wsu.edu/users-guide

Kamiak's Service Desk

hpc.wsu.edu/service-requests

SchedMD's Slurm documentation:

slurm.schedmd.com/documentation.html

- 1. My job never ran and it didn't create output files.
 - Check in the directory where you submitted the job, by default Slurm will place output files there. If you set a specific output file, did the directory it is in exist before the job was submitted? Do you have write access to that directory?
- 2. "Requested node configuration is not available"
 - Either your resource request is wrong (e.g. asks for more cores per node than exist) or the nodes with enough resources are offline (check sinfo).
- 3. My queue/partition is busy and my jobs are waiting too long.
 - If possible, use smaller jobs which are easier for Slurm to find resources for.
 - Switch to a partition with available resources, such as backfill.
- 4. My GPU job won't run, it says there are no CUDA capable devices.
 - Ensure you requested a GPU with the --gres option of sbatch.
- 5. My jobs get cancelled with a memory error.
 - Use the --mem or --mem-per-cpu options of sbatch to request more memory.



Running Jobs on Kamiak - Being a Good User

Kamiak is a shared cluster for all of WSU and your access to it is a privilege. Its resources are finite and care must be taken to ensure its continued usefulness for yourself and the greater research community.

Do

- Use /scratch and /local for your computational storage needs when possible
- Cite Kamiak in your work
- Utilize all resources of a node when possible (20 core job on one node is generally better than using 10 cores on two nodes)
- Report issues via Kamiak's Service Desk
- Utilize checkpointing in your workflow
- Abide by Kamiak's End User License Agreement and WSU policies

Don't

- Run intensive workloads (e.g. compiling) on a login node, use idev to get a compute node to work on
- Undersubscribe: Use more resources than you reserved, causing (often severe) performance problems with other jobs (and your own)
- Oversubscribe: Reserve more resources than you use, causing them to be idle but unavailable for other jobs
- Submit thousands of jobs use job arrays or an alternative
- "Game" or otherwise abuse the scheduler (Slurm)
- Give your password to anyone, ever

How best to proceed on software installation

• What if I want to install my own software?

Tips and Tricks on Software Installs

An example of Installing software package: libxc-2.2.2 \$ wget https://www.cp2k.org/static/downloads/ libxc-2.2.2.tar.gz \$ tar -zxvf libxc-2.2.2.tar.gz \$ cd libxc-2.2.2 \$ more README # in some cases it is called README.md \$ more INSTALL # you must read these files before # any attempt of installation \$ idev -c 4 --time=4:00:00 # request a idev session \$./configure -help # to see all options available Note the following statement in **README** file: "..... Furthermore, the most important contents of the src directory are: xc.h - main header file with all external definitions util.h - header file with internal definitions *.f90 *.F90 xc_f.c - Fortran 90 interface" This suggests that we need to use C and Fortran compilers

Tips and Tricks on Software Installs Cont'd

```
$ mkdir ../libxc-install # destination dir. for package
$ ./configure --prefix=/home/username/libxc-install --
enable-shared CC=icc FC=ifort
$ make -j 4 # compile
$ make check # check the compilation
$ make install # install into the destination dir.
$ make clean # remove files created in compilation
$ make distclean # remove files created by ./configure
$ Is ../libxc-install # view installation directory, should
                  # have: bin include lib
$ ls ../libxc-install/* # viewing all sub-directories
Set PATH and LD_LIBRARY_PATH in your .bash_profile file
by putting in the following lines:
export PATH=/home/username/libxc-install/bin:$PATH
export LD_LIBRARY_PATH=/home/username/libxc-
install/bin:$LD_LIBRARY_PATH
```



How to become an investor

- Everyone at WSU has access to the backfill queue, 10Gb of storage in /home, and any storage their Unit may allocate to them
- If you need more → become an investor

Service Catalogue

Standard Compute Nodes

Processors	Cores per Node	Memory	Local Disk	Networking	Budgetary Estimate
Dual Intel E5- 2660v3	20	128GB 2133MT/s DDR4 ECC	1 x 400GB SSD	2 x 10GB SFP+ single-port FDR infiniband	\$7,840 / 5yrs
Dual Intel E5- 2660v3	20	256GB 2133MT/s DDR4 ECC	1 x 400GB SSD	2 x 10GB SFP+ single-port FDR infiniband	\$9,550 / 5yrs
Dual Intel E5- 2660v3	20	512GB 2133MT/sDDR4 ECC	1 x 400GB SSD	2 x 10GB SFP+ single-port FDR infiniband	\$12,970 / 5yrs

Special Compute Nodes

If you are interested in purchasing a non-standard compute resource, i.e. an accelerator equipped node or a large memory system, please submit a request to our <u>Service Desk</u> to get an up to date budgetary estimate. For reference purposes, below are the budgetary estimates for the specialty nodes currently installed on Kamiak.

Processors	Cores per Node	Memory	Accelerator	Local Disk	Networking	Budgetary Estimate
Quad Intel E7-4880v2	60	2TB 1600MT/s DDR3 ECC	none	600 GB 10k RPM SAS 6Gbps	2 x 10GB SFP+ dual-port FDR infiniband	\$57,300 / 5yrs
Dual Intel E5-2670v3	24	256GB 2133MT/s DDR4 ECC	Dual Tesla K80 GPU (9984 CUDA cores)	2 x 60GB 6 GBps SSD 2 x 1TB 7.2k rpm SATA	2 x 10GB SFP+ dual-port FDR infiniband	\$16,500 / 5yrs
Dual Intel E5-2670v3	24	256GB 2133MT/s DDR4 ECC	256GB 2133MT/s DDR4 ECC Dual Xeon Phi 5110P coprocessors (120 physical cores)	2 x 60GB 6 GBps SSD 2 x 1TB 7.2k rpm SATA	2 x 10GB SFP+ dual-port FDR infiniband	\$16,000 / 5yrs



Storage

All users are provided with a 10GB home directory thanks to the generous contributions of our initial investors. Users may also take advantage of the performant scratch file space to temporarily store data. If you would like additional long term "Project Storage", this can be purchased through the Service Desk in either 100GB or 500GB increments.

Storage Type	Usable Storage Amount	Disk Type	Transfer Rate	Budgetary Estimate
Project Storage	100GB unit	7.2k RPM	6GBps	\$12 /year
Project Storage	500GB unit	7.2k RPM	6GBps	\$56 /year

FIN



- We will be sending out a qualtrix survey to get your feedback about this training event (its our first one and we want to get better!)
- An advanced training session will be offered at the end of the semester – let us know in the survey what topics would be of interest
- Other ways to learn more and participate in Kamiak governance:
 - Share your thoughts and ideas with the Kamiak Executive User Group (members Scott Beckman, Ananth K., Stephen Ficklin, Thomas Badman (student rep))
 - Organize! We are interested in starting a student HPC group...see the amazing things that have been done at the UW one:
 - http://students.washington.edu/hpcc/



Additional Info Beyond the Training Session

Things that need repeating

- Sometimes you may have repetitive tasks use cron!
 - · copying/Synchronizing your files every day at midnight
 - · Reporting disk usage to you at regular intervals
 - Checking job outputs on the hour
- Every user has a crontab text file as part of their account, it is modified using the crontab command
- username: man crontab to see the full list of commands
- username: *crontab -l* to list existing **crontab** file entries
- Username: *crontab -e* to edit the existing **crontab** file (opens up a text editor)



The information you must include is (in order of appearance):

- 1. A number (or list of numbers, or range of numbers), *m*, representing the minute of the hour;
- 2. A number (or list of numbers, or range of numbers), *h*, representing the hour of the day;
- 3. A number (or list of numbers, or range of numbers), *dom*, representing the day of the month;
- 4. A number (or list, or range), or name (or list of names), *mon*, representing the month of the year;
- 5. A number (or list, or range), or name (or list of names), *dow*, representing the day of the week; and
- 6. *command*, which is the command to be run, exactly as it would appear on the command line.

cron examines crontab entries once every minute.

The time and date fields are:

field	allowed values
minute	0-59
hour	0-23
day of month	1-31
month	1-12 (or names; see example below)
day of week	0-7 (0 or 7 is Sunday, or use names; see below)



The default crontab file looks like this:

```
# Edit this file to introduce tasks to be run by cron.
# Each task to run has to be defined through a single line
# indicating with different fields when the task will be run
# and what command to run for the task
#•
# To define the time you can provide concrete values for
# minute (m), hour (h), day of month (dom), month (mon),
# and day of week (dow) or use '*' in these fields (for 'any').#.
# Notice that tasks will be started based on the cron's system
# daemon's notion of time and timezones.
#•
# Output of the crontab jobs (including errors) is sent through
# email to the user the crontab file belongs to (unless redirected).
#•
# For example, you can run a backup of all your user accounts
# at 5 a.m every week with:
# 0 5 * * 1 tar -zcf /var/backups/home.tqz /home/
#•
# For more information see the manual pages of crontab(5) and cron(8)
#•
# m h dom mon dow
                     command
```

These lines all start with a # because they are comments; they are ignored by cron, and are just there for you to read.



You don't have to run the command in the crontab – you can have it point to a script

We want our job to run at 5 A.M., which would be minute **0**, hour **5**, every day of the month, every month, every day of the week. We need to add a line to the bottom of the file which looks like this:

0 5 * * * /home/myname/scripts/do-every-day.sh