Introduction to Kamiak
Training Workshop

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hpc.wsu.edu/training/slides
hpc.wsu.edu/training/follow-along
hpc.wsu.edu/cheat-sheet

These slides
Handout
Cheat Sheet

October 5, 2021
What is Kamiak

- A **cluster** of computers called **nodes**, connected by a high-speed network
- Each computer is like your laptop, but with more cores and memory
- Applications can run in **parallel** over many cores and across multiple nodes
- **Speeds up** solving large problems

Nodes: 151
Cores: 4,196
Memory: 42 TB
Storage: 1.2 PB
GPU cores: 93,056

/ home  / data  / scratch
Kamiak Storage

- Kamiak has 4 types of storage available to users
  - `/home/your.name` 100GB per user
  - `/data/lab/pi.labname` 500GB per PI lab (e.g., `/data/clark`)
    
    *Extra storage is available for rent from CIRC service center*
  - `/scratch` Temporary storage, 2-week lifetime, 10TB limit per user
  - `/local` Temporary storage on node, 2-week lifetime, ~400GB
Running Jobs on Kamiak – Key Concepts

- **Nodes** are grouped into **partitions**, each owned by a PI or college
- All nodes also belong to shared **kamiak** partition, available to all users
- You submit a **job** asking for a number of **nodes**, **tasks**, and **cores**
  - Each task is a program instance, sits on 1 node, and uses cores
  - Each core can only be used by 1 job or task at any time
- Job gets added to a **queue** to wait in line
  - One queue for each partition (i.e., group of nodes)
  - Job waits to run until resources are available
- **Slurm job scheduler** decides **who goes first, who gets what, who gets bumped**
- Investors have priority access to the nodes they own
  - You will get **preempted** from kamiak backfill (automatic cancel and requeue) if an investor’s job can’t find enough idle cores to run, and yours would allow it to start
- Resource requirements (cores, tasks, nodes) differ for each app
  - Look at the app docs, the module help, or when in doubt ask us (note cpu’s means cores)
- Applications will only run in parallel if they are built to do so
  - Kamiak will not parallelize your programs for you
What you will learn today

• Transfer files to and from Kamiak
• Logging into Kamiak
• How to run jobs on Kamiak
  – Submit batch jobs
  – Interactive compute session
  – Use job arrays
  – Find and load software modules
• How to get help
• Best practices to being a good user
• How to invest in Kamiak for nodes or storage
Transferring Files - **scp**

- Let’s transfer some files from Kamiak to our machine

  *Make sure you are on your laptop, not logged into Kamiak*
  
  *For Windows, make sure you have Ubuntu installed*

**Open a terminal window**

Terminal >> New Window *(Mac)*
Start >> Ubuntu *(Windows)*

**Transfer a folder from Kamiak to my laptop**

- `scp -r your.name@kamiak.wsu.edu:/opt/apps/samples/training .`

  Recursive, copies all files in folder

  From Kamiak

  To current folder on laptop

**Now from my laptop back to Kamiak**

- `scp -r training your.name@kamiak.wsu.edu:~/`

  From my machine

  To my home directory on Kamiak
Synchronizing Files - **rsync**

- **rsync** makes local and remote folders have same contents
  - Copies any changed files from the source to the destination
  - Only adds or replaces files, doesn’t delete them from the destination

- Let’s synchronize a folder on Kamik to our laptop
  *Make sure you are on your laptop, not logged into Kamiak*
  
- **rsync** -ravx training/ your.name@kamiak.wsu.edu:~/training

  Recursive, archive, verbose, compress
  From folder on my laptop  To folder on Kamiak

  ```
sumo(10011) %rsync -ravx training/ peter.mills@kamiak.wsu.edu:~/training
peter.mills@kamiak.wsu.edu's password:
sending incremental file list

  sent 219 bytes  received 21 bytes  43.64 bytes/sec
total size is 3,105  speedup is 12.94
sumo(10012) %
  ```
Logging into Kamiak - ssh

Open a terminal window

- Terminal >> New Window (Mac)
- Start >> Ubuntu (Windows)

Log into Kamiak

- ssh your.name@kamiak.wsu.edu
- exit

Follow along

See also: hpc.wsu.edu/users-guide/terminal-ssh
How to Run Jobs on Kamiak

There are two ways to run jobs on Kamiak

- **sbatch** `myJob.sh` *Batch job submission*
  - Says what partition to submit to, default is backfill queue
  - Says what resources your job needs (cpu’s/cores, memory, GPU’s)
  - Says what program to run

- **idev** *Interactive session on compute node*
  - Puts you on a compute node
  - Just type in commands and see them executed

Do not run compute or compile jobs on login nodes, use **sbatch** or **idev** instead
Submitting Batch Jobs to Kamiak

• Log into Kamiak
  
  ssh your.name@kamiak.wsu.edu
  cd training
  source training_only_setup.sh  # One-time setup for this training

• Create/edit a job script
  
  cat myJob.sh

• Submit the job script to the job queue
  
  sbatch myJob.sh  # sbatch --test-only myJob.sh

• View the job queue
  
  squeue -u your.name  # Shows pending and running jobs
  squeue -j jobNumber

• Cancel the job
  
  scancel jobNumber  # Cancel job

• View past and active jobs
  
  sacct -S 10/5/21 -u your.name  # Past job history
  scontrol show job jobNumber  # Job details
Viewing Information about the Cluster

- What partitions and nodes are available
  `sinfo -a | more`  # Availability (alloc, idle, mix)

- View all running and queued jobs
  `squeue -a | more`  # Queued jobs for all partitions

- View node details
  `scontrol show node cn93`  # Amount of memory, cpus, GPU’s
Interactive Jobs

- **idev** creates an interactive session on a compute node
  - Same options as **sbatch**
  - Can also **ssh** to a compute node if you have a job allocated on it

```
idev -N 1 --ntasks=1 -cpus-per-task=2 -t 360
```
Idev interactively runs commands on a compute node.
See 'man salloc' for idev options to reserve a job allocation.
To use a GPU within idev: use 'srun yourCommand', e.g. 'srun python -i'.
To use X11 forwarding from a compute node:
  Use 'ssh -Y' or more secure 'ssh -X' to log into Kamiak.
  Within idev, use 'srun --x11' to launch a task with a user interface.
Recommend using 'srun -I' to launch a task without hanging.
Default time is 60 minutes. Use '-t yourMinutes' to override.
salloc: Granted job allocation 1160832
Allocated nodes: cn32

```
cn32$ module avail
```
# Shows available apps for loaded compiler

```
cn32$ module help python/2.7.15
```
# See any app-specific instructions
# (Resources differ for each app)

```
cn32$ module load python/2.7.15
```
# Loads specific version (recommended)

```
cn32$ module list
```
# See loaded modules
Currently Loaded Modules:
  1) StdEnv
  2) intel/xe_2016_update3
  3) workspace_maker/master
  4) python/2.7.15
Interactive Jobs

Use `srun -l` to avoid hanging if resources are not available.
• Use `mkworkspace` to create a scratch directory that expires in two weeks
  
  ```bash
  export myscratch="$(mkworkspace)"
  ```
  - Can be used outside or inside a job script for a larger temporary storage space

• Use `lsworkspace` to list your scratch allocations
  
  `lsworkspace`

• Just use `rm` to delete the contents of your scratch directory when done
  
  ```bash
  rm -r -l $myscratch/*
  ```
Job Arrays

- **Template** to create multiple instances of a job
  - `#SBATCH --array=1-5`  *Creates 5 instances, one for each index 1,2,3,4,5*

- Each instance is an individual job with the same resources
  - Template holds place in queue, spawns instances as resources become available

- Each instance has a unique index `$SLURM_ARRAY_TASK_ID`
  - Can use index however you want, in different ways

- Example: run the same program over different files *(data_1.txt)*

```
#SBATCH --array=0-2:1  # Index 0,1,2 in steps of 1
srun myProgram inputs/data_${SLURM_ARRAY_TASK_ID}.txt
```

Please use job arrays instead of submitting hundreds of individual jobs
Running Job Arrays

kamiak$ cat jobArray.sh

kamiak$ sbatch jobArray.sh
Submitted batch job 1161089

kamiak$ squeue -u your.name

<table>
<thead>
<tr>
<th>JOBID</th>
<th>PARTITION</th>
<th>NAME</th>
<th>USER</th>
<th>ST</th>
<th>TIME</th>
<th>NODES</th>
<th>NODELIST (REASON)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1161089</td>
<td>_0</td>
<td>kamiak myJobArr</td>
<td>peter.mi</td>
<td>R</td>
<td>0:01</td>
<td>1</td>
<td>cn32</td>
</tr>
<tr>
<td>1161089</td>
<td>_1</td>
<td>kamiak myJobArr</td>
<td>peter.mi</td>
<td>R</td>
<td>0:01</td>
<td>1</td>
<td>cn32</td>
</tr>
<tr>
<td>1161089</td>
<td>_2</td>
<td>kamiak myJobArr</td>
<td>peter.mi</td>
<td>R</td>
<td>0:01</td>
<td>1</td>
<td>cn32</td>
</tr>
</tbody>
</table>

kamiak$ cat output/myJobArray*out
Starting job array 0 on host cn32
Processing data file: inputs/data_0.txt

Starting job array 1 on host cn32
Processing data file: inputs/data_1.txt

Starting job array 2 on host cn32
Processing data file: inputs/data_2.txt

kamiak$ scancel 1161089

See: /opt/apps/samples/training
Other Types of Jobs

- **Single node shared memory**
  - Multithreaded or OpenMP
  - Threads share memory

- **Multiple nodes**
  - MPI for message passing
  - Tasks do not share memory

- **GPU (Graphics Processing Unit) accelerators**
  - Thousands of tiny pixel cores, and matrix processors
  - Offloads kernel function to run over many data points
  - Requires CUDA, OpenCL, OpenACC

See samples in:
```
/opt/apps/samples/advanced
```
The Center for Institutional Research Computing (CIRC) provides cutting-edge high-performance computing (HPC) resources and expertise to advance computational and data-intensive research across WSU. CIRC's goal is to propel WSU into a position of national leadership in research computing by providing state-of-the-art HPC hardware and software infrastructure and a world-class team that supports its effective utilization and fosters computational literacy. Our services include support, guidance, and training in the use of the HPC cluster, application development and deployment, and investing in nodes and storage.

Upcoming Events

- **Research Week 4.0**
  - TUE 13
  - October 12 - October 16

- **External Event – Teratec Digital Forum 2020**
  - TUE 13
  - October 13 - October 14
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 research community.

Do

• Cite Kamiak in your work
• Report issues via Kamiak’s Service Desk
• Abide by Kamiak’s End User License Agreement and WSU policies
• Use accurate resource requirements (CPU, time, memory)

Don’t

• Do not run compute jobs or installs on a login node, use `sbatch` or `idev` to run on a compute node
• Do not submit thousands of jobs – use `job arrays`
• Do not give your password to anyone, ever
• All users have access to the backfill queue, /home and /scratch storage, and any /data/lab storage made available by their PI.

• If you need more → **have your PI become an investor**

• Submit a service request to purchase nodes or rent extra storage
  • *Nodes are permanently owned by the investor with a 5-year warranty*
  • *Storage can be rented annually in units of 512GB per year*

• Standard compute nodes
  • 64-cores Intel Xeon Gold, 512GB memory
  • Optional Nvidia A100 GPU’s
  • Optional large-memory, 1-2TB

• For price quotes, please submit a service request
For detailed node descriptions, please see [hpc.wsu.edu/kamiak-hpc/becoming-an-investor/](http://hpc.wsu.edu/kamiak-hpc/becoming-an-investor/)
• We will be sending out a survey to get your feedback about this training event

• Other training sessions are planned throughout the year – let us know in the survey what topics would be of interest

• Other ways to learn more and participate in Kamiak governance:
  - CIRC Advisory Committee - share your ideas with its members
  - WSU HPC club - 4 nodes purchased through Tech Fee grant
Basic Linux Commands

- There are many basic Linux commands you must master

  - `cd path` move your current position in the folder tree
  - `ls path` list contents of a folder (“ls” for current folder)
  - `cp from to` copy files, for folders use “`cp -r from to`”
  - `mv from to` move files and folders
  - `rm todelete` delete files, for folders user “`rm -r -I path`”

- Special pathnames
  - Example: `cd ~/../`
  - `.` means one level up, the parent folder
  - `.` means the current folder
  - `~` means your home directory

- For other commands see hpc.wsu.edu/cheat-sheet or Ch2 of the tutorial sent in email
Text Editors

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

  ![Bar chart showing popularity of text editors]

- There are many tutorials on different text editors as well
Transferring Files - rsync

- We can also synchronize folders between Kamiak and your laptop so that they have the same contents

```
rsync -ravx source destination
```
- Copies any changed files from the source to the destination
- Only adds or replaces files, doesn’t delete them from the destination
- Useful for data backups and mirroring

Common options used with rsync

- `-r` recursive copy, all subfolders and files
- `-a` archive mode, preserves permissions, ownership
- `-v` verbose
- `-x` don't cross filesystem boundaries
- `-z` compress file data
- `-h` print output in human-readable format
Transferring Files - \texttt{rsync}

- Different ways to use \texttt{rsync}

  - \texttt{rsync -ravx training \textit{your.name}@kamiak.wsu.edu:~/}
    
    Without slash, aligns training to ~/training (\textit{copy the folder by name})
    With a slash, aligns training/* to ~/ (\textit{copy the contents of the folder})

  - \texttt{rsync -ravx --delete training/ \textit{your.name}@kamiak.wsu.edu:~/training}
    
    Deletes non-matching items in the destination
Different Ways to Use Job Arrays

• You can use a job array index in different ways

• As a suffix to a folder or file name
  • `srun myProgram myFolder_${SLURM_ARRAY_TASK_ID}/d.txt`

• As an index into a set of names or numbers
  • `export names=("0.txt" "1.txt" "2.txt" "3.txt" "4.txt")`
  • `export names=$(ls myFolder/inputs*.txt)` (for known --array total)
  • `srun myProgram ${names[$SLURM_ARRAY_TASK_ID]}

• As an index into a script to run (only for single core jobs)
  • `srun bash myProgram_${SLURM_ARRAY_TASK_ID}.sh`

• Any combination of the above
Types of Applications

**Multithreaded** programs take *cpus-per-task*, and run on 1 node

```
#SBATCH --nodes=1 --ntasks-per-node=1 --cpus-per-task=10
myapp
```

Number of cores per running program

Runs the program once

**MPI** programs take *tasks*, and run on multiple nodes

```
#SBATCH --nodes=2 --ntasks-per-node=4 --cpus-per-task=1
srun myapp
```

Runs the program once for each task

```
#SBATCH --nodes=1-2 --ntasks=8 --cpus-per-task=1
srun myapp
```

*Dynamic layout*

Let it compact the task layout over the min-max nodes

1. Total allocated cores = ntasks * cpus-per-task
2. --ntasks-per-node is treated as max tasks per node, if --ntasks is also specified
Using Available Software on Kamiak

- Kamiak has many software packages already installed and available for use
- **module** commands set up the environment for your software to run
  - Adds programs to your executable search path
  - Pulls in any software dependencies

```bash
module avail  # See available modules for compiler
module load python3/3.4.3  # Load specific version *(Recommended)*
module list  # See loaded modules
module avail python3  # See available python3 modules
module load python3  # Load latest version
module unload python3  # Unload a module
module spider  # See all modules
module whatis anaconda3  # See what a module does
module help anaconda3  # See help for a module
which python3  # See that python is in your path
printenv PATH  # See effects of loading modules
printenv LD_LIBRARY_PATH
```
Troubleshooting

Kamiak’s User Guide  
[link]
hpc.wsu.edu/users-guide
Kamiak’s Service Desk  
[link]
hpc.wsu.edu/service-requests
SchedMD’s Slurm documentation:  
[link]
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?

2. **“Requested node configuration is not available”**  
   - 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.**  
   - 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 `--mem` or `--mem-per-cpu` options of `sbatch` to request more memory.
   - `sacct -u your.name -o jobid,reqmem,maxrss,state,nodelist` to see how much memory you used (`maxRSS` is per task).
Transferring Files - scp

sumo(10110) %scp -r peter.mills@kamiak.wsu.edu:/opt/apps/samples/training .
peter.mills@kamiak.wsu.edu's password:
data_2.txt 100% 29  10.2KB/s  00:00
data_1.txt 100% 29   8.5KB/s  00:00
data_0.txt 100% 29   8.2KB/s  00:00
setup.sh  100% 156  83.6KB/s  00:00
jobArray.sh 100% 1252 590.4KB/s  00:00
myJob.sh   100%  999  504.2KB/s  00:00
helloWorld.py 100%  611  302.3KB/s  00:00
sumo(10111) %

sumo(10116) %scp -r training peter.mills@kamiak.wsu.edu:~/
peter.mills@kamiak.wsu.edu's password:
helloWorld.py 100%  611  68.0KB/s  00:00
data_0.txt  100%  29   3.9KB/s  00:00
data_1.txt  100%  29   4.6KB/s  00:00
data_2.txt  100%  29   4.9KB/s  00:00
jobArray.sh 100% 1252 116.8KB/s  00:00
myJob.sh   100%  999  110.7KB/s  00:00
setup.sh   100%  156  18.5KB/s  00:00
sumo(10117) %
#!/bin/bash

#SBATCH --partition=kamiak  # Partition/Queue to use
#SBATCH --job-name=myJob   # Job name
#SBATCH --output=myJob_%j.out  # Output file (stdout)
#SBATCH --error=myJob_%j.err  # Error file (stderr)
#SBATCH --mail-type=ALL  # Email notification: BEGIN,END,FAIL,ALL
#SBATCH --mail-user=your.name@wsu.edu  # Email address for notifications
#SBATCH --time=7-00:00:00  # Wall clock time limit Days-HH:MM:SS

#SBATCH --nodes=1  # Number of nodes (min-max) Where (layout)
#SBATCH --ntasks-per-node=1  # Number of tasks per node (max)
#SBATCH --ntasks=1  # Number of tasks (processes) What (cpus)
#SBATCH --cpus-per-task=2  # Number of cores per task (threads)

echo "I am job $SLURM_JOBID running on nodes $SLURM_JOB_NODELIST"

module load python/2.7.15  # Load software module from Kamiak repository
srun python helloWorld.py -w  # Each task runs this program (total 1 times)

echo "Completed job on node $HOSTNAME"
Submitting, Viewing, and Canceling Batch Jobs

kamiak$ `sbatch myJob.sh`
Submitted batch job 1160269

kamiak$ `squeue -u your.name`

<table>
<thead>
<tr>
<th>JOBID</th>
<th>PARTITION</th>
<th>NAME</th>
<th>USER</th>
<th>ST</th>
<th>TIME</th>
<th>NODES</th>
<th>NODELIST(REASON)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1160269</td>
<td>kamiak</td>
<td>myJob</td>
<td>peter.mi</td>
<td>PD</td>
<td>0:00</td>
<td>1</td>
<td>(Priority)</td>
</tr>
</tbody>
</table>

kamiak$ `squeue -u your.name`

<table>
<thead>
<tr>
<th>JOBID</th>
<th>PARTITION</th>
<th>NAME</th>
<th>USER</th>
<th>ST</th>
<th>TIME</th>
<th>NODES</th>
<th>NODELIST(REASON)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1160269</td>
<td>kamiak</td>
<td>myJob</td>
<td>peter.mi</td>
<td>R</td>
<td>0:02</td>
<td>1</td>
<td>cn93</td>
</tr>
</tbody>
</table>

kamiak$ `squeue -j 1160269`

<table>
<thead>
<tr>
<th>JOBID</th>
<th>PARTITION</th>
<th>NAME</th>
<th>USER</th>
<th>ST</th>
<th>TIME</th>
<th>NODES</th>
<th>NODELIST(REASON)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1160269</td>
<td>kamiak</td>
<td>myJob</td>
<td>peter.mi</td>
<td>R</td>
<td>0:17</td>
<td>1</td>
<td>cn93</td>
</tr>
</tbody>
</table>

kamiak$ `cat myJob_1160269.out`
I am job 1160269 running on nodes cn93
Hello World! from cn93

kamiak$ `scancel 1160269`

See also: `man sbatch`
Viewing Job History and Details

kamiak$ sacct -S 10/5/21 -u your.name

<table>
<thead>
<tr>
<th>JobID</th>
<th>JobName</th>
<th>Partition</th>
<th>Account</th>
<th>AllocCPUS</th>
<th>State</th>
<th>ExitCode</th>
</tr>
</thead>
<tbody>
<tr>
<td>1160269</td>
<td>myJob</td>
<td>kamiak</td>
<td>circ</td>
<td>2</td>
<td>CANCELLED+</td>
<td>0:0</td>
</tr>
<tr>
<td>1160269.bat+</td>
<td>batch</td>
<td>circ</td>
<td>2</td>
<td>CANCELLED</td>
<td>0:20</td>
<td></td>
</tr>
<tr>
<td>1160269.0</td>
<td>python</td>
<td>circ</td>
<td>2</td>
<td>CANCELLED</td>
<td>0:20</td>
<td></td>
</tr>
</tbody>
</table>

kamiak$ scontrol show job 1160269

JobId=1160269 JobName=myJob
UserId=peter.mills(8316) GroupId=its_p_sys_ur_kam-circ(7060) MCS_label=N/A
Priority=4294680391 Nice=0 Account=circ QOS=normal
JobState=TIMEOUT Reason=TimeLimit Dependency=(null)
Requeue=1 Restarts=0 BatchFlag=1 Reboot=0 ExitCode=0:15
RunTime=00:01:20 TimeLimit=00:01:00 TimeMin=N/A
StartTime=2020-02-26T13:57:03 EndTime=2020-02-26T13:58:23 Deadline=N/A
Partition=kamiak AllocNode:Sid=login-p1n02:33414
NodeList=cn93 BatchHost=cn93
NumNodes=1 NumCPUs=2 NumTasks=1 CPUs/Task=2 ReqB:S:C:T=0:0:*:*:*
TRES=cpu=2,mem=16G,node=1
Gres=(null) Reservation=(null)
Command=/home/peter.mills/training/myJob.sh
WorkDir=/home/peter.mills/training
StdErr=/home/peter.mills/training/myJob_1160269.err
StdIn=/dev/null
StdOut=/home/peter.mills/training/myJob_1160269.out
**Viewing Available Partitions**

<table>
<thead>
<tr>
<th>PARTITION</th>
<th>AVAIL</th>
<th>TIMELIMIT</th>
<th>NODES</th>
<th>STATE</th>
<th>NODELIST</th>
</tr>
</thead>
<tbody>
<tr>
<td>cahnrs</td>
<td>up</td>
<td>7-00:00:00:00</td>
<td>1</td>
<td>mix</td>
<td>cn9</td>
</tr>
<tr>
<td>cahnrs</td>
<td>up</td>
<td>7-00:00:00:00</td>
<td>10</td>
<td>alloc</td>
<td>cn[1-8,10-11]</td>
</tr>
<tr>
<td>cahnrs_bigmem</td>
<td>up</td>
<td>7-00:00:00:00</td>
<td>1</td>
<td>mix</td>
<td>sn4</td>
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<tr>
<td>cahnrs_gpu</td>
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<tr>
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<td>2</td>
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<td>cn[23-24]</td>
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<tr>
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<td>9</td>
<td>alloc</td>
<td>cn[14-15,17-2]</td>
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<tr>
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<td>up</td>
<td>7-00:00:00:00</td>
<td>1</td>
<td>down</td>
<td>cn16</td>
</tr>
<tr>
<td>clark</td>
<td>up</td>
<td>7-00:00:00:00</td>
<td>5</td>
<td>idle</td>
<td>cn[80-84]</td>
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<tr>
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<td>up</td>
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<td>1</td>
<td>mix</td>
<td>cn32</td>
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<td>up</td>
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<td>alloc</td>
<td>cn33</td>
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<td>mix</td>
<td>sn3</td>
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<tr>
<td>free_phi</td>
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<td>7-00:00:00:00</td>
<td>1</td>
<td>resv</td>
<td>sn1</td>
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<tr>
<td>kamiak*</td>
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<td>maint</td>
<td>cn72</td>
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<td>sn1</td>
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<td>mix</td>
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<tr>
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<td>up</td>
<td>7-00:00:00:00</td>
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<td>alloc</td>
<td>cn[1-8,10-11,]</td>
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<td>1</td>
<td>down</td>
<td>cn16</td>
</tr>
</tbody>
</table>

See also: https://hpc.wsu.edu/queue-list
### Viewing the Job Queue

```bash
kamiak$ squeue -a | more
```

<table>
<thead>
<tr>
<th>JOBID</th>
<th>PARTITION</th>
<th>NAME</th>
<th>USER</th>
<th>ST</th>
<th>TIME</th>
<th>NODES</th>
<th>NODELIST(REASON)</th>
</tr>
</thead>
<tbody>
<tr>
<td>474239</td>
<td>cas</td>
<td>tp4</td>
<td>craig.te</td>
<td>PD</td>
<td>0:00</td>
<td>2</td>
<td>(Resources)</td>
</tr>
<tr>
<td>474240</td>
<td>cas</td>
<td>tp5</td>
<td>craig.te</td>
<td>PD</td>
<td>0:00</td>
<td>2</td>
<td>(Priority)</td>
</tr>
<tr>
<td>474241</td>
<td>cas</td>
<td>tp6</td>
<td>craig.te</td>
<td>PD</td>
<td>0:00</td>
<td>2</td>
<td>(Priority)</td>
</tr>
<tr>
<td>471077</td>
<td>popgenom</td>
<td>BFS.3L.i</td>
<td>joel.t.n</td>
<td>R</td>
<td>9-03:34:38</td>
<td>1</td>
<td>cn77</td>
</tr>
<tr>
<td>471078</td>
<td>popgenom</td>
<td>BFS.2R.i</td>
<td>joel.t.n</td>
<td>R</td>
<td>9-03:34:03</td>
<td>1</td>
<td>cn29</td>
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<tr>
<td>471079</td>
<td>popgenom</td>
<td>BFS.2L.i</td>
<td>joel.t.n</td>
<td>R</td>
<td>9-03:33:14</td>
<td>1</td>
<td>cn29</td>
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<tr>
<td>473678</td>
<td>kamiak</td>
<td>cle_6cma</td>
<td>tung ngu</td>
<td>R</td>
<td>6-05:07:11</td>
<td>1</td>
<td>cn7</td>
</tr>
<tr>
<td>473722</td>
<td>beckman</td>
<td>hydr-vra</td>
<td>hong.zho</td>
<td>R</td>
<td>6-04:28:26</td>
<td>2</td>
<td>cn[43-44]</td>
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<tr>
<td>473726</td>
<td>beckman</td>
<td>occ-1na3</td>
<td>hong.zho</td>
<td>R</td>
<td>5-23:37:54</td>
<td>2</td>
<td>cn[52-53]</td>
</tr>
<tr>
<td>473727</td>
<td>kamiak</td>
<td>dbl_Pt21</td>
<td>mareike</td>
<td>R</td>
<td>2-23:09:49</td>
<td>2</td>
<td>cn[3-4]</td>
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</tbody>
</table>
kamiak$ scontrol show node cn93

NodeName=cn93  Arch=x86_64  CoresPerSocket=14
  CPUAlloc=20  CPUErr=0  CPUTot=28  CPULoad=22.11
AvailableFeatures=broadwell,e5-2660-v4-2.00ghz,avx2
ActiveFeatures=broadwell,e5-2660-v4-2.00ghz,avx2
Gres=(null)
NodeAddr=cn93  NodeHostName=cn93  Version=17.02
OS=Linux  **RealMemory=128658**  AllocMem=128000  FreeMem=7234  Sockets=2  Boards=1
State=MIXED  ThreadsPerCore=1  TmpDisk=64329  Weight=62000  Owner=N/A  MCS_label=N/A
Partitions=clark,adam,storfer,bio534,kamiak
BootTime=2019-11-28T09:00:39  SlurmdStartTime=2019-11-28T09:01:34
CfgTRES=cpu=28,mem=128658M
AllocTRES=cpu=20,mem=125G
CapWatts=n/a
CurrentWatts=125  LowestJoules=15477  ConsumedJoules=1017346137
ExtSensorsJoules=n/s  ExtSensorsWatts=0  ExtSensorsTemp=n/s
Job Array Script

```bash
#!/bin/bash
#SBATCH --partition=kamiak          # Partition/Queue to use
#SBATCH --job-name=myJobArray       # Job name
#SBATCH --output=output/myJobArray_%A_%a.out # Output filename, jobid_index
#SBATCH --error=output/myJobArray_%A_%a.err # Error filename, jobid_index
#SBATCH --time=7-00:00:00            # Wall clock time limit Days-HH:MM:SS
#SBATCH --mail-type=ALL             # Email notification: BEGIN,END,FAIL,ALL
#SBATCH --mail-user=your.name@wsu.edu # Email address for notifications
#SBATCH --array=0-2:1                # Number of jobs, in steps of 1

#SBATCH --nodes=1                    # Number of nodes (min-max)
#SBATCH --ntasks-per-node=1          # Number of tasks per node (max)
#SBATCH --cpus-per-task=1            # Number of cores per task (threads)
#SBATCH --mem-per-cpu=8G             # Memory per core (gigabytes)

# Runs this job 3 times, with index SLURM_ARRAY_TASK_ID as 0,1,2
# Split your data into 3 files, name them data_0.txt, data_1.txt, data_2.txt
# Each job array step is scheduled as an individual job
# Each job array step is allocated the above resources (cores, memory)

echo "Starting job array $SLURM_ARRAY_TASK_ID on host $HOSTNAME"

module load python
srun python helloWorld.py -w "inputs/data_${SLURM_ARRAY_TASK_ID}.txt"

echo "Completed job array $SLURM_ARRAY_TASK_ID on host $HOSTNAME"
```
Available Software Modules on Kamiak

<table>
<thead>
<tr>
<th>Compilers</th>
</tr>
</thead>
<tbody>
<tr>
<td>StdEnv (L) gcc/5.2.0 intel/xen_2016_update2</td>
</tr>
<tr>
<td>gcc/4.9.3 gcc/6.1.0 (D) intel/xen_2016_update3 (L,D)</td>
</tr>
</tbody>
</table>

intel/xen_2016_update3 Software

<table>
<thead>
<tr>
<th>bazel/0.4.2</th>
</tr>
</thead>
<tbody>
<tr>
<td>fftw/3.3.4</td>
</tr>
<tr>
<td>netcdf/4</td>
</tr>
<tr>
<td>cmake/3.7.2</td>
</tr>
<tr>
<td>gromacs/2016.2_mdrun</td>
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<tr>
<td>nwchem/6.6</td>
</tr>
<tr>
<td>corset/1.06</td>
</tr>
<tr>
<td>gromacs/2016.2_mpi (D) octave/4.0.1</td>
</tr>
<tr>
<td>eems/8ee979b</td>
</tr>
<tr>
<td>hdf5/1.8.16</td>
</tr>
<tr>
<td>siesta/4.0_mpi</td>
</tr>
<tr>
<td>elpa/2016.05.003</td>
</tr>
<tr>
<td>lammmps/16feb16</td>
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<tr>
<td>stacks/1.44</td>
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<tr>
<td>espresso/5.3.0</td>
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<tr>
<td>mvapich2/2.2</td>
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Other Software

<table>
<thead>
<tr>
<th>anaconda2/2.4.0</th>
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</thead>
<tbody>
<tr>
<td>lmod/6.0.1</td>
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<tr>
<td>anaconda2/4.2.0     (D) lobster/2.1.0</td>
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<tr>
<td>anaconda3/2.4.0</td>
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<tr>
<td>mercurial/3.7.3-1</td>
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<tr>
<td>anaconda3/4.2.0     (D) music/4.0</td>
</tr>
<tr>
<td>bamtools/2.4.1</td>
</tr>
<tr>
<td>mzmine/2.23</td>
</tr>
<tr>
<td>binutils/2.25.1</td>
</tr>
<tr>
<td>netapp/5.4p1</td>
</tr>
<tr>
<td>blast/2.2.26</td>
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<tr>
<td>netapp/5.5 (D)</td>
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<tr>
<td>bonnie++/1.03e</td>
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<tr>
<td>octave/4.2.0 (D)</td>
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<tr>
<td>boost/1.59.0</td>
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<tr>
<td>openblas/0.2.18_barcelona</td>
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<td>bowtie/1.1.2</td>
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<td>openblas/0.2.18_haswell</td>
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<tr>
<td>canu/1.3</td>
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<tr>
<td>openblas/0.2.18 (D)</td>
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<tr>
<td>cast/dbf2ec2</td>
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<tr>
<td>orangefs/2.9.6</td>
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<tr>
<td>cp2k/4.1_pre_openmp</td>
</tr>
<tr>
<td>parmetis/4.0.3</td>
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</table>
Available Software Modules on Kamiak (Cont’d)

---------------------------------- Other Software ----------------------------------
  jemalloc/4.4.0                    (D)  trinity/2.2.0
  laszip/2.2.0                      valgrind/3.11.0
  libgeotiff/1.4.0                  workspace_maker/master (L,D)
  libint/1.1.4                      workspace_maker/1.1b
  libkml/1.3.0                      workspace_maker/1.2
  liblas/1.8.0                      workspace_maker/1.1
  libspatialite/4.3.0a              zlib/1.2.11
  libxsmm/1.4.4

------------------------------- Licensed Software ------------------------------
  clc_genomics_workbench/6.0.1      gaussian/09.d.01   vasp/5.4.4
  clc_genomics_workbench/8.5.1 (D)  green/1.0
  dl_polly/4.08                     stata/14

Where:
  D:  Default Module
  L:  Module is loaded

Use "module spider" to find all possible modules.
Use "module keyword key1 key2 ..." to search for all possible modules
matching any of the "keys".
The End