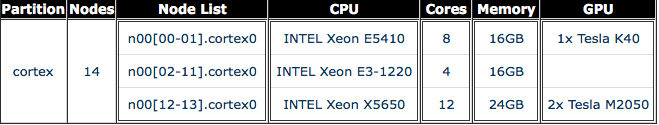
Cortex Cluster Tutorial Outline

**(A). CLUSTER GENERAL INFORMATION AND RESOURCES…**

* Resources:
  + Wiki: <http://redwood.berkeley.edu/wiki/Cluster>

Help center email: [brc-hpc-help@berkeley.edu](mailto:brc-hpc-help@berkeley.edu)

* + Redwood cluster mailing list: redwood\_cluster@lists.berkeley.edu
* Available hardware: 14 nodes with over 60 cores and 4 GPUs.



<http://research-it.berkeley.edu/services/high-performance-computing/user-guide>

**(B). HOW TO GET AN ACCOUNT AND LOGIN…**

* To request an account, email Bruno with: “FullName <emailaddress> username”
* To login to cluster, you need a 4-digit pin and a 6-digit password from Google Authenticator.
* To get a one time password for Google Authenticator, follow instructions here: <https://sites.google.com/a/lbl.gov/high-performance-computing-services-group/authentication/linotp-usage>
* How to login to cluster:
  + “ssh -Y [username@hpc.brc.berkeley.edu](mailto:username@hpc.brc.berkeley.edu)” to login to a node

**(C). NAVIGATING WITHIN AND INTERFACING WITH CLUSTER…**

* **Home directory** (/global/home/users/username) has 10 GB quota
* **Scratch space** (/clusterfs/cortex/scratch/username) has 17TB
* **Environment customization** with .bash\_profile or .bash\_rc alias.
* **Slurm Scheduler** : <https://sites.google.com/a/lbl.gov/high-performance-computing-services-group/scheduler/ucb-supercluster-slurm-migration>
* **man <some command>** - to get the documentation on any command and find what flags are important
* **sbatch** - submit bash scripts or jobs to cluster nodes. (flags below set preferences)
  + job-name=myjob1
  + partition=cortex
  + constraint=< cortex | cortex\_nogpu |other >
  + ntasks=1
  + mem-per-cpu=1G
  + time=DD:hh:mm
  + -o PvD output.out
  + -e PvD error.err
  + -x n00[00-13].cortex0
* **squeue** - look at jobs running on all cluster nodes currently.
* **scancel** - cancel a job running on cluster by its job ID
* **sinfo** - use instead of wwstats & wwtop
* **scontrol -** use instead of wwstats & wwtop
* **wwstats** - displays statistics of tasks running on cluster **(deprecated.)**
* **wwtop** - displays specific tasks currently running on cluster **(deprecated.)**
* **module load** - load a program or software on cluster to use it.
* **sshfs** [username@hadley.berkeley.edu](mailto:username@hadley.berkeley.edu):. Cortex/

(mount file system to a directory on your machine)

**(4). MY PROCESSING PIPELINE USING MATLAB**

* My pipeline:

1. Edit scripts on my local machine.
2. Copy them to cluster and run them.
3. Save output images or \*.mat files to cluster.
4. Can use mat files for next step in processing chain or copy output back to my local machine to analyze

* Construct bash scripts in MATLAB:
  + Write\_sbatch\_loop\_bench\_bsds500.m
  + Run\_scripts\_bench\_bsds
  + Script\_bench\_bsds1
  + View\_outs\_bench\_bsds
  + View\_errs\_bench\_bsds
* Copy files to cluster: [ DTN = Data transfer node (faster connection) ]
  + “while ! rsync -ravP ./scripts4cluster/\* cwarner@dtn.brc.berkeley.edu:'~/Projects'; do sleep 5; done”
  + “while ! rsync -ravP ./ImageSeg/\* cwarner@dtn.brc.berkeley.edu:'~/Projects/ImageSeg'; do sleep 5; done”
  + “while ! rsync -ravP ./Kuramoto\_DS/\* cwarner@dtn.brc.berkeley.edu:'~/Projects/Kuramoto\_DS'; do sleep 5; done”
* Copy files from cluster: while ! rsync -ravP cwarner@dtn.brc.berkeley.edu:'/clusterfs/cortex/scratch/cwarner/output/Kuramoto/NetsFromImgs/BSDS\_patch\_101x101\_ds1\_blur\_sig1/data/Kur\_PIF\_Fourier1/Mod\_SKHAdj/KurMC\*rM10\_\*kslrg\*.mat' ./output/Kuramoto/NetsFromImgs/BSDS\_patch\_101x101\_ds1\_blur\_sig1/data/Kur\_PIF\_Fourier1/Mod\_SKHAdj/ ; do sleep 5; done

**(5). USING THE CLUSTER WITH PYTHON…**

* Interfacing with the cluster in Python (Jesse)

**(6). GLOBUS FILE TRANSFER…**

* Globus (Jesse)