

# Working on UC Davis Bioinformatics Core Administrated Computing Systems

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# Outline

- Introduction/Questions
- Explain user space (home directories) vs share space (lab directories/shares).
- Working in a team, file/folder permissions.
- The module system, when to request software, when to install software yourself.
- Slurm

# Quick Introduction to the UC Davis Bioinformatics Core

The **mission** of the Bioinformatics Core facility is to facilitate outstanding omics- scale research through these activities:

### Data Analysis

The Bioinformatics Core promotes experimental design, advanced computation and informatics analysis of omics scale datasets that drives research forward.

### Research Computing

Maintain and make available high-performance computing hardware and software necessary for todays data-intensive bioinformatic analyses.

### Training

The Core helps to educate the next generation of bioinformaticians through highly acclaimed training workshops, seminars and through direct participation in research activities.

# UC Davis Bioinformatics Core in the Genome Center

**Core Facility Manager**

Dr. Matthew Settles

**Faculty Advisor**

Dr. Ian Korf

**Data Analysis Group**

**Genomics Bioinformatics**

Dr. Joseph Fass  
Dr. Monica Britton  
Nikhil Joshi

**Proteomics Bioinformatics**

Dr. Jessie Li

**Metabolomics Bioinformatics**

Dr. Kwanjeera Wanichthanarak

**Biostatistics**

Dr. Blythe Durbin-Johnson

**Research Computing Group**

**System Administration**

Michael Casper Lewis  
Richard Feltstykke

**Database/Web Programming**

Adam Schaal

**Undergraduate Assistant**

I-San Stephanie Chang

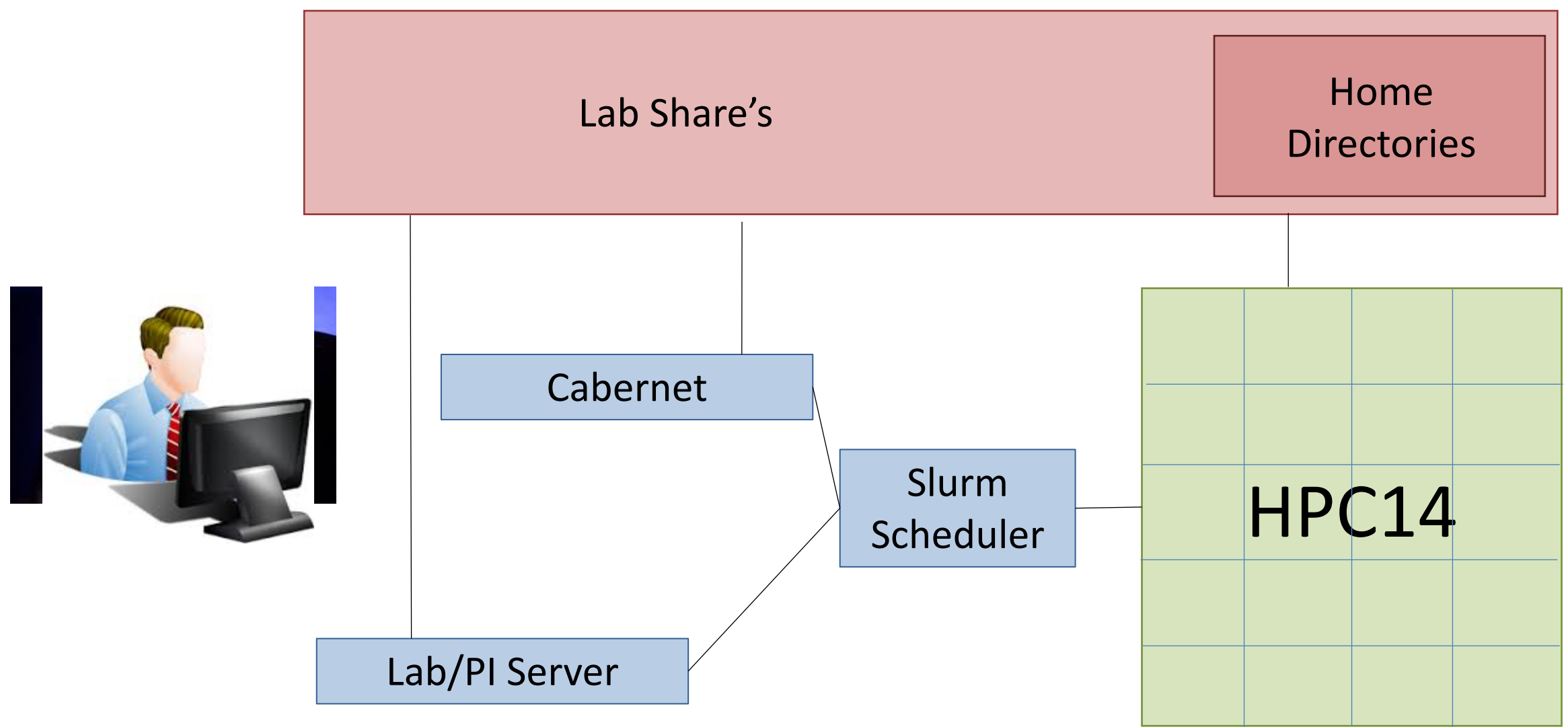
# Contacts

- Computing Issues, include but not limited to  
User account questions, equipment failure/malfunction, software install, software failures (not related to use)

[helpdesk@genomecenter.ucdavis.edu](mailto:helpdesk@genomecenter.ucdavis.edu)

- Bioinformatics related questions, include but not limited to  
bioinformatic methods questions, software use, data questions

[Bioinformatics.core@ucdavis.edu](mailto:Bioinformatics.core@ucdavis.edu)



User space vs shared space

AND

Working in a team, file/folder permissions.

Groups/Labs, etc.



# What is a user account?

- User accounts are not tied to PI/labs. Any person who has a legitimate reason for requesting an account will be provided one. **Users should only ever login as themselves and never as another user.**
- The Bioinformatics Core provides users with a home directory that is capped at 100Gb (we are exploring reducing that to 10Gb).
- User home directories are 'personal' space, special permission must be given by university administration to explore a user's home directory.
- You now presumably can login to cabernet, but because you're not yet associated with a group you can't do much. **Never ever work on cabernet.**

# Lab Groups

- The UC Davis Bioinformatics Core manages lab group data shares, top level folder associated with a collective group. **These are data storage resources purchased by a lab, or PI.**
- Groups/Labs/Collaborators work together in lab shares, found under /share/group\_name  
[ex. The Bioinformatics Core share is /share/biocore ]
- All lab associated analysis should be performed in lab shares. Virtually nothing should be done in your home directory, I personally have:
  - A link to my labs share
  - Software I've installed for me

# Linux permissions

- Users on linux system have a user id and group(s) membership(s)
  - to see your group memberships on the command line type: groups
  - You may see an 'error' groups: cannot find name for group ID 1107119953 you can safely ignore this
- Access to additional resources [data/compute] are driven by group permissions/memberships.
- More information on linux permissions

<https://www.linux.com/learn/understanding-linux-file-permissions>

# By default

- By default, you have sole access to your home directory by both user and group.
- By default the lab share is owned by the PI and the group may be the PI group id, or a special group id [ ex. subproject ].
- By default, all shares are read accessible by everyone and write accessible by the user and the group.
- By default, the group id on a share is a 'sticky' bit, this means that any files/folders created under that share folder inherit the same permission (group read/write) but are owned by the user which created them.

# Working as a team

- Groups and permissions are setup to facilitate team/group interactions.
- When working on files shared with other Users you don't have to request the other user to modify permissions, the group sticky bit takes care of that for you.
- YOU DO HAVE TO BE CAREFULL of others work! Since you have group write ability you are able to modify, delete and otherwise impact others people work/project.
- Once a file/folder has been created you can modify the permission to restrict access, however should the PI request the bioinformatics core to change it back, we will.

# Linux Permissions

Last thing about permissions, I like to be very permissive, so in addition to the lab share group sticky bit, I also set, in my `~/.bash_profile`

```
umask 0002
```

By default all files/folders I create are group read/write

# Centralized Resources

- Genomes – some genomes and mapping indexes (bwa/bowtie) are available centrally to be used by everyone, they can be found under
  - /share/genomes
    - Ensembl
    - genome\_reference\_consortium
    - lgenomes
    - Kraken
    - ncbi
    - ncbi\_genomes
    - patric

# Module system

For Software



# Modules

- The Environment Modules package provides for the dynamic modification of a user's environment via module files.
- Each module file contains the information needed to configure the shell for an application. Once the Modules package is initialized, the environment can be modified on a per-module basis using the module command which interprets module files. Typically module files instruct the module command to alter or set shell environment variables such as PATH, MANPATH, etc. module files may be shared by many users on a system and users may have their own collection to supplement or replace the shared module files.
- Modules are useful in managing different versions of applications. Modules can also be bundled into meta-modules that will load an entire suite of different applications, or ensure dependencies are loaded.

# Modules

- Users can manage their environment (software available on the path) via modules.
- Users benefit from a familiar applications environment across UC Davis Bioinformatics Core systems (on and off-campus).
- Requests for software from any user becomes available to all users.
- Efficient system administration pooling software install/testing efforts from different projects/machines.
- Additional information  
[https://en.wikipedia.org/wiki/Environment\\_Modules\\_\(software\)](https://en.wikipedia.org/wiki/Environment_Modules_(software))

```

1. ssh
msettles@ganesh: ~$module avail

----- /software/modules/3.2.10/x86_64-linux-ubuntu14.04/Modules/versions -----
3.2.10

----- /software/modules/3.2.10/x86_64-linux-ubuntu14.04/Modules/3.2.10/modulefiles -----
abyss/1.5.2      bwa/0.6.2      gmap/2015-06-23  null           samtools/1.3
abyss/1.9.0      bwa/0.7.10     gnumap/2.9.0    olb/1.9.4      samtools/default
allpaths1g/51298 bwa/0.7.12     gnumaps/0.1     pantherscore/1.03 scythe/c128b19
amos/3.1.0       bwa/0.7.13     hisat/0.1.7-beta pasa/r20140417  seqtk/1.0-r63-dirty
anytag/2.5.2     bwa/0.7.13-test hmmer/2.3.2     pbccs/34288ba   sga/0.10.13
arachne/46223    canu/1.0        hmmer/3.1b1     pbcore/1.2.7    sickle/7667f147e6
arraymaker/1.1   cdhit/4.6.1     hmmer/3.1b2     pbdagcon/ed6e2c3 singularity/3a624f3
augustus/3.0.3   cdhit/4.6.4     homer/4.7        pbsuite/15.2.20 skewer/0.1.126-g88fb913
bamtools/2.3.0   ceas/1.0.2      htseq/0.5.3p9    pear/0.9.5      snap/2013-11-29
bbcp/15.02.03.01.1 cegma/2.5      htseq/0.6.1p2    penncnv/1.0.3   soapdenovo2/2.04-r240
bcftools/1.2     cgat/0.2.4      htlib/1.1        perl/5.14.4     spades/3.5.0
bcl2fastq/1.8.4  circos/0.67-1   jellyfish/1.1.11 perl/5.14.4-mt   spades/3.9.0
bcl2fastq/2.16.0.10 cmake/3.5.1     jellyfish/2.2.3  perl/modules-5.18.2 sprai/0.9.9.10
bcl2fastq/2.17.1.14 coral/1.4        kallisto/0.42.2.1 perl-modules/5.18.2 sratoolkit/2.4.2-3
bcl2fastq/default crispresso/0.9.7 kentutils/308    plink2/1.90p    star/2.4.0h
beagle/2.1.2     cufflinks/2.2.1 khmer/1.1         poretools/0.5.1 star/2.4.2a
beast/1.8.0      cutadapt/1.8    khmer/2.0-rc1    pplacer/1.1.alpha18 star/2.5.1b
beast/1.8.3      dbg2olc/165ae2  kraken/0.10.5-beta price/1.2        stringtie/1.0.4
bedops/2.4.11    delly/0.5.9     kraken/eaf8fb6   prodigal/2.6.3  subread/1.4.6-p3
bedtools2/2.21.0 delly/0.6.7     last/621          python/2.6.9     subread/1.5.0-p1
bedtools2/2.25.0 delly/0.7.2     leehom/dfca9e6   python/2.7.6-ubuntu tabix/0.2.6
bioutils/1.0.9   deweylab-utils/0.0.2 lighter/1.0.6    qiime/1.9.1      tandem/15-04-01-1
blast/2.2.30+    diamond/0.7.9   macs2/2.1.0.20140616 quip/1.1.8        tophat/2.0.13
blast/2.2.31+    discover/52218  mafft/7.245      R/local_libs     tophat/2.0.5
blast/2.4.0+     discoverdenovo/52448 maker/2.31.8     randfold/2.0     tophat/2.1.0
blast/2.4.0+_debug discoverexp/52219 masurca/2.3.2    ray/2.3.1        torrentsuite/4.6.11
blat/v.35        dot             megahit/1.0.6    rdnatools/2a4cd4e tpp/4.8.0
blat/v.35-fastq  dwgsim/0.1.11   meme/4.10.0_1     reapr/1.0.18     transdecoder/2.0.1
boost/1.44.0     ectools/0.1     meraculous/2.0.5  repeatmasker/4.0.5 trinity/2.0.6
boost/1.60       epimine/2016-01-13 meta/galaxy/1     rosetta/latest   trinity/2.1.1
bowtie/1.1.1     express/1.5.1   methprogs/19-Oct-2015 rsem/1.2.18      trinity/r20140717
bowtie/1.1.2     falcon/0.4.2    mira4/4.0.2       rsem/1.2.20      use.own
bowtie2/2.0.0-beta7 fastphase/1.4.8  mirdeep2/2.0.0.5  rsem/1.2.28      vcflib/7f1575e

```

# Module basics

**module avail, show, load, list, unload**

\$ module avail # shows the currently available module to the system #  
format is application/version

\$ module show beast/1.8.3 # shows information, such as what-is,  
other modules loaded and path information

\$ module load beast/1.8.3 # load the module beast version 1.8.3

\$ module list # show currently loaded modules

\$ module unload beast # unload the module beast

# An Example

\$ module list # no modules are loaded by default

\$ module avail # lets see what modules are present, lets load beast

\$ which beast # currently unavailable

\$ module show beast/1.8.3 # show its load parameters

\$ module load beast/1.8.3 # load beast v. 1.8.3 into our environment

\$ module list # show the modules currently loaded

\$ which beast # now we see beast is available on our path

We can now use beast

# Modules are great for

- Modules are great for keeping track of what software and specifically what version of the software is being used in an analysis.
- You can keep track by
  - Doing an analysis from a bash script, loading the modules at the beginning of a script.
  - Copy/paste recording all commands to a file (ex. Analysis.txt) to save the commands for review later
  - Use history at the end of an analysis and save all commands including module load commands
- Note of caution: There are some applications available as a part of the system (ex. samtools) we are working to identify and remove these.

# When to install software or request a module

- Benefits to having software in a module:
  - System administrators install, with troublesome software or difficult dependencies they can solve issues others can't.
  - Modules are available to all users, to so request benefits many
- Difficulties with software in a module:
  - Can take time for a system administrators to install, we manage over 400 servers and 5 clusters, we do our best to be responsive.
  - If your just trying something out that may or may not be useful can waste valuable system administrator time.

# When to install software or request a module

- If you feel the software will be broadly applicable, request a module
- If it's a tough install, can't get it installed yourself, request a module
- If you just want to try something out, install it yourself
- If you need it right now, install it yourself
- If you installed it yourself AND requested a module, once the module is available delete your instance.



# Slurm scheduler

# SLURM

## Simple Linux Utility for Resource Management

- Manages compute resources
- Schedules jobs using those resources
- Original developed at Lawrence Livermore National Labs
- Open Source
- Supports plugins extending or enhancing functionality
- Increasingly being used at academic research computing centers and national labs
  - Berkeley
  - UCSD Super Computer

# Slurm Commands

**sinfo, squeue, sacct, srun, sbatch, scancel**

**sinfo** reports the state of partitions and nodes managed by Slurm. It has a wide variety of filtering, sorting, and formatting options.

**squeue** reports the state of jobs or job steps. It has a wide variety of filtering, sorting, and formatting options. By default, it reports the running jobs in priority order and then the pending jobs in priority order.

**sacct** is used to report job or job step accounting information about active or completed jobs.

**srun** is used to submit a job for execution or initiate job steps in real time. srun has a wide variety of options to specify resource requirements. A job can contain multiple job steps executing sequentially or in parallel on independent or shared resources within the job's node allocation.

**sbatch** is used to submit a job script for later execution. The script may contain one or more srun commands to launch parallel tasks.

**scancel** is used to cancel a pending or running job or job step. It can also be used to send an arbitrary signal to all processes associated with a running job or job step.

# Slurm Commands - SINFO

- **sinfo** reports the state of partitions and nodes managed by Slurm. It has a wide variety of filtering, sorting, and formatting options.

sinfo --summarize

- Node
- Nodes are computers/servers, multiple cpu with shared memory
- Partitions are logical groups of nodes (possibly overlapping)
  - gc64, gc128, gc256, gc512
  - Partition gc is the collection of gc64, gc128 and gc256 and is the default queue

# Slurm Commands – SQUEUE

- **squeue** reports the state of jobs or job steps. It has a wide variety of filtering, sorting, and formatting options. By default, it reports the running jobs in priority order and then the pending jobs in priority order.
- Use squeue to view jobs currently queued and running
  - --user=username
  - --states=[running or pending]
  - --long # long format
  - --start # sometimes gives approximate start time

# Slurm Commands -SBATCH

- **sbatch** is used to submit a job script for later execution [non-interactive]. The script may contain one or more srun commands to launch parallel tasks.
1. Login to cluster
  2. Create a job script
    - I use a .slurm extension so that I know it's a job script
  3. Submit the script to the cluster using sbatch
    - sbatch script.slurm
  4. Slurm will respond with a jobid:
    - Submitted batch job 311533
- See example on [github](#)

# Example Job script

```
#!/bin/bash
#SBATCH --partition=gc # partition to submit to
#SBATCH --job-name="myjob" # Job name
#SBATCH --nodes=1 # single node, anything more than 1 will not run
#SBATCH --ntasks=1 # equivalent to cpus, stick to around 20 max on gc64, or gc128 nodes
#SBATCH --mem=1G # memory pool all cores, default is 2GB per cpu
#SBATCH --time=0-01:30:00 # expected time of completion in hours, minutes, seconds, default 1-day
#SBATCH --output=my_output.out # STDOUT
#SBATCH --error=my_output.err # STDERR
#SBATCH --mail-user=you@gmail.com
#SBATCH --mail-type=ALL
# This will be run once for a single process
/bin/hostname
module load blat/v.35-fastq
echo "HELLO"
```

# Slurm Commands – SCANCEL

- **scancel** is used to cancel a pending or running job or job step. It can also be used to send an arbitrary signal to all processes associated with a running job or job step.
- To delete a job
  - `scancel <jobid>`
  - Jobs not running yet (queued) are deleted, jobs running will be killed
- To delete many jobs
  - `scancel <jobid1> <jobid2> <jobid3> ...`



# Slurm Command – srun and helper scripts

**srun** is used to submit a job for execution or initiate job steps in real time. srun has a wide variety of options to specify resource requirements. A job can contain multiple job steps executing sequentially or in parallel on independent or shared resources within the job's node allocation.

# An interactive session (preferred way)

- `slurmlogin`
  - `srun -N 1 -n 1 --pty /bin/bash`
- `slurmlogin-wholenode`
  - `srun -N1 --exclusive --pty /bin/bash`
- `Slurmlogin-gc512`
  - `srun -p gc512 --mem 500000 -N1 --exclusive --pty /bin/bash`
- If using 'screen',
  1. 'screen' on Cabernet,
  2. then `srun`,
  3. then exit when done.

# Task Arrays

Job arrays offer a mechanism for submitting and managing collections of similar jobs quickly and easily; job arrays with millions of tasks can be submitted in milliseconds (subject to configured size limits).

- Slurm parameter, `--array=a-b` , where a and b are numeric number ex. 1-5
- Sets the environment variables
  - **SLURM\_ARRAY\_JOB\_ID** will be set to the first job ID of the array.
  - **SLURM\_ARRAY\_TASK\_ID** will be set to the job array index value.
- The value of `$SLURM_ARRAY_TASK_ID` can be used to reference rows in a file containing values to use for that job
- See example on github

# Pipelines – using dependency

- sbatch returns the jobid after submission
- Can use that jobid and the sbatch argument --dependency to launch another job once the first one finishes
  - dependency=<type:job\_id[:job\_id][,type:job\_id[:job\_id]>
- See example on github

<b>after:</b> jobid[:jobid...]	job can begin after the specified jobs have started
<b>afterany:</b> jobid[:jobid...]	job can begin after the specified jobs have terminated
<b>afternotok:</b> jobid[:jobid...]	job can begin after the specified jobs have failed
<b>afterok:</b> jobid[:jobid...]	job can begin after the specified jobs have run to completion with an exit code of zero (see the <a href="#">user guide</a> for caveats).
<b>singleton</b>	jobs can begin execution after all previously launched jobs <i>with the same name and user</i> have ended. This is useful to collate results of a swarm or to send a notification at the end of a swarm.

# Coming soon

- HPC16
- UC Davis Bioinformatics Core Portal
  - Request users accounts
  - Manage groups/labs/access
  - View available modules and info
    - Request modules and see status of request
  - Request Sys Admin Support

# Account registration

Bioinformatics Core x

test.portal.genomecenter.ucdavis.edu/registration/register/

My Genome Center Log in

Register

Welcome to the portal registration page. If someone at the Genome Center directed you to register for a computing account, you've come to the right place. When registering, be sure to select the lab or group you are joining. Someone from that group will need to confirm your request. Still wondering what the Genome Center Portal is? Visit the home page.

Sponsor\*

White House

Enter group or lab sponsoring the account. If your group is not listed, please email "sysadmin@genomecenter.ucdavis.edu".

Category\*

Other

☐ UCD

Are you a UC Davis student or employee?

First name\*

Hillary

Last name\*

Clinton

Email\*

secretaryofstate@yahoo.com

Username\*

nextprez

Required. 30 characters or fewer. Lowercase letters only.

Policies

LAN policy

Introduction Modified This document sets forth standards which must be adhered to by all employees, contractors and any user granted access to any machine on the Local Area Network (LAN) at any time, whether physically present at the Firm or via remote access.

Failure to comply with the policies set forth in this document will result in disciplinary action, and may result in termination of employment.

Definitions For the purposes of this document, an "Employee" is any employee, contractor, agent, temporary worker, vendor and any other person in a position to know or obtain information about computers or devices on the LAN.

The firewall is a hardware or software device which protects the ports of computers on the LAN. For the purposes of this document, "Remote Access" shall mean access to the Local Area Network from any location outside the firewall by any method, including but not limited to Virtual Private Network (VPN), dial-in modem, frame-relay, SSH, cable-modem and any other method of accessing the LAN from outside the firewall.

Policy Scope The Policy applies to any person granted authorization to access any computer or device on the Firm's LAN (an "Authorized User"). This includes but is not limited to contractors, temporary workers, vendors, sub-contractors, employees, attorneys and partners authorized to access any of the Firm's computers, locally or via Remote Access, for any reason, including email and Internet or intranet web browsing.

Physical Security All computers and devices on the LAN must be physically secured when leaving them unattended. All servers must be additionally secured with locking devices such as keyboard locks.

Approved devices include: desktop computer, Personal Digital Assistant (PDA), Internet enabled cellular device, MAC OS enabled device or other device capable of connecting to Remote Access.

☒ Accept

Submit

# Group memberships

My Genome Center

Home


Request Forms

Software

Manage Lab ▾

Network Registration

Policies

 ▾

Manage Lab Permissions

Select lab: 

The White House ▾

Bioinformatics Core

Sponsored users

User	Email	Username	
Hillary Clinton	secretaryofstate@yahoo.com	nextprez	<div>Revoke</div>

User permissions

Add a user: 

Search users

User	Email	Username	Can approve group members	Can administer group
Joe Biden	joe@whitehouse.gov	jb	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Save

# Request help

My Genome Center

[Home](#)


[Request Forms](#)

[Software](#)

[Manage Lab](#)

[Network Registration](#)

[Policies](#)



Submit a ticket

Subject\*

Job id\*

Server\*

Command\*

Directory\*

Description\*

Submit



# Software Request

[My Genome Center](#) [Home](#) [Request Forms](#) [Software](#) [Manage Lab](#) [Network Registration](#) [Policies](#) [User](#)

## Request software

Name\*

Version\*

Link\*

Description\*

Tags\*

☐ modules ☐ data analysis ☐ libraries ☐ aligner ☐ assembler ☐ cluster ☐ databases ☐ patterns

Submit

# Software List

[My Genome Center](#)
[Home](#)
[Request Forms](#)
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[Manage Lab](#)
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## Software

Search: 
  
[Clear search criteria.](#)

Tags:
☐ analysis
☐ correction
☐ databases
☐ gpu
☐ gtf
☐ package
☐ sequence
☐ simulator
☐ aligner
☐ assembler
☐ cluster
☐ data analysis
☐ epigenomic
☐ genome
☐ gff
☐ libraries
☐ luajit
☐ modules
☐ patterns
☐ tools

Don't see the software you need? [Request new software to be installed on the cluster.](#)

[R](#)  
Versions: .3.1.0.swp, 3.0.2, local\_libs, .3.1.0.swo  
Tags:

<a href="#">abyss</a> Versions: 1.5.2, 1.9.0 Tags:	<a href="#">allpaths-lg</a> Versions: 51298 Tags:	<a href="#">amos</a> Versions: 3.1.0 Tags:
<a href="#">anytag</a> Versions: 2.5.2 Tags:	<a href="#">arachne</a> Versions: 46223 Tags:	<a href="#">arraymaker</a> Versions: 1.1 Tags:
<a href="#">augustus</a> Versions: 3.0.3 Tags:	<a href="#">bamtools</a> Versions: 2.3.0, .2.3.0.swp, .2.3.0.swo Tags:	<a href="#">bbcp</a> Versions: 15.02.03.01.1 Tags:
<a href="#">bcftools</a> Versions: 1.2 Tags:	<a href="#">bcl2fastq</a> Versions: 1.8.4, 2.16.0.10, 2.17.1.14 Tags:	<a href="#">beagle</a> Versions: 2.1.2 Tags:
<a href="#">beast</a> Versions: 1.8.3, 1.8.0, 2.4.3 Tags:	<a href="#">bedops</a> Versions: 2.4.11 Tags:	<a href="#">bedtools2</a> Versions: 2.25.0, 2.21.0 Tags:
<a href="#">biutils</a> Versions: 1.0.9 Tags:	<a href="#">blast</a> Versions: 2.2.30+, 2.2.29+, 2.2.31+, 2.4.0+, 2.4.0+_debug Tags:	<a href="#">blast-legacy</a> Versions: 2.2.26 Tags: modules
<a href="#">blat</a> Versions: v.35-fastq, v.35 Tags: data analysis	<a href="#">boost</a> Versions: 1.44.0, 1.60 Tags: libraries	<a href="#">bowtie</a> Versions: 1.1.1, 1.1.2 Tags: aligner
<a href="#">bowtie2</a>	<a href="#">bsseeker2</a>	<a href="#">busco</a>

# Contact

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