

# SCF Computing Cluster

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## Overview

Today we'll discuss the Statistical Computing Facility's (SCF) cluster, which is administrated by the Department of Statistics. Much of this material comes directly from the SCF's documentation; see the links below for more details:

- [SCF homepage](#)
- [SCF Linux cluster](#)
- [SCF FAQs and How-Tos](#)
- [SCF Parallel processing in R tutorial](#)
- [How to get help on the SCF](#)

- [SCF JupyterHub](#)

## SCF cluster capabilities and hardware

💡 Clusters, partitions, and nodes! Oh my!

A **cluster** is a collection of computing **nodes**. A node is analogous to a laptop or desktop computer, with an operating system, RAM, CPUs, and sometimes GPUs.



[Image source](#)

Nodes with similar capabilities or access policies are often grouped together as a **partition**. This allows cluster users to request the resources they need – such as number of CPU **cores** – from a pool of nodes, rather than specify a specific one.

The SCF cluster has 1064 cores, across 7 partitions with more than 26 nodes, but for this class we'll use the **low** partition. It's the default, so you won't need to do anything special to use it for your jobs (we'll explain how to submit jobs later on).

The **low** partition has the following resources:

- 8 nodes
- 32 cores per node
- 256 GB RAM per node

The SCF Linux cluster uses a batch job scheduler called [Slurm](#), commonly used by large computer centers in both academia and industry. Although the SCF cluster has much greater computational capacity than our personal computers, it is a shared resource with many users. With Slurm, the cluster is able to schedule jobs asynchronously, balancing resource allocations so that everyone gets a turn. This also means that when you submit a job, it may not run until many minutes or hours later. Be sure to give yourself enough time!

## Your ~/ on the SCF

Nodes in the SCF cluster use the Linux distribution Ubuntu. Every user has a private home directory which, as usual on Linux-based OSes, has the shortcut `~/`. In this section, we'll give an overview of access, disk space, and remote file transfers to and from your SCF home directory.

### Logging in

The SCF has a number of **login nodes** which you can access via `ssh`.

#### Note

For info on using `ssh` (including on Windows), see [here](#).

For example, I'll use `ssh` to connect to the `dorothy` node:

```
james@pop-os:~$ ssh jpduncan@dorothy.berkeley.edu
The authenticity of host 'dorothy.berkeley.edu (128.32.135.58)' can't be established.
ED25519 key fingerprint is SHA256:rOY7ED/iLiTgI++Y4XHmiEl+tC+OmSGBvWp03CSII5E.
This key is not known by any other names
Are you sure you want to continue connecting (yes/no/[fingerprint])? yes
Warning: Permanently added 'dorothy.berkeley.edu' (ED25519) to the list of known hosts.
```

Notice that upon first connecting to a server you haven't visited there is a warning that the “authenticity of the host ... can't be established”. So long as you have typed in the hostname correctly (`dorothy.berkeley.edu`, in this case), and trust the host (we trust the SCF!) then you can type `yes` to add the host to your known hosts file (found on your local machine at `~/.ssh/known_hosts`).

You'll then be asked to enter your password for the SCF cluster. For privacy, you won't see anything happen in your terminal when you type it in, so type carefully (you can use **Backspace** if you make a mistake) and press **Enter** when you're done. If you were successful, you should see a welcome message and your shell prompt, like:

```
jpduncan@dorothy:~$
```

To get your bearings, you can type `pwd` to see where your home directory is located on the SCF cluster filesystem:

```
jpduncan@dorothy:~$ pwd
/accounts/grad/jpduncan
```

Your home directory is likely also in the `/accounts/grad/` directory, as mine is.

## Other login nodes

### ! Important

Don't run computationally intensive tasks on the login nodes!  
They are shared by all the SCF users, and should only be used for non-intensive interactive work such as job submission and monitoring, basic compilation, managing your disk space, and transferring data to/from the server.

If for some reason `dorothy` is not working for you, the SCF has a number of nodes which can be accessed from your local machine with commands of the form `ssh <scf-username>@<hostname>.berkeley.edu`. Currently, these are:

- aragorn
- arwen
- dorothy
- gandalf
- gollum
- hermione
- quidditch
- radagast
- shelob

## Disk space

Your home directory has a limited amount of disk space; you can check how much you have used and available using the `quota` command, which will show your home directory usage and quota on the line for the `accounts` filesystem.

```
jpduncan@dorothy:~$ quota
FILESYSTEM  USE          QUOTA          %
accounts    5.29 G       20 G           26.5
```

The `accounts` filesystem is accessible from all the nodes on the SCF cluster. This means that regardless of which login or compute node you use, you will have access to the files in your home directory. Moreover, your home directory is backed up regularly, so you are protected from accidental data loss.

If you're running out of space, you should try to selectively delete large files that you no longer need. See [here](#) for some tips on finding large files. If all else fails, you can request additional space or request access the `/scratch` filesystem. The latter is a good place for large datasets, but note that `/scratch` is not backed up, unlike your home directory. See the previous link for more info.

For temporary files (e.g., intermediate results of a computation that you don't need to store for later), every machine has a `/tmp` filesystem. However, `/tmp` is *always linked to the specific machine* you are on, meaning that if you put something in `/tmp` on `dorothy` and then later go to `aragorn`, you won't find your files in the `/tmp` directory there. If you go back to `dorothy`, you will likely find them again, but `/tmp` is automatically wiped when a machine reboots, so only use it for files you don't care about preserving!

## Data transfer: SCP / SFTP

We can use the `scp` and `sftp` protocols to transfer files to and from any login node on the SCF cluster. `scp` is a shell program that should be available by default on macOS and Linux, while on Windows you can use [WinSCP](#). WinSCP can also do `sftp` transfers, or you can use [FileZilla](#) on any platform for `sftp`. Both WinSCP and FileZilla have a GUI that allows you to drag and drop files between your local machine and a remote host.

The syntax for `scp` is `scp <from-place> <to-place>`, and you'll typically use `scp` on your local machine. For example, we'll show how to transfer the file `data.csv` (you can find it [here](#)) :

### To SCF while on your local machine

```
# transfer to my home directory without renaming the file
scp data.csv jpduncan@dorothy.berkeley.edu:~/

# transfer to the data/ subdirectory and rename the file
scp data.csv jpduncan@dorothy.berkeley.edu:~/data/new_name.csv

# transfer to the dorothy-specific /tmp/ directory
scp data.csv jpduncan@dorothy.berkeley.edu:/tmp/
```

### From SCF while on your local machine

```
# now <from-place> is a path in my home directory on the SCF
scp jpduncan@dorothy.berkeley.edu:~/data/new_name.csv ~/Desktop/data_scf.csv
```

For more information, see [here](#). In particular, if you have a very large dataset to transfer, [Globus](#) is a better option than either `scp` or `sftp`.

## Running jobs on the SCF

### Tip

For this section, you'll need to have some of [this week's materials](#) in your home directory on the SCF cluster.

To get them, you can (and probably should) clone the course repo to your home directory on the SCF cluster:

```
# first ssh to an SCF login node: ssh <scf-username>@<host-name>.berkeley.edu

cd ~/ # or a subdirectory if you prefer

git clone https://github.com/berkeley-stat243/stat243-fall-2022.git
# or git@github.com:berkeley-stat243/stat243-fall-2022.git if you use SSH with git

# the files you need are here
cd stat243-fall-2022/labs/06/
```

As mentioned before, the SCF cluster uses Slurm to schedule jobs. We'll learn some Slurm commands now.

### Non-interactive jobs: **sbatch**

### Tip

This is the best option when you have a long-running job where no

The first command is **sbatch**. To use **sbatch**, you will first create a bash script (you can do this on the SCF cluster if you know how to use a shell text editor like **nano**, or just do it locally and transfer the file to the SCF via one of the methods discussed before).

In the course repo, you will find an example bash script called **submit.sh**. Here's what it contains:

```
#!/bin/bash

#####
# SBATCH OPTIONS
#####

#SBATCH --job-name=example # job name for queue (optional)
#SBATCH --partition=low    # partition (optional, default=low)
#SBATCH --error=ex.err     # file for stderr (optional)
#SBATCH --output=ex.out    # file for stdout (optional)
```

```
#SBATCH --time=00:01:00    # max runtime of job hours:minutes:seconds
#SBATCH --nodes=1          # use 1 node
#SBATCH --ntasks=1         # use 1 task
#SBATCH --cpus-per-task=1  # use 1 CPU core

#####
# Command(s) to run
#####

./example.sh
```

The `example.sh` script creates a file called `testFile.txt` and appends some output to that file. Note that since `submit.sh` is itself a bash script, you could have just put the contents of `example.sh` directly in `submit.sh`, but it is good practice to keep your computational code separate from your Slurm batch submission scripts.

Now we can submit the job using the Slurm command `sbatch`:

```
sbatch submit.sh
```

Once you run that, your job will be queued. To check it's status, you can use `squeue`:

```
squeue -u jpduncan # use your username, not mine
```

And now you wait. Go get a cup of coffee or get some rest! Then check back later.

## Interactive jobs

### Tip

Interactive jobs are the best option when you need to do many short but computationally intensive tasks which require your hands at the keyboard.

## `srun`

### Tip

This is the best option when you want to work at the Linux command line and don't need a GUI, e.g. when debugging components of larger non-interactive job.

To run an interactive job via Slurm, you can use the `srun` command:

```
# ssh -Y <scf-username>@dorothy.berkeley.edu
```

```
# 10 minute time limit
srun -t 00:10:00 -N 1 -n 1 -c 1 --pty /bin/bash

# uses resources already made available from the previous srun command
srun --pty --x11=first matlab # interactive matlab job
```

Here we used the `-Y` flag to `ssh` to run software with a GUI, such as MATLAB, which allows the GUI to open in our local machine while still running computations on the SCF cluster. For this to work, you'll need X server software on your own machine to manage the graphical windows. For Windows, your options include eXceed or Xming and for Mac, there is XQuartz.

## JupyterHub for RStudio or Jupyter Notebooks



Tip

This is the best option when you want to interact with the RStudio or Jupyter GUI while doing your computations or debugging.

The SCF's [JupyterHub](#) is another resource for interactive computing on the SCF, allowing you to use RStudio or Jupyter on one of the cluster's computing nodes.

## Specifying resources

If you are submitting a job that uses multiple cores or nodes, you may need to carefully specify the resources you need. The key flags for use in your job script are:

- `--nodes` (or `-N`): indicates the number of nodes to use
- `--ntasks-per-node`: indicates the number of tasks (i.e., processes) one wants to run on each node
- `--cpus-per-task` (or `-c`): indicates the number of CPUs to be used for each task

In addition, in some cases it can make sense to use the `--ntasks` (or `-n`) option to indicate the total number of tasks and let the scheduler determine how many nodes and tasks per node are needed. In general `--cpus-per-task` will be 1 except when running threaded code. When setting up parallel R code, you can find out how many cores there are on the node assigned to you with:

```
ncores <- Sys.getenv("SLURM_CPUS_ON_NODE")
```

The `SLURM_CPUS_ON_NODE` environment variable is set by Slurm when the job starts running, and therefore can be accessed within your jobs. In addition to `SLURM_CPUS_ON_NODE` here are some other variables that may be useful: `SLURM_NTASKS`, `SLURM_CPUS_PER_TASK`, `SLURM_NODLIST`, `SLURM_NNODES`.

## Monitoring your jobs

As we saw, the basic command for seeing what is running on the system is `squeue`:



```
squeue # this shows all the queued jobs!
squeue -u SCF_USERNAME # this shows your jobs
```

To see what nodes are available in a given partition, you can use `sinfo`:

```
sinfo -p low
```

Finally, you can cancel a job with `scancel`.

```
# you can find your job ID using `squeue`
scancel YOUR_JOB_ID
```

See the “How to Monitor Jobs” section of the SCF’s documentation on [this page](#) for some more info.

## Exercise

You can either do 1. on your local machine and transfer the file to the SCF cluster, or you can do it remotely. 2 - 4 should be done on the SCF.

1. Create a submission `submitBoot.sh` that will execute the code in `boot.R`. To do this I suggest copying the text from `submitR.sh` and updating a couple lines:
  - Change `job-name` to whatever you want to call this job.
  - Change `rEx.err` and `rEx.out` to `boot.err` and `boot.out`. Note these files can be useful for fixing bugs, particularly when executing shell scripts. These files show errors and output printed to the terminal.
  - Change time to `00:10:00` just in case your code runs longer than one minute.
  - Change the `--cpus-per-task` to 3. This is where you are telling Slurm to execute in parallel on 3 CPUs.
  - Change the last line `R CMD BATCH --no-save boot.R boot.Rout`. The `boot.Rout` file will contain all of code, messages, errors, etc. from the R session.
2. Call `sbatch submitBoot.sh` to execute the R script `boot.R`.
3. Check that the execution worked by examining the `.Rout` file.
4. Time allowing: Update the parallel code to use the `future` package and compare the results.