KEY: $ = command starts here, after the $ sign.

Log into Blue Waters:

Which hostname you use to log in depends on whether you have a Blue Waters project account or a temporary training account.

If you have a project account:

```
$ ssh username@bw.ncsa.illinois.edu
```

If you have a temporary training account:

```
$ ssh username@bwbay.ncsa.illinois.edu
```

Ask for resources:

Ask for an interactive job running on 4 nodes with 32 cores each (for a total of 128 cores), running for a maximum of 1 hour:

```
$ qsub -I -l nodes=4:ppn=32,walltime=01:00:00
```

Copy the GalaxSee code and compile it:

1. Copy the **bw-bccd** directory from Aaron's public web directory on the Shodor server to your account (unless you already did):

   ```
   $ wget http://shodor.org/~aweeden/bw-bccd.tar.gz
   ```

2. Extract the directory:

   ```
   $ tar -xzf bw-bccd.tar.gz
   ```

3. Go to **GalaxSee** directory under the **bw-bccd** directory:

   ```
   $ cd ~/bw-bccd/GalaxSee
   ```

4. Compile the GalaxSee module. Make sure there is no error during compilation:

   ```
   $ make NO_X11=1
   ```

Run GalaxSee:

Where you are sitting in the room will determine which of the following commands you should run.

Row 1: `$ time aprun -n XXX ./GalaxSee.cxx-mpi 10000 500 500 0`

Row 2: `$ time aprun -n XXX ./GalaxSee.cxx-mpi 5000 500 500 0`

Row 3: `$ time aprun -n XXX ./GalaxSee.cxx-mpi 2000 500 500 0`

Row 4: `$ time aprun -n XXX ./GalaxSee.cxx-mpi 1000 500 500 0`

Row 5: `$ time aprun -n XXX ./GalaxSee.cxx-mpi 500 500 500 0`

Everyone in a row will run with a different number of processors (specifically, 2 to the power of your number). So, the first person in the row (left-to-right) will run with -n 2, the second person will run with -n 4, and so on for n=2, 4, 8, 16, 32, 64, 128. Replace the "XXX" above with your number.