

POLAR SCIENCE FOR PLANET EARTH

An Introduction to High Performance Computing 2021

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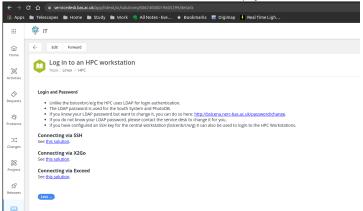


Exercise 1: Login to a BAS HPC Workstation

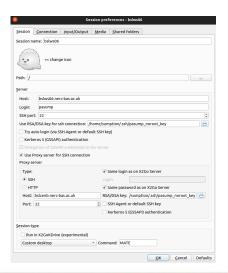
- ► Login to any of the workstations: bslws01...bslws12
- ► Configure X2go (it runs on Mac, Linux and Windows)
- ➤ X2go will also allow us to use a graphical desktop in our later exercises

Exercise 1: X2go solution

Follow the service desk solution to setup your client



Exercise 1: X2go session preferences



- ► Follow the instructions in the solution for your operating system
- Configure a session preference for a workstation
- ► My example uses ssh keys, you can just use passwords

Exercise 1: X2go session launch



- Click on a session and launch it
- You should see a MATE desktop
- **▶** Demonstration
- Troubleshooting

Exercise 2: Simple command line operations

- (a) List your current directory (folder) using Is -al. Use df -h to see the various cluster filesystems, their sizes and their current total usages. You will be on a random login node – use hostname to confirm which one, and w to find out who else is using it. Use Istopo to find out more about the internal structure of the login node.
- (b) Examine your personal filesystem quotas with the command quota.

You should see a 40GB quota on /home, a 1TB block and 1024k file quota on /rds-d2 (which corresponds to $^{\sim}$ /rds/hpc-work).

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Exercise 3: Laptop setup

Before attempting exercise 3:

- ► https://www.hpc.cam.ac.uk/training-courses
- ▶ Download the file **exercises.tgz** to your desktop.
- You will need an sftp client on your laptop to then transfer this file to the cluster.
- ► Mac users open a terminal, you can use sftp from the command line
- ► Windows users download winsftp

Exercise 3: File transfer

► Use SFTP to transfer the file **exercises.tgz** to your Research Computing Service training account directory "/rds/hpc-work.

Hints: The command is **sftp**. Use the same remote host, username and password as in the previous exercise.

Use **cd rds/hpc-work** to change the target directory, then **put exercises.tgz** to transfer the file from your desktop to the target directory on the Research Computing Service cluster. Use **quit** to close the connection.

Optionally, copy the file over again using rsync.

Exercise 3: File transfer (ctd)

► Switch back to the SSH session you created in the previous exercise. Verify that the file is now present by using **Is**.

Hints: Do **Is -al** ~/rds/hpc-work/. Note that you can often reduce typing by pressing **TAB**.

▶ Unpack the tar archive to create an exercise subdirectory.

Hints: Do cd ~/rds/hpc-work/ then tar -zxvf exercises.tgz.

Exercise 5: Modules and Compilers

► Go to the **exercises** directory of your cluster account.

Hints: Firstly you may need to review Exercise 1 in order to reconnect to your cluster account. At the remote command prompt, change to the exercises directory (cd ~/rds/hpc-work/exercises).

➤ Try to compile the **hello.c** program using the default **gcc** compiler (it will fail because there is a deliberate bug).

Hints: gcc hello.c -o hello

Exercise 5: Modules and Compilers

➤ To fix the problem, open the hello.c file in an editor (e.g. gedit, nano, emacs).

Hints: Launch gedit in the background by doing **gedit**. A gedit window should appear. Remove the word **BUG**, save the file and recompile. Do ./hello to run the program.

Exercise 5: Modules and Compilers (ctd)

► The default version of gcc on the RCS HPC clusters is 4.8.5. Compile hello.c again with gcc 5.4.0.

Hints: module av, module load, then gcc hello.c -o hello2

► Launch the Matlab GUI. Note this should work from either the SSH command-line or remote desktop sessions.

Hints: module load matlab then run: matlab&

Quit Matlab and launch it again without the graphical desktop interface. This is the way to launch it inside a batch job.

Hints: matlab -nodisplay -nojvm -nosplash

Exercise 6: Submitting Jobs (Matlab)

- Submit a job which will run matlab on the file.m command file (which contains just the Matlab ver command).
 - Hints:
- Load the matlab module at the place indicated in the file job_script in your exercises directory.
- Set the value of application to "matlab -nodesktop -nosplash -nojvm"
- 3. Set the value of options to "-r file"
- 4. Submit the job with **sbatch job_script**. The jobid is then printed.
- 5. Watch the job in the queue with **squeue**.
- After it has disappeared, open the output file slurm-jobid.out in your editor. It should contain a list of licensed Matlab features from the ver command.

Exercise 7: Submitting Jobs (serial or threaded application)

Submit a job which will run a copy of your hello program on 1 cpu.

#SBATCH -nodes=1 #SBATCH -ntasks=1 application="./hello"

- Submit the job with sbatch job_script. The jobid is then printed.
- 3. Watch the job in the queue with **squeue**.
- After it has disappeared, open the output file slurm-jobid.out in your editor. There should be exactly one "Hello, World!" message.

Exercise 7: Submitting Jobs (serial or threaded application)

- ► Experiment with varying the number of nodes and tasks.
- Note you will need to launch the application with **srun** to actually use more than 1 cpu.

Exercise 8: Submitting Jobs (R)

▶ R jobs may be serial, threaded, or even MPI parallel depending on the packages used. Submit a job which will run the trivial script **hello.r** program on 1 cpu.

```
Hints: 1. Edit the script job_script in your exercises directory. Set:

#SBATCH -nodes=1

#SBATCH -ntasks=1
application="Rscript"
options="hello.r"
```

- Submit the job with sbatch job_script. The jobid is then printed.
- ► Repeat this using a different version of R.

Exercise 9: Array Jobs

► Submit your last job in the form of an array with indices 1-64. Use -H with sbatch to mark the array as held (so that it won't run immediately).

Hints:

- 1. Use sbatch -H --array=1-64 job_script
- Use squeue -u userid to see your array job. Note that -r reports each array element individually.

Exercise 9: Array Jobs

▶ Release array element 1 and allow it to run. Then release the others.

> Hints. 1 Use scontrol release \${SLURM_ARRAY_JOB_ID}_1

- 2. Use **squeue -u userid** again to watch what happens.
- 3. Release the others with scontrol release \${SLURM_ARRAY_JOB_ID} i.e. use the array id to release the entire array.
- 4. When all the jobs complete you should have 64 slurm-\${SLURM_ARRAY_JOB_ID}_N.out files saying hello from various cpus on possibly multiple nodes.