

# An Introduction to HPC — Exercises

Stuart Rankin

`sjr20@cam.ac.uk`

Research Computing Services (<http://www.hpc.cam.ac.uk/>)

University Information Services (<http://www.uis.cam.ac.uk/>)

# Exercise 1: Login

- Log into your RCS training account.

*Hints:* Create a terminal window and use `ssh` to login to your cluster training account.

The remote host is `login.hpc.cam.ac.uk`. The user name is the same name as your MCS Desktop training account (i.e. `z4XY`).

N.B. If in doubt about the name of your training account, check the number of your station (see the label on the top of the box), then station `1XY` should correspond to account `z4XY`.

## Exercise 2: Simple command line operations

- (a) List your current directory (folder) using `ls -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 `lstopo` to find out more about the internal structure of the login node.
- (b) Examine your personal filesystem quotas with the command `quota`.
- (c) Ask the scheduler what compute resources are available to you with `mybalance`. This command may take a little while to return (the units are CPU/GPU/KNL hours).

## Exercise 2: Simple command line operations

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- (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 `~/rds/hpc-work`).

- (c) Ask the scheduler what compute resources are available to you with `mybalance`. This command may take a little while to return (the units are CPU/GPU/KNL hours).

## Exercise 3: File transfer

- ▶ Use SFTP to transfer the file [exercises.tgz](#) to your Research Computing Service training account directory `~/rds/hpc-work`.

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- 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 MCS home directory to the target directory on the Research Computing Service cluster. Use `quit` to close the connection.

Optionally, copy the file over again using `rsync`.

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- ▶ Unpack the tar archive to create an exercise subdirectory.

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

## Exercise 4: Remote desktop

- ▶ Using TurboVNC, connect to the remote desktop running on `login-gfx2.hpc.cam.ac.uk` on display `:99`. The command is `~/bin/turbovncviewer` (note that the `vncviewer` command provides a different version) and the VNC password is *“trAin99”*.

## Exercise 4: Remote desktop

- Using TurboVNC, connect to the remote desktop running on `login-gfx2.hpc.cam.ac.uk` on display `:99`. The command is `~/bin/turbovncviewer` (note that the `vncviewer` command provides a different version) and the VNC password is *“trAin99”*.

*Hints:* Because the RCS clusters only allow SSH connections, to use VNC we need to tunnel via SSH.

Use `localhost:99` as the remote display name.

Use `-via USER@login-gfx2.hpc.cam.ac.uk` to specify the gateway server, with your training account ID as `USER`.

You should be prompted first for your training account password, then for the VNC password which is *“trAin99”*. Note that this is a view-only password.

## Exercise 5: Modules and Compilers

- ▶ Go to the [exercises](#) directory of your cluster account.
- ▶ Try to compile the [hello.c](#) program using the default [gcc](#) compiler (it will fail because there is a deliberate bug).
- ▶ To fix the problem, open the [hello.c](#) file in an editor (e.g. [gedit](#), [nano](#), [emacs](#)).

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*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`).

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- ▶ Go to the `exercises` directory of your cluster account.

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- ▶ 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`

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*Hints:* `gcc hello.c -o hello`

- ▶ 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.
- ▶ Launch the Matlab GUI. Note this should work from either the SSH command-line or remote desktop sessions.
- ▶ Quit Matlab and launch it again without the graphical desktop interface. This is the way to launch it inside a batch job.



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

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*Hints:* module load matlab then run: matlab&

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*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).

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*Hints:*

1. Load the matlab module at the place indicated in the file `job_script` in your exercises directory.
2. 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`.
6. 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.
7. For more demanding work you can increase the available memory by increasing the number of cpus.

## Exercise 7: Submitting jobs (serial or threaded application)

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

Experiment with varying the number of nodes and tasks (you are limited to 4 nodes). Note you will need to launch the application with `srun` to actually use more than 1 cpu.

## Exercise 7: Submitting jobs (serial or threaded application)

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

*Hints:*

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

```
#SBATCH --nodes=1  
#SBATCH --ntasks=1  
application="./hello"
```
2. Submit the job with `sbatch job_script`. The jobid is then printed.
3. Watch the job in the queue with `squeue`.
4. After it has disappeared, open the output file `slurm-jobid.out` in your editor. There should be exactly one "Hello, World!" message.

Experiment with varying the number of nodes and tasks (you are limited to 4 nodes). 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.
- ▶ Repeat this using a different version of R.



## 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"
```

2. 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).
- ▶ Release array element 1 and allow it to run. Then release the others.

## 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`
2. Use `squeue -u userid` to see your array job. Note that `-r` reports each array element individually.

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

## 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`
2. Use `queue -u userid` to see your array job. Note that `-r` reports each array element individually.

- ▶ 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 `queue -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.