



NSCCS/ARCHER CP2K UK Workshop 2014: Instructions for running parallel jobs on ARCHER

1 Introduction

This handout contains basic instructions for how to login in to ARCHER and submit jobs to the batch system. ARCHER is the UK's National HPC Service, and consists of a 72,000 core Cray XC30 system. For more detailed instructions, please refer to the ARCHER website:

http://www.archer.ac.uk/documentation/

2 Connecting to ARCHER via SSH

Each course participant has a numbered guest account (from guest01 to guest50), the same numbering as your NSSCS guest account (msscXX). The password will be given at the start of the practical session. Please ensure you use the correct account for the duration of the course. To log in to ARCHER you should use the following details:

Server: login.archer.ac.uk

Username: guestXX Password: *As provided*

For example, using the OpenSSH client on Linux or Mac run:

ssh guestXX@login.archer.ac.uk

You should see a welcome message, and obtain a command prompt on the ARCHER front-end similar to the following:

login.archer.ac.uk

This is a private computing facility. Access to this system is limited to those who have been granted access by the operating service provider on behalf of the issuing authority and use is restricted to the purposes for which access was granted. All access and usage are governed by the terms and conditions of access agreed to by all registered users and are thus subject to the provisions of the

If you are not authorised to use this account then you must logout immediately.

Computer Misuse Act, 1990 under which unauthorised use is a criminal offence.

For assistance please contact the service helpdesk at: support@archer.ac.uk

```
guest02@eslogin005:~>
```

If you have any difficulty connecting please ask the course staff.

For Windows, we recommend the PuTTY SSH client, which can be downloaded from:

```
http://www.chiark.greenend.org.uk/~sgtatham/putty/
```

3 Running a job

3.1 Filesystems

ARCHER uses the PBS batch processing system to schedule user jobs on the back-end nodes of the system. Please do not run compute-intensive tasks (e.g. CP2K calculations) on the front-end nodes as these are shared by all users of the system.

ARCHER has two main file-systems, /home/ and /work/. Upon login, you will be placed in your home directory on the /home/ file system. This is intended for storage of files, code etc. It is not accessible to the back-end nodes where your jobs will run. /work/ is a large, high-performance parallel file system, connected to the back-end nodes, and you should use this as a location to run your jobs from, store and access job input and output files.

To access your directory on /work/ enter:

```
guest02@eslogin006:~> cd /work/y14/y14/guest02
guest02@eslogin006:/work/y14/y14/guest02>
```

Please note that data stored in the guest accounts will be erased shortly after the course ends. It is your responsibility to make copies of any data you wish to keep in another location before the course ends.

3.2 Batch system

To run a job using the batch system, you must create a batch script containing the commands you wish to execute. An example script is below, please make a copy of it in your own directory:

```
guest02@eslogin006:/work/y14/y14/guest02> cat run.pbs
#!/bin/bash --login

#PBS -N test_job
#PBS -l select=1
#PBS -l walltime=0:5:0
#PBS -A y14

cd $PBS_O_WORKDIR

module load cp2k
aprun -n 24 $CP2K/cp2k.popt --version
```

The #PBS directives give the system information about your job, in this case that the job should be called test_job, that it should use 1 ARCHER node, and will run for up to 5 minutes. All jobs run during the course should use the y14 project account. You may edit these values if you wish to run on more nodes or for longer durations, before submitting the script.

Below this are a list of commands. The cd line ensures that the job runs correctly on the /work/ filesystem. A module is then loaded to give access to the CP2K software, and finally we launch the CP2K MPI executable in parallel using 24 MPI processes. ARCHER has 24 processor cores per node, so when running your jobs make sure that the number of processors (-n 24) is less than 24 times the number of nodes (-l select=1).

guest02@eslogin006:/work/y14/y14/guest02> qsub -q Rxxxxxx run.pbs

Once the script has been created, we submit the job using:

```
230228.sdb
guest02@eslogin006:/work/y14/y14/guest02> qstat -u guest02
sdb:

Req'd Req'd Elap
Job ID Username Queue Jobname SessID NDS TSK Memory Time S Time
```

```
        Job ID
        Username Queue
        Jobname
        SessID NDS TSK Memory Time S Time

        230228.sdb
        guest02 standard test_job
        -- 1 24 -- 00:05 Q --
```

The qsub command submits the script, and returns a unique job ID. The qstat command can be used to monitor the status of the job. Q corresponds to a job which is waiting in the queue, R to a job which is running, and E to a job which is in the process of exiting. Once the job has completed it does not appear in the list.

The -q Rxxxxx argument refers to q unique Reservation ID which has been set up to give exclusive access to a set of 50 nodes for the duration of the course. This should reduce queue waiting times. Please be aware this is shared by all participants so avoid running many jobs at one time, or using many nodes at once. The following reservation ID should be used:

• Thursday 28th August 12.00-18.00: R472734

Note that jobs can still be run without the reservation ID, but will go into the main ARCHER queue along with all other jobs, so will likely queue for (much) longer before running.

The standard output and error files produced by the job will be located in the current directory, and are numbered by the Job ID, alongside any additional files produced by CP2K:

```
guest02@eslogin006:/work/y14/y14/guest02> ls -ltr
total 8
-rw-r--r- 1 guest02 y14  164 Apr 21 10:40 run.pbs
-rw----- 1 guest02 y14  0 Apr 21 10:52 test_job.e230228
-rw----- 1 guest02 y14 1523 Apr 21 10:52 test_job.o230228
```

In this case the standard output contains the version information from the CP2K executable, as specified in the batch script, along with some information about the job. The standard error file is empty:

Congratulations, you have now run a simple CP2K job on ARCHER. Please proceed with the rest of the exercises. You will need to modify your batch script as necessary.

4 Visualisation & Analysis

Some exercises require the use of VMD for visualise the psystem (e.g. Exercise 2: Geometry Optimization). To use VMD on ARCHER you will need to enabled X11 forwarding in your SSH connection. With OpenSSH this is done by adding the -X flag. You will also need to load the vmd module before running VMD:

For plotting data, ARCHER has the following tools installed:

- GNUplot: simply type gnuplot
- XMGrace: first load the xmgrace module then run xmgrace