Introduction to High Performance Computing (HPC) – Session 1

using the "Computational Shared Facility" (CSF)

Research Platforms, Research IT, IT Services

Course materials / Slides available from: https://ri.itservices.manchester.ac.uk/course/rcsf/

CSF online documentation https://ri.itservices.manchester.ac.uk/csf3/

Contact Research Platforms via the Connect Portal https://ri.itservices.manchester.ac.uk/csf3/help/

Course materials at https://ri.itservices.manchester.ac.uk/course/rcsf/

Feedback

- · Your feedback is important to us!
- Please give feedback on this course
 - Quick form at https://goo.gl/forms/zfZyTLw4DDaySnCF3 (choose "Introduction to HPC (Using CSF)")
 - Feedback is important to help us improve our courses
 - Records your attendance on the course

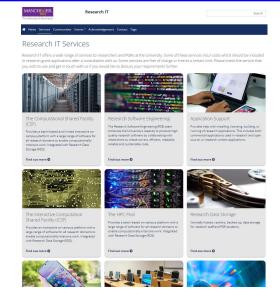
Housekeeping

- Please let me know if you're leaving
 - 10am 12:30pm (practical sessions 1, 2, & 3)
 - Lunch approx 12:30pm 1:30pm
 - 1:30pm 4pm (practical sessions 4 & 5)
- 1-to-1 help is available if needed during exercises.
- Power adapters are available for the purposes of charging laptops, please be considerate of other users and be careful of any trailing leads.
- Got a question at any point? PLEASE ASK!!

Course materials at https://ri.itservices.manchester.ac.uk/course/rcsf/

Who we are - Research IT

https://research-it.manchester.ac.uk/services/



What we'll cover today

- Brief intro to High Performance Computing (HPC) as motivation
- Using the University's HPC system The "Computational Shared Facility" (CSF)
 - What the CSF is and what it can do for you
 - Logging in
 - Running work ("jobs") on the system
 - Different types of jobs (simple to advanced)
 - Using real applications
 - Doing the above in the practical sessions today

Course materials at https://ri.itservices.manchester.ac.uk/course/rcsf/

WHY & WHAT ...

High Performance Computing: why use it & what is it

Who the course is for - everyone

- People new to HPC / research computing, or who just want to try the CSF
 - We'll introduce you to these topics and you'll try it out today
- Maybe your supervisor asked you to get a CSF account
 - We'll teach you how to use it
- Those who have used CSF already, but want to know more
 - Parallel jobs, job arrays, the batch system, ...
- Using the CSF is today's focus, so that you can use it effectively in your work
 - not theoretical aspects of HPC
 - but we'll explain some of the basics to help you make good use of the resources
 - not parallel software development or version control
 - But we'll show you how to run high-end parallel applications
 - not Linux installation / administration
 - · but we'll cover the basic Linux commands needed to use the CSF
 - not the specifics of the software you plan on using
 - ask your PI/supervisor for help with that

Invest a little time now, get results much faster!

https://ri.itservices.manchester.ac.uk/course/rcsf/

Motivation: Why use HPC (and the CSF)?

- Some (most?) research computation not suitable for your desktop/laptop
 - Takes too long to run
 - Needs more memory
 - Uses too much disk/storage space
- Use advanced, centrally-managed, UoM hardware
- Eventually, use regional / national supercomputers

Do not let the size/capacity/power of your computer dictate the size and complexity of the models/simulations/systems/problems you are solving!

What is HPC?

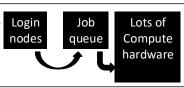
insideHPC.com

- High Performance Computing most generally refers to the practice of aggregating computing power in a way that delivers much higher performance than one could get out of a typical desktop computer or workstation in order to solve large problems in science, engineering, or business.
- HPC systems are usually a cluster of compute nodes (with some extra items such as login *nodes*, storage, networking)
 - The CSF fits this description

A new way of working!







Running on a desktop

- You can fire up a GUI, run an app immediately. BUT:
- Got enough memory, cores, storage?
- Need to keep the PC to yourself (public cluster PC?)
- For several days?!
- Only one "job" (simulation, analysis) at a time?

Logging in to the HPC system

- Submit "jobs" to the queue
- Jobs wait until selected to run
- Jobs run on high-end hardware (lots of cores, memory, disk, GPU)
- Jobs run safely for days
- Many jobs can run at once
- Can log out any time (jobs still run)
- Log in to check on progress, get results

HPC Example: Finite Element Analysis

Perform stress analysis on 3D mesh

- The app splits the *input* into chunks

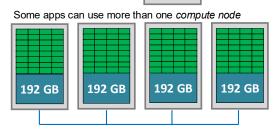
- It performs calculations on chunks, in *parallel*

• Faster and/or larger problem size





Single HPC compute node: 32 cores. 192GB ~2 days to complete



Multiple HPC compute nodes: 128 cores, 768GB RAM ~0.5 days to complete

"HTC" Example: Image Analysis

- High Throughput Computing
 - Not all s/w is "HPC" / parallel
 - But you might have lots of data
 - EG: Each image takes 1hr to process (and are independent -

Over 1 year to complete!! Desktop: 4 cores, 4 copies of software running.



Single HPC compute

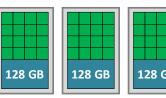
~100 days to complete!

Laptop: 1 copy of software

running on 4-core CPU.

can be processed in any order) 128 GB

node: 16 copies of software running. ~26 days to complete



128 GB 128 GB

Multiple HPC compute nodes: 64 copies of software running independently. ~6 days to complete

Example: 10,000 image scans to be analysed by an image processing application. Each image takes 1 hour to process.

Source: Professor Paul Mummery (MACE) using ParaFEM software http://parafem.org.uk

What we'll be using today - the "CSF"

- Q: who has used the Computational Shared Facility (CSF) before?
- CSF3 current config:
 - A large Linux cluster system
 - 19,544 CPU cores (AMD Genoa, some Intel Xeon CPUs)
 - 156 Nvidia GPUs (24 x v100, 76 x A100, 56 x L40s)
 - Got big datasets to process? Can run large-memory jobs (up to 4TB RAM)
 - (we'll cover all of these details throughout the course)

BUT, you <u>do not</u> need to be running huge parallel jobs, or be a Linux / HPC expert, to use our systems and to benefit from the CSF

CSF: THE BASICS...

Hardware, OS, logging in, security, home filesystem, copying files, Linux, GUIs

Who can use the CSF?

The following info is mainly for people who may want to "buy in" to the CSF. Your PI/supervisor or School may well have already done this! If interested, ask us at the end of the course.

- CSF uses a shared funding model
 - Researchers/academics/schools contribute financially to buy compute hardware
 - All h/w pooled so that all users can access the h/w
 - H/w not associated with individuals so it can always be in use as long as there are jobs to run!
- The time it takes to run all of your jobs depends on the size of the contribution with which you are associated
 - A research group that contributes more will be able to get more jobs done sooner – they have more "throughput"
 - Managed automatically by the batch system you just submit jobs!
- Some limited 'free at the point of use' access for noncontributors

What is the CSF? (more details)

Computational Shared Facility

Two main storage areas visible to *all* nodes. Your input data/files, code (python etc)

and job result files are here.

• A batch compute cluster to run your "jobs" (simulations, analysis,...)

• Here are the main components you'll learn about: 3. 100s of powerful compute nodes run your jobs (~19,000 2. All work ("jobs") is submitted 1. From your PC, cores) to the batch system's job connect to the login Compute nodes Backend compute nodes node. Submit work connected by local ("jobs") from here. network for parallel Manage your files apps & files. here. Login node /scratch GPU compute nodes home No direct access to backend compute nodes. RDS (Isilon)

Research Data Storage,

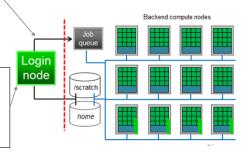
networked into the CSF.

Login Nodes

- We mostly only interact directly with the (three) CSF login nodes
 - Approximately 400 compute nodes
 - Far too many for you to find a free compute node to use
 - Instead: connect to the login node, let the job queue find a node

Key concept!

- Do: Submit work ("jobs") to be run
 - No direct access to compute nodes
 - Submit jobs to the job queue.
 - The system will run your work on available compute nodes meeting your requirements.
- Do not: run applications on the login node
 - Shared by all users, not much memory
 - For lightweight tasks (job submission, file transfer, ...)



Some pictures of the CSF



Compute Nodes

- The CSF is a cluster of powerful "compute nodes"
 - Can think of the compute nodes as very high-end PCs where your simulations / data analysis / ML training ... will run
 - Different types of compute nodes available to suit your requirements (high mem, GPU, or a standard / default node)
 - Multi-core CPUs (e.g., 32, 168 cores)
 - Lots of RAM (e.g., 512GB, ..., 2TB, 4TB!)
 - Network (possibly fast InfiniBand n/w)
 - O/S (Linux)
 - Local disk (for temp files)
 - Maybe a GPU

- Not all nodes have the same hardware.
- You can specify certain requirements for your job – e.g., "I need a node with a GPU."
 "I need extra RAM."



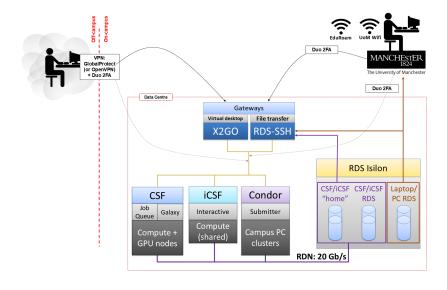
Local network connecting compute nodes. This allows:

- some applications to use more than one node (e.g., for big data / large simulations)
- all nodes to see all of your files so you don't have to copy files to the compute nodes 18

Other Benefits of the CSF

- Over 150 software applications already installed, (and compilers and libraries if writing your own s/w)
 - Abaqus, Ansys, Gromacs, Bowtie2, Gaussian, LAMMPS, MATLAB, OpenFOAM, PyTorch, StarCCM, TensorFlow, VASP + many more
- Backed-up file storage (no more risky USB disks!!!!)
- Leave computational work running for days without needing to be logged in
- 19,000+ cores & 150+ GPUs currently in the system
 - If a compute node fails, we can remove it for maintenance without you noticing. What if your laptop / workstation fails?
- Dedicated support team
 - Connect Portal tickets come directly to us

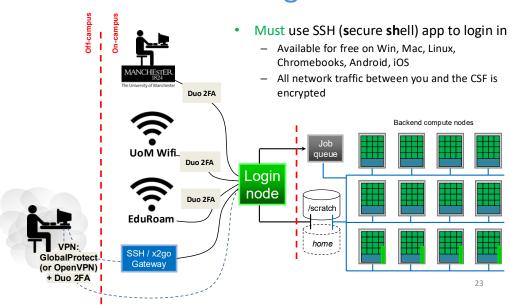
Part of the *Computationally Intensive***Research Ecosystem**



Logging in ...

Let's get access to the system

Where can I log in from?



Security (1)

- The CSF has a private (campus-only) IP address
 - Firewall also controls connections to and from the system
- When you are on-campus
 - Connect from any PC/laptop with a wired connection, or UoM WiFi, or EduRoam WiFi
 - Does not matter if using GlobalProtect or not, but you will always be asked to authenticate using your 2FA (DUO) device (see later)
- When you are off-campus
 - First, sign-in to University GlobalProtect VPN + DUO 2FA
 - Then can login as normal to CSF (won't have to DUO 2FA again)
- Further documentation: https://ri.itservices.manchester.ac.uk/csf3/getting-started/connecting/

Login Overview

- We'll soon do exercise 1 to login to the CSF
 - The exercise sheet provides all of the steps, including app installs
 - There are also reference slides here giving all of the details
- Access the CSF from a PC / laptop using a Secure Shell (SSH) app
 - Sometimes called a "terminal"
 - There's no web-based or other fancy GUI on the CSF use the "command line"
- In summary, on your PC/laptop:
 - Windows users will install a free terminal+ssh app called MobaXterm
 - Mac users will install a free app named XQuartz, then use the built-in Terminal app and ssh command
 - Linux users will use the built-in terminal and ssh command
 - In all cases you will need:
 - Your UoM IT username (like mabcxyz1, NOT your email address!)
 - Your UoM IT password (same as used for email, blackboard etc.)
 - Your DUO 2FA device (most likely your mobile phone.)
 - Everyone will use the address of the CSF:

csf3.itservices.manchester.ac.uk

What you see once you've log in

- The CSF uses Rocky Linux (c.f. Red Hat EL)
 - Command line requires the input of commands,
 can be a little scary at first to new users
 - A welcome Message of the Day announcements
 - The system awaits input/commands from you at a prompt (after you've logged in):

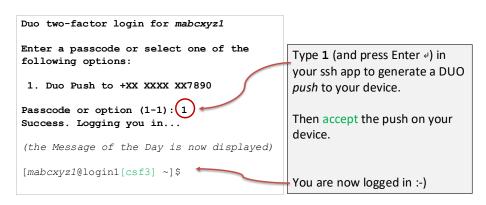
```
[username@login1[csf3] ~]$
[username@login2[csf3] ~]$

[username@login3[csf3] ~]$
```

- Learning Linux commands (more later):
 - https://www.chm.bris.ac.uk/unix/

DUO 2FA (when on-campus)

 Note: When on-campus, after you enter your password during CSF login, all login methods will then ask you to do DUO 2FA:



Security (2)

- It is **NOT** permitted to share your CSF account
- CSF uses your IT password i.e. same as needed to access UoM email, Blackboard and so on ...
 - NEVER share it with ANYONE, including IT staff and your supervisor
 - Forgotten it? You can reset it via the IT Account Manager. Will affect all systems that require it.
 - https://iam.manchester.ac.uk/
- Reminder: Other general safety measures
 - —Install a virus scanner https://www.itservices.manchester.ac.uk/cybersecurity/advice/virusprotection/
 - By aware of phishing emails https://www.itservices.manchester.ac.uk/cybersecurity/advice/phishing/

PRACTICAL SESSION 1

Logging in

Exercise 1 – Logging-in Reference Slides

See also the exercise sheet for necessary steps

Practical Session 1 – Logging in

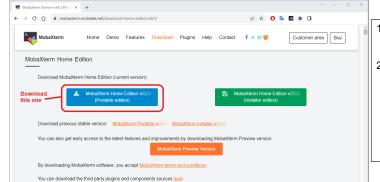
- Exercise 1 sheet (pdf) available at: https://ri.itservices.manchester.ac.uk/course/rcsf/
- See also the reference slides after this one for Windows, Mac and Linux users.
- Tip 1: During login, you'll be asked for your password. Type it carefully!
 - o The cursor will *not* be displayed.
 - You won't see any characters or ***s as you press the keys.
 - But it IS noticing what you type!

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- Tip 2: Once logged in to the CSF, you can run Linux commands "at the prompt".
 - o Many Linux commands do not display anything after you've run them.
 - o This is usually a good sign it often means your command worked.
 - o If you've got something wrong, it will usually tell you via an error message.
 - You can't do any harm. Typos / incorrect commands won't run, but also won't do any damage! Just try again.
- By the end of this exercise, everyone must have successfully logged-in to the CSF!
- PLEASE ASK FOR HELP IF YOU RUN IN TO ANY PROBLEMS WE ARE HERE TO HELP!

Connect to CSF from Windows

- Login node Recatch
- Windows users need to install a free terminal app called MobaXterm
- https://mobaxterm.mobatek.net/download-home-edition.html
 the Home edition (portable edition) does not require Administrator rights just extract the small .zip file in your P-Drive or Downloads or USB stick for example.



- Download using the blue box.
- 2. Once downloaded, right-click on the .zip file and select:

"Extract all ..."

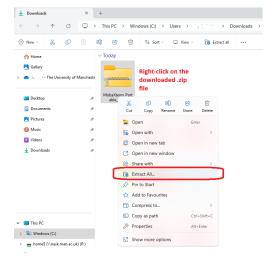
This will *unpack* the .zip file to a folder.

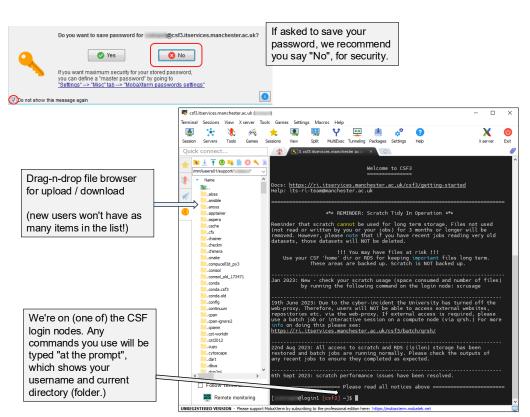
Install the MobaXterm app on your laptop/PC

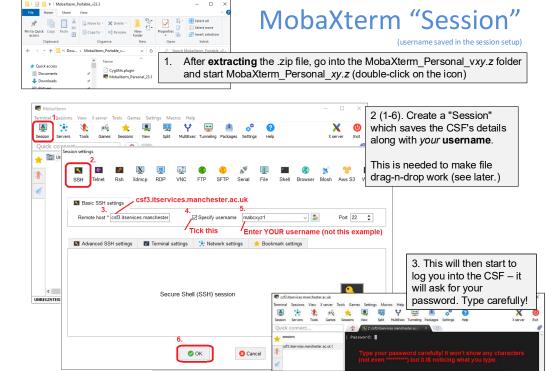
You must right-click on the downloaded .zip file, then "Extract all..."

Simple double-clicking on the .zip file to browse the contents does NOT

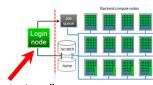
install it correctly.





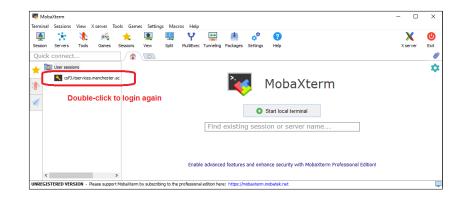


Next time you want to login to CSF from Windows

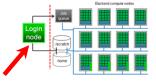


- Just double-click the csf3 "session" in the list of "User sessions"
- The CSF details are saved in the "session"
- (this also makes the file browser work, for drag-n-drop file transfers.)

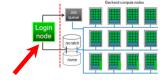
4. See slide about 2FA - you may be asked for DUO after your password



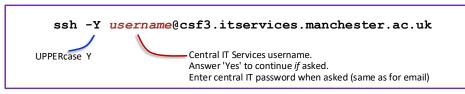
Connect to CSF from a Mac



Connect to CSF from Linux

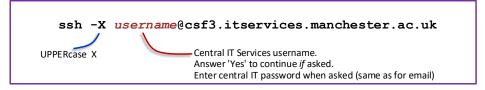


- Mac users have a terminal application by default
 - You will first need to install X-Quartz first
 https://www.xquartz.org/ (install, then you should reboot your Mac)
 - Start a Terminal app (possibly from Go > Utilities > Terminal) and then type the following command:



Finished using CSF? Log out with: logout or exit

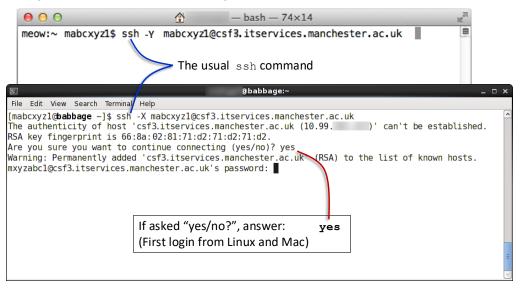
- Linux users have a terminal application available by default
 - Start a Terminal (e.g., MATE terminal) and type the following command:



Finished using CSF? Log out with: logout or exit

Linux / Mac Terminals

• You might be asked a question upon first login, before it asks for your password. It is safe to answer "yes".

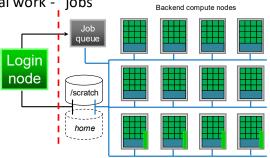


RUNNING JOBS

Doing real work on the CSF

Jobs, Jobscripts and the Batch System

We want to do computational work - "jobs"



- You decide:
 - Which program(s) to run
 - Which resources it needs (#cores, CPU type, memory, GPU?)
 - How much time the job will need to complete its work
 - Which of your folders ("directory") to run the job in
- You'll put these requirements into a *jobscript* file
- Then submit your *jobscript* to the batch system ("Slurm")
- Slurm decides when the job runs and on which compute node(s). It ensures you get all of your requested resources.

• Do *not* run computational work here:

- Not enough cores
 - Not enough memory
 - 100+ users connected, so running work causes serious problems

Reminder: The login nodes

- You *can* do the following:
 - Transfer files on and off the CSF
 - Set up and submit your jobs (covered in next few slides)
 - Basic data processing/viewing
- Computational work running on the login node will be killed without warning!

Creating a Jobscript file (1)

- You need to be able to create a small text file to describe your job
- Run gedit on the CSF login node a simple text editor
 - Creates and saves the file directly on the CSF
 - Is similar to notepad (other Linux editors: xnedit, nano, emacs, vi – only use these last two if you know how to use them.)
- Once logged in to the CSF, run one of these:

aedit & gedit filename & '&' allows you to carry on using the command-line. Try it without to see.

- (start a new file or edit an existing one. Then save it.)

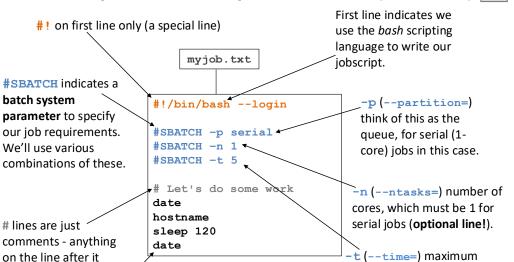
Can I Write Jobscripts on Windows?

- A warning about Windows text files (EG: in *notepad*)
 - There's an inconsistency over the (hidden) end-of-line characters in text files:
 - CR (carriage return \r) + LF (line feed \n) Windows:
 - LF (line feed \n) • Linux/Unix:
 - The extra CR from Windows is a problem in jobscripts.
 - It causes shatch to reject your job immediately.

sbatch: error: Batch script contains DOS line breaks (\r) sbatch: error: instead of expected UNIX line breaks (\n).

- Solutions
 - Use gedit on the CSF login node (writes Linux text files)
 - Or use notepad, upload, then run dos2unix myfile.txt
 - Use dos2unix only on jobscripts will break other files.
 - Do not come to rely on this it is too easy to forget to do it use gedit directly on the CSF!

A simple Jobscript – Serial (1 core)



"wallclock" time the job is

allowed to run for. Various

formats. 5 is 5 minutes. 4-0

would be 4 days (0 hours).

Submit Jobscript to Job Queue

• Submit the jobscript from the login node with:

sbatch jobscript # EG: sbatch myjob.txt

• You will be given a unique *JobID* (currently a 7-digit number). Can use this in other commands.

Submitted batch job 5980521

- You can then:
 - carry on with other work
 - check on your job queue and the jobs
 - submit more jobs, without disturbing previous jobs
 - log out of the CSF and your jobs will still run

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Check status of your jobs

• To see your job(s) in the batch system, run:

Actual Linux commands we

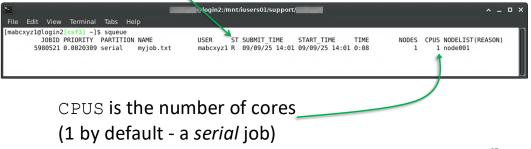
execute on a compute node.

run in our job. They will

squeue

will be ignored.

ST (state) is either pending (PD), running (R) or failed (F). These are the most common states.



Serial (1-core) Job Properties

- Our simple example job:
 - Serial (only 1 core is used)
 - Standard memory (no #SBATCH line asking for more)
 - Our job gets ~5GB RAM to work with
 - The serial partition contains node with Intel CPUs, 5GB/core
 - We said the job would need no more than 5 minutes runtime (max permitted is 7-0 i.e., 7 days)
- Standard serial jobs will be placed on: Intel nodes
 - Other nodes exist for other job types
 - The batch system looks for a free core (in a list of compute nodes in the "serial" partition).
 - That core is assigned to your job, for the requested wallclock time.

Optional Serial Job Resources

https://ri.itservices.manchester.ac.uk/csf3/batch-slurm/serial-jobs

Jobscript flag(s)	Description	
#SBATCH -C haswell	5GB/core Intel "haswell" CPU. Otherwise Slurm chooses.	
#SBATCH -C skylake	6GB/core Intel "skylake" CPU. Otherwise Slurm chooses.	
How to run serial jobs on the AMD 168-core nodes		
#SBATCH -p interactive	8GB/core AMD "Genoa" CPU. Despite the name, can be used for batch jobs. Max permitted wallclock is 1 hour. Adjust your "#SBATCH -t" line. We'll cover interactive jobs later.	

- Max permitted wallclock limit is 7-days runtime limit. You must say how long.
- Our simple jobscript did *not* use any of the above. Not needed in most cases.
- If you limit a job by node-type it may wait longer in the queue.
- You will see that the example jobscripts in the exercises have:

#SBATCH --reservation=course

- Only for use today (we have reserved nodes on a teaching day.)
- Remove if practicing after today (jobs will fail to submit otherwise.)

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Why is my job still waiting?

- Your job will wait until there are resources available (meeting your jobscript's requirements).
- Slurm keeps track of when resources will become free, based on the wallclock specified in all jobs.
 - Jobs are starting and finishing all the time
 - A more realistic wallclock time helps with scheduling
- The queue can be frustrating, but has advantages:
 - You can log off, switch off your laptop and your job will stay on the CSF. Log in later to check on job / collect the results.
 - You can submit many (100s, 1000s) jobs.
 - They might not all run at once Slurm will decide this...
 - But many jobs might run at the same time so more of your work is completed sooner
 - (you may need to use different files/folders for each job).

So where did my results go?

- If squeue returns no output means job has finished!
- Where are my results? Three possibilities:
 - 1. If your app usually prints to screen: output captured to a text file called *slurm-JOBID*.out where
 - JOBID is the number of your job
 - Previous example: slurm-5980521.out
 - 2. Output file(s) specific to your application
 - EG Abaqus: casename.dat, casename.prt,...
 - 3. Your job had a problem or failed: it may be reported in one of the above files check the *slurm-JOBID*.out file.
 - (Technically: "the std error stream is redirected to the file")
- Various ways to view the files (they are plain text):

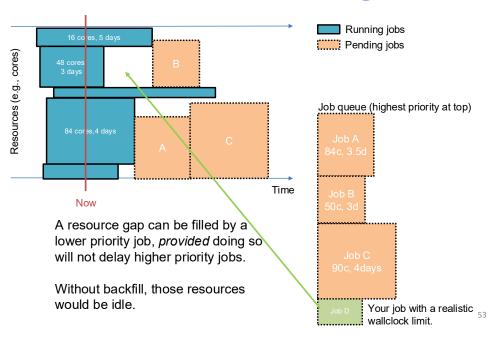
```
cat filename  # EG: cat slurm-5980521.out
less filename (allows you to page through with spacebar)
qedit filename (not recommended if it is large)
```

Why do I now need to specify a Wallclock time?

- If you've used the CSF in the past, you probably just relied on the default 7-day wallclock limit.
- This made it more difficult for the batch system to schedule jobs it had to assume that all jobs would run for the full 7 days.
- We now require that you add a wallclock time to your jobscripts:
 - #SBATCH -t 2-0 2 days (0 hours). 7 days is the max. #SBATCH -t d-hh:mm:ss Various formats accepted
- By specifying an accurate(ish) wallclock, Slurm can better plan when resources will become free.
 - Always err on side of caution too much time is better than not enough time!
 - Slurm will kill a job if still running, once the job's wallclock limit has been reached!
 - You might have to run a few jobs to get a feel for how long they take.
 - Or run the first job with 7-days then check the actual runtime.
- Can't I just request 7-days for all of my jobs (or 4-days for GPU jobs)?
 - Yes, you can. But ...
 - It might be possible to fit a shorter, small job in before larger jobs are able to use the resources.
 - Ultimately, everyone will wait longer

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Backfill Scheduling



Many Users Sharing the CSF

- 100s of users running 1000s of jobs
- Slurm gives each job a priority (number), which depends on
 - Size of research group's / school's CSF contribution
 - Amount of work already put through by that group and by you as an individual (this month)
- The time for your job to start depends on
 - Priority
 - Availability of requested resource (is CSF busy?)
- Jobs submitted after yours may start before yours!
- A few Jobs may never start
 - Slurm tries to spot invalid resource requests in jobscripts
 - Some may still get through then never run
- We try to ensure that if you submit some jobs, some of them will start within **24 hours**.
 - We make a check every morning of the waiting jobs

Checking your jobs and deleting jobs

- The CSF is always very busy!
- However, jobs frequently finish, allowing waiting ones to start

How busy is it?

- To see all the jobs for everyone (put a blackslash at the start)
 \squeue
- Note: all jobs shown as one long list misleading
 - It displays running and waiting jobs
 - Your job is not necessarily stuck behind all others above yours in the squeue output.
 - CSF is split into a few partitions the very big jobs do not compete with the smaller jobs for cores
- Do not try to guess when is a good time to submit your jobs.
 - If you have work ready to go, just **submit** it!
 - If your jobs are not in the queue, the scheduler cannot consider them
 - You will waste time, not gain it, by not submitting

- squeue reports your job as 'F' (failed)
- Or your job has finished but you suspect it failed to complete correctly
 - The slurm-JOBID.out contains errors / incomplete results
 - Ask Slurm for info about your job once it has finished
 seff JOBID Resource usage efficiency and exit code
 sacct -j JOBID LOTS of stats about job (MaxRSS is peak mem used.)
- Most common causes of errors:
 - Job ran out of memory ("OOM" error in slurm-JOBID.out)
 - Missing directory (did you rename the directory before job ran?)
 - Unusual characters or **spaces** in file and directory names
 - No disk space on the filesystem run in the scratch area to avoid this
- Detailed advice:

https://ri.itservices.manchester.ac.uk/csf3/batch-slurm/monitoring/

 To delete a job from the queue (e.g., a failed job, or you just no longer want it – pending or running):

scancel JOBID

PRACTICAL SESSION 2

Serial job

CSF STORAGE (FILESYSTEMS)

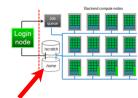
Where to store your files...

Practical Session 2 - Submitting jobs

- Follow the handout 'Practical Session 2'
 - Use sbatch to submit a simple serial job on the CSF
 - Use squeue to look at the queues
 - Use scance1 to kill jobs
 - Use sacct and seff to look at finished jobs
- Exercise sheet (pdf) available at: https://ri.itservices.manchester.ac.uk/course/rcsf/

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Storage – *Home* filesystem



Upon login, automatically placed in your home directory (folder)

/mnt/iusers01/group01/username

- Limited space, quota shared by everyone in the group
- Uses the Research Data Service (networked storage)
 - Large files can be slow-ish to read/write (implications for jobs)
- Which directory (folder) am I currently in?
- How much space am I using? (Linux commands!)

du -sh dirname # Can take a while

How big is that file?

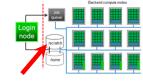
How much space is used/free overall?

df -h . # The . is important!

Storage - *Home* filesystem

- Home is backed up and mirrored to another datacentre
 - Keep important files here (results, jobscripts, source code, ...)
 - Deleted a file by mistake? We can tell you how to retrieve it
- Only you can access your home directory
 - File permissions can be used to give others access
 - Contact us if you want advice on this as they can be complex
- Do not run jobs from your home area (see later)
 - Can generate a lot of files, some of them large
 - Using up all of the shared space will make your colleagues unhappy!
 - Consider compressing large (text) files with gzip

Filesystems - Scratch



- Filesystem local to CSF for:
 - Temporary files can be huge
 - Running jobs from (it is faster!). Recommended!
- Shared by all CSF users, but we have 1.9PB
- Tidy up after each job finishes
- Clean-up policy applies: files that have not been accessed for the past 3 months may be deleted automatically
- Not backed up!
 - Move/copy important results to home area
 - Not considered safe for long term storage hardware failure could cause data loss

Filesystems - Scratch

Using scratch is easy: after log in, change to it:

cd ~/scratch

- Uses a 'symlink' (short cut) in your home dir to /scratch/username

Create a directory (now we're in scratch):

mkdir myjobdir

- Put all files relevant to your job in that directory and run your jobs from there - we'll try this out soon...
- All compute nodes see the same scratch area

Extra Storage Space (Optional)

Some research groups have extra space, example path:

/mnt/eps01-rds/group/username

No shortcut from your home? To access it use:

cd /mnt/eps01-rds/group/username

 To create a shortcut (named data) in your home area:

cd ~
ln -s /mnt/eps01-rds/group/username data

- Also backed up
- Often many TB, but again shared by everyone else from your group
 - Be fair in your usage

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DC Tall 1

File Transfer

- Transfer files to-and-from your home, scratch or additional Research Data Storage (RDS) filesystems, to your local desktop/laptop.
- Transfers will go via one of the 3x CSF3 login nodes.
- Various methods available to transfer data toand-from the CSF3.
 - File Transfer Clients (GUIs)
 - Command- Line Tools
- Covered in next practical (Practical 3)
- https://ri.itservices.manchester.ac.uk/csf3/filesy stems/file-transfer/

File Transfer Clients (GUIs)

- Offer a user-friendly intuitive graphical interface for browsing and transferring files.
- Easier to explore remote directories and allow users to drag-and-drop files.
- Provides visual progress indicators and error messages.
- Clients typically use SSH in the background in order to transfer files securely
- Various clients available
 - MobaXterm (Windows)
 - WinSCP (Windows)
 - o FileZilla (Windows, macOS, Linux)
 - CyberDuck (macOS)

File Transfer Command-Line Tools

- Fast and lightweight, ideal for large or automated transfers.
- Easily scriptable for batch operations or scheduled jobs.
- Uses secure protocols like SSH for encrypted transfers.
- Cross-platform: Works on Linux, macOS, and Windows (via terminals like MobaXterm, PuTTY).
- Examples include scp & rsync

scp myfile.txt username@csf3.itservices.manchester.ac.uk:

rsync -avz myfile.txt username@csf3.itservices.manchester.ac.uk:

 https://ri.itservices.manchester.ac.uk/csf3/filesystems/filetransfer/linux-mac/

Additional filesystem/file transfer info

- We have additional info about how to manage your files and your disk usage:
 - https://ri.itservices.manchester.ac.uk/userdocs/file-management/
- Docs about file transfer: https://ri.itservices.manchester.ac.uk/userdocs/file-transfer/
- If you need to transfer a lot of files or big files to and from the CSF please do not do it on the login node
 - Ask for an account on the RDS-SSH service
- Many file management tasks can be included in your batch jobs – see the FAQ.

Basic Linux File Commands

A good Linux tutorial is available at: https://www.chm.bris.ac.uk/unix/

- Country and -		
Command	Description	
less file1 zless file2.gz	Display the content of file1 (text file) a page at a time on screen. If you've compressed file2 with gzip, no need to uncompress first. Press space to page down through a long file Press return to scroll down a line at a time Press b to scroll back up a page Press G to go to end of file Press q to quit/exit	
cat file1 zcat file2.gz	Dump entire file to screen (a quick way to look at text files). If you've compress file2 with gzip, no need to uncompress first.	
gedit file1	Edit file1 using a simple graphical text editor (similar to notepad on Windows). See later for more on opening graphical programs on the CSF so that they display a window on your computer.	
file filenameA	Try to tell us what type of data is in filenameA. Useful to determine the output of some program where you are not sure what type of output it has generated. For example: file output.dat Might be ASCII text (so we can look at it with less or gedit) or might be data (you'll need some other program to read it)	
du -sh .	How much disk space is current directory (all files and subdirs) using?	
df -h .	How much free space is there in the current area? 69	

Basic Linux File Commands

A good Linux tutorial is available at: https://www.chm.bris.ac.uk/unix/

- Book Ellian tatoria is a tallació a ti		
Command	Description	
<pre>cd dir1 cd ~/dir1/dir2 cd cd</pre>	Change directory (go in to dir1 which is located in the current dir) Go in to dir2 in dir1 in home (~ is shorthand for home) Go up to parent directory (e.g., from ~/dir1/dir2 to ~/dir1) Go back to home (useful if you become lost)	
pwd	Lost? Print Working Directory (display current location)	
ls -lh ls -lh file1 dirA ls -lh dirA/*.dat	List content (names of files and directories) of current directory List in long form (dates, file sizes, names) current directory List in long form (dates, file sizes, names) specified files, directories List in long form all files ending in .dat in directory dirA	
mkdir dirA	Make directory named dirA (in the current directory)	
cp fileA fileB	Copy (duplicate) a file (copy fileA to a new file fileB)	
<pre>mv fileC fileD mv fileE dirA mv fileF dirA/fileG</pre>	Rename a file (from fileC to fileD). Works for directories too. Move fileE in to sub-directory dirA (dirA must exist) Move fileF AND rename it all in one go (dirA must exist)	
rm fileH	Delete (remove) a file (caution!!)	
rm -rf dir1	Delete directory and all files (and other sub-dirs) in there (caution!!!!!)	
gzip bigfile gunzip bigfile.gz	Compress a file (becomes $bigfile.gz$) to make better use of disk-space. Text files usually compress well. Uncompress previously compressed file (becomes $bigfile$). $_{70}$	

Practical Session 3 – File Transfer

- Follow the hand-out 'Practical Session 3'
 - Transfer a file: from the CSF to your PC
 - Transfer a file: from your PC to the CSF
 - Windows: use MobaXterm, Mac/Linux: use "scp"
 - Or, if time permits, Windows users can try option 2 https://winscp.net/eng/download.php
- This is not a 'real' world example, but:
 - You may need to generate files on your PC for processing on the CSF (e.g. an "abaqus" input file)
 - Your supervisor may give you files that you then need to transfer to CSF
- Exercise sheet (pdf) available at: https://ri.itservices.manchester.ac.uk/course/rcsf/

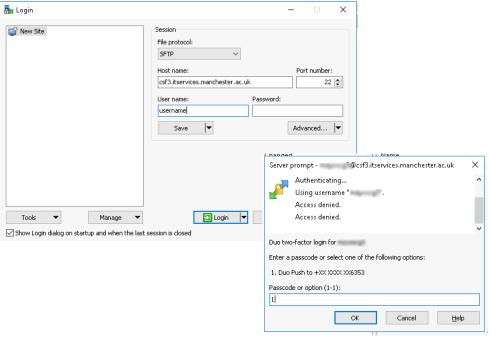
PRACTICAL SESSION 3

File Transfer

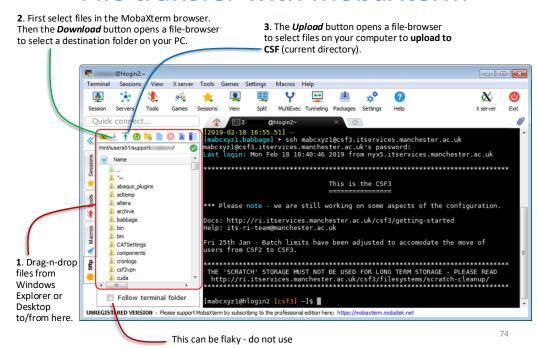
Exercise 3 – File Transfer Reference Slides

See also the exercise sheet for necessary steps

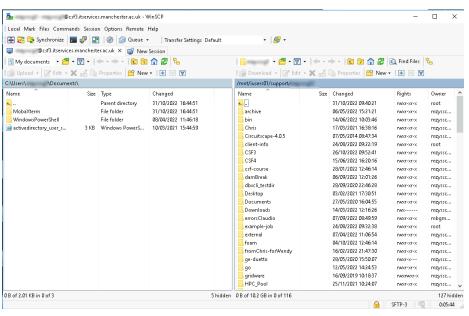
File transfer with WinSCP



File transfer with MobaXterm



File transfer with WinSCP



home file transfer with Linux / Mac

(can also type in a local MobaXterm window)

• Transfer a file from your computer to your CSF home dir

Exercise: Create a file on your PC named myfile.txt containing some text then transfer it to the CSF.

Destination directory on the CSF

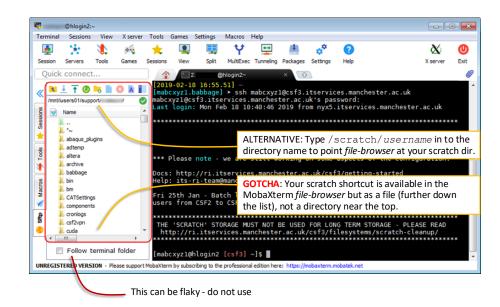
is shorthand meaning "your home directory"

If no destination after the: then uses "your home directory"

Transfer a file from your CSF home dir to your computer

Change directory & filenames...

Accessing scratch with MobaXterm



scratch file transfer with Linux / Mac

(can also type in a local MobaXterm window)

- Very similar to commands used earlier for our *home* directory
- Transfer a file from your computer to your CSF scratch dir

scp file2.txt username@csf3.itservices.manchester.ac.uk:~/scratch/

We give a destination after
the: meaning "use my scratch shortcut"
Omit the destination to transfer to home dir

• Transfer a file from your CSF scratch to your computer

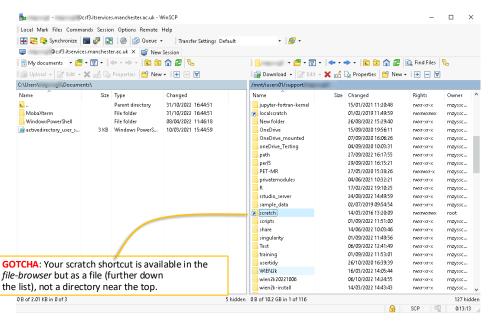
scp username@csf3.itservices.manchester.ac.uk:scratch/results2.out results2.copy

Now you get a copy with a different name on your computer.

Use . to keep the same name (results2.out)

• Change directory & filenames as required...

Accessing scratch with WinSCP



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Need more help with the CSF?

 Extensive documentation about all aspects of the service:

https://ri.itservices.manchester.ac.uk/csf3/

 Contact the Research Infrastructure Team via your Connect Portal

https://ri.itservices.manchester.ac.uk/csf3/help/

- See you:
 - After lunch (in-person courses)

Thank you!