Introduction to COSMA

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High performance computing

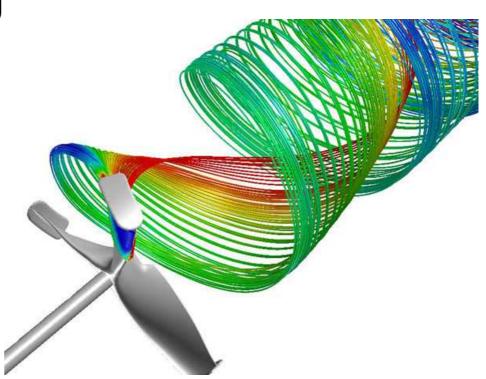
- What is HPC?
 - Use of parallel processing to run large applications
 - Typically applied to systems >10 TFLOPS
 - Aggregated computing power
 - More than can be obtained from a desktop
 - Used for solving large problems
- Cloud computing is not usually HPC
 - Typically only a single computer in the cloud is used

The TOP500

- Prestigious list of the World's most powerful supercomputers, released 6-monthly
 - Includes some DiRAC sites
- Also:
 - Green TOP500
 - Best performance/Watt
 - I/O TOP 500
 - Best I/O

HPC use cases

- Galaxy simulation
- Weather simulation
- Artificial intelligence
- Fluid dynamics modelling
- etc



DiRAC

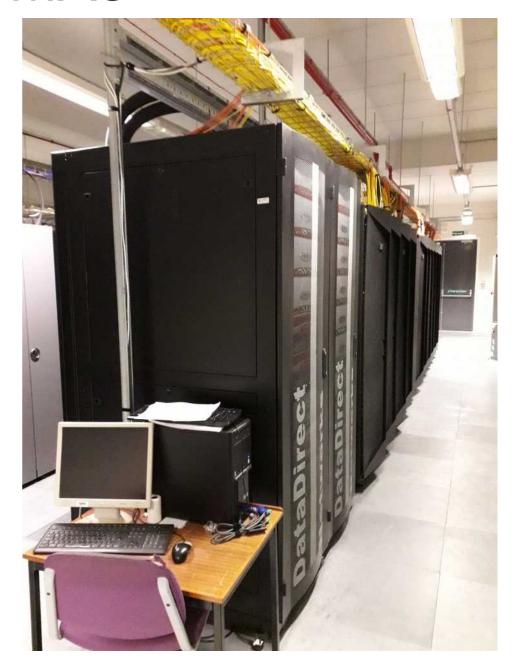
- A tier 1 HPC facility for the STFC community
 - Astronomy, cosmology and particle physics
- 4 DiRAC sites:
 - Cambridge
 - · GPU and Xeon Phi systems
 - Leicester
 - Durham
 - Memory intensive system lots of memory per core
 - (note, since memory is expensive, COSMA typically has lower total compute power than other sites, but can perform simulations not possible elsewhere)
 - Edinburgh
 - Extreme scaling system maximum compute power
- DiRAC 2 (At Durham = COSMA5) in 2012
- DiRAC 2.5 (At Durham = COSMA7) in 2018
- DiRAC 3 expected in 2020 or 2021

The COSmology MAchine

- The Durham DiRAC node
 - Now in its 7th generation
 - COSMA5, 6 and 7 available for use

COSMA5

- A Durham-only facility
 - Including collaborators
 - Was a DiRAC facility until 2018
 - If you are part of a DiRAC project, please try to use COSMA6/7
- Arrived in 2012
- ~300 nodes
 - 16 cores per node (2 CPUs)
 - 128GB RAM per node
 - Diskless
- 3x login nodes: cosma-a, -b and -c



COSMA6

- A DiRAC facility
- Arrived in 2016
 - Second-hand, originally at STFC Hartree
- Approx 575 nodes
 - Identical to COSMA6 nodes
 - But also with disks
 - 9200 compute cores



COSMA7

- A DiRAC facility
- Arrived in 2018
- Currently 147 nodes, to be 300 nodes by end October
 - ~400 nodes by March
 - Each 2x 14 core Xeon CPUs (circa 2018)
 - 768GB RAM (28GB/core)
- Also, mad01:
 - 3TB RAM
- mad02:
 - 0.75TB RAM, 4x CPUs,
 - 28 cores each (112 cores)



DiRAC3: COSMA8

- £8M due in 2020-2021
- Likely to be conventional CPU architecture
 - (not GPU/FPGA)
- May include ARM or AMD processors
- Will again be memory intensive

COSMA summary

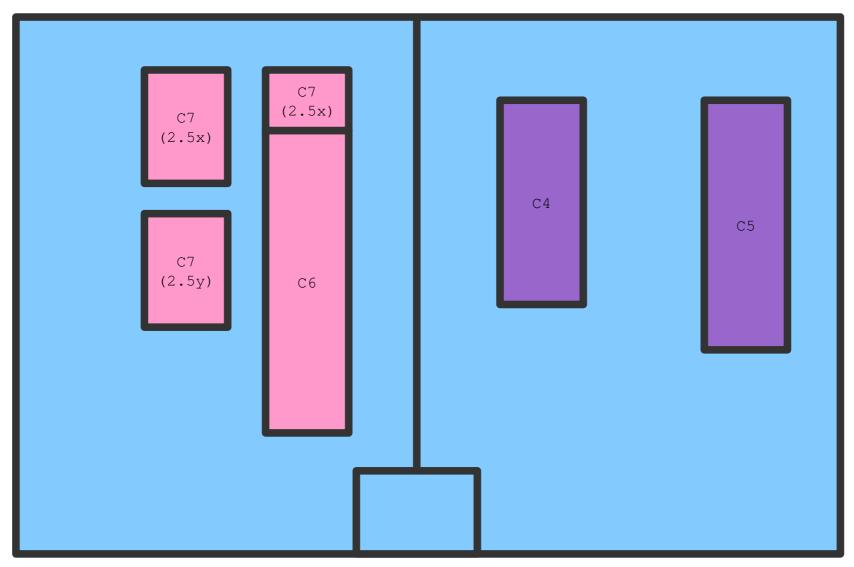
	COSMA5	COSMA6	COSMA7
Nodes	300	575	400 (in 2019)
Cores/node	16	16	28
Cores	4800	9200	11200
Memory/node (GB)	128	128	768 (may become 512 in 2019)
Memory/core (GB)	8	8	28
Total memory	38TB	74TB	230TB
Login nodes	2 (currently 3)	1 (currently 0)	2
Operating system	CentOS 7.4	CentOS 7.4	CentOS 7.4

COSMA networks

- Mostly, you don't need to know this:
 - COSMA uses Infiniband for inter-node communication (MPI) and file system access
 - FDR10 for COSMA5/6 (40Gb/s)
 - EDR for COSMA7 (100Gb/s)
 - 2:1 blocking ratio
 - All nodes also connected by 1G Ethernet for communication/control/homespace

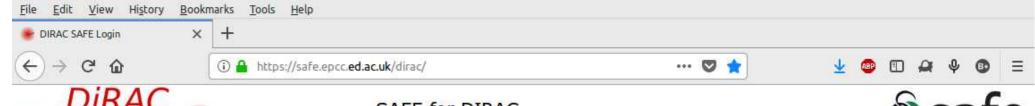
Arthur Holmes Data Centre

Location of COSMA



Accessing COSMA

- First, you need a SAFE account
 - (Service Administration From EPCC)
 - (Used for all DiRAC facilities)
 - See https://www.dur.ac.uk/icc/cosma/support/account
 - In summary:
 - https://safe.epcc.ed.ac.uk/dirac/
 - Create an account (durham email, not personal email)
 - Upload an ssh key
 - Select your project
 - e.g. hpcicc or dp004 (ask your supervisor)
 - Select COSMA (not COSMOS)
 - Wait...

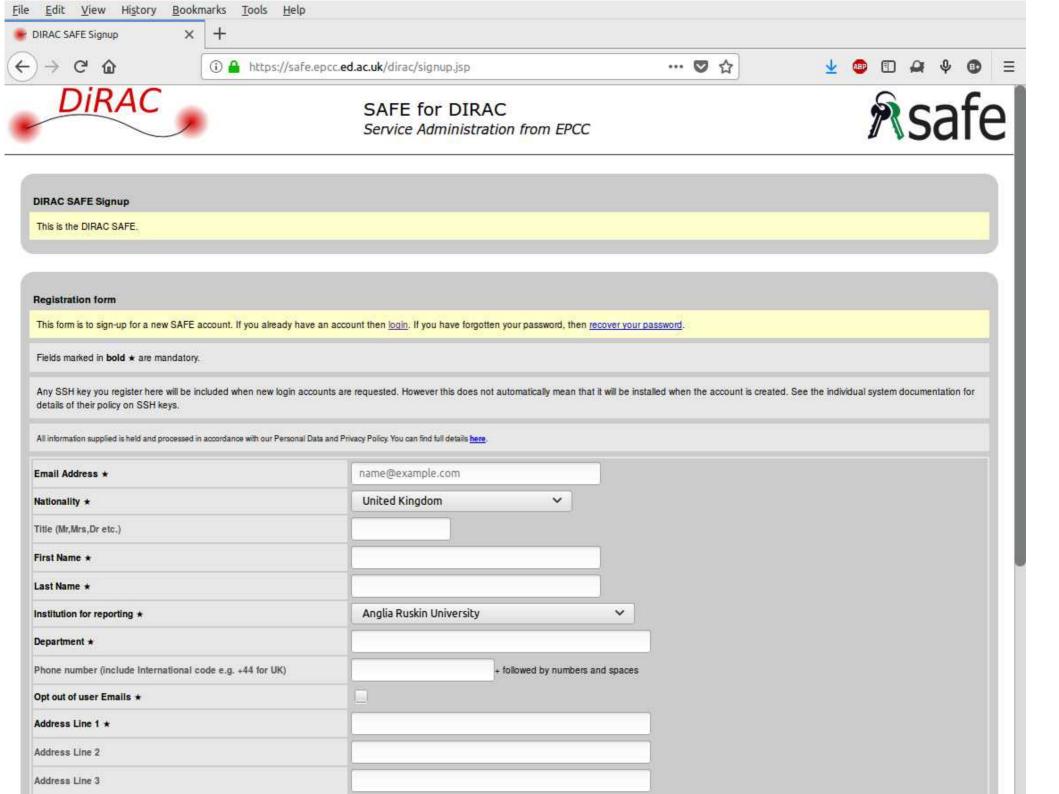


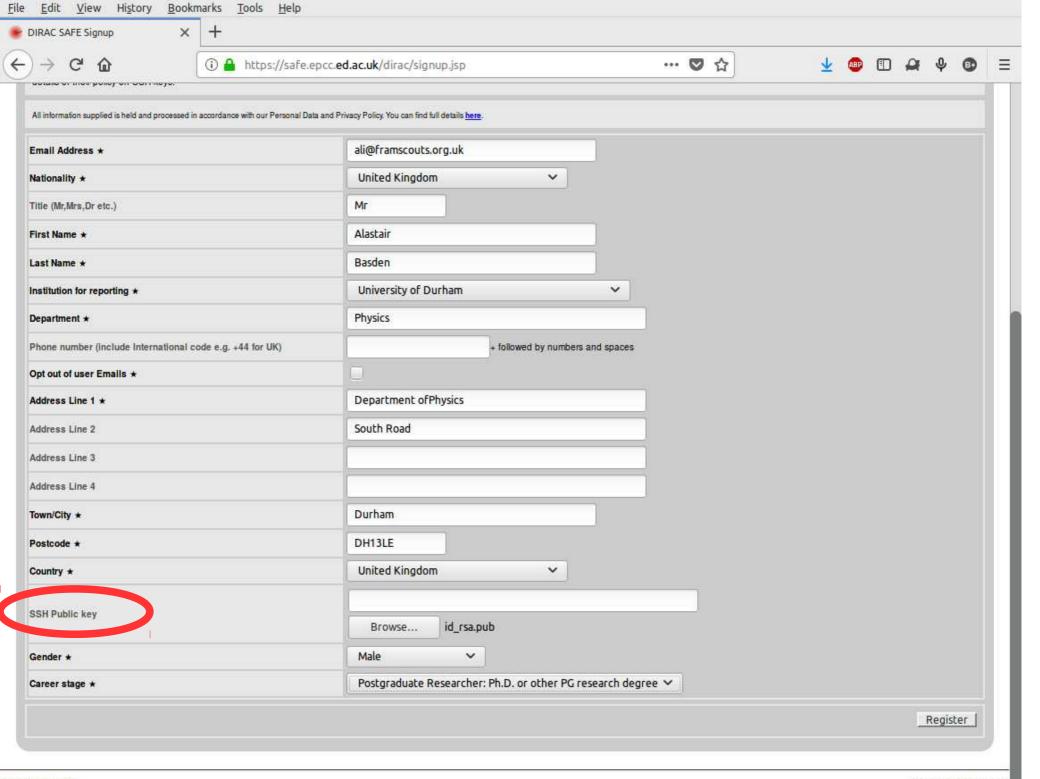


SAFE for DIRAC Service Administration from EPCC

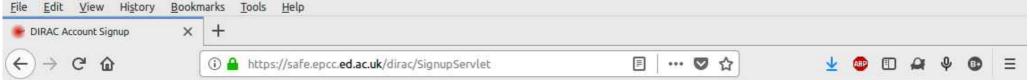


elcome to the <u>DIRAC</u> SAFE. Through the SAFE, you can ap	ply for an account on our high-performance computing system	ns, and perform other administrative tasks relating to your use of our machines.
ogin using UKAMF or		
nail or Dirac-global-id or Wiki name: *		
ssword *		Login Forgot password?





DIRAC SAFE quide





SAFE for DIRAC Service Administration from EPCC



User Access Agreement

Please read our acceptable use policy.

Before accepting the Terms and Conditions, please note: you can change any of the details you have input by clicking your browser's BACK button and then editing them. You can also change them later by returning to this website. No specific copy of these Terms and Conditions will be filled under your name, but you can look at them at any time by going to

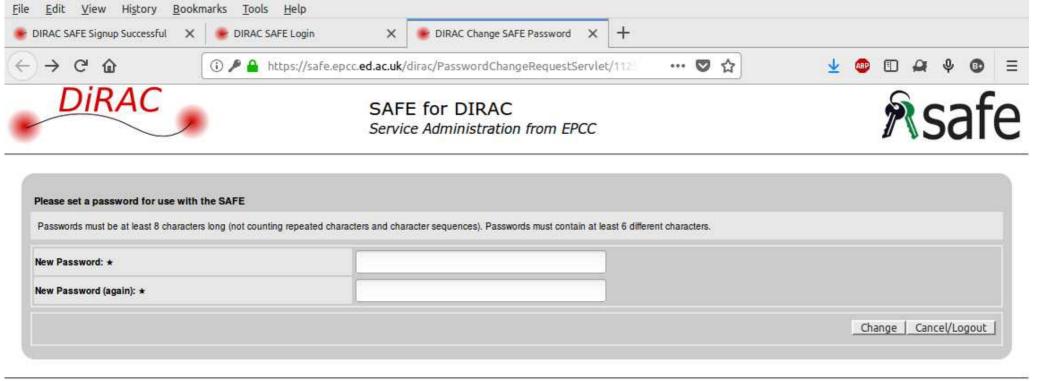
https://safe.epcc.ed.ac.uk/dirac/safe_acceptable_use.jsp.

These Terms and Conditions are offered only in English.

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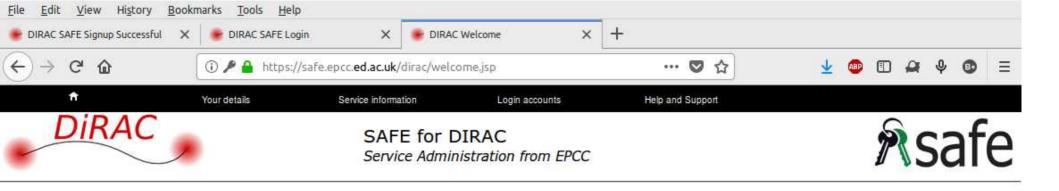
I accept the Terms and Conditions of Access

<u>DIRAC SAFE guide</u>



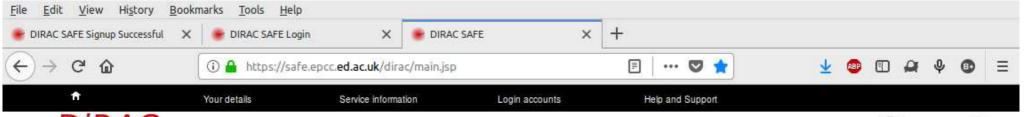
DIRAC SAFE guide SAFE is an EPCC product

After email arrives, click the link to get here...





DIRAC SAFE guide SAFE is an EPCC product





SAFE for DIRAC Service Administration from EPCC



SAFE for DIRAC

This is the DIRAC SAFE.It is a web-site used to administer the DIRAC HPC service.

You are currently recorded as a new user of the SAFE and will see a restricted view of the available information until you have been accepted into a project. To join a project you should apply for a login account on the HPC service using this link or via the Login accounts menu. You will need to select the project you are applying for. Once your login account has been approved the login account will be created.

All of the functions of the SAFE are available from the menus at the top of the page.

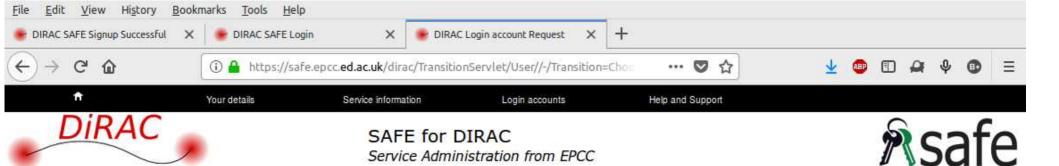
Use the Your details menu to view and update the information we hold about you or to change the settings of your SAFE account.

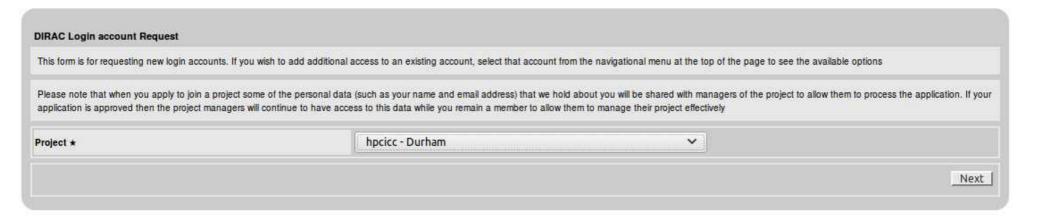
Use the Service Information menu to view information about the service or to generate reports from our database.

Use the Login Accounts menu to apply for an account on DIRAC machines. All accounts need to be part of a funded project so this request will need to be approved by a manager of the project you select before the account can be created. If you already have an account you can also use this menu to view the status of, and make changes to, your accounts.

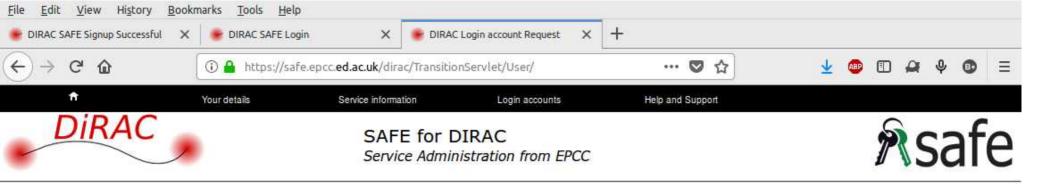
If a menu is coloured orange it indicates a pending request that needs your attention.

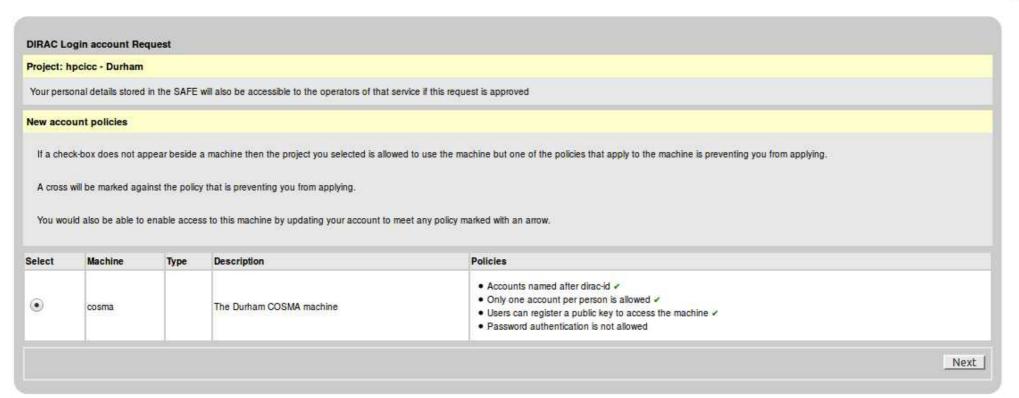
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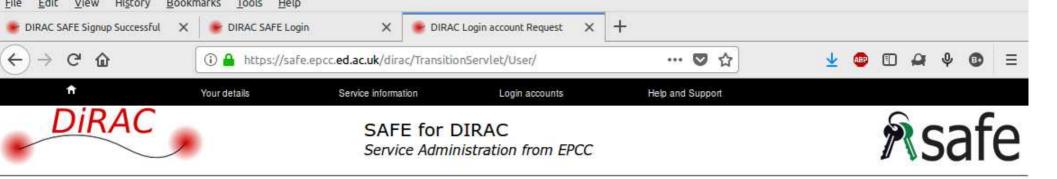


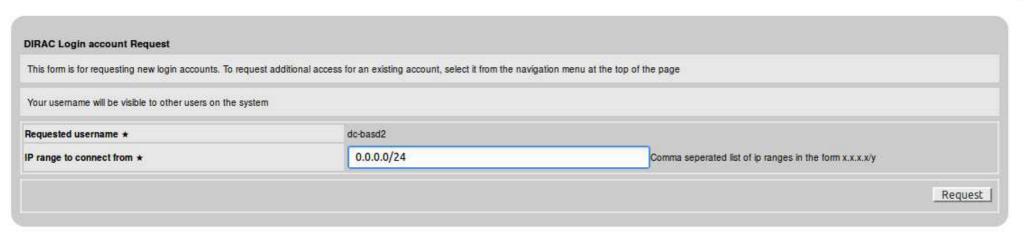
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Then wait...

- While the account is first authorised
- And then created
- Finally, you will receive an email!

Accessing COSMA...

- Login nodes
 - This is where you do your work!
 - Prepare scripts
 - Edit code
 - Compile code
 - Inspect results
 - A shared facility
 - Usually with extra RAM
 - Via ssh:
 - ssh USERNAME@login.cosma.dur.ac.uk
 - ssh USERNAME@login7.cosma.dur.ac.uk



ssh on COSMA

- Authentication requires an SSH key:
 - A key has 2 parts
 - Private part (keep this very safe!)
 - A public part (give this to COSMA or anything else)
 - Uses "public key cryptography"
 - When you try to connect:
 - COSMA will use the public key to generate a "challenge" an encrypted message
 - Only the private key can decode this
 - Your computer then sends the correct response to COSMA
 - Access is then granted

Generating an ssh key

- ssh-keygen -t rsa -b 4096
 - This will ask for a passphrase
 - Please use one this protects your private key
 - This will create:
 - id_rsa (private key keep this safe)
 - id_rsa.pub (public key upload this to SAFE)
 - We will then append your id_rsa.pub key to the .ssh/authorized_keys file in COSMA
 - You can use the same public key on any other servers that you use
 - e.g. mira.dur.ac.uk, hamilton.dur.ac.uk, your desktop, etc.

ssh key example

Could have different files for different keys

```
cosma7:~$ ssh-keygen -t rsa -b 4096
Generating public/private rsa key pair.
Enter file in which to save the key (/home/user/.ssh/id_rsa):
Created directory '/home/user/.ssh'.
Enter passphrase (empty for no passphrase):
Enter same passphrase again:
Your identification has been saved in /home/user/.ssh/id rsa.
Your public key has been saved in /home/user/.ssh/id rsa.pub.
The key fingerprint is:
SHA256:T4Ey6lfKrcFB/fjELAuV7THm/MAAis1xdY5IKLnWhFE user@computer
The key's randomart image is:
+---[RSA 4096]----+
   =E.+..
  ++0= + B
  .=+ = B B
  0.0+%+
 . . o S %
   . o * B o
    . * 0 0 .
    . 0
+----[SHA256]----+
```

A passphrase (password) was entered here

Upload this file to SAFE

After login...

- Your terminal will now be redirected to COSMA
 - Anything you type will be interpreted by COSMA (not your PC)
 - Use common Unix commands
 - e.g. ls, pwd, mkdir, cp, etc
 - Start text editors
 - e.g. vi, emacs etc
- If you want to access COSMA from other computers, upload the public key to SAFE

Some useful commands

- id
 - Gives you User ID, and the groups you are in
- finger USERNAME
 - Information about a user
- whoami
 - Your USERNAME
- w and who
 - see who else is logged on at the moment
- top and htop
 - see who is hogging resources!
- And don't forget tab-completion

X-forwarding

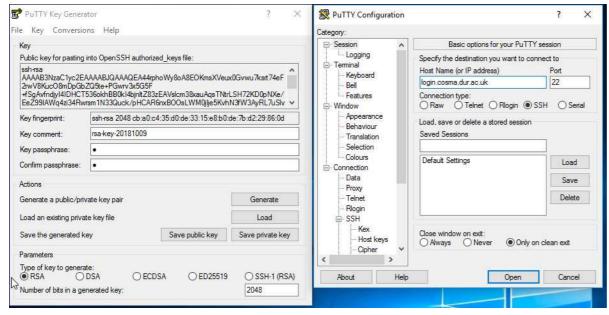
- If you want graphical access:
 - ssh -X USER@login.cosma.dur.ac.uk
 - (or -Y if that doesn't work well less secure)
- You can then start remote programs which will display windows locally, e.g.
 - text editors
 - plots of your data
 - movies etc are not recommended unless you have an excellent connection
- Note: X-forwarding is bandwidth heavy
 - Requires a good network connection to be useable
 - You might struggle from home if on a 1MBit connection
 - To edit files over a poor connection, use a terminal based editor
 - vi, emacs -nw, nano

COSMA passwords

- Are only used to authenticate with the cosma website
 - (to access usage statistics, etc)

ssh from other platforms

- On Windows, use e.g. putty
 - You will need to run puttygen first to create the ssh key pair
- On Android, use e.g. JuiceSSH
 - You will need to generate an ssh key pair (using the app)



```
11:15 🗐 98% 🗎 11:15
ast login: Tue Oct 9 10:19:27 2018 from host-92-14-183-32.as43234.net
dc-basd1@cosma-m [cosma7] ~]$ ls
                            test15113.txt
                            test15578.txt
atempo.lic
subSerial.bsub
                            test18216.txt
 subSerial.bsub~
                            tes t20165. txt
 ead letter
                            test22149.txt
 esktop
                            tes t29386, txt
                            test31771, txt
 ownloads
                            test5379.txt
 etHomeDirs.py
                            test5436.txt
                            test5504.txt
                            test5959.txt
                            test7637.txt
                            test8431.txt
installer properties
                            test8822 txt
makeLargeFiles.py
                            test.out
                            testScript.py
makeLargeFiles.py~
                            testScript.py~
 odule.txt
                            tmp2.txt
 arallel_tasks
                            tmp3.txt
                            tmp3.txt~
                            tmp4.txt
                            tmp5.txt
 oot@console51
                            tmp5.txt~
 sync-3.1.0
 sync-3.1.0.patch
                            tmnTest txt
                            tmp.txt
 syncData.py
                            tmp.txt-
syncData.py~
                            userdirs.txt
                            users.txt
                            users txt~
                            valgrind-3.13.0.tar.bz2
Videos
test11062 txt
test12984.txt
[dc-basd1@cosma-m [cosma7] ~1$ |
                                       6
         W
                                                            0
              S
                                   g
                                                                 (X)
              Z
                                          b
                                                                4
            63
   1@#
                              English (UK)
```

Typical workflow

- Log in to a login node
- Edit files and scripts
 - If you have a particular editor that isn't available, or are on a slow connection and want a graphical editor:
 - consider using sshfs to mount your COSMA file system:
 - cd && mkdir mnt
 - sshfs USER@login.cosma.dur.ac.uk:/cosma/home/PROJECT/USER ~/mnt
 - "ls mnt/" locally will then show your COSMA homespace files
 - Useful options for sshfs include -o reconnect, ServerAliveInterval=15, ServerAliveCountMax=3
- Submit jobs to the batch queue (see later)
- Monitor jobs if necessary
- If you need to access an internal webpage on COSMA, either start firefox over X (slow), or forward the ssh connection from your desktop:
 - ssh -D 1234 USER@cosma-m.cosma.dur.ac.uk
 - chromium-browser -proxy-server="socks5://localhost:1234" https://webpage.on.cosma

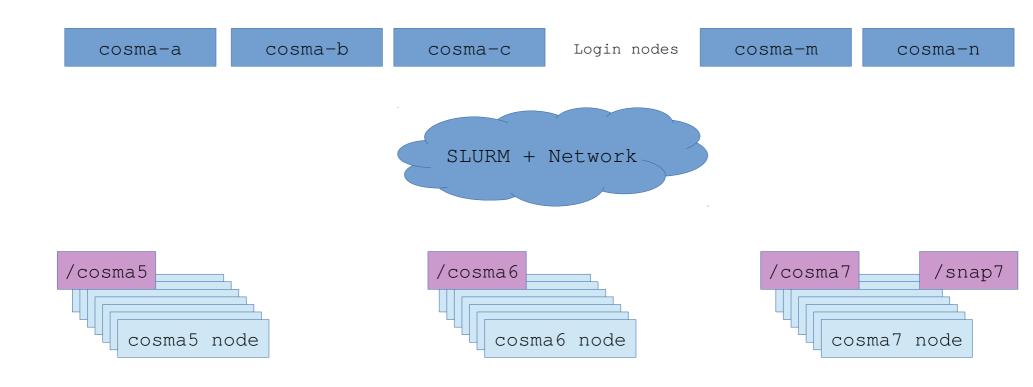
COSMA login nodes

- Currently, COSMA5 and COSMA7 have login nodes
 - COSMA5 has 3 nodes: cosma-a, cosma-b and cosma-c
 - COSMA7 has 2 nodes: cosma-m and cosma-n
- Shortly, one COSMA5 node will be moved to COSMA6
- All login nodes offer access to all facilities
 - File space, job queues, libraries, tools, compilers, etc
- In general, please use COSMA6 or 7 for DiRAC projects, and use COSMA5 for internal Durham projects
 - Ask (us or supervisor) if not sure
- login.cosma.dur.ac.uk (round-robin allocation to -a, -b, -c)
- login7.cosma.dur.ac.uk (round-robin allocation to -m, -n)

Graphical COSMA

login.cosma.dur.ac.uk

login7.cosma.dur.ac.uk



COSMA file system

- Your home folder will be in
 - /cosma/home/PROJECT/USERNAME
 - PROJECT is probably durham
 - When you first log in, typing "pwd" will show you where you are
 - You have a 10GB quota
- You will also have data space at some of:
 - /cosma5/data/PROJECT/USERNAME (10TB/2.4PB)
 - /cosma6/data/PROJECT/USERNAME (10TB/2.5PB)
 - /cosma7/data/PROJECT/USERNAME (10TB/2.1PB)
 - /snap7/scratch/PROJECT/USERNAME (Unlimited/346TB)
- Data space is optimally connected to the corresponding COSMA
 - Reading /cosma6/ from COSMA6 will be faster than from COSMA7
 - /snap7 space is temporary storage to use within a single run
 - e.g. for restart points
 - Fast SSDs
 - At one point was the fastest storage in Europe
- /cosma/local/ is where tools and libraries are located

File system quotas

• quota (for home space):

Disk quotas for user dc-basdl (uid 20957):

Filesystem blocks quota limit grace files quota limit grace
172.17.170.16:/export/voll 2256360 10485760 30000000 1208 2000000 22000000

c7quota (for /cosma7, on a C7 login node):

Quota for dc-r	basai					
Filesystem	usage	quota	limit	files	quota	limit
/madfs	0MB	0MB	0MB	0	0	0
/cosma7	0.00390625MB 0MB		0MB	1	0	0
/snap7	0MB	0MB	0MB	0	0	0

c5quota (for /cosma5, on a C5 login node):

Quota for dc-	basd1					
Filesystem	usage	quota	limit	files	quota	limit
		- 				
/apfs	0GB	0GB	0GB			
/cosma5	33.4439GB	5120GB	5200GB	23	0	0

c6quota (for /cosma6, on a C6 node):

Quota for dc-k	pasd1					
Filesystem	usage	quota	limit	files	quota	limit
/ a a a m a 7	0.00390625MB 0MB		0MB	1	0	0
/cosma7	0.003906	ZOMB UMB	UMB	1	U	U
/cosma6	31.9992G	B OMB	0MB	17	0	0

• Eventually, running "quota" should tell you all this information

Files

- Your quota is not just restricted to total storage used
 - The number of files is also important
 - Each file uses a single inode
 - Metadata about a file, e.g. name, creation time, access rights, etc
 - Total number of inodes is limited
- Lots of small files is BAD
 - If you need this, please consider tarring up files, or concatenating them during writing

Over-quota

- If you go over quota:
 - You will be sent a daily email reminder
 - You have a soft limit and a hard limit
 - You can go over your soft limit for up to 7 days
 - You cannot go over your hard limit
 - After 7 days, you will not be able to write files until you get back under quota

Group/project quotas

- Groups/projects also have quotas
 - If a project goes over quota, no one will be able to write files
 - To check group quotas:
 - c7quota -g durham
 - Worth noting: If you are within your quota, but cannot write files, check the group quota

What to put where...

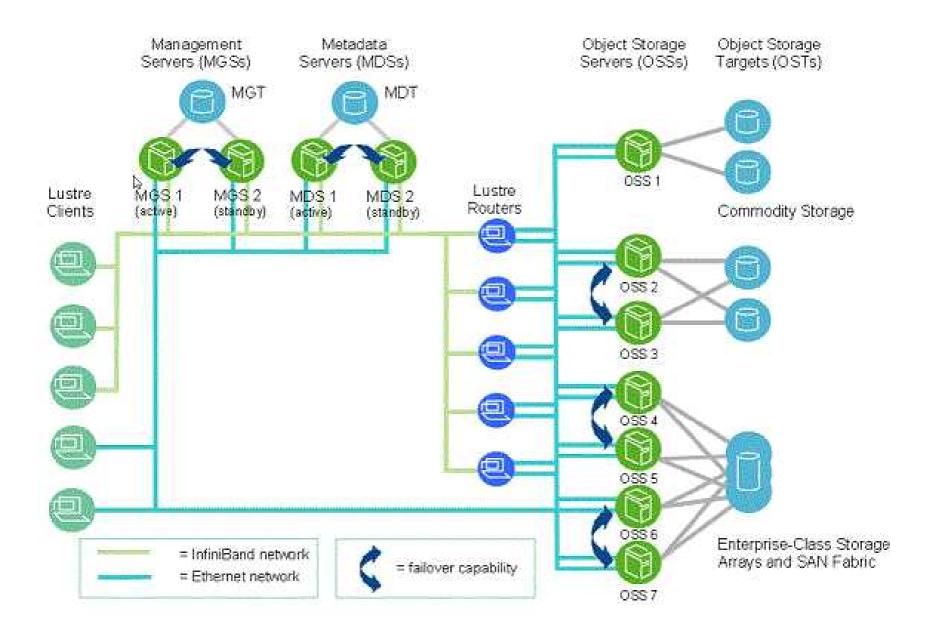
- Use /cosma/home/ for scripts, code, self-compiled libraries, python modules etc.
 - This is backed up
 - No data files from runs
 - No log files from runs
- Use /cosma[567]/data/ for input and output data produced by your runs
 - This is archived to tape
- Use /snap7/scratch/ if running on COSMA7 for staging posts, restart files etc.
 - This is not backed up, and may be removed if older than a few days.

Parallel file systems

- Storage of data across multiple servers
 - Data is distributed across these
 - Striped
- High performance access
 - Simultaneous reads/writes
- COSMA uses:
 - Lustre for /cosma6, /cosma7, /snap7
 - GPFS for /cosma5
 - NFS (not parallel) for /cosma/home and /cosma/local

The Lustre file system

- An object-based parallel file system
- Main components:
 - Metadata servers (MDS)
 - Metadata targets (MDT)
 - aka disks
 - Object Storage Servers (OSS)
 - Object Storage Targets (OST)
 - Lustre clients
 - e.g. login nodes and compute nodes



Lustre sequence

To read a file:

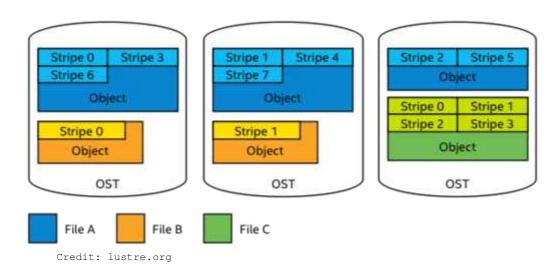
- Client requests information about the file from the MDS
- Object identifiers and layout transferred from MDS (meta-data server) to client
- Client can then directly interact with corresponding OSSs (object storage servers)
 where the object (data) is actually held
- Client can then perform I/O in parallel across multiple OSSs without further communication with the MDS
- Client then presents the file

To write a file:

- Client requires new file creation from an MDS
- Client receives details about where to write the information
- Client then writes data to the relevant OSSs.
 - which store the data on the OSTs

Lustre striping

- Strength of parallel file systems comes from ability to stripe data across multiple targets (HDDs)
 - Capacity and bandwidth scale with the number of OSSs
 - Each Lustre file specifies its own stripe count and size
- With Lustre, once a file is created, its striping cannot be changed
 - i.e. the number of stripes
 - unless the file is recreated (overwritten)
- Striping is inherited from the directory that a file is in
- Default striping for COSMA is 1 (i.e. not striped)



Writing large files

• If you are writing large files:

Size of the individual data blocks

Number of OSTs to stripe across

1) Set striping for the directory:

Ifs setstripe -S 4M -c -1 /path/to/directory All files here will then have this striping

2) "Touch" a file first:

Ifs setstripe -S 4M -c -1 /path/to/new/file (this creates an empty file)

When written to, this file will then have this striping

- For very large files, striping is essential if the file won't fit on a single HDD
- A C API also exists (#include <lustre/lustreapi.h>)
 - But don't reinvent the wheel
 - e.g. use parallel HDF5 to write files...

File striping

- To check the current striping on a file or directory:
 - Ifs getstrip /path/to/file/or/directory

```
tmp3.txt
lmm_stripe_count: 2
lmm_stripe_size:
                  2097152
lmm_pattern:
lmm_layout_gen:
lmm_stripe_offset: 10
obdidx
              objid
                            objid
                                           group
                460960
                             0x708a0
   10
                             0x713cd
    4
                463821
```

Hints for striping

- Good practice is to have dedicated directories with high striping for writing large files into
- Small files should be written with no striping
- With a file-per-process I/O pattern, best to use no striping
 - This will limit OST contention
- Accessing a single shared file with many processes, strip count is best if equalling the number of processes
 - Size and location of I/O operations can then be managed to allow stripe alignment with each process accessing a single OST
- Avoid patterns where a single process accesses all OSTs
- Open files as read-only where possible
- Try to avoid:
 - Multiple processes accessing the same small file
 - · Use a single process to broadcast the information
 - Excessive use of stdout and stderr for parallel processes
- A good stripe size is something like 0.1-1GB
 - HDDs write at ~100 200MB/s
 - Feel free to investigate best sizes for your application

General Lustre hints

- Avoid using "ls -l"
 - File size is only stored on the OSSs
 - Use "Is" to see if a file exists
 - Use "Is -I FILENAME" to get the size of a file
- Avoid having thousands of files in the same directory
- Avoid accessing small files under lustre
 - Either keep them in /cosma/home, or copy to /tmp before starting your job

COSMA Modules

- COSMA uses a "Module" environment
 - If you need specific tools/libraries/compilers, load the corresponding module
 - All this does is sets the correct environment variables
- e.g.

```
module load gnu_comp
```

- Will "load" the GNU gcc compiler module
- (actually adds /cosma/local/gnu_comp/.../.../bin to \$PATH)

```
module load fftw
```

- Will load the FFTW libraries
- (actually adds stuff to \$LDFLAGS, \$LIBRARY_PATH, \$CPATH, \$CMAKE_INCLUDE_PATH, etc)

Module commands

- module avail
 - Too see available modules
 - Can search by appending a name, e.g.
 - module avail ff → will show all modules starting with ff
- module list
 - Lists currently loaded modules
- module load MODULENAME
- module unload MODULENAME
- module purge
 - Unloads all modules
- module show MODULENAME
 - Shows information about the module
- Commands can be shortened (e.g. module av)
 - Tab completion works

Module dependencies

- Some modules depend on others
- e.g. for FFTW, you need a compiler module and an MPI module loaded first
- Others conflict
- e.g. you cannot load both python2 and python3 modules
 - (python/2.7.15 and python/3.6.5)
 - Note, if you load the python3 module, you need to use python3, rather than python (which would give you the old system python2)

Compilers and MPI libraries

- gnu_comp/7.3.0
- intel_comp/2017
- intel_comp/2018
- openmpi/3.0.1
- intel_mpi/2017
- intel_mpi/2018
- hpcx-mt/2.2 → Openmpi optimised for infiniband
- If you need new modules, please ask us to add them

Message Passing Interface (MPI)

- Most HPC codes use MPI to communicate between nodes
 - Mostly transparent to a user
 - But some knowledge required for code development
 - See other lectures/courses

SLURM

- Job scheduling system
- Used to allocate resources (nodes) to users
- Monitoring of jobs
- Maintaining a fair work queue
- COSMA has several work queues or partitions
- Useful commands:
 - sinfo, squeue, sbatch, scontrol, scancel, showq, sprio

COSMA5 partitions

- cosma
 - Standard queue
- cosma-prince
 - For users who require a large number of nodes
- cosma-analyse
 - For users of the analyse group
- cordelia
 - For single core jobs (i.e. not parallel jobs)

COSMA6 partitions

- cosma6
 - Standard cosma6 queue
- cosma6-pauper
 - A poor-mans queue for projects with no resources left
- cosma6-prince
 - When a large number of nodes are required

COSMA7 partitions

- cosma7
 - Standard queue
- cosma7-pauper
 - For users with no allocation left
- cosma7-prince
 - When a large number of nodes are required

sinfo

- sinfo
 - Shows a list of the nodes allocated to the different queues

 PARTITION AVAIL TIMELIMIT NODES STATE NODELIST COSMA 7 Up 3-00:00:00 1 down* m7037

up 3-00:00:00

up 3-00:00:00

2 drain m[7064,7143]

144 alloc m[7001-7036,7038-7063,7065-7142,7144-7147]

- sinfo -p cosma7
 - Show only cosma7 nodes
- See the man pages for further information:

cosma7

- man sinfo

squeue

- Shows the current state of the queues
- e.g. squeue -p cosma
 - Shows only cosma

```
JOBID PARTITION
                NAME
                        USER ST
                                    TIME NODES NODELIST (REASON)
86362
        cosma LWHalo dc-rega4 R 14:56
                                            36 m[5124-5136,5146-5156,5159-
86282
        cosma L400_de dc-pfei1 R 2:37:07
                                            32 m[5184,5219-5242,5244-5250
86281
        cosma L400_de dc-pfei1 R 2:37:39 32 m[5185-5212,5214,5216-5218
86363
        cosma MMHalo_N dc-rega4 R 14:42 12 m[5123,5171-5181]
        cosma RECAL-h0 rcrain R 0:54 8 m[5182-5183,5251-5256]
86376
                       arj R 4:54:39 8 m[5137-5138,5140-5145]
        cosma IC_Gen
                      likm R 5:47 1 m5262
86374
               energy
        cosma cal_all shliao R 1-05:32:27
                                            1 m5122
```

- Column ST shows state
 - Commen states are:
 - R=running, PD=pending, CA=cancelled, CF=configuring (e.g. waiting for servers to book), CG=completing, DL=deadline (job terminated on deadline), NF=node fail, TO=timeout

sbatch

- Use sbatch to submit a job:
 - sbatch /path/to/job/file
- A job file will contain the necessary information for SLURM
- Sample scripts in /cosma/home/sample-user

```
# Number of cores 1
#SBATCH -n 1
#SBATCH -J job name
#SBATCH --exclusive
                                # No sharing of node
#SBATCH -t. 10
                               # Time limit of 10 minutes
#SBATCH -p cosma
                                # Use partition (queue) cosma
#SBATCH -A durham
                                 # group durham for accounting purposes
#SBATCH -o std_%j.out
                                 # Output file
                                # Error file
#SBATCH -e stderr_%j.err
#SBATCH --mail-type=END # Notification when job ends (done or failed)
#SBATCH --mail-user=userid # Where to send emails
module load fft.w
cd /path/to/my/code
./startMyJob
```

scontrol

- Can be used to see which groups are allowed to submit to a partition
- e.g. scontrol show part cosma7

```
PartitionName=cosma7
   AllowGroups=ALL AllowAccounts=do004, dp004, dp019, dp034, dp104, dp105, ds007 AllowQos=ALL AllocNodes=ALL Default=NO QoS=N/A
   DefaultTime=NONE DisableRootJobs=NO ExclusiveUser=NO GraceTime=0 Hidden=NO
   MaxNodes=UNLIMITED MaxTime=3-00:00:00 MinNodes=1 LLN=NO MaxCPUsPerNode=UNLIMITED
   Nodes=m[7001-7147]
   PriorityJobFactor=50 PriorityTier=50 RootOnly=NO ReqResv=NO OverSubscribe=EXCLUSIVE
   OverTimeLimit=NONE PreemptMode=OFF
   State=UP TotalCPUs=4116 TotalNodes=147 SelectTypeParameters=NONE
   DefMemPerNode=UNLIMITED MaxMemPerNode=UNLIMITED
```

scancel

- Cancel submitted jobs:
 - scancel jobID

showq and sprio

- showq -I -o -p cosma7
 - Shows running and waiting jobs, ordered by priority
- sprio -l -p cosma7
 - shows information about priorities

Scheduling

- SLURM priority calculation is complex
- Consider the case of a large job requiring many nodes, and many smaller jobs.
 - Small jobs can back-fill (i.e. use unused nodes)
 - But this would mean that there are never enough jobs for the large job
 - So a priority is calculated based on many things
 - If you have short jobs, please specify their estimated runtime accurately, so that they can be used to back-fill nodes while the large jobs are waiting to start
- Command c[567]backfill shows nodes currently available for small jobs

Compiling and optimising

- Use the login nodes for compiling code
- Optimisation flags can be used to improve code performance:
 - For gcc:
 - -O3 -march=native
 - For icc:
 - -O3 -xHOST
- Other flags also available (>1000!)
- But, if compiling for a COSMA6 queue on the COSMA7 login nodes, do not optimise too far
 - C6 nodes are older and illegal instructions may result
 - (C5 node CPUs are identical to C6)
- A COSMA6 login node will be made available to alleviate this problem shortly

Jupyter hub

- A Jupyter hub will shortly be made available on the COSMA7 login nodes
 - But, this is not a good HPC paradigm and should really only be used for analysis of results

Future updates

- Singularity
 - A modularised container facility for HPC
- COSMA7 expansion
 - Up to 300 nodes by the end of October
 - Up to 400 nodes by March 2019
- COSMA8
 - Expected sometime in 2020-2021 as part of DiRAC3
- Hierarchical storage management
 - Automatic archiving of unused files
 - Debate about automatic retrieval
 - Releasing filesystem space for other users