

Table of Contents

1. [Introduction](#)
2. [Using Unix and Apocrita](#)
 - i. [What is Apocrita?](#)
 - ii. [Connecting to Apocrita](#)
 - iii. [Launching a Job on Apocrita](#)
 - iv. [Basic UNIX Navigation](#)
 - v. [Playing With Files](#)
 - vi. [Copying & Downloading Files](#)
 - vii. [Dealing with Compressed Files](#)
 - viii. [Available Software](#)
 - ix. [R](#)
 - x. [Galaxy](#)
 - xi. [Handy Shortcuts](#)
3. [Advanced](#)
4. [Contact](#)



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SBCS-Informatics

This is a README explaining how to use the Apocrita HPC resource from an SBCS perspective, it contains:

- Instructions on how to submit jobs and use Apocrita generally
- An introduction to the command line and Unix
- A slightly more advanced section with tips and tricks for the more seasoned user who has gotten to know Apocrita and Unix better

Click on the menu on the left to navigate through the website. This document is also available as a [single pdf download](#).

Contributing

There are two main ways of contributing content or asking questions about this document.

1. Using GitHub, clicking the Edit link will take you to the repository of this document. [There](#), you can either make a GitHub issue or a pull request.
2. You can find contact details [here](#) if you would rather send an email.

Using Unix and Apocrita

This section will help new users to get started using Apocrita. Here you can find information regarding:

- How to log in
- How to submit jobs
- Handy information on the system
- Common Unix commands and how to use them to navigate

The information here can also be seen as the first place to look when a question about Apocrita comes up. If there are any unanswered questions after that feel free to create a GitHub issue or use the [contact page](#).

Much of this information has been gathered from the official Apocrita docs, you can find them [here](#).



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1. What is Apocrita?

Cluster Structure

Apocrita is a High Performance Computing (HPC) cluster that consists of many interconnected computers, called **nodes**. The user logs into one specific **head node**, from which the rest of the cluster can be accessed. On Apocrita these are called **frontends**. Importantly, ***no jobs are run directly on the frontends***. Instead, whenever the user wants to run a job, the details of the job is submitted to a software that handles scheduling of work on the cluster and it is dispatched to a work node when one is available. There are also **utility servers** which the user can interactively log in to. More information on utility servers can be found below and in the [advanced section](#).

Apocrita and all the other peripheral machines are run by the [ITS Research team](#). They have a documentation site available [here](#).

Nodes

- 150 normal use nodes each with two 6-core processors, i.e. 12 cores, and 24GB RAM
- 11 so called **fat nodes** each with four 12-core processors, i.e. 48 cores, and 512GB RAM. These nodes are used for heavier calculations, in particular ones which require a lot of memory.

For more information on the specifications on Apocrita nodes, see the [advanced section](#).

Utility servers

There are a number of very specific so called utility servers that are part of the HPC resources but not the general Apocrita system. Users can SSH to these machines and use them interactively for their analysis. These servers were all purchased separately with different funding, keep this in mind as groups who have contributed to the acquisition of these machines have priority. With that said, feel free to use these resources when they are available, you can find more information in the [advanced section](#).

Galaxy

There is a Galaxy server set up on Apocrita through which you can run some general (and some more specific) analyses in a graphical web interface. For more information on Galaxy, see the [specifications here](#).

Data

Each user has a specific account on Apocrita and have a data quota of 50GB in their home directory. Often this is nowhere near enough to run the analysis needed, therefore there is a so called **scratch** space for temporary files. This is where most people do their work but it's important to note that that **scratch area is not backed up** and you should treat these as purely temporary. In the future a time-limit on files may be implemented, automatically deleting old files in the scratch space.

Home

- Is tiny
- Is backed up
- Is for your personal scripts and installations, small files you use often and want to keep safe

Scratch

- Is giant

- Is **NOT** backed up
- Is communal, you're not the only user here - keep this in mind and write only in your directories
- Is temporary - **NEVER** store files on a scratch space, they will be deleted sooner or later

Lab specific storage

- Each lab has a 1TB space, some labs have purchased additional storage
- Ask your supervisor about access to your lab space
- This is usually for medium term storage of data etc., but each lab handles their area internally

Archive

We are working on setting up an archival data space where the user can store data long term, for things like raw and processed data from finished projects that cannot be deleted but probably won't be used a lot in the future. In many cases there is project specific storage implemented.

Archive will be:

- Large
- Backed up
- For storing files you cannot delete for some reason
- Please, remember to **zip** your files before transferring them to the archive

System

Apocrita is running [Scientific Linux 6.2](#).



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2. Connecting to Apocrita

Get an account on the cluster

To get an Apocrita account you need to make a [request to ITS Research](#). Once this has been set up you can continue to log in with the details provided.

Logging in from Mac (or other Unix systems)

OS X (and indeed all Linux distributions) have an application called Terminal. On your Mac you can find it in Applications -> Utilities.

1. Open Terminal
2. Enter the following

```
ssh -X [youruserID@login.hpc.qmul.ac.uk
```

e.g.

```
ssh -X btw000@login.hpc.qmul.ac.uk
```

3. Enter your password when prompted (It will not appear as you type, this is by design, your keystrokes are being registered.)

To avoid having to type your password each time you log in You can also set up SSH keys that will be used when you log in from your computer instead of a password. There are instructions on how to set up SSH keys in the [advanced section](#).

Logging in from Windows

The simplest way of doing things on Windows is using a program called [MobaXterm](#).

1. [Download](#) the newest version of MobaXterm
2. Create a session
3. Enter the address to Apocrita which is `login.hpc.qmul.ac.uk`
4. You can also enter username and password to save them here
5. Connect and enter your username and/or password when prompted

If you would rather use PuTTY.

1. [Download](#) PuTTY
2. In the host name window enter the server address `login.hpc.qmul.ac.uk`
3. Enter the correct port number (22) and check on correct connection type (SSH)
4. Now go to the data tab under connection and in auto-login username box enter your username (e.g. btw000)
5. Go back to the session tab and in the saved sessions box enter a name for this log in (e.g. apocrita)
6. Save!
7. Double click the session name and enter your password where prompted

Display

If you're planning on using any graphical interface, e.g. plotting in R, you need the X11 forwarding flag, `-X`. This instructs the terminal forward display items to your computer, that will allow you to see your plots or other graphical user interfaces.

You might as well always have this option set - to simplify things. MobaXterm uses X11 forwarding by default.

```
ssh -X btw000@login.hpc.qmul.ac.uk
```

Keep your terminal as you log out or lose network connection

When you shut your laptop down the connections it has made with Apocrita (and the rest of the outside world) will be interrupted. This can happen randomly at other times as well and the implication is that anything you were running in your terminal on Apocrita will be shut down too, along with the connection.

Screen

Usefully, the program `screen` allows you to keep a process running on a server without the need to be consistently connected to the network. It sets up a session that will stay active even if you quit your terminal, you can just connect to the session later and you will find yourself exactly where you left off.

- `screen -ls` # list all your sessions
- `screen -r` # reconnect to a session
- `CTRL+A`, `CTRL+D` # pressing these two key bindings will detach you from the current screen session
- `CTRL+D` # `CTRL+D` without `CTRL+A` first will terminate the session instead
- `man screen` # manual for screen - explaining every option

Disconnect a command from the terminal

When a terminal is shut down, a so called hang-up signal is sent to any process running in that terminal telling it to quit. There is a way you can make your process ignore that specific signal with `nohup`. It is very simple to use; you add `nohup` before your command as such:

```
bwa mem -t 10 -p inputreference.fa inputfasta.fastq > outputfile.sam &           #if this is your command
nohup bwa mem -t 10 -p inputreference.fa inputfasta.fastq > outputfile.sam &     #do this instead
nohup nice bwa mem -t 10 -p inputreference.fa inputfasta.fastq > outputfile.sam &  #it's a good idea to add a nice va
```

An ampersand, `&`, at the end of a command will send it to the background, however this is not enough as it will still be sent the hang-up signal when the terminal is closed, you need the `nohup` addition.

The last example includes the `nice` command as well. `nice` tells the computer that your process should be run with a lower priority, a good idea if you are leaving your process unattended! This does not mean it will take any longer than normal as long as there is available CPUs on the machine.

Keep in mind that `nohup` will redirect the output if it is a set to a terminal - use `man nohup` for more information. `nohup` does not prevent other signals and will not make your process unkillable!



3. Launching a Job on Apocrita

When you log in to Apocrita you will be accessing a **frontend**. It is very important that you do not simply run your scripts here. These nodes are there to accommodate logins to the cluster, not workload. Instead, there is a scheduling program running on the cluster which takes instructions to your job and distributes the total load over all the worker nodes. You can also use the utility servers interactively by SSHing to them from the frontend.

Interactive use

These modes will log you in directly to a machine, allowing you to test, develop and try different things out in a single session. This is useful if for example you are trying a new tool out and need to test different parameters or if you are unsure about the syntax of the program.

Using the queueing system on Apocrita

qlogin

These commands will connect you to one of the worker nodes with the requested resources available for you to use. This will allow you to run your scripts/jobs interactively on a command line. This can be useful if you want to have more freedom in what you are doing than a script allows, but should be avoided for longer jobs as the frontends are rebooted fairly frequently which may kill your job. These commands take the arguments on how what resources you need. For more details, have a look at the [ITS research website](#)

Here is an example of logging onto a machine using qlogin:

```
ssh -X btw000@login.hpc.qmul.ac.uk      #log in to Apocrita
qlogin -l h_rt=3600                     #request a session 3600s (1h) long
qlogin -l h_rt=10:0:0,h_vmem=4G        #request 10h and 4G memory
exit                                    #just type exit to logout
```

Do keep in mind that the frontends are rebooted reasonably frequently to be able to handle all the traffic on them. For this reason, it's best to keep interactive jobs fairly short. Use the utility servers or `qsub` described below for longer runs.

SSHing to a utility server

frontend5, frontend6 and SM11

Once you have logged into a frontend of Apocrita, all you need to do to log in to one of these servers is to SSH to that particular name. These machines have all been bought by different groups of academics and priority remains with these groups. This only means that you need to check carefully before you start to work here, if it is free everyone is allowed to make use of the resource.

```
ssh -X frontend5
ssh -X frontend6
ssh -X sm11
```

These machines are all different, to find out how and why, head to the [advanced section](#). It is **VERY** important that you do not overload these servers, it is up to the user to figure out what the load on the machine is and determine if there is room for their job. Use commands such as `top`, `htop` `free` etc. to make sure.

Non-interactive use

Submitting a job script to the queue

This is the easiest way to run your job on the Apocrita cluster. Even so, it is not as simple as running your command. Remember, don't run jobs on the frontends. This method uses a command called `qsub` which takes a script as input. Inside the script you define the resources your job needs.

You need to write the script with the instructions for your job, below you find the simplest version of such a script. Use this as a template and add options as needed. There are several more options you can add to the header of your script which for example allows for more cores to be used.

```
#!/bin/sh
#$ -cwd           # Set the working directory for the job to the current directory
#$ -V
#$ -l h_rt=24:0:0 # Request 24 hour runtime
#$ -l h_vmem=1G   # Request 1GB RAM
./code           # Your code goes here
```

After you have written and saved the script you feed it to `qsub` as such

```
qsub job_script.sh
```

For more details, have a look at the [ITS research website](#), or if you feel like you can take it, the [qsub man page](#).

Monitoring your job

Use `qstat` to show the status of all your jobs in the queue on Apocrita, and `qdel` to delete a job from the queue.

To monitor a job running in an interactive session or on a utility server use a program like `top`. It lists all processes currently running on the machine and allows you to sort them by various criteria like CPU or memory usage. There is an arguably better version of the same type of tool called `htop`. You will need to load it with `module load htop/1.0.3` before you can use it though. Both `top` and `htop` have an argument `-u` taking a username so that you can inspect only your own processes if you want, `htop -u btw000` will show only btw000's processes.



4. Basic Unix Navigation

This section contains some extremely basic commands that you can run while logged onto Apocrita (or in your own Unix terminal if you are a Mac user.) There are much better guides available online if you want to learn about Linux and the command line. One such is [Learn Linux the Hard Way](#). That link will take you a version which, although long, could be very useful. Some parts of it are even interactive.

Where am I?

Files are organised in your allocated server space into folders, or 'directories', just like on your regular computer. You can check your current working directory (i.e. where you are) with the 'print working directory' command, `pwd`.

Checking the contents of directory

It's easy to check the contents of the directory you're currently in, using the list command, `ls`. Typing `ls` alone will list the filenames. However, if you require extra information you can add 'flags' after the command to give the computer further instructions:

```
ls          #prints filenames in a list
ls -a       #prints all filenames, including hidden files
ls -l       #'long' list, displays info including permissions.
ls -h       #prints the sizes of files in units you can read
ls -tr      #t for time sorted, r for reverse
```

The above flags (amongst others) can be combined together in one string for convenience. You may use one `-` (to indicate a flag) followed by all required characters, or separate them individually:

```
ls -lhatr    #has the same effect as
ls -l -h -a -t -r
```

This bit will print a list of files with all of the above information.

Changing directories

Navigate through directories using the 'change directory' command, `cd`. It will assume you're looking for a directory name that is within your current working directory

Change directory

```
cd directory_name/
```

Go back "up" one directory:

```
cd ../
cd ../../          #you can go several at a time
cd ../../antr_dir/subdir2  #as many up and down as you want
```

Return to home directory

```
cd ~/
```

or just

```
cd
```

Note: On Mac, it's possible to click and drag the desired location of a directory or file from the finder (by the icon) to the terminal. Just type `cd` followed by a space, click & drag, hit enter. You can do this from any starting point.



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5. Playing with Files

Creating a new directory

The `mkdir` command will create a directory inside your current location.

```
mkdir newdirectoryname
```

Moving files in local machine

The `mv` command will move a file or directory from its current location and place it elsewhere. The syntax is, `mv current_location new_location`. It can also be used to rename files.

If the new location is a file, the file is renamed:

```
mv oldfile newfile
```

or if the target is a directory, the file is moved:

```
mv oldfile newdirectory/
```

Delete files or directories

Delete files with the 'remove' command, `rm`:

```
rm filename
```

or for a directory `rmdir`, the directory has to be empty:

```
rmdir directory/
```

You can use `rm` to remove directories with the `-r` option, it removes files in a directory recursively. **Be careful** when using `rm`, once you hit enter, the files are gone. After adding or removing files and directories, you can check and make sure it worked using the `ls` command.

Viewing different parts of an existing file

`less` shows a small portion of the file, `more` shows a larger portion (according to the manual, it will display your file 'one screen's worth of lines at a time'). `head` displays the first ten lines, and `tail` displays the last ten lines. Both `head` and `tail` have several useful options like how many lines to display.

```
less filename.txt          #look through file with less
tail -n35 filename.txt     #print last 35 lines of file
```

Searching for a pattern within a file

The `grep` function searches for a particular pattern of characters. The syntax for the `grep` function is: `grep pattern file-to-look-in`. `grep` will by default print the whole line in which it found the pattern. There are options to have it print only the

match, line numbers, or just a count of how many times the pattern was found.

e.g.

```
grep "scaffold" genome.fasta #prints all lines with "scaffold" in them
grep ">" genome.fasta -c     #counts the number of ">" characters in the file
```



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6. Copying & Downloading Files

Files can be copied in and around your computer, in and around your space on the servers, and between the two. The basic copy function, `cp`, is for within locations (i.e. your computer or the server). To go between the two, use 'secure copy', `scp`.

The basic syntax is 'cp, original file location, new file'.

Between a remote server and local machine

From local file to server:

```
scp /path/to/local/file.txt server:/path/to/server/directory_or_newfile.txt
```

For example:

```
scp /Users/bob/Desktop/data.csv btw000@frontend1.apocrita.hpc.qmul.ac.uk:/home/btw000/archive/2013/data.csv
```

From server to local directory on local machine:

```
scp btw000@frontend1.apocrita.hpc.qmul.ac.uk:/home/btw000/myoutput.pdf .
```

Note, "." means "current directory".

Within your home computer, or the servers

This is just the same, except replace `scp` with `cp`.

```
cp /path/to/file.extension /new/directory/
```

Using a graphical user interface (GUI)

[Cyberduck](#) (on Mac) or [FileZilla](#) (on Windows). These two are GUI programs which offer file-sharing via a straightforward drag-and-drop or by menu navigation.

Both programs have a facility for attaching your account and passwords to them so they'll log in automatically. Make sure you check in the preferences/options/settings to set the file transfer protocol to "ssh", as that's not usually the default.

Note that while these systems are convenient for moving and organising your files, they will not let you schedule jobs or run anything on the server. Alas, it's back to the command line to do anything using the Apocrita computational resources.

Mounting your Apocrita file system on your computer

You can use some third party software to easily mount your Apocrita file system on your computer, that way you can manipulate your files in your operating system, and programs on your personal computer will be able to read and write files on Apocrita.

[Here is a good guide for every OS.](#)

Downloading files from the web

`wget` is short for "web-get", and will download a target file into your current working directory, e.g.

```
wget http://ftp.gnu.org/gnu/wget/wget-1.5.3.tar.gz
```

Here wget is used to download an old version of itself. You often find links to software you are keen on installing that you can use wget to directly transfer the code to the server.



7. Dealing with Compressed Files

As disk space is always limited and factoring in the large number of users, it is vital that everyone takes care storing their data properly on Apocrita. Always compress and archive files that aren't used.

Files

In genomics it is very common to have big files which contain sequence information or mapping files that can tell software and user where each sequence read fits against a certain reference. These files are essentially text files like any other and are often human-readable (for your convenience). Unfortunately, that means these types of files take up an enormous amount of space, but there are ways to mitigate this issue. Compression really just means that files are manipulated in such a way that information is denser, making them smaller, although this also means that they cannot be viewed/read unless you reverse the process. The simpler the file, the smaller it gets after compression because there wasn't much information to begin with. It is important to **compress anything that you are not currently using**, as this will save a lot of space on the cluster.

Remember that some tools and applications are able to work with compressed files. You might not have to unzip that `sequence_reads.fastq.gz` file you've got.

Directories

In some cases, it's not a single large file that is causing storage issues. Some programs create a large system of folders filled with lots and lots of tiny files. This can add up quickly and because of the way file systems work there is a "minimum size" that a file can occupy on disk ([if you want to know more about block size](#)). The solution to this problem is to make an archive of the directory. In a Linux/Unix environment the most common archiver is a program called `tar`. `tar` was created to handle problems with block size and writes a single new file, often called tarball, containing everything in the directory. This is not compressed so what you often see is compressed tar archives where the tarball has been run through `gzip`. You should do this as well.

Archiving

Use the `tar` command to create, and extract, archives of folders.

```
tar -c directory/ > directory.tar
```

`-c` is for create. This creates a new file called `directory.tar` but the original directory is still there. You can now remove the directory.

Compressing

Gzip is the go-to program to use for compressing files on any Unix system. Here is how simple it is to use:

```
gzip file
```

This zips the file up and gives it the `.gz` extension, note that this replaces the file with the compressed version.

Use `tar` to convert your analysis folder into an archive, followed by `gzip` to compress it making it as small and easy to handle as possible.

Extracting compressed files, e.g. `.zip` `.tar.gz` `.tgz`

The command for unzipping a file depends on the type of archive it is (i.e. its extension). `tar` can decompress several types of files as well, so you do not have to `gunzip` your `archive.tar.gz` file before using `tar`. `tar` handles it all by itself.

```
unzip file.zip          #for .zip  
gunzip file.gz          #for .gz  
tar -zxvf file.tar.gz   #for .tar.gz  
tar -zxvf file.tgz      #for .tgz  
tar -jxvf file.tar.bz   #for .tar.bz
```

Notable is that a file may have any extension, it is actually just a part of the file name. However, using proper extensions is a way of letting the user know what kind of file it is. When you move, archive and unzip files etc., make sure that you keep correct extensions on your files, or maybe you wont remember how to open it next time.



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8. Available Software

What is installed on Apocrita?

Software installed on the cluster is handled through something called the `module` command. Each tool installed is a module which can be loaded into your session. `module` has a number of subcommands which you can see by running just `module`. These are the most commonly used:

```
module avail                #prints a long list of available modules
module avail py             #prints all available modules starting with "py"
module load python/3.4.3    #loads python 3.4.3
module unload python/3.4.3  #unloads python to return to to sweet 2.X
module clear                #unloads all loaded modules
```

All `module` commands work with tab-completion, that way you can type `module load java` and press twice to see all available java versions.

The only problem with these modules is that they are not always up to date. Often you will have to ask for a new version to be installed if you want to be on the bleeding edge.

Installing new software

If you need a tool that is not currently available there are essentially two ways to get new software on Apocrita. Either request an installation by ITS Research, or install it yourself in your home directory.

Requesting installation by ITS Research

If you are looking into a piece of software that you think/know other users will have much use of it is best to have it installed for everyone, available through the `module` commands. The easiest way to create a ticket with ITS Research is by sending an email to its-research-support@qmul.ac.uk explaining what software you want installed and providing relevant links to the software webpage.

Compiling software yourself

If you are in a rush, or if the software is experimental, etc. it might be better to compile it yourself and keep it in your home directory.

Software for Unix systems is generally distributed as archives. To install a software package:

Download it (perhaps with `wget`). Then decompress it (perhaps with `unzip` or `tar`). Then check the installation instructions, usually in an `INSTALL` or `README` file. A lot of the time this will involve running a script called `configure` followed typing `make` in the directory.

Keep in mind that by default most software will try to install in directories in which you do not have permissions (you need `sudo`). In almost all cases there are options to instead install the tool in an alternate location. Use these options to install software in your home directory. Often this includes using the `--prefix` parameter in the `configure` script.

Some readme files are more useful than others. If there is no help in the readme, but there is a file called `makefile` in the directory, just type `make` and that should work. What happens usually in this case is that the compiled software is created in the same directory.



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9. R

You can run R in the Unix command line. To do this, simply type `R`. If you have X11 forwarding on in your ssh session, using the `-X` option, you will be able to see graphical devices that R opens when you for example plot something

This essentially turns the command window into the R console you're familiar with. From here, you can do all of the same things as you can in regular R. There are a few things worth noting:

Reading files

Alas, the command line is completely mouseless, so the `file.choose()` command for reading data using `read.table()` or `read.csv()` is no longer available. Instead, type in the name of the file you want in inverted commas. Fortunately, R will look for the file in the working directory you were in when you started the console, so it may actually be even more straightforward. However, if you're not in the same directory, you'll need to type the path the same way as you would when you're copying, moving, or navigating files & folders.

```
mydata <- read.table("data.txt", header=T)
otherdata <- read.csv("work-monthly/RData/data.csv")
```

Creating pdf file of a plot

Unless you're using X11 forwarding, you won't be able to see any plots you've made in R. Even if you are, once you've made the plot you want for your paper, you'll still need to save it. R can do this by opening its own workspace inside a pdf file, called a 'device'. Other devices include the Quartz & X11 windows you're already familiar with looking at your plots on.

First, call the `pdf()` function to tell it what the file should be called, then make your plot as you like it. To stop working in that file call the `dev.off()` function. You can then download it from the server to view it.

```
pdf("plot.pdf")
plot(object)
dev.off()
```

More information on R's ability to use devices (it can do more than just PDFs, and also have several open at once) can be found in the help files.



10. Galaxy

There is a Galaxy server set up on Apocrita.

Login

<https://galaxy.hpc.qmul.ac.uk/> - This is the link to the web interface.

To log in, use your entire QMUL email address i.e. j.doe@qmul.ac.uk as username and your Apocrita password.

SFTP

You can use SFTP to transfer large files to the Galaxy server. Use a [GUI program](#) to connect to the server using SFTP and transfer your files. The hostname is the same as the website, galaxy.hpc.qmul.ac.uk.

Remember to set SFTP and not FTP.

Specifics

The actual server runs on frontend2 but it uses DRMAA to submit jobs to the cluster queue. It will run jobs as the "galaxy" user, that means that the user starting the job is not the one that executes it on the cluster, but the username is listed in the job name in the queue.

For an unknown reason the command line version of sftp may or may not work for transferring files. There seems to be some issue with permissions of files sometimes. Use Cyberduck if you can. Contact Adrian Lärkeryd or ITS-Research if you're having issues with the file transfer.

This server is still very much experimental and things change. If something is not working or you need a new tool installed do not hesitate to [contact](#) Adrian.

Repeatexplorer

Is set to use almost an entire fat node on Apocrita. Unfortunately, it doesn't allow for dynamically changing the resource requirement, thus even a small job will request a lot of resources from the cluster and be stuck in the SGE queue for longer than necessary. The main requirement of this tool seems to be memory and the biggest nodes on the cluster have 512GB of RAM. It is possible that some very large jobs could exceed that limit and be killed.



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11. Handy Shortcuts

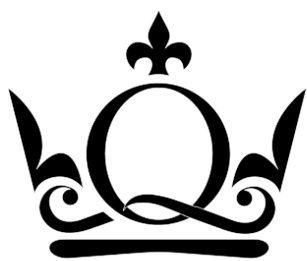
- Get your quota information `qquota -s`
- Make a soft link to a file `ln -s /path/to/source/file.txt ./destination_file.txt`
- Find username or information on a user with `finger <search-term>`
- Peek into the head of a gzipped file with `zcat zippedupfile.gz | head`
- You can use `bc` to do precision calculations like so `bc -l <<< "sqrt(2)-5/7+18"`

Apocrita job stats

ITS-R has a webpage for statistics where you can see the load on the cluster but more importantly you can see your completed jobs.

stats.hpc.qmul.ac.uk

On the left hand menu there is a View your job detail in which you can see all the jobs ran on the cluster recently.



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Advanced

This section contains more advanced information as well as tips and tricks for users who know their way around. Make sure you know what a command found here does before running it. If you are curious about something and want to know if it can be applied to your situation or research, [contact us](#).

1. Apocrita Specifications

Apocrita cluster nodes

Thin nodes

- 150 Nodes
- Dual 6-core Intel Westmere (E5645) - 2.4GHz
- Memory 24GB

Hyperthreading is currently disabled on the thin nodes.

Fat Nodes

- 11 Nodes
- Four 12-core AMD Bulldozer (6234) - 2.4GHz
- Memory 512GB

Frontends

- frontend1.apocrita.hpc.qmul.ac.uk - This is the one you should be using to connect to Apocrita. `login.hpc.qmul.ac.uk` currently points to frontend1.
- frontend2.apocrita.hpc.qmul.ac.uk - Sometimes, frontend1 is unavailable, in this case try frontend2. Galaxy runs on frontend2.
- There are other servers with the naming convention frontend# which in fact are **utility servers**, listed below.

Other information on Apocrita

- OS - [Scientific Linux 6.2](#)
- Interconnect - Gigabit Ethernet
- Queueing system - Sun Grid Engine 8.0.0e
- Compilers - Intel, Solaris Studio, Open64, Portland
- Parallel libraries - OpenMPI

Utility servers (SSH-able nodes)

sm11

- Purchased by Nichols, Leitch, Rossiter, Buggs, Wurm, Chelala, Clayton and Le Comber

A "set free" fat node that SBCS users can ssh directly into. The GPFS is mounted and it should work like any other part of Apocrita, just that the Sun Grid Engine doesn't schedule jobs here so that it is free for users to handle themselves. Check whether or not the machine is free (top, htop) before you start something, and maybe use a [nice value](#). To log in, just type `ssh sm11` when logged into a frontend. You can also make an ssh shortcut in your config file, explained below.

- Four 12-core AMD Opteron(TM) Processor 6234 - 2.4GHz
- Mem 512GB
- 16TB local scratch disk

Prometheus

- Purchased with NERC money by Nichols & Wurm.

This machine is not connected to Apocrita. It runs Ubuntu 14.04 and is administrated by SBCS users. A user has to be created for anyone who wants to use this hardware, see below for contact details.

- 2 10-core Intel Xeon CPU E5-2680 v2s clocked at Min:1199.953Mhz Max:2538.265Mhz with hyperthreading ON
- Kernel 3.18.9-031809-generic x86_64
- Mem 512GB
- 13TB local scratch disk
- Runs Ubuntu
- Docker installed

Contact: a.larkeryd@qmul.ac.uk, y.wurm@qmul.ac.uk, r.a.nichols@qmul.ac.uk

frontend5 and frontend6

- Purchased with NERC money by Nichols & Wurm.

These two identical machines are similar to sm11 but are running on newer hardware. For this reason, these two machines are slightly more powerful than sm11. The only difference between the machines is that frontend5 has hyperthreading (HT) turned on and frontend6 has it turned off. If you are aware of your tools running better on HT on/off, you can use the appropriate machine. Please feel free to use the /tmp catalogue on these machines for your temporary analysis files, but remember to move off it as soon as you are done as your files may be deleted during reboots etc.

- Four 10-core Intel Xeon E5-4640 v2 - 2.20GHz. This means 40 threads with HT off and 80 with HT on.
- Mem 630GB
- 13TB local scratch disk located on /tmp - do NOT store things here, it is ephemeral will be deleted.
- cachecade using a 100GB SSD. This is a caching of the local spinning disks onto the SSD. In principle it should increase performance on /tmp.

GPU

There are no GPUs on Apocrita, if you need this for your analysis you should talk to you PI about acquisition.

2. SSH Keys

Keys

You can set up a pair of SSH keys for a more secure as well as password-less login to Apocrita. This is done by having a private key on your machine, and a matching public key on the remote server, when you try to log in these two match up and let you in without having to type the user password. The private key should never be shared with anyone as it will allow that person access to your login. This is why you should always **protect your private key** with a passphrase.

Key Generation

1. Open a terminal window (on Windows, use MobaXterm)
2. Enter `ssh-keygen` and hit enter

3. You will see `Enter file in which to save the key (/home/username/.ssh/id_rsa):` on the screen. Just hit enter here which will save the keys in their default location.
4. The program will now ask you for a passphrase. Please enter one (it is possible to create a key without it but don't, it's to protect from someone getting hold of your private key.)
5. There is a message telling you that the key pair has been created, the public key is now located in `/home/my_username/.ssh/id_rsa.pub` and the private key is `/home/my_username/.ssh/id_rsa`.
6. You are now ready to copy the **public key** to Apocrita

Public Key Copy

The process is different depending on which operating system you are using.

Windows and Linux

Here it's very simple, open a terminal (or MobaXterm window) and type in `ssh-copy-id btw000@login.hpc.qmul.ac.uk` using your own username. That's it. Now try your connection `ssh -X btw000@login.hpc.qmul.ac.uk !`

Mac

If you have [Homebrew](#) installed on your Mac you can use it to install `ssh-copy-id` and go from there.

One of the few times having a mac will make you suffer extra work. You will have to manually copy your **public key** to a file located in your home directory on Apocrita.

1. Open a terminal and go to your home directory with `cd`
2. Use `scp` to copy the public key to Apocrita with this command `scp .ssh/id_rsa.pub btw000@login.hpc.qmul.ac.uk:~/`
3. Login to Apocrita `ssh btw000@login.hpc.qmul.ac.uk`
4. `cat ~/id_rsa.pub >> ~/.ssh/authorized_keys`
5. You can now log out and try the connection again to see if your keys work!

Shortcuts

Another convenience tip is to add shorthand names for your ssh logins. The address to the Apocrita head node is quite long and arguably tedious to write. So, this being computer science, of course there is a setup that will allow you to simply type something like `ssh apocrita` on the command line to connect.

1. `cd ~/.ssh`
2. Open or create the config file `nano config`
3. Add the following, you may call the Host whatever you like, here I'm using "apocrita":

```
Host apocrita
  Hostname frontend1.apocrita.hpc.qmul.ac.uk
  IdentityFile ~/.ssh/id_rsa
  User btw000
  ServerAliveInterval 300
```

4. Save and quit the editor
5. Change permissions of the file `chmod 600 ~/.ssh/config`
6. Try `ssh apocrita`

Another example, using apocrita (our newly created shortcut to frontend1) as a proxy to connect to SM11. This way all you need to connect to SM11 is `ssh sm11`.

```
Host sm11
  Hostname sm11
  User btw000
```

```
ProxyCommand ssh apocrita nc %h %p
ForwardX11 yes
```

You may or may not want X11 forwarding and there are other [options](#).

3. zsh defaults

These are instructions to set up your shell with some useful `zsh` settings like better auto completion and history etc. It also contains a small set of useful aliases.

All you need to do

Save your old `.bash_profile` and `.zshrc` files

These files control settings which should be set up as you log in. They are located in your home directory and control bash and zsh respectively (You may not have a `.zshrc` file if you haven't tried that shell before). You will need to remove them in order for this to work, but it is highly recommended that you save them in case you want to go back.

```
cd
mv .bash_profile .bash_profile.BAK # this file runs every time you log in with bash
mv .zshrc .zshrc.BAK              # this file runs every time you log in with zsh
```

Run the small installation

```
source /data/SBCS-Informatics/zsh_extensions
```

You should find yourself in a helpful shell. Have fun.

What happened was that a new `.bash_profile` was created which launches `zsh`. This in turn reads a new `.zshrc` file.

Features

Prompt directory information

`zsh` will show you an abbreviated version of the full path to where you are, giving you better sense of the file system.

```
/data/scratch/btw000/folder1 # pwd - this is the directory
[btw000@frontend1 folder1]$  # prompt with default bash settings
btw000@frontend1 /d/s/b/folder1> # here is how it looks with the new settings
```

Better tab completion

Case insensitive tab completion and you can tab between the different options.

```
btw977@frontend1 ~> cd /data/sbcs # pressing TAB twice
sbcs/
SBCS-BessantLab/ SBCS-ClareLab/ SBCS-EizaguirreLab/ SBCS-GreyLab/ SBCS-LeitchLab/ SBCS-OsmanLab/
SBCS-BuggsLab/ SBCS-ClaytonLab/ SBCS-ElphickLab/ SBCS-HirstLab/ SBCS-MarinakisLab/ SBCS-RossiterL
SBCS-BuggsLab/ SBCS-CrespoOtero/ SBCS-EvansLab/ SBCS-HurdLab/ SBCS-McElligottLab/ SBCS-RubanLab/
SBCS-ChassLab/ SBCS-DiTommasoLab/ SBCS-ForniliLab/ SBCS-Irys/ SBCS-MSc-BioInf/ SBCS-Stollewer
SBCS-ChittkaLab/ SBCS-DuffyLab/ SBCS-GoldupLab/ SBCS-LeComberLab/ SBCS-NicholsLab/ SBCS-WurmLab/
```

zsh 5.0.7

The default version of zsh that every SBCS user has (unless explicitly changed) is version 4.3.10 which doesn't contain all the functionality used here. Because of that a check is made when logging in and if the version of `zsh` isn't 5.0.7, it is loaded.

Oh My Zsh

[Oh My Zsh](#) is a large package of settings, plugins and themes for zsh which is used as foundation for these defaults. It has a ton of options but it is kept fairly simple here, including the theme. It does allow for much more customisation which you can do for yourself.

Per directory history

This plugin is enabled to give you a command line history that is specific to the directory you are in. That way when you go back to the folder where you carried out your analysis all those months ago you can just press the up-arrow on your keyboard and it will go through what last happened in this particular directory (instead of the failed installation of that python package you were wrestling with yesterday.) Please keep in mind that this is not retroactive!

Customising further

Perhaps you want some more fancy features than what is provided here? There are a multitude of themes that change appearance of your shell, or maybe it's syntax highlighting you crave. The setup followed above inserted a sourcing of our general `.zshrc` file in your local version. That file is located in your home directory.

If you are adding things like `module load` commands, aliases, changing your `$PATH` variable or something similar, the easiest way is to just add it to the end of your new `.zshrc` file which is in your home.

You can also copy all the contents of the general SBCS-zshrc (/data/SBCS-Informatics/SBCS-zshrc) to your own `.zshrc`. That way you can change anything you like! Add plugins, try the random theme, or even build your own functions. You can of course write your own `.zshrc` and use [other](#) packages.

There are other shells available as well. `fish` for example, which claims to be "Finally, a command line shell for the 90s". However, `fish` does have slightly different syntax than `bash` and `zsh`, the two of which are very similar. Feel free to keep looking, there are other more obscure things out there.

4. Oneliners

- [Long list of bioinformatic and non-bio oneliners](#)
- Get all sbcs users: `ldapsearch -x cn=sbcs | grep memberId | sort`. Can email to @qmul.ac.uk directly



Contact

Please send an email if you need anything. If you have a question, or more information, you would like to add to the documentation, feel free to use the EDIT link up top and create a GitHub issue or pull request.

Adrian Lärkeryd

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