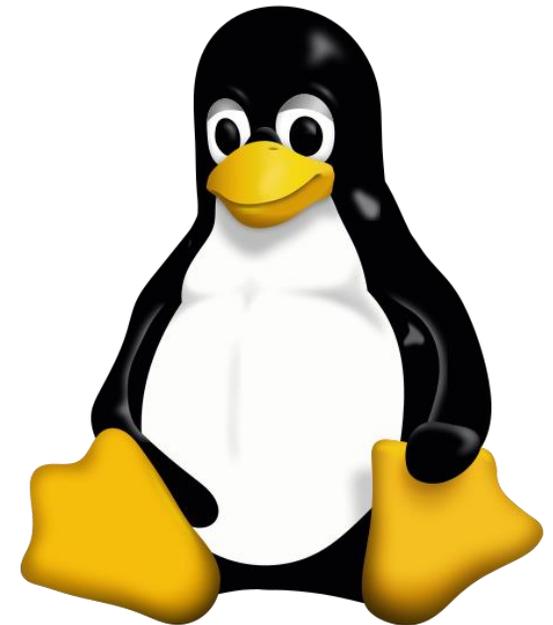


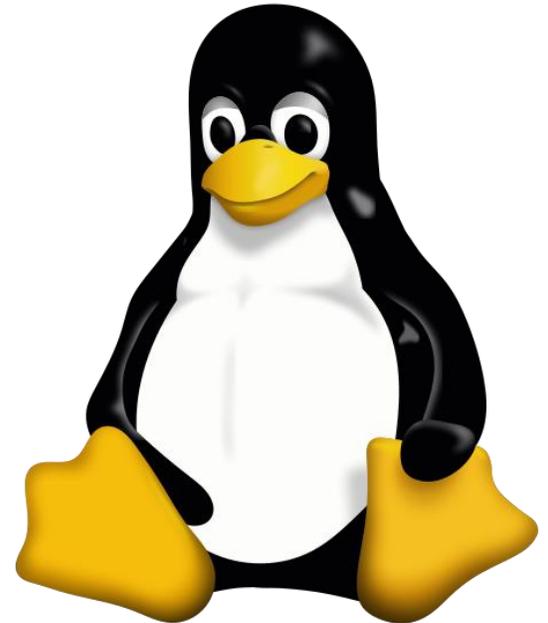
An Introduction to Unix

Sarah Inglesfield, Simon Andrews

v2024-08

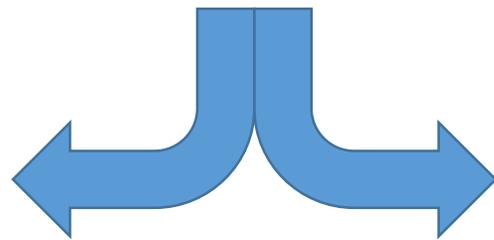
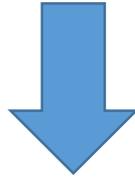


Terminology and Distributions



UNIX®

00011110 00011110 00011110 00011110 00011110 00011110 00011110 00011110



 **debian**
 **ubuntu**

- Admin tools
- Bundled Software
- Support duration / cost



Types of Linux installation

Bare Metal



- Physical hardware
- CD / DVD / USB / Network installation
- Can be physically accessible (desktop) or remote (server / cluster)

Virtual Machine



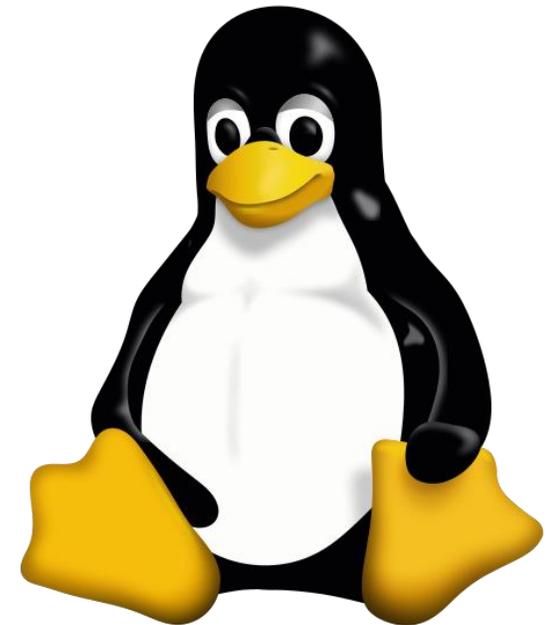
- Runs within another operating system
- Portable / disposable
- Install from ISO / Network

Cloud

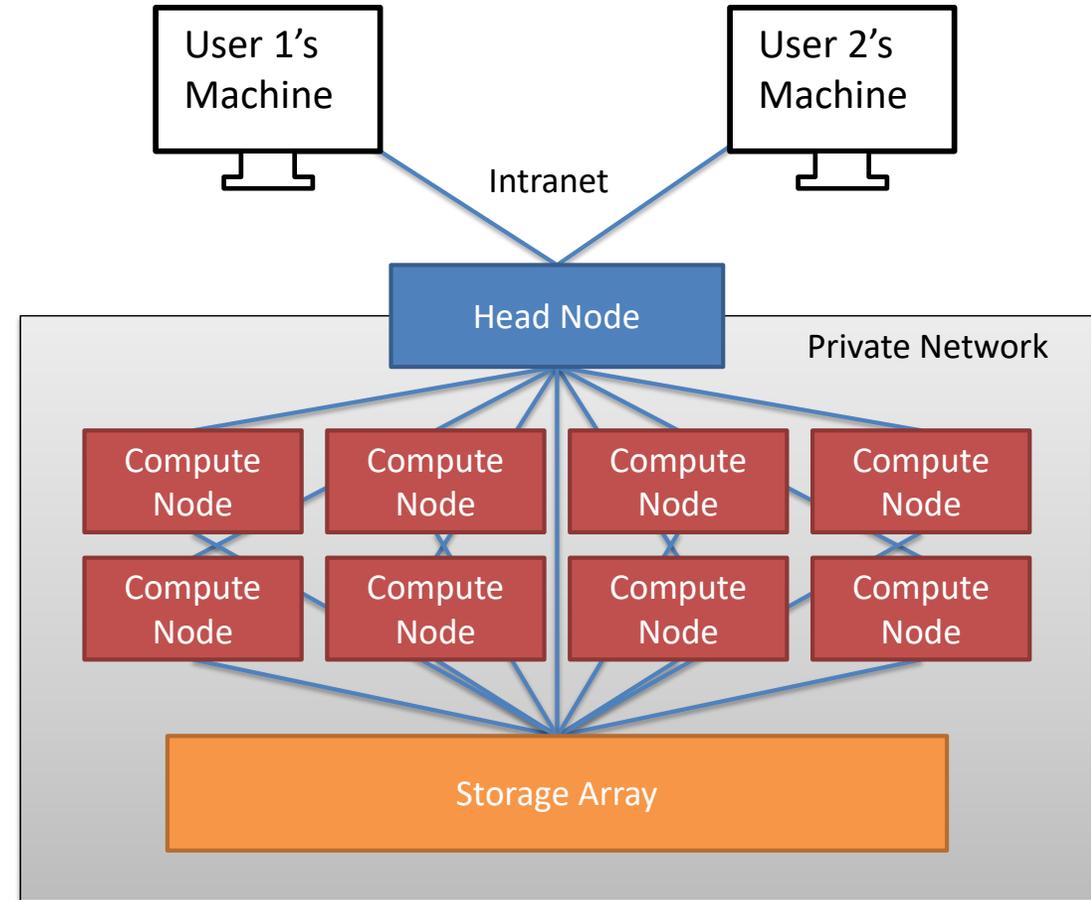
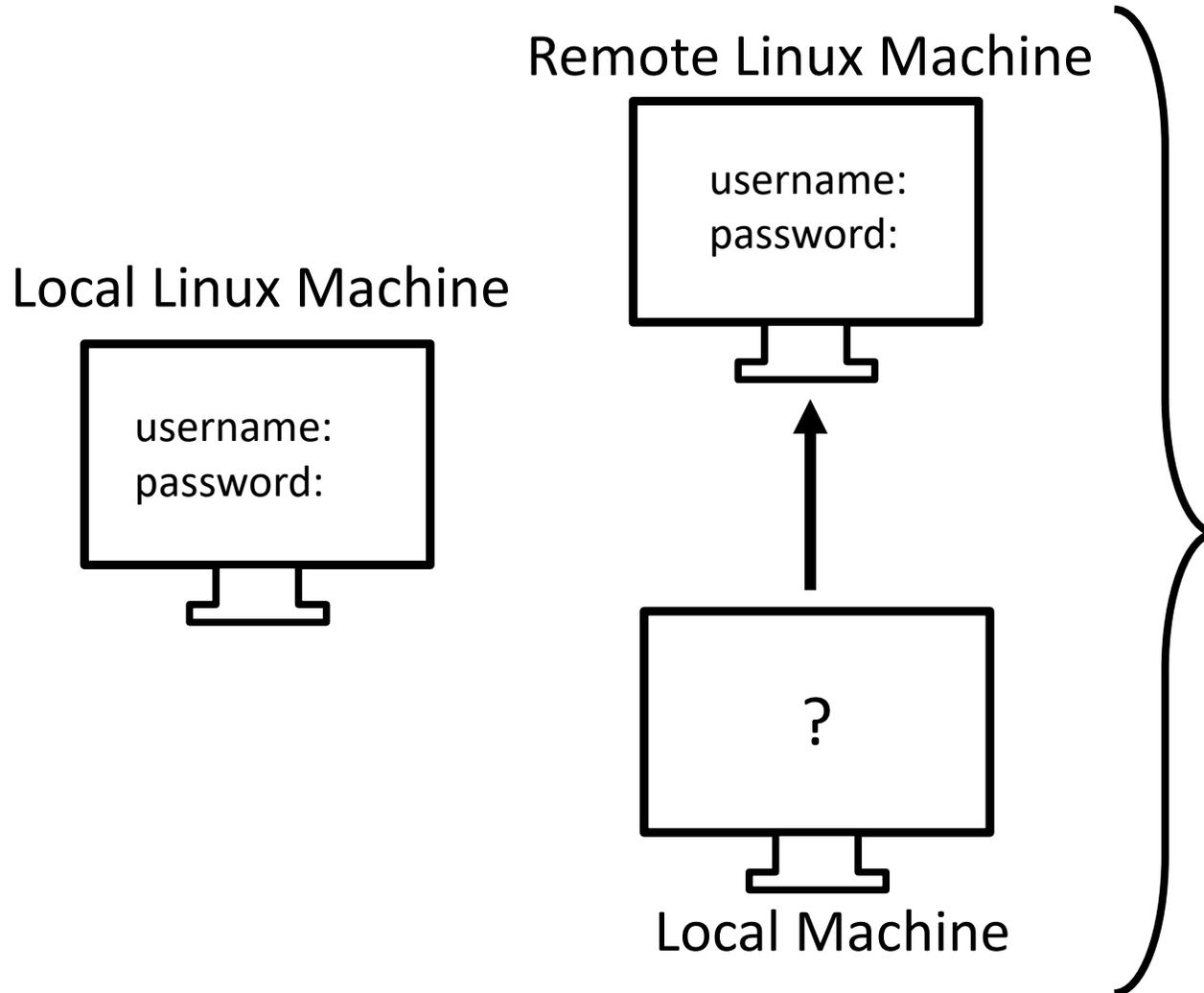


- Virtual machine on someone else's hardware
- Amazon / Google are the main providers
- Range of available hardware

Connecting to Linux Installations

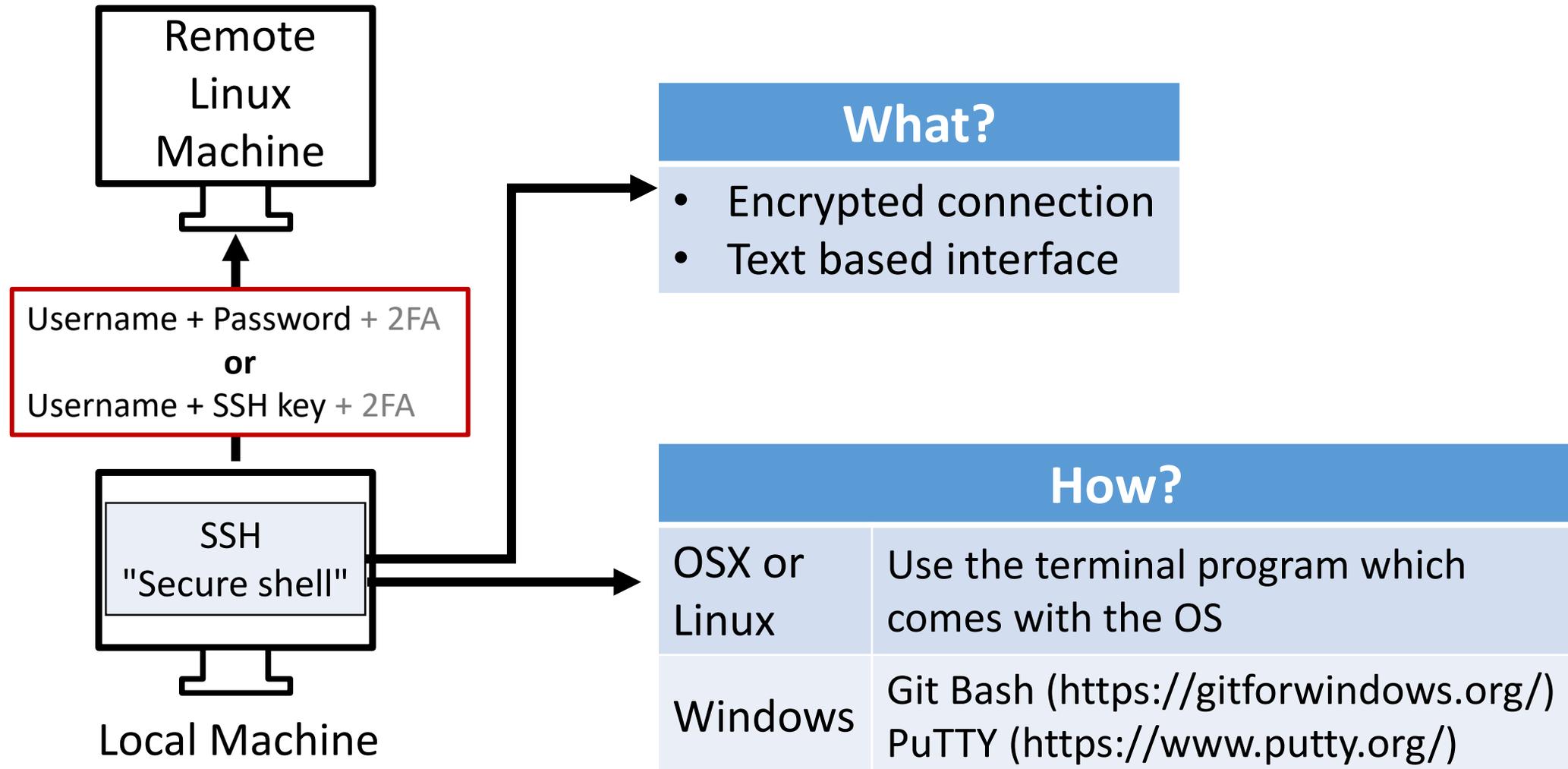


Local vs Remote Connections



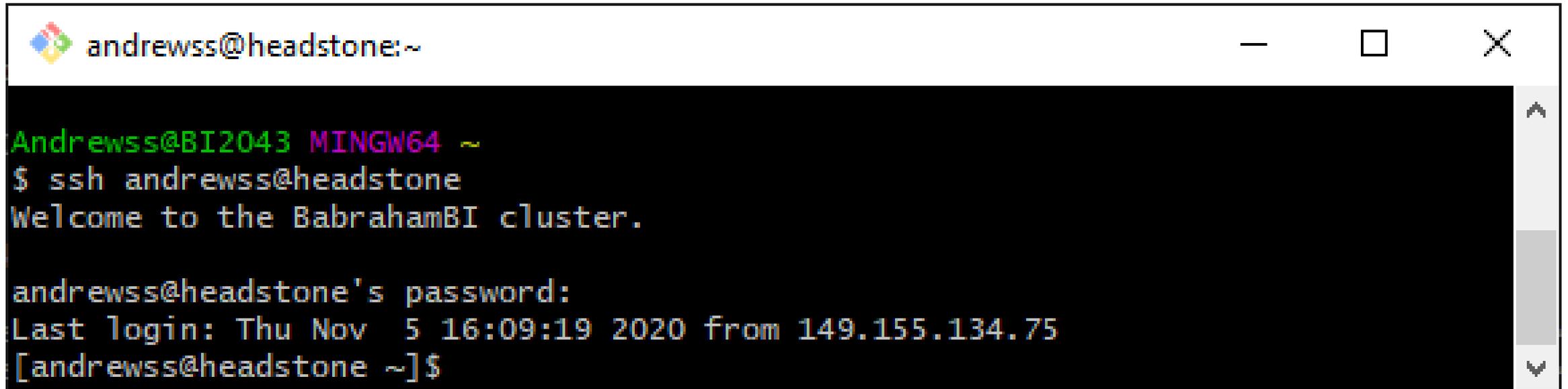
e.g. working on clusters

Connecting to a remote Linux installation



SSH + Password connection

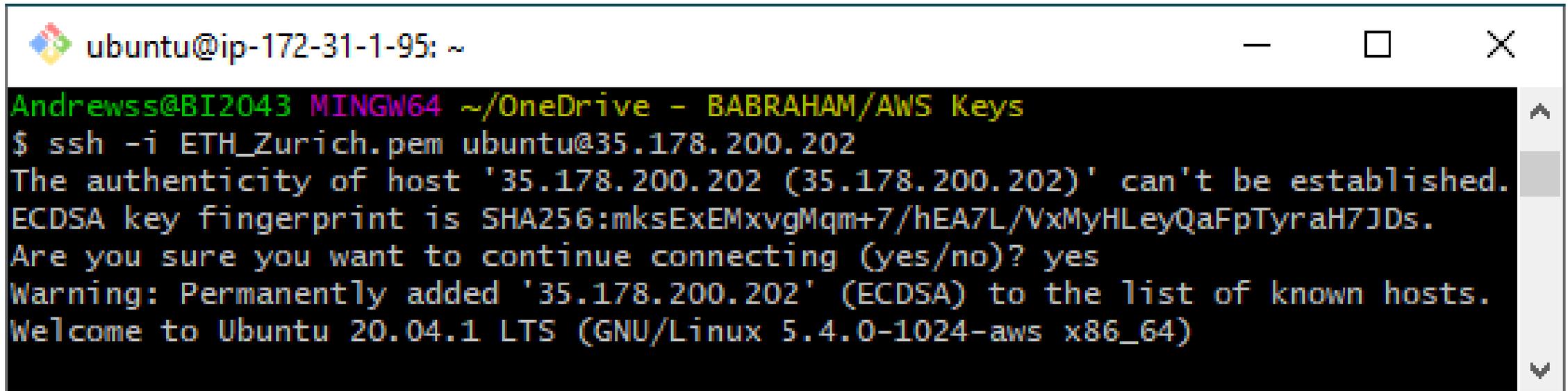
- `ssh username@server.address`
- [Will be promoted for password]



```
andrewss@headstone:~  
Andrewss@BI2043 MINGW64 ~  
$ ssh andrewss@headstone  
Welcome to the BabrahamBI cluster.  
  
andrewss@headstone's password:  
Last login: Thu Nov  5 16:09:19 2020 from 149.155.134.75  
[andrewss@headstone ~]$
```

SSH + Key connection

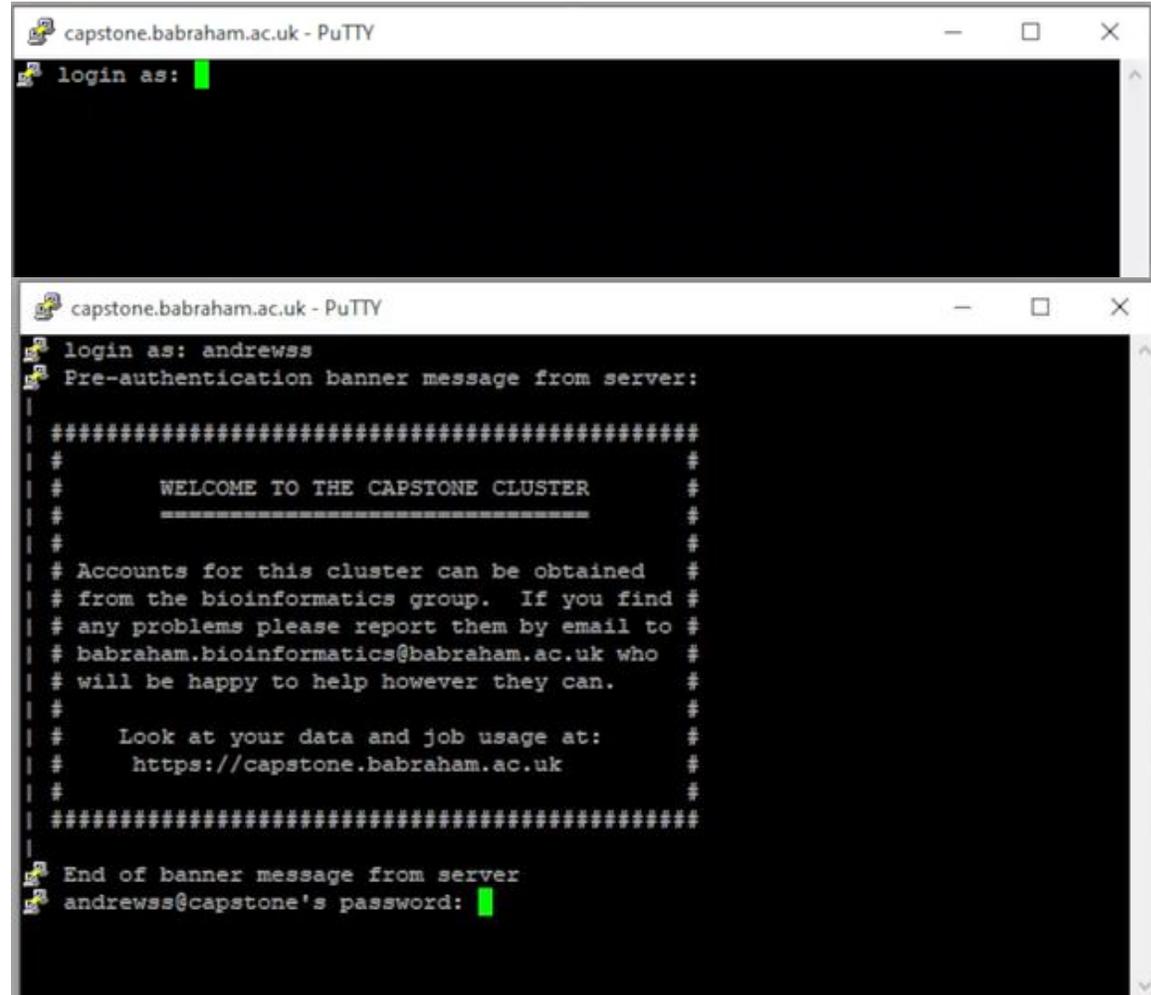
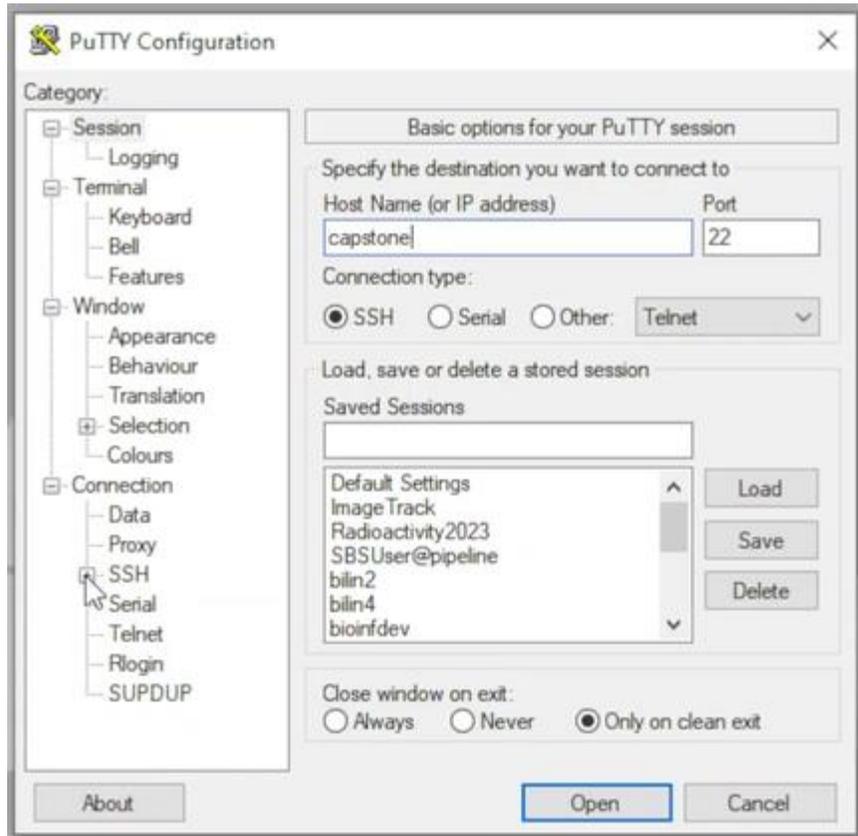
- `ssh -i [key_file.pem] username@server.address`



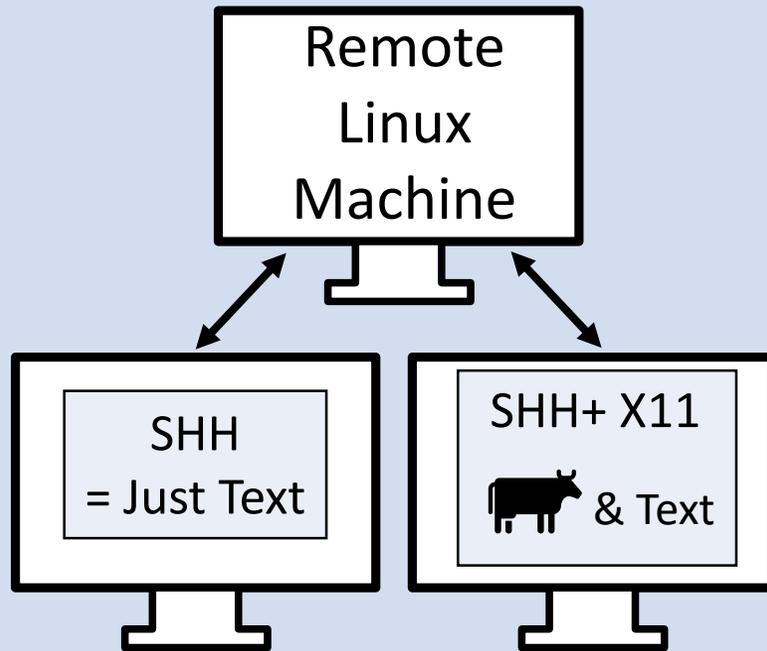
The image shows a terminal window with a title bar that reads "ubuntu@ip-172-31-1-95: ~". The terminal content is as follows:

```
Andrewss@BI2043 MINGW64 ~/OneDrive - BABRAHAM/AWS Keys
$ ssh -i ETH_Zurich.pem ubuntu@35.178.200.202
The authenticity of host '35.178.200.202 (35.178.200.202)' can't be established.
ECDSA key fingerprint is SHA256:mksExEMxvgMqm+7/hEA7L/VxMyHLeyQaFpTyrAH7JDs.
Are you sure you want to continue connecting (yes/no)? yes
Warning: Permanently added '35.178.200.202' (ECDSA) to the list of known hosts.
Welcome to Ubuntu 20.04.1 LTS (GNU/Linux 5.4.0-1024-aws x86_64)
```

SSH Using PuTTY



SSH with Graphical Connections



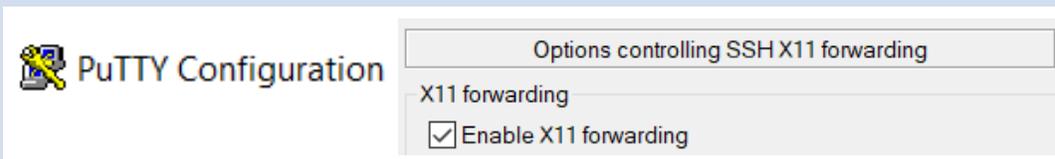
Single application windows

- X11
- Sits on top of SSH



<https://www.xquartz.org/>
<https://sourceforge.net/projects/vcxsrv/>

```
ssh -YC -i [key_file.pem] username@server.address
```

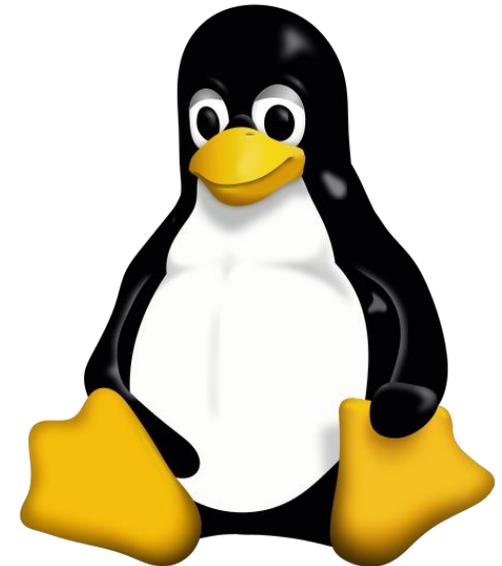


Virtual Desktop

- VNC
- Stand alone application or
- Browser based desktop

Exercise 1

Running programs in the BASH shell



Launching programs in Linux

Two major methods:

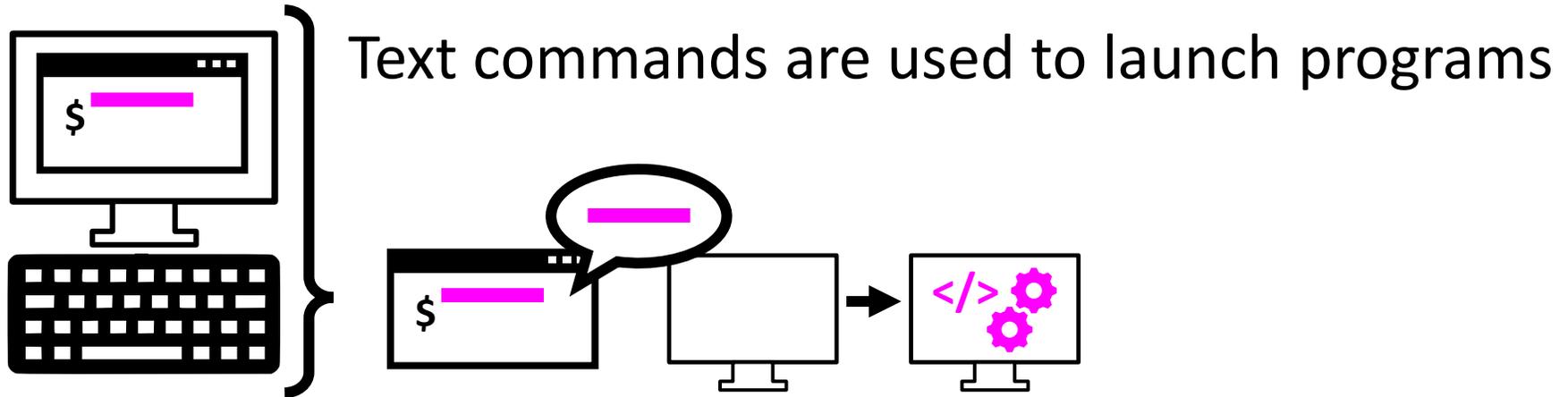
| | Graphical | Command Line |
|--|---|--|
| Requires? | Full Graphical Environment e.g. virtual desktop | Command Line Linux Environment |
| How to Launch a program? | Click an icon | Type commands into an interpreter |
| Works for: Graphical Programs Non-Graphical Programs | <input checked="" type="checkbox"/> <input type="checkbox"/> | <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> |

Most data processing and remote access will be command line based

For this we need an interpreter....

Shells

A shell is a command line interpreter, used to launch software in Linux

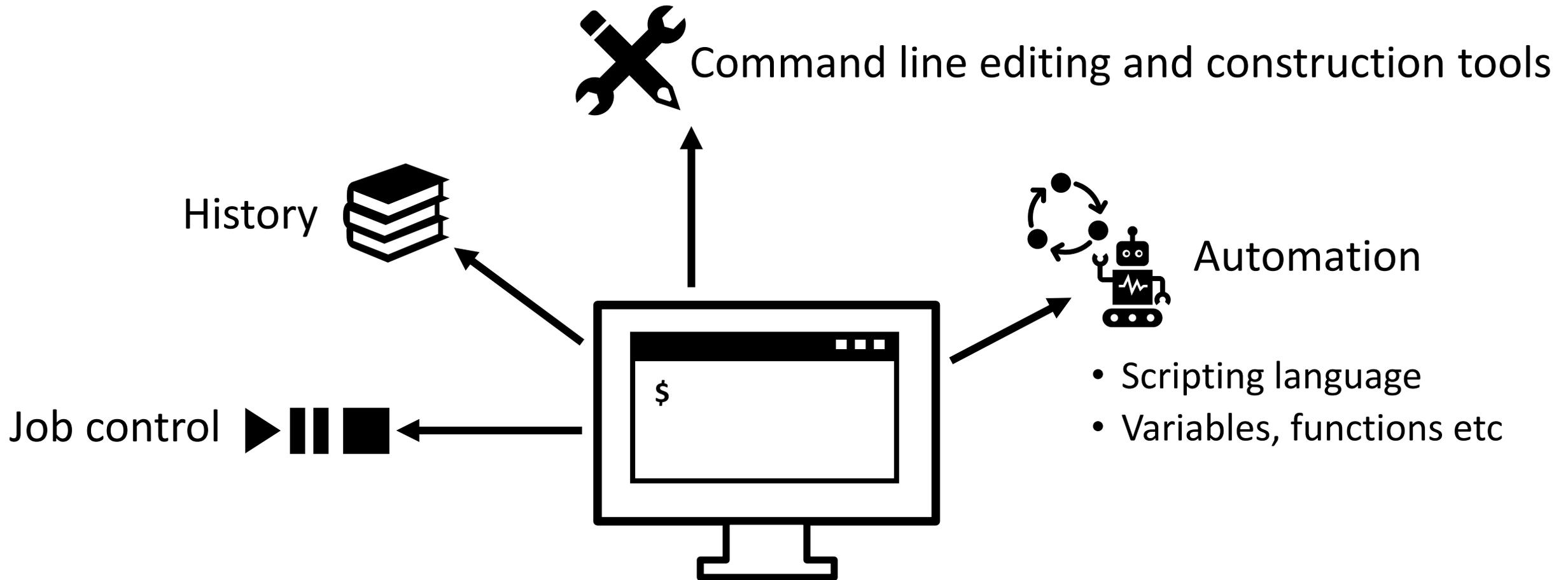


Many different shells available:

- Largely similar in how they launch programs
- Differ in some of their automation/ other clever functions

We will use the most popular shell: **BASH**

What Does a Shell Provide?



What does a Shell look like?



We will be using a graphical terminal running BASH

Running programs

Type the name of the program you want to run



Add on any options the program needs



Press return - the program will run



When the program ends control will return to the shell



Run the next program!

Running programs

```
student@ip1-2-3-4:~$ ls  
Desktop  Documents  Downloads  examples.desktop  Music  
Pictures  Public  Templates  Videos  
  
student@ip1-2-3-4:~$
```

- Command prompt - you can't enter a command unless you can see this
- The command we're going to run (`ls` in this case, to list files)
- The output of the command - just text in this case

Running graphical programs

```
student@ip1-2-3-4:~$ xeyes
```



```
student@ip1-2-3-4:~$
```

Note that you can't enter another command until you close the program you launched

Command line switches

To change the behaviour of the program must write the appropriate switch

- Different options are represented by short and/or long forms (usually both)

| Short Form | Long Form |
|--|---|
| Minus plus single letter <code>-x -c -z</code> Can be combined <code>-xcz</code> | Two minuses plus a word <code>--extract --gzip</code> Can't be combined |

- Switches can be binary (on/off) or take an additional value

| Binary (on/off) | + Additional Value |
|---|---|
| Switch alone specifies the behaviour <code>--gzip</code> | An additional value is provided after the switch <code>-f somfile.txt</code> (specify a filename) <code>--width=30</code> (specify a value) Use a [space] or = to separate |

Figuring Out Options...

Programmes usually come with documentation for their options and usage

| Core Programs | Non-Core Programs |
|----------------------------|--|
| Included with the install | Additional installs e.g analysis tools |
| Manual page (always) | Help Page (usually) |
| <code>man [program]</code> | <code>[program] --help (or -h)</code> |

These pages all follow a very similar structure...

Manual Pages

vs

Help Pages

```
CAT(1) User Commands CAT(1)
NAME
  cat - concatenate files and print on the standard output

SYNOPSIS
  cat [OPTION]... [FILE]...

DESCRIPTION
  Concatenate FILE(s) to standard output.

  With no FILE, or when FILE is -, read standard input.

  -A, --show-all
      equivalent to -vET

  -b, --number-nonblank
      number nonempty output lines, overrides -n

  -e
      equivalent to -vE

  -E, --show-ends
      display $ at end of each line

  -n, --number
      number all output lines

  -s, --squeeze-blank
      suppress repeated empty output lines

  -t
      equivalent to -vT

  -T, --show-tabs
      display TAB characters as ^I

  -u
      (ignored)

  -v, --show-nonprinting
      use ^ and M- notation, except for LFD and TAB

  --help display this help and exit

  --version
      output version information and exit

EXAMPLES
  cat f - g
      Output f's contents, then standard input, then g's contents.
```

Name

Synopsis

Description

Examples

```
FastQC - A high throughput sequence QC analysis tool

SYNOPSIS
  fastqc seqfile1 seqfile2 .. seqfileN

  fastqc [-o output dir] [--(no)extract] [-f fastq|bam|sam]
         [-c contaminant file] seqfile1 .. seqfileN

DESCRIPTION
  FastQC reads a set of sequence files and produces from each one a quality control report consisting of a number of different modules, each one of which will help to identify a different potential type of problem in your data.

  If no files to process are specified on the command line then the program will start as an interactive graphical application. If files are provided on the command line then the program will run with no user interaction required. In this mode it is suitable for inclusion into a standardised analysis pipeline.

  The options for the program as follows:

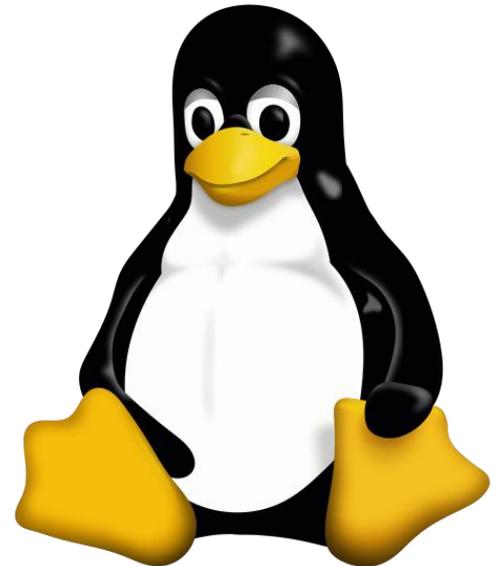
  -h --help      Print this help file and exit

  -v --version   Print the version of the program and exit

  -o --outdir    Create all output files in the specified output directory. Please note that this directory must exist as the program will not create it. If this option is not set then the output file for each sequence file is created in the same directory as the sequence file which was processed.
```

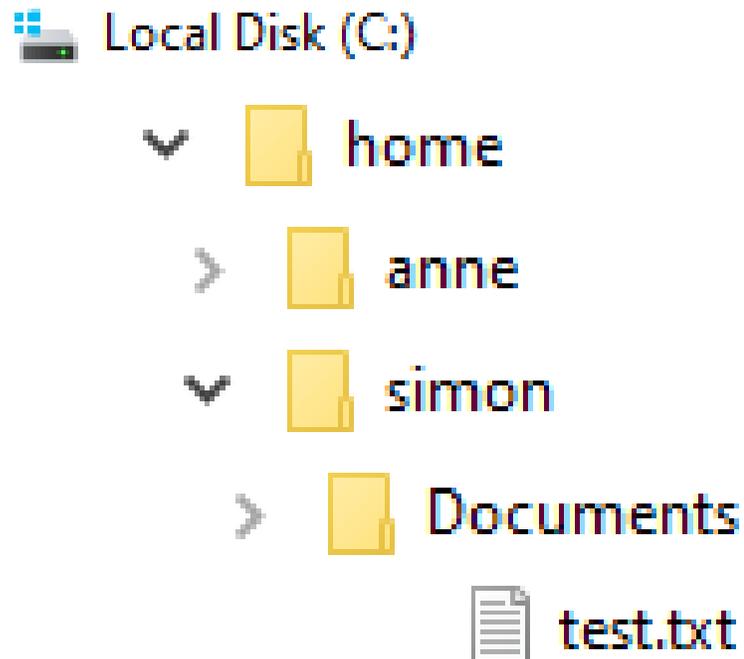
Exercise 2

Understanding Unix File Systems



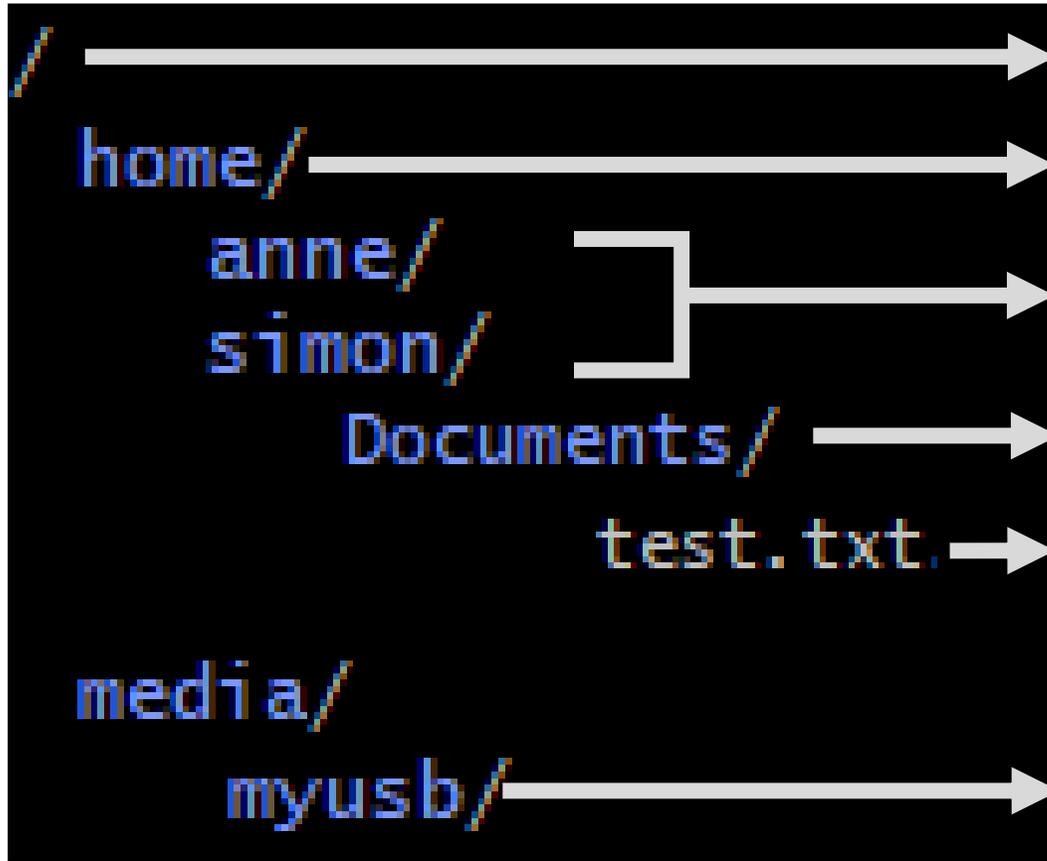
Unix File Systems vs Other File Systems

A Familiar Picture...



| Standard OS File System | Same in Unix? |
|----------------------------------|-------------------------------------|
| Hierarchical Directories | <input checked="" type="checkbox"/> |
| Each Directory can contain files | <input checked="" type="checkbox"/> |
| Use drive Letters | <input type="checkbox"/> |
| Need file extensions e.g. .txt | <input type="checkbox"/> |

A Simple Unix Filesystem



= Root Directory = Always the top of the file system

= Directory containing all users home directories

= Directory containing all users home directories

= A Directory – note names are case sensitive

= A text file we want to work with

= A USB stick added to the system

How do we write this in our shell? = Path

```
$ ls /home/simon/Documents/test.txt
```

Navigating The File System

- Every Unix session has a '**working directory**'
 - This is a folder where the shell looks for file paths
- Your initial working directory will normally be your home directory (eg `/home/user`)
- There are some useful commands to help navigate the system:

| Task | Command |
|---|--|
| What is my current working directory? | pwd |
| I want to make a new directory | mkdir [name of directory to make] |
| I want to move into a different directory | cd [location to move to] |
| I want to go home | cd |

Navigating The File System – An Example

```
[andrewss@server ~]$ pwd  
/home/andrewss
```

```
[andrewss@server ~]$ mkdir simon
```

```
[andrewss@server ~]$ cd simon  
[andrewss@server simon]$ pwd  
/home/andrewss/simon
```

```
[andrewss@server simon]$ cd  
[andrewss@server ~]$ pwd  
/home/andrewss
```

Specifying File Paths

Options:

1. Absolute paths from the top of the file system e.g.

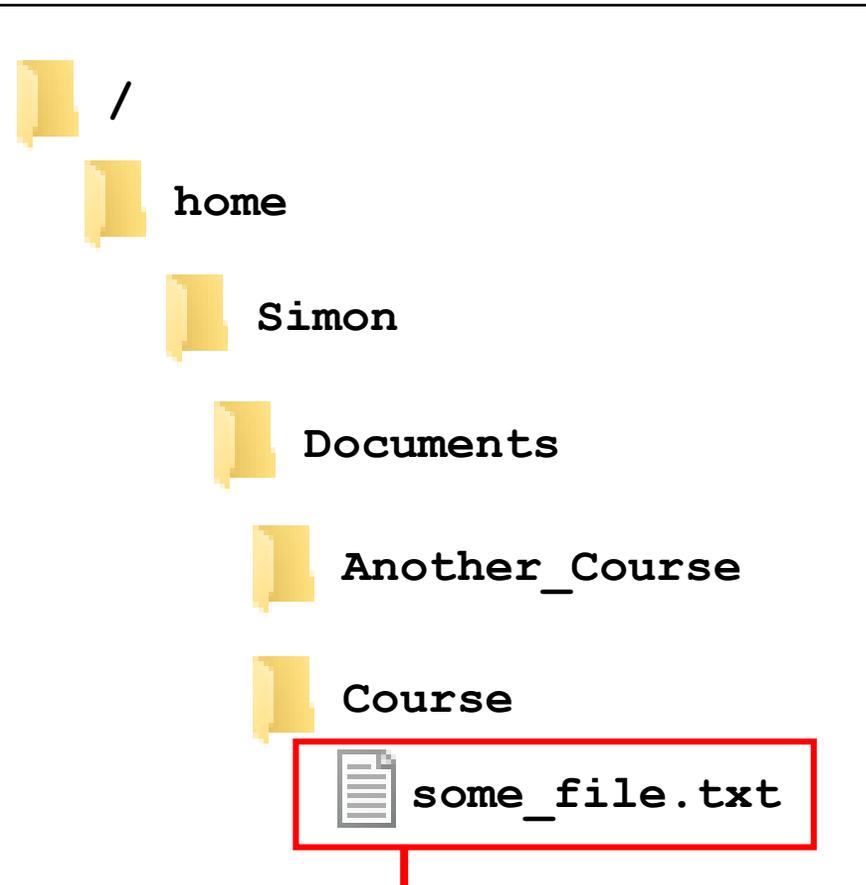
`/home/simon/Documents/Course/some_file.txt`

2. Relative paths from your current directory e.g.

if we are in Course = `some_file.txt`

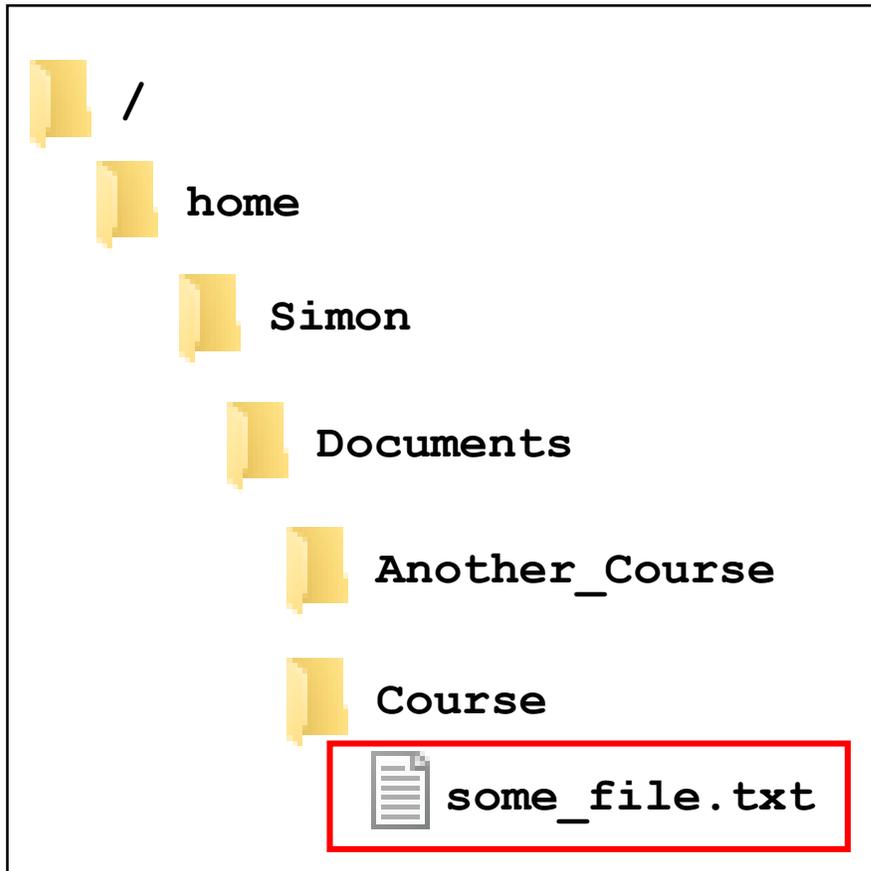
if we are in Documents = `Course/some_file.txt`

3. Paths using typing shortcuts



How can we refer to this file?

Specifying file paths - Shortcuts



Some Useful Shortcuts:

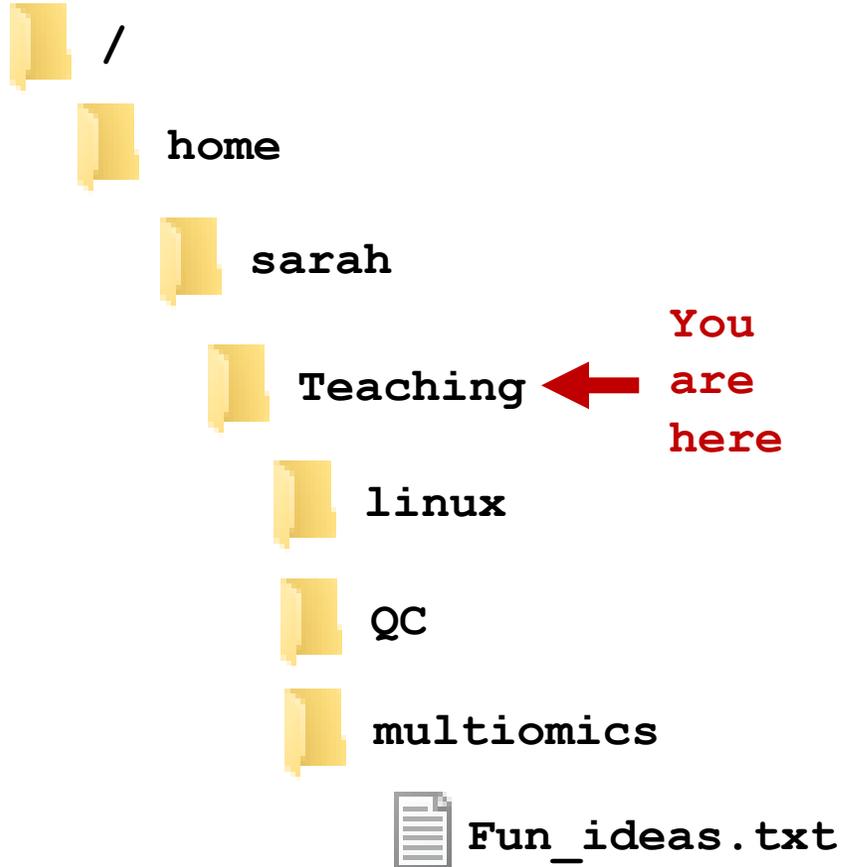
| | |
|----|---|
| ~ | The current user's home directory |
| . | The current directory |
| .. | The directory immediately above the current directory |

If we were in **Another_Course**

```
~/Documents/Course/some_file.txt
```

```
../Course/some_file.txt
```

Specifying File Paths – Question:

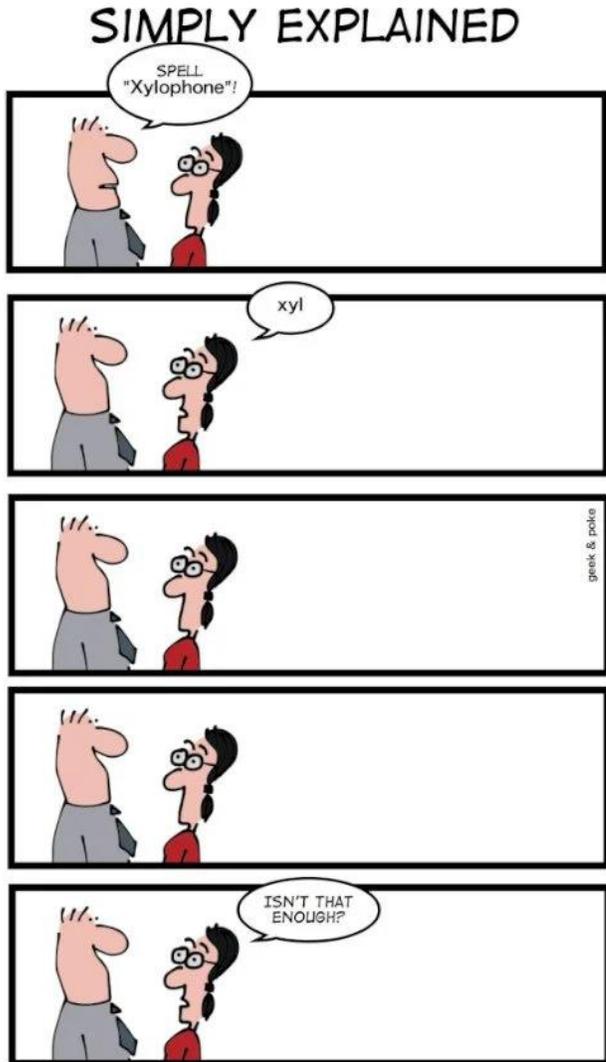
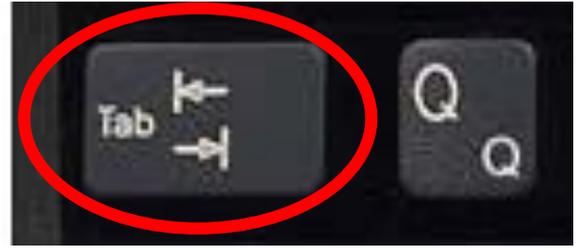


Which Path (or Paths!) will specify my “Fun_ideas.txt”?

- A** `/home/sarah/teaching/multiomics/Fun_ideas.txt`
- B** `~/Teaching/multiomics/Fun_ideas.txt`
- C** `multiomics/Fun_ideas.txt`

It's easy to make mistakes when typing paths

Command line completion...



...Is Basically the shell's version of Autocomplete

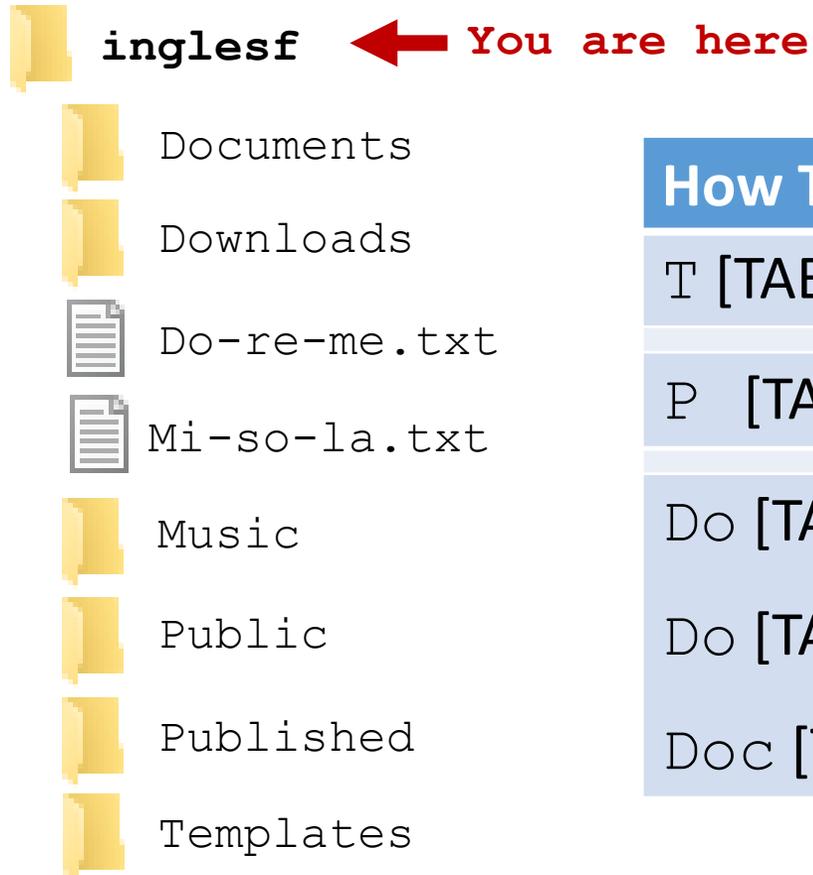
- Most errors in commands are typing errors in either program names or file paths
- Shells (ie BASH) can help by completing paths for us

How?

Type a partial path then press the TAB key

Hooray for the TAB Key!

Command line completion- Examples



How Tab Complete Will Work:

T [TAB] → Templates

P [TAB] → Publi

Do [TAB] → [beep]

Do [TAB] [TAB] → Documents Downloads Do-re-me.txt

Doc [TAB] → Documents

You should **ALWAYS** use TAB completion to fill in paths for locations **which exist** so you can't make typing mistakes

(so it won't work for output files!)

Command line completion- Question



Which Is the Shortest Way to Specify Mi-so-la.txt?

- A** M[TAB]
- B** Mi [TAB]
- C** Mi-so-la [TAB]

Specifying Multiple File Paths – Wildcards

Sometimes we want to refer to more than one file / location

 2024_report.txt  2023_report.txt  2019_report.txt

Common part of name
Unique part of name

Use Wild cards to substitute for unique parts of related file paths

- Shell will expand them before passing them on to the program

| Wildcard | Meaning | Example |
|----------|------------------------------|-----------------|
| ? | One of Any character | 202?_report.txt |
| * | Any number of Any characters | 20*_report.txt |



Could be more ambiguous here e.g. **20*** , ***.txt** or even *****

But it depends what else this path would capture!

Using Wildcards

How do we use them:

At any point in the path



Multiple wildcards can be in the same path



Do make sure expression captures files of interest specifically!



Command line completion won't work after the first wildcard



```
ls -ltd --reverse D*
```



Program
name

Switches

Data
(normally files)

Using Wildcards - Questions



My Working Directory:



Monday



mon_1.txt



mon_2.txt



mon_3.txt



mon_500.txt



Tuesday



tue_1.txt



tue_2.txt



tue_3.csv

How can I list only text files from Tuesday?

A `ls Tuesday/*`

B `ls Tuesday/*.txt`

C `ls Tuesday/*.txt`

Using Wildcards - Questions



My Working Directory:



Monday



mon_1.txt



mon_2.txt



mon_3.txt



mon_500.txt



Tuesday



tue_1.txt



tue_2.txt



tue_3.csv

What files will “`ls Monday/mon_?.txt`” return?

A mon_1.txt mon_2.txt mon_3.txt

B mon_1.txt mon_2.txt mon_3.txt mon_500.txt

C tue_1.txt tue_2.txt tue_3.csv

Using Wildcards - Questions



My Working Directory:



Monday



mon_1.txt



mon_2.txt



mon_3.txt



mon_500.txt



Tuesday



tue_1.txt



tue_2.txt



tue_3.csv

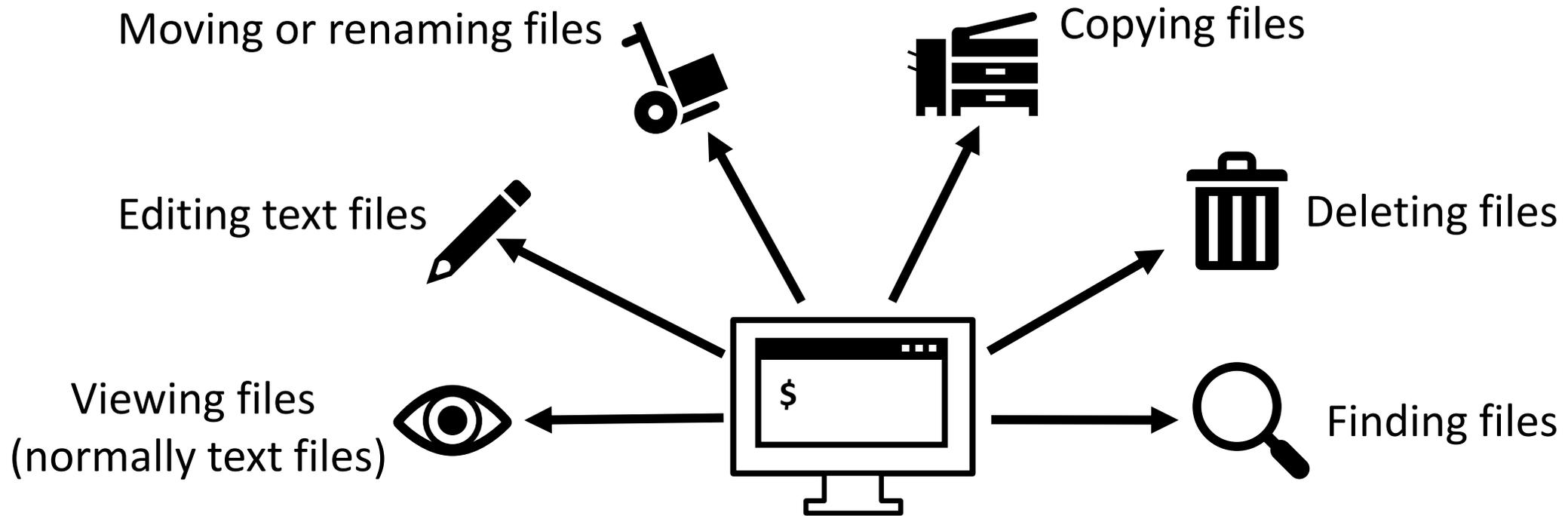
How can I list all the text files in both Monday and Tuesday?

A `ls ?day/*`

B `ls *`

C `ls */*txt`

Manipulating files



You will spend a lot of time managing files on a Linux system

Viewing Files

Simplest solution

| | |
|-------------------------|--|
| <code>cat [file]</code> | Sends the entire contents of a file (or multiple files) to the screen. |
|-------------------------|--|

Quick look

| | |
|------------------------------------|---------------------------------------|
| <code>head -[number] [file]</code> | Look at the first X lines of the file |
|------------------------------------|---------------------------------------|

| | |
|------------------------------------|--------------------------------------|
| <code>tail -[number] [file]</code> | Look at the last X lines of the file |
|------------------------------------|--------------------------------------|

More scalable solution

| | |
|--------------------------|--|
| <code>less [file]</code> | A 'pager' program, sends output to the screen one page at a time |
|--------------------------|--|

| | |
|-----------------|--|
| <code>-s</code> | A useful switch that stops line wrapping |
|-----------------|--|

Navigation inside less:

Return / j = move down one line

k = move up one line

Space = move down one page

b = go back one page

/[term] = search for [term] in the file

q = quit back to the command prompt

Editing files

- Lots of text editors exist, both graphical and command line
- Many have special functionality for specific content (C, HTML etc)
- nano is a simple command line editor which is always present

nano [filename]

edits if file exists, creates if it doesn't

```
GNU nano 2.9.3 test.txt Modified
This is the nano text editor.
You can type stuff in here...
The options at the bottom are commands, the ^ means the control key
eg: Control+K cuts the current line of text and Control+U will paste it.
Control+O will write out the current contents of the editor,
and Control+X will exit back to the shell.
[]
^G Get Help      ^O Write Out    ^W Where Is    ^K Cut Text    ^J Justify     ^C Cur Pos
^X Exit          ^R Read File   ^\ Replace     ^U Uncut Text  ^T To Spell    ^  Go To Line
```

Moving / Renaming files

- Use `mv` command for both (renaming = moving from one name to another)

```
mv [existing file or directory] [new name/location]
```

- Good to Know....
 - If “location” is an existing directory, the file is moved there with its existing name
 - Moving a directory moves all of its contents as well
 - Shortcuts can help to form the path of where you want to move files to/from

The return of useful shortcuts!

| | | |
|-----------------|---|-------------------------|
| <code>.</code> | The current directory | Useful for “pull” moves |
| <code>..</code> | The directory immediately above the current directory | Useful for “push” moves |

Moving / Renaming files – “Push”

| Start | Command | Outcome |
|--|--|--|
| | <pre>mv old.txt new.txt</pre> |  my_dir  new.txt |
| <p>You are here →  my_dir  old.txt  Saved</p> | <pre>mv old.txt ../Saved/</pre> |  my_dir  Saved  old.txt |
| | <pre>mv old.txt ../Saved/new.txt</pre> |  my_dir  Saved  new.txt |

Moving / Renaming files – “Pull”

| Start | Command | Outcome |
|--|--|---|
| <p data-bbox="96 701 211 851">You are here</p>  <p data-bbox="321 508 741 836"> my_dir  old.txt  Saved</p> | <pre data-bbox="932 658 1556 701">mv ../my_dir/old.txt .</pre> | <p data-bbox="1663 515 2053 836"> my_dir  Saved  old.txt</p> |

Copying a file

- Use `cp` command on a single file

```
cp [existing file] [new name/location]
```

| Start | Command | Outcome |
|---|-------------------------------|---|
|   my_dir  old.txt | <pre>cp old.txt new.txt</pre> |  my_dir  old.txt  new.txt |

Copying Directories with recursive copy

```
cp -r [existing directory] [new name/location]
```

| Start | Command | Outcome |
|---|---|--|
|   my_dir  Saved  test.txt | <pre>cp -r ../Saved NewDir</pre> |  my_dir  NewDir  test.txt |
|   my_dir  ExistingDir  Saved  test.txt | <pre>cp -r ../Saved ExistingDir/ (only if ExistingDir exists)</pre> |  my_dir  ExistingDir  Saved  test.txt |

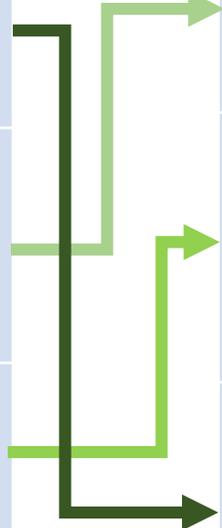
*remember the original "Saved" directory will also still exist

Copying files: Match the Command with the Desired Action



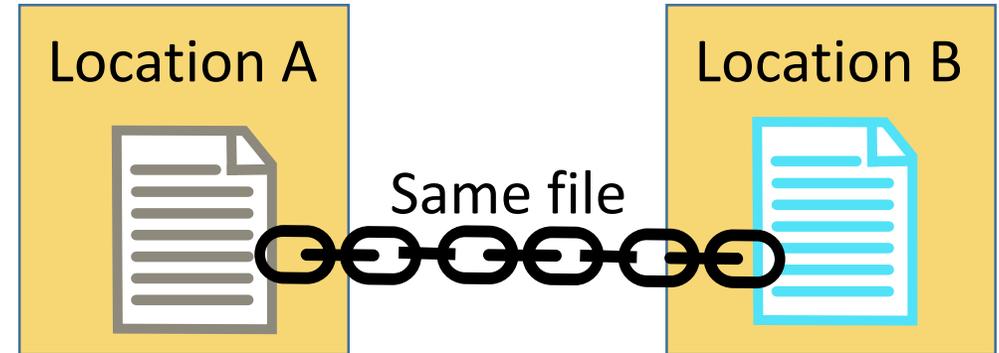
| Working Directory | Action |
|-------------------|--|
| my_dir | 1) Copy old.txt to Saved |
| my_dir | 2) Copy old.txt to Saved and call it new.txt |
| Saved | 3) Copy old.txt to Saved |

| Command |
|---|
| A) <code>cp old.txt ../Saved/new.txt</code> |
| B) <code>cp ../Saved/old.txt .</code> |
| C) <code>cp old.txt ../Saved/</code> |



Linking rather than copying

- Copy duplicates the data in a file
 - Can be a problem with big data files
- Links are a way to do 'virtual' copies
- Two types of link, hard links and soft (or symbolic) links
 - We will always use soft links as they're more flexible



```
ln -s [from] [to]
```

| Start | Command | Outcome |
|--|-------------------------------------|---|
|  mydir  test.txt | <pre>ln -s test.txt test2.txt</pre> |  mydir  test.txt  test2.txt |

Working with symbolic links

When you list a link you can see where it points...

```
$ ls -l test2.txt
```

```
lrwxrwxrwx 1 babraham babraham 8 Sep 11 16:27 test2.txt -> test.txt
```

...but you can use it like a file

```
$ cat test.txt
```

```
This is a test file
```

=

```
$ cat test2.txt
```

```
This is a test file
```

Finding Things with `find`

find [starting point] [global options] [other arguments]

Location to start from

modify the behaviour of find

Tests of what to look for

- How to handle symbolic links
`-H`, `-L`, `-P`
- How to handle how deep to search in the filesystem
`-maxdepth` `-mindepth`

- Find a given file name
`-name [filename]`
- Find matches belonging to a user
`-user [username]`
- Find matches of a certain type
`- d -f`



mydir



file1.txt



file3.txt



file2.txt



file4.csv



mysubdir



yet_another_file.txt

Example:

```
find .-maxdepth 1 -name '*.txt'
```

Deleting files



Linux has no undo.
Deleting files has no recycle bin.
Linux will not ask you "are you sure"



Use the `rm` command to delete files and directories (and all of their contents)

```
rm [name(s) of file to delete]
```

```
rm -r [name(s) of directory to delete]
```

Examples

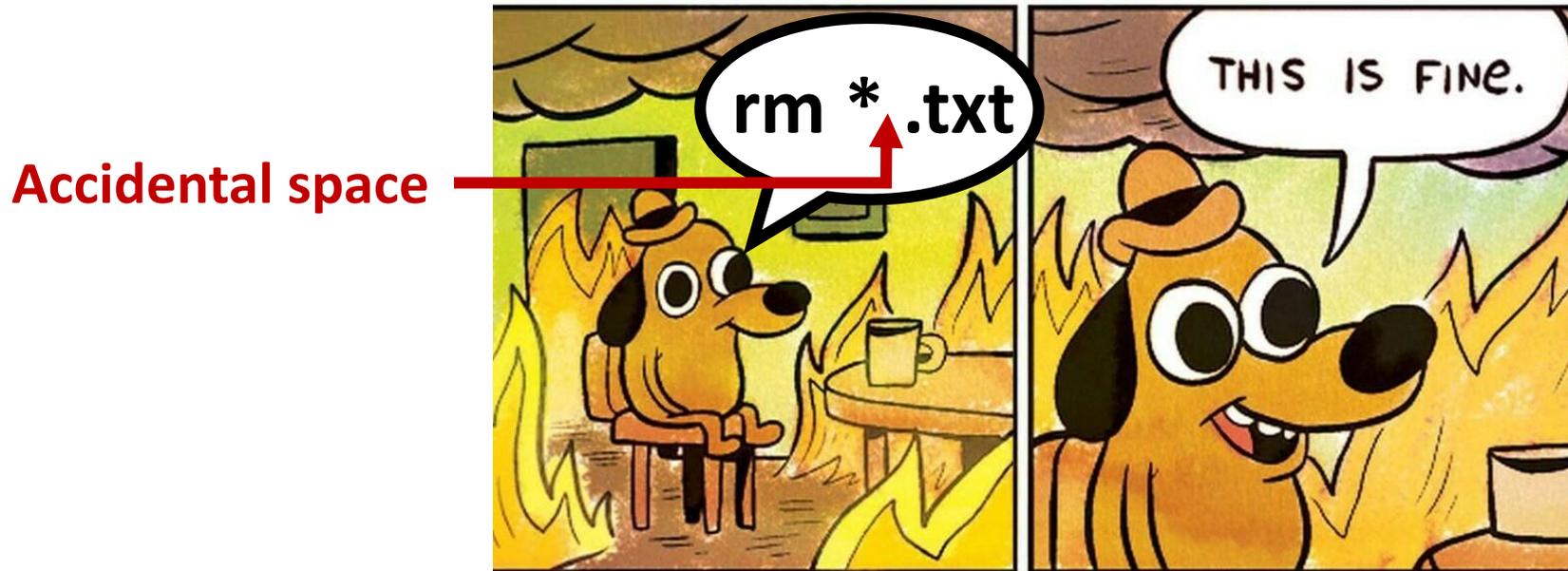
- `rm test_file.txt test_file2.txt`
- `rm -r Old_directory/`

Deleting files – With Wildcards

You can use the wildcard shortcuts to delete multiple files or directories

```
rm *.txt
```

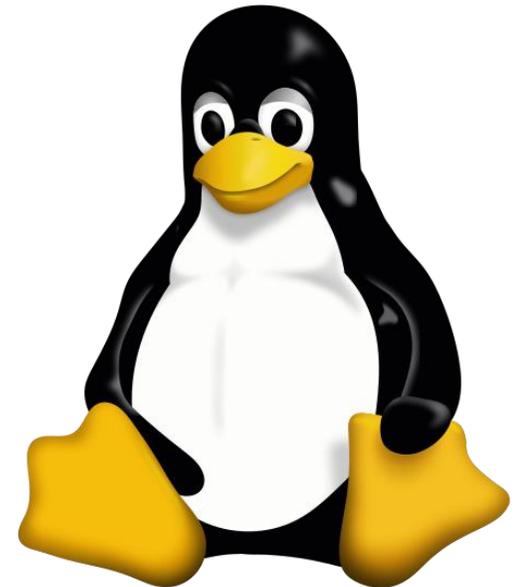
be **VERY** careful using wildcards



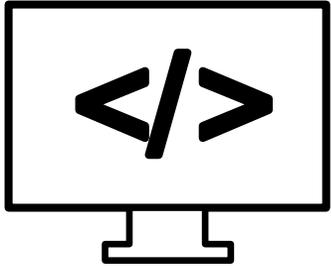
Always run `ls` first to see what will go

Exercise 3

More advanced BASH usage



What we know already

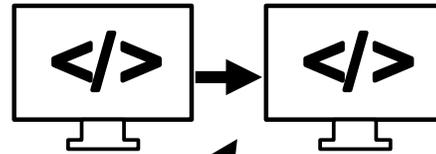


- How to run programs
 - How to modify the options for a program using switches
 - How to supply data to programs using file paths and wildcards

How Can we Usefully Build on this?

What else can we do...

Check for errors in programs
which are running



Link programs together
into small pipelines

Record the output
of programs

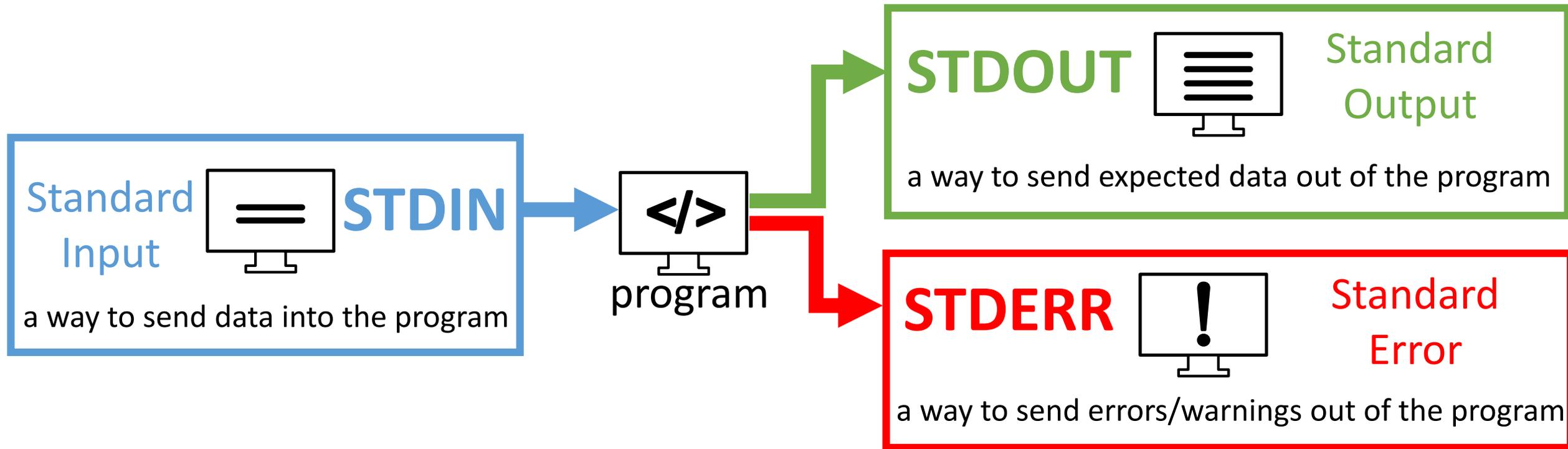


Automate the running of
programs over batches of files

All possible with a bit more knowledge of the BASH Shell

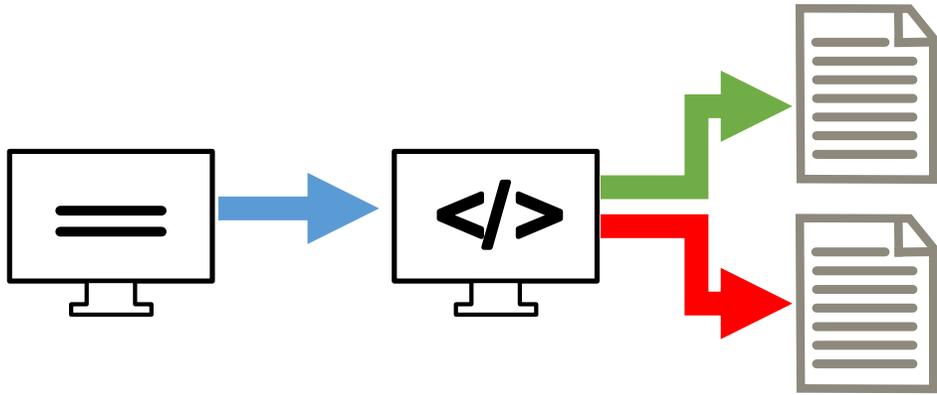
Communicating with Programs

Three data streams exist for all Linux programs:

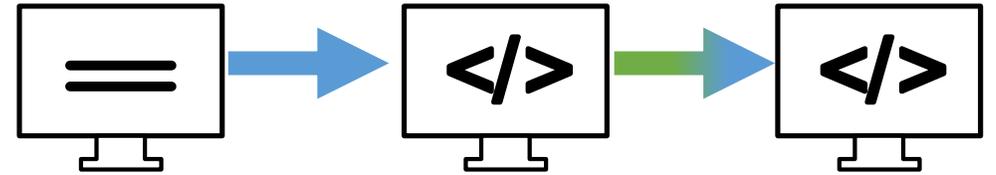


By default **STDOUT** and **STDERR** are connected to your shell
so when you see text coming from a program it's from these streams

Communicating with Programs

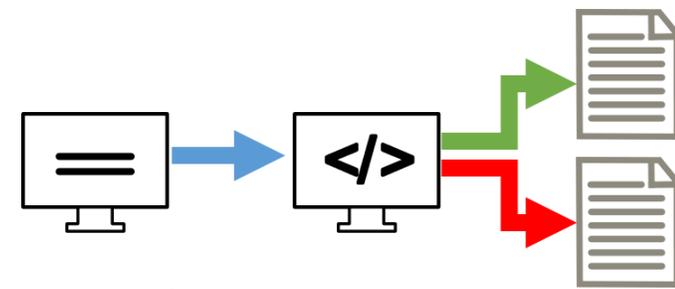


Redirecting standard streams to files



Redirecting standard streams to other programs

Redirecting standard streams



You can redirect using arrows at the end of your command

| | |
|---------------|--------------------------|
| > [file] | Redirects STDOUT |
| 2> [file] | Redirects STDERR |
| > [file] 2>&1 | Sends STDERR into STDOUT |
| < [file] | Redirects STDIN |

```
$ find . -print > file_list.txt 2> errors.txt
```

```
$ ls
```

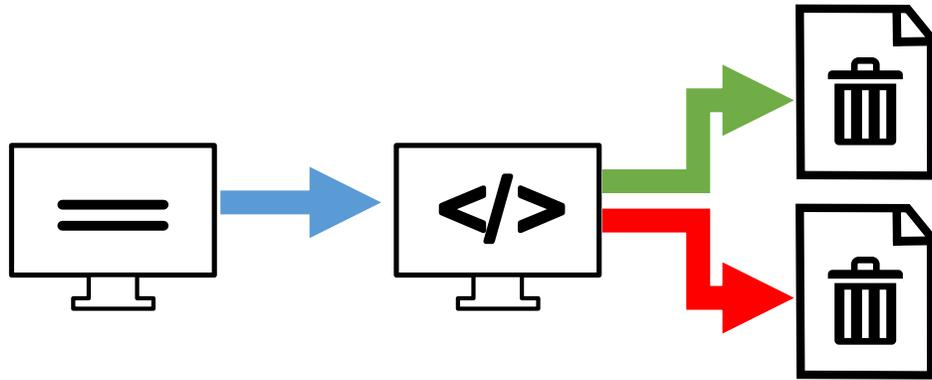
```
Data Desktop Documents Downloads errors.txt examples.desktop file_list.txt  
Music Pictures Public Templates Videos
```

```
$ head file_list.txt
```

```
.  
./Downloads  
./Pictures  
./Public  
./Music
```

Throwing stuff away

- Sometimes you want to be able to hide output
 - **STDOUT** - I just want to test whether something worked
 - **STDERR** - I want to hide progress / error messages



Linux defines a special file `/dev/null`
Which just discards all data sent to it

Throw away the STDOUT

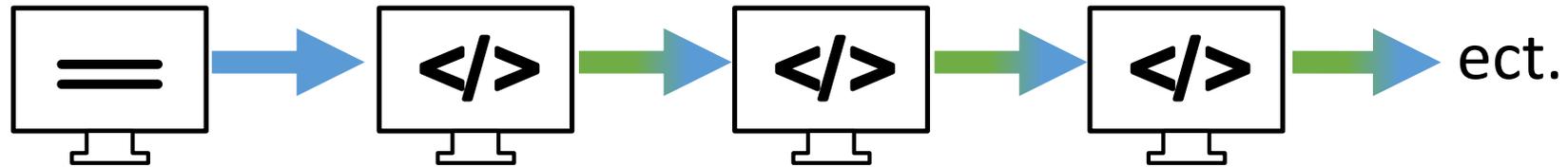
```
program > /dev/null
```

Throw away the STDERR

```
program 2> /dev/null
```

Linking programs together with pipes

UNIX was designed to have lots of small programs doing specific jobs
Which could be linked together to perform more advanced tasks



Do this by connecting STDOUT from one program to STDIN on another

This is done with Pipes |



```
$ ls | head -2
```

```
Data
```

```
Desktop
```

Useful programs for pipes

- You can theoretically use pipes to link any programs
- But there are some which are particularly useful, like:

| | |
|-------------------------------|------------------------------------|
| <code>wc</code> | to do word and line counting |
| <code>grep</code> | to do pattern searching |
| <code>sort</code> | to sort things |
| <code>Uniq</code> | to deduplicate things |
| <code>less</code> | to read large amounts of output |
| <code>zcat/gunzip/gzip</code> | to do decompression or compression |

Small example pipeline

Take a compressed fastq sequence file, extract from it all of the entries containing the telomere repeat sequence (TTAGGG) and count them

Decompress the fastq file → Find the pattern → Count the matches

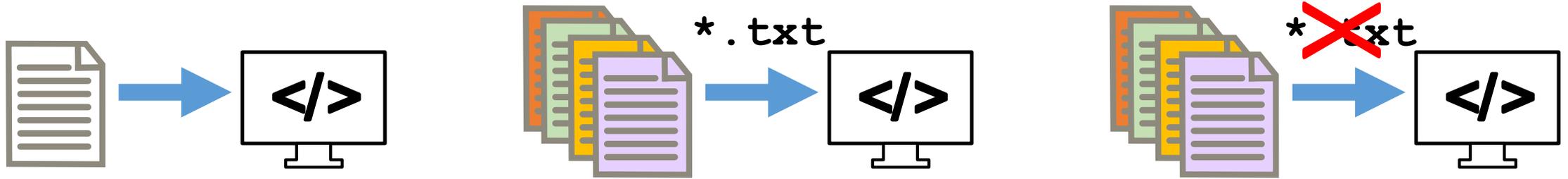
```
zcat file.fq.gz | grep TTAGGGTTAGGG | wc -l
```

```
$ zcat file.fq.gz | wc -l  
179536960
```

```
$ zcat file.fq.gz | grep TTAGGGTTAGGG | wc -l  
3925
```

Iterating over files

When processing data often need to re-run the same command multiple times for different input/output files.



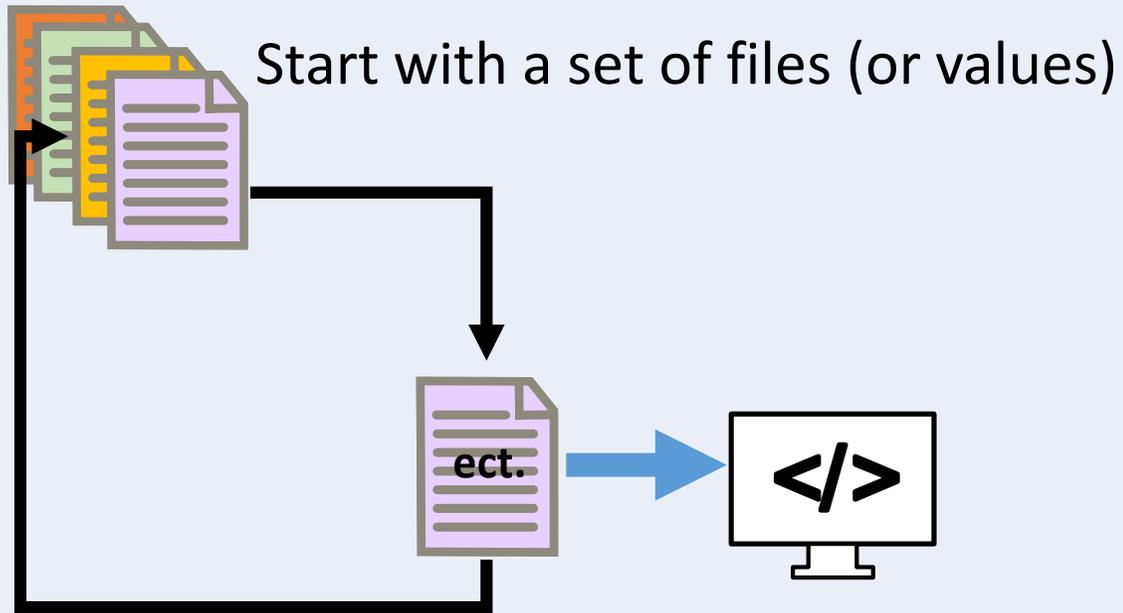
Some programs support being provided with multiple input files i.e. wildcards!

BUT MANY DON'T!

Instead we use the automation features of the BASH shell to automate running these programs

The BASH `for` loop

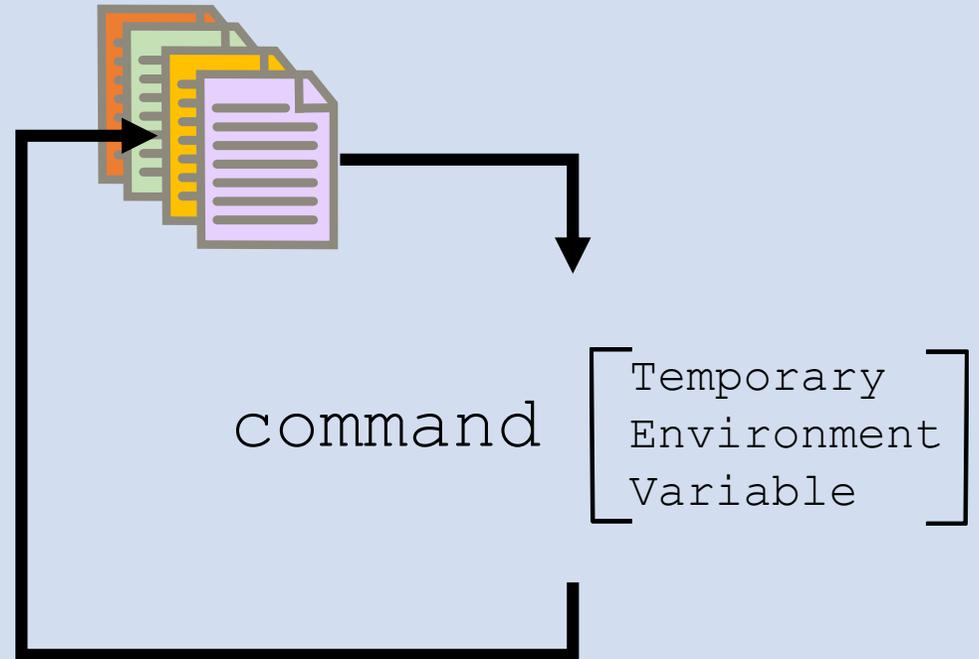
What?



Loop over these to do some function
for each in turn

How?

Use Simple looping construct



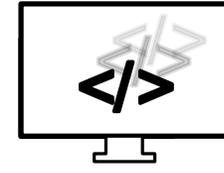
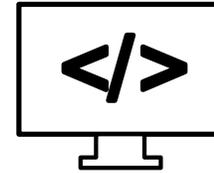
Write commands using a special variable
Takes on the value of each item in turn

Example of BASH **for** loops

```
for file in *txt  
  do  
    echo $file  
    grep .sam $file | wc -l  
  done
```

Job Control

- By default you run one job at a time in a shell
- Shells support multiple running jobs



jobs lists the jobs in this shell

States of job:

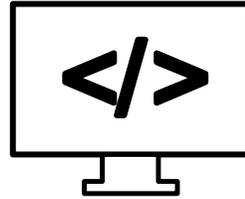
| | |
|------------------------|---|
| Running - foreground | shell has the attention of the job |
| Running - background | output goes to the shell but other jobs can run |
| Suspended | job exists but is paused, consumes no CPU |
| Running - disconnected | output is no longer attached to the shell |

Job Control

| Working Directory | |
|---|--|
| <code>prog_to_run</code> | starts in foreground |
| <code>prog_to_run &</code> | starts in background |
| <code>Control + Z</code> | suspends the current job |
| <code>bg</code> <code>fg</code> | Send a job to the background Bring a job to the foreground |
| <code>nohup prog_to_run</code> <code>nohup prog_to_run > log.txt &</code> | disconnects, logs to <code>nohup.out</code> ... or redirect to your choice of file Means it can't be killed when terminal exits |

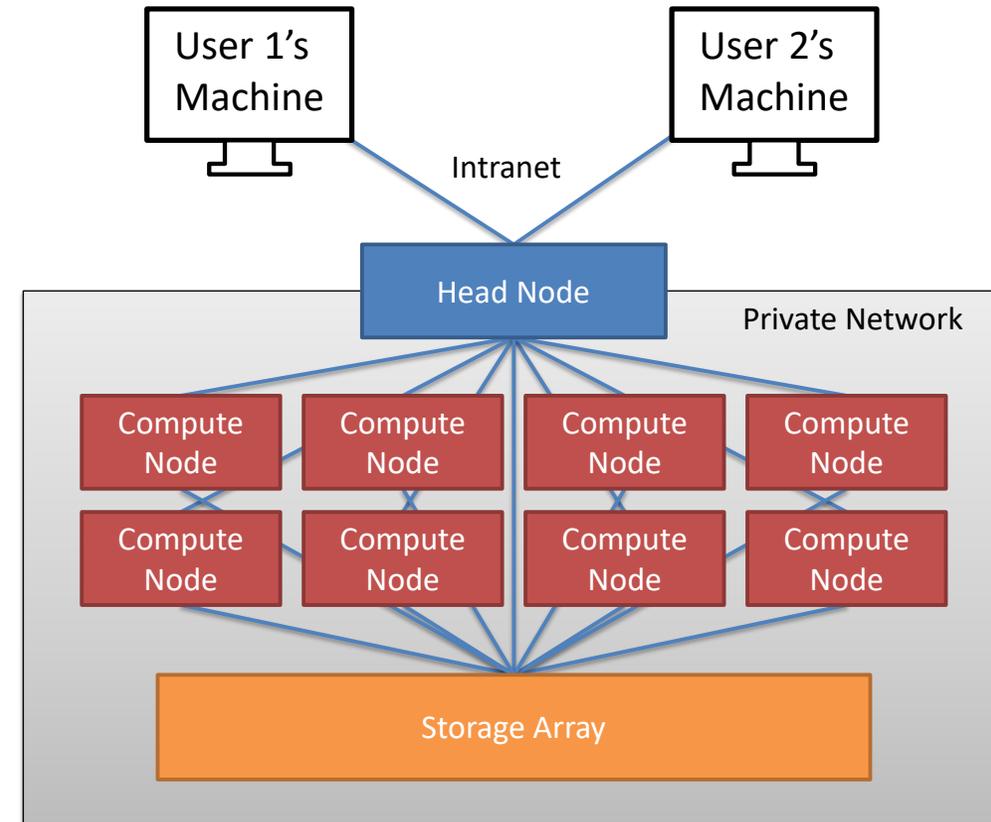
More Extended Job Control on Clusters

Control on a single machine



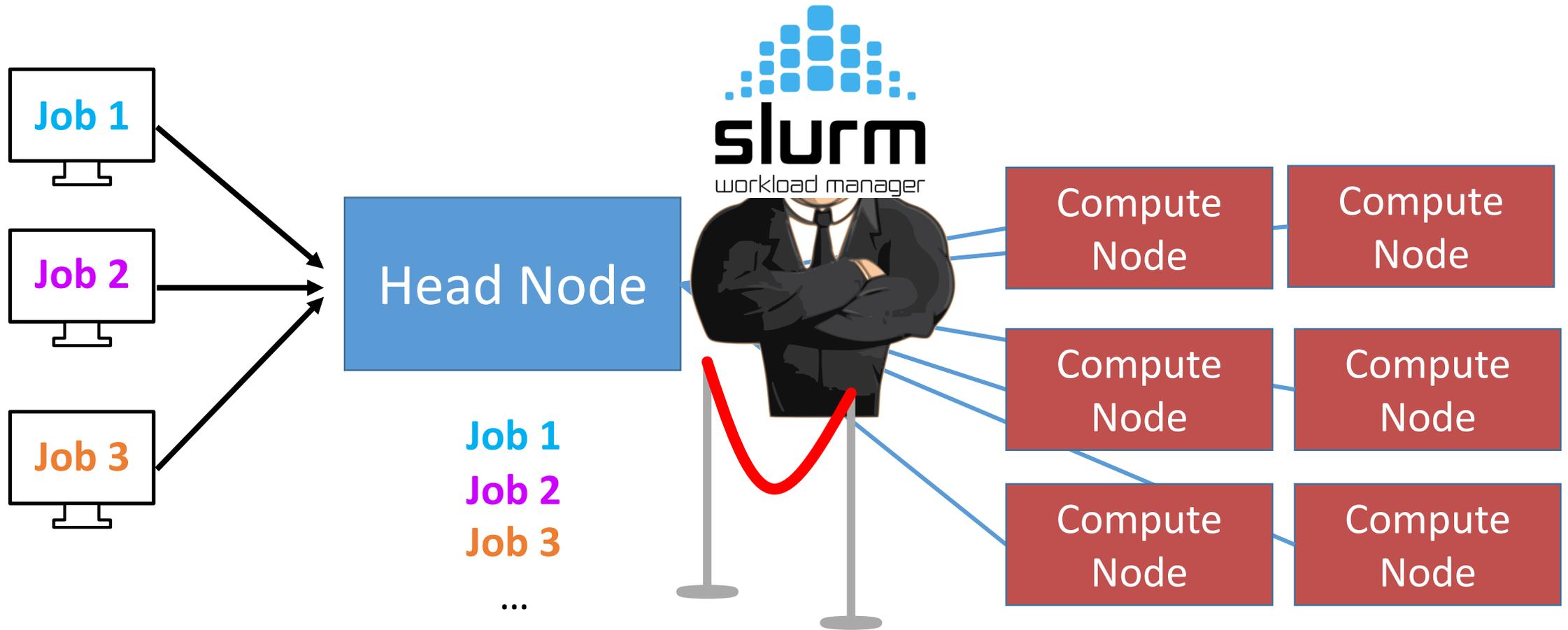
vs

Control on a Cluster



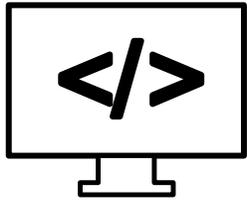
- Same for small jobs we can run on the Head Node
 - e.g. nohup, fg, bg
- Need a bit more control for bigger jobs
 - Workload managers
 - Workflow managers

Workload managers – Cluster Queues



Workload managers – Cluster Queues

Submitting a job directly



```
fastqc data.fq.gz
```

Submitting a job to a workload manager



```
srun
```

```
-o f.log
```

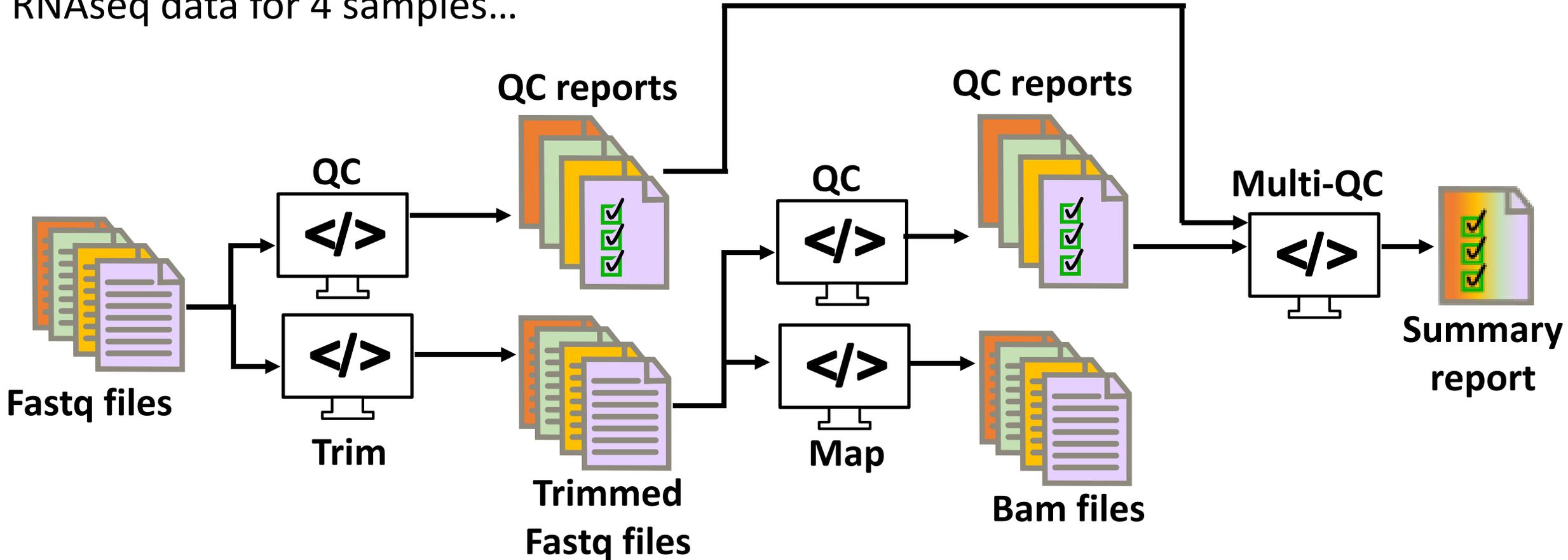
```
--cores=2
```

```
--mem=5G
```

```
fastqc data.fq.gz
```

Workflow Mangers – Beyond 1 job...

Imagine you have generated
RNAseq data for 4 samples...



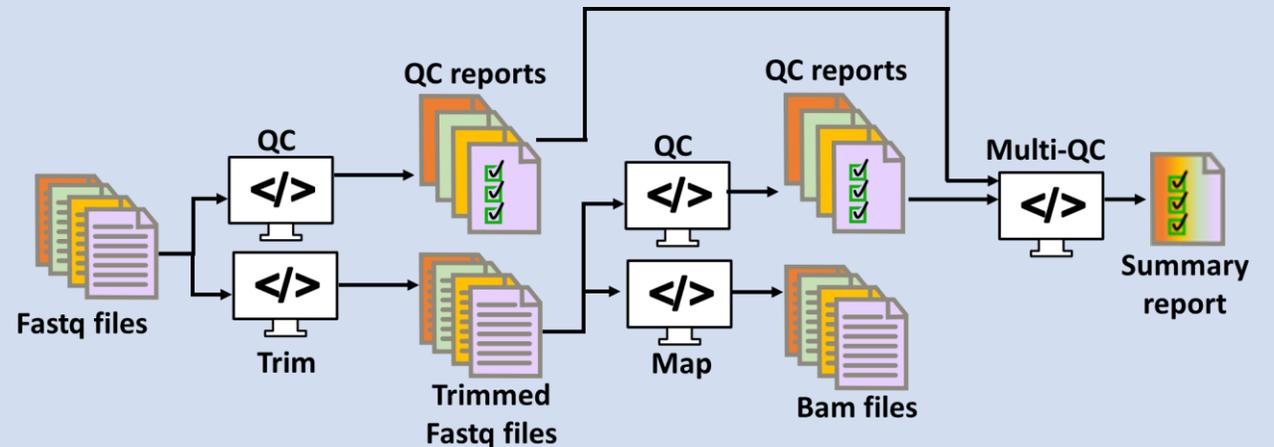
...A lot to coordinate!

Workflow Mangers

- Larger Scale Automation
- Multiple Programs
- Multiple Files
- Integrates with Clusters



Turn this...



...Into this!

```
nf_rnaseq --genome GRCh38 *fastq.gz
```

```

executor > slurm (21)
[15/929bd5] process > FASTQC (lane8_DD_P9_TGACCA_L008)
[b9/674ced] process > FASTQ_SCREEN (lane8_FF_P4_ATCACG_L008)
[ca/b39d14] process > TRIM_GALORE (lane8_FF_P9_CGATGT_L008)
[c0/4dcaf9] process > FASTQC2 (lane8_FF_P9_CGATGT_L008)
[58/879cf5] process > HISAT2 (lane8_FF_P9_CGATGT_L008)
[c4/cfe1f1] process > MULTIQC
Completed at: 05-Feb-2021 08:47:47
Duration      : 4m 2s
CPU hours    : 1.9
Succeeded    : 21

```

Workflow completion notification

Run Name: jovial_bartik

Execution completed successfully!

The command used to launch the workflow was as follows:

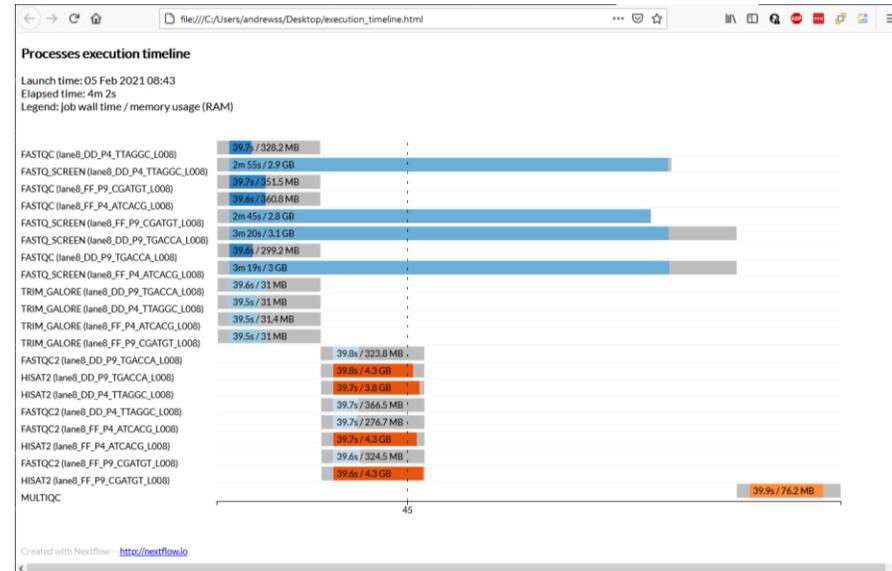
```

nextflow /bi/apps/nextflow/nextflow_pipelines/nf_rnaseq --genome GRCh38
lane8_DD_P4_TTAGGC_L008_R1.fastq.gz lane8_DD_P4_TTAGGC_L008_R2.fastq.gz
lane8_DD_P9_TGACCA_L008_R1.fastq.gz lane8_DD_P9_TGACCA_L008_R2.fastq.gz
lane8_FF_P4_ATCACG_L008_R1.fastq.gz lane8_FF_P4_ATCACG_L008_R2.fastq.gz
lane8_FF_P9_CGATGT_L008_R1.fastq.gz lane8_FF_P9_CGATGT_L008_R2.fastq.gz

```

Execution summary

Launch time 05-Feb-2021 08:43:45
 Ending time 05-Feb-2021 08:47:46 (duration: 4m 1s)
 Total CPU-Hours 1.9
 Tasks stats Succeeded: 21 Cashed: 0 Ignored: 0 Failed: 0



Exercise 4