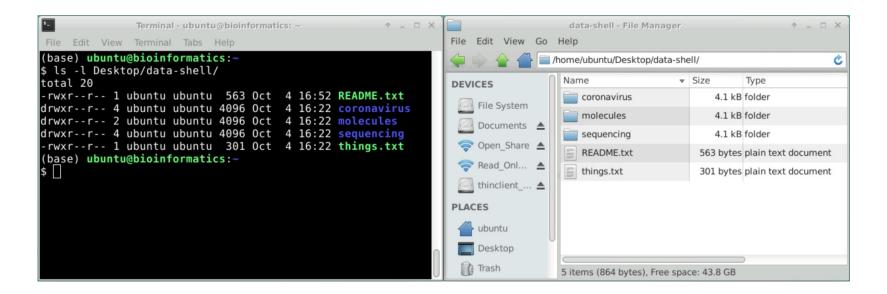
Introduction to UNIX and bash shell

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UNIX command line vs. Graphical user interface (GUI)



Unix command line

- Text-based interaction
- Powerful and flexible
- Scriptable
- Resource-Efficient

GUI

- Visual interaction
- User-friendly
- Less scriptable
- Resource-intensive



Nomenclature

- Unix a family of operating systems that includes Linux and Mac OS
- Terminal a program that allows interaction with the computer using textbased commands (i.e., a command-line interface)
- Unix Shell the command-line interpreter that enables interaction with a Unix-like operating system
- Bash a programming language used to interact with the Unix Shell

Don't worry too much about the terminology!

People interchangeably use terms like "shell", "command line", "bash", "terminal", "unix", "linux", "ubuntu" to mean broadly the same thing:

a (non-Windows) command line







Why do we need to learn UNIX and bash shell?

- Ubiquitous in computing applications and used in remote servers (like HPC)
- Most bioinformatics software is written for Linux
- Wide range of commands allow complex file manipulations, such as finding/replacing text patterns → very useful in bioinformatics
- Commands can be saved in script files → automation and reproducibility



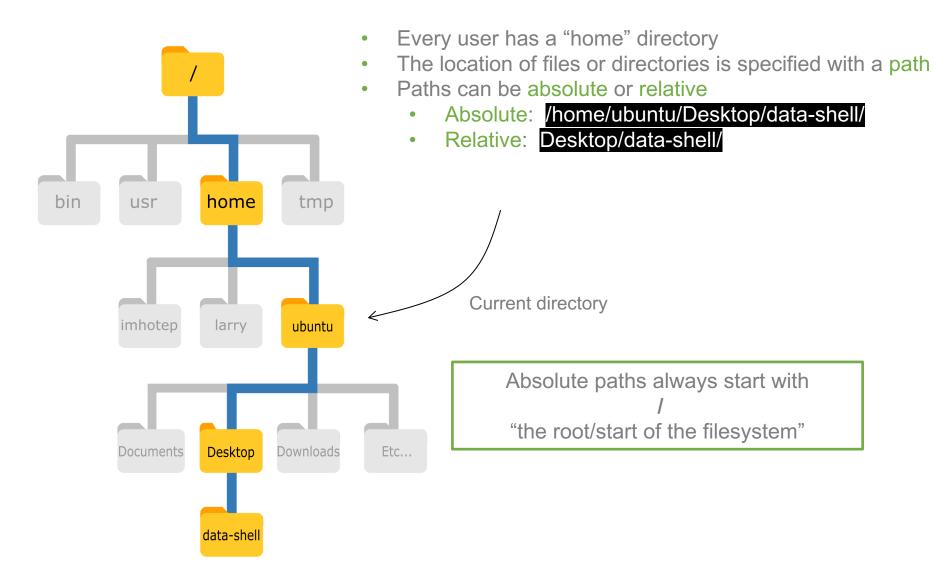
Motivating example

Combine two files search for lines count number of together that start with '>' lines in the output file1.fa 6 >S19249 >S19249 >S19249 >S23123 AACGCGTGGTTTGCA AACGCGTGGTTTGCA >S23391 >S23123 >S23123 >S44192 AACGCGTGGTTTGCA AACGCGTGGTTTGCA >S55652 >S23391 >S23391 >S15973 AACGCGTGGTTTGCA AACGCGTGGTTTGCA >S44192 file2.fa AACGCGTGGTTTGCA >S44192 >S55652 AACGCGTGGTTTGCA How many sequences are there AACGCGTGGTTTGCA >S55652 in a collection of FASTA files? >S15973 AACGCGTGGTTTGCA AACGCGTGGTTTGCA >S15973 AACGCGTGGTTTGCA

cat *.fa | grep ">" | wc -1



Files, directories and paths





Terminal layout

```
robin@computer-name:~$ pwd
/home/robin

robin@computer-name:~$ cd Desktop

robin@computer-name:~/Desktop$ cd Desktop

robin@computer-name:~/Desktop$
```

pwd → "print working directory"~ → "short for home directory"



Terminal layout

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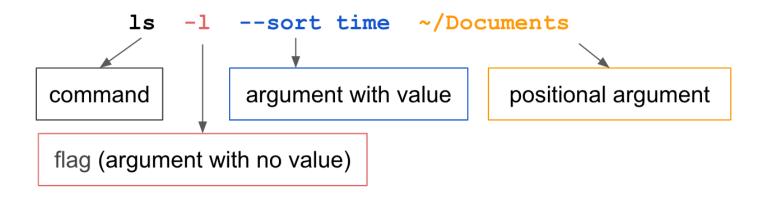
robin@computer-name:~/Desktop$ cd Desktop

robin@computer-name:~/Desktop$
```

cd → "change directory"



Basic command structure



List the files
in a long format
sorted by time of creation/modification
in the directory Documents

Documentation

man Is

```
NAME
      ls - list directory contents
SYNOPSIS
      ls [OPTION]... [FILE]...
DESCRIPTION
      List information about the FILEs (the current directory by default). Sort
entries alphabetically if none of
       -cftuvSUX nor --sort is specified.
      Mandatory arguments to long options are mandatory for short options too.
       -a, --all
             do not ignore entries starting with .
       -A, --almost-all
             do not list implied . and ..
       --author
             with -1, print the author of each file
             use a long listing format
       -1
       --sort=WORD
              sort by WORD instead of name: none (-U), size (-S), time (-t),
             version (-v), extension (-X)
```



Combining commands using pipe |

```
cat example.csv | cut -d "," -f 3
cat example.csv | cut -d "," -f 3 | sort
cat example.csv | cut -d "," -f 3 | sort | uniq
```

What is a "for loop"?

- A programming language technique which allows a piece of code to be repeated multiple times
- A "for loop" statement is usually called an "iterative statement"
- A typical example of a repetitive task is to read and process a list of files

```
$ bash count_atoms.sh cubabe.pdb
$ bash count_atoms.sh methane.pdb
$ bash count_atoms.sh ethane.pdb
$ bash count_atoms.sh pentane.pdb
```

```
for variable in item1 item2 item3
do
   some_command_using ${variable}
done
```

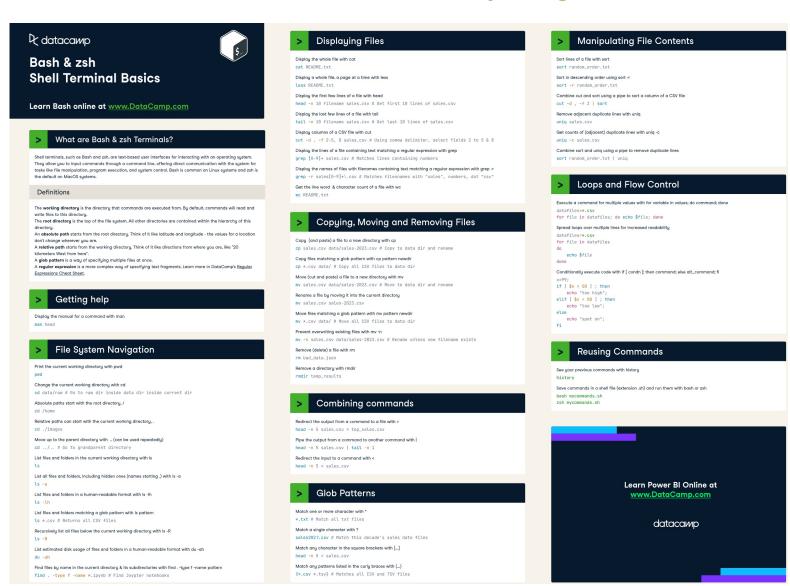


What is a shell script?

```
#!/bin/bash
pattern=$1
for filename in example_sub1.csv example_sub2.csv example_sub3.csv
do
   bash count_input.sh $pattern $filename
done
```



You don't need to remember everything...





Reference

Most of the content presented here is based on the following references with a few modifications, from the Bioinformatics Training Facility, University of Cambridge.

- https://docs.google.com/presentation/d/1q9Wy77wg_QrN5iP_wYD_TpX7iurs2eFYliOId1owj1A/edit#s lide=id.g149f6c2cfa3 0 0
- https://github.com/cambiotraining/unix-shell/tree/main/materials

