

What is a 'shell'?

The Shell

Unix Shell



BASH

THE BOURNE-AGAIN SHELL

Why bother?

- Automate repetitive tasks
- Manage large sets of information
- Easily combine smaller tasks into larger, more powerful workflows
- Interface with remote systems (including High Performance Computing systems)
- Reproducibility

Nelle's pipeline

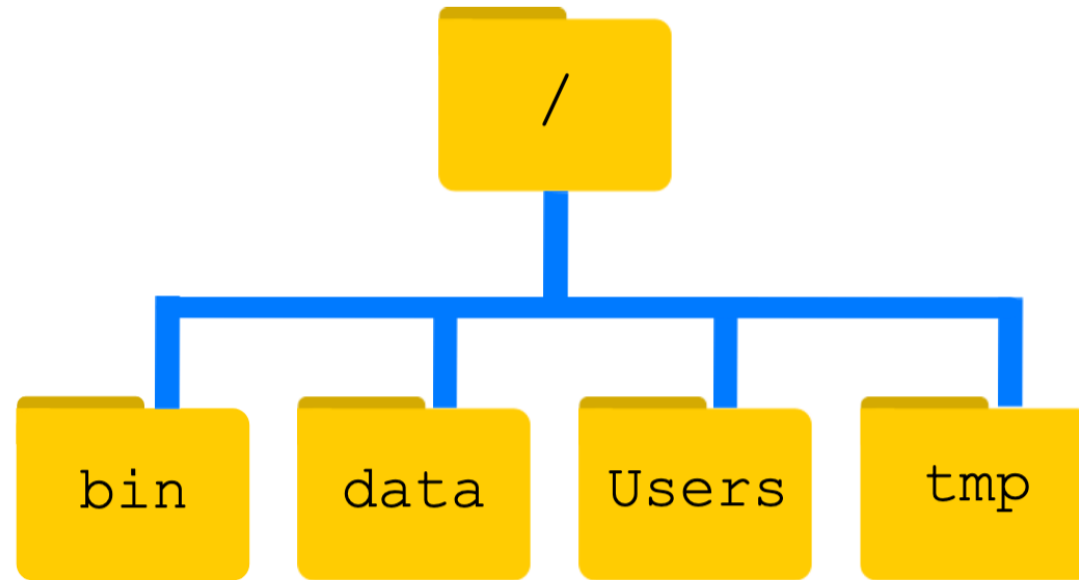
- 1520 samples with 300 data points (protein abundance)
- Need to process this data before analyzing
- ***Highly repetitive task***
- Point-and-click (i.e. GUI-based) software would take hours of hands-on work
- A series of jobs on a high-performance computing cluster (HPCC) could take seconds-minutes

Outline

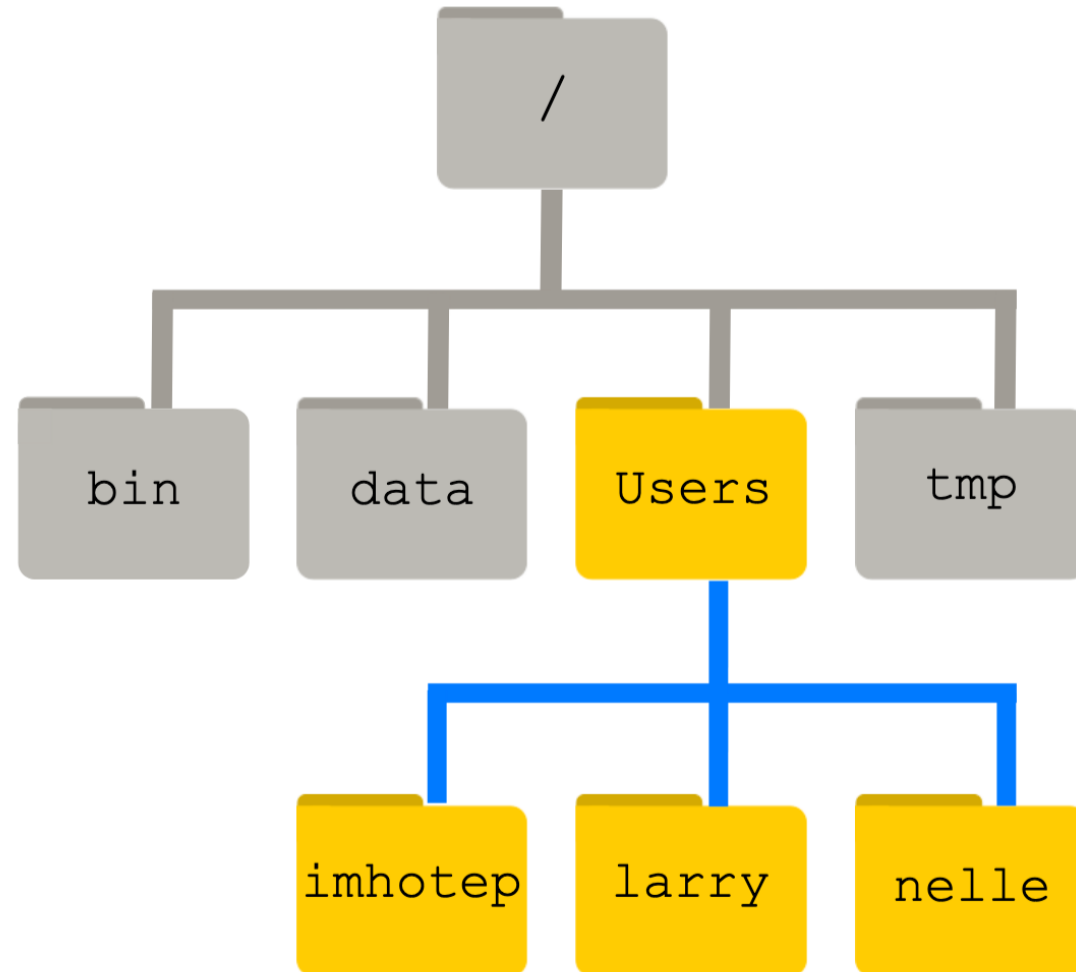
1. Navigating the directory structure
2. Creating files and folders
3. Combining commands to process files
4. Writing and executing scripts

****Skipping loops, but the concept will be covered in R modules***

Navigating the directory structure

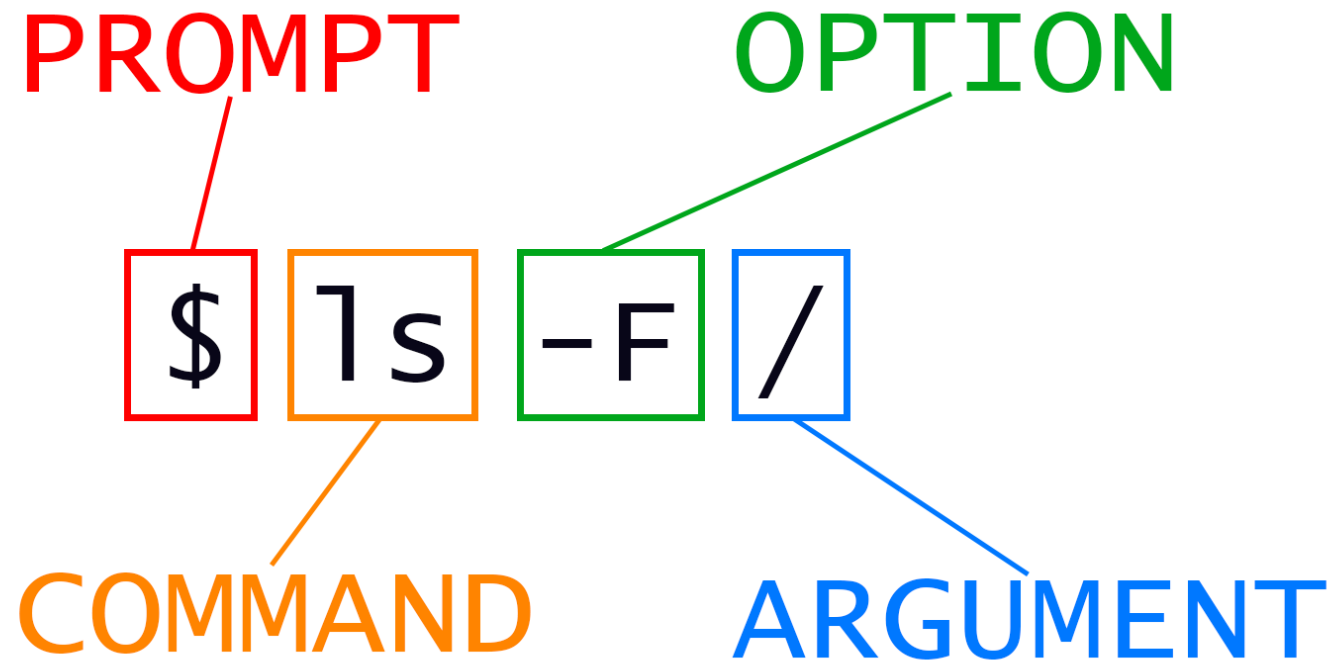


Navigating the directory structure



Navigating the directory structure

Anatomy of a command



Navigating the directory structure

Key commands:

- **pwd** – print working directory
- **cd** – change directory
- **ls** – list contents of directory
- **man** – manual entry for command

Creating files and folders

Key commands:

- **mkdir** – make directory
- **nano** – open nano text editor
- **less** – view contents of file
- **rm** – remove file or directory
- **mv** – move file or directory
- **cp** – copy file or directory

Combining commands

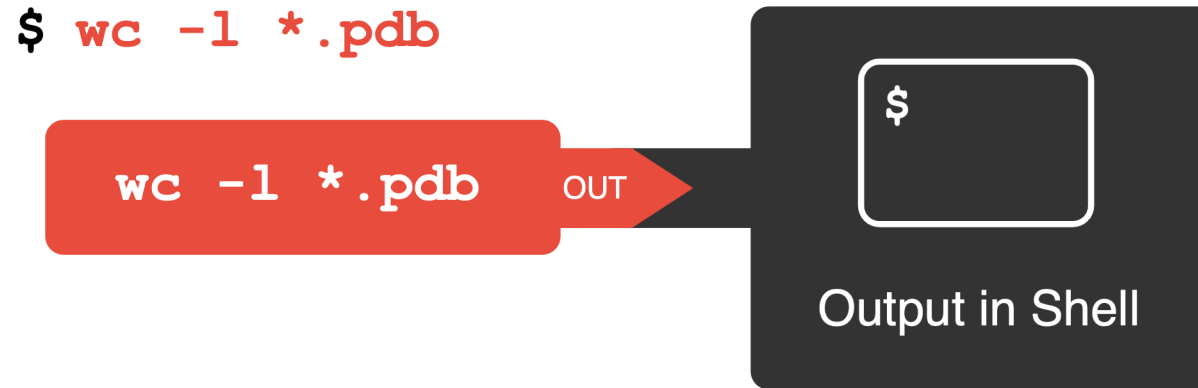
```
$ wc -l *.pdb
```

```
wc -l *.pdb
```

OUT

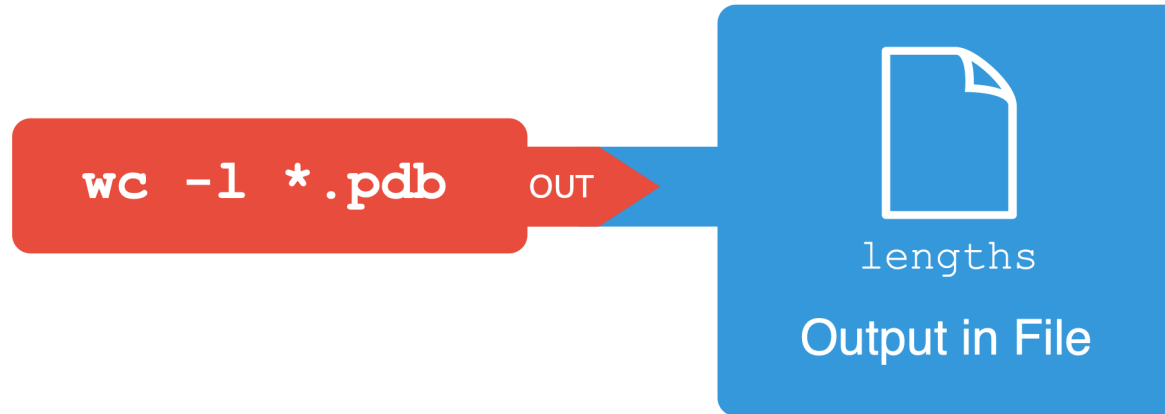
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$
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Output in Shell



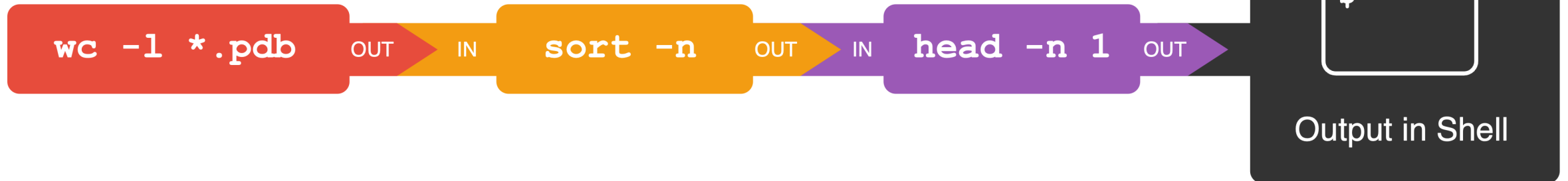
Combining commands

```
$ wc -l *.pdb > lengths
```



Combining commands

```
$ wc -l *.pdb | sort -n | head -n 1
```



Combining commands

Key commands:

- **wc** – count words/lines in file
- **cat** – print file to standard output/concatenate files
- **head** – view first lines of file
- **tail** – view last lines of file
- **sort** – sort lines of file