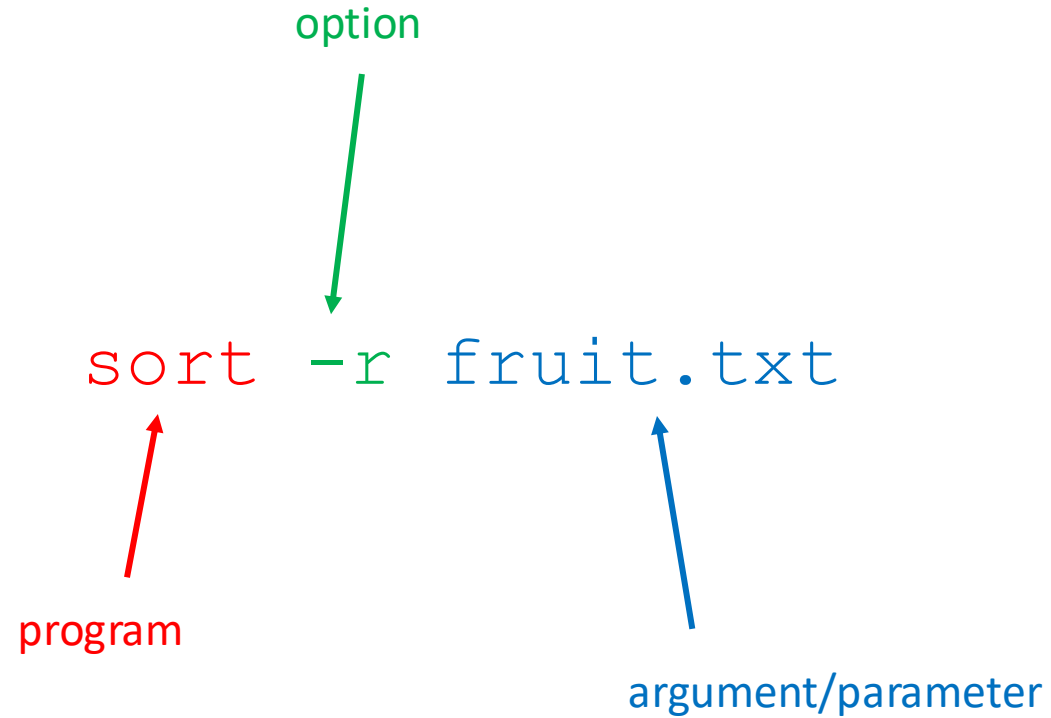


Introduction to the command line

Anatomy of a command

```
sort -r fruit.txt
```

Anatomy of a command



Anatomy of a command

The diagram illustrates the components of the command `sort -r fruit.txt > sortedfruit.txt`. It features three colored arrows pointing to specific parts of the command:

- A red arrow points from the word **program** to the word `sort`.
- A green arrow points from the word **option** to the flag `-r`.
- A blue arrow points from the word **argument/parameter** to the file `fruit.txt`.

The command itself is displayed with color-coding: `sort` is red, `-r` is green, `fruit.txt` is blue, `>` is purple, and `sortedfruit.txt` is blue.

Anatomy of a command

```
sort -f -r fruit.txt
```

```
sort -fr fruit.txt
```

```
sort -rf fruit.txt
```

```
sort --reverse --ignore-case fruit.txt
```

Anatomy of a command

```
fastp --in1 ERR5386380_1.fastq.gz --in2  
ERR5386380_2.fastq.gz --out1  
ERR5386380_1.trimmed.fastq.gz --out2  
ERR5386380_2.trimmed.fastq.gz --  
length_required 40 --cut_front --cut_tail --  
cut_mean_quality 25
```

Anatomy of a command

```
fastp --in1 ERR5386380_1.fastq.gz --in2  
ERR5386380_2.fastq.gz --out1  
ERR5386380_1.trimmed.fastq.gz --out2  
ERR5386380_2.trimmed.fastq.gz --  
length_required 40 --cut_front --cut_tail --  
cut_mean_quality 25
```

Anatomy of a command

```
fastp --in1 ERR5386380_1.fastq.gz --in2  
ERR5386380_2.fastq.gz --out1  
ERR5386380_1.trimmed.fastq.gz --out2  
ERR5386380_2.trimmed.fastq.gz --  
length_required 40 --cut_front --cut_tail --  
cut_mean_quality 25
```


Anatomy of a command

```
fastp --in1 ERR5386380_1.fastq.gz --in2  
ERR5386380_2.fastq.gz --out1  
ERR5386380_1.trimmed.fastq.gz --out2  
ERR5386380_2.trimmed.fastq.gz --  
length_required 40 --cut_front --cut_tail --  
cut_mean_quality 25
```

Anatomy of a command

```
fastp --in1 ERR5386380_1.fastq.gz --in2  
ERR5386380_2.fastq.gz --out1  
ERR5386380_1.trimmed.fastq.gz --out2  
ERR5386380_2.trimmed.fastq.gz --  
length_required 40 --cut_front --cut_tail --  
cut_mean_quality 25
```

- The command line is case-sensitive!

- `-S` is not the same as `-s`

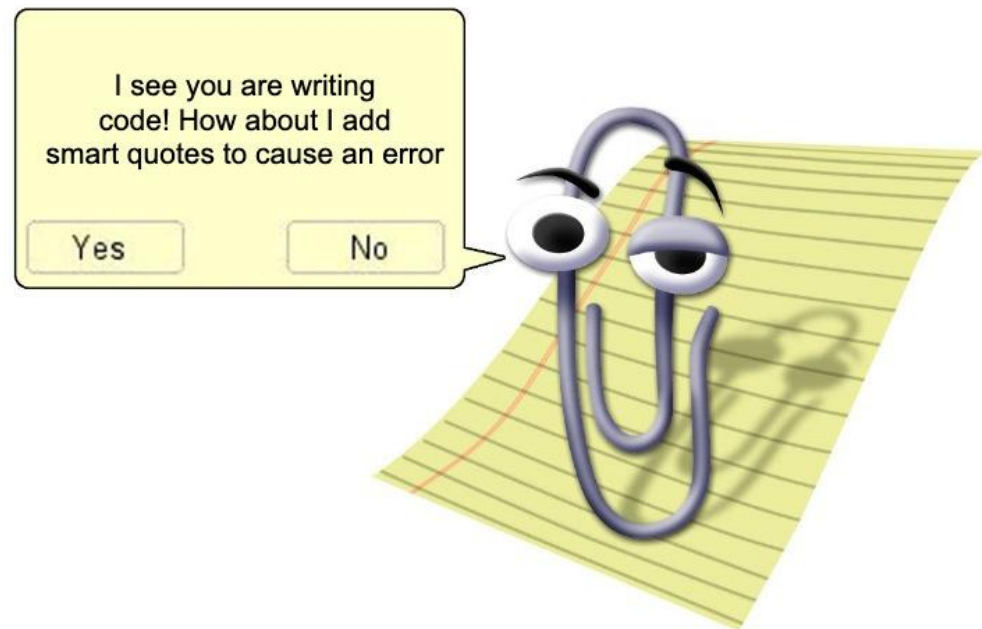
- Your filenames must be exactly correct

`ERR10741_1.fastq.gz` is not the same file as
`ERR10741-1.fastq.gz` or
`ERR10741_I.fastq.gz`

- Files will be over-written without warning by the `mv` and `cp` commands
 - Did you type `mv a.txt b.txt`? If `b.txt` exists already it will be overwritten
 - Double-check your commands
 - The `-i` option will ask you before overwriting
 - The `-n` option will stop you overwriting a file

```
(base) MIC-MBpro-06:test Elizabeth$ mv -i a.txt b.txt
overwrite b.txt? (y/n [n])
not overwritten
(base) MIC-MBpro-06:test Elizabeth$
```

- Avoid spaces in your filenames
 - The command line cannot tell that `list of fruit.txt` is one file
 - Use underscores instead: `list_of_fruit.txt`
- Watch out for quotes
 - ``` is not the same as `“`
 - Word will add smart quotes which are not the same as regular quotes



What is the error message telling me?

- Can it find the program I am trying to run?
- What directory am I running my command from? `pwd` is your friend
- Is there a file it cannot find? Does the file exist and am I using the right path?
- Check you have permission to read and write the files and directory
- Did I forget to give a necessary option?
- Break down the command to work out what is causing the error