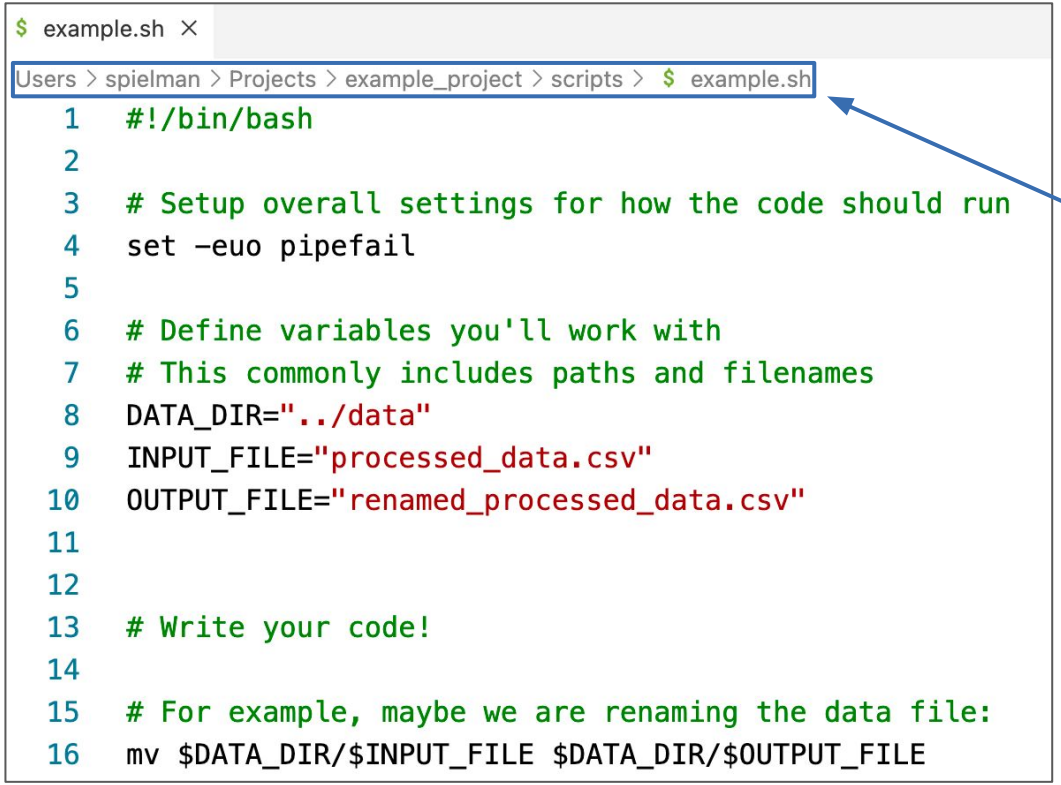
Shell scripting

Childhood Cancer Data Lab

The anatomy of a shell script



We generally like to run scripts from the directory where they are saved to avoid path confusion

```
cd ~/Projects/example_project/scripts
```

Once in the right directory, we run this script from the terminal as:

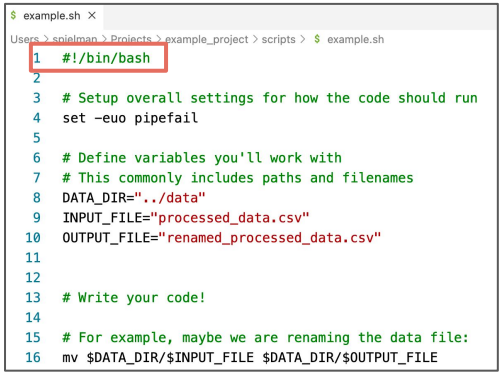
```
bash example.sh
```

We can also add the following to the top of our shell scripts to ensure they use the directory where they are saved as the working directory:

```
cd "$(dirname "${BASH_SOURCE[0]}")"
```

Best practices in scripting

```
1   #!/bin/bash
```



The very first line of shell scripts often contain a **shebang (#!)** indicating which shell interpreter be used when running this shell script.

This script will use the **BASH** shell

The **path to the given shell interpreter** immediately follows (no spaces!) the **#!**

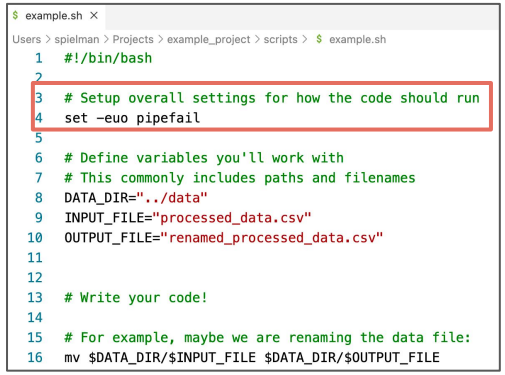
The shebang can be generally used to make any script *executable*, for interpretable languages.
It also cues you in to what language the code is in.

```
#!/usr/local/bin/python3
```

```
#!/usr/bin/env python
#!/usr/bin/env bash
```

Best practices in scripting

```
3   # Setup overall settings for how the code should run
4   set -euo pipefail
```



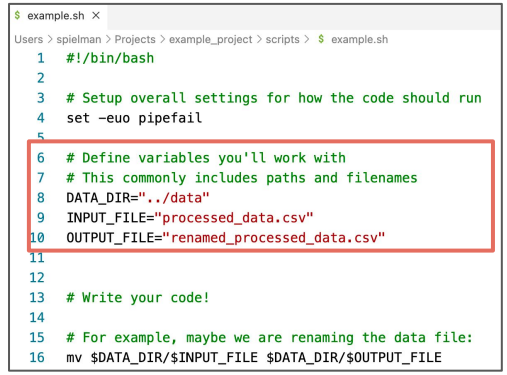
We like to use **`set`** to define preferences for how errors should be handled while running this script

- The **`-e`** flag causes the script to exit if any step has an error
- The **`-u`** flag causes the script to exit if a variable isn't defined
- The **`-o pipefail`** option causes the entire script to fail if any step in a pipeline fails

Note these can be used one-at-a-time, or pick only some options! All of these are legit (but **`o pipefail`** has to be kept together, and usually last):

```
set -e
set -u
set -o pipefail
set -eo pipefail
```

Defining variables




```
6   # Define variables you'll work with
7   # This commonly includes paths and filenames
8   DATA_DIR="../data"
9   INPUT_FILE="processed_data.csv"
10  OUTPUT_FILE="renamed_processed_data.csv"
```

Variables are *defined* as `VARIABLE_NAME="CONTENT"` ***without any spaces!!***

(Using quotes when defining variables is not strictly required, but it is best practice.)

Variables are *used* with **dollar signs:** `$VARIABLE_NAME`, and sometimes braces: `${VARIABLE_NAME}`

(Note there are more types of variables, like arrays, which are defined and used slightly differently! We'll just focus on single-value variables here).

Use double quotes when referring to variables

```
DATA_DIR=data
```

✅

```
echo $DATA_DIR

data
```

❌

```
echo '$DATA_DIR'

$DATA_DIR
```

```
echo "$DATA_DIR"

data
```

Variations on a variable

```
6   # Define variables you'll work with
7   # This commonly includes paths and filenames
8   DATA_DIR="../data"
9   INPUT_FILE="processed_data.csv"
10  OUTPUT_FILE="renamed_processed_data.csv"
```

You can combine variables with strings directly:

```
DATA_DIR="../data"
INPUT_FILE="processed_data.csv"
OUTPUT_FILE="renamed_$INPUT_FILE"
```

You can set up your variables to contain the path, if you want *(and it makes sense for the code!)*

```
DATA_DIR="../data"
INPUT_PATH="$DATA_DIR/processed_data.csv"
OUTPUT_PATH="$DATA_DIR/renamed_processed_data.csv"
```

Use curly braces { } to combine variables safely

```
DATA_DIR="../data"
INPUT_FILE="processed_data.csv"
PREFIX="renamed"
OUTPUT_FILE="${PREFIX}_${INPUT_FILE}"
```

Curly braces protect the variable

```
INPUT_FILE="processed_data.csv"
PREFIX="renamed"
```

✅

```
echo "${PREFIX}_${INPUT_FILE}"
renamed_processed_data.csv
```

❌

```
echo "$PREFIX_$INPUT_FILE"
processed_data.csv
```

Putting it all together

$ example.sh ×

Users > spielman > Projects > example_project > scripts > $ example.sh

```
#!/bin/bash

# Setup overall settings for how the code should run
set -euo pipefail

# Define variables you'll work with
# This commonly includes paths and filenames
DATA_DIR="../data"
INPUT_FILE="processed_data.csv"
OUTPUT_FILE="renamed_processed_data.csv"


# Write your code!

# For example, maybe we are renaming the data file:
mv $DATA_DIR/$INPUT_FILE $DATA_DIR/$OUTPUT_FILE
```

Now let's write a script to…

- Download paired FASTQ reads (R1 and R2 files) programmatically - no "point-and-click" in browser!!
  - https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP255885

- Save these files to the appropriate directory in your forked repository

- Ask how many lines are in each FASTQ file

URLs to use for downloads

Full size files from ENA:

```
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR115/089/SRR11518889/SRR11518889_1.fastq.gz
ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR115/089/SRR11518889/SRR11518889_2.fastq.gz
```

Or truncated versions if the internet is slow:

```
https://raw.githubusercontent.com/AlexsLemonade/reproducible-research/main/instructor_notes/fastq_subset/subset-SRR11518889_1.fastq.gz
https://raw.githubusercontent.com/AlexsLemonade/reproducible-research/main/instructor_notes/fastq_subset/subset-SRR11518889_2.fastq.gz
```