Achieve this short story with the command line alone.
Create your copy of the file and enter your command in the terminal space ($) below each action

N/B: The story here is fictional and the files are just hypothetical. Please don't use it for any serious research work.

Please note the following names of directories have the correct codes:
Ishak-instead if Ishaku (my name)
bayocomputin-instead of biocomputing
compaya-instead of compare

1. ~~Login to the server~~

```
$
```

2. Create a new folder titled your name

```
$ mkdir Ishak
```

3. Create another new directory titled biocomputing and change to that directory with one line of command

```
$ mkdir bayocomputin && cd bayocomputin
```

4. Download these 3 files:
a. https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.fna
b. https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk
c. https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk

Hint: Google search for "command for download file in linux"

```
$ wget https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.fna

$ wget https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk

$ wget https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk
```

5. OH! You made a mistake. You have to move the .fna file to the folder titled your name directly. (Do this with one command. Hint: See our cheatsheet)

```
$ mv wildtype.fna ../Ishak/
```

6. OH No! The gbk file is a duplicate, they are actually the same thing. Please delete it.

```
$ rm wildtype.gbk.1
```

7. The .fna file is actually from a bacteria, and it should definitely have a TATA (tata) box for initiating gene transcription. The molecular biologist is trying to understand the implication of dual TATA sequences. The files got mixed up and we are not sure which is wildtype and which is mutant. The mutant should have "tatatata" while the normal should have just "tata". Can you confirm if the file is mutant or wild type

```
$ grep 'tatatata' wildtype.fna
```

8. If it is mutant, print all the lines that show it is a mutant into a new file
ishakuharuna03@cloudshell:~$ grep 'tatatata' wildtype.fna > mutant
atccacagcacctactactattactaagaacttaaaacctatataattatatataaacga
aattacttgaatattattcataatatattaacaactttattatactgctctttatatata
actatatataagtaaaacaatgatggacaatgactgtgaaaaagtatgtgatagaaacgt
aaggtatatataagattaaacattttaccttagataaagaaaatggtgcattatttaatc
gtatatatatttgccacgattgcatgtggttgtagtgcgatactgcaaggtttagcgacg
attatatatatcaattagaacattgatggttgttattacaggggaaggctcaaggtagtc
attatgcaaggtttagaagcagattcagattactaatatatataaaatttgggagtgata
gaaaaatatatataagtcattaactgtctctgcaattgttgcaacggtatcattaagtgc
aatactatatatataataccaattttaatgaaaattttaagggagtgaaataatggaaa
tagttgtcgcgcttatatatatcttcttcaaagtaattttgataagcgaattaaagatg
aatcgcccgggacgtattttaataattttcagcagttatatatataggtagaggtgttt
ctttatccataatgatagcccccctatatatatctttatttacttataccctaacattatt
atctttagcggatattgaaattttttccacatcaacacgggttcaaaattatatataacag

```
$ grep 'tatatata' wildtype.fna > mutant
```

9. Clear your terminal space and print all the commands you have used today.

```
$ clear
```

10. List the files in the two folders and share a screenshot of your terminal below

```
$ ls && ls ../bayocomputin/
```

Your pictures go here:

```
ishakuharuna03@cloudshell:~/Ishak$ ls
mutant  wildtype.fna
ishakuharuna03@cloudshell:~/Ishak$ cd ../bayocomputing/
-bash: cd: ../bayocomputing/: No such file or directory
ishakuharuna03@cloudshell:~/Ishak$ cd bayocomputin
-bash: cd: bayocomputin: No such file or directory
ishakuharuna03@cloudshell:~/Ishak$ ../bayocomputin
-bash: ../bayocomputin: Is a directory
ishakuharuna03@cloudshell:~/Ishak$ ls && ls ../bayocomputin/
mutant  wildtype.fna
wildtype.gbk
ishakuharuna03@cloudshell:~/Ishak$ █
```

Bonus Task: Exit the terminal

```
$ exit ()
```

1. Use the `figlet` command to draw a graphical representation of your **name**.

```
 ___   __            _      _            _
|_ _| / _|          | |    |_|          | | __
 | | | |_   _  __   | |     _    _ __   | |/ /
 | | |  _| | |/ _\  | |    | |  | '_ \  |   <
|___||_|   |_|\__|  |__|   |_|  |_| |_| |_|\_\
```

sudo apt-get install figlet

then run: figlet Ishak

~~2.   xcowsay is a stupid program for making a cow talk. Tell the cow to say your name~~

~~a.   Specify -t 0 for xcowsay. What does it mean?~~

3.   In your home directory, create a folder called `compare`.

Mkdir compaya && cd compaya

.   Download this file [5MB] into your the `compare` directory:
https://www.bioinformatics.babraham.ac.uk/training/Introduction%20to%20Unix/unix_intro_data.tar.gz

The file will be directly downloaded into the compaya directory

a.   Unzip using `gunzip` command

gunzip unix_intro_data.tar.gz

and the gunziped folder will be unix_intro_data.tar without the .gz

b.   Then, untar the *.tar* file with `tar` command

c.   Get into `seqmonk_genomes/Saccharomyces cerevisiae/EF4` and identify the rRNAs present in `Mito.dat`.

cd Saccharomyces cerevisiae

d.   Using `cp` copy `Mito.dat` into the `compare` directory.

cp Mito.dat ../../../compaya/

e.   Use nano to effect the following edits:

nano Mito.dat

i.Change `Mito` to `Mitochondrion` in the `ID` and `AC` header lines

ii.Save the file and exit `nano`

CTR + O

iii.Rename the file from `Mito.dat` to `Mitochondrion.txt`

4.   In task 3, in your `compare` directory, `cd` into `FastQ_Data` directory.

cd ../

cd ../

cd ../

cd `FastQ_Data`

.   Calculate the total number of lines in `lane8_DD_P4_TTAGGC_L008_R1.fastq.gz`

gunzip -c lane8_DD_P4_TTAGGC_L008_R1.fastq.gz | wc -l

`400,000 lines`

a.   Print the total number of lines in all `fastq.gz` files and save it as a new file.