

Exercise:

1. Unzip the archive 'linux-exercise.zip'
2. A new directory called 'bioinformatics' has been created. How many directories are contained in 'bioinformatics'?
3. Enter the directory 'bioinformatics' and delete 'testme'
4. Run the script called 'generator.sh'
5. Enter the directory 'exercise'
6. Find the only file containing the four nucleotides sequence 'AATG'. What is the name of the file?
7. Copy this file in 'bioinformatics'
8. Rename the file in 'sequence.txt'
9. Edit 'sequence.txt' changing the G in the sequence into an A, then save the file and exit
10. Run the script 'cleanup.sh'
11. Using the command line, create the directory structure shown below in the figure.

Hint: you may use, but make sure you understand what happens:

```
for i in *; do
    mkdir $i/GO
    mkdir $i/Pfam
    mkdir $i/SCOP
    mkdir $i/blast
done
```

12. Use your favorite file browser (e.g. Nautilus) to check what you did.
13. Close the terminal, you are ready to start scripting.

