BASh Task 0: Paschal Ugwu

1. Write a simple Bash program where your first name and last name are assigned to different variables, and the script prints out your full name.
2. Create a new folder titled your name.
3. Create another new directory titled biocompute and change to that directory with one line of command.
4. Download these 3 files:
https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.fna
https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk
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 the cheatsheet).
6. OH No! The gbk file is a duplicate, they are actually the same thing. Please delete it.
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.
8. If it is mutant, print all the lines that show it is a mutant into a new file.
9. Clear your terminal space and print all the commands you have used today.
10. List the files in the two folders and share a screenshot of your terminal below.
11. Use the figlet command to draw a graphical representation of your name.
12. In your home directory, create a folder called compare.
13. Download this file [5MB] into your the compare directory:
https://www.bioinformatics.babraham.ac.uk/training/Introduction%20to%20Unix/unix_intro_data.tar.gz
14. Unzip using gunzip command.
15. Then, untar the .tar file with tar command.
16. Get into seqmonk_genomes/Saccharomyces cerevisiae/EF4 and identify the rRNAs present in Mito.dat.
17. Using cp copy Mito.dat into the compare directory.
18. Use nano to effect the following edits:Change Mito to Mitochondrion in the ID and AC header lines, Save the file and exit nano, Rename the file from Mito.dat to Mitochondrion.txt (Check how to do this in the cheat chart. You can also browse and watch YouTube videos).
19. Copy and save your codes in a notebook (.txt extension) for submission.
20. Bonus Task: Exit the terminal.