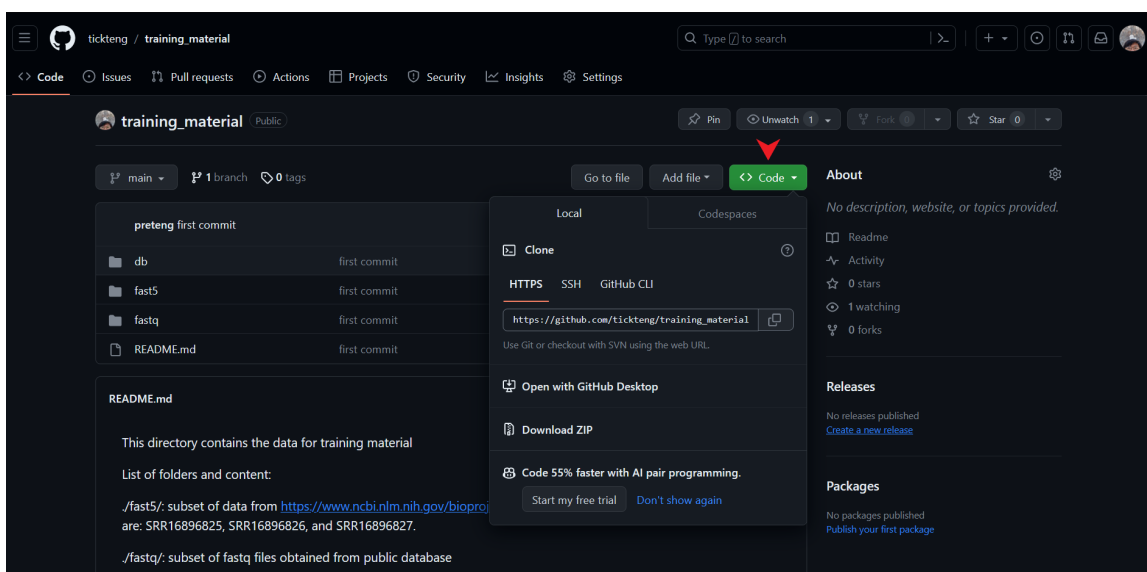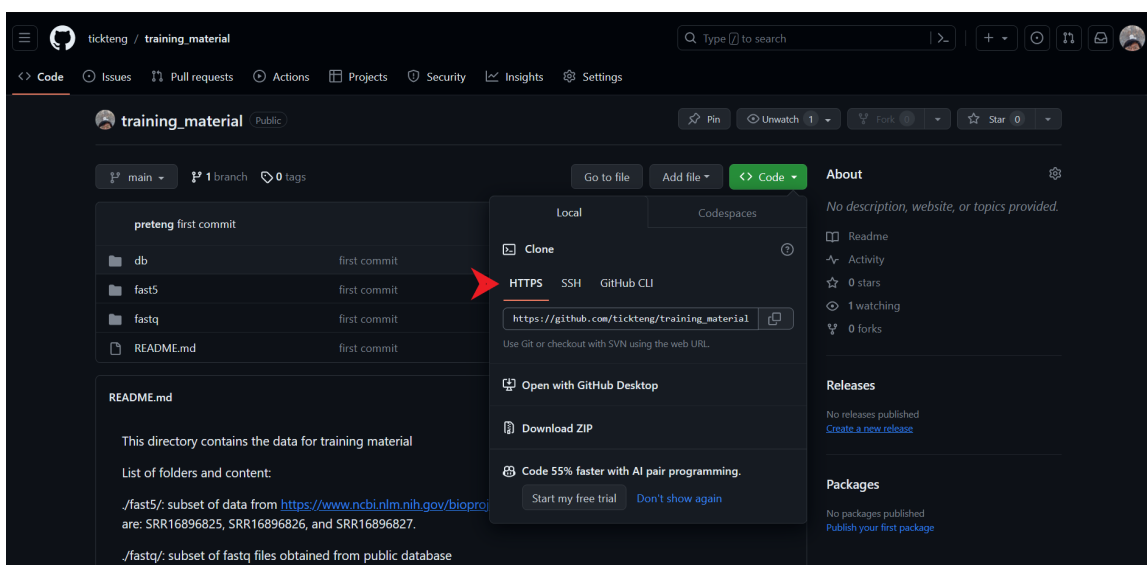# Basic Linux Command

## Clone the training material

1. Go to https://github.com/tickteng/training_material.git

2. Click the "Code" button.



3. A pop up will open. Make sure you select "https", then copy the provided link.

4. In your terminal, type the following:

```
git clone <link>
```

## Practice

1. Check your username.

```
whoami
```

2. Print the current directory.

```
pwd
```

3. Check the description for grep command.

```
man grep
grep --h
```

4. Print the help message for grep command into a file name grep.txt.

```
grep --h > grep.txt
```

5. Preview the newly created file.

```
cat grep.txt
more grep.txt
```

6. Create a directory named training in the home directory.

```
mkdir folder
```

7. Move the grep_manual.txt into the training directory.

```
mv ./grep.txt ./folder/
```

8. Moving around directories

```
cd ./training_material/
pwd
cd ../
pwd
cd ~/
pwd
```

Can you navigate back to the the ./folder/ directory?

9. Create a copy of the grep.txt.

```
cp grep.txt grep_cp.txt
```

10. List all the files (compare both commands).

```
ls
ls -l
```

12. Count how many lines and character in the grep_manual_cp.txt file.

```
wc -l grep_cp.txt
wc -m grep_cp.txt
```

13. Create a copy of training directory in the home directory

```
cd ..
cp -r folder folder2
```

14. Delete the training2 directory

```
rm -r folder2
```

15. Delete the copy file

```
rm ./folder/grep_cp.txt
```

16. Preview the file named Animals and Birds in the practice folder

```
more ./training/practice/Animals
more ./training/practice/Birds
```

17. Sort the lines in Animals

```
sort ./training/practice/Animals
cat ./training/practice/Animals | sort
```

18. Print only the non-redundant line.

```
sort ./training/practice/Animals | uniq
```

19. A) Print only lines containing the string "Duck"
    B) Print only the non-redundant lines

```
grep "duck" ./training/practice/Animals
grep "duck" ./training/practice/Animals| sort | uniq
```

20. A) Print the lines that contain the string  "horse"
    B) Print only the line that match the whole word

```
grep "horse" Animals
grep -w "horse" Animals
```

21. Count how many lines has "duck" in Animals

```
grep "duck" Animals | wc -l
```

22. A) Print only the lines containing string found in file "Birds"
    B) Redirect the output to "output1.txt"

```
sort Animals | grep -wf Birds
sort Animals | grep -wf Birds > output1.txt
```

23. Find strings containing cat, dog, and horse, using loop and print the output into a file name output2.txt

```
for mammals in cat dog horse; do grep ${mammals} Animals; done > output2.txt
```

23. Concatenate the file output1.txt and output2.txt into a file named BirdsandMammals.txt

```
cat output1.txt output2.txt > BirdsandMammals.txt
```

24. Print a certain column:

```
cut -f1 blastres.txt
awk '{print $1}'
```

25. Print only lines when the value in column 2 is higher than 90.

```
awk '$3>90' blastres.txt
```

26. Print only lines when the string in column 5 equal to "A-seg2"

```
awk '$5=="A-seg2"' blastres.txt
```

27. Print the first column of each lines whose column 5 equal to "A-seg8"

```
#option 1
awk '$5=="A-seg8"{print $1}' blastres.txt
#option 2
awk '$5=="A-seg8"' blastres.txt | cut -f1
#option 3
grep -w "A-seg8" blastres.txt | cut -f1
grep -w "A-seg8" blastres.txt | awk '{print $1}'
```

Multiple solutions for one problem.

In computer programming "=" is not the same as "==", the first one is to assign variables and the latter is to compare two variables.

28. Print only lines when the string in column 5 equal to "A-seg1" and sort the order based on the value in column 3.

```
awk '$5=="A-seg1"' blastres.txt | sort -k3
```

Tips: order will be from lower to higher. Use `-r` to reverse the order.

PRACTICE

1. How many reads are in the file sample01.fastq - sample03.fastq?

2. Can you find this read "@e69b9e08-b70c-4e0d-bbd8-95cf096da6cc" (all four lines) in the file sample01.fastq.gz? (all 4 lines)

3. Can you print the last read in the file sample01.fastq.gz?

4. Can you print the first three reads in the file sample01.fastq.gz?

5. Can you create a file name "practice.txt" that has 1) the first three reads in sample01.fastq.gz, 2) the last read in sample01.fastq.gz, and 3) the read with this id "@b7a6906d-f154-4fcf-b429-64ab6f2a689a" in sample01.fastq.gz?

6. Can you print lines that has the string "A-seg2" in column 5 and output only the first 5 lines?

Hint: for zipped files (.gz extension), use zgrep, zmore, zcat.