

Fill in with a list of commands

1. In doppelganger_names.txt file count the line which has the most repeats?

- Command

- Lines with most repeats

2. Use the printf command to make this script_sbatch as an output

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

```
#Written by YOUR NAME here!
```

```
#Sep 9th, 2021
```

```
#SBATCH --partition=BINF2111
```

```
#SBATCH --job-name=sg-program
```

```
#SBATCH --output=stout_090721.txt
```

```
#SBATCH --error=sterr_090721.txt
```

```
#SBATCH --time=0-08:00:00
```

```
#SBATCH --nodes=1
```

```
#SBATCH --ntasks-per-node=1
```

- Command here

3. Using the any command you would like count the number of times abdul is repeated in line 2 doppelganger_names.txt

- Command here

- Answer here

4. In the doppelganger_names.txt provide two unique commands to convert all from lower case to upper case? They cannot start with the same command (For example, grep/sed, grep/awk, grep/tr, tr/sed etc).

- Command 1 here:

- Command 2 here:

5. Provide two unique commands to convert a tsv to csv? They cannot start with the same command (For example, sed/tr, grep/tr etc)

- Command 1 here:

- Command 2 here:

6. Using any command you want convert whitespace into tabs?

Command here:

7. In the name_game.csv print all the columns but 2nd and 4th columns into a new file?

- Command here:

8. In example2.fasta count the number of start (ATG) and stop (TAG) codons in the file and convert them (Stop) and (Start) as single or multiple commands?

- Command 1:

- Command 2:

9. Write a command that deletes all lines that start with lower case 'o'

With this file:

Rat,steven,bear,Xi

Olf,thor,flower,Ton

Lazy,aaron,larry,jose

old,thor,flower,Ton

Command:

10. Extract the sequence in example2.fasta that has more than one ATG?

Command:

BONUS (3pts):

- In the doppelganger_names.txt count how many times the name 'chi' is left to the name 'bill' in the file?

Using grep only command/with count:

Using grep with printf command/with count:

Only awk/with count:

EXTRA BONUS (5 pts):

Convert all of example2.fasta into it's amino acids using any command(s) you want?

- Script here