Day 1 Exercise

Log on to logrus server

Enter the following command to log on to logrus: **ssh -p 44111 <username>@gateway.training.ncgr.org**

Substitute your personal username in for <username>

Make a new directory under your home directory:
```
mkdir fastq_files
```

Enter the new directory:
```
cd fastq_files
```

Move the fastq file file from yesterday to the present working directory:
```
mv ~/linuxc/SP1.fq .

ls -ltr
## total 0
## lrwxrwxrwx 1 elavelle elavelle 28 Aug 17 22:50 SP1.fq -> /home/fds/unix_basics/SP1.f
```

How can we count the number of records in a fastq file?
```
grep -c "@cluster" SP1.fq
## 250
```

If you want to determine the number of lines in a file, you can use the "wc" command.
```
cat SP1.fq | wc -l
## 1000
```

Why does the first command output 250 and the second 1000?

Exercises

1. With one command, send a copy of table1.txt in the linuxc directory to your home directory with the name table1_bu.txt

2. Print to standard output the last line of table1.txt

3. Use a loop to count the number of lines in all files in the linuxc directory.

4. Print to standard output the last names of music artists with album prices less than or equal to $7.30

5. Create a file with only the accession numbers of the sequences contained in the covid.fasta file (with no additional spaces or symbols).