

Activity: Basic shell scripting, Oct 26

Modify the following shell script to count the number of records in the fasta files linked below:

[Link to data](#)

```
#!/bin/bash
set -e
set -u
set -o pipefail

for file in *.fa
do
echo "$file: " $(awk '/>/ { count++ } END { print count }' $file)
done
```

1. How many fasta records in each file?

In the below exercises, you will work with the find command and answer some questions

Step 1: Make some files to play with

```
$ mkdir -p zmays-snps/{data/seqs,scripts,analysis}
$ cd data
$ touch seqs/zmays{A,B,C}_R{1,2}.fastq
$ cd ..
$ cd ..
```

Step 2: Find your files

```
$ find zmays-snps
```

1. What was returned to you?
2. What happens if you run the following command: `$ find zmays-snps max-depth -2`

3. List 2 ways to run the command if you wanted to find only files that were marked either 'A' or 'C'.