

## Bash Script to count the number of sequences in a series of files.

This Bash script counts the number of sequences in a series of files and displays the results by file. The program can be created in any text editor and saved with an .sh extension.

**count\_fasta\_sequences.sh** script:

```
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#!/bin/bash  
  
# Folder where your files are located  
folder_path=""  
  
# Loop over all the files with the pattern matches_BCF*.fasta  
for fasta_file in "$folder_path"/matches_BCF*.fasta; do  
  # Count how many lines start with '>' (FASTA headers) in each file  
  count=$(grep -c "^>" "$fasta_file")  
  
  # Print the filename and the count  
  echo "$fasta_file: $count sequences"  
done
```

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To run the program, make it executable by navigating to the folder that it is in and running the following command from the command line:

- `chmod +x count_fasta_sequences.sh`

Then type the following command:

- `./count_fasta_sequences.sh`