Basic Structure of a QIIME Script

```
python_script.py -i input_filepath -o output_filepath

python_script.py -i input_filedirectory/ -o output_filedirectory/
```

Your command that starts a task within QIIME

The path to the file or directory that gets processed by your command

The path to the file or directory of where you want the output of the command to be saved

Example:
```
align_seqs.py -i computer/desktop/analysis/picked_otus.fasta -o computer/desktop/analysis/aligned_seqs/
```
Basic Unix Commands Used in this Workshop

Change directory – this allows you to move between directories within your terminal. This example would move you working within the directory “QIIME_analysis” on the desktop of Julia’s computer:

```
cd /Users/Julia/Desktop/QIIME_analysis
```

Change mode – when you write the looping program for converting fastq files to fasta files, this command will make that program executable, allowing it to run properly

```
chmod +x convert_fastq.sh
```
Basic Unix Commands Used in this Workshop

Make new directory – make a new directory within the directory you are currently located. This example would make the directory “otu_output” within the directory “QIIME_analysis”

mkdir QIIME_analysis/otu_output/

Copy – makes a copy of files and can move them into a new location. This example would put a copy of the file “97_otu.fasta” into the “otu_output” directory

cp 97_otu.fasta otu_output/97_otu.fasta