

Basic Unix command

Folder: gencommand_proj1_data

Module 1 Exam – Command Line Tools for Genomic DS

```
(base) Chaus-MacBook-Air:Downloads aaaz$ cd
```

```
/Users/aaaz/Downloads/gencommand_proj1_data
```

```
-bash: cd: /Users/aaaz/Downloads/gencommand_proj1_data: No such file or directory
```

```
(base) Chaus-MacBook-Air:Downloads aaaz$ cd
```

```
/Users/aaaz/Downloads/gencommand_proj1_data
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ ls
```

```
apple.conditionA apple.conditionC apple.genome
```

```
apple.conditionB apple.genes
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ grep -c ">" apple.genome
```

```
3
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1 apple.genes | uniq | wc -l
```

```
5453
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f2 apple.genes | uniq | wc -l
```

```
5456
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1 apple.genes | uniq -c | grep
```

```
"1" | wc -l
```

```
5451
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1 apple.genes | uniq -c | grep
```

```
-v "1" | wc -l
```

```
2
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,4 apple.genes | grep "+" |
```

```
uniq | wc -l
```

```
cut: apple: No such file or directory
```

```
cut: genes: No such file or directory
```

```
-bash: wc-l: command not found
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,4 apple.genes | grep "+" |  
uniq | wc -l
```

2662

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,4 apple.genes | grep "-" |  
uniq | wc -l
```

2791

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,3 apple.genes | grep "chr1" |  
uniq | wc -l
```

-bash: wc-l: command not found

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,3 apple.genes | grep "chr1" |  
uniq | wc -l
```

-bash: wc-l: command not found

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,3 apple.genes | grep "chr1" |  
uniq | wc -l
```

1624

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,3 apple.genes | grep "chr2"  
|uniq| wc -l
```

2058

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1,3 apple.genes | grep "chr3"  
|uniq| wc -l
```

1771

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f2,3 apple.genes | grep "chr1"  
|uniq |wc -l
```

1625

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f2,3 apple.genes | grep "chr2" |  
uniq | wc -l
```

2059

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f2,3 apple.genes | grep "chr3" |  
uniq | wc -l
```

1772

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1 apple.conditionA | sort -u >
conditionA
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1 apple.conditionB | sort -u >
conditionB
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -1 -2 conditionAconditionB |
wc -l
```

```
usage: comm [-123i] file1 file2
```

```
0
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -1 -2 conditionA conditionB |
wc -l
```

```
2410
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -2 -3 conditionA conditionB |
wc -l
```

```
1205
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -1 -3 conditionAconditionB |
wc -l
```

```
usage: comm [-123i] file1 file2
```

```
0
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -1 -3 conditionA conditionB |
wc -l
```

```
1243
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -1 -2 conditionA conditionB
> conditionAB
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ cut -f1 apple.conditionC | sort -u >
conditionC
```

```
(base) Chaus-MacBook-Air:gencommand_proj1_data aaaz$ comm -1 -2 conditionAB conditionC
| wc -l
```

```
1608
```