

# Some CLI commands

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## `./notebooks/grep`

### 1 `grep`

For finding occurrences within files

#### 1.1 Useful flags

1. `grep -w` to only get exact occurrence/whole word instead of part of another.
2. `grep -c` to print number of occurrences (line counts) to stdout instead of the actual occurrences
3. `grep -A NUM` for NUM count of lines after `grep` target to stdout

#### 1.2 Example uses

```
$ cat vombaticus.gff3 | cut -f 3 | grep tRN
```

```
tRNA
tRNA
tRNA
tRNA
tRNA
tRNA
tRNA
tRNA
```

```
$ cat vombaticus.gff3 | cut -f 3 | grep -c tRN
```

```
8
```

```
$ grep -A1 ">" file.fa
```

To find header of new fasta when separated by >

`./notebooks/wc`

## 2 ‘wc’

For printing wordcount, newline count, and byte counts of file

### 2.1 Useful flags

`wc -l`

→ Line counts

`wc -w`

→ Word counts

`wc -c`

→ Byte counts

`wc -m`

→ Character counts (UTF-8)

### 2.2 Example uses

`wc -l file.txt`

→ Outputs line count for file.txt

`cat file.txt | wc -l`

→ Pipe into word count (same output as above)

`grep "apple" file.txt | wc -l`

→ Counts how many lines contain `apple`