title: The Unix Shell
subtitle: Pipes and Filters
ANSWERS

Exercises

Challenge 1

Create a file under my_files called "sorts.txt" that contains these data

```
10
2
19
22
6
```

Sort it numerically and place the output in a file called "nsorts.txt". Then, sort it alphabetically and place the output in a file called "asorts.txt". Are these files the same? Why or why not?

```
cd my_files
touch sorts.txt
nano sorts.txt
```

add numbers

```
sort -n sorts.txt > nsorts.txt
sort sorts.txt > asorts.txt
```

No, the are different because BASH will not sort the numbers if you sort alphabetically.

Challenge 2

The command `uniq` removes adjacent duplicated lines from its input.
For example, if a file `salmon.txt` contains:

```
coho
coho
steelhead
coho
steelhead
steelhead
```

then `uniq salmon.txt` produces:

```
coho
steelhead
coho
steelhead
```

You have a file called `data/animals.txt` contains the following data:

```
deer
rabbit
raccoon
rabbit
deer
fox
rabbit
bear
```

Process this list such that there is only one value for each animal, and save it in a file under my_files/ called "unique_animals.txt"

```
sort ../data/animals.txt | uniq > unique_animals.txt
```

Challenge 3

The command cut will cut out a sequence, for characters the argument -c must be added.

```
$ echo hello
hello
```

```
$ echo hello | cut -c 2-4
ell
```

How would you count all of the words contained in articles about asia found in data/articles/? Store this number under my_files/ in a file called "asia_count".

```
cd my_files
wc -w ../data/articles/asia*.txt | tail -1 | cut -c 4-8 > asia_count
```

NB: In Windows Git Bash the cut will be 2-6.