

## FINAL EXERCISE!

Your final task is to create a script that when you change the variable "Chrom", you are able to calculate the average gene length for that chromosome.

Sample script:

```
#!/bin/bash
```

```
Chrom=chr1
```

```
...
```

```
...
```

```
...
```

This exercise does not have one way of solving the problem! Use all the tools that you have gathered so far such as: awk, grep, storing variables, line count, etc. to solve the problem.