

C_HW6 (GC)

Ken Youens-Clark

Abstract

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Protocol

Step 1.

Checkout or "git pull" the [Metagenomics Book repo](#)

Step 2.

Copy the "problems/gc" into your repo:

```
$ cp -r metagenomics-book/problems/gc /abe487/problems
```

Step 3.

Write a Perl script that will parse a FASTA file. For each read, print the GC content and whether it is "anthrax" or "burkholderia" based on the whether the percent GC falls above or below a given threshold (default = 30%).

Sample output

```
$ ./gc.pl6 burk.fa
0.52: burkholderia
0.51: burkholderia
0.50: burkholderia
0.47: burkholderia
0.51: burkholderia
0.46: burkholderia
0.50: burkholderia
0.44: burkholderia
0.49: burkholderia
```

```
$ ./gc.pl6 --threshold=.5 burk.fa
```

0.52: burkholderia
0.51: burkholderia
0.50: anthrax
0.47: anthrax
0.51: burkholderia
0.46: anthrax
0.50: anthrax
0.44: anthrax
0.49: anthrax

Step 4.

A passing test suite should look like this:

```
$ make test
./test.pl6
1..3
ok 1 - Bad arg gives usage
ok 2 - Burkholderia
ok 3 - Anthrax
```