

C_HW3 (Hello, Perl) Version 3

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Abstract

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Protocol

Step 1.

Clone the "metagenomics-book" repo if necessary (NOT in your own "abe487" repo):

```
$ git clone https://github.com/kyclark/metagenomics-book.git
```

Then pull to get the latest code and copy the "problems/greeting" directory into your "/abe487/problems" (assuming your repo is located in your \$HOME):

```
$ cd metagenomics-book
```

```
$ git pull
```

```
$ cp -r problems/greeting /abe487/problems
```

Step 2.

Edit the existing 'greeting.pl6' file to take a single, positional (not named) argument called 'name.' If you type 'make,' it will execute the script with \$USER like so:

```
$ make
```

```
./greeting.pl6 kyclark
```

```
Hello, kyclark, your name has 7 characters.
```

```
$ ./greeting.pl6 'John Coltrane'
```

```
Hello, John Coltrane, your name has 13 characters.
```

The argument you are getting from the command line is a string, so you will want to read the docs on the "Str" type:

<https://docs.perl6.org/type/Str>

If your program is given no arguments, it should print a "usage" statement. If you use the "MAIN" subroutine with a proper signature, this will happen automatically; otherwise, you will need to handle this yourself.

Step 3.

Your solution is correct when "make test" looks like this:

```
$ make test
./test.pl6
ok 1 - No args gives usage
ok 2 - Correct output
```

Step 4.

Commit and push your work to Github for checking:

```
$ git commit -m 'works now' greeting.pl6
$ git push
```