C_HW5 (wc)

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Abstract

Protocol

Step 1.

Update your checkout of the "metagenomics-book" Git repo and copy "problems/wc" to your "abe487/problems" directory:

```
$ ssh hpc

$ (cd metagenomics-book && git pull)

$ cp -r metagenomics-book/problems/wc abe487/problems

$ cd !$

$ git add wc

$ git commit -m 'wc homework' wc

$ git push
```

■ ANNOTATIONS
Emma Skidmore 15 Oct 2016

What does it mean to have unmerged files?

```
[service2@~]$ (cd metagenomics-book && git pull)
A perl6/hangman/Hangman.pm6
A perl6/hangman/hangman1.pl6
A perl6/hangman/hangman2.pl6
D perl6/palindrome/palindrome.pl6
M perl6/palindrome/palindrome1.pl6
M perl6/palindrome/palindrome2.pl6
```

M perl6/palindrome/palindrome3.pl6
M perl6/palindrome/palindrome4.pl6
M perl6/palindrome/palindrome5.pl6
M perl6/palindrome/palindrome6.pl6
M perl6/palindrome/palindrome7.pl6
D problems/cat-n/test.pl6
U problems/greeting/greeting.pl6
Pull is not possible because you have unmerged files.
Please, fix them up in the work tree, and then use 'git add/rm <file>'
as appropriate to mark resolution, or use 'git commit -a'.
[service2@~]$

Amy Hudson 16 Oct 2016

don't forget the ~ in:

cp -r metagenomics-book/problems/wc ~abe487/problems

Step 2.

Write a Perl version of 'wc' that will report the lines, words, and characters in a given file. E.g., for the given 'const.txt' file, you should see:

$ ./wc.pl6 const.txt

lines (872) words (7652) chars (45119)

For any given file, you output should match the same numbers as the standard 'wc':

$ wc const.txt
872 7652 45119 const.txt

Try your script with other input files.

🔖 ANNOTATIONS

Farideh Farahnak 15 Oct 2016

Hello Ken,

How the punctuations are handled in this script?.

Step 3.

A passing test suite looks like this:

```
$ make test
./test.pl6
1..2
ok 1 - Bad arg gives usage
ok 2 - Correct output
```