protocols.io

C_HW4 (tac) Version 3

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Abstract

Create a script that is the reverse of 'cat' in that it will print the lines from a given input file in reverse order:

```
$ cat input.txt
foo
bar
baz
quux
$ ./tac.pl6 input.txt
quux
baz
bar
foo
```

The script should accept a single unnamed "input" argument that should be a file. If provided no arguments or an argument that is not an existing file, the script should produce a "usage" statement:

```
$ ./tac.pl6
Usage:
  ./tac.pl6 <input>
$ ./tac.pl6 this-does-not-exist
Usage:
  ./tac.pl6 <input>
```

If given an input that does not exist, it should print a usage statement.

A passing test suite should look like this:

```
$ make test
./test.pl6
1..3
ok 1 - No args gives usage
ok 2 - Bad arg gives usage
ok 3 - Correct output
```

If you "make jabber," you should see this:

```
  And the mome raths outgrabe.
All mimsy were the borogoves,
  Did gyre and gimble in the wabe;
'Twas brillig, and the slithy toves
```

```
   He chortled in his joy.
O frabjous day! Callooh! Callay!'
   Come to my arms, my beamish boy!
"And, has thou slain the Jabberwock?

   He went galumphing back.
He left it dead, and with its head
   The vorpal blade went snicker-snack!
One, two! One, two! And through and through

   And burbled as it came!
Came whiffling through the tulgey wood,
   The Jabberwock, with eyes of flame,
And, as in uffish thought he stood,

   And stood awhile in thought.
So rested he by the Tumtum tree,
   Long time the manxome foe he sought --
He took his vorpal sword in hand:

   The frumious Bandersnatch!"
Beware the Jubjub bird, and shun
   The jaws that bite, the claws that catch!
"Beware the Jabberwock, my son!

   And the mome raths outgrabe.
All mimsy were the borogoves,
   Did gyre and gimble in the wabe:
'Twas brillig, and the slithy toves

JABBERWOCKY -- Lewis Carroll
```

Protocol

Step 1.

Connect to the UA HPC via ssh.

Step 2.

In your $HOME directory, you should have the 'metagenomics-book' and your own 'abe487' Git repos already checked out. If you do not have the 'metagenomics-book' directory, then do this:

```
$ (cd && git clone https://github.com/kyclark/metagenomics-book.git)
```

If you do have the directory, then do this:

```
$ (cd metagenomics-book && git pull)
```

Step 3.

Copy the new problem set into your 'problems' directory and then add to your Git repo:

```
$ (cd && cp metagenomics-book/problems/tac abe487/problems)

$ cd abe487/problems

$ git add tac

$ git commit -m 'tac problem' tac

$ git push
```

BE SURE TO WORK IN YOUR REPO AND NOT MINE!

Step 4.

You will receive full points (20) when the output of 'make test' looks like this:

```
$ make test
./test.pl6
1..3
ok 1 - No args gives usage
ok 2 - Dies on "Not a file"
ok 3 - Correct output
```

Here is what it looks like on another input:

```
$ head -10 /usr/share/dict/words > words

$ cat words
```

```
A
a
aa
aal
aalii
aam
Aani
aardvark
aardwolf
Aaron

$ ./tac.pl6 words
Aaron
aardwolf
aardvark
Aani
aam
aalii
aal
aa
a
A
```