

Trim Sequences HW

Review chapters 2-4 in “Python for Biologists”. At the end of chapter 4 there are two exercises. Complete these exercises on your own. The files you need for input as well as the solutions to the exercises are in `week4/from_the_book/`. Please work through these exercises without copying the final code. If you’re stuck you can look over the solution guide, which takes you step by step.

Your homework is to extend the script generated in the first exercise. The script you will turn in will trim the sequences in `Python/HW_1/sequences1.txt`. Your script must:

- 1) Take a command line argument for the trimming length and print that length to the screen.
 - a. I showed you how to incorporate command line arguments in class and an example script is found the `sys_argv.py`
- 2) Function properly on any length between 0 and 12.
- 3) Generate two output files:
 - a. The first file is the trimmed sequences and should be called:
 - i. `trimmed_seqs.txt`
 - ii. All sequences should be in upper case!
 - b. The second will contain stats on the trimmed sequences all on separate lines.
 - i. File should be called: `trim_stats.txt`
- 4) The trimmed stats file must contain please include useful descriptions as well as the numbers:
 - a. The length of the sequence before trimming.
 - b. The length of the sequence after trimming
 - c. The AT content of the trimmed sequence
- 5) Extra credit: Return only 3 digits for the AT content.

Testing

Your script should be named as follows:

`<your name>_HW_4.py`