Due: 23rd Sept

CMPSC 300
Bioinformatics
Fall 2019

Lab 3:
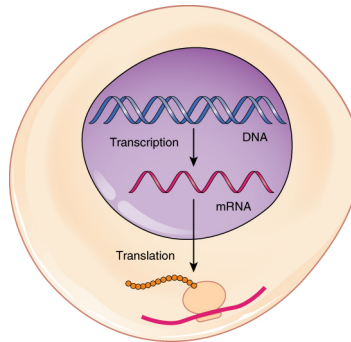**Translation with Python3**

Figure 1: The central dogma of biology in a nutshell (i.e., DNA → RNA → Protein.)

GitHub starter link

https://classroom.github.com/a/zn0wOF2R

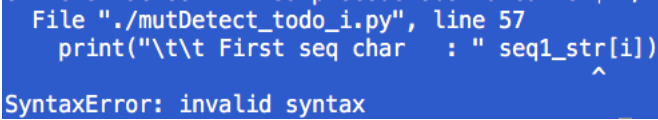To use this link, please follow the steps below.

- Click on the link and accept the assignment.

- Once the importing task has completed, click on the created assignment link which will take you to your newly created GitHub repository for this lab.

- Clone this repository (bearing your name) and work on the practical locally.

- As you are working on your practical, you are to commit and push regularly. You can use the following commands to add a single file, you must be in the directory where the file is located (or add the path to the file in the command):

  - `git add -A`
  - `git commit -m ``Your notes about commit here''`
  - `git push`

  Alternatively, you can use the following commands to add multiple files from your repository:

  - `git commit <`*nameOfFile*`> -m ``Your notes about commit here''`
  - `git push`

Be sure to read the `README.md` file in the GitHub Classroom repository for instructions on how to complete your first assignment.

HANDED OUT: 16th SEPT. 2019

```
File "./mutDetect_todo_i.py", line 57
    print("\t\t First seq char   : " seq1_str[i])
                                     ^
SyntaxError: invalid syntax
```

Figure 2: Finding bugs in code is a normal part of programming.

Objectives

To strengthen the understanding of the transcription, translation and mutation. To learn to debug Python3 code that performs a basic analysis of sequences using transcription and translation.

Reading Assignment

In addition to following the specified sections of the Python tutorial outlined below, please read Chapter 3 in the "ThinkPython" book. You should also review class slides and videos on the topics of transcription, translation and mutation.

Analysis Program

The program that you have been given in the src/mutDetect_todo_i.py is supposed to compare sequences and to perform basic translations of two user-entered sequences. It is then supposed to compare the protein sequences of the two DNA sequences to find changes in product. Unfortunately, this code was written hastily and, as a result, contains TWELVE (12) basic coding bugs (i.e., typographical errors) that prevent the code from working properly. **Your task is to complete the code by fixing the errors to allow it to run and to display the output shown below.**

Your output should look like the following.

```
bioinformaticsNumberOneFan$ ./mutDetect.py s

 Welcome to mutDetect!
 A program to compare DNA, make protein and compare protein sequences.
 __Getting a sequence__
Enter a sequence :atgatgatggcc
 __Getting a sequence__
Enter a sequence :atgatgatgggg
 + Length of first sequence  : 12
 + Length of second sequence : 12

 __Comparing sequences__
 + Bases not the same at pos:  10
 First seq char   :  c
 Second  seq char :  g
```

```
+ Bases not the same at pos:  11
First seq char    : c
Second  seq char :  g
+ Sequences are same length:  True

__Translation__
+ Original DNA        : atgatgatggcc , length is : 12
+ PROTEIN from RNA    : MMMA
+ protein1 sequence   : MMMA

__Translation__
+ Original DNA        : atgatgatgggg , length is : 12
+ PROTEIN from RNA    : MMMG
+ protein2 sequence   : MMMG

__Comparing sequences__
+ Bases not the same at pos:  3
First seq char    :  A
Second  seq char :  G
```

Required Deliverables

- Your completed activity should be saved as src/mutDetect_todo_i.py in the repository that you will push to GitHub.

- Write a reflection of about 100 words to describe your approach to finding the errors of the code. Record your reflection in the markdown document; writing/reflections.md.

Please see the instructor if you have questions about the assignment submission.