

<https://github.com/999Path/DNA-dissect>

DESCRIPTION OF THE CLASS

The RNA class purpose is to take in a DNA name and Strand. The user then can call on the methods of each class to generate the answer into a txt file. The method must be called to get an output. If none of the method is called, then the only output would be the original DNA strand. The `__init__` constructor allows the class to initialize the attributes of the class, which are `self.Name`, `self.DNA`, `self.CDNA`, `self.RNA`, `self.New_RNA`, `self.New_CDNA`, `self.A_content`, `self.G_content`, `self.C_content`, `self.U_content` and `self.gc_content`.

DESCRIPTION OF EACH OF THE CLASS AND DATA VARIABLES

`self.Name` = a string variable: the name of the DNA strand. The default would be set to unknown if there's no input.

`self.DNA` = a string variable: the DNA strand that the user wants.

DESCRIPTION OF EACH OF THE METHODS

`__init__` method take in the identifier and store it. The input for both `self.Name` and `self.DNA` must be a string.

`transcribe_seq` method returns nothing, but stores the new variable, this method must be called or else the other methods would not work.

`count_seq` method returns nothing, but stores the new variable

`gc_content` method returns nothing, but stores the new variable

`complementing_DNA` method returns nothing, but stores the new variable

`save` method print out the results of the function that was called

DESCRIPTION OF DEMO PROGRAM

Testing is set as RNA with the input "testing" and "ATGAT...". `Transcribe_seq`, `count_seq`, `gc_content`, `complementing_DNA`, and `save` methods has been called. The output will be "testing.txt" txt file. To find the file, search up "testing.txt" on your desktop. Testing2 is set as RNA with the input "" and "ATG...". However, since Testing2 name input = "" the txt file that's created is named as "unknown.txt". Testing3 inputs are "Error" and "", "Error: Input a DNA sequence" will pop up in the terminal.

HOW TO RUN THE DEMO PROGRAM

The user don't have to do anything to run the demo program since it's already running in the main() function and it's already tested to run automatically. However, the user can modify the input that's inside the main function. For example:

```
Tublin = RNA("TUBA1A", "GCAGGTTCTCTTA")
Tublin.transcribe_seq()
Tublin.count_seq()
Tublin.gc_content()
Tublin.complementing_DNA()
Tublin.save()
```