

Biomedical Software Engineering

Mount Sinai School of Medicine

Graduate School of Biomedical Sciences

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Grading sheet for Assignment 2: Write a Python program that uses the genetic code

Student:	Mu Li			
Feature category	Feature	Points	Points earned	Notes
General	Input multiple mini-chromosomes	6	5	Instead of hard-coding them, would be better to input them from a file or on the command line
	Outputs the proteins encoded by the mini-chromosomes	6	2	Does this only for one mini-chromosome
	Use the "#!/usr/bin/env python" line so your program can be run from the command line	2	1	Not done; but not very important
	Run under Python 3	2	2	
	Input all of the mini-chromosomes provided in the assignment	5	3	
	Hard-code a dictionary literal that maps all possible codons into their role in the genetic code, mapping each codon into one of the 1 letter amino acid abbreviations or 'STOP'	8	8	
	Execute a loop that scans each mini-chromosome	8	8	
	Properly transcribe proteins as encoded by any sequence of codons on the DNA that immediately follows a START codon and immediately precedes a STOP codon	8	3	Doesn't output the amino acid sequence of each protein. See "use the codon dictionary to determine and print the amino acid sequence of each encoded protein"
	Properly encode proteins containing a methionine encoded by ATG	4	2	Cannot tell
Maintain and report the following values for the input DNA	The number of encoded proteins	4	4	
	The length, in amino acids, of the shortest protein	4	2	If no proteins are encoded, get "inf" but should report "unknown", or "no proteins are encoded".
	The length, in amino acids, of the longest protein	3	3	
	The mean protein length in amino acids	4	4	
	The number of DNA failures	4	3	
	The total amount of non-coding DNA, in nucleotides	4	3	
	Output these values with text labels that identify them	5	4	
	Include the variables' units	2	2	
Make your program general purpose:	Report the mean protein length as undefined when the DNA contains no proteins	4	1	Not done
Include some test input data:	Test data contains DNA and the output expected when processing it	4	4	
	Each test case tests a particular feature of your program	5	5	
	Make at least a six test cases	4	4	
	Make a test case with no mini-chromosomes	2	0	Not done
	Handle arbitrary DNA	2	1	Unclear
Total		100	74	
Overall comments	See comments in "# APG: " in your program.			
	Large amounts of debugging output, like your "codon to amino acid" lines, hide the important output. I used "grep -v ' ' to " to see just the rest.			
	You passed in two versions of the program. I reviewed Assignment2_MuLi_Ver2.py ,			