Introduction to Bioinformatics HW 1

Submission deadline: 10 April 2022

PS: HWs submitted after the deadline will not be accepted

Please upload your HW to YTU-LMS:

Any question should be addressed to naydin@yildiz.edu.tr

You must name your Perl file by using your matriculation number (for example, 07011068.pl)

Write a Perl program that takes a DNA sequence in FASTA format and implements DNA sequence translation to amino acit sequence process.

Please note that the input data file must be in FASTA format.

(An example data file that can be used as input is provided as DNA-ex.txt)

FASTA format: A sequence file in FASTA format can contain several sequences. One sequence in FASTA format begins with a single-line description, followed by lines of sequence data. The description line must begin with a greater-than (">") symbol in the first column.

An example sequence in FASTA format is:

>U03518 Aspergillus awamori internal transcribed spacer 1 (ITS1)

Second letter							
		U	С	Α	G		
First letter	υ	UUU } Phe UUA } Leu	UCU UCC UCA UCG	UAU Tyr UAC Stop UAG Stop	UGU Cys UGC Stop UGG Trp	UCAG	Third letter
	O	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU His CAA GIn CAG	CGU CGC CGA CGG	UCAG	
	A	AUU AUC AUA He AUG Met	ACU ACC ACA ACG	AAU Asn AAC AAA AAA Lys	AGU Ser AGA AGG	UCAG	
	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC Asp GAA GAG	GGU GGC GGA GGG	UCAG	

A=Ala=Alanine
C=Cys=Cysteine
D=Asp=Aspartic acid
E=Glu=Glutamic acid
F=Phe=Phenylalanine
G=Gly=Glycine
H=His=Histidine
I=Ile=Isoleucine
K=Lys=Lysine
L=Leu=Leucine

M=Met=Methionine
N=Asn=Asparagine
P=Pro=Proline
Q=Gln=Glutamine
R=Arg=Arginine
S=Ser=Serine
T=Thr=Threonine
V=Val=Valine
W=Trp=Tryptophan
Y=Tyr=Tyrosine