

Indraprastha Institute of Information Technology Delhi (IIITD)

Department of Computational Biotechnology

BIO213 – Introduction to Quantitative Biology

ASSIGNMENT-2 (April 06, 2023)

Instructions:

1. You are required to submit the assignments by next **Saturday, 15 April 2023**.
2. Use Python to write your program.
3. Compile everything into a single PDF. Use <roll no.-name> to label and save the file.
4. You are also required to submit a well commented working code.
5. Requests for extension of submission deadline will NOT be entertained.

Question 1. Write a program to implement Chou and Fasman method of secondary structure prediction (Helix and Beta strand) for the following protein sequence.

SGFRKMAFPSGKVEGCMVQVTCGTTTLNGLWLDDTVYCPRHVICTAEDMLNPNYEDL
LIRKSNHSFLVQAGNVQLRVIGHSMQNCLRLKVDTSNPKTPKYKFVRIQPGQTFSVLA
CYNGSPSGVYQCAMRPNHTIKGSFLNGSCGSVGF

- a) Provide a well commented code for the same. **(30 marks)**
- b) Display the output using the notation – H: Helix, S: Beta strand. **(10 marks)**

Chou and Fasman parameters to be used for the prediction are as following:

Residue	P α	Residue	P β
Glu	1.53	Met	1.67
Ala	1.45	Val	1.65
Leu	1.34	Ile	1.60
His	1.24	Cys	1.30
Met	1.20	Tyr	1.29
Gln	1.17	Phe	1.28
Trp	1.14	Gln	1.23
Val	1.14	Leu	1.22
Phe	1.12	Thr	1.20
Lys	1.07	Trp	1.19
Ile	1.00	Ala	0.97
Asp	0.98	Arg	0.90
Thr	0.82	Gly	0.81
Ser	0.79	Asp	0.80
Arg	0.79	Lys	0.74
Cys	0.77	Ser	0.72
Asn	0.73	His	0.71
Tyr	0.61	Asn	0.65
Pro	0.59	Pro	0.62
Gly	0.53	Glu	0.26

Question 2. Elaborate upon the major differences between the following two categories of secondary structure prediction methods/tools? **(10 marks)**

Category I: Chou and Fasman and GOR method

Category II: DSSP, P-curve and Stride