Major Examination - SBV 887: Current Topics in Computational Biology

Semester II, 2015 - 2016

Time: 2 hrs

Maximum Marks: 40

Brevity is the soul of communication. Extraneous information will be penalized.

1. Recently a method was developed to transform 3-D structural data of protein sequences into 2-D data of the form $Y = Y_{Max}(1-e^{-kX})^n$, where "Y" defines the number of neighbours for a given amino acid residue within a spherical zone of radius "X" Å (with that particular amino acid residue as the centre of the sphere). Develop an algorithm (either as a diagram/flow chart or in form of steps – *paragraphs will be penalized*) to extract 3-D structural data back from 2-D data given the values of "n" and "k". After writing the algorithm, carry out a dry-run assuming n = 4 and k = 0.025 – show your results in a tabulated form.

(8 + 2 = 10)

2. Utilizing the central dogma, draw a diagram of a cell labelling the following – (i) Genome (ii) Proteome (iii) Transcriptome (iv) Exome. Will this diagram be different for eukaryotes and prokaryotes? Why or why not?

({2 x 4} + 1 + 1 = 10)

3. Following is a scale of free energies that we wish to utilize for identifying trans-membrane helices:

Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val
0.3	-1.4	-0.5	-0.6	0.9	-0.7	-0.7	0.3	-0.1	0.7	0.5	-1.8	0.4	0.5	-0.3	-0.1	-0.2	0.3	-0.4	0.6

If a trans-membrane domain of a protein is assumed to be an alpha-helix, and the thickness of the membrane of a newly discovered organism is found to be 5.4 nm, what is the window size required to prepare a hydropathy plot for predicting trans-membrane domains of membrane proteins in this organism? Note that in an alpha-helix there are 3.6 residues per turn and pitch of the helix is 5.4 Angstroms.

(5)

4. Referring to Dill et al., 1995, Principles of protein folding -A perspective from simple exact models, draw all possible states for a hexamer toy model utilized for developing a statistical mechanics framework for understanding protein folding. Calculate the density of states, and use the results obtained to plot h vs. g(h). **Note:** Points will be awarded for the plot only if the drawings and calculations are collect (i.e. copying/regurgitation of the plot from the reference is not acceptable).

(10 + 5 = 15)

EXTRA CREDIT: How does the answer to Q. 4 demonstrate (a) "complexity" of the protein folding problem and (b) a possible direction for overcoming the complexity?

(2.5 x 2 = 5)