No. of Printed Pages : 4+1

MBOI-006

M.S. IN BIOTECHNOLOGY

(MSBOMM/MSBOCC)

Term-End Examination

00121

December, 2014

MBOI-006 : COMPUTATIONAL MOLECULAR BIOLOGY

Time : 3 hours *Maximum Marks : 100*

Note :

(i) *Section I is* ***compulsory****.*

(ii) *In Section II, solve any* ***five*** *questions.*

(iii) *Assume suitable data wherever required.*

(iv) *Draw suitable sketches wherever required.*

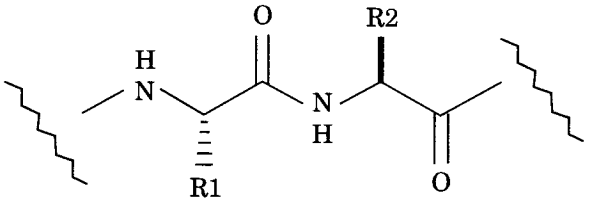
(v) *Italicized figures to the right indicate maximum marks.*

SECTION I

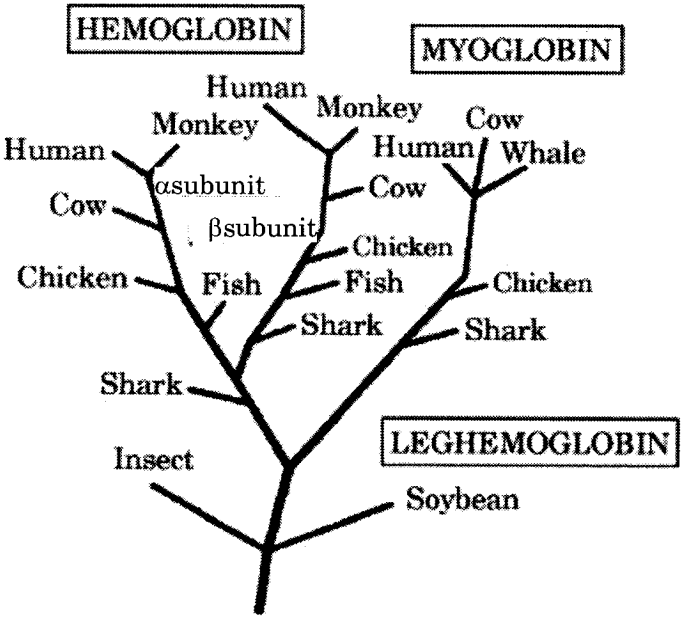
1. Differentiate a gene from an ORF. Explain the methods used for Gene Prediction. What is Alternative Splicing ? What steps would you devise to enable the software to predict alternative splicing from a given gene sequence ?

2+4+2+2

2. What are proteins ? Define primary structure, secondary structural elements and tertiary structure observed in protein structures giving an example. Explain the need for a new metric such as torsional angle to understand proteins. Identify the atoms involved which define phi, psi and omega torsion angles in the diagram given below. *1+3+2+4*



3. What is Phylogenetic Tree analysis ? Explain the various methods to draw a phylogenetic tree. What biological information can be deduced from the following phylogenetic tree : *3+3+4*



SECTION II

4. Do a Global and Local alignment of the following hypothetical signal peptides with the following parameters/recommendations. Assume gap penalty : -1. Substitution Matrix is provided at the end of the question paper. Interpret the results.

Protein 1 : MYSPVLS

Protein 2 : LFTPILP *14*

5. What is Homology modelling ? Write the steps involved in Homology modelling. Explain the relevant reasons for having ~ 7,00,000 protein sequences but only ~ 1,00,000 protein 3D structures. *2+8+4*

6. Explain multiple sequence alignment. What is the difference between a consensus sequence and a conserved sequence ? Explain the various algorithms used to perform a multiple sequence alignment. What type of biological information does a scientist look for in a multiply aligned sequence output ? *3+1+5+5*

7. List the various experimental techniques used to deduce protein 3D structure. Write the limitation of each of the techniques. Explain one of the techniques in your own words. *4+5+5*

8. Expand BLAST. List the various variants of BLAST algorithm. Explain the algorithm of BLAST. Comment on the unique steps in the algorithm which contribute to time savings when using BLAST as compared to DPA. *1+3+6+4*

9. Expand DPA. Describe the algorithmic steps of DPA in detail. What is the differentiating step between Global and Local alignment algorithm ? List the fundamental assumptions behind alignment algorithms. *1+6+2+5*

10. List four biological structure visualization software tools. Explain the salient features of SPDB Viewer. List four new features you would propose in the next version of SPDB Viewer. *4+6+4*

Use the following Substitution Matrix

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	B	Z	X	*
A	4	−1	−2	−2	0	−1	−1	0	−2	−1	−1	−1	−1	−2	−1	1	0	−3	−2	0	−2	−1	0	−12
R	−1	5	0	−2	−3	1	0	−2	0	−3	−2	2	−1	−3	−2	−1	−1	−3	−2	−3	−1	0	−1	−12
N	−2	0	6	1	−3	0	0	0	1	−3	−3	0	−2	−3	−2	1	0	−4	−2	−3	3	0	−1	−12
D	−2	−2	1	6	−3	0	2	−1	−1	−3	−4	−1	−3	−3	−1	0	−1	−4	−3	−3	4	1	−1	−12
C	0	−3	−3	−3	9	−3	−4	−3	−3	−1	−1	−3	−1	−2	−3	−1	−1	−2	−2	−1	−3	−3	−2	−12
Q	−1	1	0	0	−3	5	2	−2	0	−3	−2	1	0	−3	−1	0	−1	−2	−1	−2	0	3	−1	−12
E	−1	0	0	2	−4	2	5	−2	0	−3	−3	1	−2	−3	−1	0	−1	−3	−2	−2	1	4	−1	−12
G	0	−2	0	−1	−3	−2	−2	6	−2	−4	−4	−2	−3	−3	−2	0	−2	−2	−3	−3	−1	−2	−1	−12
H	−2	0	1	−1	−3	0	0	−2	0	−3	−3	−1	−2	−1	−2	−1	−2	−2	2	−3	0	0	−1	−12
I	−1	−3	−3	−3	−1	−3	−3	−4	−3	4	2	−3	1	0	−3	−2	−1	−3	−1	3	−3	−3	−1	−12
L	−1	−2	−3	−4	−1	−2	−3	−4	−3	2	4	−2	2	0	−3	−2	−1	−2	−1	1	−4	−3	−1	−12
K	−1	2	0	−1	−3	1	1	−2	−1	−3	−2	5	−1	−3	−1	0	−1	−3	−2	−2	0	1	−1	−12
M	−1	−1	−2	−3	−1	0	−2	−3	−2	1	2	−1	5	0	−2	−1	−1	−1	−1	1	−3	−1	−1	−12
F	−2	−3	−3	−3	−2	−3	−3	−3	−1	0	0	−3	0	6	−4	−2	−2	1	3	−1	−3	−3	−1	−12
P	−1	−2	−2	−1	−3	−1	−1	−2	−2	−3	−3	−1	−2	−4	7	−1	−1	−4	−3	−2	−2	−1	−2	−12
S	1	−1	1	0	−1	0	0	0	−1	−2	−2	0	−1	−2	−1	4	1	−3	−2	−2	0	0	0	−12
T	0	−1	0	−1	−1	−1	−1	−2	−2	−1	−1	−1	−1	−2	−1	1	5	−2	−2	0	−1	−1	0	−12
W	−3	−3	−4	−4	−2	−2	−3	−2	−2	−3	−2	−3	−1	1	−4	−3	−2	11	2	−3	−4	−3	−2	−12
Y	−2	−2	−2	−3	−2	−1	−2	−3	2	−1	−1	−2	−1	3	−3	−2	−2	2	7	−1	−3	−2	−1	−12
V	0	−3	−3	−3	−1	−2	−2	−3	−3	3	1	−2	1	−1	−2	−2	0	−3	−1	4	−3	−2	−1	−12
B	−2	−1	3	4	−3	0	1	−1	0	−3	−4	0	−3	−3	−2	0	−1	−4	−3	−3	4	1	−1	−12
Z	1	0	0	1	−3	3	4	−2	0	−3	−3	1	−1	−3	−1	0	−1	−3	−2	−2	1	4	−1	−12
X	0	−1	−1	−1	−2	−1	−1	−1	−1	−1	−1	−1	−1	−1	−2	0	0	−2	−1	−1	−1	−1	−1	−12
*	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	−12	1