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PG/IIS/MCB—204/11(X)

M.Sc. 2nd Semester Examination, 2011

MICROBIOLOGY

PAPER—X

Full Marks : 40

Time : 2 hours

The figures in the right-hand margin indicate marks

Candidates are required to give their answers in their own words as far as practicable

Illustrate the answers wherever necessary

GROUP – A

(*Computer and Bioinformatics*)

[*Marks* : 20]

Answer any *two* questions : 10 × 2

1. Describe the five important components, such as input unit, output unit, CPU, memory and ALU of a computer and draw a logical diagram mentioning the connection among these components. 5 × 2

2. What do you mean by operating system ? Give example of two operating system. What are the differences between system software and application software ? What are the differences between programming languages and packages ? Mention name of two programming language and one package. 2 + 1 + 3 + 2 + 2

3. (*a*) What is Windows ? Explain a method to create a folder in C drive. How the content of a folder can be copied to another folder ? 2 + 2 + 2

   (*b*) Write a brief note about 'for' statement in C. 4

GROUP – B

[*Marks* : 20]

Answer any *two* questions : 10 × 2

4. (*a*) What is the full form of BLAST ? Who has developed the algorithm and in which year ? What is the significance of e-value ? 2 + 1 + 2

(*b*) (*i*) Provide the name of a database focusing on biomedical literature.

(*ii*) What is the reverse complement of the following DNA sequence ? GTGGTGAAATCT.

(*iii*) Draw a plot (dot) for the following two sequences : CACGAC and GATCACG. Assume a window and stringency of 1.

(*iv*) Do you think if two genes are homologous they always have similar functions ? Give examples. 1 + 1 + 2 + 1

5. (*a*) (*i*) If you were performing pairwise comparisons of protein sequences of the same highly conserved gene from *E.coli* and human, which scoring matrix and pairwise alignment algorithm would you use and why ?

(*ii*) Write any two differences between PAM and BLOSUM. 2 + 3 (*b*) (*i*) Define similarity , identity and homology, "Two sequences are 10% homologous". Explain the meaning of the above statement.

(*ii*) Define orthologous and paralogous sequences. 3 + 2

6. (*a*) What is the difference between phylogram and cladogram ? 2

(*b*) Suppose you have given two sets of sequences. One is a set of closely related sequences and the other is distantly related. Which of the two approaches maximum passimony or maximum likelihood do you think better for the analysis and why ? Does gene tree and species tree represent the same tree ? 3

(*c*) (*i*) Difference between local and global alignment.

(*ii*) Suppose you have the following matrix for the Needleman Wunch dynamic programming algorithm. The scores are

+3 for a match, –1 for a mismatch, and –2 for a gap. Fill in the final entry of the matrix. 2 + 3

$$\begin{array}{ccccccc}
 & & A & C & A & C & G \\
 & 0 & -2 & -4 & -6 & -8 & -10 \\
G & -2 & -1 & -3 & -1 & -3 & -5 \\
C & -4 & -3 & +2 & 0 & 2 & 0 \\
A & -6 & -5 & 0 & 5 & 3 & 5 \\
C & -8 & -7 & -2 & 3 & 8 & 6 \\
A & -10 & -5 & -4 & 1 & 6 &
\end{array}$$