CS/B.Sc.(H)/BT/Gen/Micro-Bio/Mol-Bio/SEM-4/CBB-402/2013

2013

COMPUTATIONAL BIOLOGY & BIO-INFORMATICS

Time Allotted : 3 Hours   *Full Marks* : 70

The figures in the margin indicate full marks.

Candidates are required to give their answers in their own words

as far as practicable.

GROUP – A
(Multiple Choice Type Questions)

1. Choose the correct alternatives for any *ten* of the following :

$$10 \times 1 = 10$$

   i)   Which of these is not a protein sequence database ?

   a)   PIR   b)   GenBank

   c)   PDB   d)   Swiss-Prot.

   ii) BCA stands for

   a)   Bacteria Artifice Chromosome

   b)   Bacterial Artifice Chromosome

   c)   Bacterial Artificial Chromosome

   d)   Bacterial Artificial Chromatid.

   iii) Which step is omitted in whole genome sequencing ?

   a)   Random shqedding of genome

   b)   Making phage library

   c)   Computational analysis

   d)   None of these.

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iv) Which of the following is not primary nucleotide sequence database ?

a) DDBJ   b) OWL

c) GEN BANK   d) EMBL.

v) URL for NCBI is

a) www.ncbi.nlm.nih.gov   b) www.ncbi.nih.nlm.gov

c) www.ncbi.gov   d) www.ncbi.nlm.gov.

vi) Clastal *W*

a) multiple sequence alignment tool

b) protein secondary structure predicting tool

c) data retrieving tool

d) nucleic acid sequence analysis tool.

vii) Which is data retiring tool ?

a) KEGG   b) EMBL

c) ENTERZ   d) PHD.

viii) BLAST & FASTA are used for

a) global similarity

b) end free space alignment

c) local similarity

d) gap penalty.

ix) Information of all known nucleotide & protein sequel are available on

a) NCBI gene bank   b) DDBJ

c) EMBL   d) all of these.

x) What is the primary goals of databases ?

a) Minimizing data redundancy

b) Achieving data independence

c) Both (a) and (b)

d) None of these.

xi) Phylogenetic relationship can be shown by

a) Dendogram   b) Data search tool

c) Data retrieving   d) Gene bank.
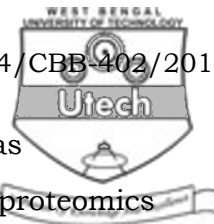
xii) Proteomics research can be categorized as

   a) structural proteomics & functional proteomics

   b) structural functional & comparative functional

   c) functional & comparative proteomics

   d) none of these.

GROUP – B

(Short Answer Type Questions)

Answer any *three* of the following.   3 × 5 = 15

2. Define WWW, HTTP, HTML, URL.

3. What is substitution matrix ? Write down the difference between PAM & BLOSUM matrix.   2 + 3

4. What is sequence alignment ? Write about *E* value & *Z* score.

          2 + 3

5. Write down the difference between FASTA & BLAST.   2 + 3

6. Write about data retrieval tool. What is sequin & bankit ?

          2 + 3

GROUP – C

(Long Answer Type Questions)

Answer any *three* of the following.   3 × 15 = 45

7. a) What is Secondary Database ? Name two Secondary Databases.

   b) What is the difference between Accession Number and Gi Number ?

   c) What are the basis of database searching in bioinformatics ?

   d) What do you mean by BankIT ?   1 + 2 + 4 + 5 + 3

8. a) Compare the features between Primary, Secondary and Tertiary database.

   b) What is PFAM and BLOCKS ?

   c) Write down the differences between Flat File and Hierarchical files.

   d) Why Biological Database are important ?   5 + 3 + 4 + 3

9. What is Dynamic Programming ? What are the general steps of it ? Name two database searching tools. Fill the matrix for DP and align the following sequences :

   GAATTCAGTTA (sequence#1) (Upto Matrix fill step only)

   GGATCGA (sequence#2)   2 + 1 + 2 + 7 + 3

10. What is substitution matrix ? In "PAM 250" the 250 stands for what ? Write down the difference of PAM 250 and BIOSSM 62 matrix. What is humming and levenstein distance ? Write down one name of two small molecule database. What is Pubmed ? What is the name of the database where you get the inheritable disease of human ? What is word size ? Comment on sensitivity and selectivity ?

                    1 + 1 + 3 + 4 + 1 + 1 + 1 + 1 + 2

11. State the difference between homology and similarity ? Write down 6 emerging fields in bioinformatics. You have given a sequence of African elephant and Indian elephant how would you draw the phylogenetic relation between them ? What would you expect the result. What is relative mutability ?

                    3 + 3 + 4 + 2 + 3

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