

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 × 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 shquedding of genome

b) Making phage library

c) Computational analysis

d) None of these.

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](http://www.ncbi.nlm.nih.gov) b) [www.ncbi.nih.nlm.gov](http://www.ncbi.nih.nlm.gov)
- c) [www.ncbi.gov](http://www.ncbi.gov) d) [www.ncbi.nlm.gov](http://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.  $3 \times 5 = 15$

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.  $3 \times 15 = 45$

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 BLOSUM 62 matrix. What is hamming 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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