



NBH-1603220001020300 Seat No. _____

B. Sc. (Bioinformatics) (Sem. II) (CBCS) Examination

April / May - 2017

BI - 203 : Introduction to Bioinformatics

(New Course)

Time : $2\frac{1}{2}$ Hours]

[Total Marks : 70

- Instructions :** (1) All questions are compulsory.
(2) The right side figure indicates total marks of the question.

- 1 Attempt the following : **14**
- (a) Answer the following short questions : (All Compulsory) **4**
- (1) The Smallest known vertebrate genome
 - (2) _____ deals with the study of messenger RNA molecules produced in an individual or population of a particular cell type.
 - (3) The study of relationships between the genomes of different species is known as _____.
 - (4) _____ differs from cell to cell and from time to time.
- (b) Answer Any One of the following short questions : **2**
- (1) Cheminformatics
 - (2) Neuroinformatics
- (c) Answer Any One of the following short questions : **3**
- (1) Classification of Biological databases
 - (2) Human Genome Project
- (d) Explain Any One of the following questions in details : **5**
- (1) Application of Bioinformatics
 - (2) DDBJ

- 2** Attempt the following : **14**
- (a) Answer the following short questions : (All Compulsory) **4**
- (1) What is the full form of INSDC?
 - (2) Give examples for protein family and domain databases.
 - (3) Which are the sequence databases that coordinate with NCBI / GenBank?
 - (4) What are the online submission tools for GenBank?
- (b) Answer Any **One** of the following short questions : **2**
- (1) Define Literature database
 - (2) PDB
- (c) Answer Any **One** of the following short questions : **3**
- (1) Explain software used in 3D structure comparison
 - (2) Give a note on the growth of GenBank.
- (d) Explain Any **One** of the following questions in details : **5**
- (1) GenBank
 - (2) PyMol
- 3** Attempt the following : **14**
- (a) Answer the following short questions : (All Compulsory) **4**
- (1) The NCBI assigns a unique _____ to each species of organism.
 - (2) The GenBank staff examines the originality of the data and assigns an _____ to the sequence and performs quality assurance checks.
 - (3) Which type of alignment is generally used to compare distantly related sequence?
 - (4) EST is the abbreviation of _____.
- (b) Answer Any **One** of the following short questions : **2**
- (1) BLOSUM
 - (2) Fingerprint
- (c) Answer Any **One** of the following short questions : **3**
- (1) Difference between PAM and BLOSUM Matrix
 - (2) Global Alignment

- (d) Explain Any **One** of the following questions in details : 5
- (1) Align the following sequences :
- Sequence 1 G G G G U U C G C U C A
Sequence 2 A G A G G U U G C U C U
Sequence 3 C G A G G C U G C U C
Sequence 4 U G A G G C U C G C U C A
- (2) What are the sequence comparison methods available?

4 Attempt following : 14

(a) Answer the following short questions : (All Compulsory) 4

- (1) Full form of BLAST.
(2) VecScreen BLAST use to identify _____.
(3) _____ search the sequence against the genome of specific organism.
(4) Which are the similarity search tools?

(b) Answer Any **One** of the following short questions : 2

- (1) FASTA
(2) Similarity vs Identity

(c) Answer Any **One** of the following short questions : 3

- (1) Explain the tools for MSA
(2) Relationship between MSA and Phylogenetic tree.

(d) Explain Any **One** of the following questions in details : 5

- (1) BLAST
(2) Multiple Sequence Alignment algorithms

5 Attempt the following : 14

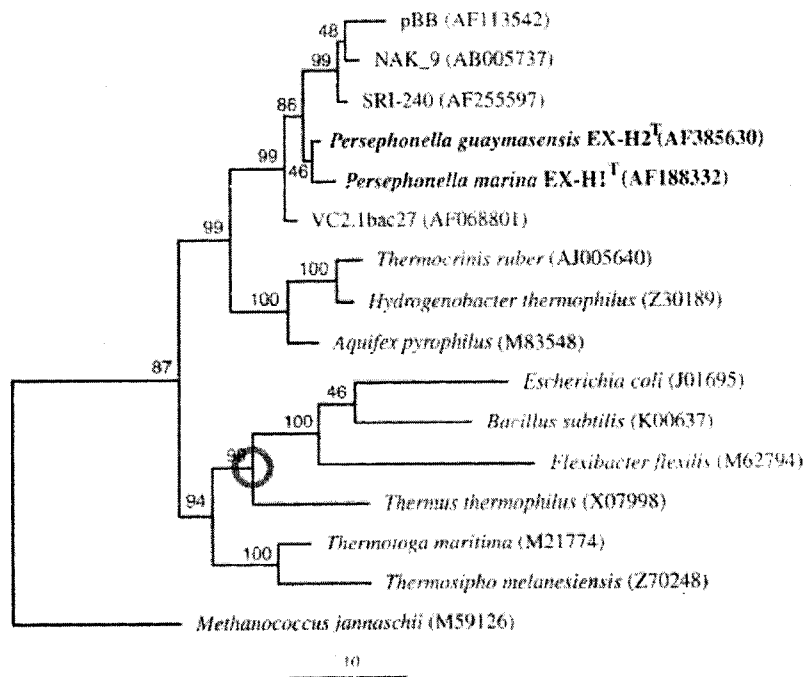
(a) Answer the following short questions : (All Compulsory) 4

- (1) TreeFam is a database composed of _____
(2) Multiple sequence alignment is used for
(3) If the scale of the phylogenetic tree is mentioned then it is called Scaled, Dendogram or _____ tree.
(4) Abbreviation of CATH is _____.

(b) Answer Any **One** of the following short questions : 2

- (1) Rooted Tree
(2) Unit of Phylogenetic tree construction

- (c) Answer Any **One** of the following short questions : **3**
- (1) Define: Tree, Node, Bifurcating node, Scaled tree, Dendrogram (Phylogram), and Cladogram
 - (2) List out a few Phylogenetic tree visualization software
- (d) Explain Any **One** of the following questions in details : **5**
- (1) Explain character based methods to construct phylogenetic tree.
 - (2) Tree interpretation: answer the following questions based on this ssu-rRNA-based phylogenetic tree. The scale bar (0.10) represents evolutionary distance. Sequences/organisms without names (i.e.pBB, Nak_9, SRI-240, and VC2.1 bac27) are from uncultivated species.



- (a) Is this a dendrogram or a phenogram?
- (b) Which sequence(s) is/are presumably the outgroup?
- (c) Which sequence is most closely related to *Bacillus subtilis*?
- (d) The Circle (on the tree above) is the last common ancestor of _____ and _____
- (e) Except for the outgroup, which two sequences in this tree are the most distantly related?
- (f) Which branch(es) would you have the least confidence in?