BRAINWARE UNIVERSITY

Term End Examination 2019 – 20

Programme – Master of Science in Biotechnology

Course Name – Bioinformatics and Computer Application

Course Code – MBT105

(Semester – 1)

Time allotted: 2 Hours 30 Minutes   Full Marks: 60

[The figure in the margin indicates full marks. Candidates are required to give their answers in their own words as far as practicable.]

Group –A

(Multiple Choice Type Question)   20 x 1 = 20

1.   Answer any *twenty* from the following

(i)   Dynamic programming is applicable to

    a.   Diverged alignment   b.   Local alignment

    c.   Parallel alignment   d.   None.

(ii)   When characters are homologous due to conserved function?

    a.   Homologous   b.   Analogous.

    c.   Orthologous.   d.   Paralogous.

(iii)   The first bioinformatics database was created by

    a.   Richard Durbin   b.   Dayhoff

    c.   Michael J.Dunn   d.   Pearson

(iv)   An example of Homology & similarity tool?

    a.   PROSPECT   b.   EMBOSS

    c.   RASMOL   d.   BLAST

(v)   Analyzing or comparing entire genome of species (tick the most appropriate answer)

    a.   Bioinformatics   b.   Genomics

    c.   Proteomics   d.   Pharmacogenomics

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(vi)   Two-dimensional gels are used to _____.

    a. separate DNA fragments   b. separate RNA fragments

    c. separate different proteins   d. observe a protein in two dimensions

(vii)   You do a BLAST search on a DNA sequence and it identifies it as 'Exon 1' of a certain gene. An exon is

    a. a section of a eukaryotic gene that is translated into protein.   b. a section of a eukaryotic gene that is NOT translated into protein.

    c. a regulatory sequence that turns genes on and off.   d. DNA that has no genetic role, but does maintain the physical structure of a chromosome.

(viii) Each record in a database is called as

    a. entry   b. file

    c. record   d. ticket

(ix)   Literature database include

    a. MEDILINE and PUBMED   b. MEDILINE and PDB

    c. PUBMED and PDB   d. MEDILINE and PDS

(x)   The stepwise method for solving problems in computer science is called as

    a. flowchart   b. sequential design

    c. procedure   d. Algorithm

(xi)   The term used for refer something performed on computer

    a. dry lab   b. web lab

    c. wet lab   d. insilico

(xii)   A compound that has desirable properties to become a drug

    a. lead   b. find

    c. fit drug   d. fit compound

(xiii) Alignment method suitable method for align closely related sequence is called as

    a. MSA   b. Pairwise alignment

    c. global alignment   d. local alignment

(xiv)   All are sequence alignment tool except

    a. RASMOL   b. BLAST

    c. FASTA   d. CLUSTAL W

(xv)   Operating system is a

    a. Collection of hardware components   b. Collection of input devices

    c. Collection of software routine   d. all

(xvi)   BLOSSOM matrices are used in
      a. MSA
                    b. Pairwise Sequence Alignment
      c. Phylogenic alignment
                    d. all

(xvii) Which is model organism database
      a. GOLD
                    b. PROMISE
      c. SGD
                    d. SCOP

(xviii) FASTA was published by
      a. Joseph Sambrooke
                    b. Pearson and Lippman
      c. Sanger
                    d. Altschul

(xix)   Which of the following options is protein data base
      a. DDBz
                    b. SWISSPORT
      c. GENE bank
                    d. PDB

(xx)   Which of the following statements is wrong WRT SWISSPORT
      a. Curated protein sequence data
                    b. Data is redundant
      c. provide high level annotation
                    d. Maintained by Swiss institute of bioinformatics and EBI

(xxi)   PAM matrices are derived by noting evolutionary changes in protein sequences that are more than -------- similar
      a. 80%
                    b. 60%
      c. 90%
                    d. 40%

(xxii) Which alignment is used to predict whether two sequences are homologous or not?
      a. Local
                    b. Global
      c. Pairwise
                    d. all

(xxiii) Which of the following terms describe SNP, s that result in an amino acid change in the protein?
      a. synonymous change in the non-coding region
                    b. synonymous change in the coding region
      c. Non-synonymous change in the non-coding region
                    d. Non-synonymous change in the coding region

(xxiv) Which of the following information is not found in SWISSPORT
      a. 3-D coordinates of crystal structure
                    b. Tissue and sub cellular localization.
      c. amino acid in active site
                    d. alternate name for the protein

(xxv)   An E-value is
      a. a. The expected number of codon in a sequence of nucleotide length
                    b. b. An expression of likelihood that a QTL exits in a genome interval
      c. c. The expected number of equally good sequence matches in a sequence database
                    d. d. An expression of goodness of fit of a gene prediction to DNA sequence

Group – B

(Short Answer Type Questions)   4 x 5 = 20

Answer any *four* from the following

2. (a) What are the different integrated retrieval platform of Entre through which user can access in to different database?   2

    (b) How protein profile is determined by Hidden Markov Model?   3

3.   Give the formula by which similarity between two sequences can be calculated   5

4. (a) Explain curated database   2

    (b) What is Hidden Markov Model   2

    (c) Distinguish between E-score and P-score   1

5. (a) What is structural database? Explain with suitable example   2

    (b) What are advantages of NMR spectroscopy?   3

6. (a) Briefly mention the fundamental consideration in designing and using biological database.   2

    (b) Distinguish between flat file and relational database.   3

7. (a) What is pattern recognition?   2

    (b) How pattern matching software allow several option for making the pattern search more efficient?   3

Group – C

(Long Answer Type Questions)   2 x 10 = 20

Answer any *two* from the following

8. (a) What main function of microarray?   5

    (b) How normalization of microarray is performed?   3

    (c) Mention the factors that contribute to experimental errors in microarray   2

9. (a) Give short notes on homologous, analogous , orthologous and paralogous type of sequence similarity   5

    (b) Give brief history of development of Entrez   5

10. (a) Distinguish between Blastp and Blastn and Blastx   5

    (b) How scoring of alignment is made by Dynamic Programming?   2

    (c) Explain domain and motif with suitable example   3

11.   Briefly enumerate the different application of bioinformatics   10