BRAINWARE UNIVERSITY

ODD Semester Examinations 2021- 22

Programme – Bachelor of Technology in Computer Science & Engineering - 2018 [B.Tech.(CSE)]

Course Name – Biology

Course Code – BSC(CSE)701

(Semester VII)

Time allotted : 1 Hour 25 Minutes   Full Marks : 70

(Multiple choise type question)   70 x 1 = 70

Choose the correct alternative from the following

(I) Double-helical structure of DNA is analysed by Data obained from which techniques?

    A) Electrophoresis   B) Chromatography

    C) X-ray crystallography   D) Centrifugation

(II) What is a fingerprint?

    A) A protein family discriminator built from a set of regular expressions.   B) A protein family discriminator built from a set of conserved motifs.

    C) A cluster of protein sequences gathered from a BLAST search.   D) A cluster of protein sequences gathered from a FASTA search.

(III) Sanger sequencing is based in

    A) Nucleotide base in DNA   B) Nucleotide base in RNA

    C) m-RNA sequence   D) Amino acid sequence

(IV) 1. Which of these analyses needs a stretched grid?

    A) Transient flow over a flat plate   B) Incompressible flow over a flat plate

    C) Viscous flow over a flat plate   D) Subsonic flow over a flat plate

(V) By using which method sorting is not possible?

    A) Insertion   B) Selection,

    C) deletion,   D) exchange

(VI) Distance matrix method for making phylogenetic tree are done by

    A) Normal algorythemic sequence   B) Data base maintain sequence

    C) UPGMA   D) None of them

(VII) Sanger Sequence Teniques are

    A) 1st generation techniques   B) 2nd Generation techniques

    C) 3rd Generation techniques   D) next Gen technique

(VIII) The sequence alignment of amino acid for making phylogenetic tree are done by

    A) Gene bank   B) PDB

    C) BLAST   D) Oracle

(IX) The radial structure generelly observed in

    A) Rooted tree   B) Unrooted tree

    C) Phylogenetic tree   D) Living tree

(X) Human genome project employed .... for sequencing Data

    A) Needleman-Wunsch algorithm   B) Clasical algorhythem

    C) artificial intelegence   D) None of them

(XI) Gene bank Include

    A) Only DNA sequence   B) Potein level expression

C) information about the locus name, length of the sequence,   D) None of them

(XII) The backbone of nucleic acid structure is constructed by

A) Peptide bonds   B) Phosphodiester bridges

C) Glycosidic bonds   D) All of them

(XIII) Which one is the secondary data bases

A) Prosite-   B) Uni prot

C) NCBI   D) EMBL

(XIV) Point out the wrong statement.

A) k-means clustering is a method of vector quantization   B) k-means clustering aims to partition n observations into k clusters

C) k-nearest neighbor is same as k-means   D) none of them

(XV) In which year did the SWISSPROT protein sequence database begin?

A) 1988   B) 1985

C) 1986   D) 1987

(XVI) The main function of primary database are

A) A Collection of Data   B) Analysing Data

C) Storage of Data   D) Collection and storage of DaTa

(XVII) The Branch point denotes

A) divergence event   B) Convergence event

C) Multivergence event   D) No eventual significance

(XVIII) The term Bioinformatics was coined by

A) J.D Watson   B) Pauline Hogeweg

C) Margaret Dayhoff   D) Frederic Sanger

(XIX) Replication occurs once every cell generation during

A) S phase   B) T phase

C) C phase   D) A phase

(XX) Human genome project run

A) 10 years   B) 13 years

C) 15 years   D) Still running

(XXI) One aromatic amino acid

A) Tyrosine   B) Alanine

C) Lysine   D) Arginine

(XXII) What does elliptic grid generation mean?

A) Grids generated for elliptic equations   B) Grids transformed with elliptic equations

C) The computational domain is elliptic   D) The object under consideration is ellipti

(XXIII) Basic amino acid is

A) Glutamic acid   B) Aspertic acid

C) Arginine,   D) Glycine

(XXIV) Synthesis of DNA from RNA is known as

A) Reverse transcriptase   B) Reverse transcription

C) Reverse Replication   D) Reverse Translation

(XXV) all of the mentioned

A) defined distance metric   B) defined distance metric

C) defined distance metric   D) defined distance metric

(XXVI) "Rooted bifurcating"-This term used to denoted

A) two descendants arising from each interior node   B) two descendants arising from different node

C) two descendants arising from different species   D) None of them

(XXVII) For making Phylogenetic Tree, we prefered Data obtained from

A) DNA micro array   B) m-RNA

C) Protein Data Base   D) None of them

(XXVIII) Which technique was used to determine the double-helical structure of DNA?

A) Electrophoresis   B) Chromatography

C) Centrifugation   D) X-ray crystallography

(XXIX) Which of the following combination is incorrect?

A) Continuous – euclidean distance   B) Continuous – correlation similarity

C) Binary – manhattan distance   D) None of the mentioned

(XXX)   Natural pace maker is

A) SA node   B) AV node

C) Perkinji Fiber   D) Hiss Bundle

(XXXI) Hydrophobic side chain generally present in

A) Outer Periphery region   B) hydrophobic sidechain do not form bond

C) Core region   D) randomly assorted

(XXXII) The highest number of gene present in human chromosome are

A) Chromosome 1   B) Chromosone X

C) Chromosome Y   D) Chromosome 21

(XXXIII) next Gen sequencing technology is primarily applied for

A) Gene therapy   B) Pharmaco econimics study

C) terget oriented drug therapy   D) none of them

(XXXIV) The vector used for Human genome project are

A) BAC   B) ECORI

C) BAMHIII   D) Ti Plasmid

(XXXV) Which of the following RNAs bind to an amino acid?

A) mRNA   B) tRNA

C) rRNA   D) hnRNA

(XXXVI) The larest lymph gland is

A) Spllen   B) Liver

C) Tonsil   D) Gastric gland

(XXXVII) The laboratory work using computers and associated with web-based analysis generally online is referred to as _____.

A) In silico   B) Dry lab

C) Wet lab   D) All of the above

(XXXVIII) Which of the following is finally produced by Hierarchical Clustering?

A) final estimate of cluster centroids   B) tree showing how close things are to each other

C) assignment of each point to clusters   D) all of the mentioned

(XXXIX) Identify Incorrect statement, Algorithms can be represented:

A) as pseudo codes   B) as syntax

C) as programs   D) as flowcharts

(XL) Identify the amino acids containing nonpolar, aliphatic R groups

A) Phenylalanine, tyrosine, and tryptophan   B) Lysine, arginine, histidine

C) Glycine, alanine, leucine   D) Serine, threonine, cysteine

(XLI) Comperative genomics is use for study in

A) between difference into species   B) Relation between two species

C) similarity between two species   D) Genome study for one individual

(XLII) Salivery gland mostly present in

A) Stomach   B) Oesophagus

C) Mouth   D) Intestine

(XLIII) Adaptive grids change automatically based on _____

A) flow field gradients   B) time rate of change of the flow properties

    C) grid gradients   D) time rate of change of the grid points

(XLIV) Which of the following are the spatial clustering algorithms?

    A) Partitioning based clustering   B) K-means clustering

    C) Grid based clustering   D) All of the above

(XLV) Distant relation between species focused on

    A) Rooted tree   B) Unrooted tree

    C) Phylogenetic tree   D) Living tree

(XLVI) The cell formed after fusion of sperm and ovum is known as

    A) Embryo   B) Brastula

    C) Zygote   D) Infant

(XLVII) The muscle attatched with skeleton is known as

    A) Smooth Muscle   B) Cardiac muscle

    C) Bone marrow   D) Striated Muscle

(XLVIII) Coordinates for known protein structures are housed in?

    A) CATH   B) SCOP

    C) PDBsum   D) PDB

(XLIX) Which of the following are not the application of bioinformatics?

    A) Drug designing   B) Data storage and management

    C) Understand the relationships between organisms   D) None of the above

(L) Why are colour schemes important in creating and analysing sequence alignments?

    A) They look pretty   B) To make clearer printouts and presentations

    C) To allow you to distinguish conserved residues and residue groups more easily   D) To allow you to detect active sites of proteins

(LI) Which of the following is an example of Homology and similarity tool?

    A) BLAST   B) RasMol

    C) EMBOSS   D) PROSPECT

(LII) The gray matter and White matter is present in

    A) Spinal cord only   B) Brain Only

    C) Both Spinal Cord and Brain   D) none of them

(LIII) The identification of drugs through the genomic study is called_____.

    A) Genomics   B) Pharmacogenomics

    C) Pharmacogenetics   D) Proteomics

(LIV) Well-conserved regions in multiple sequence alignments:

    A) reflect areas of structural importance.   B) reflect areas of functional importance

    C) reflect areas of both functional and structural importance.   D) reflect areas of both functional and structural importance.

(LV) Bayesian Belief Network is also known as ?

    A) belief network   B) decision network

    C) Bayesian model   D) All of the above

(LVI) Human genome project was completed on

    A) 1990   B) 2000

    C) 2003   D) Contineously running

(LVII) How many bones are present in our body

    A) 206   B) 306

    C) 106   D) 602

(LVIII) Human genome project employed

    A) Expressed sequence tags only   B) Sequence Annotation only

    C) Both The techniques   D) None of them

(LIX) DNA replication is

A) Conservative

B) Non-conservative

C) Semi-conservative

D) None

(LX) Which base is not found in RNA?

A) adenine

B) cytosine

C) thymine

D) uracil

(LXI) Amino acid are linked together by

A) Glycosidic bond

B) peptide bond

C) Di ester bond

D) phosphate bond

(LXII) Origin of species is written by

A) Jean-Baptiste Lamarck

B) Charles Darwin

C) Edward Hitchcock.

D) Gregor Mendel

(LXIII) Pick the right difference between a DNA and RNA

A) Sugar and phosphate

B) Purines and phosphate

C) Sugar and pyrimidines

D) Sugar and purines

(LXIV) How many terms are required for building a bayes model?

A) 1

B) 2

C) 3

D) 4

(LXV) Where does the bayes rule can be used?

A) Solving queries

B) Increasing complexity

C) Decreasing complexity

D) Answering probabilistic query

(LXVI) Human genome contain

A) 6 billion base pairs.

B) 3.3 billion base pairs.

C) 3.3 billion base

D) 3.3 billion amino acid sequence

(LXVII) All of the followings are protein sequence databases except.

A) PIR

B) PSD

C) EMBL

D) SWISS PORT

(LXVIII)   Which of the following tools is used for the identification of motifs?

A) BLAST

B) COPIA

C) PROSPECT

D) Pattern hunter

(LXIX) The ribosomes are composed of

A) proteins

B) RNA

C) both (a) and (b)

D) lipids

(LXX) Two sequences are said to be homologous if:

A) they have diverged from a common ancestor.

B) their alignments share 30% identity or more.

C) they belong to the same fold family.

D) they have converged to share similar functional properties.