Online Examinations (Even Sem/Part-I/Part-II Examinations 2020 - 2021

Course Name - Bioinformatics
Course Code - BBT603C2A

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8.　　*

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( ) LLM

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( ) M.SC.(MSJ)

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( ) M.SC.CS)

( ) M.SC.(ANCS)

( ) M.SC.(MM)

( ) B.A.(Eng)

Answer all the questions. Each question carry one mark.

9.   1. In which year did the SWISSPROT protein sequence database begin?

Mark only one oval.

( ) 1988

( ) 1985

( ) 1986

( ) 1987

10.   2. The human genome contains approximately_____.

Mark only one oval.

( ) 6 billion base pairs

( ) 3 billion base pairs

( ) 4 billion base pairs

( ) 4.5 billion base pairs

11.   3. Which of the following compounds has desirable properties to become a drug?

Mark only one oval.

( ) Fit drug

( ) Lead

( ) Fit compound

( ) All of the above

12.   4. The stepwise method for solving problems in computer science is called_____

Mark only one oval.

( ) Algorithm

( ) Flowchart

( ) Procedure

( ) Sequential design

13.   5. GeneBank, a nucleotide sequence database is maintained by

Mark only one oval.

- ⬭ DDBJ
- ⬭ NCBI
- ⬭ EMBL
- ⬭ CSIR

14.   6. The information retrieval tool for NCBI Gene Bank is -

Mark only one oval.

- ⬭ Entrez
- ⬭ SeqIn.
- ⬭ Text Search.
- ⬭ STAG.

15.   7. PRINTS are software used for

Mark only one oval.

- ⬭ detection of genes from genome sequence
- ⬭ detection of tRNA genes
- ⬭ prediction of function of a new gene
- ⬭ Identification of functional domains/motifs of proteins

16.　8. Which of the following is not a gene expression database?

Mark only one oval.

◯ GEO

◯ Array Express

◯ FASTA

◯ All of the above

17.　9. The human genes produce more than one transcripts by the process of

Mark only one oval.

◯ Replication

◯ Transcription

◯ Alternative splicing

◯ Translation

18.　10. _____ is a primary protein structure database.

Mark only one oval.

◯ PDB

◯ PubChem

◯ ChemBank

◯ SCOP

19. 11. FASTA format starts with?

Mark only one oval.

○ /

○ }

○ >

○ *

20. 12. If a single organism contains two loci encoding homologous genes as a result of gene duplication, the encoded proteins are said to be?

Mark only one oval.

○ Orthologous

○ Xenologous

○ Paralogous

○ Heterologou

21. 13. Which of the following is a mismatch?

Mark only one oval.

○ Polymerase – Taq polymerase

○ Template – double stranded DNA

○ Primer – oligonucleotide

○ Synthesis – 5' to 3' direction

22.   14. Polymerase used for PCR is extracted from _____.

Mark only one oval.

⬭ Escherichia coli

⬭ Homo sapiens

⬭ Thermus aquaticus

⬭ Saccharomyces cerevisiae

23.   15. At what temperature do denaturation of DNA double helix takes place?

Mark only one oval.

⬭ 60°

⬭ 54°

⬭ 74°

⬭ 94°

24.   16. Which of the following is incorrect about a microarray?

Mark only one oval.

⬭ It is a slide attached with a high-density array of immobilized DNA oligomers representing the entire genome of the species.

⬭ Array of immobilized DNA oligomers cannot be cDNAs

⬭ Each oligomer is spotted on the slide and serves as a probe for binding to a unique complementary cDNA.

⬭ It is the most commonly used global gene expression profiling method

25.   17. Which of the following is incorrect about Microarray Data Collection?

Mark only one oval.

◯ The two-color microarray uses multiple dyes at times

◯ The most common type of microarray protocol is the two-color microarray

◯ The cDNAs are obtained by extracting total RNA or mRNA from tissues or cells and incorporating fluorescent dyes in the DNA strands during the cDNA biosynthesis

◯ The expression of genes is measured via the signals from cDNAs hybridizing with the specific oligonucleotide probes on the microarray

26.   18. Which of the following is incorrect about Classification of microarray data?

Mark only one oval.

◯ For microarray data, clustering analysis identifies coexpressed and coregulated genes.

◯ For microarray data, clustering analysis identifies coexpressed but not coregulated genes.

◯ For microarray data, clustering analysis identifies and coregulated but not coexpressed genes.

◯ Genes within a category have more similarity in expression than genes from different categories.

27.   19. Which of the following is incorrect about Hierarchical Clustering?

Mark only one oval.

◯ The tree-branching pattern illustrates a higher degree of relationship between related gene groups.

◯ It is not similar to the distance phylogenetic tree-building method

◯ It produces a treelike structure that represents a hierarchy or relative relatedness of data groups.

◯ In the tree leaves, similar gene expression profiles are placed more closely together than dissimilar gene expression profiles.

28.   20. The classic protein separation methods involve

Mark only one oval.

⬭ Two-dimensional gel electrophoresis followed by gel image analysis.

⬭ One-dimensional gel electrophoresis followed by gel image analysis.

⬭ Westen Blot

⬭ None of them

29.   21. Which of the following is incorrect regarding Mass Spectrometry Protein Identification?

Mark only one oval.

⬭ The proteolysis doesn't generate a pattern according to molecular weight.

⬭ Proteins can be identified and characterized using MS.

⬭ The proteins from a two dimensional gel system are first digested in situ with a protease.

⬭ Protein spots of interest are excised from the two-dimensional gel.

30.   22. Which of the following is incorrect regarding the Protein Identification through Database Searching?

Mark only one oval.

⬭ MS characterization of proteins is highly dependent on bioinformatic analysis.

⬭ Bioinformatics programs can be used to search for the identity of a protein in a database of theoretically digested proteins.

⬭ the protease digestion is always perfect in MS

⬭ The purpose of the database search is to find exact or nearly exact matches.

31. 23. Which of the following is incorrect regarding Differential In-Gel Electrophoresis?

Mark only one oval.

◯ Proteins are mixed together before electrophoresis on a two-dimensional gel.

◯ Differentially expressed proteins in both conditions can't be visualized in the same gel.

◯ In this, Differences in protein expression patterns can be detected in a similar way as in fluorescent-labeled DNA microarrays.

◯ Proteins from experimental and control samples are labeled with differently colored fluorescent dyes.

32. 24. An alternative approach to determining protein–protein interactions is to use a large-scale affinity purification technique involves

Mark only one oval.

◯ Attaching fusion tags to proteins and purifying the associated protein complexes.

◯ Attaching fluorescence tags to proteins and purifying the associated protein complexes.

◯ Attaching reporter gene tags to proteins and purifying the associated protein complexes.

◯ Option 4

33. 25. When the two domains are located in two different proteins, to preserve the same functionality---

Mark only one oval.

◯ Their close proximity and interaction have to be preserved as well.

◯ They are called homologs.

◯ They are hydrophobic in nature

◯ They are hydrophilic in nature

34.   26. Which of the following is untrue regarding the STRING?

Mark only one oval.

◯ Search Tool for the Retrieval of Interacting Genes/Proteins.

◯ Functional associations include only the direct protein-protein interactions

◯ It is based on combined evidence of gene linkage, gene fusion and phylogenetic profiles.

◯ It is a web server that predicts gene and protein functional associations.

35.   27. Which of the following is not one of the training sets in SignalP?

Mark only one oval.

◯ Prokaryotes

◯ Eukaryotes

◯ Gram-positive bacteria

◯ Gram-negative bacteria

36.   28. Which of the following is incorrect regarding GeneQuiz?

Mark only one oval.

◯ It is a web server for protein DNA annotation.

◯ It is a web server for protein sequence annotation.

◯ It compares a query sequence against databases using BLAST and FASTA to identify homologs with high similarities.

◯ It performs domain analysis using the PROSITE and Blocks databases.

37. 29. The remote homology detection helps to shed light on the possible functions of the proteins---

Mark only one oval.

- that previously have no functional information at all.
- that previously have no functional information.
- that are from different orgasims always
- which are more than 100 kDa molecular weight.

38. 30.Conserved functional sites can be identified by profile and hidden Markov model–based motif and domain search tools such as.

Mark only one oval.

- SMART
- InterPro
- BLAST
- Both (a) & (b)

39. 31. Gene set enrichment analysis can be performed by

Mark only one oval.

- GSEA
- GO
- KEGG
- None of them

40.   32. Why is it possible to have two homologous proteins separated by more than 100 PAMs (percent accepted mutations)

Mark only one oval.

⬭ The two proteins are paralogous

⬭ Some sites mutate more than once

⬭ It is due to convergent evolution

⬭ These is a direct correspondence between PAM and evolutionary distance

41.   33. Which of the following is TRUE??

Mark only one oval.

⬭ Local alignment techniques are useful only for nucleotide alignments

⬭ tis most useful when two sequences are distantly related

⬭ Local alignment can identify only paralogues, global alignment can identify only orthologues

⬭ Local alignment is used when querying a database

42.   34. Which branching diagram is assumed to be an estimate of a phylogeny when branching lengths are proportional to the amount of inferred evolutionary change?

Mark only one oval.

⬭ Phylogram

⬭ Cladogram

⬭ A guide tree

⬭ Cardiogram

43. 35. When you are comparing two or more than two sequences of same or different organisms, what is the type of alignment?

Mark only one oval.

( ) Global

( ) Local

( ) Pairwise

( ) Multiple sequence

44. 36. Which alignment is useful to detect the highly conserved sequences?

Mark only one oval.

( ) Local

( ) Global

( ) Pairwise

( ) Multiple Sequence

45. 37. Multiple sequence alignment method is called as an_____alignment method?

Mark only one oval.

( ) Global

( ) Local

( ) Progressive

( ) Non-progressive

46. 38. Pfam-A and Pfam-B is automatically generated from the _____database?

Mark only one oval.

( ) SMART

( ) PRINTS

( ) PROSITE

( ) PRODOM

47. 39. The tool of identification of motifs

Mark only one oval.

( ) COPIA

( ) Pattern Hunter

( ) PROSPECT

( ) BLAST

48. 40. In sequence alignment by BLAST, each word from query sequence is typically _____ residues for protein sequences and _____ residues for DNA sequences

Mark only one oval.

( ) ten, eleven

( ) three, three

( ) three, eleven

( ) three, ten

49.   41. Which of the following is not a variant of BLAST?

Mark only one oval.

◯ BLASTN

◯ BLASTP

◯ BLASTX

◯ TBLASTNX

50.   42. Which of the following is not correct about BLAST?

Mark only one oval.

◯ The BLAST web server has been designed in such away as to simplify the task of program selection

◯ The programs are organized based on the type of query sequences

◯ The programs are organized based on the type of nucleotide sequences, or nucleotide sequence to be translated

◯ BLAST is not based on heuristic searching methods

51.   43.Genetic linkage maps, also called genetic maps, identify_____ on a chromosome.

Mark only one oval.

◯ the relative positions of genetic markers

◯ the gene sequence

◯ the relative position of promoters and enhancers.

◯ All of them

52.   44. Physical maps are constructed by using_____

Mark only one oval.

◯ chromosome walking

◯ genetic recombination

◯ gene epistasis

◯ all of them

53.   45. Which of the following is untrue about DNA sequencing?

Mark only one oval.

◯ It is now routinely carried out using the Sanger method

◯ This doesn't make use of DNA polymerases

◯ This involves the synthesis of DNA chains of varying length

◯ The DNA synthesis is stopped by adding dideoxynucleotides

54.   46. Which of the following is incorrect regarding gene annotation?

Mark only one oval.

◯ The gene annotation of the human genome employs a combination of theoretical prediction and experimental verification

◯ Gene structures are first predicted by ab initio exon prediction programs

◯ The predicted genes are compared with experimentally determined cDNA and EST sequences

◯ The pairwise alignment programs are not involved

55.   47. RNA-Sequencing is performed to study

Mark only one oval.

( ) Gene expression

( ) Isoform identification

( ) Both (a) &(b)

( ) None of them

56.   48. All are sequence alignment tool except-

Mark only one oval.

( ) Rasmol

( ) BLAST

( ) BWA

( ) Clustal W

57.   49. Which of the following is multiple sequence alignment tool.

Mark only one oval.

( ) Clustal W

( ) Chime

( ) Dismol

( ) PDB

58.   50. Building phylogenetic tree involves_____

Mark only one oval.

◯ bifurcation

◯ multifurcation

◯ Both (a) & (b)

◯ None of them

59.   51. SRS is:

Mark only one oval.

◯ A website for sequence similarity searches

◯ A Website specialising in mapping mutations related to human disease

◯ A Website that indexes many biological databases and is searchable by keywords.

◯ A Website for protein family database searches

60.   52. Which of the following is incorrect statement about Molecular Markers?

Mark only one oval.

◯ For studying very closely related organisms, protein sequences are preferred

◯ The decision to use nucleotide or protein sequences depends on the purposes of the study

◯ For constructing molecular phylogenetic trees, one can use either nucleotide or protein sequence data

◯ The decision to use nucleotide or protein sequences depends on the properties of the sequences

61.   53. Which of the following is untrue?

Mark only one oval.

⬭ Eukaryotic nuclear genomes are much larger than prokaryotic ones.

⬭ They tend to have a very high gene density.

⬭ Eukaryotic nuclear genomes' sizes range from 10 Mbp to 60 Gbp

⬭ All of the above

62.   54. A genomic DNA possesses functioning units, a group of genes under the influence of promoters known as

Mark only one oval.

⬭ Genes

⬭ Operon

⬭ Codon

⬭ Anti-codon

63.   55. Which of the following is untrue about Ab Initio–Based Programs for Gene Prediction?

Mark only one oval.

⬭ The goal of the ab initio gene prediction programs is to discriminate exons from noncoding sequences

⬭ The goal is joining exons together in the correct order

⬭ The main difficulty is correct identification of exons

⬭ To predict exons, the algorithms rely solely on gene signals.

64.   56. Which of the following is untrue about GeneMark?

Mark only one oval.

( ) It is a suite of gene prediction programs based on the fifth-order HMMs.

( ) The main program is trained on a number of complete microbial genomes.

( ) A GeneMark heuristic program can be used to improve accuracy

( ) If the sequence to be predicted is from a non-listed organism, the most closely related organism can be chosen as the basis for computation

65.   57. Why are colour schemes important in creating and analysing sequence alignments?

Mark only one oval.

( ) They look pretty

( ) To make clearer printouts and presentations

( ) To allow you to distinguish conserved residues and residue groups more easily

( ) To allow you to detect active sites of proteins

66.   58. Protein-coding genes can be identified by

Mark only one oval.

( ) Transposon tagging

( ) ORF scanning

( ) Zoo-blotting

( ) Nuclease S1 mapping

67.   59. ORF scanning is performed

Mark only one oval.

○ To find exon

○ To find intergenic sequence

○ To find gene homologies

○ To find protein-coding genes.

68.   60. GEO is affiliated with

Mark only one oval.

○ NCBI

○ EBI

○ Both

○ None

69.   61. Which of the followings is not related to GO terms?

Mark only one oval.

○ Biological processes

○ Molecular function

○ Cellular components

○ Cell size

70.　62. Which of the followings is a protein interaction database?

Mark only one oval.

◯ STRING

◯ BioExpress

◯ GEO

◯ ENSEMBLE

71.　63. Which one is a markup language?

Mark only one oval.

◯ HTML

◯ MySQL

◯ R

◯ Python

72.　64. EMBL-EB is located in

Mark only one oval.

◯ France

◯ England

◯ Germany

◯ Japan

73.   65. Alternative splicing generates multiple variants of

Mark only one oval.

⬭ Transcripts

⬭ Protein

⬭ Both (a) and (b)

⬭ None of them

74.   66.Human genome only contains

Mark only one oval.

⬭ Protein coding sequences

⬭ Non-coding sequences

⬭ Peudogenes

⬭ All of the above

75.   67. A comprehensive database to study the human genetics and molecular biology is

Mark only one oval.

⬭ PDB

⬭ OMIM

⬭ ENTREZ

⬭ SWISS PROT

76. 68. Which database of Pfam is having high quality data?

Mark only one oval.

- ⬭ Pfam-A
- ⬭ Pfam-B
- ⬭ Pfam-C
- ⬭ Pfam-D

77. 69. Which of the following is genome alignment tool?

Mark only one oval.

- ⬭ FastQC
- ⬭ Bowtie
- ⬭ Chomatogram
- ⬭ None of them

78. 70. Human genome contains _Gbp data.

Mark only one oval.

- ⬭ 3.3
- ⬭ 1
- ⬭ 0.5
- ⬭ 0.2

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