

1. Which of the following is the type of software that has self-replicating software that causes damage to files and system?

A) Viruses B) Trojan horses C) Bots D) **Worms**

2. McAfee is an example of

A. Photo Editing Software

B. Quick Heal

C. Virus

**D. Antivirus**

3. Which of the following is known as Malicious software?

A. illegalware

B. badware

**C. malware**

D. software

**4. To protect a computer from virus, you should install ----- in your computer.**

A. backup wizard

B. disk cleanup

**C. antivirus**

D. disk defragmenter

**5. VIRUS stands for**

A. Very Intelligent Result Until Source

B. Very Interchanged Resource Under Search

**C. Vital Information Resource Under Siege**

D. Viral Important Record User Searched

**6. Which of the following is not an antivirus software?**

A. AVG

B. Avast

**C. Code Red**

D. McAfee

**7. software designed to disrupt computer operation, gather sensitive information, or gain unauthorized access to computer systems**

**A. Malware**

B. Moleculewar

C. Malisoft

D. Malairasoft

**8. Which of the following is/are threats for electronic payment systems?**

A. Computer worms

B. Computer virus

C. Trojan horse

**D. All of the above**

**9. Key logger is a**

A. Firmware

B. Antivirus

**C. Spyware**

D. All of the above

**10. To protect yourself from computer hacker, you should turn on a**

A. Script

**B. Firewall**

C. VLC

D. Antivirus

**11. Firewalls are used to protect against -----**

- A. data driven attacks
- B. fire attacks
- C. virus attacks

**D. unauthorised access**

12. Code red is a(n) -----

- A. Word Processing Software
- B. Antivirus
- C. Virus**
- D. Photo Editing Software

13. ----- software are programs that are installed onto your computer and can scan and remove known viruses which you may have contracted.

- A. Firmware
- B. Adware
- C. Keylogger

**D. Antivirus**

14. Which of the following describes programs that can run independently travel from system to system and disrupt computer communication?

- A. Viruses
- B. Trojans
- C. Droppers

**D. Worm**

15. A ----- is a computer program that can replicate itself and spread from one computer to another.

- A. Antivirus
- B. PenDrive
- C. Mouse

**D. Computer Virus**

16. Authentication is

- A. modification
- B. insertion

**C. hard to assure identity of user on a remote system**

D. none of the above

17. A ----- is a computer program that can replicate itself and spread from one computer to another.

A) PenDrive

**B) Computer Virus**

C) Antivirus

D) Mouse

18. ----- are attempts by individuals to obtain confidential information from you to falsifying their identity.

A. Computer viruses

**B. Phishing scams**

C. Phishing trips

D. Spyware scams

19. ----- are often delivered to a PC through an email attachment and are often designed to do harm.

A. Spam

B. Email

C. Portals

**D. Virus**

20. The altering of data so that it is not usable unless the changes are undone is
- A. ergonomics
  - B. compression
  - C. biometrics
  - D. encryption**
21. When a logic bomb is activated by a time related event, it is known as -----
- A. virus
  - B. trojan horse
  - C. time related bomb sequence
  - D. time bomb**
22. A ----- is a computer program that can invade computer and perform a variety of functions ranging from annoying(e.g. popping up messages as a joke) to dangerous (e.g. deleting files or destroying your hard disk).
- A. Ms Word
  - B. Ms Access
  - C. Antivirus
  - D. Computer Virus**
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- A. Spam
  - B. Email
  - C. Portals
  - D. Virus**
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- A. Ms Word
  - B. Ms Access
  - C. Antivirus
  - D. Computer Virus**
26. Which of the following virus overtake computer system, when it boots and destroy information?
- A. Stealth virus**
  - B. Trojan
  - C. Boot infectors
  - D. System infectors
27. To protect yourself from computer hacker, you should turn on a
- A. Firewall**
  - B. Script
  - C. Antivirus
  - D. VLC
28. Primary databases of three-dimensional structures of biological molecules, included:

- A. PDB
- B. SCOP
- C. EMBL
- D. Both A and B**

29. Levels between CPU and main memory were given a name of

- A. Hit time
- B. Miss rate
- C. Locality in time
- D. Cache**

30. Allowing processor for continuing execution of instructions, that access data-cache while having cache miss, is known as

- A. Nonblocking cache**
- B. Blocking cache
- C. Cache buffer
- D. None of above

31. A queue holding data while data are waiting to be written in memory, is known as

- A. Read buffer
- B. Queue buffer
- C. Write buffer
- D. Data buffer**

33. Spatial locality, is also known as

- A. Temporal locality
- B. Locality in space**
- C. Locality in time
- D. Spectral Locality

34. Main memory of a computer can act as a 'cache' for secondary memory, usually implemented by magnetic disks, technique is called

- A. Virtual memory**
- B. Main memory
- C. Cache
- D. Buffer

35. Principle of locality that was used; implementing memory of computer as

- A. Locality in time
- B. Locality in space
- C. Memory hierarchy**
- D. Temporal locality

36. Address location in main memory, is referred to as

- A. Logical address
- B. Physical address**
- C. Static address
- D. Block associative

37. An asymmetric-key (or public-key) cipher uses

- A. 1 Key
- B. 2 Key**
- C. 3 Key
- D. 4 Key

38. We use Cryptography term to transforming messages to make them secure and immune to

- A. Change
- B. Idle
- C. Attacks**

- D. Defend
39. Substitutional ciphers are
- Monoalphabetic
  - Semi alphabetic
  - polyalphabetic
  - both a and c**
40. DES stands for
- Data Encryption Standard**
  - Data Encryption Subscription
  - Data Encryption Solutions
  - Data Encryption Slots
41. In Cryptography, original message, before being transformed, is called
- Simple Text
  - Plain Text**
  - Empty Text
  - Filled Text
42. Original message, before being transformed, is
- Cipher text
  - plaintext**
  - decryption
  - None
43. Data Encryption Standard (DES), was designed by
- Intel
  - IBM**
  - HP
  - Sony
44. **Why would a hacker use a proxy server?**
- To create a stronger connection with the target.
  - To create a ghost server on the network.
  - To obtain a remote access connection.
  - To hide malicious activity on the network.**
45. **The first phase of hacking an IT system is compromise of which foundation of security?**
- Availability
  - Confidentiality**
  - Integrity
  - Authentication
46. Trademark can be used as domain name
- Yes** (b) No (c) Yes in some cases (d) None of the above
47. Geographical Indication is
- Private right (b) Community right
  - Intellectual property right (d) **both (b) and (c)**
48. Certification mark can be registered in
- Trademark Registry** (b) Certification Board
  - Quality Control Board (d) MHRD
49. Which of the following statements best describes a white-hat hacker?
- Security professional**
  - Former black hat
  - Former grey hat
  - Malicious hacker

50. What type of ethical hack tests access to the physical infrastructure?

- A. Internal network
- B. Remote network
- C. External network

**D. Physical access**

51. Human genome project was officially started in:

- A. 1984
- B. 1990**
- C. 1991
- D. 1859

52. Term bioinformatics emerged in year;

- A. 1989
- B. 1988
- C. 1985

**D. 1990**

53. Bioinformatics' is also be regarded as part of the;

- A. Computational biology**
- B. Computational biotechnology
- C. Computer biology
- D. Computer knowledge

54. Primary databases of three-dimensional structures of biological molecules, included:

- A. PDB
- B. SCOP
- C. EMBL

**D. Both A and B**

55. The first bioinformatics database was created by

- A. Richard Durbin
- B. Dayhoff**
- C. Michael j.Dunn
- D. Pearson

56. The BLAST program was developed in \_\_\_\_\_

- a) 1992
- b) 1985**
- c) 1990
- d) 1991

57. In sequence alignment by BLAST, each word from query sequence is typically \_\_\_\_\_ residues for protein sequences and \_\_\_\_\_ residues for DNA sequences.

- a) ten, eleven
- b) three, three
- c) three, eleven**
- d) three, ten

58. Which of the following is not a variant of BLAST?

- a) BLASTN
- b) BLASTP
- c) BLASTX
- d) TBLASTNX**

59. Which is the default scoring matrix used in BLAST?

- a) PAM62
- b) BLOSUM 62**

- c) BLOSUM 60
  - d) BLOSUM 80
60. PAM matrices are derived by noting evolutionary changes in protein sequences that are more than:
- a) **80% similar** b) 60% similar
  - c) 40% similar d) 25% similar
61. Which alignment is used to predict whether two sequences are homologous or not?
- a) Local **b) Global** c) Pair-wise d) multiple
62. In a PHYLIP output, the first line is two numbers, what do they indicate?
- a) **Number of sequences, length of alignment**
  - b) Length of alignment, number of sequences
  - c) Number of gaps, number of sequences
  - d) Number of sequences, number of gaps
63. Homology modeling may be distinguished from ab initio prediction because:
- a) Homology modeling requires a model to be built
  - b) Homology modeling requires alignment of a target to a template**
  - c) Homology modeling is usefully applied to any protein sequence
  - d) The accuracy of homology modeling is independent of the percent identity between the target and the template
64. What is PROSITE?
- a) a database of protein structures
  - b) a database of interacting proteins
  - c) a database of protein motifs**
  - d) a search tool
65. Which is the best annotated database?
- a) Genbank
  - b) PDB
  - c) Prodom
  - d) Swissprot**
66. If you want literature information, which is the best website to visit?
- a) OMIM
  - b) Entrez
  - c) PubMed**
  - d) PROSITE
67. Which of the following amino acids is least mutable according to PAM scoring matrix?
- a) Alanine
  - b) Glutamine
  - c) Methionine
  - d) Cysteine**
68. You have two distantly related proteins. Which of the following sets is the best for comparing them?
- a) BLOSUM45 or PAM250**
  - b) BLOSUM45 or PAM1
  - c) BLOSUM80 or PAM250
  - d) BLOSUM80 or PAM1
69. Which alignment is used to predict whether two sequences are homologous or not?
- a) Local
  - b) Global
  - c) Pair-wise
  - d) Multiple

70. BLOCKS refers to

- a) gapped, aligned motif in a multiple sequence alignment
- b) ungapped, aligned motif in a multiple sequence alignment**
- c) coding sequences
- d) non-coding sequences

71. CpG islands and codon bias are tools used in eukaryotic genomics to identify open reading frames

**a) differentiate between eukaryotic and prokaryotic**

- b) DNA sequences
- c) Look for DNA-binding domains
- d) determine STS

72. The type of algorithm that GENSCAN tool employs is

- a) Neural network
- b) Rule-based system
- c) Hidden Markovs model**
- d) Statistics based

73. Which of the following is a retrieval system?

- a) Entrez**
- b) Bioedit
- c) Vecscreen
- d) Rasmol

74. Homology modeling involves

- a) alignment of the target sequence to the sequence of a template structure**
- b) alignment of the target sequence with multiple sequences with no structural information
- c) ab initio structure prediction
- d) no input of sequence information

75. Quantitative Structure Activity Relationship (QSAR) is used for

- a) Drug design**
- b) Protein modelling
- c) Aligning two sequences
- d) Molecular Dynamics simulation

76. In protein modeling, molecular mechanics force field is used, because

- a) it takes less time as compared to others**
- b) it is more accurate
- c) it guarantees global minimum
- d) it explicitly represents the electrons in a calculation

77. Which of the following algorithms implements “once a gap, always a gap” policy?

- a) ClustalW**
- b) Needleman & Wunsch
- c) Chou & Fasman
- d) FASTA

78. The Ramachandran map of a protein representation allows you to identify

- a) The most stable structure
- b) The tertiary allowed structure
- c) The sterically disallowed conformations**
- d) the secondary structure elements

79. The collection of proteins that can be produced by a given species is:

- A) Considered that species' genetic complement.
- B) Correlated with the size of the organism.

C) **Called the proteome.** ✓

D) All of these.

80. How many potential open reading frames are present in a DNA sequence?

A) One

B) Three

C) **Six** ✓

D) More than Six

81. Drug designing approaches are of \_\_\_\_\_ types

a) **4**

b) 2

c) 1

d) 6

82. Expressed portion of gene

a) protein

b) lipids

c) aminoacids

d) **exons**

83. Non –coding regions are called as

a) gene

b) chromatin

c) **intron**

d) none of these

84. ORF stands for

a) **Open reading frame**

b) open real frame

b) ordinary realistic frame

d) original reoccurring frame

85. Proteomics the term coined by

a) Mark Wilkins

b) Crick

c) Watson

d) Kornberg

86. Databases such as CATH and SCOP are used to identify:

A. the structural family to which a protein belongs

B. the genic family to which a protein belongs

C. homologous proteins

D. analogous proteins

87. Bootstrapping repeats the phylogenetic analysis several times, each time reshuffling the columns of the initial alignment, in order to:

A. build a consensus tree, where the number of times each branch reforms is counted and used to estimate its probability

B. generate a random model from which to benchmark phylogenetic data

C. produce a graphical representation of the tree

D. assess the probability that the sequences in the alignment are unrelated

88. Why might you want to search a database for a protein motif?

A) **A specific motif may impart a specific function to the molecule. You could then identify groups of proteins that may have similar functions.**

B) Presence of a specific motif in several proteins indicates that they are likely to be all from the same species.

C) Absence of a specific motif from one of a pair of otherwise similar proteins indicates that they are produced by alternative splicing of the same gene.

D) All of the above.

89. In an analysis of eukaryotic gene, you identify several nonoverlapping open reading frames, but they are not all in the same frame. Which explanation makes the most sense?

A) By random chance, a second reading frame within the gene also has an open reading frame.

**B) This gene includes introns which are not multiples of three. ✓**

C) This is a mutant allele that has had several small insertions.

D) All of these.

90. Homologous genes:

**A) Would be expected to have very similar sequences in related organisms.**

B) Would be expected to be more similar in distantly related organisms than in organisms that are closely related.

C) May have become similar to each other by random mutation.

D) All of these.

91. Secondary structure of RNA molecules:

**A) Depends on complementary base pairing.**

B) Is generated by covalent bonding between sections of the RNA molecule.

C) Can be described as interactions between portions of the backbone of the molecule.

D) Does not have an impact on function of the molecule.

92. The collection of proteins that can be produced by a given species is:

A) Considered that species' genetic complement.

B) Correlated with the size of the organism.

**C) Called the proteome.**

D) All of these.

93. A cDNA library:

A) Can also be called an expressed sequence tag (EST) library.

B) Consists of coding sequences from genes that are expressed.

C) Is specific to the set of conditions under which the original mRNA was generated.

**D) All of these.**

94. Which of the following statements regarding the proteome is the most correct?

A) A large proportion of the proteome is expressed by each cell of a species.

B) Levels of gene expression at the mRNA level generally correlate highly with levels of functional protein.

**C) The proteins produced by a specific cell depend on cell type and environmental conditions.**

D) All of the above.

95. Which of these conclusions might be drawn from the results of a 2D gel electrophoresis experiment?

A) Levels of mRNA expression for two different genes are lower under one set of conditions than another.

B) In a mutant cell, the lack of protein expression is due to production of unstable mRNA, which is rapidly degraded.

C) A mutation prevents proper posttranslational modification of a protein.

**D) None of these are reasonable conclusions.**

96. If computers were not able to access the entire genomic sequence of an organism, which of the following techniques might allow determination of the gene sequence that encodes a particular protein?

A) PCR amplification of related gene sequences.

**B) Hybridization of a genomic library with a degenerate probe.**

C) Production of synthetic peptides.

D) All of these.

97. Human genome contains about

A. 2 billion base pairs

**B. 3 billion base pairs**

C. 4 billion base pairs

D. 5 billion base pairs

98. The identification of drugs through genomic study

A. Genomics

B. Cheminformatics

**C. Pharmagenomics**

D. Pharmacogenetics

99. Analysing or comparing entire genome of species

A. Bioinformatics

**B. Genomics**

C. Proteomics

D. Pharmacogenomics

100. CpG islands and codon bias are tools used in eukaryotic genomics to \_\_\_\_\_.

a. **identify open reading frames**

b. differentiate between eukaryotic and prokaryotic DNA sequences

c. find regulatory sequences

d. look for DNA-binding domains

K2 questions

## **Unit I**

1. Write short notes on Cyber security
2. What is CIA triad explain briefly.
3. What are Confidentiality, integrity and availability
4. Write briefly about malicious software
5. Write short notes on viruses, Trojans, root kits, worms, botnets.
6. Explain briefly about memory exploits
7. Give an account on buffer overflow, heap overflow and integer overflow.
8. Write a short essay on cryptography authentication
9. Explain windows security and its importance.

## **Unit II**

1. Write briefly network security
2. Write short notes on network intrusion and detection systems.
3. Explain software security with brief examples
4. Write short notes on vulnerability auditing, penetration testing
5. Give an brief account on web security

6. Write short notes on intellectual property rights, copyrights, patents in cyber crime.
7. Explain the following trade secret, hacking and intrusion and privacy in cyber crime

### **Unit III**

1. Explain briefly about biological databases.
2. Write short notes on Primary and secondary databases used in bioinformatics.
3. Give short notes on Gen bank and DDBJ sequences.
4. Write short notes on Biological information portal.
5. Briefly explain NCBI and EMB net.
6. Give an overview of BLAST tools of NCBI.
7. Write short notes on Conserved domains of proteins and its significance.
8. Explain briefly about CpG islands and its significance.

### **Unit IV**

1. Write short notes on gene prediction methods
2. Give an brief accout on Homology, ab initio, and comparative method
3. Briefly explain about pairwise alignments and its significance.
4. What are scoring matrices? Give significance on it.
5. Explain Pair wise and multiple sequence alignment
6. Write short notes on BLOSUM
7. Give an brief account on PAM
8. Write short notes on Molecular phylogeny
9. Explain briefly about Cladistics and phenetic methods of molecular phylogeny
10. Write briefly about CLUSTAL and PHYLIP tools in constructing a phylogenetic tree
11. Write short notes on phylogenetic tree, types and its significance.

### **Unit V**

1. Write briefly about proteomics and its importance
2. Give an account on Levels of protein structure.
3. Write briefly about Protein secondary structure prediction.
4. Write briefly about Molecular visualization tool
5. Explain role of Rasmol and Swiss PDB Viewer in molecular visualization
6. Write briefly about Protein modeling methods.
7. Write short note on Comparative and De novo methods.

8. Give an brief Over view of SWISS PROT and its significance
9. Write briefly about Outline of computer aided drug designing.
10. Give a brief account on Systems biology - concept and applications.

#### **K4 questions**

##### **Unit I**

1. Write an essay on cyber security
2. Give a detailed account on confidentiality, integrity and availability in cyber security
3. Explain properties of malicious software in detail. Add notes on viruses, Trojans, rootkits, worms, botnets
4. Discuss memory exploits add notes on buffer overflow, heap overflow and Integer overflow, Write an essay on cryptography, authentication, password system.
5. Give a detailed account on windows security.

##### **Unit II**

1. Write an essay on network intrusion detection and prevention systems. Add notes on firewalls.
2. Explain software security in detail
3. Give an account on vulnerability auditing, penetration testing, sandboxing and control flow integrity
4. Explain user authentication - legal and ethical issues in web security
5. Write an essay on cyber crime,
6. Give an detailed account on intellectual property rights, copyright, patent, trade secret, hacking and intrusion, privacy, identity threat.

##### **Unit III**

1. What is bioinformatics? Explain the Scope of bioinformatics in detail
2. Write an essay on Biological databases add notes on Primary and secondary databases with examples.
3. Give a detailed account on Genomics
4. Write an essay on Gen Bank and DDBJ.
5. Discuss biological information portal NCBI AND EMB net in detail.
6. Explain the role of BLAST tool in NCBI add notes on pair wise alignments

## **Unit IV**

1. Write an essay Gene prediction methods (Homology, ab initio, and comparative method). What is alignment? Explain Pair wise and multiple sequence alignment and its significance, Write an essay on scoring matrices add notes on PAM and BLOSUM.
2. What is Molecular phylogeny? Explain the Cladistics and phenetic methods in understanding molecular phylogeny
3. Discuss the tools like CLUSTAL and PHYLIP in constructing the phylogenetic tree. Add notes on types of tree.

## **Unit V**

1. Discuss the various Levels of protein structure and its importance.
2. Write an essay on Protein secondary structure prediction. Give an account on tools like SOPMA and JPRED in predicting and visualizing the protein.
3. Write essay on Molecular visualization tools.
4. Write an essay on Rasmol and Swiss PDB Viewer in visualising the proteins.
5. Give an detailed account on Protein modeling methods Comparative and De novo methods.
6. Write an essay on SWISS PROT.
7. Discuss computer aided drug designing in detail
8. What is Systems biology? Add notes on its concept and applications.