

## Bioinformatics MCQ

1-..... is the **field of science** in which biology, computer science, and information technology merge.

- **Bioinformatics**
- Image processing
- Computer vision
- None

2-**Bioinformatics** describes use of computers to **handle biological information**.

- **True**
- False

3-Our body **contain** ..... **Cell**.

- **75 trillion**
- 50 thousands
- 24
- None

4- Bioinformatics is the interference between biology, computer science and mathematics and statistics.

- **True**
- False

5-**Bioinformatics** describes use of computers to **handle biological** information.

- **True**
- False

6-..... collect molecular data: **DNA & Protein sequences, gene expression, etc.**

- **Biologists**
- Computer scientists

- Bioinformaticians
- None

7- ..... is (+Mathematicians, Statisticians, etc.) Develop tools, software, algorithms to store and analyze the data.

- Biologists
- Computer scientists
- Bioinformaticians
- None

8- ..... Study biological questions by analyzing molecular data.

- Biologists
- Computer scientists
- Bioinformaticians
- None

9- We express with human body by .....

- Mathematical model
- Statistical model
- None.

10- Bioinformatics is also called molecular evolution

- True
- False

11- We need bioinformatics because information becomes larger and more complex, more computational tools are needed to sort these data.

- True
- False

**12- Bioinformatics Goals:**

- Development of software tools and efficient algorithms to solve biological problems
- Creation and management of databases
- Use of software tools and biological databases to extract new knowledge.
- **All**

**13- ..... Anything biology can do with experiments.**

- **Theoretical Biology**
- Computational Biology
- None

**14- Refer to biology replacing experiments by computers.**

- Theoretical Biology
- **Computational Biology**
- None

**15- Cell is the smallest structural unit of an organism.**

- **True**
- False

**16-..... all information (DNA) which every cell in body needs to grow and carry out its various functions.**

- **Genes**
- Genome
- None

**17- Genome is Organism's complete set of DNA.**

- **True**
- False

18- Human genome has ..... distinct chromosomes.

- 20
- **24**
- 22
- None

23

19- Each chromosome contains many genes.

- **True**
- False

20- **Proteins are Large, complex** molecules made up of smaller subunits called amino acids.

- **True**
- False

21- Nucleic acid represents biological molecules (RNA and DNA).

- **True**
- False

22- ..... **Hold** information on how cell works.

- **DNA**
- RNA
- Protein
- None

23- ..... **Transfer** information to different parts of cell.

- DNA
- **RNA**
- Protein
- None

24-..... Form body's major components (e.g. hair, skin, etc.).

- DNA
- RNA
- **Protein**
- None

25- ..... has a double structure which is composed of sugar molecule, phosphate group and a base (A, C, G, T)

- **DNA**
- RNA
- Protein
- None

26-..... is a double helix.

- **DNA**
- RNA
- Protein
- None

27 ..... is a single helix.

- DNA
- **RNA**
- Protein
- None

28- Refer to the knowledge of one assures the knowledge of the other.

- **Double helix**
- Single helix
- None

29- DNA is converted to protein by a process of transcription and translation.

- True
- False

30- Information is passed from RNA to protein and from protein to RNA.

- True
- False

31- DNA can replicate

- True
- False

32- ..... The process of making RNA from DNA.

- Transcription
- Translation.
- None

33 -..... the process of converted RNA to protein is .....

- Transcription
- Translation
- None

34- In RNA, the base Uracil (U) is used instead of thymine (T).

- True
- False

35- Each amino acid encoded by 3 DNA bases.

- True
- False

36- ..... is a **sequence of amino acids**

- DNA
- RNA
- **Protein**
- None

37- **Amino acids** are coded by codons – **triplets** of nucleotides

- **True**
- False

38- **protein** contains .....**alphabet**.

- 4
- 3
- 7
- **20**

39- protein contains .....codon

- 4
- 3
- **7**
- 20

40- Codons can **overlap**.

- True
- **False**

41- Refer to **Theoretical** development of algorithms used for bioinformatics

- **Computational Biology**
- Bioinformatics
- None

42-refer to Development and application of computational tools in managing all kinds of biological data.

- Computational Biology
- **Bioinformatics**
- None

43- Bioinformatics considered as *computational molecular biology*

- **True**
- False

44- Understanding functions of a cell by analyzing sequence data because the flow of genetic information is dictated by .....

- **Central dogma of biology**
- Sequence alignment
- Pairwise

45- The difference in the brain size is mainly related their content.

- True
- **False**

46-..... Procedure of comparing two (pairwise) or more (multiple) sequences by searching for a series of individual characters that is in the same order in the sequences.

- **Sequence alignment**
- Central dogma
- Bioinformatics
- None

47- Sequence comparison is the heart of bioinformatics analysis.

- **True**
- False



48- Fundamental process of **comparison** is **sequence alignment**.

- **True**
- False

49- ..... Process by which **sequences are compared** by searching for common character patterns and correspondence among related sequences.

- **Sequence alignment**
- Central dogma
- Bioinformatics
- None

50-..... process of **aligning two sequences** and is the basis of database similarity searching and multiple sequence alignment.

- **Pairwise sequence alignment**
- Multi sequence alignment
- None

51- **Sequence alignment** provides inference for the relatedness of **two** sequences under study

- **True**
- False

52- When **two** sequences are descended from a common evolutionary origin, they are said to have

- Homologous relationship
- Share homology
- Ortholog
- **A and B**

53-..... is conclusion about relationship **drawn** from sequence similarity comparison when the two sequences share a high enough degree of similarity.

- **Sequence homology**
- Similarity
- Ortholog

None

54- It is correct to say that the two sequences share **60% homology**.

- True
- **False**

55- It is correct to say that the two sequences share **60% similarity**.

- **True**
- False

56-..... **displays all possible sequence matches**. However, it is often up to the user to construct a full alignment with insertions and deletions by linking nearby diagonals.

- **Dot matrix method**
- Dynamic programming method
- Word method
- None

57- **Needleman/ Wunsch** techniques is

- **Global sequence alignment**
- Local sequence alignment
- None

58- The first step in Needleman/ Wunsch technique is **trackback**.

- True
- **False**

59- The size of the matrix in Needleman/ Wunsch technique is .....

- **M+1, N+1**
- M, N+1
- M+1, N
- M, N

60- We **filling the first row and Column** in Needleman/ Wunsch technique by helping the value of .....

- **Gap**
- Match
- Mismatch
- None

61-When we use the **substitution method in the sequence modification** we count the number of match and mismatch and gap.

- True
- **False**

62-We filling the first row and Column in **Smith–Waterman** algorithm .....

- **Zeros**
- Ones
- None

63- **Smith–Waterman** algorithm is .....

- Global sequence alignment
- **Local sequence alignment**
- None

64-..... contain original biological data. They are archives of **raw sequence** data.

- **Primary databases**
- Secondary databases
- Specialized databases
- None

65-..... contain processed information, **based on original information** from primary databases.

- Primary databases
- **Secondary databases**
- Specialized databases
- None

66- Which of the following is example of **secondary** databases?

- **SWISS-Prot**
- GenBank
- Protein Data Bank (PDB)
- None

67-which of the following is example of **primary** databases.

- Flybase
- HIV sequence database
- Ribosomal Database Project
- **None**

68- Which of the following is example of **specialized** databases?

- Flybase
- HIV sequence database
- Ribosomal Database Project
- **All**

69- FASTA algorithm is.....

- Local alignment
- Global alignment
- None

70- BLAST is .....

- Local alignment
- Global alignment
- None

71- FASTA algorithm derives from the logic of DOT PLOT.

- True
- False

72- FASTA determinates the best segment of similarity between the query sequence and the search set sequence.

- True
- False

73- Is the alignment of N sequences (amino acids/nucleotides), where  $N > 2$

- Multiple Sequence Alignment
- Pairwise Sequence Alignment
- None

74- Star Algorithm is .....

- Multiple Sequence Alignment
- Pairwise Sequence Alignment

75- Sum of pair is .....

- Multiple Sequence Alignment
- Pairwise Sequence Alignment

76- **Star** Algorithm Proposed by **Gusfield**.

- **True**
- False

77- An approximation algorithm for the sum of pairs multiple sequence alignment problems.

- Needleman/ Wunsch Algorithm
- Smith-waterman Algorithm
- **Star Algorithm**
- None

78- Given a set  $S$  of  $k$  sequences, the center of this set of sequences is the sequence which **maximize**  $\min$

- True
- **False**

79- **MST** Preservation preserves.....

- **K-1**
- K
- K-2
- None

80- **NCBI** stands for **National Center for Biotechnology Information**.

- **True**
- False

البطل الحقيقي وصل ..  
يريت دعوة حلوة ملبسش 3 سنين ظابط عاوز اتجوز