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1. Which of the following is an example of Homology and similarity tool?

(a) BLAST

(b) RasMol

(c) EMBOSS

(d) PROSPECT

Sol:(a) BLAST.

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

(a) 1988

(b) 1985

(c) 1986

(d) 1987

Sol: (d) 1987.

3.Which of the following scientists created the first Bioinformatics database?

(a) Dayhoff

(b) Pearson

(c) Richard Durbin

(d) Michael.J.Dunn

Sol:(a) Dayhoff.

4. The human genome contains approximately_____.

(a) 6 billion base pairs

(b) 5 billion base pairs

(c) 3 billion base pairs

(d) 4 billion base pairs

Sol: (c) 3 billion base pairs.

5. Which of the following tools is used for the identification of motifs?

(a) BLAST

(b) COPIA

(c) PROSPECT

(d) Pattern hunter

Sol: (b) COPIA.

6. The first molecular biology server expasy was in the year _____.

(a) 1992

(b) 1993

(c) 1994

(d) 1995

Sol: (b) 1993.

7. What is the deposition of cDNA into the inert structure called?

(a) DNA probes

(b) DNA polymerase

(c) DNA microarrays

(d) DNA fingerprinting

Sol: (c) DNA microarrays.

8. The identification of drugs through the genomic study is called_____.

(a) Genomics

(b) Pharmacogenomics

(c) Pharmacogenetics

(d) Cheminformatics

Sol: (b) Pharmacogenomics.

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

(a) Fit drug

(b) Lead

(c) Fit compound

(d) All of the above

Sol:(b) Lead.

10. Proteomics refers to the study of _____.

(a) Set of proteins in a specific region of the cell

(b) Biomolecules

(c) Set of proteins

(d) The entire set of expressed proteins in the cell

Sol: (d) The entire set of expressed proteins in the cell.

11. The process of finding the relative location of genes on a chromosome is called _____.

(a) Gene tracking

(b) Genome walking

(c) Genome mapping

(d) Chromosome walking

Sol:(c) Genome mapping.

12. The computational methodology that tries to find the best matching between two molecules, a receptor and ligand are called _____.

(a) Molecular fitting

(b) Molecular matching

(c) Molecular docking

(d) Molecule affinity checking

Sol: (c) Molecular docking.

13. 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

Sol: (d) None of the above.

14. The term "invitro" is the Latin word which refers to_____.

(a) Within the lab

(b) Within the glass

(c) Outside the lab

(d) Outside the glass

Sol: (b) Within the glass.

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

(a) Flowchart

(b) Algorithm

(c) Procedure

(d) Sequential design

Sol:(b) Algorithm.

16. The term Bioinformatics was coined by _____.

(a) J.D Watson

(b) Pauline Hogeweg

(c) Margaret Dayhoff

(d) Frederic Sanger

Sol: (b) Pauline Hogeweg.

17. 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

Sol: (c) In silico.

18. Which of the following is the first completed and published gene sequence?

(a) ΦX174

(b) T4 phage

(c) M13 phage

(d) Lambda phage

Sol: (a) ΦX174.

19. The laboratory work using computers and computer-generated models generally offline is referred to as _____.

(a) Insilico

(b) Wet lab

(c) Dry lab

(d) All of the above

Sol: (c) Dry lab.

20. The computer simulation refers to _____.

(a) Dry lab

(b) Invitro

(c) In silico

(d) Wet lab

Sol:(c) In silico.

21. What are bioinformatics databases?
a) Repositories of biological samples
b) Online platforms for sharing research papers
c) Resources that store biological data and provide tools for analysis
d) Platforms for conducting laboratory experiments
Answer: c) Resources that store biological data and provide tools for analysis

22. Which type of bioinformatics database stores DNA and RNA sequences?
a) Protein databases
b) Gene expression databases
c) Sequence databases
d) Structural databases
Answer: c) Sequence databases

23. Which of the following databases is widely used for storing and retrieving DNA and protein sequence information?
a) GenBank
b) PubMed
c) UniProt
d) PDB
Answer: a) GenBank

24. Which bioinformatics database focuses on protein structure information?
a) GenBank
b) PubMed
c) UniProt
d) PDB
Answer: d) PDB (Protein Data Bank)

25. When did Smith–Waterman first describe the algorithm for local alignment?
a) 1950
b) 1970
c) 1981
d) 1925
Answer: c

26. Which of the following does not describe local alignment?
a) A local alignment aligns a substring of the query sequence to a substring of the target sequence
b) A local alignment is defined by maximizing the alignment score, so that deleting a column from either end would reduce the score, and adding further columns at either end would also reduce the score
c) Local alignments have terminal gaps
d) The substrings to be examined may be all of one or both sequences; if all of both are included then the local alignment is also global

Answer: c

27. Which of the following does not describe local alignment algorithm?
a) Score can be negative
b) Negative score is set to 0
c) First row and first column are set to 0 in initialization step
d) In traceback step, beginning is with the highest score, it ends when 0 is encountered
Answer: a

28. Local alignments are more used when _____
a) There are totally similar and equal length sequences
b) Dissimilar sequences are suspected to contain regions of similarity
c) Similar sequence motif with larger sequence context
d) Partially similar, different length and conserved region containing sequences
Answer: a.

29. Which of the following does not describe BLOSUM matrices?
a) It stands for BLOcksSUbstitution Matrix
b) It was developed by Henikoff and Henikoff
c) The year it was developed was 1992
d) These matrices are logarithmic identity values
Answer: d

30. Among the following which one is not the approach to the local alignment?
a) Smith-Waterman algorithm
b) K-tuple method
c) Words method
d) Needleman-Wunsch algorithm
Answer: d

31. Which of the following does not describe k-tuple methods?
a) k-tuple methods are best known for their implementation in the database search tools FASTA and the BLAST family
b) They are also known as words methods
c) They are basically heuristic methods to find local alignment
d) They are useful in small scale databases
Answer: d

32. Which of the following does not describe BLAST?
a) It stands for Basic Local Alignment Search Tool
b) It uses word matching like FASTA
c) It is one of the tools of the NCBI
d) Even if no words are similar, there is an alignment to be considered
Answer: d

33. Which of the following is untrue regarding BLAST and FASTA?
a) FASTA is faster than BLAST
b) FASTA is the most accurate
c) BLAST has limited choices of databases
d) FASTA is more sensitive for DNA-DNA comparisons

Answer: a

34. Which of the following is not a software for dot plot analysis?
a) SIMMI
b) DOTLET
c) DOTMATCHER
d) LALIGN

Answer: a.

35. The softwares for dot plot analysis perform several tasks. Which one of them is not performed by them?
a) Gap open penalty
b) Gap extend penalty
c) Expectation threshold
d) Change or mutate residues
Answer: d

36. For palindromic sequences, what is the structure of the dot plot?
a) 2 intersecting diagonal lines at the midpoint
b) One diagonal
c) Two parallel diagonals
d) No diagonal
Answer: a

37. For significantly aligning sequences what is the resulting structure on the plot?
a) Intercrossing lines
b) Crosses everywhere
c) Vertical lines
d) A diagonal and lines parallel to diagonal
Answer: d

38. When was this method, first described?
a) 1959
b) 1966
c) 1970
d) 1982
Answer: c

39. Who were the inventors of this method?
a) Smith-Waterman
b) Margaret Preston
c) Gibbs and McIntyre
d) Needleman-Wunsch
Answer: c

40. Which of the following is true for EMBOSS Dottup?
a) Allows you to specify threshold
b) Doesn't allow you to specify threshold
c) Doesn't allow you to specify window size
d) If all cells in the window are identity, it colors in some specific cells in the window

Answer: b

41. This phenomena can be induced in those responsible for the horizontal elements of this phylogeny

(a) mitosis

(b) point mutations

(c) S phase of the cell cycle

(d) endosymbiosis

Answer: (d)

42. If cladistics were used to build a phylogenetic tree of cats, this would be the most appropriate outgroup

(a) tiger

(b) leopard

(c) wolf

(d) domestic cat

Answer: (c)

43. To construct a phylogenetic tree in order to apply parsimony, choose

(a) tree with fewest branch points

(b) tree representing fewest evolutionary changes either in morphology or DNA sequences

(c) tree in which branch points are based on as many shared characters possible

(d) tree assuming all evolutionary changes with equal probability

Answer: (b)

44. This is used to know the phylogeny

(a) mRNA

(b) rRNA

(c) DNA

(d) none of these

Answer: (b)

45. On the basis of cladistics, this eukaryotic kingdom is polyphyletic and hence unacceptable

(a) Monera

(b) Protista

(c) Animalia

(d) Fungi

Answer: (b)

46. Possessing four appendages when comparing mammals with birds is

(a) a character used to sort bird species

(b) example of analogy rather than homology

(c) a shared derived character

(d) a shared ancestral character

Answer: (d)

47. Pick the incorrect statement concerning the terminologies of phylogenetics

(a) branches are the lines in the tree

(b) tips of the branches have long lost sequences or species

(c) node indicate inferred ancestor of extant taxa

(d) connecting point joining two adjacent branches is a node

Answer: (b)

48. This is not a vestigial organ in man

(a) coccyx

(b) nails

(c) third molar

(d) homologous

Answer: (b)

49. Pick the incorrect option for the blank

Recent uses of phylogenetic analysis is to analyse _____ in addition to tracing the evolutionary history of specific genes

(a) physical separation methods

(b) proteomes

(c) genomes

(d) gene families

Answer: (a)

50. This is incorrect about the merits of molecular data for Phylogenetics study

(a) sampling bias is involved

(b) with the help of molecular data more robust and clear-cut phylogenetic tree can be constructed

(c) much easier to obtain in comparison to fossil records

(d) more in number compared to fossil records

Answer: (a)

Short answers

1. What is bio informatics?

2. What are biological data bases?

3. What is NCBI?

4. What are secondary data bases?

5. What is sequence alignment?