1.When you are comparing two sequences of the same or different organisms, what is the type of the alignment?

A .Global, B. Local C. Pairwise sequences D. Multiple sequences

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

A .Global, B. Local C. Pairwise sequences D. Multiple sequences

3.Which alignment is useful to detect the highly similar sequences?

A .Global, B. Local C. Pairwise sequences D. Multiple sequences

4. Which alignment is useful to detect the highly conserved regions?

A .Global, B. Local C. Pairwise sequences D. Multiple sequences

5. The optimal alignment of two similar sequences is usually that …….number of matches and …. The number of gaps.

A. minimize, maximize B. maximize, minimize C. degrade, upgrade D. upgrade, degrade

6. Multiple sequence alignment method is called as …… alignment method

A. global B. local C. progressive d. non-progressive

7. Cells are different because of differential gene expression.

A) true B)False

8. Gene is expressed by transcribing DNA exons into single-stranded mRNA

A) true B)False

9. In FASTA, For a Z-score > 15, the match can be considered extremely_____ with _____of a homologous relationship. a) insignificant, uncertainty b) significant, uncertainty c) significant, certainty d) insignificant, certainty

11. Which of the following is not a benefit or a factual of FASTA over BLAST?

a) FASTA scans smaller window sizes

b) It gives more sensitive results

c) It gives less sensitive results

d) It gives results with a better coverage rate for homologs.

12. The use of low-complexity masking in the BLAST procedure means that it may have higher specificity than FASTA because potential false positives are reduced.

a) True b) False Answer:

14. BLAST might not find matches for very short sequences. a) True b) False Answer:

15. BLAST often produces several short HSPs rather than a single aligned region. a) True b) False

16. FASTA is derived from logic of the dot plot.

a) True

b) False

17. The gapped portion in the diagonals represents matches in FASTA.

a) True

b) False

18. The initiation of FASTA format has ____ symbol.

a) >

b) <

c) /

d) *

19. Which of the following is incorrect about a microarray?

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

the species under study

b) Array of immobilized DNA oligomers cannot be cDNAs

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

d) It is the most commonly used global gene expression profiling method

20. In the analysis of microarray data–If replicated datasets are available, rigorous statistical tests such as t-test

and analysis of variance (ANOVA) can be performed to test the null hypothesis that a given data point is not

significantly different from the mean of the data distribution.

a) True

b) False

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

a) For microarray data, clustering analysis identifies coexpressed and coregulated genes

b) For microarray data, clustering analysis identifies coexpressed but not coregulated genes

c) For microarray data, clustering analysis identifies and coregulated but not coexpressed genes

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

22. A supervised analysis refers to classification of data into a set of predefined categories. For example,

depending on the purpose of the experiment, the data can be classified into predefined 'diseased' or 'normal'

categories.

a) True

b) False

23. When did Needleman-Wunsch first describe the algorithm for global alignment?

a) 1899

b) 1970

c) 1930

d) 1950

26. The rigorous dynamic programming method is normally not used for database searching, because it is slow and computationally expensive.

a) True

b) False

27. FASTA and BLAST are _____ but _____ for larger datasets.

a) faster, more sensitive

b) faster, less sensitive

c) slower, less sensitive

d) slower, more sensitive

28. In Smith–Waterman algorithm, in initialization Step, the _____ row and _____ column are subject to gap penalty.

a) first, first

b) first, second

c) second, First

d) first, last

30. One of the challenges in SWA is obtaining correct alignments in regions of low similarity between distantly related biological sequences.

a) True

b) False

31. Score can be negative in Smith–Waterman algorithm.

a) True

b) False

33. in dot matrix Isolated dots that are not on the diagonal represent exact matches.

a) True

b) False

34. Alignment algorithms, both global and local, are fundamentally similar and only differ in the optimization strategy used in aligning similar residues.

a) True

b) False

35.Every person inherits one set of --------from the mother and one set ------- from the father.

A) 23 genes

B) 100 DNA

C)1000 DNA

D) 23 chromosomes

36.Each human cell contains approximately -------base pairs of DNA

A)300 million

B)300 thousands

C) 3 billion

D)23 pairs

37.Sequence alignment helps scientists--------

a) Trace out evolutionary relationships

b) infer the functions of newly genes

c) predict new members of gene families

d)all of these

38.An example of Homology & similarity tool-------.

a) PROSPECT

b) EMBOSS

c) RASMOL

d) BLAST

39.The final result of Central Dogma is -------

A)transcription

B) mRNA

C) Protine

D)Gene

40.Proteins are the end result of translation of mRNA by ----------.

A)Nucleus

B) ribosomes

C)RNA

D)Cell sap

41.A gene is defined to be a sequence of ----------that code for a specific function.

A)DNA B)RNA C) Protein D)All

42. ---------- Carries instructions for a protein outside of the nucleus to the ribosome

A) cDNA B) tRNA C) mDNA D) mRNA

43. Cells are different because of differential gene expression. A) True B) False

44. Gene is expressed by transcribing DNA introns into single-stranded mRNA.

A) True B) False

45. RNA is translated into a protein. A) True B) False

46. Microarrays measure the level of RNA expression by analyzing cDNA binding.

A) True B) False

47. Genes open reading frames start with ATG and end with TAA. A) True B) False

48. Protein is a linear sequence of 4 amino acids. A) True B) False

49. Needleman-Wunsch algorithm use local dynamic programming. A) True B) False

50. Process of making an amino acid sequence from mRNA. A) Translation B) Transcription

51. Proteins are the end result of translation of mRNA by ----

A)Nucleus B) ribosomes C)RNA D)Cell sap

52. A gene is defined to be a sequence of ----- ------that code for a specific function.

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A )Global, B) Local

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58. Which alignment is useful to detect the highly conserved regions?

A)Global, B) Local

C)Pairwise sequences D) Multiple sequences

59. The optimal alignment of two similar sequences is usually that …….number of matches and …. The number of gaps.

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C) degrade, upgrade D) upgrade, degrade

60. Multiple sequence alignment method is called as …… alignment method.

A) global B) local C) progressive D) non-progressive

61. Sequence alignment helps scientists--------

A) Trace out evolutionary relationships B) infer the functions of newly genes

C) Predict new members of gene families D) all of these

62. An example of Homology & similarity tool-------.

A) PROSPECT B) EMBOSS C) RASMOL D) BLAST

63. There are twenty-three chapters called ……..

A) genes B) chromosomes C) introns D) exons

64. Each chapter contains several thousand stories called ……..

A) genes B) chromosomes C) introns D) exons

65. Each story is made up of paragraphs called ……..,

A) genes B) chromosomes C) introns D) exons

66. which are interrupted by advertisements called ……

A) genes B) chromosomes C) introns D) codons

67. Each paragraph is made up of words called ……..

A) bases B) chromosomes C) introns D) codons

68. Each word is written in letters called ……

A) genes B) bases C) introns D) codons

69. BLAST Uses “look-up” tables to shorten search time. A) True B) False

70. If you want to BLAST the non-redundant database using a new protein sequence as query, which is the BEST search program to use? A) blastp, B) blastn, C) tblastx, D) blastx .

71. Usually BLAST E- values smaller than a certain threshold are considered to demonstrate homology. This threshold is usually about .A) about 104

, B) about 10-4

, C) about 10-40

73. Who coined the term Bioinformatics and when?

A. Paulien Hogeweg, 1979.

B. Dr Margaret Oakley Dayhoff, 1976.

C. Robert Ledley, 1978.

D. David W Mount, 1977.

74. Which one of the following is not a primary nucleic acid database?

A. GenBank.

B. DDBJ.

C. EMBL.

D. TREMBL.

76. _____ is a secondary database. .

A. DDBJ.

B. PROSITE.

C. NRDB.

D. OWL.

77. _____is a composite database.

A. PROSITE.

B. DDBJ.

C. NRDB.

D. EMBL.

78. _____ is a primary protein structure database.

A. PDB.

B. PubChem.

C. ChemBank.

D. SCOP.

79. Which one of the following is a secondary protein structure database?

A. PubChem.

B. PDB.

C. ChemBank.

D. SCOP.

80. FASTA format starts with _____ symbol.

A. /.

B. *.

C. >.

D. #.

82. _____ is a bibliographic database.

A. PubMed.

B. Entrez.

C. PIR.

D. EBI.

84. _____ is a biomedical literature database which is used to retrieve full text content.

A. Entrez

B. Pubmed

C. PubMed central

D. Medscape

85. Entrez, a life science search engine used to search across databases is maintained by _____.

A. SWISS-PROT.

B. EMBL.

C. DDBJ.

D. NCBI.

86. Which Boolean operator find documents that contain terms on both sides of the operator?

A. AND.

B. OR.

C. NOT.

D. ALL THREE

87. Which Boolean operator find documents those contain either any one term?

A. NOT

B. OR

C. AND.

D. AND, NOT.

88. Which Boolean operator finds documents that contain the term on the left but not the term on the right of the operator?

A. OR.

B. AND.

C. NOT.

D. AND, NOT.

89. _____ is a similarity search tool.

A. BLAST.

B. CLUSTALW.

C. CLUSTALX.

D. RASMOL.

91. _____ compares protein sequence against protein databases.

A. blastp.

B. blastn.

C. blastx.

D. tblastx.

92. The _____ tool compares nucleotide sequence against DNA databases.

A. blastn.

B. blastp.

C. tblastx.

D. tblastn.

93. The _____ tool compares translated nucleotide query sequence against protein databases.

A. blastp.

B. tblastn.

C. blastx

D. tblastx.

94. The _____ tool compares protein sequence against translated nucleotide databases.

A. blastp.

B. tblastx.

C. blastn.

D. tblastn.

97. PIR was established by _____.

A. NBRF.

B. NCBI.

C. SIB.

D. DDBJ.

98. Swiss-Prot is maintained by _____.

A. NCBI.

B. NBRF.

C. SIB.

D. DDBJ.

99. ExPASy stands for _____.

A. Expert Protein Analysis Server.

B. Exponential Protein Analysis Server.

C. Expert Protein Analysis System.

D. Exponential Protein Analysis System.

100. EST stands for _____.

A. Expressed Sequence Tag.

B. Expressed Site Tag.

C. Expressed Structure Tag.

D. Expressed Symbol Tag.

101. SNP stands for _____.

A. Small Nucleic Polymorphism.

B. Single Nucleic Polymorphism.

C. Single Nucleotide Polymorphism

D. Small Nucleotide Polymorphism.

102. What is PROSITE?

A. A database of protein structures.

B. A database of protein sequences.

C. A database of protein motifs.

D. option a and b.

103. The family that consists of related genes within an organism is called_____.

A. orthologs.

B. zoologs.

C. paralogs.

D. xenologs.

104. The family that consists of related genes in another organism is called_____.

A. orthologs.

B. zoologs.

C. paralogs.

D. xenologs.

105. When you are comparing two sequences of same or different organisms, what is the type of the alignment?

A. Global.

B. Local.

C. Pairwise sequence.

D. Multiple sequence.

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

A. Global.

B. Pairwise sequence.

C. Local.

D. Multiple sequence.

107. Which alignment is useful to detect the highly similar sequences?

A. Pairwise sequence.

B. Local.

C. Global.

D. Multiple sequence.

108. Which alignment is useful to detect the highly conserved regions?

A. Local.

B. Global.

C. Pairwise sequence.

D. Multiple sequence.

109. The optimal alignment of two similar sequences is usually that _____ number of matches and _____ the number of gaps.

A. minimize, maximize.

B. maximize, minimize.

C. degrade, upgrade.

D. upgrade, degrade.

110. Multiple sequence alignment method is called as _____alignment method.

A. global.

B. local.

C. progressive.

D. non-progressive.

111. Dot-matrix representations denote the sequences _____.

A. as the coordinates of a two-dimensional graph.

B. are represented in the form of trees.

C. as the coordinates of a 3D graph.

D. not represented as graph.

.112Which algorithm is used by local alignment?

A. Needleman and Wunsch.

B. PAM.

C. Smith-Waterman.

D. All the above.

113. Which algorithm is used by global alignment?

A. Needleman and Wunsch.

B. Smith-Waterman.

C. BLAST.

D. PAM .

114-Which method of multiple sequence alignment uses genetic recombination?

A. Progressive.

B. Dynamic Programming.

C. Genetic Algorithm.

D. Hidden Markov Model.

115.Coordinates for known protein structures are housed in?

A. CATH.

B. SCOP.

C. PDBsum.

D. PDB.

117. Which server is used to deposit the protein structures in PDB?

A. ClustalW.

B. ClustalX.

C. ExPASy.

D. ADIT.

118. Which one of the following method predicts the protein structure based on fold recognition?

A. Comparative modeling.

B. Threading.

C. Abinitio.

D. Homology modeling.

119. The study of evolutionary relationships is _____.

A. Phylogenics.

B. Molecular Evolution.

C. Cladogenesis.

D. Cladistics.

120. Which one of the following tools can be used for both modeling the protein and structure visualization?

A. Swiss-PDB Viewer.

B. QMol.

C. RasMol.

D. ChemSketch.

123. The first step in the drug discovery process is _____. Answer: A.

A. target identification.

B. target isolation and purification.

C. target structure determination.

D. analyzing the targets structure for potential ligand binding site

124. Mechanism of action of DNA is _____.

A. agonist and antagonist.

B. reversible and irreversible.

C. blockers and openers.

D. alkylating agents.

125. is the process by which a drug enters the bloodstream without being chemically altered.

A. Absorption.

B. Distribution.

C. Excretion.

D. Metabolism.

127. _____ is the process that excretes the drug through the kidney.

A. Absorption.

B. Distribution.

C. Excretion.

D. Metabolism.

128. _____ is the fifth step in the drug discovery process.

A. Lead Optimization.

B. Preclinical trials.

C. Clinical trials.

D. Drug approval.

129. _____ is the sixth step in the drug discovery process.

A. Lead Optimization.

B. Preclinical trials.

C. Clinical trials.

D. Drug approval.

130. _____ is the seventh step in the drug discovery process.

A. Lead Optimization.

B. Preclinical trials.

C. Clinical trials.

D. Drug approval.

132. Fitting a ligand from a 3D structure database into the binding site of a target protein is called _____.

A. modeling.

B. docking.

C. threading.

D. comparative modeling.

134.Gene is expressed by ----------DNA exons into single-stranded mRNA

A. transcribing B. Translated C. Replicated D. All

135.Microarrays measure the level of mRNA expression by analyzing -------binding

A.cDNA B.DNA C.RNA D.mRNA

136.Which of the following is not a benefit or a factual of FASTA over BLAST?

a) FASTA scans smaller window sizes

b) It gives more sensitive results

c) It gives less sensitive results

d) It gives results with a better coverage rate for homologs

137.In the GCG and FASTA program suites, the scoring matrix itself is formatted in a way that includes default _____

a) gap additions

b) alignment scores

c) score penalties

d) gap penalties

138. The positional difference for each word between the two sequences is obtained by _____the position of the ____ sequence from that of the ____ sequence and is expressed as the offset.

a) subtracting, second, first

b) adding, second, first

c) adding, first, second

d) subtracting, first, second

139. The number of possible global alignments between two sequences of length N is _____

140. Which of the following is not one of the requirements for implementing algorithms for sequence databasesearching?

a) Size of the dataset

b) Sensitivity

c) Specificity

d) Speed

141. Which of the following is incorrect?

a) Smith–Waterman algorithm is the fastest

b) Smith–Waterman algorithm is comparatively slower method

c) To speedup up comparison, heuristic methods are used

d) Heuristic algorithms perform faster searches

142.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

143. Who were the inventors of this method?

a) Smith-Waterman

b) Margaret Preston

c) Gibbs and McIntyre

d) Needleman-Wunsch

144. Which of the following is not a software for dot plot analysis?

a) SIMMI

b) DOTLET

c) DOTMATCHER

d) LALIGN

145-An ORF is a sequence of DNA that starts with a start codon, usually “ATG", and ends with any of the three termination codons

: a)TAA b) TAG c) TGA d) one of them

146.In FASTA, neighboring high-scoring segments along the same diagonal are selected and joined to form a single alignment. A) True B) False