

DAYANAND SCIENCE COLLEGE, LATUR.
Department of Biotechnology
M.Sc. Biotechnology (Revised) Second-Year

SEM-IV SUB- Computational Biology & Biostatistics- (BT –XV)
Teacher- Mr. Gangavane S.C. MCQ-100 MARKS

1. Who coined the term Bioinformatics and when?
A. PaulienHogeweg, 1979.
B. Dr Margaret Oakley Dayhoff, 1976.
C. Robert Ledley, 1978.
D. David W Mount, 1977. ANSWER: A

2. Which one of the following is not a primary nucleic acid database? A.
GenBank.
B. DDBJ.
C. EMBL.
D. TREMBL. ANSWER: D

3. Which one of the following is a primary protein database?
A. SWISS-PROT.
B. EMBL.
C. DDBJ.
D. NCBI.
ANSWER: A

4. _____ is a secondary database.
A. DDBJ.
B. PROSITE.
C. NRDB.
D. OWL.
ANSWER: B

5. _____ is a composite database.
A. PROSITE.
B. DDBJ.
C. NRDB.
D. EMBL.
ANSWER: C

6. _____ is a primary protein structure database.
A. PDB.
B. PubChem.
C. ChemBank.
D. SCOP.
ANSWER: A

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

- A. PubChem.
- B. PDB.
- C. ChemBank.
- D. SCOP.

ANSWER: D

8. FASTA format starts with _____ symbol.

- A. /.
- B. *.
- C. >.
- D. #.

ANSWER: C

9. Which one of the following is a complementary DNA database?

- A. Swiss-Prot.
- B. GenBank.
- C. UniSTS.
- D. NRDB.

ANSWER: C

10. HTGS is a division maintained by _____.

- A. NCBI.
- B. PDB.
- C. SCOP.
- D. OWL.

ANSWER: A

11. _____ is a bibliographic database.

- A. PubMed.
- B. Entrez.
- C. PIR.
- D. EBI.

ANSWER: A

12. Which one of the following is a life science search engine?

- A. PubMed.
- B. Entrez.
- C. Mozilla.
- D. EBI.

ANSWER: B

13. PubMed is one of the popular resources of _____.

- A. NCBI.
- B. EMBL.
- C. DDBJ.
- D. SWISS-PROT. ANSWER: A

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

- A. Entrez
- B. Entrez.
- C. PubMed central.

D. Medscape.

ANSWER: C

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

_____.

A. SWISS-PROT.

B. EMBL.

C. DDBJ.

D. NCBI.

ANSWER: D

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

A. AND.

B. OR.

C. NOT.

D. AND, NOT. ANSWER: A

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

A. NOT.

B. OR.

C. AND.

D. AND, NOT. ANSWER: B

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

A. OR.

B. AND.

C. NOT.

D. AND, NOT. ANSWER: C

19. _____ is a similarity search tool.

A. BLAST.

B. CLUSTALW.

C. CLUSTALX.

D. RASMOL. ANSWER: A

20. How many programs are there in BLAST?

A. Four.

B. Five.

C. Six.

D. Seven.

ANSWER: B

21. What is the input sequence format in BLAST?

A. GenBank.

B. EMBL.

C. FASTA.

D. PIR.

ANSWER: C

22. _____ compares protein sequence against protein databases.

A. blastp.

- B. blastn.
- C. blastx.
- D. tblastx.

ANSWER: A

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

- A. blastn.
- B. blastp.
- C. tblastx.
- D. tblastn.

ANSWER: A

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

- A. blastp.
- B. tblastn.
- C. blastx
- D. tblastx.

ANSWER: C

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

- A. blastp.
- B. tblastx.
- C. blastn.
- D. tblastn.

ANSWER: D

26. The _____ tool compares translated nucleotide query sequence against translated nucleotidedatabases.

- A. blastp.
- B. blastn.
- C. tblastx.
- D. tblastn.

ANSWER: C

27. The _____ the E-value, the more significant the hit.

- A. lower.
- B. higher.
- C. average.
- D. superior.

ANSWER: A

28. PIR was established by _____.

- A. NBRF.
- B. NCBI.
- C. SIB.
- D. DDBJ.

ANSWER: A

29. Swiss-Prot is maintained by _____.

- A. NCBI.
- B. NBRF.

- C. SIB.
- D. DDBJ.

ANSWER: C

30. ExPASy stands for _____.
- A. Expert Protein Analysis Server.
 - B. Exponential Protein Analysis Server.
 - C. Expert Protein Analysis System.
 - D. Exponential Protein Analysis System.

ANSWER: C

31. _____ is a web resource maintained by NCBI which facilitates the retrieval of gene based information.
- A. LocusLink.
 - B. PDB.
 - C. MSD.
 - D. PRF.

ANSWER: A

32. Which one of the following databases gives immunoglobulin information?
- A. HTGS.
 - B. PIR.
 - C. IMGT.
 - D. PDB.

ANSWER: C

33. EST stands for _____.
- A. Expressed Sequence Tag.
 - B. Expressed Site Tag.
 - C. Expressed Structure Tag.
 - D. Expressed Symbol Tag.

ANSWER: A

34. SNP stands for _____.
- A. Small Nucleic Polymorphism.
 - B. Single Nucleic Polymorphism.
 - C. Single Nucleotide Polymorphism.
 - D. Small Nucleotide Polymorphism.

ANSWER: C

35. When performing a database search, what is the definition of an E-value?
- A. The chance that a random sequence could achieve a better score than the query.
 - B. The chance that a homologous sequence could achieve a similar score to the query.
 - C. The chance that a random sequence could achieve a worse score than the query.
 - D. The chance that a homologous sequence could achieve a better score than the query.

ANSWER: B

36. 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.

ANSWER: C

37. What is a fingerprint?
- A. A protein family discriminator built from a set of regular expressions.
 - B. A protein family discriminator built from a set of conserved motifs.
 - C. A cluster of protein sequences gathered from a BLAST search.
 - D. A cluster of protein sequences gathered from a FASTA search.

ANSWER: B

38. Which area is considered to be the well-conserved regions in multiple sequence alignments?
- A. Reflect areas of structural importance.
 - B. Reflect areas of functional importance.
 - C. Reflect areas of both functional and structural importance.
 - D. Reflect areas likely to be of functional and/or structural importance.

ANSWER: B

39. Results from multiple motif database searches are biologically more meaningful than single motif searches, why?
- A. Multiple motif databases store more motifs, and thus there is a greater chance of a hit.
 - B. The alignments and the selection of motifs in single motif databases is performed using automatic rather than manual methods, adding more errors.
 - C. Multiple motif databases are annotated.
 - D. A single motif may be present in several, otherwise unrelated, families and it is only when put in context with other motifs that families of related proteins are apparent.

ANSWER: D

40. Are profiles and hidden Markov models more potent discriminators than regular expressions?
- A. No, because they are used for domain databases and, having a different area of application, they can't be compared.
 - B. Yes, as they contain probability data for each position in the motif, this can be used to calculate match statistics such as E-values.
 - C. No, because even though they are more sensitive, they are less selective.
 - D. Yes, because they are fine tuned to individual protein domains.

ANSWER: B

41. Which tool can be used for the identification of motifs?
- A. COPIA.
 - B. Patternhunter.
 - C. PROSPECT.
 - D. BLAST.

ANSWER: A

42. In PROSITE, the term PATTERN indicates that the entry describes a _____.
- A. block.
 - B. profile.
 - C. regular expression.
 - D. fuzzy regular expression.

ANSWER: C

43. When searching the BLOCKS and PRINTS databases, a match is judged significant, when?
- A. Single motif is matched.

- B. Two motifs are matched.
- C. The E-value is above e^{-4} .
- D. A combined E-value above a given threshold is reported for a multiple-motif match.

ANSWER: D

44. InterPro is an _____ database.
- A. integrated protein family.
 - B. integrated protein sequence.
 - C. integrated protein structure.
 - D. integrated protein interaction.

ANSWER: A

45. Which alignment contains more than two sequences?
- A. Multiple sequence.
 - B. Pairwise sequence.
 - C. Global.
 - D. Local.

ANSWER: A

46. The most commonly used algorithms that produce multiple alignments are derived from the progressive alignment method of _____ and _____.
- A. Krogh and Eddy.
 - B. Baldi and Birney.
 - C. Da-Fei Feng and Russell Doolittle.
 - D. Schultz and Ponting.

ANSWER: C

47. The family that consists of related genes within an organism is called _____.
- A. orthologs.
 - B. zoologs.
 - C. paralogs.
 - D. xenologs.

ANSWER: C

48. The family that consists of related genes in another organism is called _____.
- A. orthologs.
 - B. paralogs.
 - C. xenologs.
 - D. zoologs.

ANSWER: A

49. _____ characterizes a protein family are defined by the existence of a multiple sequence alignment of a group of homologous sequences.
- A. Domains.
 - B. DNA.
 - C. Proteins.
 - D. RNA.

ANSWER: A

50. Clustal W program accepts the input sequences only in the _____ format.
- A. genbank.
 - B. embl.

- C. pdb.
- D. fasta.

ANSWER: D

51. 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.

ANSWER: C

52. When you are comparing two or more than two sequences of same or different organisms, what is the type of the alignment?
- A. Global.
 - B. Pairwise sequence.
 - C. Local.
 - D. Multiple sequence.

ANSWER: D

53. Which alignment is useful to detect the highly similar sequences?
- A. Pairwise sequence.
 - B. Local.
 - C. Global.
 - D. Multiple sequence.

ANSWER: C

54. Which alignment is useful to detect the highly conserved regions?
- A. Local.
 - B. Global.
 - C. Pairwise sequence.
 - D. Multiple sequence.

ANSWER: A

55. 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.

ANSWER: B

56. Multiple sequence alignment method is called as _____ alignment method.
- A. global.
 - B. local.
 - C. progressive.
 - D. non-progressive.

ANSWER: C

57. Which branching diagram is assumed to be an estimate of a phylogeny when branching lengths are proportional to the amount of inferred evolutionary change?
- A. Phylogram.

- B. Cladogram.
- C. A guide tree.
- D. Cardiogram.

ANSWER: A

58. Profile Hidden Markov Models (HMMs) are important because they provide a powerful way to search databases for _____ related homologs.
- A. closely.
 - B. distantly.
 - C. new.
 - D. extra.

ANSWER: B

59. Pfam-A and Pfam-B is automatically generated from the _____ database.
- A. SMART.
 - B. PRINTS.
 - C. PROSITE.
 - D. PRODOM.

ANSWER: D

60. Which database of Pfam is having high quality data?
- A. Pfam-A.
 - B. Pfam-B.
 - C. Pfam-C.
 - D. Pfam-D.

ANSWER: A

61. Which database of Pfam is having low quality data?
- A. Pfam-D.
 - B. Pfam-B.
 - C. Pfam-A.
 - D. Pfam-C.

ANSWER: B

62. SMART stands for _____.
- A. Simple Molecular Architecture Research Tool.
 - B. Simple Molecular Alignment Research Tool.
 - C. Simple Modular Architecture Research Tool.
 - D. Simple Modular Alignment Research Tool.

ANSWER: C

63. CDD stands for _____.
- A. Conserved Domain Database.
 - B. Conserved Dictionary Database.
 - C. Conserved Domain Dictionary.
 - D. Conserved Dictionary Database.

ANSWER: A

64. Which BLAST program is used by conserved domain database?
- A. BLASTN.
 - B. BLASTP.
 - C. SNP-BLAST.
 - D. PSI-BLAST.

ANSWER: D

65. Which BLAST is related to RPS (Reverse Position Specific) BLAST?
A. PHI-BLAST.
B. PSI-BLAST.
C. BLASTN.
D. TBLASTX. ANSWER: B
66. The PRINTS database consists of protein finger prints that define families in the _____ databases.
A. SwissProt/TrEMBL.
B. SwissProt/EMBL.
C. PIR/TrEMBL.
D. PIR/EMBL. ANSWER: A
67. PopSet stands for _____.
A. Population Set.
B. Population Study Sets.
C. Population Data Study Sets.
D. Population Study Data Sets.
ANSWER: D
68. 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.
ANSWER: A
69. Define PAM?
A. Parallel Align Mutation.
B. Point Altered Mutation.
C. Point Accepted Mutation.
D. Point Arranged Mutation.
ANSWER: C
70. Which algorithm is used by local alignment?
A. Needleman and Wunsch.
B. PAM.
C. Smith-Waterman.
D. All the above.
ANSWER: C
71. Which algorithm is used by global alignment?
A. Needleman and Wunsch.
B. Smith-Waterman.
C. BLAST.
D. PAM .
ANSWER: A
72. Who developed PAM matrices and in which year?
A. Needleman and Wunsch, 1976.
B. Smith-Waterman, 1978.
C. Dayhoff et al., 1978.

D. Henikoff 1992.

ANSWER: C

73. What is the full form of BLOSUM?

- A. Blocks of Amino Acid Substitution Mutation.
- B. Basic Amino Acid Substitution Mutation.
- C. Blocks of Amino Acid Substitution Matrix.
- D. Basic Amino Acid Substitution Matrix. ANSWER: C

74. PAM matrices are based on _____ of protein evolution.

- A. Needleman and Wunsch.
- B. Smith-Waterman.
- C. Dayhoff model.
- D. Markov model. ANSWER: C

75. SRS is _____.

- A. a website for sequence similarity searches.
- B. a website specialized in mapping mutations related to human disease.
- C. a website that indexes many biological databases and is searchable by keywords.
- D. a website for protein family database searches.

ANSWER: C

76. Sequences that share an arbitrary, threshold level of similarity determined by the alignment of mismatching bases are termed as _____ sequences.

- A. homologous.
- B. heterologous.
- C. mismatched.
- D. matched.

ANSWER: A

77. If a mismatch occurs in the sequence alignment of two protein sequences, there occurs _____.

- A. gap.
- B. deletion.
- C. insertion.
- D. transition.

ANSWER: A

78. Gene duplication results in _____.

- A. orthologs.
- B. paralogs.
- C. xenologs.
- D. zoologs.

ANSWER: B

79. Speciation event results in _____.

- A. zoologs.
- B. paralogs.
- C. xenologs.
- D. orthologs.

ANSWER: D

80. The paired dot in the sequence alignment represents _____.
A. conserved substitutions.
B. semi-conserved substitutions.
C. gaps.
D. identity.

ANSWER: A

81. Single dot in the sequence alignment represents _____.
A. identity.
B. semi-conserved substitutions.
C. conserved substitutions.
D. gaps.

ANSWER: B

82. BLAST2 compares _____ number of sequences.
A. two.
B. three.
C. four.
D. five.

ANSWER: A

83. Two principal ways to construct guide tree in progressive alignment is _____.
A. UPGMA and Neighbor joining method.
B. Maximum Parsimony.
C. Maximum Likelihood.
D. all the above.

ANSWER: A

84. An asterisk mark indicated above the sequences to mark every _____ base pairs.
A. 5.
B. 10.
C. 15.
D. 20.

ANSWER: B

85. Which method of multiple sequence alignment uses genetic recombination?
A. Progressive.
B. Dynamic Programming.
C. Genetic Algorithm.
D. Hidden Markov Model. ANSWER: C

86. Which matrix uses the data on accepted mutations and the probabilities of occurrence of each aminoacid to generate a mutation probability?
A. PAM250.
B. PAM1.
C. PAM45.
D. PAM60.

ANSWER: B

87. Which matrix is based upon the alignments of closely related protein sequences?
A. PAM1.
B. PAM45.

- C. PAM60.
- D. PAM250. ANSWER: A

88. Which one of the PAM matrix represents amino acid substitutions that occur in distantly related proteins?
- A. PAM1.
 - B. PAM250.
 - C. PAM60.
 - D. PAM45.

ANSWER: B

89. What is the Twilight Zone?
- A. Where alignments appear plausible and are statistically significant.
 - B. Where alignments may appear plausible to the eye, but are no longer statistically significant.
 - C. Where alignments neither appear plausible nor statistically significant.
 - D. Where alignments share 30% identity.

ANSWER: C

90. In pairwise alignment result, sequences reported as related homologous represents _____ result.
- A. true positive.
 - B. true negative.
 - C. false negative.
 - D. false positive.

ANSWER: A

91. In pairwise alignment result, sequences reported as similar due to chance represents _____ result.
- A. true positive.
 - B. true negative.
 - C. false positive.
 - D. false negative.

ANSWER: C

92. What kind of information present in the middle portion of the BLAST result?
- A. General description about the sequence, database and the type of BLAST program.
 - B. Graphical color coded summary of the similar sequences.
 - C. Description line of the similar sequences.
 - D. Pairwise alignments of the query and the target sequences.

ANSWER: B

93. A term used to classify protein domains according to their secondary structural content and organization is _____.
- A. class.
 - B. architecture.
 - C. taxonomy.
 - D. homologs.

ANSWER: A

94. Hydropathy plots are usually used to predict _____.
- A. beta secondary structure.
 - B. transmembrane domains.
 - C. alpha secondary structure.

D. tertiary structure.

ANSWER: B

95. Databases such as CATH and SCOP are used to identify_____.

- A. the structural family to which a protein belongs.
- B. the generic family to which a protein belongs.
- C. homologous proteins.
- D. analogous proteins.

ANSWER: A

96. Coordinates for known protein structures are housed in?

- A. CATH.
- B. SCOP.
- C. PDBsum.
- D. PDB.

ANSWER: D

97. Homology modeling is a procedure whereby?

- A. Due to low sequence similarity between proteins of unknown and known structure, the structure is predicted from first principles.
- B. Due to high sequence similarity between proteins of unknown and known structure, the same function is assumed for both.
- C. Due to high sequence similarity between proteins of unknown and known structure, the structure of the latter is used as a template to model the former.
- D. A protein of unknown structure is compared against a library of fold templates to find the best match.

ANSWER: C

98. Threading is a procedure whereby?

- A. Due to low sequence similarity between proteins of unknown and known structure, the structure is predicted from first principles.
- B. Due to high sequence similarity between proteins of unknown and known structure, the same function is assumed for both.
- C. Due to high sequence similarity between proteins of unknown and known structure, the structure of the latter is used as a template to model the former.
- D. A protein of unknown structure is compared against a library of fold templates to find the best match.

ANSWER: D

99. With homology modeling, if there are minor errors in the template, the model will be?

- A. Very good.
- B. Just as good as the template is unable.
- C. Built using current modeling programs.
- D. Completely wrong. ANSWER: B

100. With homology modeling, if there are major errors in the template, the model will be?

- A. Very good.
- B. Just as good as the template is unable.
- C. rejected.
- D. Completely wrong. ANSWER: D

101. Which is a repository for the 3-dimensional structure data for large biomolecules?

- A. NCBI.
- B. EMBL.
- C. Swiss-Prot.
- D. PDB.

ANSWER: D

102. How many methods are there to predict 3-dimensional structure of a protein?

- A. 1.
- B. 3.
- C. 5.
- D. 7.

ANSWER: B

103. Which symbol represents the termination line of the PDB file?

- A. //.
- B. #.
- C. MASTER.
- D. END.

ANSWER: D

104. Which of the following is the distance based method?

- A. PGMA.
- B. Maximum parsimony.
- C. Maximum likelihood.
- D. Neighbor-Joining.

ANSWER: D

105. PDBID is a _____ representation.

- A. SMILES.
- B. ROSDAL.
- C. WLN.
- D. ALPHANUMERIC. ANSWER: D

106. PDBID is a combination of _____ number of letters.

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

ANSWER: D

107. Which experimental structures cannot be deposited in PDB?

- A. X-ray crystallography.
- B. NMR.
- C. Mass spectrometry.
- D. Comparative modeling. ANSWER: D

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

- A. ClustalW.
- B. ClustalX.
- C. ExPASy.
- D. ADIT.

ANSWER: D

109. Which one of the following method predicts the protein structure based on fold recognition?
- A. Comparative modeling.
 - B. Threading.
 - C. Abinitio.
 - D. Homology modeling. ANSWER: B

110. SCOP stands for _____.
- A. Similar Classification of Proteins.
 - B. Structural Classification of Proteins.
 - C. Similar Characterization of Proteins.
 - D. Similar Classification of Proteins.

ANSWER: B

111. A _____ is defined in SCOP as a collection of superfamilies.
- A. primary structure of protein.
 - B. secondary structure of protein.
 - C. protein fold.
 - D. mutated protein sequences.

ANSWER: C

112. DDD stands for _____.
- A. Dali Domain Dictionary.
 - B. Distance Matrix Alignment Server.
 - C. Distance Matrix Domain Dictionary.
 - D. Distance Domain Dictionary.

ANSWER: A

113. Which one of the following helps to calculate a structural similarity measure between pairs of structures of protein chains taken from the PDB?
- A. CATH.
 - B. SCOP.
 - C. FSSP.
 - D. DALI.

ANSWER: D

114. Template based protein modeling techniques is called as _____.
- A. comparative modeling.
 - B. surface modeling.
 - C. threading.
 - D. abinitio prediction.

ANSWER: A

115. Which is the only method that permits for the incorporation of alignable gaps as characters?
- A. Maximum parsimony.
 - B. Maximum likelihood.
 - C. Neighbor Joining.
 - D. Unweighted pair group method with arithmetic mean. ANSWER: A

116. Which of these methods is a distance-based method in tree construction?

- A. Unweighted pair group method with arithmetic mean.
- B. Jukes-Cantor.
- C. Minimum evolution.
- D. Maximum parsimony. ANSWER: A

117. Which one of the following is not a character-based method in tree construction?

- A. Maximum parsimony.
- B. Minimum likelihood.
- C. Minimum evolution method.
- D. Neighbor joining.

ANSWER: D

118. PAUP stands for _____.

- A. Phylogenetic Analysis Using Parsimony.
- B. Phylogenetic Analysis Using Pairwise.
- C. Proteomic Analysis Using Parsimony.
- D. Phylogenetic Analysis Using Protein.

ANSWER: A

119. A tree representation of a family showing the relationships between members and pattern of inheritance of a given trait is known as _____.

- A. pedigree.
- B. physical Map.
- C. genetic map.
- D. population studies.

ANSWER: A

120. The study of evolutionary relationships is _____.

- A. Phylogenics.
- B. Molecular Evolution.
- C. Cladogenesis.
- D. Cladistics.

ANSWER: A

121. A bifurcating branch point in the phylogenetic tree is known as _____.

- A. node.
- B. clade.
- C. branch.
- D. taxon.

ANSWER: A

122. 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.

ANSWER: A

123. Expand UPGMA.

- A. Unweighted Pair Group Method with Arithmetic Mean.
- B. Unweighted Pair Group Method with All Mean.
- C. Upregulated Gene Method with Arithmetic Mean.
- D. Unregulated Genome Method with All Mean. ANSWER: A

124. Single substitution in the nucleotide sequence is called _____.

- A. single substitution.
- B. simple substitution.
- C. single nucleotide polymorphism.
- D. simple nucleotide polymorphism. ANSWER: C

125. Which one of the following is more weighted mutation?

- A. Transitions.
- B. Transversions.
- C. Transitions and transversion.
- D. Deletion.

ANSWER: A

126. One of the most common errors in making and analyzing phylogenetic tree is _____.

- A. using a bad multiple sequence alignment as input.
- B. trying to infer the evolutionary relationship of genes or proteins in the tree.
- C. trying to infer the age at which genes or proteins diverged from each other.
- D. assuming that clades are monophyletic.

ANSWER: A

127. Which one of the following tool can be used to generate neighbor joining trees with or without bootstrap values?

- A. ClustalX.
- B. BLAST.
- C. Swiss-PDB viewer.
- D. ChemSketch. ANSWER: A

128. If you have 200 viral DNA sequences of 500 residues each and you want to know if there are any pairs that are identical or nearly identical. Which of the following is the most efficient method to use?

- A. BLAST.
- B. Maximum-likelihood phylogenetic analysis.
- C. Neighbor-joining phylogenetic analysis.
- D. PopSet.

ANSWER: C

129. 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. ANSWER: A

130. Homology modeling can be done using _____.

- A. Swiss-PDB Viewer.
- B. QMol.
- C. Raswin.

D. Babel.

ANSWER: A

131. Energy minimization of a modeled protein can be done using _____.

- A. ChemSketch.
- B. Moldraw.
- C. RasMol.
- D. Swiss-PDB Viewer. ANSWER: D

132. Which tool can be used for viewing molecular structures and animating molecular trajectories?

- A. Chimera.
- B. QMol.
- C. Arguslab.
- D. ChemSketch.

ANSWER: B

133. Which one of the following is actually based on MolView?

- A. Raswin.
- B. QMol.
- C. RasMol.
- D. Moldraw.

ANSWER: B

134. Molecular phylogeny can be performed with _____ sequences.

- A. only DNA.
- B. only RNA.
- C. only protein.
- D. DNA, RNA and protein. ANSWER: D

135. Which one of the following is a command based offline tool for molecular structural visualization?

- A. Swiss-PDB Viewer.
- B. RasMol.
- C. QMol.
- D. PyMol.

ANSWER: B

136. Who is the father of Genetics?

- A. Tom Roderick.
- B. Gregor Mendel.
- C. Julio Celis.
- D. Craig Venter.

ANSWER: B

137. A phylogenetic tree that explicitly represents number of character changes through its branchlengths is _____.

- A. dendogram.
- B. cladogram.
- C. phylogram.
- D. chronogram.

ANSWER: C

138. Which of the following statements about phylogenetic methods is correct?
- A. The Maximum Likelihood method determines the tree for which the likelihood of the tree given the data is largest.
 - B. The Maximum Likelihood tree may sometimes contain branches of zero length.
 - C. If the trees from Maximum Likelihood, Parsimony and Neighbor-Joining methods all have the same topology, this must be the correct topology.
 - D. In Bayesian phylogenetic methods, if the prior probabilities of two trees are equal, then the posterior probabilities must also be equal.

ANSWER: C

139. Which of the following is the character based method?
- A. UPGMA.
 - B. Maximum Parsimony and Maximum Likelihood.
 - C. Maximum Likelihood and Neighbor-Joining.
 - D. Neighbor-Joining.

ANSWER: B

140. Who is the father of Genomics?
- A. Altschul.
 - B. Gregor Mendel.
 - C. Richard.
 - D. Craig Venter

ANSWER: D

141. Which of the following model account for nucleotide substitutions?
- A. Jukes-Cantor.
 - B. Kimuras.
 - C. Complex.
 - D. Option a, b and c.

ANSWER: D

142. Which method is used for predicting protein tertiary structure in the absence of homology to a known structure?
- A. Comparative modeling.
 - B. Ab initio prediction.
 - C. Threading.
 - D. Surface modeling.

ANSWER: B

143. Which one of the following is an experimental method to determine the three-dimensional structure of the protein?
- A. Threading.
 - B. X-ray crystallography.
 - C. Homology modeling.
 - D. Ab initio method.

ANSWER: B

144. Which one of the following is a computational method to predict the three-dimensional structure of the protein?
- A. X-ray crystallography.
 - B. NMR.
 - C. UV Spectroscopy.

D. Threading.

ANSWER: D

145. Homology modeling is also called as _____.

- A. comparative modeling.
- B. abinitio prediction.
- C. threading.
- D. surface modeling.

ANSWER: A

146. Which one of the following tool uses comparative modeling method to predict the threedimensional structure of a protein?

- A. Rosetta.
- B. Threader.
- C. CASP.
- D. Modeller.

ANSWER: D

147. Which one of the following tool is not used to predict the three-dimensional structure of a protein?

- A. GLIDE.
- B. Swiss-PDB Viewer.
- C. JACKAL.
- D. Modeller.

ANSWER: A

148. Which one of the following tool is used to predict the three-dimensional structure of a protein?

- A. AutoDock.
- B. Gromacs.
- C. ChemSketch.
- D. Modeller.

ANSWER: D

149. Which server is used to compare three-dimensional protein structures?

- A. DALI.
- B. FSSP.
- C. SCOP.
- D. CATH.

ANSWER: A

150. Which is a repository for the 3-dimensional structure data for large biomolecules?

- A. NCBI.
- B. EMBL.
- C. Swiss-Prot.
- D. PDB.

ANSWER: D