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BIF501 - Bioinformatics II

MCQs mid term

1. Human Genome Project Start In..... **(1886)**
2. Motif Are found in..... **(DNA or proteins)**
3. Wardenburg's Syndron is disordered in **(human)**
4. Systic Fibrosis Gene found on Chromosome No....**(02)**
5. NCBI Stand for..... **..(National Center for Biotechnology Information)**
6. PIR Stand for..... **(Protein Information Resource)**
7. Structure of RNA..... **(single strand)**
8. Choufasman Algorithm based on **(statistical occurance of amino acids)**
9. Probe Length..... **.(8-32)**
10. There are Steps in homology modeling loops formation. **(4th)**
11. 3D1d alogorithm form in **.(1991)**
12. PDGF Stand for..... **(Platelet derived growth factor)**
13. Hmm Stand for **...(Hidden Markov Model)**
14. Which RNA converted into protein **.....(primary)**
15. Genomic Rearrangement results in change of.....**(gene ordering)**
16. Uniprot is data of protien..... **.(sequence)**
17. A drug targetprotien.(**about 50**
18. HGP Revealed thatDiseases are hereditary . **(3000-4000)**
19.is good for gapped alingment . **(BLOSUM50)**
20. When senger Sequence insulin.....(**1955**
21. Neddleman alignment published in **(1970)**
22.Size Fragment can be lighted into BAC Vector.**(large)**
23. Brute Force is Called..... **(Exhaustive search algorithms)**
24. 3D1d Bowie Algorithm at el in **(1991)**
25.Help in finding global minimum.**(Global Energy Optimization)**
26. BLOSUM Means... **(BLOCK Substitution Matrix)**
27. Log Odd PAM Matric..... **(250)** Substitution matrices are the log-odds matrices used for scoring amino acid substitutions in pairwise alignments.
28. Dayhoff PAM matrices.....Dayhoff, Schwartz and Orcutt (1978) presented their famous PAM **(Point accepted mutations)** using substitution data from similar proteins then extrapolating this information to longer evolutionary distances.
29. BLOSUM62 is good for.....Alignment. **(ungapped alignment)**
30. Loops are small consistingAmino Acids **(3-4)**
31. The NeedlemanWunsch algorithm finds.....Alignment. **(best global)**
32. Substitution scores can be derived from.....Model **(probabilistic)**
33. Dayhoff PAM matrices..... **year (1978)**
34. Which notation of spectral similarity shared peaks counts**(P1and P2- S1and S2)**
35.methods for lead validation **(5)**
36. MS2 has **codons (49)**
37. TIGR stand for what **The Institute of Genome Research)**
38. XML stand for what **Extensible Markup Language)**
39. chou fasman algorithm were firstly used in..... **year (1973)**
40. Nation spectral similarity shared peak count.....**(P1and P2- S1and S2)**
41. PDB stands **... Protein Data Bank**
42. PDGF stands **PDGF (Platelet derived growth factor)**
43. HMM stands **Hidden Markov Model**

44. Which rna converted into protein **mRNA:**
45. Hamming distance - ---- **technology for dna similarity**
46. Genomic rearrangements results in change of.... **gene order**
47. Uniprot is database of.... **Protein sequence**
48. Motif facilitate for binding.....:
49. A drug targets..... Proteins. **about 500**
50. HGP revealed that.... Disease are hereditary **3000-4000**
51. Nation spectral similarity shared **peak count....**
52. **BLOSUM50**..... Is good for gapped alignment:
53. When sanger sequence insulin....???? **1955:**
54. Needleman alignment published in....???? **1970: .**...
55. Size fragment can be ligated into BAC vector **150–350 kbp (not confirmed)**
56. Programming language for modellers.... **Python script file, (not confirmed)**
57. Brute force is called.... **Exhaustive search algorithms**
58. 3D-1D bowie algorithm at el in.... **1991**
59. **Global Energy Optimization**.... Help in finding global minimum
60. The Needleman and wunch found best alignment between two sequence) **global**
61. ----- is used to find optimal alignment of two sequence **Dynamic programing**
62. More mutable amino acid **Asparagine (Asp),**
63. 4salamander genome is larger then human genome **10 times**
64. humn genome project whole genome assembly paradigm (**james weber and gene myers**)and **celera genomics** _____ mate pair read sekwinving technik.
65. 6)chou fasmin algorithem used for **predict secondary structures of proteins**
66. secondary structure of protein is formed due to **Hydrogen bonds**
67. Alpha helices finalized if their propensity higher then **5 amino acid**
68. 9)Due to duplication of gene **paralogy**
69. 10)GCG stand for **Genetic computer genome**
70. 11) step of homology modeling.... **7**
71. 3D AND ID alorithem **1991**
72. uniport is tool or **database**
73. 14) local versus global minima..... **helps find global minimum**
74. AG and GT are region of..
- A. Exon flauking**
- B. Intron
- C. Both
75. GT-AG nucleotides -----% in gene.
- A. 99.24%**
- B. 98%
- C. 92%
- D. None of the above
76. -----% human gene consists on gene.
- A. 6
- B. 5
- C. 8
- D. 3**
77. Gene is for embryonic development.
- A. Jeobok
- B. Theobox
- C. Serenbox
- D. Homeobox**
78. HGP revealed that -----diseases are hereditary.**3000-4000**
79. Endosymbiont hypothesis was approved in
- A. 1805
- B. 1883**
- C. 1956

D. 1989

80. More than 95% human gene

- A. Repeats
- B. Exon

C. Intron

81. Horizontal transfer of gene is

- A. Fast
- B. Slow**
- C. Reliable
- D. Fast and reliable

82. MS2 genome has amino acid

- A. 122
- B. 344
- C. 156

D. 129

83. Restriction enzymes are breakdown DNA molecule at???????

84. RNA is converting into proteins

- A. tRNA
- B. mRNA
- C. rRNA
- D. Amino acid

85. Bypass is a type of ----- algorithm. **Brunch and bound**

86. Median string problem is one of the ways to find **Motif**

87. Next vertex algorithm provide as an output **Next subtree**

88. Motifs are found in **Promoters**

89. PAM stands For **Point Accepted Mutation**

90. Endosymbiont hypothesis proposed in **1883**

91. Q3: Median string problem is one of the ways to find **Motif**

92. EMBL stands for **European Molecular Biology Lab**

93. GEO stands for **Gene Expression Omnibus**

94. XML stands for **Extensible Markup Language**

95. SINES stands for **Short Interspersed Nuclear Elements**

96. Horizontal Gene Transfer is -----Process **Slow**

97. MS2 Genome is **129 amino acids**

98. Two Amino Acids joins together by **Peptide Bond**

99. Gel Electrophoresis may be used to measure-----of restriction fragment **Size**

100. Cystic Fibrosis gene is found on chromosome number **7**

101. Similar proteins having 1% mutation analyzed with **PAM matrix**

102. -----gene regulate the embryonic development **Homeobox**

103. Genes present in two different organisms in orthologs have-----function **Similar**

104. Introns starts as 5' end -----and ends on 3' end as **GT-----AG**

105. SINES are **80-300 bp long**

106. Motifs are found in **Promoter regions**, and regulatory motifs are in transcription factors

107. Next Vertex Algorithm is **Branch and Bound**

108. Next Vertex Algorithm is very **Efficient**

109. Salamander Genome is -----times larger than human **10**

110. The accuracy of GENSCAN-----for genes with many short exons or with unusual codon usage
Decreases

111. Simple motif Search Algorithm is based on **Brute Force**

112. Pre-order Algorithm is **Recursive**

113. Regulatory motifs are generally found in **Promoter Region of DNA**

114. Accuracy of gene scan decreases for gene having.....axon. **Short**

115. Less edit distance shows.....**solution**

116. Hamming distance is**technique for DNA similarity**

BIF501 CURRENT MCQS FOR MIDTERM (UPDATED)

Created by irtaza ali

1. ORF stands for _____ Open Reading Frame
2. IUB stands for _____ International Union of Biochemistry
3. PAM stands for _____ Pointed accepted mutation
4. FTP stands for _____ File Transfer Protocol
5. LINE stands for _____ Long Interspersed Nuclear Elements
6. SINE stands for _____ Short Interspersed Nuclear Elements
7. PIR stands for _____ Protein information resource
8. HMM stands for _____ Hidden Markov Model
9. GCG stands for _____ Genetic computer group
10. TIGR stands for _____ The institute of genome research
11. XML stands for _____ Extensible Markup Language
12. PDGF stands for _____ (Platelet derived growth factor)
13. NCBI stands for _____ National Center for Biotechnology Information
14. EMBL stands for _____ European Molecular Biology Lab
15. DDBJ stands for _____ DNA Data Bank of Japan
16. GEO stands for _____ Gene Expression Omnibus
17. STS stands for _____ Sequence Tag Sites
18. BLOSUM stands for _____ Block substitution Matrix
19. PSSM stands for _____ position specific scoring matrices
20. Model plant is _____ Arabidopsis thaliana
21. human genome project started in _____ 1886
22. Endosymbiosis hypothesis proposed in _____ 1883
23. SINES are ... Bp long _____ 80-300BP
24. RNA is ____ stranded molecule _____ Single
25. In order to predict exon we need to get _____ ORF or Splice Site
26. Bypass is the type of algorithm _____ Branch and bound

27. Median string problem is one of the way to find Motifs
28. Aminoacids in MS2 genes 129 Amino acids
29. MS2 genome has ___ codons 49
30. The accuracy of GENSCAN decrease for genes with many short exons
31. Paralogs genes are originated from Gene duplication
32. Human mitochondria ___ kb 17Kb
33. Waardenburg's syndrome Gene present on chromosome 2
34. Genes present in different organisms Horizontal Transfer
35. Motif facilitate for binding NF-kB sites
36. Uniport finds Protein sequences
37. AG and GT are _____ Region Exon flanking
38. ___% human genome consist of gene consecutive 3%
39. Three nucleotides code for ___ Amino acid 1
40. Genebank is a ___ database DNA
41. H.Influenza was the ___ published genome 1st
42. Gene mapping is determining the ___ on chromosome location
43. Which RNA is converted in to proteins mRNA
44. In RNA thymine is replaced by Uracil
45. Regulatory Motifs are generally found in Promoter region of DNA
46. Pre order algorithm is a recursive
47. Cystic Fibrosis gene is present on chromosomes no 7
48. A drug can target about _____ proteins 500
49. Orthologs genes have same function and Evolutionl history
50. Median string is used to find Motif
51. EMBL begins with sequeunce/ ID
52. Less edit graph means Relation is closely related
53. Restriction enzymes break DNA molecules at specific sites
54. Brute force approach is good for ___ data. Small data
55. Insertion in an alignmnet shows.....in edit graph space in the top
56. Each common subsequence belong to an alignment that no mismatches

57. Symbols of the pattern and the searched text are chosen from a predetermined finite set, called an alphabet
58. Next vertex algorithm provides as an output Next subtree
59. simple motif search algorithm is based on Brute force
60. Consensus score is defined as score(s.DNA)
61. Gel electrophoresis may be used to measure Size of restriction fragments
62. Waardenburg's syndrome is disorder in Humans
63. Hamming distance is not typically used to compare DNA or protein sequences it is used for DNA Similarity
64. Genomic rearrangement results in a change of gene ordering
65. HGP revealed that.... Disease are hereditary 3000-4000
66. Brute force is called... Exhaustive search Algorithm
67. Insulin was sequenced by sanger in 1951
68. Uniprot is a database of protein a) sequence b) structure c) annotation d) All
69. Gene mapping is determining....on chromosomes location and relative distance
70. Genetic map distances are measured in Centi-Morgans (CM)
71. Proteins that are 1% different may be termed as one unit diverged. PAM
72. DNA and histone together are called Nucleosome
73. Which bond exist between 2 amino acids Peptide bond
74. Gene expression data means Rna seq(b) microarray data (c) mRNA d)all
75. More than 90% of in E.Coli Exon
76. Horizontal transfer of gene...process Slow
77. Deletion in alignment show...in edit graph Horizontal edge
78. Salamdar genome is... time larger than human genome 10 (ten times)
79. When transfer of gene occurs from parents to offspring is called Vertical Transfer
80. TCGGGATTCC sequence in Drosophila in the activation of....gene Immunity Gene
81. Ab Initio method is based on Gene prediction and repeat masker
82. Next vertex algorithm is very..... algorithm precise
83. Less edit distance shows..... solution Better
84. Brute force Algorithm was devised by Stephon

85. Which notation of spectral similarity shared peaks counts P1
86. Growth of sequence in database is exponential
87. 95% of human genome is intron
88. if two gene are equal they are called homologus
89. MSA is used to find Comparison
90. Next vertex output is efficient
91. Aspartate is more mutable
92. A pattern is an ordered sequence of symbols
93. Columns of an alignment containing spaces in top row are called ----- Insertions
94. Genes present in diff organisms having diff structure may have----- function similar
95. ----- gene for embryonic development Homeobox
96. To carry out the steps of an algorithm humans are generally slow
97. A linear time algorithm for string matching avoid useless shift of the Pattern
98. Which theory help us to find DNA motif Gold bug
99. Generally Longer ORF are preferred.
100. Random mutagenesis change sequence Amino acids