

(BIF 401) "MCQ" FOR MID TERM

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1. Humans have over _____ genes
 - a. 30,000
 - b. 25,000
 - c. 35,000
 - d. 39,000
2. The genes may produce _____ different proteins
 - a. <250,000
 - b. >25,000
 - c. >250,000
 - d. <25,000
3. Modern biological experiments produce data which is stored on _____.
 - a. Internet
 - b. Computers
 - c. Labs
 - d. None of these
4. Data is being accumulated at an _____ rate
 - a. Exponentially increasing
 - b. Double increasing
 - c. Decreasing
 - d. Stable
5. Since genome and _____ information is publically available, you can process this information after downloading it.
 - a. Proteome
 - b. Evolutionary studies
 - c. System biology
 - d. Both b and c
6. Biology easily has _____ years of exciting problems to work on.
 - a. 550
 - b. 500
 - c. 450
 - d. 1000
 - e. 850
7. "Biology easily has 500 years of exciting problems to work on" is saying of _____?
 - a. Donald trump
 - b. William Knuth

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- c. Donald knuth
 - d. William Edwin
8. If we observe the growth of gene bank than from 1982 it comprised _____ base pairs.
- a. 3 billions
 - b. 2 billions
 - c. 3 millions
 - d. 2 millions
9. By year 2002 growth of gene bank had risen to _____ base pairs.
- a. 25 billions
 - b. 65 billions
 - c. 56 billions
 - d. 52 billions
10. Phylogenetic " tree of life " basically consists of following three domains:
- a. Bacteria, archae, monera
 - b. Plantae , animalia, fungi
 - c. Bacteria, archae, eucarya
 - d. Eucarya , viruses, protozoa
11. Bioinformatics can be specifically applied to genomics through?
- a. Post translational modification
 - b. Transcription data
 - c. Genome assembly
 - d. Both b and c
12. Bioinformatics can be specifically applied to proteomics through?
- a. Protein Sequencing
 - b. Post-translational Modifications
 - c. Database Development
 - d. All of above
13. Bioinformatics can be specifically applied to evolutionary studies through:
- a. Evolutionary relationships, Evolutionary distances, Phylogenetics, Tree of life
 - b. Evolutionary relationships, Evolutionary distances
 - c. Evolutionary distances, Phylogenetics, Tree of life
 - d. None of above options is right.
14. Bioinformatics techniques have enabled us to generate _____ data and its utilization!
- a. Anic
 - b. Onic
 - c. Omic
 - d. Amic
15. Step by step applications of bioinformatics are expanding from genome level to entire _____?
- a. Metabolism

- b. Biosphere
 - c. **Biosystem**
 - d. Protein level
16. Bioinformatics helps us to understand the systems from small to big like gene finding to _____?
- a. Sequence finding
 - b. Location finding
 - c. **Function prediction**
 - d. Both a and b
17. _____ integrate biological data
- a. Simulation
 - b. **Model**
 - c. Disease prediction
 - d. Both a and c
18. Simulations help validate testable hypotheses
- a. **Simulation**
 - b. Model
 - c. Disease prediction
 - d. Both a and c
19. Bioinformatics not only organizes, stores and analyzes biological data, but can also validate novel hypotheses
- a. Genomic data
 - b. Proteomic data
 - c. **Biological data**
 - d. Phylogenetic data
20. Recent trends in bioinformatics involve development of personalized therapeutics for _____?
- a. Cancer and ulcer
 - b. Obesity and cancer
 - c. Diabetes and obesity
 - d. **Cancer and obesity**
21. NGS stands for _____?
- a. New generating sequence
 - b. New generation sequencing
 - c. **Next generation sequencing**
 - d. Next genomic sequence
22. Massive amount of biological data is in _____?
- a. Megabyte files
 - b. **Terabyte files**

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- c. Gigabyte files
 - d. All of these
23. Identification of hitherto unknown types as well as roles of RNA is considered as frontier of bioinformatics in _____?
- a. Genomics
 - b. Proteomics
 - c. Transcriptomics
 - d. Both a and b
24. Identification of known as well as novel post-translational modifications is considered as frontier of bioinformatics in _____?
- a. Genomics
 - b. Proteomics
 - c. Transcriptomics
 - d. Both a and b
25. Accurate solution of _____ is one of the toughest problems.
- a. Amino acid structure
 - b. Protein structure
 - c. Gene structure
 - d. Chromosome structure
26. _____ century is the century of Bioinformatics
- a. 20th
 - b. 21st
 - c. 19th
 - d. 18th
27. _____ provides the blueprint for building cells
- a. DNA
 - b. RNA
 - c. Proteins
 - d. Both a and b
28. _____ dictates the production of cell's proteins, carbohydrates & vitamins
- a. DNA
 - b. RNA
 - c. Proteins
 - d. Both b and c
29. DNA codes for _____
- a. Gene
 - b. Protien
 - c. RNA

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- d. Nucleuse
30. _____ along with some other molecules form cells including their organelles and membrane.
- a. Lipids
- b. Nucleotides
- c. **Proteins**
- d. DNA
31. Molecules like proteins and carbohydrate are produced after _____ of DNA into proteins
- a. Transcription
- b. Degradation
- c. Upgradation
- d. **Transformation**
32. DNA is constituted by _____ bases
- a. 2
- b. 3
- c. 4
- d. 5
33. _____ pairs with T only and _____ pairs with G
- a. A, G
- b. **A, C**
- c. C, A
- d. G, A
34. Process of transcription _____ nucleotides bases in the DNA
- a. Encodes
- b. **Decodes**
- c. Intercalates
- d. None of above options is right
35. Based on the information received after decoding DNA, an RNA molecule is _____. a. Translated
- b. Decoded
- c. **Encoded**
- d. Degraded
36. RNA is constituted by four bases. These are _____?
- a. A, C, T, G
- b. T, G, A, T
- c. **A, C, U, G**
- d. U, G, C T
- i. name of pentose sugar present in DNA.

- a. 3-deoxyribose
 - b. 5-deoxyribose
 - c. **2-deoxyribose**
 - d. 4. Deoxyribose
37. Protein and carbohydrates are produced as a result of transformation of RNA molecules. This transformation is called _____
- a. **Trascriptomics**
 - b. **Translation**
 - c. **Transcriprion**
 - d. **Replication**
38. Ribosome reads an RNA transcript and _____ amino acids according to that from the cell's cytosol
- a. Arranges
 - b. **Collects**
 - c. Makes
 - d. Assigns
39. _____ nucleotides are read at a time from the RNA
- a. **2**
 - b. **3**
 - c. **4**
 - d. **5**
40. Each codon corresponds to a specific _____
- a. Protein
 - b. Gene
 - c. **Amino acid**
 - d. Peptide bond
41. Translation involves coding of proteins by RNAs at _____?
- a. **Cytosol**
 - b. **Nucleus**
 - c. **Ribosome**
 - d. **Endoplasmic reticulum**
42. When _____ of amino acids takes, place water is formed .
- a. **Isomerization**
 - b. **Polymerization**
 - c. **Hydrogenation**
 - d. **Condensation**
43. The amino acids are joined with each other with peptide bonds and then fold with each pther in___ form they make protein structure.
- a. **2D**

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b. 3D

c. 4D

44. RNA sequences can be a little less than the _____ but they are in a much larger variety a.
Genes

b. Proteins

c. DNA

d. Both b and c

45. Proteins have long sequences and are _____ in number

a. Small

b. Very small

c. Very large

d. Large

46. Both genbank and Uniprot are online databases and DNA, RNA and Protein sequences are available here online for _____

a. Scientists

b. Researchers

c. Public

d. Both b and c

47. _____ is online database where researchers can get access to sequence of DNA, RNA and proteins..... no option Ans.....genBank

48. GenBank can be searched by:

- Sequence
- ID
- Name
- Species etc.

49. Other information includes:

- Locus
- Accession number
- Authors
- Journal etc.

50. Uniprot is the public database which is being used to search the sequence of _____? a. DNA

b. RNA

c. Both a and b

d. Proteins

51. Ubiquitin plays an important role in _____ for recycling the proteins

a. Ribosome

b. Nucleuse

c. Cytosol

d. DNa

52. In Uniprot home page there is a box named _____

- a. Blast
- b. Prot
- c. **Swiss prot**
- d. Swiss blast

53. _____ include complete matching in terms of residues and their order

- a. Inexact matcing
- b. **Exact matching**
- c. Both a and b
- d. Optimum matching

54. _____ includes partial matching in terms of residues and order with room for variations in both.

- a. **Inexact matcing**
- b. **Exact matching**
- c. **Both a and b**
- d. **Optimum matching**

55. In prosite pattern _____ separate the elements of the pattern

- a. Latter

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b.

X

c. Hyphen

d. Dot

56. Bracketed numbers denote

- a. Specific amino acid
- b. Any amino acid
- c. the elements of the pattern
- d. the repeat length of a residue,

57. If the repeat length varies, the _____ of this variation is quoted in the brackets.

- a. Range
- b. Numbers
- c. Domain
- d. Both a and b

58. How many types of matching?

- a. 5
- b. 4
- c. 3
- d. 2

59. In exact matching includes _____ matching in terms of residues and order with room for variations in both.

- a. Complete
- b. Partial
- c. Half
- d. Impartial

60. The process of inexact matching while keeping in view the _____ residues is called sequence "Alignment"

- a. Experimental
- b. Conserved
- c. Under observation
- d. Both a and b

61. Pairwise sequence alignment is therefore alignment of a pair of _____ sequences

- a. 2
- b. 3
- c. 2 or 3

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- b.
- d. d. More than 3
62. Pairwise sequence alignment takes into consideration _____ matching
- a. Exact
 - b. Inexact
 - c. Optimum
 - d. Both b and c
63. In pairwise sequence alignment _____ are coloured.
- a. Mismatches
Indels
 - c. Insertions
 - d. Matches
64. In pairwise sequence alignment _____ are denoted by '.'
- a. Matching nucleotides
 - b. Mismatching nucleotides
 - c. Substituted nucleotides
 - d. None of above
65. _____ could be inserted to account for insertions and deletions
- a. gaps
 - b. hyphens
 - c. dots
 - d. both a and b
66. Gaps ('.') may carry a penalty for _____ scores from unreasonable alignments
- a. Reducing
 - b. Increasing
 - c. Equalizing
 - d. Increasing as well as equalizing
67. How many types of pairwise alignment?
- a. 4
 - b. 3
 - c. 2
 - d. 1
68. The alignment with highest score is _____?
- a. Global
 - b. Local

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- b.
- c. **Optimal**
- d. Both a and b
69. _____ maximizes the number of matches between the query and source sequences along the entire length of both the sequences
- a. **Global alignment**
- b. Local alignment
- c. Optimal alignment
- d. Both a and b
70. _____ includes **Finding similar domains, motifs, detecting distant homology**
- a. Global alignment
- b. **Local alignment**
- c. Optimal alignment
- d. Both a and b
71. **Gaps are inserted in a sequence being aligned to _____ missing amino acids or nucleotides**
- a. Add
- Exclude
- c. **Accommodate**
- d. Delete
72. _____ **lead to Gaps in alignments**
- a. Mismatches
- b. Matches
- c. **Indels**
- d. Substitutions
73. **Sequences are written on _____ side of a dot matrix grid**
- a. Top and right
- b. **Top and left**
- c. Bottom and left
- d. In middle
74. _____ **is the number of nucleotides or amino acids which match exactly between two biological sequences"**
- a. Similarity
- b. Dissimilarity
- c. **Identity**

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- b.
- d. In some cases identity and in some cases similarity
75. For computing similarity between sequences, you will need to first _____ the two sequences using pairwise sequence alignment!
- a. Copy
 - b. Remove the gaps
 - c. Align
 - d. Remove the shorter sequence of
76. _____ is the comparison between sequences calculated by using alignment approach
- a. Similarity
 - b. Identity
 - c. Global alignment
 - d. Local alignment
77. Non-diagonal broken dots are _____ matches
- a. Exact
 - b. Mismatches
 - c. Random matches
 - d. Non random
78. Aligned portions of sequence can be considered in varying orders and the process is called _____?
- a. Domain alignment
 - b. Domain shuffling
 - c. Domain alteration

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d. Domain consideration

79. Local alignments have the power to detect small regions of high _____ between two sequences

- a. Identity
- b. **Similarity**
- c. Consideration
- d. Alignment

80. _____ can be elicited from proteins belonging to different families

- a. Query domain
- b. **Conserved domain**
- c. Alternating domain
- d. Experimental domain

81. Alignment of insertions and deletions can be performed by insertion of _____ in either the template or the target sequence

- a. Matches
- b. Mismatches
- c. **Gaps**

82. _____ were addition or removal of amino acids from protein sequences OR nucleotides from DNA or RNA sequences

- a. Matches
- b. Mismatches
- c. Panalties
- d. **Indels.**

83. No _____ is inserted in template or target

- a. Indel
- b. Matrix
- c. **Gap**
- d. Mismatch

84. Mutations are treated with _____ penalties

- a. Gap penalty
- b. **Substitution penalty**
- c. Varying penalty
- d. Point penalty

85. _____ are treated using gaps and gap penalties

- a. **Indels**
- b. **Mutations**
- c. **Substitutions**
- d. **Alignments**

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86. To perform an alignment by sliding sequences across each other, we used _____ to find matching nucleotides and amino acids

- a. Grid
- b. Matrix
- c. Dot plot
- d. Both b and c

87. Matches are labelled by _____ instead of a dot

- a. 0
- b. +1
- c. -1
- d. i

88. _____ can be included in the dot plot as -1

- a. Indels
 - b. Substitutions
 - c. Both a and b
 - d. None of above
- a. c

89. Calculation steps determine the time taken by an _____?

- a. Alignment
- b. Computation
- c. Algorithm
- d. Both a and c

90. _____ is a costly process.

- a. Extracting DNA
- b. Extraction of RNA
- c. Web programming
- d. Sequence analysis

91. _____ helps to reduce costs of sequence analysis..... no options
Ans is dynamic programming

92. DP stands for _____?

- a. Designing primer
- b. Dynamic pathadology
- c. Dynamic programming
- d. Dynamic progression

93. DP uses a _____ to deal with matches, mismatches and gaps!

- a. Scoring functionality

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- b. Scoring function
- c. Scoring penalty
- d. Possibility function

94. Alignments are represented by _____ in the dot matrix plot

- a. Vertical components
- b. Horizontal components
- c. Diagonals
- d. Dots

c

95. Which cell is diagonal to any given cell i.e (i , j)

- a. (i , j-1)
- b. (i-1 , j)
- c. (i-1 , j-1)
- d. (1-i , j)

96. Which option is correct is there is gap on y-indices

- a. (i , j-1)
- b. (i-1 , j)
- c. (i-1 , j-1)
- d. (1-i , j)

97. Which option is correct is there is gap on x-indices

- a. (i , j-1)
- b. (i-1 , j)
- c. (i-1 , j-1)
- d. (1-i , j)

98. In NEEDLEMAN WUNSH ALOGRITHM _____ is match score.

- a. Alpha
- b. Beta
- c. Gamma
- d. None of these

99. In NEEDLEMAN WUNSH ALOGRITHM _____ is mis-match penalty

- a. Alpha
- b. Beta
- c. Gamma
- d. None of these

100. In NEEDLEMAN WUNSH ALOGRITHM _____ is gap penalty.

- a. Alpha
- b. Beta

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- c. **Gamma**
- d. None of these

101. NEEDLEMAN WUNSH ALOGRITHM finds optimal combination of aligned_____.

- a. Left position eliment
- b. Upper position element
- c. Left position element
- d. **Diagonals**

102. According to NEEDLEMAN WUNSH ALOGRITHM diagonal move is a _____?

- a. **Match**
- b. Mis match
- c. Gap
- d. mutation

103. After completely calculating the matrix, we need to do _____

- a. Alignment
- b. Programming
- c. **Traceback**
- d. Computing values

104. Traceback allows us to extract the _____ alignment

- a. Global
- b. Local
- c. **Optimal**
- d. Both a and b

105. Blosum matrices are used to align:

- a. DNA sequences
- b. **protein sequences**
- c. amino acids sequences
- d. none

106. pair wise sequence alignment consists comparison of-----sequences:

- a. **2**
- b. 3
- c. 4
- d. 5

107. pair wise alignment may be:

- a. local
- b. global
- c. somewhat specific
- d. **both a and b**

108. dynamic programming cannot work after:

- a. 2 sequences
- b. 4 sequences
- c. 6 sequences
- d. **9 or 10**

sequences

109. for multiple sequence alignment we use:

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a.dynamic programming b.progressive alignments c.slective alignments
d.none of these

110.MSA involves the comparison of:

a.less than 3 sequences b.more than 3 sequences
c.more than 5 sequences d.more than 10 sequences

111. there are --- types of scoring matrices:

a.2 b.3 c.4 d.5

112.blosum matrices were first purposed in:

a.1772 b..1862 c.1992 d .1872

113.gaps are not allowed in:

a.pam sequences b.blosum sequences c.both a and b d.none

114.in computiong of blosum matrices if i=j then it means:

a.simillar amino acids b.different amino acids c.mutational substitutions d.none c

115 =characterize protein families based on regions

a)=MULTIPLE gene b)= homologous c)= heterzyous d)= none of these

116= Evaluate evolutionary order of species or

a)= Phylogeny b)= phasmids c)= bacteria d)= both b and c

117=Pairwise alignment is the alignment of

a)= Multiple sequence b)= single sequence c)= two sequence d)= all of these

4=..... can help to perform MSA!

a)= Progressive alignment b)= multiple alignment c)= both 118=ln

multiple sequence of Alignment ----- is required to remove sequence

a)= 30% b)= 40% c)= 57% d)=80%

119= pairwise alignment include the sequence which is ...

a)=S1 &S2 B)= S3 &S4 C)= All

120=similar materics =.....

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a)= matches/ comparisons

b)= camparisons / matches

c)= matches/ frequency

d)= Comparisons/frequency

121=----- is the free tool which do all the process of MSA for our body .

a)= Gene

b)= DNA

c)=clustal

d)=RNA

122=Clustal is developed by Molecular lab

a)= Russians

b)= American

c)= assians

d)=european

123=Clustal perform alignment sequence in

a)= slow and accurate

b)=fast/ approximate

c)= fast/accurate

d)= both a and b

124= Clustalw can use multiple file formats including

a)= EMBL

b)= swissprot

c)= pearson(fasta)

d)=All of these

125=Blast developed in

a)=1980

b)=1970

c)=1990

d)1956

126=blast stand for? No option

Basic local alignment search tool

127=Blast is used for...

a)= search databases for query protein and nucleotide sequence

b)= search for translational products

c)= online search to blast.ncbi.nlm.nih.gov/blast.cgi

d)= All of these

128=----- can align complete sequence of Blast.

a)= Edward

b)= Smith waterman

c)= Frenklin d)=

Griffth

129=BLAST use in

a)= For approximate sequence matching

b)= Input to BLAST is FASTA formatted sequence

c)= In search of parameters

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d)= All of these

130=Output of BLAST is

a)=Result are shown in HTML, plan text, and XML formats

b)=A table list the sequence hits found along with scores

c)= Users can read this table off and evaluate results

d)= All of these

131=..... can search sequence databases and identify unknown sequence by comparing them to the known sequence .

a)= BLAST

B)= Algorithm BLAST

C)= INPUT BLAST

D)= OUTPUT BLAST

132=Blast help in identify the

a)= parent organism

b)= function & evolutionary history

c)= both a and b

d)= none of these

133= the protein have list of all possible words

a)= PQQ(score 15)

b)= QGE (Score 9)

C)= GEL(Score 12) & PEG(score 13)

d)= both a and c

134= Blast performs searches by alignments on sequence.

a)= Slow

b)= quick

c)= normal

d)= All

135= Compares the six-frame translated proteins of a nucleotide query sequence against the six – frame translated proteins of a nucleotide sequence database. Is called

a)= Tblastx

b)= Tblastn

c)= Blastx

d)= none of these

136= Multiple types of BLAST exist which assist in

a)= Aligning nucleotide

b)= Amino acid sequence

c)= protein

d)= both a and b

137= For known sequence we use website

a)= NCBI

B)= UCSC

C)= BINC

D)= Both a and b

138=For unknown sequences we use

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A)= NGS or Mass spectrometry b)= UCSC C)= NCBI D)=
NONE OF THESE

139= Fasta developed in

a)= 1988 b)=1984 c)=1989 d)=1982

140=Structure of FASTA is obtained from.....

a)=X-ray crystallography b)= microscopy & nuclear Spectroscopy

c)= both a & b d)= none of these

141=The famous data store is called

a)= uniprot & swiss prot b)= blast c)= fasta
d)= none of these

142=----- contains human curated protein information .

a)= Uniprot b)= Swiss prot c)= FASTA D)= BLAST

143=Over protein structures are reported and present in this database .

a)= 80,000 b)= 60,000 c)= 30,000 d)= 50,000

144=Protein sequence contain

a)= Mass spectrometry b)= Edman Degradation c)= online website
d)= both a and b

145=Sequence data can be used to obtain

a)= similarity of sequences b)= evolutionary history c)= predict the
function of molecules d)= All of these

146=In gene bank public database of nucleotide sequences for over Organisms.

a)= 200,000 c)= 300,000 c)= 400,000 d)= 100,000

147= phylogenetics has led to the creation of relationship trees between various species of

a)= Bacteria b)= Archaea c)= eukaryote d)= All

148= DNA gets modified by

a)= mutation & substitution b)= insetion c~)= deletion d)= all of
these

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149=what is root node? No option

Root node is the ancestor of all other nodes! The direction of evolution is from ancestor to the terminal nodes.

150= rooted and unrooted trees can be used to showrelationship between sequence.

a)=phylogenetic b)= genetic c)= genomic d)= none of these

16= least squares distance method.....

a)= D(HUMAN , CHIMP)=0.3 B)= D(HUMAN GORILLA)=0.4

C)= D(CHIMP, GORILLA)=0.5 D= ALL OF THESE

1.UPGMA stands for:

a.unweighted pair_group method using arithmetic averages

b.undifferentiated pair—group method arithmetic averages

c.unweighted pair—general method arithmetic averages

d.unidirectional pair—general method arithmetic averages

2.the distance matrix is obtained by:

a.multiple sequence alignment b.single sequence alignment

c.pair wise sequence alignment d.all

3.UPGMA is used to calculate:

a.maximum linkage b.least square distance

c.maximum likelihood d.maximum parsimony

4. _____ 1

$$d_{XY} = \frac{1}{N} \sum_{i \in X} \sum_{j \in Y} d_{ij}$$

This formula is to find:

a.distance of clusters b.distance between trees

c.distance between sequences d.distance between cluster and sequence

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5.in the above formula I have shown you the N_x is:

- a.number of clusters b.number of trees
c.number of sequences d.none

6.component of UPGMA are:

- a.2 b.3 c.4 d.5

_____ 1

7. $d_{XY} = \frac{1}{N} \sum_{i \in X, j \in Y} d_{ij}$ In

d_{zw} the w is:

- a.cluster b.new sequence c.mixed cluster d.tree

8.in the second component of UPGMA we add:

- a.two clusters b.cluster+sequence
c.two sequences d.none of these

10.cluster+sequence will make:

- a.sequence b.cluster
c.may be a cluster or sequence d.phylogenetic tree

1= Application of UPGMA resulted in formation of Sub trees

- a)= 2 b)= 4 c)= 6 d)=8

2=Un-weighted pair group method using is a clustering method to construct phylogenetic trees.

- a)=Average b)= Airthmetic average c)= frequency d)= ALL

3=In earlier days, RNA was only considered as a passive intermediary between and

- a)= DNA AND RNA B)= RNA and protein c)= DNA and protein d)=

None of these

5=More so, that they perform irtical functions in ,, and ,, expression

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a)= Dna and gene

b)= RNA and GENE

C)= Gene and protein d)=

Protein and DNA

6=The two hydroxyl groups make RNA less stable than DNA bcoz it's more prone to

A)= Hybridization

b)= Hydrolysis

c)= none of these

7=..... has a short life span and is more prone to degradation .

A)= DNA

B)= RNA

C)= BOTH A & B

D)= GENE

8=Diverse form of RNA ...

a)= RNA molecules are the same

b)= RNAs differ in nucleotide sequence

c)= RNA have multiple role in cells

d)= All of these

10=Only of RNA content in a cell

a)= 5-80%

B)= 5-10%

C)= 5-64%

D)= 5-30%

11=..... carry genetic information from DNA to ribosomes where proteins are being assembled.

a)= m RNA

B)= r RNA

C)= t RNA

D)= NONE OF THESE

12=THE 5' can help identify mRNAs at the ,,,,,,

a)= Chromosome

b)= Ribosomes

c)= DNA

D)=RNA

13=The 3' end of mRNA has a polyA tail around adenylate residues which help shield against 3' exonucleases.

a)= 30-200

b)=30-400

c)=20-200

d)=20-300

14=THE 5' -3' regions are both cushioned with.....regions

a)= RTRs

b)= UTRs

c)= DSAs

d) all

15=RNAs can adopt complexstructures.

a)= 3D

B)= 2D

C)=4D

D)=6D

17=Nucleotide can make Bonds themselves

a)= carbon

b)= oxygen

c)= hydrogen

d)= All

20=..... Is the energy of an RNA molecule available for reaction. RNA have low energy .

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a)= kinetic energy

b)= potential energy

c)= gibbs free energy d)=

ALL

1. If nucleotides could not make pair together there will be formation of.....

- a) Helix b) disjunction c) loops d) pseudoknots 2.

Loop of hair pin must be at least bases long

- a) 3 b) 4 c) 20 d) 8

3. include two or more double stranded regions converging to form a closed structure.

- a) Bulge b) loop c) junction d) a+b

4. When unpaired bases formed H bonds with other unpaired bases which structure originates

- a) Primary b) secondary c) tertiary d) all

5. When RNA molecule fold upto itself within tertiary structure it may result formation of...

- a) Double stranded RNA b) stable RNA c) pseudoknots d) loops

6. helps us to detect pseudoknots,

- a) Linear plot b) dot plot c) circular plot d) pseudo plot

7. In circular plot are represent pseudoknots,

- a) Circular arc b) vertical arc c) perpendicular arc d) intersecting arc

8. Which is quite expensive procedure to determine the structure of RNA?

- a) NMR b) RNA bricks c) x-ray crystallography d) a+b

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9. Commonly RNA has extremely structure.

- a) Stable b) strong c) sturdy **d) fragile**

10. formation of H bond b/w nucleotides result in release of energy,

- a) -7. K cal/mol b) -17.0 K cal/mol **c) -12.0 K cal/mol** d) -5.0 K cal/mol

14. which work according to principal of diffraction?

- a) atomic force microscopy **b) x-ray crystallography** c) NMR d) A+B

1 : Several algorithms exist for predictingstructure?

- A) One **B) Two** C) Three D) Four

2 :implements an ungraded version of Zuker,s Algorithms?

- A) MFOLD** B) MOFLD C) MFODL D) MOFDL

3: MDOLDset of possible structure? NO option?

Ans) Outputs

4: Order.....complexity for sequence of length N?

- A) N^2 **B) N^3** C) N^4 D) N^5

5: MFOLD used to predict structure of sequences less than?

- A) 8000 nuclei B) 7000 nucleotides **C) 8000 nucleotides** D) 8000 nucleolus

6: MFOLD helps fold an.....Nucleotides sequences?

- A) DNA **B) RNA** C) mRNA D) SRNA

7: RNA nucleotides fold to formstructure?

- A) Two** B) Three C) Four D) Five

8: which occur in wide verity of.....?

- A) CUCUGG , RNA B) CUCGG , DNA C) CUUCGG ,DNA **D) CUUCGG , RNA**

9: CUUCGG mostly form a stable.....loop?

- A) D **B) hairpin** C) G D) T

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10: RNA bricks is a database of RNAstructure motifs?

- A) 4D B) 3D C) 2D D) 6D

11: DNA comprises oftypes of nucleotides bases?

- A) Two B) Three C) Four D) Five

12: Which is correct about translation?

- A) DNA < RNA B) RNA < Protein C) Protein < Modification D) DNA < Protein 13:

Which protein chains fold to take 3D structure?

- A) H1 B) H2 C) H3 D) All of these

14: Nucleotides codons comprises of.....code for protein?

- A) A , C & G , T B) A , U & G , C C) A , C & G , C D) A , U & G , T

15: How many start and stop codon? No option?

- A) 1 start codon and 3 stop codons

16: ORF is stand for.....? No option?

- A) Open Reading Frame

17: How many ORFs exist for each DNA sequences?

- A) Four B) Five C) Six D) Seven

18: The valid ORFs will have the longest.....read?

- A) RNA B) DNA C) SRNA D) a and b

19: Which stop codon will mark the end of the protein sequences?

- A) First B) Second C) Third D) Fourth

20: PhNCS attaches to the free amino group atterminal residue?

- A) B B) N C) A D) a and b

21: How many amino acid is removed as a PhNCS?

- A) One B) Two C) Three D) Four

22: Restricted to chain ofresidues?

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A) 40

B) 50

C) 60

D) 70

23: Protein can be charged with

A) Proton

B) Electron

C) a and b

D) Neutron

24: Write formula of Lorentz force law? No option?

A) $F = Q (E + v \times B)$

25: Each protein is deflected in proportion to its.....?

A) Molecules

B) Molecular weight

C) a and b

D) none

26: Give example of protein sequences? No option?

A) Uniprot , Swissprot

27: MS- based proteomics helps sequencesprotein?

A) Larger

B) Smaller

C) Bigger

D) a and c

29: How many peptides is selected at a time for sequencing?

A) One

B) Two

C) Three

D) Four

1 : Which enzyme are used to cleavage proteins into peptides?

A) Trypsin

B) Pepsin

C) Rennin

D) Ligase

2: Number ofdepend on number of sites at which enzyme are cut?

A) Protein

B) Peptides

C) Amino acid

D) Sequences

3: Each peptide is measured for its mass.....?

A) MS4

B) MS3

C) MS2

D) MS1

4: Each peptide is searched insequences?

A) Amino acid

B) MS3

C) Protein

D) a and b

5: Bottom up proteomics measure theof peptides?

A) Mass

B) Length

C) Sequences

D) protein

6: BUP stand for.....?No Option?

A) Bottom up proteomics

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8: Peptide mass fingerprint followed byprotein peptide analysis?

- A) Single B) Double C) Triple D) a and b

9: Protein carry typically Post.....modification?

- A) Transcriptional B) Translational C) Transformation D) a and b 10:

After.....,one protein is selected at a time?

- A) MS1 B) MS2 C) MS3 D) MS4

11: Peptides are measured for their mass.....?

- A) MS4 B) MS3 C) MS2 D) MS1

12: Which measure the mass of intact protein?

- A) BUP B) TDP C) a and b D) peptides

13:Mass spectrometer are used to measure the molecular weight of.....?

- A) Protein B) Peptides C) a and b D) None

14: Scoring Schemes are required to.....represent the quality of result?

- A) Qualitatively B) Quantitatively C) Protein sequences D) a and b 15:

Ionization result in an decrease or increase of the.....mass?

- A) Protein B) Peptide C) a and b D) None

16: How many Salient ionization technique include....ionization?

- A) One B) Two C) Three D) Four

17: MALDI & ESI stand for.....?

- A) Matrix Assisted Laser Desorption Ionization & Electro Spray ionization

18: MALDI typically adds ato the protein or peptides?

- A) Electron B) Proton C) Neutron D) a and b

19: The molecular weight of the molecule increase by.....?

- A) One B) Two C) Three D) Number of proton added

20: MS reports the molecule at?

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A) Mass + 1

B) Mass + 2

C) Mass + 3

D) Mass + 4

21: In which difficult to find molecules with +1 charge?

A) MALDI

B) ESI

C) MS

D) MS1

22: which data from MALDI ionization is easier to handle as the product ions?

A) ESI

B) MS

C) MS1

D) MS3

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