

BIF 401 MCQ FOR MID TERM

Objective

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Welcome To vuways Study Help

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 publicly available, you can process this information after downloading it.
 - a. Proteome
 - b. Evolutionary studies

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- 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 11982 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

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- 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. Proteins

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.

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- 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. Transcriptomics
b. Translation
c. Transcription
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
- a. RNA 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. Hydrolysis
c. Condensation
d. Oxidation

Polymerization

Hydrogenation d.

Condensation

43. The amino acids are joined with each other with peptide bonds and then fold with each other 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

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52. In Uniprot home page there is a box named _____
- Blast
 - Prot
 - Swiss prot
 - Swiss blast
53. _____ include complete matching in terms of residues and their order
- Inexact matching
 - Exact matching
 - Both a and b
 - Optimum matching
54. _____ includes partial matching in terms of residues and order with room for variations in both.
- Inexact matching
 - Exact matching
 - Both a and b
 - Optimum matching
55. In prosite pattern _____ separate the elements of the pattern
- Latter

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

- 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

- 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

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. cNon-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

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. Penalties
- 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