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BIF401 - Bioinformatics I.

1. What Are Uses Of Mass Spectrometry? 2

Mass spectrometry (MS) is an analytical technique that ionizes chemical species and sorts the ions based on their mass-to-charge ratio. In simpler terms, a mass spectrum measures the masses within a sample. Mass spectrometry is used in many different fields and is applied to pure samples as well as complex mixtures.

2. Need For Chou Fasman Algorithms? 2

The Chou-Fasman algorithm is simple in principle.The conformational parameters for each amino acid were calculated by considering the relative frequency of a given amino acid within a protein, its occurrence in a given type of secondary structure, and the fraction of residues occurring in that type of structure.

3. Three individual scores Integrative Scoring Scheme? 2

Three individual scores can be obtained including

1. MW Match Score
2. PST Match Score
3. In vitro & In silico Match Score.

4. Write benefits of phylogenetic studies marks • 03

5. Advantage of Folded Protein over Denatured Protein. 5

Difference Between Folding Protein and Denature Protein, / What Factors Are Used For Folding Proceeds?

Protein folding is the physical process by which a protein chain acquires its native 3-dimensional structure, a conformation that is usually biologically functional, in an expeditious and reproducible manner.

Denaturation of proteins involves the disruption and possible destruction of both the secondary and tertiary structures. Since denaturation reactions are not strong enough to break the peptide bonds, the primary structure (sequence of amino acids) remains the same after a denaturation process.

Protein folding is a process by which a polypeptide chain folds to become a biologically active protein in its native 3D structure. Protein structure is crucial to its function. Folded proteins are held together by various molecular interactions. ... The amino acid sequence of a protein determines its 3D structure.

The forces involved in protein folding include: • Electrostatic interactions, • van der Waals interactions, • Hydrogen bonds, • Hydrophobic interactions

6. Score in Silico fragment scoring?.5

- Count the matches between in silico and in vitro peaks.
- Give an equivalent score to the candidate protein.
- Weigh each of the aforementioned match by the mass error.
- Accumulate the score

7. How Loops Are Found After The Finding Of Alpha And Beta Sheets?5

Alpha helices and beta strands are connected by these turns and loops. ... Loops and turns generally lie on the surfaces of proteins so they often participate in interactions between proteins and other molecules. In a loop, there are no regular structures as can be found in helices or beta strands.

8. Tandem mass spectrometry

Tandem mass spectrometry (MS-MS) is a related technology in which compounds are separated by molecular weight by one **mass spectrometer**, fragmented as they exit, and identified on the basis of their fragments by a second **mass spectrometer**

9. Advantage and disadvantage of Ab initio method?

Advantages:

Ab Initio methods can fold any target sequence using only physical atomic properties. Predictions are mostly accurate and correctly describe the natural folding process.

Disadvantages:

Ab initio methods are the very difficult to design (energy function). These methods are slow due to the huge possibilities.

10. Types of secondary structures of RNA:

1. Single stranded:

3'end may fold on to the 5' end.

2. Helices:

Double stranded RNA helix of stacked base pairs

3. Hairpin loop:

The loop of the hairpin must at least four bases long to avoid steric hindrance with base-pairing in the stem part of the structure

4. Bulge Loops:

Bulges, are formed when a double-stranded region cannot form base pairs perfectly.

5. Interior loop:

Interior loops are formed by an asymmetric number of unpaired bases on each side of the loop.

6. Junctions or intersections:

Junctions include two or more double-stranded regions converging to form a closed structure. The unpaired bases appear as a bulge

11. How homology modeling is used for knowing the sequence of unknown protein sequence?

If another protein which has a similar sequence also has its structure known, the structure of an unknown protein can be predicted based on that similar protein. So, it is then possible to identify unknown protein structures by just examining the homologous protein sequences. Good sequence alignment and identity ensures that homology modelling will give accurate results. Thus, Homology modeling is used to predict structures of proteins having high sequence similarity with other proteins with known structures:

12. Role of Amino Acid?

Protein plays a crucial role in almost all biological processes and amino acids are the building blocks of it. A large proportion of our cells, muscles and tissue is made up of amino acids, meaning they carry out many important bodily functions, such as giving cells their structure.

13. Write Down The Following Terms Of PDB (3)

Title (Title of the structure)
Source (Identify which organism structure from)
COMPND (Brief detail of the structure)
REVEDAT (The data of last revision

14. What Happend When Ph Is Less Than The Pk Value?

If the pH is higher than the pKa, then the compound will be deprotonated. A further consideration is the charge on the compound. Acids are neutral when protonated and negatively charged (ionized) when deprotonated. Bases are neutral when deprotonated and positively charged (ionized) when protonated.

15. Chou Fasman Algorithm?

The Chou–Fasman method is an empirical technique for the prediction of secondary structures in proteins, originally developed in the 1970s by Peter Y. Chou and Gerald D. Fasman.

16. Function of Tandem MS?

Tandem MS helps in measurement of mass to the fragments as well. This process provides another step in further scoring and ranking and Protein identification thus becomes easier.

17. Factors That Participate In Folding Protein?

The external factors involved in protein denaturation or disruption of the native state include temperature, external fields (electric, magnetic), molecular crowding, and even the limitation of space, which can have a big influence on the folding of proteins

18. Need For Chou Fasman Algorithms?

The Chou-Fasman algorithm is simple in principle.The conformational parameters for each amino acid were calculated by considering the relative frequency of a given amino acid within a protein, its occurrence in a given type of secondary structure, and the fraction of residues occurring in that type of structure.

19. Optimal Energy Function In Protein?

Results: For a single protein sequence, the probability of success (i.e. the probability that the folded state is the lowest energy state) is derived. We then maximize the average probability of success for a set of proteins to obtain the optimal potential energy function

20. Silico Fragments Comparison?

Matching experimental fragments with in silico fragments is the final resort in protein search & identification

21. Chou – Fasman method?

It is a technique for the prediction of secondary structures in proteins i.e. Alpha Helices, Beta Sheets and Turns is Chou – Fasman technique. The method is based on analyses of the relative frequencies of each amino acid in alpha helices, beta sheets, and turns based on known protein structures solved with X-ray crystallography. From these frequencies a set of probability parameters (in our handouts, it is propensity table) were derived

For the appearance of each amino acid in each secondary structure type. To predict the probability that a given sequence of amino acids would form a helix, a beta strand, or a turn in a protein.

Chou-fasman algorithm (alpha helix):

For Alpha Helices, 4 contiguous amino acids are required.

 Their Alpha-Helix propensity should be more than 1.0

 Once this propensity falls below 1.0, Alpha-Helix stops.

22. Improvements Of Chou Fasman Algorithm?

The Chou-Fasman algorithm, one of the earliest methods, has been successfully applied to the prediction. ... We improved Chou-Fasman method in three aspects. (a) Replace the nucleation regions with extreme values of coefficients calculated by the continuous wavelet transform.

23. What is hydrophobicity of amino acid?

In chemistry, hydrophobicity is the physical property of a molecule that is seemingly repelled from a mass of water. In contrast, hydrophiles are attracted to water. Hydrophobic molecules tend to be nonpolar and, thus, prefer other neutral molecules and nonpolar solvents.

24. how propensity table can helps us?

25. Seven Steps present in flow chart of homology modeling? 10

1. Template recognition and initial alignment.
2. Alignment correction.
3. Backbone generation.
4. Loop modeling.
5. Side-chain modeling.
6. Model optimization.
7. Model validation

26. Role of Amino Acid?

Protein plays a crucial role in almost all biological processes and amino acids are the building blocks of it. A large proportion of our cells, muscles and tissue is made up of amino acids, meaning they carry out many important bodily functions, such as giving cells their structure.

27. Role of Global Protein?

Global protein function prediction from protein-protein interaction networks. ... The availability of entire genome sequences and of high-throughput capabilities to determine gene coexpression patterns has shifted the research focus from the study of single proteins or small complexes to that of the entire proteome.

28. Acidic and Basic Amino Acid?

There are three amino acids that have basic side chains at neutral pH. These are arginine (Arg), lysine (Lys), and histidine (His). Their side chains contain nitrogen and resemble ammonia, which is a base. Their pKa's are high enough that they tend to bind protons, gaining a positive charge in the process.

29. Points of Bottom up Proteomic?

The major alternative workflow used in high-throughput proteomics is called top-down proteomics and does not use proteolytic digestion. Essentially, bottom-up proteomics is a means of determining the protein make- up of a given sample of cells, tissues, etc. (Internet)

30. Varies RNA Secondary Structure?

Types of RNA Secondary Structures - I

• RNA Complementary bases in primary structure bond together to fold RNA into a secondary structure

Types of RNA Secondary Structures – II

• RNA 1’ sequence (5’ – 3’) can fold onto itself to make 2’ structures.

• Two previous examples of 2’ structures include Helix and Hairpin structures.

Types of RNA Secondary Structures - III

• RNA can be fold to form helices, bulge loops, and interior loops. An other 2’ RNA structure is the Junction or Intersection.

31. Objective Base Method and Clustering Approach?

Clustering Approach UPGMA WPGMA Neighbor Joining Single Linkage Complete Linkage Objective based Methods Least Square Distances Maximum Likelihood Maximum Parsimony

32. Shot Gun and Peptide Mass Finger Printing?

Shotgun proteomics digests the entire protein mix 1st followed by peptide analysis & protein database search Peptide mass fingerprinting involves protein separation followed by a single protein’s peptide analysis.

33. substitution and Indels?

Substitution at adjacent nucleotides (primarily substitutions at two adjacent nucleotides, but substitutions at three adjacent nucleotides have been observed.

Indels, being either insertions, or deletions, can be used as genetic markers in natural populations, especially in phylogenetic studies.

34. Prediction of Protein Structure?

Protein structure prediction is the inference of the three-dimensional structure of a protein from its amino acid sequence—that is, the prediction of its folding and its secondary and tertiary structure from its primary structure.

35. How Can We Predict Amino Acid In Alpha Helix And Beta Sheets?

Proteins that convert from alpha helix to beta sheet: implications for folding and disease. The sequence of a protein normally determines which amino acid residues will form alpha helices, and which one beta sheets, to an extent that allows secondary structure prediction to be made with a reasonable reliability..

36. Rooted Un Rooted Tree?

Rooted Tree:

Each node with descendants represents the inferred most recent common ancestor of the descendants.

- The edge lengths in some trees may be interpreted as time estimates.
- Rooted trees can show temporal evolutionary direction.
- Expensive.

Unrooted:

- Only the relatedness of the leaf nodes.
- Do not require the ancestral root to be known or inferred.
- Less expensive.

Uses: In bioinformatics, such as

 Rooted and unrooted trees can be used to show phylogenetic relationships between sequences..

37. Molecular biology?

It is the branch of biology that deals with the structure and function of the macromolecules (e.g. proteins and nucleic acids) essential to life. Molecular biology is the study of biology at a molecular level.

38. Protein Fragmentation techniques?

- Electron Capture Dissociation (ECD).
- Electron Transfer Dissociation (ETD).
- Collision Induced Dissociated (CID).

39. Protein structure prediction?

There are three different strategies for structure prediction

1. Homology Modelling
2. Threading/Fold Recognition
3. Ab Initio Modelling

MCQS

1) Fasta Was Develop In(**Ans1988)**
2) In Corey Paulin Modal Of The Protein Each Atom Is Represented By(**Solid Sphere)**
3) How Many Storages Use For Structural Modling (**3)**
4) Modeler Software Use For Homology Modling Which Use(Phython File Format,Not Confrm)
5) Mass Of The Based Proteomic Begin With Measure Of(**Intact Protein Amino Acid)**
6) Protein Sequence Obtained From(**Uni Port**)
7) During The Formation Of The 5 Nucleotide Hydrogen Bond Energy Release(-**12kcal/Mol**)
8) Which Method Is Not Use For Making Polygenatic???**Msa**
9) Rna Dont Have Structer???**Quatnaryy**
10) Large Numbr Of Sequence Availble??**Publically**
11) Coding Region Of Dna Is???**Exon**
12) Blast Use For???**Unknown And Known Protein**
13) Expasy Develop By???**Sib**
14) Variation In Sequence Develop By??? **Insertion,Deletion And Substituin**
15) Bond Form Between C And N Terminas??? **Hydrogen Bond**
16) X.Y.Z Position Of Protein Are Available By??? **Pdb**
17) Technique Use To Measure The Mass Of Protein??? **Mass Spactrometry**
18) Large Amino Acid??? **Tryptophan**
19) Positive Charge Amino Acid??? **Lysine And Arginine**
20) Mrna Has??? **Single Strand**
21) C.Alpha Atom Are Traced To Recreat??? **3d Structer Of Protein**
22) Bond Form Between Two Atom??? **Energy Release**
23) Provide Clue Of Precurser Protein Peptide Sequence?**?Pst**
24) Amino Acid Requird For Betasheet??? **3-5**
25) .....Are Formed By Bonding Betweenci And Ni+4n Protein Backbone??? **Alpha Halix**
26) Blasta Stand For??? **Basic Local Alignment Search Tool**
27) Amino Acid Have Uniwe Trait Which Can Help In??? **Protein Folding**
28) Align Comparison Betweendna/Dna Anddna/Protein??? **Fasta.**
29) Ratio Use To Calculate Mass Of Protein??? **M/Q.**
30) Treading Not Requied For??? **Structer Of Entire Backbone.**
31) Needle Man Wounch Man Or Smith Water Man Algorithm Use For??? **Local And Global Alignmnt.**
32) Dianamic Programing Recombinant Nucleotide By??? **Traseback.**
33) Insertion And Deletion Cause??? **Gap.**
34) Information Required For Follding Of Amino Acid Is Present In??? **Amino Acid.**
35) Mgf Use For??? **Proteomic.**
36) Nj Algorith Use To Pridict The??? **2nd Structer Of Rna..**
37) Genomics, evolutionary studies and system biology are application of **bioinformatics**

38) Exact matching require which type of nucleotide-**same number of nucleotide**

39) Accurate solution of protein structure is one of the ___ **toughest problems**

40)Tract back is overlap matches can start from any position in scoring matrix

41) The matrix has ……scores. **Positive and negative**

42)MASCOT___can search people mass finger printing and shotgun proteomics data set

43) Spectrometer measures the protein by _____ **Mass/charge**

44) Simulation of the folding process depends _____ **Energy function**

45) Information about **DNA/RNA i**s available on gene bank

46)TDP is used to measure the molecules weight of intact proteins.

47) Coordinates of **alpha carbon** in the protein backbone can be used for structural visualization.

48)in structure visualization c-alpha atoms are traced to recreate a _____**3D protein structure**

49)in UPGMA distance is calculated btw _____ **two clusters and between two trees**

50)pk value of Aspartic acid **3.9**

51) Largest amino acid …… **Tryptophan**

52)2nd STRUCTURE of proteins can be obtained by using_____ **Chou Fasman algorithm**

53)NJ Algorithm strategy is used to predict __ **RNA 2` structure**

54) The loop of hair pin must be at least ___ in length **2 aminoacids**

55) Fold recognition is also called …….**threading**

56) Ab initio method in contrast ,base their prediction on **low energy model**.

57) Bioinformatics require…….smart mind, and connected to internet, **both**,

58) Sequence alignment tool is…….**PROSIGHT and MASCOT**

59)MS1,MS2 provide us data identifying unknown…….**Proteins sequence**.

60)MGF files develop as an open standard for……. **proteomics data**.

61)PDB coordinates alpha carbon in protein back bone can be used for comparison .

62) Alpha carbon atom can be obtained from…**…PDB**

63)in formation of 2nd structure of protein C & N can make……**Hydrogen bonds**

64)information for protein folding is into its native structure is in…….. **protein's amino acid sequence**!

65) Energy **released** during bond formation.

66)hydrogen bonding occur in …**secondary** ..Protein structure

67) Bond between C and H in alpha helices____**Hydrogen bonding**

68) Amino acid having 3 codons_____ **isoleucine**

69)MALDI typically adds a …… to protein or peptide. **Proton**

70)low quality match gets_____**lower score**

71)____ are sequences of amino acids produced during MS2. **PST** (**peptide sequence tags**)

72) MS2 data can be used to extract…… **peptide sequence tags**.

73) The alpha helices propensity should be more than____(**1.0)**

74) How many types are of protein sequencing techniques__ **(2)**

75) Blast can find sequences of _____**nucleotides amino acid**

76) If a protein sequence of 26 amino acids is fragmented at 11 amino acid **C11, Z25**

77) To find out unknown sequence of nucleotide we use . **NGS or Mass spectrometry**

78) How many types of peptide May be injected in mass spectrometry chamber.. . **three hundred thousand to four hundred thousand**

79).**MASCOT**.can search peptide mass finger printing and shotgun proteomics dataset.

80) Stabilizing and destabilizing energy give us **…….. quality of 2nd structure** .

81) The Fasman algorithm is based on **statistical occurrence** of Amino Acids in known structures.

82)DP recombinant the nucleotide recombination through process of ..... **Traceback**

83) MALDI.....add proton to a protein and a peptide..

84) Positively charged amino acids are..... **3**

85) Aromatic amino acid include ..... . **phenylalanine, tyrosine tryptophan**

86) Homology modelling fail to predict …… **quality structure**

87) How many forces are involved in protein folding.

88) Pairwise alignments tells the similarity between sequence**... by maximizing the matches.**

89) Dot plots employ dot matrix with two sequence plotted represents.....**pairwise alignment and comparison**.

90) Differentiate b/w DNA and RNA sequence…….. **RNA has more variety of sequence**

91) Cell molecule are produced after transformation of …… **DNA to protein**

92) Dot plot cannot deal with……. **Insertion, deletion and gaps.**

93) Exons are may be more …… **conserved**.

94) In dynamic algorithm we can do comparison …… of more sequence. **Three**

95) Mass/Charge ratio helps calculate the mass of the …. **Protein**

96) In scale tree branches lengths are equal to the magnitude of change in the …….. **nodes**.

97) How many types of peptides mix in MS chamber…….. **300,000 – 400,000**

98)mRNA is a …… structure. **Planer**

99) When unpaired bases of 2´ stricture join to form…….. **3´ structure**

100) N Jackobson use to pridict **2´structure.**

101) Aromatic amino acid ……. **Tyrosine**

102) Positive charge amino acids……. **Lysine, arginine, histidin**

103) MS begins with the measure of …….. **intact protein**

104) Amount of amino acids in alpha helix…….(**4**)

105) Intact mass of protein can be found by….. **MS1**

106) MSA can be done by……. **CLUSTAL**

107) Which is used as sequence alignment tool……. **PROSIT**

108) MS1 and MS2 help to identify …… (**PST**)

109) MGF is used for …….. **proteomics**

110) X,Y,Z positions of alpha carbon available online on …… (**PDB**)

111) Method to determine RNA structure …….. **NMR, X-Ray crystallography**

112) CLUSTLA runs……. **Slow accurate/ fast appropriate**

113) Which give info about precursor protein……. **PSTS**

114) Raw data files format can be converted to ……. **Open format**

115) Which of the following is cartoonic figure…….. **Ribbon diagram**

116) In CATH protein recognize according to their…….. **structural similarity**

117) Method for obtaining 1´ structure**…… (Edman Degradation Tandem Mass Spectrometry).**

1. FASTA achieves alignment by using **short lengths of exact matches.**
2. Dot plots cannot capture **insertions, deletions and gap indications**
3. Dot plots employ dot matrix with two sequences plotted on **top and left of the matrix**
4. In multiple sequencing, we have **both**
5. CLUSTALW can run in two modes **slow/accurate, fast/appropriate.**
6. The correct order of progressive alignment for multiple sequencing alignment is **Pair wise alignment, Guide tree, branching order in tree.**
7. Blast can find sequencing from protein or nucleotide database **it can find known and unknown sequencing.**
8. : **Next generation sequencing** is used to known about unknown sequences of nucleotide.
9. In multiple sequence algorithm **doing so many progressive alignment can be slow.**
10. : Structural information of a molecule obtained by **X ray crystallography & Nuclear magnetic resonance.**
11. Before starting to mach nucleotide or amino acid are need to find the **Location of conserved residues.**
12. Bioinformatics is an interdisciplinary relative new development of **biology, mathematics, computer science, chemistry and physics.**
13. Fasta online software Can also perform genome and proteome similarity search .**true**
14. From Fasta we can obtain the information **on the parent organism, function and evolution history.**
15. name any two frequently used scoring matrix **Blosum and pam**.
16. Amino acids are chained together by **peptide bonds**
17. To find out the unknown sequence of nucleotide and protein we use **blast.**
18. GenBank and Uniprot, have **A large number of sequences are available in publically .**
19. Protein databank is a **data base**
20. In dynamic programming we can do multiple sequence alignment upto **21 sequence** .
21. How many types of secondary structure can be formed possible of RNA? **5.**

22. RNA structures have the **lowest (or close)** quantity of free energy.

23. RNA can play role due to its structure . **all of above.**
24. Rna contains **ribose** sugar?
25. Thymine is replaced by **uracil** in rna.

26. RNA molecules readily degrade due to their **short** shelf life .

27. Each Nucleotide in rna has **covalently bonded** to the backbone .

28. **Gibbs Free Energy"** is the free energy of an RNA molecule available for reaction .
29. The structure of rna sampled can be measured by.**Atomic Force Microscopy**
30. The 3'-end of **mRNA** has a poly A tail
31. The role of **mRNA** Carry genetic information from DNA to Ribosomes where proteins are being assembled .
32. Messenger rna is only **5-10%** of rna content in the cell.
33.

FOR MID TERM PREPARATION

1: Gaps are produced by insertion or deletion.

2: Example of energy base Zuker algorithm.

3: Two forms of DNA rending sequence.

4: Translation involves coding of protein by RNA at ribosome.

5: some medicine have side effect on certain patient Frontiers in personalized medicine.

6: By comparing sequence we can get similarity, specific difference, relationship, evolutionary insight.

7: Non clustering method include Maximum parsimony.

8: Destabilizing energy of a nucleotide has (+) value.

9: Comparison of protein sequence can be done with…Uniprot

10: Function is a property of the RNA structure,which is formed from the RNA sequences.

11: Structural information of a molecule obtained by X ray crystallography & Nuclear magnetic resonance.

12: Protein have 20 amino acid.

13: If sequence are 9 then according formula it will be 9^2.

14: Fast is available online.

15 Fasta was developed in 1988.

16: Bioinformatics is the inter disciplinary relative new developing field.

17: Genbank can be reached by…online website or www.ncbi.nim.nih.gov/genebank.

18: Before starting to mach nucleotide or amino acid are need to find the Location of conserved residues.

19: some medicine have side effect on certain patient Frontiers in personalized medicine.

20: Identity is the number of nucleotide or amino acid which match exactly between two biological sequence.

21: Alignment are represented by diagonals in dot matrix.

22: Needleman wunsch man algorithm we use for…… Global alignment.

23: Exons in protein tend to be more conserved then the intron.

24: In MSA the distance between 2 sequences in equal to NO of identical residue/number of aligned residue.

25: All the changes which accrued in our cell …….. metabolism

26: The loop of the hairpin must be least 4 bases lo

28: NJ algorithm is used to produc ……. Optimal RNA 2´ sturucture.

29: energy base algorithm type is Zuker algorithm.

30: Types of RNA…present in organism. (5)

31: The online search is for DNA and RNA is…….. genebank

32: Rooted tree is computational expensive.

33: In multiple sequence algorithm doing so many progressive alignment can be slow.

34: DNA dictates the production of cell protein and carbohydrate

35: protein have long sequences …in no?

36: In Exact partial matching of residue and order with room for variation in both.

37: DNA/RNA sequence is available on…. GENE BANK 38:

Martine algorithm predict for structure 2 RNA.

39: In extraction of ORF, 1st step is obtained the 3 codons.

40: Example of energy based algorithm Zukar algorithm.

41: Dynamic programming help us to……. reduce computational cost.

43: When unpaired bases in 2 region binds is result form Buldges.

44: which one of following is not objective based method of phylogenic … UPGMA

45: protein sequencing can be done by Swiss prot & UniProt.

46: Drugs can be better developed after understanding molecular basis of …… Disease

47: Online tools are available for homology modeling.

48: Insertion and deletion in alignment cause…… gaps.

49: Alligment of insertion and deletion can be performed by ……. dynamic programming

50: Exons in proteins tend to be more conserved than ……. intron.

51: Blast confined sequences from—— ID,name,spcies

52: ribosmes read RNA and collect amino acid from…… cell cytosol.

53: Simulation can predict diseases progression & outcomes.

54: For exact maching …….required. Traceback 55: trackback is

start from high score on couple nucleotide.

56: Motif protein chain fold to take . 3D structure

57: Next generation sequencing is used to known about unknown sequences of nucleotide.

58: RNA fold to form 2 structure.

59: MFOLD implement are ungraded version of Zuker.

60: Which has less computational cost …… Dynamic programming

61: In scoring matrics, we score with maximum 4 matrix.

62: We compare all length of nucleotides in …. Global alignment.

63: we compare smaller fragment Local alignment.

64: Destabilized RNA molecule have (+)value.

65: In Zukar algorithm, we need construct all possible combination.

66: We use Zukar algorithm to sum up energy to find lowest matrix.

67:Swiss prot.is a box in uniprot.

68: In comparing RNA structure, we used to select which having lowest energy.

69: Addition of nucleotide is done by ….. hydrogen bondi

71: Adman degradationis used for protein sequencing.

72: Why do we create all possible combination of diagonals in zukar algorithm with overall lowest energy is selected.

73: We can do repeated sequences alignment by slight modification in waterman model.

74: Length of hairpin loop is 4 bases.

75: ‘’T" Thrionine is an basic element....true

76: To align sequence what will be necessary firstly..... . to find conserved rigion

77: Sequence of biomolecules can be known by using ..... . uniprot or gene bank

78: Defination of Expasy: Expasy provide access to variety of online database and tools.

79: Structural information of a molecule can be obtained by X.ray crystallography , nuclear magnetic sequence.

80: Compare a protein query sequence against a nucleotide sequence database…..tBlastn

81: Protein formation of abnormal folding called Pseudoknots.

82: By using uniprot we can find sequence of…..(protein)

83: The 5´ end of molecule caped with 7 Methyl Guanosine Triphosphate.

84: DNA provide blue print for building.

85: DNA get modified by mutation, substitution, insertion, deletion.

86: UPGMA is used to calculate the distance of each cluster.

87: Global alignment used to determin overall conversation.

88: if the sequence is multiple there can be several possible alignment.

89: can we identify the post translational modifications by . Expacy

90: scoring scheme has an extremely crucial role in producing optical alignment.

91: why is there need to predict RNA structures to know about its function

92: DP recombines the nucleotide recombination through a process of Traceback.

93: .how many open reading frame exist for each DNA sequence.6ORFs

94: tblastn search translated nucleotide using...Protein query

95: Blast can find sequencing from protein or nucleotide database it can find known and unknown sequencing.

96: name any two frequently used scoring matrix Blosum and pam.

97: From Fasta we can obtain the information on the parent organism, function and evolution history.

98: The correct order of progressive alignment for multiple sequencing alignment is Pair wise alignment, Guide tree, branching order in tree.

99: CLUSTALW can run in two modes slow/accurate, fast/appropriate.

100: Gene bank and UniProt have Large number of sequencing publically.

101: In multiple sequencing, we have Global alignment.

102: Ubiquitin play important role recycling protein.

103: 6 form of DNA ending sequencing.

104: Non-clustering method such as maximum parsimony may be used for making trees.

105: If in needleman and Smith watermark algorithm along '0' place is in……relationship. 1st row and 1st column.

107: Faster active alignment by using local alignment and protein nucleotide. pairwise alignment

109: Expasy was develop by Swiss Bioinformatics Institute (SIB)

110: .In phylogenetics tree , ancestor are placed at Root/bottom/ancestor node trees.

111: .In UPQMA two sequence are .

112: .When unpaired bases in 2 region binds itself form Buldges.

113: Zukers algorithm is use to predict computational and destabilizing energy?

114: In Nussinov Jacob algorithm which turn is added to compare to score for diagonal position set diagonal and lower tri diagonal to zero.

115: Trackback begins from the position in Nussinov Jacobson score matrix. 4rth possition

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1. Genomics, evolutionary studies and system biology are application of **bioinformatics.**

1) Exact matching require which type of nucleotide-**same number of nucleotide.**

2) Accurate solution of protein structure is one of **the toughest problems** 3)

Tract back is overlap matches can start from any position in scoring matrix.

5) The matrix has .....scores. **Positive and negative.**

6) **MASCOT**….._can search people mass finger printing and shotgun proteomics data set 7) Spectrometer measures the protein by_____ **Mass/charge**

8) Simulation of the folding process depends_____**Energy function**

9) Information about **DNA/RNA** is available on gene bank

1.Domain are----

2RNA brick database-----

3.overcome homology modelling limitations by-----

4.homology predicts structure of protein-------

5.aromatic amino acids-----

- 6.DNA/RNA sequence----database

7.mRNA does not have------

- 8. BLAST can find sequences----------

- 9.MS based protemics begins measurement of ----------

10. alpha carbon atom can be obtain by---

11. Ab Initio methods can predict the sytructure on the bases of _____, charg volume mass.

12. The value of one angstrom _____.

13. _____- amino acid are required for alpha helices.

14. Blosum aberration_____.

15. The pka value of valin_____-.

16. The sequences that are similar we _____ modeling.

17. Exact matching require wchich type of nucleotide_____-

18. _____- cordinats the alpha carbon.

19. We start from ___**top right**__ in global alignment.

19. In structr visualization the sequence are visibal as cartoon_____.

20. pk value of Aspartic acid **3.9**

21. expasy was made by _____-.

22. Dot plots employ dot matrix with two sequence plotted represents.....**pairwise**

23. Which give info about precursor protein……. **PSTS**

24. mgf files format can be converted to …….

25. Molecular evolution can be caused by ….insertion deletion substitution.

26. Xyz position of position is available in _____

27. We can predict better by _____.

28. The amino acid join togather by _____bond.

29. One and 4 amino in alpha helix joind by ____bond.

30. Cn3d is an online tool used for_____.

31. Dot plots employ dot matrix with two sequences plotted on_____-

40. Fasta Was Develop In(**Ans1988)**

41. In Corey Paulin Modal Of The Protein Each Atom Is Represented By(**Solid Sphere**)
42. How Many Storages Use For Structural Modling **(3)**
43. Modeler Software Use For Homology Modling Which Use(Phython File Format,Not Confrm)
44. Mass Of The Based Proteomic Begin With Measure Of(**Intact Protein Amino Acid)**
45. Protein Sequence Obtained From(**Uni Port)**
46. During The Formation Of The 5 Nucleotide Hydrogen Bond Energy Release(-**12kcal/Mol)**
47. Which Method Is Not Use For Making
48. Rna Dont Have Structer???**Quatnaryy**
49. Large Numbr Of Sequence
50. Coding Region Of Dna
51. Blast Use For???**Unknown And Known Protein**
52. Expasy Develop

A. Bond Form Between C And N Terminas??? **Hydrogen Bond**
B. X.Y.Z Position Of Protein Are Available By??? **Pdb**
C. Technique Use To Measure The Mass Of Protein???**Mass Spactrometry**
D. Large Amino Acid??? **Tryptophan**
E. Positive Charge Amino Acid??? **Lysine And Arginine**
F. Mrna Has???**Single Strand**
G. C.Alpha Atom Are Traced To Recreat??? **3d Structer Of Protein**
Bond
H. Form Between Two Atom??? **Energy Release**
I. Provide Clue Of Precurser Protein Peptide Sequence??**Pst**
J. Amino Acid Requird For Betasheet??? **3-5**
K. Are Formed By Bonding Betweenci And Ni+4n Protein Backbone??? **Alpha Halix**
L. Blasta Stand For??? **Basic Local Alignment Search Tool**
Amino Acid
M. Have Uniwe Trait Which Can Help In??? **Protein Folding Align**
N. Comparison Betweendna/Dna Anddna/Protein??? **Fasta.**
O. Ratio Use To Calculate Mass Of Protein**??? M/Q**.
P. Treading Not Requied For??? **Structer Of Entire Backbone.**
Q. Needle Man Wounch Man Or Smith Water Man Algorithm Use For**??? Local And Global Alignmnt.**