

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.

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.nlm.nih.gov/genbank.
- 18: Before starting to match 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 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 is 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' structure.**
- 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: ribosomes read RNA and collect amino acid from..... cell cytosol.
- 53: Simulation can predict diseases progression & outcomes.
- 54: For exact machingrequired. Traceback 55:
- trackback is start from high score on couple nucleotide.
- 56: Motif protein chain fold to 3D structure take .
- 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 matrices, we with maximum 4 score 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 Zuker 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" Threonine is an basic element....true
- 76: To align sequence what will be necessary to find conserved firstly..... region
- 77: Sequence of biomolecules can be known by uniprot or gene bank using
- 78: Definition 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 capped 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 determine overall conversation.
- 88: if the sequence is multiple there can be several possible alignment.
- 89: can we identify the post translational Expasy modifications by .
- 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 developed by **Swiss Bioinformatics Institute (SIB)**

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

111: In UPQMA two sequence N_x &
are N_y

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

113: **Zukers algorithm** is used 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. **4th position**

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

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

Accurate solution of protein structure is one of **the toughest problems**

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

The matrix hasscores. **Positive and negative**.

MASCOT.....can search people mass finger printing and shotgun proteomics data set

7) Spectrometer measures the protein by_____ **Mass/charge**

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

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