MTH718



- Question 1: Define benchmarking and its method
- Question 2: What are Substitutions & Indel
- Question 3: What are the methods for clustring the phylogenetic trees.
- Question 4: What dose role of 5' cap and 3' role A poly tail
- Question 5: What is dot plots?
- Question 6: What is the bioinformatics promise to the society
- Question 7: What is the phenomineon of reduency of amino acid and what us the name of the amino acid which has three codos.
- Question 8: What is the role of 5' cap and poly A tail
- Question 9: Why unpaired nucleotides should make the structure of RNA destabilized
- Question 10: Write down Four Steps of FASTA.
- Question 11: Write formula for finding distance between two sequences and elaborate it.
- Question 12: Write the four objectives of the comparing sequensing?
- Question 13: Write URL of ncbi?
- Question 14: Challenges of ab initio modelling
- Question 15: Define pharmacology and pharmacogenomics and write three applications of pharmacogenomics
- Question 16: Differentiate between supervised and unsupervised machine learning
- Question 17: Explain gene expression omnibus
- Question 18: Explain RNA (definition, structure, secondary structure, prediction, types of RNA and their function etc)
- Question 19: How sanger method solved Edman degradation problemof protein identification
- Question 20: Longest common subsequence problem (only single strip) with example
- Question 21: needleman-wunsch algorithm complete
- Question 22: What is primary medical databaselist four databases.
- Question 23: Why Edman degradation strategy was failed in protein identification.
- Question 24: write and explain 2 approaches of target discovery
- Question 25: Differentiate between Artery, veins and capillaries.
- Question 26: Formation of seeds and fruits in plants.
- Question 27: Importance of Mitosis.
- Question 28: Labeling the organelles of cell. (Animal cell).
- Question 29: Name all the parts in Alimentary canal.