Papers year 2018  
1) online tools for homology modelling 2 marks  
2) short note on IUB 2 marks  
3) what James weber and gene myers proposed about read size 2 marks  
4) diff b/w FAST & NBRF with example 3 marks  
5) define homology, paralogy n orthology  
6) pharmacology, pharmacogenesis+3 application of pharmacogenesis 3 marks  
7) diff b/w satellite DNA, microsatellite,minisatellite 5 marks  
8 ) write n explain 2 approches of target discovery 5 marks  
9) lexicographic order of TAT,ATG,TGG,GGT,GTG,TGC 5 marks  
10) rna, structure, types of rna with function, processing of rna , sec. structure and prediction 10  
marks  
1)genequiz  
2)structure annotation and technique  
3)homology, orthology, paraology  
4)Pharmacology and pharmacogenomics  
5)needle wunsch algorithm(5)  
6)protein translation(5)  
7)Target discovery(5)  
8)RNA structure, types, prediction, processing (10)  
9) why bac is used(3)  
1:Write a short note on cystic fibrosis gene? 2mks  
2: Limitation of Ab-Initio method? 2  
3: Why we are interested to obtaining superstrings? 2  
4: Explain spiceosome? 3mks  
5: Explian the following function with example:  
DELETE(y, L)? 3  
6: Explain the digital resolution in recent time? 3  
7: List the stop and start codons and their functions? 5mrks  
8: Write two approaches of target discovery? 5  
9: Find the prefix function of pattern using KMP Algorithm? 5  
10: RNA,RNA Structure, its types with functions,Secondary structure and how we predict and  
RNA processing?  
note swiss port 2  
limitation of ab intio 2  
why sanger awaed noble prize 2  
challenge of limitation 3  
why bac used for sequence 3  
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fasta and BBRF formats and example 3  
fragment aessmbly algorithms 5  
edit distance? With examples  
RNA structure, types, processing,  
Start and stop codon  
KMP Matcher  
Two target approaches  
Method for four different groups sequencing  
Digital resolution  
Limitations of Ab initio  
Challenges of AB initio  
Total questions 45. in which 34 were mcqs rest of others were following questions.  
Q.1 explain RNA(definition,structure,secondary structure,prediction,types of RNA and their  
function etc). 10 marks.  
Q.2 needleman-wunsch algorithm complete (5 marks)  
Q.3 write and explain 2 approaches of target discovery (5 marks).  
Q.4 explain gene expression omnibus (5 marks)  
Q.5 challenges of ab initio modelling (3 marks)  
Q.6 why Edman degradation strategy was failed in protein identification.(3 marks)  
Q.7 longest common subsequence problem (only single strip) with example (3 marks)  
Q.8 define pharmacology and pharmacogenomics and write three applications of  
pharmacogenomics (3 marks)  
Q.9 what is primary medical database??? list four databases.(2 marks)  
Q.10 how sanger method solved Edman degradation problemof protein identification (2 marks)  
Q.11 differentiate b/w supervised and unsupervised machine learning (2 marks)  
Mcqs  
mcqs from ab initio modelling, RNA structure, chou fasman algorithm, DNAsequencing  
pharmacogenomics homolgy modelling, orthology paralogy,  
1Explain RNA in detail 10  
2 components of KMP algorithim 5  
3 explain 2 approaches of target discovery 5  
4 five tasks of genome analysis 5  
5 define folliwing term homology,paralogy,orthology 3  
6 define pharmacology and pharmacogenomics and its applications 3  
7 explain two computational prblms which are used identify proteins 3  
8 generalize algorithim for pattern finding in genome 3  
9 in human T cella how many fragments of tryptosin gene are present 2  
10 online tools for homology modeling 2  
11four aminoacids that are mutable 2  
Mcqs  
1Which notation of spectral similarity shared peaks counts  
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A p1 b p2 c m1 d m2  
2\_layer of neural network has classifiers  
3 methods for lead validation  
4 MS2 has \_ codons  
4 TIGR stand for what  
5 XML stand for what  
Current MCQ's year 20181.human genome project start in...? (1886)  
2.matif are found in ...?(DNA or proteins)  
3. Waardenburg's syndron is disorder in???(human)  
4. Systic fibrosis gene found in.. (childrens) ansd on chromosome no….. (2)  
5.NCBI stand for?? (National Center for Biotechnology Information)  
6.PIR stand for?(Protein Information  
Resource)  
7.forth step of homology modeling? (Loop modeling)  
8.Which notation of spectral similarity shared peaks counts  
(P1 and p2 - s1 and s2)  
9methods for lead validation (5)  
10. MS2 has \_ codons  
11. TIGR stand for what( The Institute of  
Genome Research (TIGR))  
12 XML stand for what.(Extensible Markup  
Language)  
13.chou fasman algorithm were firstly used in..... year(1974)  
14.Model plant.(Arabidopsis thaliana)  
15.3D1d @algorithm form in (1991)  
16. Sturucture of rna -(single strand)  
17.Choufashman algorithm based on (statistical occurance of amino acids)  
18.Four step in homologyodeling (loop formation)  
19.Wardenberg syndrome in (human)  
Probe length (8-32)  
20.PDB stands(protein data bank)  
21.PDGF stands((Platelet derived growth factor)  
22.Hmm stands(Hidden Markov Model  
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23.Hamming distance is not used to campare DNA protein sequences in dna similarity.and is  
uses for DNA similarity.  
24. Genomic rearrangements results in change of.... (gene ordering)  
25. Uniprot is database of protein....(sequenc)  
26. A drug target..... Protein(only about 500)  
27. HGP revealed that.... Disease are hereditary(3000-4000)  
28. Nation spectral similarity shared peak count....(P1and P2- S1and S2)  
29. ..... Is good for gapped alignment(BLOSUM50)  
30. When sanger sequence insulin....????(1955)  
31. Needleman alignment published in....????(1970)  
32. .... Size fragment can be ligated into BAC vector(large)  
33.Brute force is called.... (exhaustive search Algorithms)  
35..3D-1D bowie algorithm was proposed by bowie at el in.....(1991)  
36..... Help in finding global minimum(Global Energy Optimization)  
Mising ans:  
Mcqs no 2.(sequence)  
Mcqs no 7.(PAM)