Bio Informatics Interview Questions And Answers Guide.

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Bio Informatics Job Interview Preparation Guide.

Question # 1

What is e value?

Answer:-

Expectation value. lower the e value more significant is the match. it gives the statistical significance of a match to signify whether a match has taken by chance alone or not.

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Question # 2

How is the respiratory system applied to the sport paintball?

Answer:-

Paintball is a sport in which players eliminate opponents by hitting them with pellets containing paint (referred to as a "paintball"), usually propelled from a CO2 or compressed-gas (HPA or Nitrogen) powered paintball gun.

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Question # 3

How to identify highly mutated aminoacid from clustalw?

Answer:-

By Calculating the distance score between two nodes(Taxon)

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Question # 4

Can isolation of DNA done with perfection? how?

Answer:-

For isolating the DNA from specific source,we first know the behavior of cell morphology because cell wall playing important role in protecting the inner content. By using various chemicals and there composition helps in isolating the DNA from source cell.

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Question # 5

What are databases used in bioinformatics?

Answer:-

NCBI,
DDBJ,
EMBL for nucleic acids and PDB,
Swissprot for protein

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Question # 6

Explain it is a common experience that if we go on burping simultaneously and consciously(i.e.purposely,as in a non- natural action),our stomach starts aching. Why does this happen?

Answer:-

Due to improper digestion, diaphagrm get misplaced

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Question # 7

Which field have wider prospective of job M.sc bioinformatics or M.sc biotechnology?

Answer:-

see as the biochemistry is the basic thing for each and every subject opening for any process or in any stream in biology feild starts with the Biochem only

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Question # 8

What are the responsible factors for extinction of flora and fauna?

Answer:-

Deforestation,hence habitat of wildlife is ruined.
Hunting International market of animal organs.

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Question # 9

What is the difference between present and oldest drug discovery methods?

Answer:-

in oldest drug discovery we use to do hit and trial method for drug discovering we use to make a formula manually and then to design a drug but now that work has been reduce by new softwares and tools now we can avoid this hit and trial method now we can design a drug and can create an hypothesis about that drug and can also predict its efficiency for targetting to the receptor

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Question # 10

WHY YOU SELECT BIOINFORMATICS AS YOUR MAJOR FIELD?

Answer:-

i like this field because advanced technique of biology,combined of biotechnology and information technology,mainly use for drug designing and research, if anybody research in biological science use for bioinformatics

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Question # 11

Derive e-value?

Answer:-

Expect value. The E-value is a parameter that describes the number of hits one can â€œexpectâ€• to see by chance when searching a database of a particular size. It decreases exponentially with the score (S) that is assigned to a match between two sequences. Essentially, the E-value describes the random background noise that exists for matches between sequences. For example, an E-value of 1 assigned to a hit can be interpreted as meaning that in a database of the current size, one might expect to see one match with a similar score simply by chance. This means that the lower the E-value, or the closer it is to â€œ0â€•, the higher is the â€œsignificanceâ€• of the match. However, it is important to note that searches with short sequences can be virtually identical and have relatively high E-value. This is because the calculation of the E-value also takes into account the length of the query sequence. This is because shorter sequences have a high probability of occurring in the database purely by chance

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Question # 12

How to run DOCK 6 using cygwin?

Answer:-

1.install the needed package such as bison, perl etc.....
2.Configure the gnu file using ./configure gnu....
3.Download the accessary programs, such as dms, sphgen, chimera....
4.Prepare the structure and form the spheres and then built the grid for the ligand.....
5.Dock the molecule, by selecting the rigid dcking or flexible docking...

6.Give the input file for the selected docking and obtain
the output.....

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Question # 13

What are the main signals used for gene finding in prokaryotic genomes? How are these signals introduced into the search algorithms?

Answer:-

The main signals used are the TATA Box and the GC rich
regions present ahead of promoters in prokaryotes. Since,
the genes in prokaryotes are organised as operons so by
using comparative genomics we can find new genes.

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Question # 14

Explain Homology modelling?

Answer:-

if the crystal structure of any protein is unavailable,
then one can use the tools of homology modelling to
determine the structure. the logic is that a similar
structure arises becuse of a similar sequence of amino
acids. for homology modelling to be accurate an identity
match of 70% is desirable.basically, one does a FASTA
search of A.A sequences in the PDB database (A.A sequences
whose structures are known), does a CLUSTAL alignment to
check for conserved residues. then the structure of the
unknown A.A sequence is built up on the basis of the
structure of the best matches in FASTA and CLUSTAL by
programs like LLOOP and HHPRED. this structure can be
visualized in programs like DEEPVIEW,Protein Explorer
etc.

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Question # 15

What is the meaning of science?

Answer:-

Science is the term given to the powerfull branch which
forces a living thing to struggle and win the obstacles
existing in the mother earth. A dragging power which
motivates the life.

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Question # 16

Which of the following sequences contains the pattern [AG]-x
(4)-G-K-[ST] from the PROSITE database?
seq. A: VAGWGKST
seq B: GVLKRGKS
seq. C: AGVLKGRT
seq. D: AGVGKSTP?

Answer:-

seq. C: AGVLKGRT
[AG]-x (4)-G-K-[ST]
decodin the pattern:
A or G in the first position,(note both sequence C and D
start with the same)
X any amino acid follows the next four positions (2-5)
G in the sixth position (note seq C alone satify)
k in the seventh position
S or T in the eigth position (note seq C alone satify)

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Question # 17

What is the main idea of maximum parsimony in phylogenetic tree construction? What are the drawbacks?

Answer:-

The Maximum Parsimony (MP) problem aims at reconstructing a
phylogenetic tree from DNA sequences while minimizing the
number of genetic transformations. To solve this NP-
complete problem, heuristic methods have been developed,
often based on local search. In this paper, we focus on the
influence of the neighborhood relations

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Question # 18

What are the main approaches of predicting protein interactions using genomic context analysis?

Answer:-

We have developed an approach using Bayesian networks to predict protein-protein interactions genome-wide in yeast. Our method naturally weights and combines into reliable predictions genomic features only weakly associated with interaction (e.g., messenger RNAcoexpression, coessentiality, and colocalization). In addition to de novo predictions, it can integrate often noisy, experimental interaction data sets. We observe that at given levels of sensitivity, our predictions are more accurate than the existing high-throughput experimental data sets

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Question # 19

How you calculate sensitivity and selectivity of Blast?

Answer:-

Suppose the Blast search returned 100 hits. Of these, 17 were false positives and we knew that there were 165 sequences in
the database which should have returned a hit with our sequence.
To calculate the sensitivity and selectivity, we must determine the number of true positives (ntp), the number of false
positives (nfp) and the number of false negatives (nfn). We are told that the number of false positives was 17, hence the
number true positives must have been 100-17 = 83, as there were 100 hits. Therefore we know that the search algorithm found
83 of the 165 sequences it should have found, hence the number of false negatives was 165-83 = 82. So, we know that ntp = 83,
nfp = 17 and nfn=82. Using the equations in the notes, we can calculate:
Sensitivity = ntp/(ntp+nfn) = 83/(83+82) = 83/165 = 0.50 (2 d.p)
Selectivity = ntp/(ntp+nfp) = 83/(83+17) = 83/100 = 0.83

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Question # 20

Suppose you used the NCBI Blast server to look for a match to a fruit-fly gene. Suppose further that the best alignment contained this section of an alignment:
Hit from database: XXXXXXXXXXXXXXNFSTSQ
user sequence: SLEAEAAPASISPSNFSSSQ
What do the Xs signify?

Answer:-

unknown amino acid

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