Bioinformatics Interview Questions And Answers Guide.

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Bioinformatics Job Interview Preparation Guide.

Question # 1

What are the bioinformatic tools applied to micromolecular evolution?

Answer:-

When sequence data for microbial genomes first became available, we adapted available software and also designed new programs for analyzing these data. This approach allowed us quickly to identify probable trans membrane proteins, estimate their topologies, and determine the likelihood that they function in transport, a topic of particular interest to our research group. This work allowed us to expand previously recognized families of such proteins and to identify dozens of new families.

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Question # 2

Did integral membrane transport proteins arise as an independent protein class or from other types of proteins?

Answer:-

Among the more than 400 families of transport systems in our TC system, very few include integral membrane homologues that function in a capacity other than transport. Moreover, almost all these exceptions are receptors. In some cases, transporters gained receptor functions while retaining their transport functions but in other cases they gained this function while losing the capacity to transport. A loss of transport capacity typically is accompanied by the gain or loss of specific protein domains, in a few cases, another protein with high affinity for the transport protein homologue accounts for the loss of function. Dissociation of such protein-protein complexes or losing the extra domains may restore the lost transport functions.

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Question # 3

Can independent origins be established for two families of transport systems having no sequence or motif similarities without three-dimensional structural data?

Answer:-

Many integral membrane transport proteins contain 6 or 12 TMSs. For example, both mitochondrial carrier (MC) family members and the aquaporins and glycerol facilitators within the major intrinsic protein (MIP) family contain six TMSs per polypeptide chain. Sequence analyses reveal that MIP family members arose by duplication of a three-TMS-encoding genetic element, while members of the MC family arose by triplication of a two-TMS-encoding element.
The MIP family arose before the three domains of life (bacteria, archaea, and eukaryotes) diverged from each other, whereas the MC family arose late within eukaryotes, after endosymbiotic proteobacteria became permanent denizens of eukaryotic cells. The advent of mitochondria evidently required a new mode of communication between the mitochondrial matrix and the cytoplasmic compartment of such cells. Thus, mitochondrial carriers depend on a distinctive solute. Solute exchange mechanism rather than on the cation symport mechanisms that bacteria use for ingesting nutrients.

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Question # 4

Did bacteria, archaea, and eukaryotes exchange transporter genes appreciably during the past two billion years?

Answer:-

After analyzing dozens of large transport protein families, we find several examples of horizontal transfer between distinct kingdoms within these domains, such as between gram-positive and gram-negative bacteria. However, we find little evidence of horizontal transfer of transporter genes among the three domains occurring any time during the past two billion years. Thus, although hundreds of members of the MC family are found in eukaryotes, not a single such member is found in a prokaryote. Moreover, of the hundreds of sequenced homologues of the phosphoenolpyruvate, sugar phosphotransferase system (PTS), every one is in a bacterium, without a single example in an archaeon or a eukaryote.

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Question # 5

Did shuffling of protein constituents occur between systems for multicomponent transport systems such as the ATP-binding-cassette or complex protein secretion systems?

Answer:-

After analyzing numerous multicomponent transport systems phylogenetically, we found little evidence for shuffling of protein constituents during their late evolutionary divergence. We included several protein secretion systems, such as types I, II, III, and IV as well as ABC-type solute uptake systems. The protein secretion systems consist of many proteins that were often transferred laterally among gram-negative bacteria. Although several such multicomponent systems may be found within a single bacterial cell, the systems apparently did not exchange protein constituents, even though they can be exchanged experimentally by genetic

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manipulation. One important caveat: phylogenetic analyses may overlook constituent shuffling between closely related systems.
These observations suggest to us that complex multicomponent transport systems depend on extensive protein-protein interactions, which probably arose through coevolution of the protein constituents. Once any two systems have diverged appreciably in sequence, the constituents in one system no longer can interact properly with those in another, effectively preventing shuffling between the two.

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Question # 6

Are all members of transporter families confined to a particular organelle or to the plasma membrane, or are some family members found throughout cellular compartments in eukaryotes?

Answer:-

Mitochondrial carriers are restricted to certain eukaryotic organelles. Not a single one appears to be a constituent of the plasma membrane, endoplasmic reticulum, Golgi apparatus, or nuclear membrane. Instead, they are found in a subset of organelles, including mitochondria, peroxisomes, amyloplasts, and hydrogenosomes. Are other families similarly restricted? Some of them, such as members of the cystine transporter family, are probably restricted to the intracellular vesicular membranes of eukaryotes, whereas other families can be found in the plasma membrane as well as in various organelles.

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Question # 7

What is computational biology?

Answer:-

Computational biology is an interdisciplinary field that applies the techniques of computer science and applied mathematics to problems inspired by biology.

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Question # 8

What technique is used to measure the number of copies of a gene or an RNA molecule in human tissues?

Answer:-

PCR or polymerase chain reaction in real time, as opposed to the conventional method, because the number of copies of the target molecule can be monitored for each PCR cycle.

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Question # 9

What are the limitations of blotting techniques?

Answer:-

The major limitation of blotting procedures is the length of time needed and the fact that they can accommodate only one probe at a time. DNA microchip technology permits the analysis of thousands of genes at the same time. DNA molecules are attached to the wafers in an organized array and are called the probes. DNA molecules taken from tissues are hybridized to the chips and are called targets, which are labeled with fluorescent light. The probes that have hybridized to the fluorescent targets are then identified by fluorescence microscopy.

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Question # 10

How will you value a biotech company as opposed to a consumer products company?

Answer:-

Most companies are valued based on their growth prospects. That is what determines their stock price and overall dollar value, when they are sold. Biotech companies, as are other pharmaceutical companies, are valued based on the perceived quality of the products in their pipelines. That is what determines if they are going to have sustainable revenues and earnings. It is also why so many Analysts on The Street pay such close attention to FDA pronouncements.

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Question # 11

Tell me about the mass number of nuclear?

Answer:-

The mass number of a nucleus is sometimes more than and sometimes equal to its atomic number.

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Question # 12

What is protein sequencing?

Answer:-

Protein sequencing is a technique to determine the amino acid sequence of a protein, as well as which conformation the protein adopts and the extent to which it is complexed with any non-peptide molecules.

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Question # 13

Have the proteins of a family generally acquired distinctive properties within each of these three kingdoms for ancient families that arose before bacteria, archaea and eukaryotes diverged?

Answer:-

Proteins from 20 large ubiquitous families represented in all three domains to see if proteins from each domain exhibit distinctive characteristics. The archaeal

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integral membrane proteins are consistently smaller than their bacterial homologues, while the eukaryotic homologues are much larger. Moreover, among transporters in the three major eukaryotic kingdoms of plants, animals and fungi, the animal and fungal homologues are of comparable size, whereas the plant homologues are substantially smaller. Although these surprising observations presumably reflect evolutionary pressures during protein sequence divergence, we do not know what those pressures were.

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Question # 14

What kinds of metrics would you gauge to determine the financial, strategic and operational health of a prospective alliance partner?

Answer:-

Several metrics are available in each sector you mention. To gauge the financial health of a prospective partner, I would look at product sales growth or I might look at whether they have met their milestones. To gauge strategic health, I would consider their market share growth or how well their customers have access to the company. For operational health, I would again look to see whether they have met their milestones, how well they make decisions as gauged by the rating we give them and how quickly they resolve conflicts. Good evaluations in these areas suggest that the prospective alliance will be viable for both parties.

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Question # 15

Does multidrug resistance (MDR) arise by activation of stable genes encoding drug efflux pumps or by mutations of genes encoding other types of transporters in bacterial pathogens?

Answer:-

MDR efflux pumps began causing clinical problems relatively recently, in parallel with the extensive use of antibiotics in medicine and as supplements in animal feeds. However, our analyses indicate that these MDR efflux pumps did not arise through recent mutations in genes encoding transporters that changed their substrate specificities.
Instead, such MDR pumps are encoded within the genomes of virtually all microorganisms, so these genes are present and thus need only to be activated to become problematic. Moreover, lateral transfer of genes among bacteria has occurred frequently, particularly for plasmid-encoded systems, suggesting that such genes can be acquired fairly readily even if they are not initially present. Finally, although mutations that enable transporters to act on different types of substrate are rare, experiments and phylogenetic analyses indicate that simple point mutations can readily narrow or broaden a particular transporter's specificity toward a single class of compounds. These findings provide clues for developing strategies to control MDR among bacterial pathogens.

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Question # 16

What is the science of bioinformatics?

Answer:-

The science of bioinformatics, which is the melding of molecular biology with computer science, is essential to the use of genomic information in understanding human diseases and in the identification of new molecular targets for drug discovery.

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Question # 17

What is the informatics in bioinformatics?

Answer:-

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Question # 18

What is bioinformatics?

Answer:-

The mathematical, statistical and computing methods that aim to solve biological problems using DNA and amino acid sequences and related information is known as Bioinformatics.

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Question # 19

Why do you think that bioinformatics is important?

Answer:-

Today, we can use computers to access much more biological data than ever before. You can learn a lot by analysing this data. For example, you can identify genes by comparing genomic data across organisms and identifying patterns in the data. Insights as to the structure of proteins can be obtained through computer analyses of the protein sequences. These approaches are a lot faster and a lot cheaper than relying solely on wet lab or X-ray crystallographic techniques. Of course, computational techniques are often not as reliable as getting the first-hand view of the molecules. Clearly, you need both worlds: you need to take advantage of the computer tools when you know the predictions are reliable and use the more expensive techniques (in the wet lab) when you can't get away from it.

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Question # 20

what is a Homologue?

Answer:-

One chromosome of a pair is called homologue.In Homologous pair two identical chromosomes are present. Each one chromosome in a Homologous pair is called Homologue.

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Question # 21

What do you think are the more interesting areas of bioinformatics?

Answer:-

Looking at what the academic world is publishing, microarray research is really hot right now, and people haven't quite figured out what the best way is (some might argue if we should even be trying) to store, process, and understand this data, but there are lots of interesting ideas.

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Question # 22

How can you have an accession number?

Answer:-

Accession number (bioinformatics), a unique identifier given to a biological polymer sequence (DNA, protein) when it is submitted to a sequence database.

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Question # 23

In the next two or three years what will the important advances in the field be?

Answer:-

The sequencing of the human genome has just been completed and in the next two or three years I expect progress will be made in identifying the genes. Right now, we don't even know how many genes we have! Also, in the next two or three years, we'll be learning more about the structure and function of proteins in the cell. Hopefully, in the longer term we'll be able to piece together that information to get a more complete picture of regulatory networks in the cell.

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Question # 24

Tell us about three kinds of DNA?

Answer:-

There are three kinds of DNA sequences. Genomic DNA comes from the genome and includes both genes and extragenic material.
cDNA is reverse transcribed from mRNA and corresponds only to the expressed parts of the genome.
Recombinant DNA is man-made and is composed of artificial DNA.

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Question # 25

How did you get into the field of bioinformatics?

Answer:-

My background is in computer sciences, including design of algorithms and theoretical computer science. I got interested in this because of some work in an area called DNA computing. That idea is to build computers out of DNA. The person who started that line of work - is a computer scientist who spent a quite a bit of time in a biology lab. His work really caught the attention of many people in the computer science community. But then, as I got more interested in some of the algorithmic problems that come up, I realized they are also relevant in the more traditional biological areas. You have to talk to chemists and biochemists if you want to understand DNA and RNA - you can't get the right level of understanding just from reading papers. I got more interested in their perspectives and problems.

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Question # 26

What is a clean and run reaction?

Answer:-

This means that purchase a BigDye terminator kit from our facility and run the cycle sequencing reaction and post clean-up. We recommend using Princeton Separations Centri-Sep spin columns or Abgene Dye Terminator Removal Plates.
Drop off your sample in the form of a dried pellet in 1.5 ml eppendorf tube along with your request form. Your dnalims request order will have Seq_Drop_Off selected under Service Requested, and have no selected under Spin-Column Clean-up.

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Question # 27

How much template do you need for sequencing?

Answer:-

For PCR product size of product(bp)/50 = ng DNA. For plasmid up to 10.0 kb 250-300 ng. For genomic DNA 2.0 microgram.

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Question # 28

How do you customise database for blast?

Answer:-

Step 1. Assemble your sequences.
Put all your sequences in Fasta format in a single file.
This file should be located in a suitably named
subdirectory of your home directory on the UBiC Blast
server. The definition line for each sequence should start
with a unique identifier for that sequence.
Step 2. Convert this sequence file to a Blastable database.
The command formatdb converts your Fasta file of sequences

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to a set of files that can be queried with command-line BLAST.
Step 3. Test Blast on your database.
See the UBiC tutorial, Using Command-line BLAST. In the blastall command-line you will need to specify the location of your database by typing: -
d /disk2/home/myhome/blastdbs/custom.aa.

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