What is PROB?
???????

Explain Primary Tertiary and Quaternary Structure of Protein?
Primary Structure: the **primary structure** of a **protein** is the linear sequence of amino acids. Together, this linear sequence is referred to as a polypeptide chain. The amino acids in the **primary structure** are held together by covalent bonds, which are made during the process of **protein** synthesis (translation).

Tertiary Structure: the tertiary **structure** will have a single polypeptide chain "backbone" with one or more **protein** secondary **structures**, the **protein** domains. Amino acid side chains may interact and bond in a number of ways. The interactions and bonds of side chains within a particular **protein** determine its tertiary **structure**.

Quaternary Structure: Protein quaternary structure is the number and arrangement of multiple folded **protein** subunits in a multi-subunit complex. It includes organisations from simple dimers to large homo oligomers and complexes with defined or variable numbers of subunits.

Discus RNA (10) RNA Structure and types and SecondaryStructure and Process? (10)
RNA, abbreviation of **ribonucleic acid**, complex compound of high molecular weight that functions in cellular protein synthesis and replaces DNA (deoxyribonucleic acid) as a carrier of genetic codes in some viruses. RNA consists of ribose nucleotides (nitrogenous bases appended to a ribose sugar) attached by phosphodiester bonds, forming strands of varying lengths. The nitrogenous bases in RNA are adenine, guanine, cytosine, and uracil, which replaces thymine in DNA.

RNA Structure: RNA is typically single stranded and is made of ribonucleotides that are linked by phosphodiester bonds. A ribonucleotide in the **RNA** chain contains ribose (the pentose sugar), one of the four nitrogenous bases (A, U, G, and C), and a phosphate group.

RNA Types and Function:
* mRNA - Messenger RNA: Encodes amino acid sequence of a polypeptide.
* tRNA - Transfer RNA: Brings amino acids to ribosomes during translation.
* rRNA - Ribosomal RNA: With ribosomal proteins, makes up the ribosomes, the organelles that translate the mRNA.
* snRNA - Small nuclear RNA: With proteins, forms complexes that are used in RNA processing in eukaryotes. (Not found in prokaryotes.)

Supervised and Unsupervised Machine Learning?
Supervised: Supervised Learning Prediction of future cases Knowledge extraction Compression Outlier detection.
Un Supervised: Learning "what normally happens" No output.
Clustering: Grouping similar instances.
Applications Customer segmentation in CRM Image compression Bioinformatics.

Swiss Port?
Swissport International Ltd. is the world's largest ground handling company, **Swissport's** activities encompass everything an airline needs on the ground to move passengers and cargo efficiently and safely. The company also performs such services as line maintenance, aircraft cleaning, and fueling.

Secondary Structure prediction process?
Secondary structure prediction is a set of techniques in bioinformatics that aim to **predict** the local **secondary structures** of proteins based only on knowledge of their amino acid sequence.

Mate Pair Sequencing Strategy Sequencing?
Mate-pair **sequencing** can also provide a powerful alternative for whole genome **sequencing** as the longer DNA fragments can be used to bridge together DNA fragments even in the presence of highly repetitive DNA **sequences** which are rife in human and many other complex genomes.

Homology, Paralogy and Orthalogy? Homology Modeling?

Homology modeling, also known as comparative **modeling** of **protein**, refers to constructing an atomic-resolution **model** of the "target" **protein** from its amino acid sequence and an experimental three-dimensional structure of a related **homologous protein** (the "template").

orthology and **paralogy** relationships between two sequences are derived from such trees based on which evolutionary event (speciation or duplication, respectively) is assigned for their last common ancestor.

What method used for sequence?
DNA sequencing methodsFred Sanger and Walter Gilbert Cells make copies of DNA DNA fragments of different lengths- if one base is missing. **(PPTS)**

Limitation of AB intio?
Computationally expensive • Suitable for proteins with less than 100 residues. Conclusion • Ab initio methods rely on computing the energies of folded proteins • The protein structures with the lowest energy are deemed as plausible predictions. **(PPTS)**

Challenge of AB intio?
Very hard to accurately describe energy functions that can reliably discriminate native and non-native structures. Enormous amount of computations. **(PPTS)**

Two target discovery approaches?
Target discovery to clinical application saga • Physiology-based approach • Target-based approach.

Physiology-based approach Is a disease-centric approach in which target is not identified, multiple targets are involved. In vivo screening is done by using drugs, siRNAor antisense oligonucleotides.

Target-centric approach Target based discovery starts with the identification of genes and their protein products. Aim to develop drugs affecting one gene or a molecular mechanism.

Pharmacology and Pharmacogenomics?
Pharmacology: Pharmacology (science of drugs) Genomics (the study of genes and their functions) Develop effective, safe medications & doses tailored to a person's genetic makeup.
Pharmacogenomics: Detection of genetic variability of drug effects on the genome level • Agent selection • Analysis of drug reactions and drug toxicity on gene expression • Development of new indications for already approved drugs. Discovery of new drug targets • Identification of (non) responders in clinical trials of phase I-IV • Identification of genotype dependent adverse drug reactions • Identification of individuals at risk for severe adverse drug effects.

Homology Folding recognition Steps? Folding recognition process of homology modeling and its important?
Homology / fold recognition predict protein structures without computing fundamental physical/chemical properties of the mechanisms and driving forces in structure formation. Ab initio methods, in contrast, base their predictions on physical models for these mechanisms • Energy released during the folding process is computed for predicting structure.
Importants:
Homology modeling is **the** most accurate computational method to create reliable structural **models** and is commonly used in many biological applications. **Homology modeling** predicts **the** 3D structure of a query protein through **the** sequence alignment of template proteins. **(Internet)**

What is the simple way of scoring and algorithm?
Scoring: A simple way (but not the best) to score an alignment is to count 1 for each match and 0 for each mismatch, **(PPT)**

Algorithm: Algorithms can be written in ordinary language, and that may be all a person needs. In computing, an **algorithm** is a precise list of operations that could be done by a Turing machine. For the purpose of computing, **algorithms** are written in pseudocode, flow charts, or programming languages. **(INTERNET)**

Three step of needlman wunch algorithm?

Three steps • Initialization • Matrix filling • Traceback.

Initialization • The cell of first row and first column of the matrix is initially filled with zero • Add gap penalty for each shift to the right.

Matrix Fill • Move through the cells row by row, calculating the score for each cell • Compute three scores: – A match score – Vertical gap score – Horizontal gap score.

Traceback • The final step in the algorithm is the trace back for the best alignment • Start at the bottom-right corner • Follow where maximum value comes from

Structure of Protein?

Protein structure is the three-dimensional arrangement of atoms in an amino acid-chain molecule. **Proteins** are polymers – specifically polypeptides – formed from sequences of amino acids, the monomers of the polymer. ... Very large aggregates can be formed from **protein**subunits.

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Needleman Algorithm?

The **Needleman**–Wunsch **algorithm** is an **algorithm**used in bioinformatics to align protein or nucleotide sequences. It was one of the first applications of dynamic programming to compare biological sequences. The **algorithm** was developed by Saul B. **Needleman**and Christian D. Wunsch and published in 1970.

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