## Biological sequence analysis probabilistic models of proteins and nucleic aci

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What is the application of bioinformatics in sequence analysis? Bioinformatics helps us understand complex biological problems by investigating similarities and differences that exist at sequence levels in poly-nucleic acids or proteins. Alignment algorithms such as dynamic programming, basic local alignment search tool and HHblits are discussed.

What is nucleotide sequence analysis in bioinformatics? Nucleotide sequence analyses identify functional elements like protein binding sites, uncover genetic variations like SNPs, study gene expression patterns, and understand the genetic basis of traits. It helps to understand mechanisms that contribute to processes like replication and transcription.

What is an example of a biological sequence? A biological sequence is a sequence with a small fixed alphabet, and represents a naturally occurring or experimental generated fragment of genetic or protein material or any intermediate product (like the messenger RNA). Example: A DNA fragment has the 4 character alphabet 'A', 'C', 'T', 'G'.

What is the purpose of sequence analysis? Sequence analysis is a term that comprehensively represents computational analysis of a DNA, RNA or peptide sequence, to extract knowledge about its properties, biological function, structure and evolution.

What is sequence analysis of proteins and nucleic acids? Sequence analysis of protein and nucleic acid databases by exhaustive string-matching algorithms is

effectively implemented on large processor-array machines, such as the I.C.L. DAP. An improved method of assessing the significance of the best alignments for proteins is described.

What is sequence analysis of proteins? Protein sequencing is the practical process of determining the amino acid sequence of all or part of a protein or peptide. This may serve to identify the protein or characterize its post-translational modifications.

What is a nucleic acid sequence in bioinformatics? Nucleic acid sequence is important material of bioinformatics research. Nucleic acid sequences provide the fundamental starting point for describing and understanding the structure, function, and development of genetically diverse organisms.

What is a real life example of sequencing? We come across sequences in many places in real life. For example, the house numbers in a row, salary in successive years (by a fixed amount or a by a fixed percentage), page numbers of a book, etc represent sequences.

What are the different types of sequences used in bioinformatics? Data types in bioinformatics can be DNA sequences, RNA sequences, amino acid sequences, methylation sequences, three-dimensional protein structures, and more.

What is an example of biological analysis? For example, if the goal is to identify molecular mechanisms that link a genotype to a phenotype, biological analysis is the crucial approach that links gene expression changes in cancer cells to the observed cellular phenotype or related disease phenotype.

What does analysis of DNA sequences tell us? In most cases, DNA sequencing is employed in order to identify and analyze genetic variants. These variants can be small nucleotide substitutions, insertions, deletions, copy-number alterations or structural variants. Futhermore, they may be heritable polymorphisms or somatic mutations.

How to analyse a DNA sequence?

What are the tools used in bioinformatics?

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