

Sr and protein binding sites in dna.

Design



**ASSIGN
BUSTER**

Sr no. Tool Description References 1. CLUSTAL Omega Multiple sequence alignment of biological sequences using algorithms. 2 2.

MEGA Reconstruct or rebuild evolutionary relatedness among organisms. 3

3. MEME To find motifs in biomolecules, domains in proteins and protein binding sites in DNA. 4 4. JALVIEW To edit, analyze and visualize the multiple sequence alignment in biological sequences, predict secondary structures in protein molecules. 5 5.

MUSCLE Alignment of protein sequences by multiple sequence alignment, phylogenetic analysis and predict protein structures. 6 6. Taverna Comforts

bioinformaticians who are not skillful in web services and programming by providing interface between different tools and databases. 7 7. GENSCAN

Find whole genome structures of human, predict exons, introns, transcriptional, translational signals and intergenic regions, find gene or multiple genes in DNA. 8 It is such a tool used to find and search whole structures present in genomic DNA of humans. GENSCAN used to predict exons, introns, transcriptional, translational signals and intergenic regions in the DNA.

Gene or multiple genes present in DNA can also be predicted by using this tool. This tool proved to be accurate as it predicted 75 to 80 % exons precisely. (Chris Burge, Samuel Karlin, 1997) 8. 7. GENSCAN Taverna has number of uses in constructing and performing a sequence of activities that comforts bioinformaticians who are not skillful in web services and programming languages. It provides interface between bioinformaticians and

web services that helps to communicate between different tools and databases for sequence analyses.

Taverna has many services and one of them provided by INSDC (<http://www.insdc.org/>). (Duncan Hull et. al, 2006) 7. 6. Taverna is a protein sequence alignment tool used to build alignments of protein sequences by multiple sequence alignment with great accuracy.

It is reported to be the fastest sequence alignment tool compared with other alignment tools e. g., T-Coffee, CLUSTALW etc. It has wide range of uses including phylogenetic analysis, to predict protein structure etc. The most important thing of this tool is to show the evolution of sequences by graphs. (Robert C. Edgar, 2004) 6. 5.

MUSCLE is a tool used to edit, analyze and visualize the multiple sequence alignment of biological sequences and refine the sequences. It is used to align the sequences and predict the secondary structures of the protein molecules. It shows the alignment results by showing figures and construct phylogenetic trees of sequences. JALVIEW 1. 0 is not able to analyze the huge and detailed tasks, so JALVIEW 2 is constructed by bioinformaticians to perform greater tasks. (Andrew M. Waterhouse et.

al, 2009) 5. 4. JALVIEW is a bioinformatics tool used to find out motifs in biological sequences of biomolecules e. g., proteins and DNA. It is also used to discover domains in proteins and protein binding sites in DNA. It can also be used to find out repeated sequences in proteins and DNA when query sequences are submitted into it.

(Timothy L. Bailey et. al, 2006) 4. 3.

MEME (Multiple EM For Motif Elicitation) It is a bioinformatics tool used to reconstruct or rebuild evolutionary relatedness among the species or organisms. MEGA's important feature is the use of graphical user interface (GUI), that shows the graphical representation of the given data, phylogenetic trees and results. (Sudhir Kumar et. al, 2012) 3. 2.

MEGA (Molecular Evolutionary Genetics Analysis) CLUSTAL Omega is a latest version of the CLUSTAL programs for multiple sequence alignment of biological sequences. It uses algorithms for construction of guide trees. The software has proved to be better than earlier CLUSTAL series and it has great precision. The larger alignments can be done using this tool even on home computers.

(Sievers F., Higgins D. G., 2014) 2. 1. CLUSTAL Omega Bioinformatics tools for biological sequence analyses These sequences are the information stored in DNA and proteins in the form of letters. These letters are instructions and have specific arrangements given by the nature to our DNA and from DNA to proteins. The nucleotides in DNA are instructions that pass from generation to generation.

The proteins are macromolecules made of amino acid sequences and perform many functions of the body. The sequences came into existence due to molecular attractions of different molecules. Sequence analysis is the comprehension of novel arrangement and characteristics of codes in a biomolecule like nucleic acid and protein, that are responsible for their operation and function. (Mehmood MA et. al, 2014) 1.

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For carrying out sequence analyses, the sequences after retrieval from different databases are refined and submitted to various tools that speculate their features important for their function, structure and evolutionary history with extreme precision. (Mehmood MA et. al, 2014) 1. The objective of this review is to encompass all the tools being used for biological sequence analyses. Introduction