

A Comparison of Methods for Aligning Genomic Sequences

Genomic sequence analysis is becoming increasingly important in the identification of genomic regulatory regions. Many algorithms have been designed to search through chromosomes for genes, pieces of DNA that contain instructions for the assembly of proteins. A typical gene is regulated by proteins, known as transcription factors, that bind to specific DNA sites, generally found in close proximity to the gene itself. CLUSTALW and DiAlign are two computational approaches that have been developed to identify functional DNA in non-coding regions by sequence comparison. CLUSTALW is a program that uses the progressive method of multiple sequence alignment. It uses a global sequence alignment algorithm to construct an alignment of the entire length of sequences. Then, it uses the neighbor-joining algorithm to construct a guide tree and progressively aligns the sequences starting with the sequences that are most closely related. DiAlign is a program that uses the iterative method of multiple sequence alignment. It uses a local alignment approach to construct multiple alignments based on segment-to-segment comparisons rather than residue-to-residue comparisons. The segments are then incorporated into a multiple alignment using an iterative procedure. These two programs were compared to a new computational approach developed at Oak Ridge National Laboratory within the last year. This new approach is applied to genomic sequences in two phases. Phase one consists of the collection of complete small subsequences that match specified criteria. Phase two involves the assembly of pieces from the phase-one collection into larger patterns. The final result will be a better understanding of the way genes are regulated, which will aid in the development of treatments for genetic diseases.

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