

Sequence Analysis

Pubrica's Bioinformatics team supports identifying a specific sequence, sequence conversion and gene prediction of the relevant information in a given area.

The goal of computational sequence analysis is to identify sequence similarities that could indicate structural and functional conservation and evolutionary relationships between the sequences. Because the sequence alignment score commonly measures the degree of similarity, it is essential to understand whether a score is high enough to indicate a physiologically relevant alignment. The examination of the statistical significance of alignments is a reliable way of determining score cutoffs. The importance of an alignment score is often determined by its P-value, which is the probability that this score or a higher one might happen by chance, given the probabilistic models for the sequences.

P-value estimations of broad function in sequence analysis, as well as a discussion of theoretical methodologies and computer approaches for estimating statistical significance for significant kinds of sequence analysis problems.

We concentrate on P-value estimation methodologies for single sequence studies (both score-based and score-free), multiple alignments, sequence-to-profile alignments, and hidden Markov model alignments in particular. The review will be valuable to both professional bioinformatics researchers and biological scientists interested in implementing standard DNA and protein sequence analysis. Sequence analysis techniques and databases can be used to identify genes and functional components in newly sequenced genomes. Computational sequence analysis also provides a foundation for the rapidly emerging subject of systems biology. It may anticipate protein-protein interactions and interactions in transcriptional regularity networks using sequence comparison and motif analysis approach.

Our comprehensive Bioinformatics Database services

- Find out the coding regions and non coding regions
- Find the evolutionary relationship of two sequences
- Identified subfamily
- Identified introns and exons in genomic sequences

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