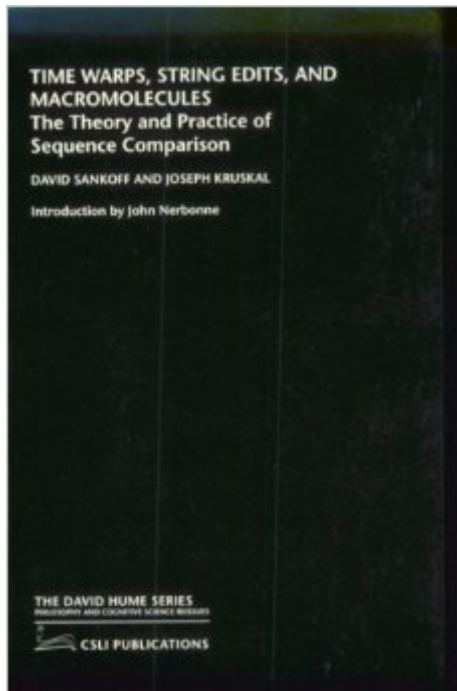


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Time Warps, String Edits, And Macromolecules: The Theory And Practice Of Sequence Comparison



Synopsis

Time Warps, String Edits and Macromolecules is a young classic in computational science. The computational perspective is that of sequence processing, in particular the problem of recognizing related sequences. The book is the first, and still best compilation of papers explaining how to measure distance between sequences, and how to compute that measure effectively. This is called string distance, Levenshtein distance, or edit distance. The book contains lucid explanations of the basic techniques; well-annotated examples of applications; mathematical analysis of its computational (algorithmic) complexity; and extensive discussion of the variants needed for weighted measures, timed sequences (songs), applications to continuous data, comparison of multiple sequences and extensions to tree-structures. This theory finds applications in molecular biology, speech recognition, analysis of bird song and error correcting in computer software.

Book Information

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Customer Reviews

This book, originally published in 1983, was reissued in 1999, no doubt because of the importance of genetic sequencing in recent years. What is neat about the book is it shows how algorithms from one field can be applied to solve problems in another, possibly totally disparate field, one example being computational linguistics and sequence algorithms in computational biology. A general overview of sequence comparison is given in chapter 1 with applications to molecular biology, human speech, computer science, coding theory, gas chromatography, and bird songs discussed. The author discusses how deletion-insertion, compression-expansion, and substitution are

employed in sequence comparison. Different metrics are introduced, such as the Levenshtein distance. Dynamic programming, which pretty much dominates the book, is introduced here also. Part 1 of the book discusses sequence comparison in molecular biology. The use of dynamic programming is emphasized and its importance continues to this day. The advantages of using the dynamic programming method are outlined, and it is shown how to find the substring in a longer sequence with most optimum agreement to a shorter sequence. In addition, given an RNA molecule with a known nucleotide sequence, methods are discussed for predicting the way different parts of the molecule will bond to each other. These methods are based on dynamic programming.

Mathematicians considering doing research on or about entering the field will profit from the section on the biological background. The treatment of RNA secondary structures is excellent. In part 2, the emphasis is on speech processing and what is called "time-warping", which is a technique for comparing functions by altering the time axis.

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