



Smith-Waterman algorithm

By Lambert M. Surhone

Betascript Publishers Jan 2010, 2010. Taschenbuch. Condition: Neu. Neuware - High Quality Content by WIKIPEDIA articles! The Smith-Waterman algorithm is a well-known algorithm for performing local sequence alignment; that is, for determining similar regions between two nucleotide or protein sequences. Instead of looking at the total sequence, the Smith-Waterman algorithm compares segments of all possible lengths and optimizes the similarity measure. The algorithm was first proposed by Temple Smith and Michael Waterman in 1981. Like the Needleman-Wunsch algorithm, of which it is a variation, Smith-Waterman is a dynamic programming algorithm. As such, it has the desirable property that it is guaranteed to find the optimal local alignment with respect to the scoring system being used (which includes the substitution matrix and the gap-scoring scheme). 92 pp. Englisch.



READ ONLINE
[1013.02 KB

Reviews

This kind of publication is every thing and taught me to seeking ahead and a lot more. It really is rally interesting throgh reading through time. I realized this ebook from my i and dad recommended this publication to understand.

-- **Dax Herzog**

This composed publication is fantastic. This is certainly for all those who statte that there was not a well worth reading through. You will not truly feel monotony at whenever you want of your respective time (that's what catalogs are for regarding when you ask me).

-- **Prof. Mark Ratke Jr.**