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High speed database sequence comparison

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Abstract

Database sequence comparison applications compare a query sequence with each sequence in a database to find the closest match. These applications are high consumers of computation time because they use dynamic programming algorithms to perform the large number of required sequence comparisons. Traditional methods perform the comparisons on the entire set of sequences in the database. In this work, we introduce a novel high-speed technique that reduces the number of database sequences to which the time-consuming matching algorithm is applied. The selection of the target database sequences is based on similarity measures that will be introduced in this contribution as well. Using the proposed technique and the proposed similarity measures, we are able to accelerate the database sequence comparison by 65% compared to traditional exhaustive methods.

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1. Introduction

Database sequence comparison applications are widely used in different research fields. In Biology^{10, 12} for example, rapid analysis of DNA and Protein sequences are performed to search a large database of sequences for

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