



Direct Suffix Sorting

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Condition: New. Publisher/Verlag: VDM Verlag Dr. Müller | Basics, Concepts and Applications | Pattern matching plays a central role in different aspects of biological sequence analysis, and has been used in applications as diverse as short-read sequencing, multiple sequence alignments, gene finding, analysis of repetition structures, searching for unique oligonucleotides, prediction of protein function and structure, sequence homology search, finding DNA-binding protein motifs, etc. Suffix trees and suffix arrays are primary data structures used in rapid pattern matching. And the problem of suffix sorting is a fundamental problem in constructing suffix arrays. This book presents the basics, concepts of suffix trees, suffix arrays and suffix sorting and proposes a direct suffix sorting algorithm which rearranges the biological sequences of interests and facilitates high throughput pattern query, retrieval and storage in linear time. The direct suffix sorting algorithm is then applied to solve practical problems in multiple sequence alignment and data compression. The book serves both as a reference for computer scientists, computational biologists and bio-informatics professionals and as essential study materials for graduate and advanced courses on computational biology. | Format: Paperback | Language/Sprache: english | 108 pp.



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Reviews

It is great and fantastic. Better than ever, though I am quite late in starting to read this one. It has been written in an extremely simple way and is particularly only right after I finished reading this ebook where it actually changed me, affected the way I really believe.

-- **Orin Blick**

Unquestionably, this is the very best operated by any author. It had been written extremely flawlessly and beneficial. You can expect to like the way the blogger publishes this publication.

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