

Needleman And Wunsch Algorithm

Qiang Xue

Reducing the Search Space and Time Complexity of Needleman-Wunsch Algorithm (Global Alignment) and Smith-Waterman Algorithm (Local Algorithm) for DNA Sequence Alignment Fatimah Noni Muhamad, 2011 The main research in this project is to align the DNA sequences by using the Needleman-Wunsch algorithm for global alignment and Smith-Waterman algorithm for local alignment based on the Dynamic Programming algorithm.

Rough Sets and Current Trends in Computing Shusaku Tsumoto, Roman Slowiński, Jan Komorowski, Jerzy W. Grzymala-Busse, 2004-05-21 In recent years rough set theory has attracted the attention of many researchers and practitioners all over the world, who have contributed essentially to its development and applications.

We are observing a growing research interest in the foundations of rough sets, including the various logical, mathematical and philosophical aspects of rough sets. Some relationships have already been established between rough sets and other approaches, and also with a wide range of hybrid systems. As a result, rough sets are linked with decision system modeling and analysis of complex systems, fuzzy sets, neural networks, evolutionary computing, data mining and knowledge discovery, pattern recognition, machine learning, and approximate reasoning. In particular, rough sets are used in probabilistic reasoning, granular computing (including information granule calculi based on rough mereology), intelligent control, intelligent agent modeling, identification of autonomous systems, and process specification. Methods based on rough set theory alone or in combination with other approaches have been discovered with a wide range of applications in such areas as: acoustics, bioinformatics, business and finance, chemistry, computer engineering (e.g., data compression, digital image processing, digital signal processing, parallel and distributed computer systems, sensor fusion, fractal engineering), decision analysis and systems, economics, electrical engineering (e.g., control, signal analysis, power systems), environmental studies, informatics, medicine, molecular biology, musicology, neurology, robotics, social science, software engineering, spatial visualization, Web engineering, and Web mining.

Advanced Parallel Processing Technologies Ming Xu, Yinwei Zhan, Jiannong Cao, Yijun Liu, 2007-11-07 This book constitutes the refereed proceedings of the 7th International Workshop on Advanced Parallel Processing Technologies, APPT 2007, held in Guangzhou, China, in November 2007. The 78 revised full papers presented were carefully reviewed and selected from 346 submissions. All current aspects in parallel and distributed computing are addressed ranging from

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Concepts in Bioinformatics and Genomics Jamil Momand, Alison McCurdy, 2017 Concepts in Bioinformatics and Genomics takes a conceptual approach, balancing biology, mathematics, and programming while highlighting relevant real-world applications and providing students with the tools to compute and analyze biological data. Through many thought-provoking exercises, students will develop a deeper understanding of the molecular biology, basic probability, software programs, and program-coding methodology underpinning this exciting field.

Mobile Computing, Applications, and Services Yuyu Yin, Ying Li, Honghao Gao, Jilin Zhang, 2019-09-24 This book constitutes the thoroughly refereed post-conference proceedings of the 10th International Conference on Mobile Computing, Applications, and Services, MobiCASE 2019, held in Hangzhou, China, in June 2019. The 17 full papers were carefully reviewed and selected from 48 submissions. The papers are organized in topical sections on mobile application with data analysis, mobile application with AI, edge computing, energy optimization and application

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well as genomes. The book has been rewritten to make it more accessible to a wider audience, including advanced undergraduate and graduate students. New features include chapter guides and explanatory information panels and glossary terms. New chapters in this second edition cover statistical analysis of sequence alignments, computer programming for bioinformatics, and data management and mining. Practically oriented problems at the ends of chapters enhance the value of the book as a teaching resource. The book also serves as an essential reference for professionals in molecular biology, pharmaceutical, and genome laboratories.

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