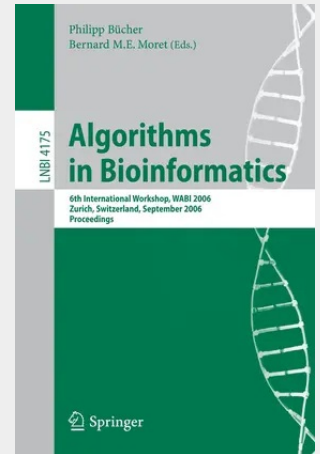


Algorithms in Bioinformatics

6th International Workshop, WABI 2006, Zurich, Switzerland, September 11-13, 2006, Proceedings

Here are the refereed proceedings of the 6th International Workshop on Algorithms in Bioinformatics, WABI 2006, held in the course of the ALGO 2006 conference meetings. The book presents 36 revised full papers addressing all current issues of algorithms in bioinformatics, from mathematical tools to experimental studies of approximation algorithms and reports on significant computational analyses. For the first time, coverage extends to machine-learning approaches along with combinatorial optimization.

We are very pleased to present the proceedings of the Sixth Workshop on Algorithms in Bioinformatics (WABI 2006), which took place in Zurich September 11-13, 2006, under the auspices of the International Society for Computational Biology (ISCB), the European Association for Theoretical Computer Science (EATCS), and the Eidgenössische Technische Hochschule Zürich (ETHZ). The Workshop on Algorithms in Bioinformatics covers research on all aspects of algorithmic work in bioinformatics. The emphasis is on discrete algorithms that address important problems in molecular biology, that are founded on sound models, that are computationally efficient, and that have been implemented and tested in simulations and on real datasets. The goal is to present recent research results, including significant work-in-progress, and to identify and explore directions of future research. Specific topics of interest include, but are not limited to: – Exact, approximate, and machine-learning algorithms for genomics, sequence analysis, gene and signal recognition, alignment, molecular evolution, population genetics and nucleotide polymorphism, structure determination or prediction, gene expression and gene networks, proteomics, functional genomics, and drug design. – Methods, software and dataset repositories for the development and testing of such algorithms and their underlying models. – High-performance approaches to computationally hard problems in bioinformatics, particularly optimization problems.



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