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this book is the first of its kind to provide a large collection of bioinformatics problems with accompanying solutions notably the problem set includes all of the problems offered in biological sequence analysis by durbin et al cambridge 1998 widely adopted as a required text for bioinformatics courses at leading universities worldwide although many of the problems included in biological sequence analysis as exercises for its readers have been repeatedly used for homework and tests no detailed solutions for the problems were available bioinformatics instructors had therefore frequently expressed a need for fully worked solutions and a larger set of problems for use on courses this book provides just that following the same structure as biological sequence analysis and significantly extending the set of workable problems it will facilitate a better understanding of the contents of the chapters in bsa and will help its readers develop problem solving skills that are vitally important for conducting successful research in the growing field of bioinformatics all of the material has been class tested by the authors at georgia tech where the first ever msc degree program in bioinformatics was held

the exponentially increasing amounts of biological data along with comparable advances in computing power are making possible the construction of quantitative predictive biological systems models this development could revolutionize those biology based fields of science to assist this transformation the u s department of energy asked the national research council to recommend mathematical research activities to enable more effective use of the large amounts of existing genomic information and the structural and functional genomic

information being created the resulting study is a broad scientifically based view of the opportunities lying at the mathematical science and biology interface the book provides a review of past successes an examination of opportunities at the various levels of biological systemsâ from molecules to ecosystemsâ an analysis of cross cutting themes and a set of recommendations to advance the mathematics biology connection that are applicable to all agencies funding research in this area

discover how to streamline complex bioinformatics applications with parallel computing this publication enables readers to handle more complex bioinformatics applications and larger and richer data sets as the editor clearly shows using powerful parallel computing tools can lead to significant breakthroughs in deciphering genomes understanding genetic disease designing customized drug therapies and understanding evolution a broad range of bioinformatics applications is covered with demonstrations on how each one can be parallelized to improve performance and gain faster rates of computation current parallel computing techniques and technologies are examined including distributed computing and grid computing readers are provided with a mixture of algorithms experiments and simulations that provide not only qualitative but also quantitative insights into the dynamic field of bioinformatics parallel computing for bioinformatics and computational biology is a contributed work that serves as a repository of case studies collectively demonstrating how parallel computing streamlines difficult problems in bioinformatics and produces better results each of the chapters is authored by an established expert in the field and carefully edited to ensure a consistent approach and high standard throughout the publication the work is organized into five parts algorithms and models sequence analysis and microarrays phylogenetics protein folding platforms and enabling technologies researchers educators and students in the field of bioinformatics will discover how high performance computing can enable them to handle more complex data sets gain deeper insights and make new discoveries

dynamical systems for biological modeling an introduction prepares both biology and mathematics students with the understanding and techniques necessary to undertake basic modeling of biological systems it achieves this through the development and analysis of dynamical systems the approach emphasizes qualitative ideas rather than explicit computa

so called string problems are abundant in bioinformatics and computational biology new optimization problems dealing with dna or protein sequences are constantly arising and researchers are highly in need of efficient optimization techniques for solving them one obstacle for optimization practitioners is the atypical nature of these problems which require an interdisciplinary approach in order to solve them efficiently and accurately

no detailed description available for thermodynamic bases of biological processes

methodological pluralism is advocated in this book which takes students on an investigative tour of uncertainty in the social sciences with particular emphasis on the scientific response to uncertainty much of the material is drawn from the disciplines of international relations and politics

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