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A suite of databases and tools to conducting genome and metagenome studies. Nucleotide. The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

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Aimed at students of
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Databases and Algorithms describes the methods used to store, retrieve, and derive data from databases using various tools. Bioinformatics. Experiments, Tools, Databases, and Algorithms. Orpita Bosu and Simminder Kaur Thukral. Description.

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Bioinformatics: Experiments

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Bioinformatics isn't just about storing biological data in databases, it also concerns conducting experiments on that data. Finding a database entry you are interested in is database searching, but as soon as you want to draw a conclusion from your search – inferring homologues of a protein of interest for example – you are conducting an experiment and need to apply the same scientific methodologies in terms of controls etc. that you would

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to an experiment in the
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Aimed at students of biotechnology, this work describes the methods used to store, receive, and derive data from databases using various tools.

This textbook presents mathematical models in bioinformatics and describes biological problems that inspire the computer science tools used to manage the enormous data sets involved. The first part of the book covers mathematical and computational methods, with

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Practical applications presented in the second part. The mathematical presentation avoids unnecessary formalism, while remaining clear and precise. The book closes with a thorough bibliography, reaching from classic research results to very recent findings. This volume is suited for a senior undergraduate or graduate course on bioinformatics, with a strong focus on mathematical and computer science background.

The field of statistics not only affects all areas of scientific activity, but also many other matters such

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as public policy. It is branching rapidly into so many different subjects that a series of handbooks is the only way of comprehensively presenting the various aspects of statistical methodology, applications, and recent developments. The Handbook of Statistics, a series of self-contained reference books. Each volume is devoted to a particular topic in statistics with Volume 28 dealing with bioinformatics. Every chapter is written by prominent workers in the area to which the volume is devoted. The series is addressed to the entire community of statisticians

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and scientists in various disciplines who use statistical methodology in their work. At the same time, special emphasis is placed on applications-oriented techniques, with the applied statistician in mind as the primary audience. Comprehensively presents the various aspects of statistical methodology. Discusses a wide variety of diverse applications and recent developments. Contributors are internationally renowned experts in their respective areas.

The field of statistics not only affects all areas of

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Scientific activity, but also many other matters such as public policy. It is branching rapidly into so many different subjects that a series of handbooks is the only way of comprehensively presenting the various aspects of statistical methodology, applications, and recent developments. The Handbook of Statistics, a series of self-contained reference books. Each volume is devoted to a particular topic in statistics with Volume 28 dealing with bioinformatics. Every chapter is written by prominent workers in the area to which the volume is devoted. The series is

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addressed to the entire community of statisticians and scientists in various disciplines who use statistical methodology in their work. At the same time, special emphasis is placed on applications-oriented techniques, with the applied statistician in mind as the primary audience. Comprehensively presents the various aspects of statistical methodology
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"This reference expands the field of database technologies through four-volumes of in-depth, advanced research articles from nearly 300 of the world's leading professionals"--Provided by publisher.

Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools provides a coherent and friendly treatment of bioinformatics for any student or scientist within biology who has not routinely performed bioinformatic analysis. The book discusses the relevant

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principles needed to understand the theoretical underpinnings of

bioinformatic analysis and demonstrates, with examples, targeted analysis using freely available web-based software and publicly available databases.

Eschewing non-essential information, the work focuses on principles and hands-on analysis, also pointing to further study options. Avoids non-essential coverage, yet fully describes the field for beginners Explains the molecular basis of evolution to place bioinformatic analysis in biological context Provides useful

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Links to the vast resource of publicly available bioinformatic databases and analysis tools Contains over 100 figures that aid in concept discovery and illustration

Bioinformatics is an integrative field of computer science, genetics, genomics, proteomics, and statistics, which has undoubtedly revolutionized the study of biology and medicine in past decades. It mainly assists in modeling, predicting and interpreting large multidimensional biological data by utilizing advanced computational methods. Despite its

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enormous potential, bioinformatics is not widely integrated into the academic curriculum as most life science students and researchers are still not equipped with the necessary knowledge to take advantage of this powerful tool. Hence, the primary purpose of our book is to supplement this unmet need by providing an easily accessible platform for students and researchers starting their career in life sciences. This book aims to avoid sophisticated computational algorithms and programming. Instead, it focuses on simple DIY analysis and interpretation of biological

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data with personal computers. Our belief is that once the beginners acquire these basic skillsets, they will be able to handle most of the bioinformatics tools for their research work and to better understand their experimental outcomes. Our second title of this volume set In Silico Life Sciences: Medicine provides hands-on experience in analyzing high throughput molecular data for the diagnosis, prognosis, and treatment of monogenic or polygenic human diseases. The key concepts in this volume include risk factor assessment, genetic tests and result

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interpretation, personalized medicine, and drug discovery. This volume is expected to train readers in both single and multi-dimensional biological analysis using open data sets, and provides a unique learning experience through clinical scenarios and case studies.

" The main focus of this publication is on technologies, solutions and requirements that interest the grid and the life-science communities to foster the integration of grids into health. The

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Proceedings are especially interesting for grid middleware and grid application developers, biomedical and health informatics users, and security and policy makers with a common focus on the application in the health domain. Topics in this publication are: State-of-the-art of the grid research and use at molecule, cell, organ, individual and population levels; and security and imaging. In security, data protection and pseudonymization are being discussed. In imaging, theres Globus MEDICUS, which federates DICOM devices through a grid architecture

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and KnowARC on facilitating grid networks for the biomedical research community. Finally, there's a report on the successful use of multimodal workflows in diabetic retinopathy research. "

"This book offers research articles focused on key issues concerning the development, design, and analysis of databases"--Provided by publisher.

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