

Building Bioinformatics Solutions With Perl R And Mysql

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Building Bioinformatics Solutions

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Building Bioinformatics Solutions provides a comprehensive introduction to this methodology, explaining how to acquire and use the most popular development tools, how to apply them to build processing pipelines, and how to make the results available through visualizations and web-based services for deployment either locally or via the Internet. The main development tools covered in this book are the MySQL database management system, the Perl programming language, and the R language for ...

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Bioinformatics encompasses a broad and ever-changing range of activities involved with the management and analysis of data from molecular biology experiments. Despite the diversity of activities and applications, the basic methodology and core tools needed to tackle bioinformatics problems is common to many projects. This unique book provides an invaluable introduction to three of the main tools used in the development of bioinformatics software - Perl, R and MySQL - and explains how these can be used together to tackle the complex data-driven challenges that typify modern biology. These industry standard open source tools form the core of many bioinformatics projects, both in academia and industry. The methodologies introduced are platform independent, and all the examples that feature have been tested on Windows, Linux and Mac OS. Building Bioinformatics Solutions is suitable for graduate students and researchers in the life sciences who wish to automate analyses or create their own databases and web-based tools. No prior knowledge of software development is assumed. Having worked through the book, the reader should have the necessary core skills to develop computational solutions for their specific research programmes. The book will also help the reader overcome the inertia associated with penetrating this field, and provide them with the confidence and understanding required to go on to develop more advanced bioinformatics skills.

Despite the diversity of activities and applications of modern bioinformatics, the basic methodology needed to tackle problems is common to most projects. The aim of this book is to provide a comprehensive introduction to this methodology to aid the management and analysis of data from molecular biology experiments.

With its highly developed capacity to detect patterns in data, Perl has become one of the most popular languages for biological data analysis. But if you're a biologist with little or no programming experience, starting out in Perl can be a challenge. Many biologists have a difficult time learning how to apply the language to bioinformatics. The most popular Perl programming books are often too theoretical and too focused on computer science for a non-programming biologist who needs to solve very specific problems.Beginning Perl for Bioinformatics is designed to get you quickly over the Perl language barrier by approaching programming as an important new laboratory skill, revealing Perl programs and techniques that are immediately useful in the lab. Each chapter focuses on solving a particular bioinformatics problem or class of problems, starting with the simplest and increasing in complexity as the book progresses. Each chapter includes programming exercises and teaches bioinformatics by showing and modifying programs that deal with various kinds of practical biological problems. By the end of the book you'll have a solid understanding of Perl basics, a collection of programs for such tasks as parsing BLAST and GenBank, and the skills to take on more advanced bioinformatics programming. Some of the later chapters focus in greater detail on specific bioinformatics topics. This book is suitable for use as a classroom textbook, for self-study, and as a reference.The book covers: Programming basics and working with DNA sequences and strings Debugging your code Simulating gene mutations using random number generators Regular expressions and finding motifs in data Arrays, hashes, and relational databases Regular expressions and restriction maps Using Perl to parse PDB records, annotations in GenBank, and BLAST output

Bioinformatics encompasses a broad and ever-changing range of activities involved with the management and analysis of data from molecular biology experiments. Despite the diversity of activities and applications, the basic methodology and core tools needed to tackle bioinformatics problems is common to many projects. This unique book provides an invaluable introduction to three of the main tools used in the development of bioinformatics software - Perl, R and MySQL - and explains how these can be used together to tackle the complex data-driven challenges that typify modern biology. These industry standard open source tools form the core of many bioinformatics projects, both in academia and industry. The methodologies introduced are platform independent, and all the examples that feature have been tested on Windows, Linux and Mac OS. Building Bioinformatics Solutions is suitable for graduate students and researchers in the life sciences who wish to automate analyses or create their own databases and web-based tools. No prior knowledge of software development is assumed. Having worked through the book, the reader should have the necessary core skills to develop computational solutions for their specific research programmes. The book will also help the reader overcome the inertia associated with penetrating this field, and provide them with the confidence and understanding required to go on to develop more advanced bioinformatics skills.

Offers a structured approach to biological data and the computer tools needed to analyze it, covering UNIX, databases, computation, Perl, data mining, data visualization, and tailoring software to suit specific research needs.

Working on the assumption that the reader has no formal training in programming, Perl Programming for Biologists demonstrates how Perl is used to solve biological problems. Each chapter opens with a set of learning objectives, provides numerous review questions and self-study exercises, and concludes with a bulleted summary of key points. The author incorporates numerous real-life examples throughout the text. Upon completing the book, readers are able to quickly perform such tasks as correcting recurring errors in spreadsheets, scanning a Fasta sequence for every occurrence of an EcoRI site, adapting other writers' scripts to one's own purposes, and most important, writing reusable and maintainable scripts that spare the rote repetition of code.

Historically, programming hasn't been considered a critical skill for biologists. But now, with access to vast amounts of biological data contained in public databases, programming skills are increasingly in strong demand in biology research and development. Perl, with its highly developed capacities in string handling, text processing, networking, and rapid prototyping, has emerged as the programming language of choice for biological data analysis.Mastering Perl for Bioinformatics covers the core Perl language and many of its module extensions, presenting them in the context of biological data and problems of pressing interest to the biological community. This book, along with Beginning Perl for Bioinformatics, forms a basic course in Perl programming. This second volume finishes the basic Perl tutorial material (references, complex data structures, object-oriented programming, use of modules--all presented in a biological context) and presents some advanced topics of considerable interest in bioinformatics.The range of topics covered in Mastering Perl for Bioinformatics prepares the reader for enduring and emerging developments in critical areas of bioinformatics programming such as: Gene finding String alignment Methods of data storage and retrieval (SML and databases) Modeling of networks (graphs and Petri nets) Graphics (Tk) Parallelization Interfacing with other programming languages Statistics (PDL) Protein structure determination Biological models of computation (DNA Computers) Biologists and computer scientists who have conquered the basics of Perl and are ready to move even further in their mastery of this versatile language will appreciate the author's well-balanced approach to applying Perl's analytical abilities to the field of bioinformatics. Full of practical examples and real-world biological problem solving, this book is a must for any reader wanting to move beyond beginner level Perl in bioinformatics.

Explains many computational molecular biology problems and how to implement solutions to them in Perl.

Written for biomedical professionals and hospital practitioners interested in creating their own programs, Perl Programming for Medicine and Biology, discusses and reviews biomedical data resources, data standards, data organization, medicolegal and ethical conduct for data miners, and grants-related data sharing responsibilities. It teaches readers the basic Perl programming skills necessary for collecting, analyzing, and distributing biomedical data and provides solutions to in-depth problems that face researchers and healthcare professionals. Non-technical "Background" sections open each chapter to help non-programmers easily comprehend programming procedures. Explanations are provided for the biomedical issues underlying the Perl scripts that follow, and examples of real-world implementation are provided. Perl Programming for Medicine and Biology will show you how to transform, merge, and examine large and complex databases with ease.

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