Bioinformatics Programming Using Python Practical Programming For Biological Data By Mitchell L Model Dec 22 2009

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Managing Your Biological Data with Python - Allegra Via 2014-03-18
Take Control of Your Data and Use Python with ConfidenceRequiring no prior programming experience, Managing Your Biological Data with Python empowers biologists and other life scientists to work with biological data on their own using the Python language. The book teaches them not only how to program but also how to manage their data. It shows how

Beginning Python - Magnus Lie Hetland 2006-11-07
* Totaling 900 pages and covering all of the topics important to new and intermediate users, Beginning Python is intended to be the most comprehensive book on the Python ever written. * The 15 sample projects in Beginning Python are attractive to novice programmers interested in learning by creating applications of timely interest, such as a P2P file-sharing application, Web-based bulletin-board, and an arcade game similar to the classic Space Invaders. * The author Magnus Lie Hetland, PhD, is author of Apress' well-received 2002 title, Practical Python, ISBN: 1-59059-006-6. He's also author of the popular online guide, Instant Python Hacking (http://www.hetland.org), from which both Practical Python and Beginning Python are based.

Bayesian Analysis with Python - Osvaldo Martin 2016-11-25
Unleash the power and flexibility of the Bayesian frameworkAbout This Book- Simplify the Bayes process for solving complex statistical problems using Python; - Tutorial guide that will take the you through the journey of Bayesian analysis with the help of sample problems and practice exercises; - Learn how and when to use Bayesian analysis in your applications with this guide.Who This Book Is ForStudents, researchers and data scientists who wish to learn Bayesian data analysis with Python and implement probabilistic models in their day to day projects. Programming experience with Python is essential. No previous statistical knowledge is assumed.What You Will Learn- Understand the essentials Bayesian concepts from a practical point of view- Learn how to build probabilistic models using the Python library PyMC3- Acquire the skills to sanity-check your models and modify them if necessary- Add structure to your models and get the advantages of hierarchical models- Find out how different models can be used to answer different data analysis questions - When in doubt, learn to choose between alternative models.- Predict continuous target outcomes using regression analysis or assign classes using logistic and softmax regression.- Learn how to think probabilistically and unleash the power and flexibility of the Bayesian frameworkIn DetailThe purpose of this book is to teach the main concepts of Bayesian data analysis. We will learn how to effectively use PyMC3, a Python library for probabilistic programming, to perform Bayesian parameter estimation, to check models and validate them. This book begins presenting the key concepts of the Bayesian framework and the main advantages of this approach from a practical point of view. Moving on, we will explore the power and flexibility of generalized linear models and how to adapt them to a wide array of problems, including regression and classification. We will also look into mixture models and clustering data, and we will finish with advanced topics like non-parametrics models and Gaussian processes. With the help of Python and PyMC3 you will learn to implement, check and expand Bayesian models to solve data analysis problems.Style and approachBayes algorithms are widely used in statistics, machine learning, artificial intelligence, and data mining. This will be a practical guide allowing the readers to use Bayesian methods for statistical modelling and analysis using Python.

Bioinformatics Programming in Python - Ruediger-Marcus Flaig 2011-10-05
This first introductory book designed to train novice programmers is based on a student course taught by the author, and has been optimized for biology students without previous experience in programming. By interspersing theory chapters with numerous small and large programming exercises, the author quickly shows readers how to do their own programming, and throughout uses anecdotes and real-life examples from the biosciences to 'spice up' the text. This practical book thus teaches essential programming skills for life scientists who want -- or need -- to write their own bioinformatics software tools.

Python Programming in Context - Bradley N. Miller 2014
"The user-friendly, object-oriented programming language Python is quickly becoming the most popular introductory programming language for both students and instructors ... Building on essential concepts of computer science and offering a plentitude of real-world examples, Python programming in context, Second edition offers a thorough overview of multiple applied areas, including image processing, cryptography, astronomy, the Internet, and bioinformatics. The text's emphasis on problem solving, extrapolation, and development of independent exploration and solution building provides students with a unique and innovative approach to learning programming." --

Python for the Life Sciences - Alexander Lancaster 2019-09-27
Treat yourself to a lively, intuitive, and easy-to-follow introduction to computer programming in Python. The book was written specifically for biologists with little or no prior experience of writing code - with the goal of giving them not only a foundation in Python programming, but also the confidence and inspiration to start using Python in their own research. Virtually all of the examples in the book are drawn from across a wide spectrum of life science research, from simple biochemical calculations and sequence analysis, to modeling the dynamic interactions of genes and proteins in cells, or the drift of genes in an evolving population. Best of all, Python for the Life Sciences shows you how to implement all of these projects in Python, one of the most popular programming languages for scientific computing. If you are a life scientist interested in learning Python to jump-start your research, this is the book for you. What You'll Learn Write Python scripts to automate your lab calculations Search for important motifs in genome sequences Use object-oriented programming with Python Study mining interaction network data for patterns Review dynamic modeling of biochemical switches Who This Book Is For Life scientists with little or no programming experience, including undergraduate and graduate students, postdoctoral researchers in academia and industry, medical professionals, and teachers/lecturers. "A comprehensive introduction to using Python for computational biology... A lovely book with humor and perspective" -- John Novembre, Associate Professor of Human Genetics, University of Chicago and MacArthur Fellow "Fun, entertaining, witty and darn useful. A magical portal to the big data revolution" -- Sandro Santagata, Assistant Professor in Pathology, Harvard Medical School "Alex and Gordon's enthusiasm for Python is contagious" -- Glenys Thomson Professor of Integrative Biology, University of California, Berkeley

Python for Bioinformatics - Jason Kinser 2010-10-25
Python for Bioinformatics provides a clear introduction to the Python programming language and instructs beginners on the development of simple programming exercises. Important Notice: The digital edition of this book is missing some of the images or content found in the physical edition.

Introduction to Bioinformatics with R - Edward Curry 2020-11-02
In biological research, the amount of data available to researchers has increased so much over recent years, it is becoming increasingly difficult to understand the current state of the art without some experience and understanding of data analytics and bioinformatics. An Introduction to Bioinformatics with R: A Practical Guide for Biologists leads the reader through the basics of computational analysis of data encountered in modern biological research. With no previous experience with statistics

or programming required, readers will develop the ability to plan suitable analyses of biological datasets, and to use the R programming environment to perform these analyses. This is achieved through a series of case studies using R to answer research questions using molecular biology datasets. Broadly applicable statistical methods are explained, including linear and rank-based correlation, distance metrics and hierarchical clustering, hypothesis testing using linear regression, proportional hazards regression for survival data, and principal component analysis. These methods are then applied as appropriate throughout the case studies, illustrating how they can be used to answer research questions. Key Features: · Provides a practical course in computational data analysis suitable for students or researchers with no previous exposure to computer programming. · Describes in detail the theoretical basis for statistical analysis techniques used throughout the textbook, from basic principles · Presents walk-throughs of data analysis tasks using R and example datasets. All R commands are presented and explained in order to enable the reader to carry out these tasks themselves. · Uses outputs from a large range of molecular biology platforms including DNA methylation and genotyping microarrays; RNA-seq, genome sequencing, ChIP-seq and bisulphite sequencing; and high-throughput phenotypic screens. · Gives worked-out examples geared towards problems encountered in cancer research, which can also be applied across many areas of molecular biology and medical research. This book has been developed over years of training biological scientists and clinicians to analyse the large datasets available in their cancer research projects. It is appropriate for use as a textbook or as a practical book for biological scientists looking to gain bioinformatics skills.

Beginning Perl for Bioinformatics - James Tisdall 2001-10-22
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 with Python Cookbook - Tiago Antao 2015-06-25
If you are either a computational biologist or a Python programmer, you will probably relate to the expression "explosive growth, exciting times". Python is arguably the main programming language for big data, and the deluge of data in biology, mostly from genomics and proteomics, makes bioinformatics one of the most exciting fields in data science. Using the hands-on recipes in this book, you'll be able to do practical research and analysis in computational biology with Python. We cover modern, next-generation sequencing libraries and explore real-world examples on how to handle real data. The main focus of the book is the practical application of bioinformatics, but we also cover modern programming techniques and frameworks to deal with the ever increasing deluge of bioinformatics data.

Mastering Python for Bioinformatics - Ken Youens-Clark 2021-05-05
Life scientists today urgently need training in bioinformatics skills. Too many bioinformatics programs are poorly written and barely maintained--usually by students and researchers who've never learned basic programming skills. This practical guide shows postdoc bioinformatics professionals and students how to exploit the best parts of Python to

solve problems in biology while creating documented, tested, reproducible software. Ken Youens-Clark, author of Tiny Python Projects (Manning), demonstrates not only how to write effective Python code but also how to use tests to write and refactor scientific programs. You'll learn the latest Python features and toolsâ??including linters, formatters, type checkers, and testsâ??to create documented and tested programs. You'll also tackle 14 challenges in Rosalind, a problem-solving platform for learning bioinformatics and programming. Create command-line Python programs to document and validate parameters Write tests to verify refactor programs and confirm they're correct Address bioinformatics ideas using Python data structures and modules such as Biopython Create reproducible shortcuts and workflows using makefiles Parse essential bioinformatics file formats such as FASTA and FASTQ Find patterns of text using regular expressions Use higher-order functions in Python like filter(), map(), and reduce()

Python Programming for Biology - Tim J. Stevens 2015-02-12
Do you have a biological question that could be readily answered by computational techniques, but little experience in programming? Do you want to learn more about the core techniques used in computational biology and bioinformatics? Written in an accessible style, this guide provides a foundation for both newcomers to computer programming and those interested in learning more about computational biology. The chapters guide the reader through: a complete beginners' course to programming in Python, with an introduction to computing jargon; descriptions of core bioinformatics methods with working Python examples; scientific computing techniques, including image analysis, statistics and machine learning. This book also functions as a language reference written in straightforward English, covering the most common Python language elements and a glossary of computing and biological terms. This title will teach undergraduates, postgraduates and professionals working in the life sciences how to program with Python, a powerful, flexible and easy-to-use language.

Explorations in Computing - John S. Conery 2014-09-24
An Active Learning Approach to Teaching the Main Ideas in Computing Explorations in Computing: An Introduction to Computer Science and Python Programming teaches computer science students how to use programming skills to explore fundamental concepts and computational approaches to solving problems. Tbook gives beginning students an introduction to

Practical Computing for Biologists - Steven Harold David Haddock 2011
To help with the increasingly large data sets that many scientists deal with, this book illustrates how to use many freely available computing tools to work more powerfully and effectively. The book was born out of the authors' experiences developing tools for their research and to fix other biologist's computational problems.

Bioinformatics Data Skills - Vince Buffalo 2015-07
Learn the data skills necessary for turning large sequencing datasets into reproducible and robust biological findings. With this practical guide, youâ??ll learn how to use freely available open source tools to extract meaning from large complex biological data sets. At no other point in human history has our ability to understand lifeâ??s complexities been so dependent on our skills to work with and analyze data. This intermediate-level book teaches the general computational and data skills you need to analyze biological data. If you have experience with a scripting language like Python, youâ??re ready to get started. Go from handling small problems with messy scripts to tackling large problems with clever methods and tools Process bioinformatics data with powerful Unix pipelines and data tools Learn how to use exploratory data analysis techniques in the R language Use efficient methods to work with genomic range data and range operations Work with common genomics data file formats like FASTA, FASTQ, SAM, and BAM Manage your bioinformatics project with the Git version control system Tackle tedious data processing tasks with with Bash scripts and Makefiles

Bioinformatics - Frédéric Dardel 2007-01-11
This book is an excellent introductory text describing the use of bioinformatics to analyze genomic and post-genomic data. It has been translated from the original popular French edition, which was based on a course taught at the well-respected École Polytechnique in Palaiseau. This edition has been fully revised and updated by the authors. After a brief introduction to gene structure and sequence determination, it describes the techniques used to identify genes, their protein-coding sequences and regulatory regions. The book discusses the methodology of comparative genomics, using information from different organisms to deduce information about unknown sequences. There is a comprehensive

chapter on structure prediction, covering both RNA and protein. Finally, the book describes the complex networks of RNA and protein that exist within the cell and their interactions, ending with a discussion of the simulation approaches that can be used to model these networks. Praise from the reviews: "In context of the new developments the genomic era has brought, Bioinformatics: Genomics and Post-Genomics becomes a fundamental and indispensable resource for undergraduate and early graduate students...insightfully authored...will immensely help students...in establishing important foundations while shaping their careers." NEWSLETTER, BRITISH SOCIETY OF CELL BIOLOGY

Bioinformatics Programming Using Python - Mitchell Model 2009-12-15
Powerful, flexible, and easy to use, Python is an ideal language for building software tools and applications for life science research and development. This unique book shows you how to program with Python, using code examples taken directly from bioinformatics. In a short time, you'll be using sophisticated techniques and Python modules that are particularly effective for bioinformatics programming. Bioinformatics Programming Using Python is perfect for anyone involved with bioinformatics -- researchers, support staff, students, and software developers interested in writing bioinformatics applications. You'll find it useful whether you already use Python, write code in another language, or have no programming experience at all. It's an excellent self-instruction tool, as well as a handy reference when facing the challenges of real-life programming tasks. Become familiar with Python's fundamentals, including ways to develop simple applications Learn how to use Python modules for pattern matching, structured text processing, online data retrieval, and database access Discover generalized patterns that cover a large proportion of how Python code is used in bioinformatics Learn how to apply the principles and techniques of object-oriented programming Benefit from the "tips and traps" section in each chapter

R Bioinformatics Cookbook - Dan MacLean 2019-10-11
Over 60 recipes to model and handle real-life biological data using modern libraries from the R ecosystem Key FeaturesApply modern R packages to handle biological data using real-world examplesRepresent biological data with advanced visualizations suitable for research and publicationsHandle real-world problems in bioinformatics such as next-generation sequencing, metagenomics, and automating analysesBook Description Handling biological data effectively requires an in-depth knowledge of machine learning techniques and computational skills, along with an understanding of how to use tools such as edgeR and DESeq. With the R Bioinformatics Cookbook, you'll explore all this and more, tackling common and not-so-common challenges in the bioinformatics domain using real-world examples. This book will use a recipe-based approach to show you how to perform practical research and analysis in computational biology with R. You will learn how to effectively analyze your data with the latest tools in Bioconductor, ggplot, and tidyverse. The book will guide you through the essential tools in Bioconductor to help you understand and carry out protocols in RNAseq, phylogenetics, genomics, and sequence analysis. As you progress, you will get up to speed with how machine learning techniques can be used in the bioinformatics domain. You will gradually develop key computational skills such as creating reusable workflows in R Markdown and packages for code reuse. By the end of this book, you'll have gained a solid understanding of the most important and widely used techniques in bioinformatic analysis and the tools you need to work with real biological data. What you will learnEmploy Bioconductor to determine differential expressions in RNAseq dataRun SAMtools and develop pipelines to find single nucleotide polymorphisms (SNPs) and IndelsUse ggplot to create and annotate a range of visualizationsQuery external databases with Ensembl to find functional genomics informationExecute large-scale multiple sequence alignment with DECIPHER to perform comparative genomicsUse d3.js and Plotly to create dynamic and interactive web graphicsUse k-nearest neighbors, support vector machines and random forests to find groups and classify dataWho this book is for This book is for bioinformaticians, data analysts, researchers, and R developers who want to address intermediate-to-advanced biological and bioinformatics problems by learning through a recipe-based approach. Working knowledge of R programming language and basic knowledge of bioinformatics are prerequisites.

Natural Language Processing with Python - Steven Bird 2009-06-12
This book offers a highly accessible introduction to natural language processing, the field that supports a variety of language technologies, from predictive text and email filtering to automatic summarization and

translation. With it, you'll learn how to write Python programs that work with large collections of unstructured text. You'll access richly annotated datasets using a comprehensive range of linguistic data structures, and you'll understand the main algorithms for analyzing the content and structure of written communication. Packed with examples and exercises, Natural Language Processing with Python will help you: Extract information from unstructured text, either to guess the topic or identify "named entities" Analyze linguistic structure in text, including parsing and semantic analysis Access popular linguistic databases, including WordNet and treebanks Integrate techniques drawn from fields as diverse as linguistics and artificial intelligence This book will help you gain practical skills in natural language processing using the Python programming language and the Natural Language Toolkit (NLTK) open source library. If you're interested in developing web applications, analyzing multilingual news sources, or documenting endangered languages -- or if you're simply curious to have a programmer's perspective on how human language works -- you'll find Natural Language Processing with Python both fascinating and immensely useful.

Python for Bioinformatics - Sebastian Bassi 2017-08-07
In today's data driven biology, programming knowledge is essential in turning ideas into testable hypothesis. Based on the author's extensive experience, Python for Bioinformatics, Second Edition helps biologists get to grips with the basics of software development. Requiring no prior knowledge of programming-related concepts, the book focuses on the easy-to-use, yet powerful, Python computer language. This new edition is updated throughout to Python 3 and is designed not just to help scientists master the basics, but to do more in less time and in a reproducible way. New developments added in this edition include NoSQL databases, the Anaconda Python distribution, graphical libraries like Bokeh, and the use of Github for collaborative development.

A Primer on Scientific Programming with Python - Hans Petter Langtangen 2016-07-28
The book serves as a first introduction to computer programming of scientific applications, using the high-level Python language. The exposition is example and problem-oriented, where the applications are taken from mathematics, numerical calculus, statistics, physics, biology and finance. The book teaches "Matlab-style" and procedural programming as well as object-oriented programming. High school mathematics is a required background and it is advantageous to study classical and numerical one-variable calculus in parallel with reading this book. Besides learning how to program computers, the reader will also learn how to solve mathematical problems, arising in various branches of science and engineering, with the aid of numerical methods and programming. By blending programming, mathematics and scientific applications, the book lays a solid foundation for practicing computational science. From the reviews: Langtangen ... does an excellent job of introducing programming as a set of skills in problem solving. He guides the reader into thinking properly about producing program logic and data structures for modeling real-world problems using objects and functions and embracing the object-oriented paradigm. ... Summing Up: Highly recommended. F. H. Wild III, Choice, Vol. 47 (8), April 2010 Those of us who have learned scientific programming in Python 'on the streets' could be a little jealous of students who have the opportunity to take a course out of Langtangen's Primer." John D. Cook, The Mathematical Association of America, September 2011 This book goes through Python in particular, and programming in general, via tasks that scientists will likely perform. It contains valuable information for students new to scientific computing and would be the perfect bridge between an introduction to programming and an advanced course on numerical methods or computational science. Alex Small, IEEE, CiSE Vol. 14 (2), March /April 2012 "This fourth edition is a wonderful, inclusive textbook that covers pretty much everything one needs to know to go from zero to fairly sophisticated scientific programming in Python..." Joan Horvath, Computing Reviews, March 2015

Practical Programming - Paul Gries 2017-12-06
Classroom-tested by tens of thousands of students, this new edition of the bestselling intro to programming book is for anyone who wants to understand computer science. Learn about design, algorithms, testing, and debugging. Discover the fundamentals of programming with Python 3.6--a language that's used in millions of devices. Write programs to solve real-world problems, and come away with everything you need to produce quality code. This edition has been updated to use the new language features in Python 3.6.

Bioinformatics with Python Cookbook - Tiago Antao 2018-11-30
Discover modern, next-generation sequencing libraries from Python

ecosystem to analyze large amounts of biological data Key FeaturesPerform complex bioinformatics analysis using the most important Python libraries and applicationsImplement next-generation sequencing, metagenomics, automating analysis, population genetics, and moreExplore various statistical and machine learning techniques for bioinformatics data analysisBook Description Bioinformatics is an active research field that uses a range of simple-to-advanced computations to extract valuable information from biological data. This book covers next-generation sequencing, genomics, metagenomics, population genetics, phylogenetics, and proteomics. You'll learn modern programming techniques to analyze large amounts of biological data. With the help of real-world examples, you'll convert, analyze, and visualize datasets using various Python tools and libraries. This book will help you get a better understanding of working with a Galaxy server, which is the most widely used bioinformatics web-based pipeline system. This updated edition also includes advanced next-generation sequencing filtering techniques. You'll also explore topics such as SNP discovery using statistical approaches under high-performance computing frameworks such as Dask and Spark. By the end of this book, you'll be able to use and implement modern programming techniques and frameworks to deal with the ever-increasing deluge of bioinformatics data. What you will learnLearn how to process large next-generation sequencing (NGS) datasetsWork with genomic dataset using the FASTQ, BAM, and VCF formatsLearn to perform sequence comparison and phylogenetic reconstructionPerform complex analysis with protemics dataUse Python to interact with Galaxy serversUse High-performance computing techniques with Dask and SparkVisualize protein dataset interactions using CytoscapeUse PCA and Decision Trees, two machine learning techniques, with biological datasetsWho this book is for This book is for Data data Scientistsscientists, Bioinformatics bioinformatics analysts, researchers, and Python developers who want to address intermediate-to-advanced biological and bioinformatics problems using a recipe-based approach. Working knowledge of the Python programming language is expected.

Mastering Perl for Bioinformatics - James Tisdall 2003-09-25
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.

High Performance Python - Micha Gorelick 2020-04-30
Your Python code may run correctly, but you need it to run faster. Updated for Python 3, this expanded edition shows you how to locate performance bottlenecks and significantly speed up your code in high-data-volume programs. By exploring the fundamental theory behind design choices, High Performance Python helps you gain a deeper understanding of Python's implementation. How do you take advantage of multicore architectures or clusters? Or build a system that scales up and down without losing reliability? Experienced Python programmers will learn concrete solutions to many issues, along with war stories from companies that use high-performance Python for social media analytics, productionized machine learning, and more. Get a better grasp of

NumPy, Cython, and profilers Learn how Python abstracts the underlying computer architecture Use profiling to find bottlenecks in CPU time and memory usage Write efficient programs by choosing appropriate data structures Speed up matrix and vector computations Use tools to compile Python down to machine code Manage multiple I/O and computational operations concurrently Convert multiprocessing code to run on local or remote clusters Deploy code faster using tools like Docker

Applied Bioinformatics - Paul Maria Selzer 2008-01-18
At last, here is a baseline book for anyone who is confused by cryptic computer programs, algorithms and formulae, but wants to learn about applied bioinformatics. Now, anyone who can operate a PC, standard software and the internet can also learn to understand the biological basis of bioinformatics, of the existence as well as the source and availability of bioinformatics software, and how to apply these tools and interpret results with confidence. This process is aided by chapters that introduce important aspects of bioinformatics, detailed bioinformatics exercises (including solutions), and to cap it all, a glossary of definitions and terminology relating to bioinformatics.

Computing for Biologists - Ran Libeskind-Hadas 2014-09-22
Computing is revolutionizing the practice of biology. This book, which assumes no prior computing experience, provides students with the tools to write their own Python programs and to understand fundamental concepts in computational biology and bioinformatics. Each major part of the book begins with a compelling biological question, followed by the algorithmic ideas and programming tools necessary to explore it: the origins of pathogenicity are examined using gene finding, the evolutionary history of sex determination systems is studied using sequence alignment, and the origin of modern humans is addressed using phylogenetic methods. In addition to providing general programming skills, this book explores the design of efficient algorithms, simulation, NP-hardness, and the maximum likelihood method, among other key concepts and methods. Easy-to-read and designed to equip students with the skills to write programs for solving a range of biological problems, the book is accompanied by numerous programming exercises, available at www.cs.hmc.edu/CFB.

Python Pocket Reference - Mark Lutz 2014-01-22
Updated for both Python 3.4 and 2.7, this convenient pocket guide is the perfect on-the-job quick reference. You'll find concise, need-to-know information on Python types and statements, special method names, built-in functions and exceptions, commonly used standard library modules, and other prominent Python tools. The handy index lets you pinpoint exactly what you need. Written by Mark Lutz—widely recognized as the world's leading Python trainer—Python Pocket Reference is an ideal companion to O'Reilly's classic Python tutorials, Learning Python and Programming Python, also written by Mark. This fifth edition covers: Built-in object types, including numbers, lists, dictionaries, and more Statements and syntax for creating and processing objects Functions and modules for structuring and reusing code Python's object-oriented programming tools Built-in functions, exceptions, and attributes Special operator overloading methods Widely used standard library modules and extensions Command-line options and development tools Python idioms and hints The Python SQL Database API

Python for Biologists - Martin Jones 2013
Python for biologists is a complete programming course for beginners that will give you the skills you need to tackle common biological and bioinformatics problems.

Python for Scientists - John M. Stewart 2017-07-20
Scientific Python is taught from scratch in this book via copious, downloadable, useful and adaptable code snippets. Everything the working scientist needs to know is covered, quickly providing researchers and research students with the skills to start using Python effectively.

Computational Genomics with R - Altuna Akalin 2020-12-16
Computational Genomics with R provides a starting point for beginners in genomic data analysis and also guides more advanced practitioners to sophisticated data analysis techniques in genomics. The book covers topics from R programming, to machine learning and statistics, to the latest genomic data analysis techniques. The text provides accessible information and explanations, always with the genomics context in the background. This also contains practical and well-documented examples in R so readers can analyze their data by simply reusing the code presented. As the field of computational genomics is interdisciplinary, it requires different starting points for people with different backgrounds. For example, a biologist might skip sections on basic genome biology and

start with R programming, whereas a computer scientist might want to start with genome biology. After reading: You will have the basics of R and be able to dive right into specialized uses of R for computational genomics such as using Bioconductor packages. You will be familiar with statistics, supervised and unsupervised learning techniques that are important in data modeling, and exploratory analysis of high-dimensional data. You will understand genomic intervals and operations on them that are used for tasks such as aligned read counting and genomic feature annotation. You will know the basics of processing and quality checking high-throughput sequencing data. You will be able to do sequence analysis, such as calculating GC content for parts of a genome or finding transcription factor binding sites. You will know about visualization techniques used in genomics, such as heatmaps, meta-gene plots, and genomic track visualization. You will be familiar with analysis of different high-throughput sequencing data sets, such as RNA-seq, ChIP-seq, and BS-seq. You will know basic techniques for integrating and interpreting multi-omics datasets. Altuna Akalin is a group leader and head of the Bioinformatics and Omics Data Science Platform at the Berlin Institute of Medical Systems Biology, Max Delbrück Center, Berlin. He has been developing computational methods for analyzing and integrating large-scale genomics data sets since 2002. He has published an extensive body of work in this area. The framework for this book grew out of the yearly computational genomics courses he has been organizing and teaching since 2015.

An Introduction to Python Programming for Scientists and Engineers - Johnny Wei-Bing Lin 2022-05-31
Python is one of the most popular programming languages, widely used for data analysis and modelling, and is fast becoming the leading choice for scientists and engineers. Unlike other textbooks introducing Python, typically organised by language syntax, this book uses many examples from across Biology, Chemistry, Physics, Earth science, and Engineering to teach and motivate students in science and engineering. The text is organised by the tasks and workflows students undertake day-to-day, helping them see the connections between programming tools and their disciplines. The pace of study is carefully developed for complete beginners, and a spiral pedagogy is used so concepts are introduced across multiple chapters, allowing readers to engage with topics more than once. "Try This!" exercises and online Jupyter notebooks encourage students to test their new knowledge, and further develop their programming skills. Online solutions are available for instructors, alongside discipline-specific homework problems across the sciences and engineering.

Python by Example - Nichola Lacey 2019-06-06
A refreshingly different and engaging way of learning how to program using Python. This book includes example code and brief user-friendly explanations, along with 150 progressively trickier challenges. As readers are actively involved in their learning, they quickly master the new skills and gain confidence in creating their own programs.

Python Cookbook - David Beazley 2013-05-10
If you need help writing programs in Python 3, or want to update older Python 2 code, this book is just the ticket. Packed with practical recipes written and tested with Python 3.3, this unique cookbook is for experienced Python programmers who want to focus on modern tools and idioms. Inside, you'll find complete recipes for more than a dozen topics, covering the core Python language as well as tasks common to a wide variety of application domains. Each recipe contains code samples you can use in your projects right away, along with a discussion about how and why the solution works. Topics include: Data Structures and Algorithms Strings and Text Numbers, Dates, and Times Iterators and Generators Files and I/O Data Encoding and Processing Functions Classes and Objects Metaprogramming Modules and Packages Network and Web Programming Concurrency Utility Scripting and System Administration Testing, Debugging, and Exceptions C Extensions

EMBOSS Developer's Guide - Jon C. Ison 2011-06-16
The European Molecular Biology Open Software Suite (EMBOSS) is a high quality, well documented package of open source software tools for molecular biology. EMBOSS includes extensive and extensible C programming libraries, providing a powerful and robust toolkit for developing new bioinformatics tools from scratch. The EMBOSS Developer's Guide is the official and definitive guide to developing software under EMBOSS. It includes comprehensive reference information and guidelines, including step-by-step instructions and real-world code examples: • Learn how to write fully-featured tools guided by the people who developed EMBOSS • Step-by-step guide to writing EMBOSS applications, illustrated with functional, deployed code • ACD

file development - learn how to customise existing tools without coding, or design and write entirely new application interfaces • EMBOSS API programming guidelines - quickly master application development • Wrapping and porting applications under EMBOSS - learn how to incorporate third-party tools

R Programming for Bioinformatics - Robert Gentleman 2008-07-14
Due to its data handling and modeling capabilities as well as its flexibility, R is becoming the most widely used software in bioinformatics. R Programming for Bioinformatics explores the programming skills needed to use this software tool for the solution of bioinformatics and computational biology problems. Drawing on the author's first-hand experiences as an expert in R, the book begins with coverage on the general properties of the R language, several unique programming aspects of R, and object-oriented programming in R. It presents methods for data input and output as well as database interactions. The author also examines different facets of string handling and manipulations, discusses the interfacing of R with other languages, and describes how to write software packages. He concludes with a discussion on the debugging and profiling of R code. With numerous examples and exercises, this practical guide focuses on developing R programming skills in order to tackle problems encountered in bioinformatics and computational biology.

Hands on Data Science for Biologists Using Python - Yasha Hasija 2021-04-09
Hands-on Data Science for Biologists using Python has been conceptualized to address the massive data handling needs of modern-day biologists. With the advent of high throughput technologies and consequent availability of omics data, biological science has become a data-intensive field. This hands-on textbook has been written with the inception of easing data analysis by providing an interactive, problem-based instructional approach in Python programming language. The book starts with an introduction to Python and steadily delves into scrupulous techniques of data handling, preprocessing, and visualization. The book concludes with machine learning algorithms and their applications in biological data science. Each topic has an intuitive explanation of concepts and is accompanied with biological examples. Features of this book: The book contains standard templates for data analysis using Python, suitable for beginners as well as advanced learners. This book shows working implementations of data handling and machine learning algorithms using real-life biological datasets and problems, such as gene expression analysis; disease prediction; image recognition; SNP association with phenotypes and diseases. Considering the importance of visualization for data interpretation, especially in biological systems, there is a dedicated chapter for the ease of data visualization and plotting. Every chapter is designed to be interactive and is accompanied with Jupyter notebook to prompt readers to practice in their local systems. Other avant-garde component of the book is the inclusion of a machine learning project, wherein various machine learning algorithms are applied for the identification of genes associated with age-related disorders. A systematic understanding of data analysis steps has always been an important element for biological research. This book is a readily accessible resource that can be used as a handbook for data analysis, as well as a platter of standard code templates for building models.

Integer Linear Programming in Computational and Systems Biology - Dan Gusfield 2019-06-13
This hands-on tutorial text for non-experts demonstrates biological applications of a versatile modeling and optimization technique.

Developing Bioinformatics Computer Skills - Cynthia Gibas 2001
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.

Bioinformatics Programming Using Python - Mitchell L Model 2009-12-08
Powerful, flexible, and easy to use, Python is an ideal language for building software tools and applications for life science research and development. This unique book shows you how to program with Python, using code examples taken directly from bioinformatics. In a short time, you'll be using sophisticated techniques and Python modules that are particularly effective for bioinformatics programming. Bioinformatics Programming Using Python is perfect for anyone involved with bioinformatics -- researchers, support staff, students, and software developers interested in writing bioinformatics applications. You'll find it useful whether you already use Python, write code in another language, or have no programming experience at all. It's an excellent self-

instruction tool, as well as a handy reference when facing the challenges of real-life programming tasks. Become familiar with Python's fundamentals, including ways to develop simple applications Learn how to use Python modules for pattern matching, structured text processing, online data retrieval, and database access Discover generalized patterns that cover a large proportion of how Python code is used in bioinformatics Learn how to apply the principles and techniques of object-oriented programming Benefit from the "tips and traps" section in each chapter