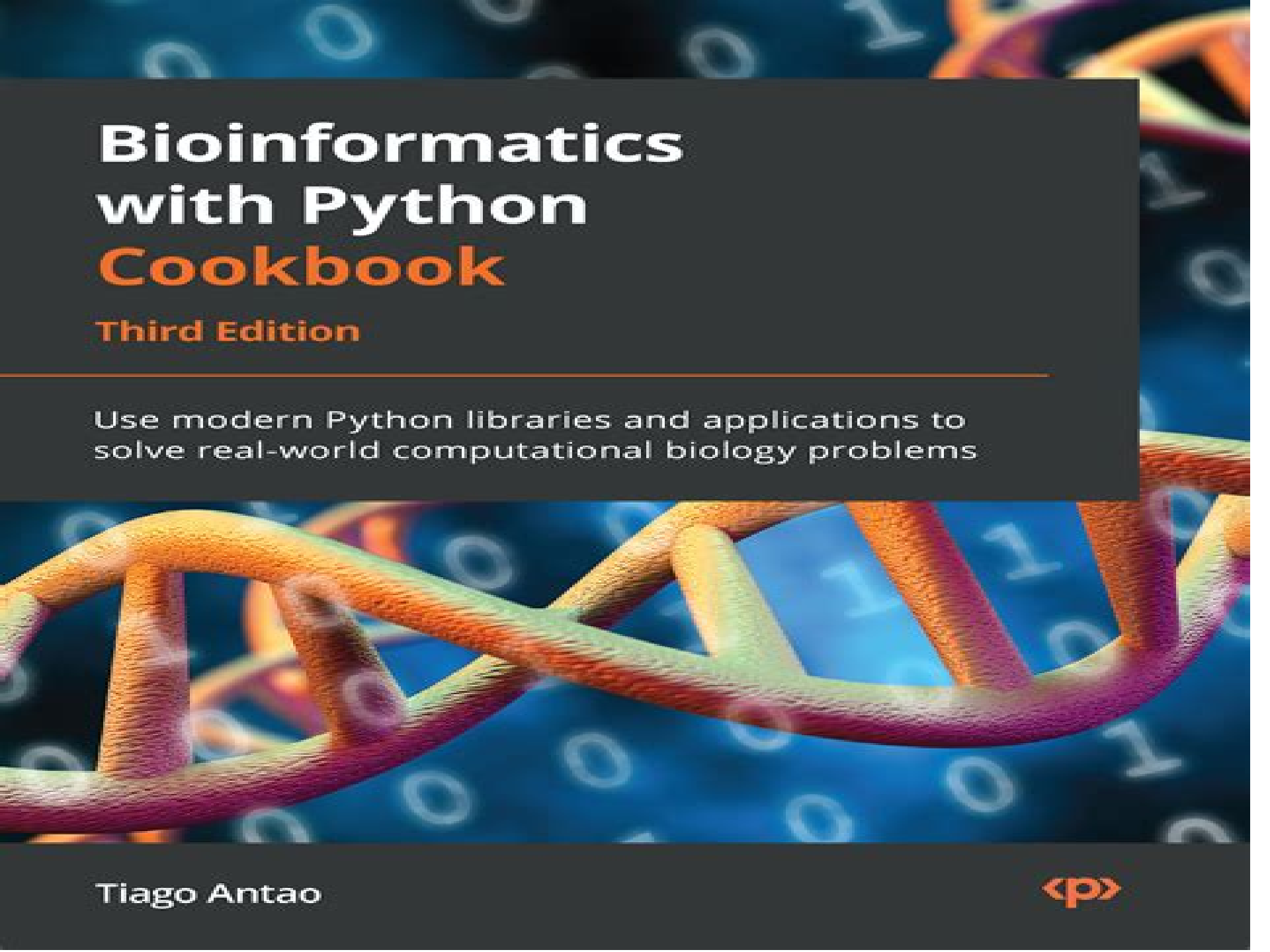




Bioinformatics with Python **Cookbook**

Third Edition

Use modern Python libraries and applications to
solve real-world computational biology problems

Tiago Antao



Bioinformatics With Python Cookbook

Tiago Antao



Bioinformatics With Python Cookbook:

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

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 Features Perform complex bioinformatics analysis using the most important Python libraries and applications Implement next generation sequencing metagenomics automating analysis population genetics and more Explore various statistical and machine learning techniques for bioinformatics data analysis Book 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 learn Learn how to process large next generation sequencing NGS datasets Work with genomic dataset using the FASTQ BAM and VCF formats Learn to perform sequence comparison and phylogenetic reconstruction Perform complex analysis with proteomics data Use Python to interact with Galaxy servers Use High performance computing techniques with Dask and Spark Visualize protein dataset interactions using Cytoscape Use PCA and Decision Trees two machine learning techniques with biological datasets Who 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

Bioinformatics with Python Cookbook Tiago Antao, 2022-09-27 Discover modern next generation sequencing libraries from the powerful Python ecosystem to perform cutting edge research and analyze large amounts of biological data Key

Features Perform complex bioinformatics analysis using the most essential Python libraries and applications Implement next generation sequencing metagenomics automating analysis population genetics and much more Explore various statistical and machine learning techniques for bioinformatics data analysis Book Description Bioinformatics is an active research field that uses a range of simple to advanced computations to extract valuable information from biological data and this book will show you how to manage these tasks using Python This updated third edition of the Bioinformatics with Python Cookbook begins with a quick overview of the various tools and libraries in the Python ecosystem that will help you convert analyze and visualize biological datasets Next you ll cover key techniques for next generation sequencing single cell analysis genomics metagenomics population genetics phylogenetics and proteomics with the help of real world examples You ll learn how to work with important pipeline systems such as Galaxy servers and Snakemake and understand the various modules in Python for functional and asynchronous programming This book will also help you explore topics such as SNP discovery using statistical approaches under high performance computing frameworks including Dask and Spark In addition to this you ll explore the application of machine learning algorithms in bioinformatics By the end of this bioinformatics Python book you ll be equipped with the knowledge you need to implement the latest programming techniques and frameworks empowering you to deal with bioinformatics data on every scale What you will learn Become well versed with data processing libraries such as NumPy pandas arrow and zarr in the context of bioinformatic analysis Interact with genomic databases Solve real world problems in the fields of population genetics phylogenetics and proteomics Build bioinformatics pipelines using a Galaxy server and Snakemake Work with functools and itertools for functional programming Perform parallel processing with Dask on biological data Explore principal component analysis PCA techniques with scikit learn Who this book is for This book is for bioinformatics analysts data scientists computational biologists researchers and Python developers who want to address intermediate to advanced biological and bioinformatics problems Working knowledge of the Python programming language is expected Basic knowledge of biology will also be helpful **Bioinformatics with Python Cookbook** Tiago Antao,2022

Bioinformatics is an active research field that uses a range of simple to advanced computations to extract valuable information from biological data and this book will show you how to manage these tasks using Python This updated third edition of the Bioinformatics with Python Cookbook begins with a quick overview of the various tools and libraries in the Python ecosystem that will help you convert analyze and visualize biological datasets Next you ll cover key techniques for next generation sequencing single cell analysis genomics metagenomics population genetics phylogenetics and proteomics with the help of real world examples You ll learn how to work with important pipeline systems such as Galaxy servers and Snakemake and understand the various modules in Python for functional and asynchronous programming This book will also help you explore topics such as SNP discovery using statistical approaches under high performance computing frameworks including Dask and Spark In addition to this you ll explore the application of machine learning algorithms in bioinformatics

By the end of this bioinformatics Python book you ll be equipped with the knowledge you need to implement the latest programming techniques and frameworks empowering you to deal with bioinformatics data on every scale

BIOINFORMATICS WITH PYTHON COOKBOOK SHANE. BRUBAKER,2025 Bioinformatics with Python Cookbook - Second Edition Tiago Antao,2018 Discover modern next generation sequencing libraries from Python ecosystem to analyze large amounts of biological data Key Features Perform complex bioinformatics analysis using the most important Python libraries and applications Implement next generation sequencing metagenomics automating analysis population genetics and more Explore various statistical and machine learning techniques for bioinformatics data analysis Book 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 learn Learn how to process large next generation sequencing NGS datasets Work with genomic dataset using the FASTQ BAM and VCF formats Learn to perform sequence comparison and phylogenetic reconstruction Perform complex analysis with proteomics data Use Python to interact with Galaxy servers Use High performance computing techniques with Dask and Spark Visualize protein dataset interactions using Cytoscape Use PCA and Decision Trees two machine learning techniques with biological datasets Who 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 Downloading the example code for this book You can download the example code files for all Packt books you have purchased from your account at <http://www.it-ebooks.info> **R Bioinformatics Cookbook** Dan MacLean,2023-10-31 Discover over 80 recipes for modeling and handling real life biological data using modern libraries from the R ecosystem Key Features Apply modern R packages to process biological data using real world examples Represent biological data with advanced visualizations and workflows suitable for research and publications Solve real world bioinformatics problems such as transcriptomics genomics and phylogenetics Purchase of the print or Kindle book includes a free PDF eBook Book DescriptionThe updated second edition of R Bioinformatics Cookbook takes a recipe based approach to show you how to conduct practical research and analysis in computational biology with R

You'll learn how to create a useful and modular R working environment along with loading, cleaning, and analyzing data using the most up-to-date Bioconductor, ggplot2, and tidyverse tools. This book will walk you through the Bioconductor tools necessary for you to understand and carry out protocols in RNA-seq and ChIP-seq, phylogenetics, genomics, gene search, gene annotation, statistical analysis, and sequence analysis. As you advance, you'll find out how to use Quarto to create data-rich reports, presentations, and websites, as well as get a clear understanding of how machine learning techniques can be applied in the bioinformatics domain. The concluding chapters will help you develop proficiency in key skills such as gene annotation, analysis, and functional programming in purrr and base R. Finally, you'll discover how to use the latest AI tools, including ChatGPT, to generate, edit, and understand R code and draft workflows for complex analyses. By the end of this book, you'll have gained a solid understanding of the skills and techniques needed to become a bioinformatics specialist and efficiently work with large and complex bioinformatics datasets.

What you will learn:

- Set up a working environment for bioinformatics analysis with R.
- Import, clean, and organize bioinformatics data using tidyr.
- Create publication-quality plots, reports, and presentations using ggplot2 and Quarto.
- Analyze RNA-seq, ChIP-seq, genomics, and next-generation genetics with Bioconductor.
- Search for genes and proteins by performing phylogenetics and gene annotation.
- Apply ML techniques to bioinformatics data using mlr3.
- Streamline programmatic work using iterators and functional tools in the base R and purrr packages.
- Use ChatGPT to create, annotate, and debug code and workflows.

Who 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 via a recipe-based approach. Working knowledge of the R programming language and basic knowledge of bioinformatics are prerequisites.

Functional Python Programming Steven F. Lott, Ricardo Banffy, 2022-12-30

Python isn't all about object-oriented programming. Discover a valuable way of thinking about code design through a function-first approach and learn when you need to use it. Now with detailed exercises at the end of every chapter. Purchase of the print or Kindle book includes a free eBook in PDF format.

Key Features:

- Learn how, when, and why to adopt functional elements in your projects.
- Explore the Python modules essential to functional programming, like itertools and functools.
- Revised to cover new features of Python 3.10.
- Exercises at the end of every chapter and more.

Book Description: Not enough developers understand the benefits of functional programming or even what it is. Author Steven Lott demystifies the approach, teaching you how to improve the way you code in Python and make gains in memory use and performance. Starting from the fundamentals, this book shows you how to apply functional thinking and techniques in a range of scenarios, with examples centered around data cleaning and exploratory data analysis. You'll learn how to use generator expressions, list comprehensions, and decorators to your advantage. You don't have to abandon object-oriented design completely, though you'll also see how Python's native object orientation is used in conjunction with functional programming techniques. By the end of this book, you'll be well-versed in the essential functional programming features of Python and understand why and when functional thinking helps.

You'll also have all the tools you need to pursue any additional functional topics that are not part of the Python language

What you will learn

- Use Python's libraries to avoid the complexities of state-changing classes
- Leverage built-in higher-order functions to avoid rewriting common algorithms
- Write generator functions to create lazy processing
- Design and implement decorators for functional composition
- Make use of Python type annotations to describe parameters and results of functions
- Apply functional programming to concurrency and web services
- Explore the PyMonad library for stateful simulations

Who this book is for

The functional paradigm is very useful for programmers working in data science, but any Python developer who wants to create more reliable, succinct, and expressive code will have much to learn from this book. No prior knowledge of functional programming is required to get started, though Python programming knowledge is assumed. A running Python environment is essential.

Fast Python Tiago Antao, 2023-07-04

Master Python techniques and libraries to reduce run times, efficiently handle huge datasets, and optimize execution for complex machine learning applications.

Fast Python is a toolbox of techniques for high-performance Python, including:

- Writing efficient pure Python code
- Optimizing the NumPy and pandas libraries
- Rewriting critical code in Cython
- Designing persistent data structures
- Tailoring code for different architectures
- Implementing Python GPU computing

Fast Python is your guide to optimizing every part of your Python-based data analysis process, from the pure Python code you write to managing the resources of modern hardware and GPUs.

You'll learn to rewrite inefficient data structures, improve underperforming code with multithreading, and simplify your datasets without sacrificing accuracy.

Written for experienced practitioners, this book dives right into practical solutions for improving computation and storage efficiency. You'll experiment with fun and interesting examples, such as rewriting games in Cython and implementing a MapReduce framework from scratch.

Finally, you'll go deep into Python GPU computing and learn how modern hardware has rehabilitated some former antipatterns and made counterintuitive ideas the most efficient way of working.

About the Technology Face it: Slow code will kill a big data project. Fast, pure Python code, optimized libraries, and fully utilized multiprocessor hardware are the price of entry for machine learning and large-scale data analysis. What you need are reliable solutions that respond faster to computing requirements while using less resources and saving money.

About the Book *Fast Python* is a toolbox of techniques for speeding up Python, with an emphasis on big data applications. Following the clear examples and precisely articulated details, you'll learn how to use common libraries like NumPy and pandas in more performant ways and transform data for efficient storage and I/O. More importantly, *Fast Python* takes a holistic approach to performance, so you'll see how to optimize the whole system, from code to architecture.

What's Inside

- Rewriting critical code in Cython
- Designing persistent data structures
- Tailoring code for different architectures
- Implementing Python GPU computing

About the Reader

For intermediate Python programmers familiar with the basics of concurrency.

About the Author

Tiago Antao is one of the co-authors of Biopython, a major bioinformatics package written in Python.

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Machine Learning in Biotechnology and Life Sciences Saleh Alkhalifa, 2022-01-28 Explore all the tools and templates needed for data scientists to drive success in their biotechnology careers with this comprehensive guide

Key Features Learn the applications of machine learning in biotechnology and life science sectors Discover exciting real world applications of deep learning and natural language processing Understand the general process of deploying models to cloud platforms such as AWS and GCP

Book Description The booming fields of biotechnology and life sciences have seen drastic changes over the last few years With competition growing in every corner companies around the globe are looking to data driven methods such as machine learning to optimize processes and reduce costs This book helps lab scientists engineers and managers to develop a data scientist's mindset by taking a hands on approach to learning about the applications of machine learning to increase productivity and efficiency in no time You'll start with a crash course in Python SQL and data science to develop and tune sophisticated models from scratch to automate processes and make predictions in the biotechnology and life sciences domain As you advance the book covers a number of advanced techniques in machine learning deep learning and natural language processing using real world data By the end of this machine learning book you'll be able to build and deploy your own machine learning models to automate processes and make predictions using AWS and GCP

What you will learn Get started with Python programming and Structured Query Language SQL Develop a machine learning predictive model from scratch using Python Fine tune deep learning models to optimize their performance for various tasks Find out how to deploy evaluate and monitor a model in the cloud Understand how to apply advanced techniques to real world data Discover how to use key deep learning methods such as LSTMs and transformers

Who this book is for This book is for data scientists and scientific professionals looking to transcend to the biotechnology domain Scientific professionals who are already established within the pharmaceutical and biotechnology sectors will find this book useful A basic understanding of Python programming and beginner level background in data science conjunction is needed to get the most out of this book

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