



Bioinformatics with Python Cookbook

Tiago Antao

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Learn how to use modern Python bioinformatics libraries and applications to do cutting-edge research in computational biology

About This Book

- Discover and learn the most important Python libraries and applications to do a complex bioinformatics analysis
- Focuses on the most modern tools to do research with next generation sequencing, genomics, population genetics, phylogenomics, and proteomics
- Uses real-world examples and teaches you to implement high-impact research methods

Who This Book Is For

If you have intermediate-level knowledge of Python and are well aware of the main research and vocabulary in your bioinformatics topic of interest, this book will help you develop your knowledge further.

What You Will Learn

- Gain a deep understanding of Python's fundamental bioinformatics libraries and be exposed to the most important data science tools in Python
- Process genome-wide data with Biopython
- Analyze and perform quality control on next-generation sequencing datasets using libraries such as PyVCF or PySAM
- Use DendroPy and Biopython for phylogenetic analysis
- Perform population genetics analysis on large datasets
- Simulate complex demographies and genomic features with simuPOP

In Detail

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.

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Crystal Freeman:

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