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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 Il 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 II 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 II explore the application of machine learning algorithms in bioinformatics by the end of this bioinformatics python book you II 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

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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

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