



# Bioinformatics with R Cookbook

*Paurush Praveen Sinha*

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# Bioinformatics with R Cookbook

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**Bioinformatics with R Cookbook** Paurush Praveen Sinha

**Over 90 practical recipes for computational biologists to model and handle real-life data using R**

## About This Book

- Use the existing R-packages to handle biological data
- Represent biological data with attractive visualizations
- An easy-to-follow guide to handle real-life problems in Bioinformatics like Next Generation Sequencing and Microarray Analysis

## Who This Book Is For

This book is ideal for computational biologists and bioinformaticians with basic knowledge of R programming, bioinformatics and statistics. If you want to understand various critical concepts needed to develop your computational models in Bioinformatics, then this book is for you. Basic knowledge of R is expected.

## What You Will Learn

- Retrieve biological data from within an R environment without hassling web pages
- Annotate and enrich your data and convert the identifiers
- Find relevant text from PubMed on which to perform text mining
- Find phylogenetic relations between species
- Infer relations between genomic content and diseases via GWAS
- Classify patients based on biological or clinical features
- Represent biological data with attractive visualizations, useful for publications and presentations

## In Detail

Bioinformatics is an interdisciplinary field that develops and improves upon the methods for storing, retrieving, organizing, and analyzing biological data. R is the primary language used for handling most of the data analysis work done in the domain of bioinformatics.

Bioinformatics with R Cookbook is a hands-on guide that provides you with a number of recipes offering you solutions to all the computational tasks related to bioinformatics in terms of packages and tested codes.

With the help of this book, you will learn how to analyze biological data using R, allowing you to infer new knowledge from your data coming from different types of experiments stretching from microarray to NGS and mass spectrometry.

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