

1. Record Nr.	UNINA9910739430503321
Autore	Wunschiers Robbe
Titolo	Computational Biology : A Practical Introduction to BioData Processing and Analysis with Linux, MySQL, and R / / by Röbbe Wünschiers
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2013
ISBN	9783642347498 3642347495
Edizione	[2nd ed. 2013.]
Descrizione fisica	1 online resource (449 p.)
Classificazione	42.10
Disciplina	570.285
Soggetti	Bioinformatics Proteins Biochemistry Application software Biophysics Computational and Systems Biology Protein Biochemistry Computer and Information Systems Applications
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Considerably revised new edition.
Nota di bibliografia	Includes bibliographical references (pages 433-435) and index.
Nota di contenuto	Part I Whetting Your Appetite -- 1 Introduction -- 2 Content of this Book -- Part II Computer & Operating Systems -- 3 Unix/Linux -- Part III Working with Linux -- 4 The First Touch -- 5 Working with Files -- 6 Remote Connections -- 7 Playing -- 8 Using the Shell -- 9 Installing BLAST+ and ClustalW -- 10 Shell Programming -- 11 Regular Expressions -- 12 Sed -- Part IV Programming -- 13 AWK -- 14 Perl -- 15 Other Programming Languages -- Part V Advanced Data Analysis -- 16 Relational Databases with MySQL -- 17 The Statistics Suite R -- Part VI Worked Examples -- 18 Genomic Analysis of the Pathogenicity Factors from <i>E. coli</i> Strain O157:H7 and EHEC Strain O104:H4 -- 19 Limits of BLAST & Homology Modeling -- 20 Virtual Sequencing of pUC18c -- 21 Querying for Potential Redox-Regulated Enzymes -- Part VII Additional Material -- References -- A Supplementary Information -- Solutions -- Index.

Sommario/riassunto

This greatly expanded 2nd edition provides a practical introduction to - data processing with Linux tools and the programming languages AWK and Perl - data management with the relational database system MySQL, and - data analysis and visualization with the statistical computing environment R for students and practitioners in the life sciences. Although written for beginners, experienced researchers in areas involving bioinformatics and computational biology may benefit from numerous tips and tricks that help to process, filter and format large datasets. Learning by doing is the basic concept of this book. Worked examples illustrate how to employ data processing and analysis techniques, e.g. for - finding proteins potentially causing pathogenicity in bacteria, - supporting the significance of BLAST with homology modeling, or - detecting candidate proteins that may be redox-regulated, on the basis of their structure. All the software tools and datasets used are freely available. One section is devoted to explaining setup and maintenance of Linux as an operating system independent virtual machine. The author's experiences and knowledge gained from working and teaching in both academia and industry constitute the foundation for this practical approach.
