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	Autore	Wunschiers Robbe
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	Nota di contenuto	Part I: Whetting Your Appetite -- Chapter 1: Introduction -- Chapter 2: Content of this Book -- Part II: Learning and Setting Up Our Playground -- Chapter 3: The World of Linux -- Part III: Working with Linux -- Chapter 4: The First Touch -- Chapter 5: Working with Files -- Chapter 6: Remote Connections -- Chapter 7: Playing with Text and Data Files -- Chapter 8: Get More Out of the Shell -- Chapter 9: Installing BLAST+ and ClustalW -- Part IV: Processing and Programming -- Chapter 10: Shell Programming -- Chapter 11: Regular Expressions -- Chapter 12: Sed -- Chapter 13: AWK -- Chapter 14: Other Programming Languages -- Part V: Advanced Data Analysis -- Chapter 15: GitHub Repositories and Jupyter Notebooks -- Chapter 16: Relational Databases with MariaDB -- Chapter 17: The Statistics Suite R -- Part VI: Worked Examples -- Chapter 18: BLASTing Forensic PCR Primers -- Chapter 19: In Search of Differences in Proteomes -- Chapter 20: Virtual Sequencing of mtDNA -- Chapter 21: DNA Sequence Analysis of

	MinION Nanopore Reads -- Chapter 22: Querying for Potential Redox-Regulated Enzymes -- Chapter 23: Exploring of Early SARS-CoV2 Mutations. Chapter 24: Genome-Wide Association Studies (GWAS).
Sommario/riassunto	This extensively expanded third edition offers a practical introduction to Bio Data Science. With a hands-on approach to learning, this book offers ample opportunities to practice: - Installing and utilizing Linux as a virtual machine or remotely - Processing bio data with the programming language AWK - Managing data with the relational database system MariaDB - Analyzing and visualizing data with R - Implementing good bioinformatics practices with Jupyter Notebook and GitHub This book targets both students and professionals in the life sciences. While it is aimed at beginners, it also provides valuable tips and tricks for experienced researchers dealing with large datasets. Worked examples illustrate how to utilize various bioinformatics tools such as BLAST, Clustal, PLINK, IGV, SAMtools, BCFtools, Mason2, Minimap, NCBI Datasets, Velvet, Jmol, and more for: - Identifying bacterial proteins potentially associated with pathogenicity - Querying molecular structures for redox-regulated enzymes - Mapping and assembling real or simulated sequence reads - Identifying and mapping molecular structure mutations in viruses - Conducting genome-wide association studies All software tools and datasets mentioned are freely available, and all code is accessible as Jupyter Notebooks on GitHub. Drawing from the author's experiences and knowledge gained from both academia and industry, this book provides a practical and comprehensive approach to bioinformatics. .