1. Record Nr.   UNINA9911018651603321

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   Titolo   Practical Bioinformatics : A Laboratory Manual / / by Sufang Wang,
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   Pubbl/distr/stampa   Singapore : , : Springer Nature Singapore : , : Imprint : Springer, , 2025

   ISBN   9789819679492

   Edizione   [1st ed. 2025.]

   Descrizione fisica   1 online resource (143 pages)

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   Disciplina   616.042072

   Soggetti   Genetics - Research
                       Biology - Technique
                       Genetics
                       Molecular biology
                       Biotechnology
                       Genetics Research
                       Biological Techniques
                       Genetics and Genomics
                       Molecular Biology

   Lingua di pubblicazione   Inglese

   Formato   Materiale a stampa

   Livello bibliografico   Monografia

   Nota di contenuto   Chapter 1. Introduction to Bioinformatics -- Chapter 2. Introduction to
                       Antibiotic Resistance -- Chapter 3. Introduction to Evolution and
                       Homology -- Chapter 4. Preparing your sequences -- Chapter 5.
                       Investigating sequence comparison statistics -- Chapter 6. Finding
                       homologous sequences using Blast -- Chapter 7. Finding homologous
                       sequences using UniProt -- Chapter 8. Multiple Sequence Alignment --
                       Chapter 9. Identifying conserved sequence motifs -- Chapter 10.
                       Building a phylogenetic tree -- Chapter 11. Gene expression analysis in
                       RNA-seq -- Chapter 12. Machine learning methods in RNA-seq.

   Sommario/riassunto   This book is a lab manual which can be integrated with bioinformatics
                       course. The field of bioinformatics is advancing at a remarkable rate.
                       With the development of new analytical techniques that make use of the
                       latest advances in machine learning and data science, today's biologists
                       are gaining fantastic new insights into the natural world's most

complex systems. This book includes a lab-based manual that can assist students handling large biological data. It aims to help students and researchers understand (1) the importance of horizontal transfer in the spread of antibiotic resistance, and in biology more broadly; (2) how protein and nucleic acid sequences are used to determine phylogenetic trees and the genetic relationship between organisms; (3) how sequence comparisons can be used to infer protein function; and (4) how to analyze high-throughput sequencing data to do gene expression analysis. This book is valuable for researchers, teachers and students, as well as any readers who are interested in bioinformatics.