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Titolo	Bioinformatic and Statistical Analysis of Microbiome Data [[electronic resource]] : From Raw Sequences to Advanced Modeling with QIIME 2 and R // by Yinglin Xia, Jun Sun
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ISBN	9783031213915 9783031213908
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Descrizione fisica	1 online resource (716 pages)
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Soggetti	Bioinformatics Biometry Big data Mathematical statistics - Data processing Biotechnology Biomedical engineering Biostatistics Big Data Statistics and Computing Biomedical Engineering and Bioengineering
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Chapter 1. Introduction to Linux and Unix -- Chapter 2. Introduction to R, Rstudio -- Chapter 3. Bioinformatic Analysis of Next-Generation Sequencing -- Chapter 4. Bioinformatic Analysis of Metagenomics -- Chapter 5. Alpha Diversity -- Chapter 6. Beta Diversity -- Chapter 7. Differential Abundance Analysis -- Chapter 8. Analyzing Zero-Inflated Microbiome Data -- Chapter 9. Compositional Analysis of Microbiome Data -- Chapter 10. Longitudinal Data Analysis of Microbiome -- Chapter 11. Meta-analysis of Microbiome Data (optional).
Sommario/riassunto	This unique book addresses the bioinformatic and statistical modelling and also the analysis of microbiome data using cutting-edge QIIME 2

and R software. It covers core analysis topics in both bioinformatics and statistics, which provides a complete workflow for microbiome data analysis: from raw sequencing reads to community analysis and statistical hypothesis testing. It includes real-world data from the authors' research and from the public domain, and discusses the implementation of QIIME 2 and R for data analysis step-by-step. The data as well as QIIME 2 and R computer programs are publicly available, allowing readers to replicate the model development and data analysis presented in each chapter so that these new methods can be readily applied in their own research. Bioinformatic and Statistical Analysis of Microbiome Data is an ideal book for advanced graduate students and researchers in the clinical, biomedical, agricultural, and environmental fields, as well as those studying bioinformatics, statistics, and big data analysis.
