1.	Record Nr.	UNINA9910568298003321
	Titolo	Comparative Genomics : 19th International Conference, RECOMB-CG 2022, La Jolla, CA, USA, May 20–21, 2022, Proceedings / / edited by Lingling Jin, Dannie Durand
	Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2022
	ISBN	3-031-06220-5
	Edizione	[1st ed. 2022.]
	Descrizione fisica	1 online resource (344 pages)
	Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 13234
	Disciplina	570.285 572.86
	Soggetti	Biomathematics Bioinformatics Algorithms Computer networks Computer science - Mathematics Application software Mathematical and Computational Biology Computational and Systems Biology Design and Analysis of Algorithms Computer Communication Networks Mathematics of Computing Computer and Information Systems Applications
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di bibliografia	Includes bibliographical references and index.
	Nota di contenuto	Evolution -- On the Comparison of Bacteriophage Populations -- Syntenic Dimensions of Genomic Evolution -- Phylogenetics -- Fast and Accurate Branch Support Calculation for Distance-based Phylogenetic Placements -- The Sackin Index of Simplex Networks -- Phylogenetic Placement Problem: A Hyperbolic Embedding Approach -- Phylogenetic Network Dissimilarity Measures That Take Branch Lengths Into Account -- Homology and Reconciliation -- The Complexity of Finding Common Partitions of Genomes with Predefined Block Sizes --

Reconciliation with Segmental Duplication, Transfer, Loss and Gain -- Quantifying Hierarchical Conflicts in Homology Statements -- On Partial Gene Transfer and its Impact on Gene Tree Reconstruction -- Genome Rearrangements -- Sorting by k-Cuts on Signed Permutations -- A New Approach for the Reversal Distance with Indels and Moves in Intergenic Regions -- Chromothripsis Rearrangements Are Informed by 3D Genome Organization -- Metagenomics -- Using Computational Synthetic Biology Toolsto Modulate Gene Expression within a Microbiome -- Metagenomics Binning of Long Reads Using Read-Overlap Graphs -- A Mixed Integer Linear Programming Algorithm for Plasmid Binning -- Genomic Sequencing -- Benchmarking Penalized Regression Methods in Machine Learning for Single Cell RNA Sequencing Data -- Deciphering the Tissue-speci c Regulatory Role of Intronless Genes Across Cancers.

| Sommario/riassunto | This book constitutes the refereed proceedings of the 19th Annual RECOMB Satellite Workshop on Comparative Genomics, RECOMB-CG which took place in La Jolla, USA, during May 20-21, 2022. The 18 full papers included in this book were carefully reviewed and selected from 28 submissions. The papers were organized in topical sections on evolution; phylogenetics; homology and reconciliation; genome rearrangements; metagenomics; and genomic sequencing. . |