1.	Record Nr.	UNISALENTO991000873429707536
	Autore	Tomarelli, Franco
	Titolo	Esercizi di metodi matematici per l'ingegneria : funzioni analitiche di una variabile complessa. Trasformata di Fourier. Trasformata di Laplace / F. Tomarelli
	Pubbl/distr/stampa	Rozzano (Mi) : CittàStudi, 1993
	ISBN	8872590280
	Edizione	[2. ed]
	Descrizione fisica	146 p. ; 24 cm.
	Classificazione	AMS 30-01 AMS 42-01 AMS 44-01
	Disciplina	515.93
	Soggetti	Fourier analysis-textbooks Functions of a complex variable-textbooks
	Lingua di pubblicazione	Italiano
	Formato	Materiale a stampa
	Livello bibliografico	Monografia

2. Record Nr.	UNINA9910847595103321
Titolo	Comparative Genomics : 21st International Conference, RECOMB-CG 2024, Boston, MA, USA, April 27–28, 2024, Proceedings / / edited by Celine Scornavacca, Maribel Hernández-Rosales
Pubbl/distr/stampa	Cham : , : Springer Nature Switzerland : , : Imprint : Springer, , 2024
ISBN	9783031580727 3031580729
Edizione	[1st ed. 2024.]
Descrizione fisica	1 online resource (XII, 272 p. 70 illus., 58 illus. in color.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 14616
Disciplina	572.80285
Soggetti	Biomathematics Bioinformatics Computer networks Computer science - Mathematics Application software Algorithms Mathematical and Computational Biology Computer Communication Networks Mathematics of Computing Computer and Information Systems Applications Design and Analysis of Algorithms
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	-- Phylogenetic Networks. -- Statistically Consistent Estimation of Rooted and Unrooted Level-1 Phylogenetic Networks from SNP data. -- Galled Perfect Transfer Networks. -- Homology and Phylogenetic Reconstruction. -- Inferring Transcript Phylogenies from Transcript Ortholog Clusters. -- Gene-Adjacency-Based Phylogenetics under a Stochastic Gain-Loss Model. -- Tools for Evolution Reconstruction. -- REvolutionH-tl : Reconstruction of Evolutionary Histories tool. -- Gene tree parsimony in the presence of gene duplication, loss, and incomplete lineage sorting. -- Assessing the potential of gene tree parsimony for microbial phylogenomics. -- Genome Rearrangements.

	-- Maximum Alternating Balanced Cycle Decomposition and Applications in Sorting by Intergenic Operations Problems. -- On the Distribution of Synteny Blocks under a Neutral Model of Genome Dynamics. -- Sampling gene adjacencies and geodesic points of random genomes. -- Genome Evolution. -- Transcription factors across the Escherichia coli pangenome: a 3D perspective. -- Revisiting the effects of MDR1 Variants using computational approaches. -- Evidence of increased adaptation of Omicron SARS-CoV-2 codon to humans.
Sommario/riassunto	This book constitutes the proceedings of the 21st International Conference on Comparative Genomics, RECOMB-CG 2024, which was held in Boston, MA, USA, during April 27–28, 2024. The 13 full papers presented in this book were carefully reviewed and selected from 21 submissions. The papers are divided into the following topical sections: phylogenetic networks; homology and phylogenetic reconstruction; tools for evolution reconstruction; genome rearrangements; and genome evolution. .