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Record Nr.	UNINA9910404118403321
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Titolo	Pan-genome diversity, dynamics and evolution of genomes / / editors, Hervé Tettelin, Duccio Medini
Pubbl/distr/stampa	Cham, : Springer Nature, 2020 Cham : , : Springer International Publishing : , : Imprint : Springer, , 2020
ISBN	3-030-38281-8
Edizione	[1st edition 2020.]
Descrizione fisica	1 online resource (XIV, 307 p. 47 illus., 43 illus. in color.)
Disciplina	579.135
Soggetti	Genomes Genomics Biologia molecular Llibres electrònics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Part 1: Genomic diversity and the pan-genome concept -- Chapter 1: The pan-genome: a data-drivendiscovery in biology -- Chapter 2: The prokaryotic species concept and challenges -- Chapter 3: Bacterial guide on how to design a diversified gene portfolio -- Chapter 4: A review of pan-genome tools and recent studies -- Part 2: Evolutionary biology of pan-genomes -- Chapter 5: Structure and dynamics of bacterial populations: pan-genome ecology -- Chapter 6: Bacterial microevolution and the pan-genome -- Chapter 7: Pan-genomes and selection: the public goods hypothesis -- Chapter 8: A pan-genomic perspective on the emergence, maintenance and predictability of antibiotic resistance -- Part 3: Pan-genomics: an open, evolving discipline -- Chapter 9: Metapangenome: at the crossroad of pangenomics and metagenomics -- Chapter 10: Pan-genome flux balance analysis towards pan-phenomes -- Chapter 11: Bacterial epigenomics: epigenetics in the age of population genomics -- Chapter 12: Eukaryotic pan-genomes -- Chapter 13: Computational strategies for eukaryotic pan-genome analyses.
Sommario/riassunto	This open access book offers the first comprehensive account of the

pan-genome concept and its manifold implications. The realization that the genetic repertoire of a biological species always encompasses more than the genome of each individual is one of the earliest examples of big data in biology that opened biology to the unbounded. The study of genetic variation observed within a species challenges existing views and has profound consequences for our understanding of the fundamental mechanisms underpinning bacterial biology and evolution. The underlying rationale extends well beyond the initial prokaryotic focus to all kingdoms of life and evolves into similar concepts for metagenomes, phenomes and epigenomes. The book's respective chapters address a range of topics, from the serendipitous emergence of the pan-genome concept and its impacts on the fields of microbiology, vaccinology and antimicrobial resistance, to the study of microbial communities, bioinformatic applications and mathematical models that tie in with complex systems and economic theory. Given its scope, the book will appeal to a broad readership interested in population dynamics, evolutionary biology and genomics.