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	Nota di contenuto	Chapter 1 Bioinformatics and Intellectual Property Rights: An Introduction -- Chapter 2 Next Generation Sequencing: Technology, Advancements and Applications -- Chapter 3 Sequence Analysis -- Chapter 4 Understanding Genomic Variations in the Context of Health and Disease -- Chapter 5 Metagenomics: A Long Way to Go -- Chapter 6 Computational Epigenomics and Its Application in Regulatory Genomics -- Chapter 7 Data Mining to Detect Common, Unique and Polymorphic Simple Sequence Repeats -- Chapter 8 R-programming for Genome-wide Data Analysis -- Chapter 9 Phylogenetic Analysis -- Chapter 10 Structural Bioinformatics: Life Through the 3D Glasses -- Chapter 11 An Introduction to the Protein Folding Process and Survey of the Structural Parameters of Proteins Used for Computational Predictions -- Chapter 12 Quality Assessment of Protein Tertiary Structures: Past, Present and Future -- Chapter 13 Predicting Protein Function Using Homology Based Methods -- Chapter 14 Drug Discovery: An In Silico Approach -- Chapter 15 Advanced In-silico

	Tools for Designing of Antigenic Epitope as Potential Vaccine Candidates Against Corona Virus -- Chapter 16 Machine Learning: What, Why & How? -- Chapter 17 Command Line Tools in Linux for Handling Large Data Files.
Sommario/riassunto	This book provides a comprehensive overview of the concepts and approaches used for sequence, structure, and phylogenetic analysis. Starting with an introduction to the subject and intellectual property protection for bioinformatics, it guides readers through the latest sequencing technologies, sequence analysis, genomic variations, metagenomics, epigenomics, molecular evolution and phylogenetics, structural bioinformatics, protein folding, structure analysis and validation, drug discovery, reverse vaccinology, machine learning, application of R programming in biological data analysis, and the use of Linux in handling large data files.