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	Nota di contenuto	1. Introduction -- 2. NGS file formats -- 3. Related algorithms and data structures -- 4. NGS read mapping -- 5. Genome assembly -- 6. Single nucleotide variation (SNV) calling -- 7. Structural variation calling -- 8. RNA-seq -- 9. Peak calling methods -- 10. Data compression techniques used in NGS files.
	Sommario/riassunto	Advances in sequencing technology have allowed scientists to study the human genome in greater depth and on a larger scale than ever before - as many as hundreds of millions of short reads in the course of a few days. But what are the best ways to deal with this flood of data? Algorithms for Next-Generation Sequencing is an invaluable tool for students and researchers in bioinformatics and computational biology, biologists seeking to process and manage the data generated by next-generation sequencing, and as a textbook or a self-study resource. In addition to offering an in-depth description of the algorithms for processing sequencing data, it also presents useful case studies describing the applications of this technology.