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Sommario/riassunto	In recent years, technological breakthroughs have greatly enhanced our ability to understand the complex world of molecular biology. Rapid developments in genomic profiling techniques, such as high-throughput sequencing, have brought new opportunities and challenges to the fields of computational biology and bioinformatics. Furthermore, by combining genomic profiling techniques with other experimental techniques, many powerful approaches (e.g., RNA-Seq, Chips-Seq, single-cell assays, and Hi-C) have been developed in order to help explore complex biological systems. As a result of the increasing availability of genomic datasets, in terms of both volume and variety, the analysis of such data has become a critical challenge as well as a topic of great interest. Therefore, statistical methods that address the problems associated with these newly developed techniques are in high demand. This book includes a number of studies that highlight the state-of-the-art statistical methods for the analysis of genomic data and explore future directions for improvement.