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Nota di contenuto	Contents; Contributors; Preface; 1 Identification of Structural Variation; Introduction; Defining structural variants; Causes of structural variation; Early methods for SV identification; Identification of structural variation from sequencing data; Discussion; Future trends; 2 Methods for RNA Isolation, Characterization and Sequencing (RNA-Seq); A brief history of RNA; Principles of RNA isolation; Methods of RNA sequencing; Using RNA sequencing to define transcriptional landscapes; RNA sequencing to discover RNA modifications; RNA base modifications and epitranscriptomics; Conclusions 3 Transcriptome Reconstruction and Quantification from RNA Sequencing DataIntroduction; Transcriptome reconstruction; Transcriptome quantification; Future trends; Conclusions; 4 Identification of Small Interfering RNA from Next-generation Sequencing Data; Introduction; Applying sequencing technologies to siRNAs; Experimental designs; Available tools for analysis of siRNA-seq data; Processing of siRNA-seq data; Locus finding; Association of siRNA loci with genomic features; Differential expression in siRNAs; Phased siRNAs; Post-analysis visualization; Target finding and small RNA networks Discussion5 Motif Discovery and Motif Finding in ChIP-Seq Data; Introduction; ChIP-Seq data: advantages and challenges for sequence analysis bioinformatics; Cooking recipes for motif analysis of ChIP-Seq data; Conclusion: the present and the future of motif analysis for the

ChIP-Seq technology; 6 Mammalian Enhancer Prediction; Introduction; Transcriptional enhancers; Computational prediction of enhancers; Discussion and conclusions; Future trends; 7 DNA Patterns for Nucleosome Positioning; Nucleosome as the basic unit of chromatin; Role of nucleosome positioning in gene regulation
Different nucleosome sequence patternsEarly history (pre-genomic and genomic era); Post-genomic era and high-throughput data; Positive versus negative, combining and splitting the patterns; Discussion and conclusions; 8 Hypermethylation in Cancer; Introduction: hypermethylation in the context of other epigenetic modifications; Types of DNA methylation; Hypermethylation machineries: the role of DNMTs; Epigenetic factors contribute to tumourigenesis and cancer progression; Biological pathways of frequently methylated genes in cancer
The relevance of high-throughput technologies as accelerating discovery means of epigenetic events in cancerTranslational applications of methylome analyses as a source of cancer biomarkers; Conclusions; Acknowledgements; References; 9 Identification and Analysis of Transposable Elements in Genomic Sequences; Introduction; Classic detection methods for TEs in genome sequences; TEs in the next-generation sequencing data era; What do NGS data bring to TE analyses?; Conclusions; Future trends; 10 The Current State of Metagenomic Analysis; Introduction; Metagenome sequencing Metagenome sequencing protocols

Sommario/riassunto

In recent years, there have been tremendous achievements made in DNA sequencing technologies and corresponding innovations in data analysis and bioinformatics that have revolutionized the field of genome analysis. In this book, an impressive array of experts highlight and review current advances in genome analysis. The book provides an invaluable, up-to-date, and comprehensive overview of the methods currently employed for next-generation sequencing (NGS) data analysis. It also highlights their problems and limitations, and it demonstrates the applications and indicates the developing trends i