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Nota di contenuto	Contents; Current books of interest; Contributors; Preface; 1; An Overview of Next-generation Genome Sequencing Platforms; Introduction; Second generation sequencing platforms; Third-generation sequencing platforms; Concluding remarks; 2: Attomole-level Genomics with Single-molecule Direct DNA, cDNA and RNA Sequencing Technologies; Introduction; Materials; Methods; 3: SNP Assessment on Draft Genomes from Next-generation Sequencing Data; Background; Single nucleotide polymorphisms (SNPs); SNP calling with one sample on draft genomes with ACCUSA Head-to-head comparisons of sequenced samples with ACCUSA 2Conclusions; 4: Processing Large-scale Small RNA Datasets in Silico; Introduction; Library preparation and sequencing; Helper tools; Analysis tools; Visualization tools; Discussion; 5: Utility of High-throughput Sequence Data in Rare Variant Detection; What is a rare variant?; Why is variant detection needed?; Utility of non-HTS methods for minority and rare variant detection; Status of rare variant detection by analysis of HTS data; How much HTS data is needed to accurately detect rare variants?

Testing the feasibility of analysing HTS for rare SNP detectionSources of errors; Experimental validation of correction approaches; Conclusions; 6: Detecting Breakpoints of Insertions and Deletions from Paired-end Short Reads; Introduction; Pindel: a pattern growth method to identify precise breakpoints of indels and SVs; Performance on real data (NA18507); Recent developments; Further advances of split-read approaches; Conclusion and future perspectives; 7: Novel Insights from Re-sequencing of Human Exomes Through NGS; Introduction; The protocol; Exome capture platforms and kits
Quality control and performance evaluationBioinformatics analysis; Applications in human disease research; Perspective; 8: Insights on Plant Development Using NGS Technologies; Introduction; Use RNA-seq to dissect transcription at the cellular resolution; Use ChIP-seq to dissect transcriptional networks; Use ChIP-seq to analyse the epigenome; Conclusions and perspectives; 9: Next-generation Sequencing and the Future of Microbial Metagenomics; Introduction; Tracking microbial diversity; Applying omics technologies; Designing experiments; Modelling microbial diversity; Concluding remarks
10: Next-generation Sequencing, Metagenomes and the Human MicrobiomeIntroduction; Marker-specific microbial community surveys; Metagenomics - high-throughput shotgun (HTS sequencing) of microbial communities; Applications of metagenomics to the study of human health and disease; Beyond the omes - systems biology views onto the host-microbiome interactions; The new generation of cloud-based informatics solutions for next-generation sequencing; Conclusion; Index

Sommario/riassunto

High-throughput, next generation sequencing (NGS) technologies are capable of producing a huge amount of sequence data in a relatively short time and have revolutionized genome research in recent years. The powerful and flexible nature of NGS has made it an indispensable tool for a broad spectrum of biological sciences, and NGS technologies have transformed scientific research in many fields. Written by experts from around the world, this book explores the most recent advances in NGS instrumentation and data analysis. The book begins with a comprehensive description of current NGS platforms, t