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Descrizione fisica	1 online resource (VIII, 428 p. 70 illus., 58 illus. in color.)
Disciplina	570.285
Soggetti	Bioinformatics Data mining Statistics Biomathematics Computational Biology/Bioinformatics Data Mining and Knowledge Discovery Statistics for Life Sciences, Medicine, Health Sciences Genetics and Population Dynamics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Introduction to Statistical Methods for Integrative Analysis of Genomic Data -- Robust Methods for Expression Quantitative Trait Loci Mapping -- Causal Inference and Structure Learning of Genotype-Phenotype Networks using Genetic Variation -- Genomic Applications of the Neyman-Pearson Classification Paradigm -- Improving Re-annotation of Annotated Eukaryotic Genomes -- State-of-the-art in Smith-Waterman Protein Database Search -- A Survey of Computational Methods for Protein Function Prediction -- Genome Wide Mapping of Nucleosome Position and Histone Code Polymorphisms in Yeast -- Perspectives of Machine Learning Techniques in Big Data Mining of Cancer -- Mining Massive Genomic Data for Therapeutic Biomarker Discovery in Cancer: Resources, Tools, and Algorithms -- NGC Analysis of Somatic Mutations in Cancer Genomes -- OncoMiner: A Pipeline for Bioinformatics Analysis of Exonic Sequence Variants in Cancer -- A Bioinformatics Approach for Understanding Genotype-Phenotype Correlation in Breast Cancer.

This contributed volume explores the emerging intersection between big data analytics and genomics. Recent sequencing technologies have enabled high-throughput sequencing data generation for genomics resulting in several international projects which have led to massive genomic data accumulation at an unprecedented pace. To reveal novel genomic insights from this data within a reasonable time frame, traditional data analysis methods may not be sufficient or scalable, forcing the need for big data analytics to be developed for genomics. The computational methods addressed in the book are intended to tackle crucial biological questions using big data, and are appropriate for either newcomers or veterans in the field. This volume offers thirteen peer-reviewed contributions, written by international leading experts from different regions, representing Argentina, Brazil, China, France, Germany, Hong Kong, India, Japan, Spain, and the USA. In particular, the book surveys three main areas: statistical analytics, computational analytics, and cancer genome analytics. Sample topics covered include: statistical methods for integrative analysis of genomic data, computation methods for protein function prediction, and perspectives on machine learning techniques in big data mining of cancer. Self-contained and suitable for graduate students, this book is also designed for bioinformaticians, computational biologists, and researchers in communities ranging from genomics, big data, molecular genetics, data mining, biostatistics, biomedical science, cancer research, medical research, and biology to machine learning and computer science. Readers will find this volume to be an essential read for appreciating the role of big data in genomics, making this an invaluable resource for stimulating further research on the topic.

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