1. Record Nr. UNINA9910299980703321

Titolo	Statistical Analysis of Next Generation Sequencing Data / / edited by Somnath Datta, Dan Nettleton
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2014
ISBN	3-319-07212-9
Edizione	[1st ed. 2014.]
Descrizione fisica	1 online resource (438 p.)
Collana	Frontiers in Probability and the Statistical Sciences, , 2624-9987
Disciplina	572.8633015195
Soggetti	Statistics Human genetics Cancer research Statistics for Life Sciences, Medicine, Health Sciences Human Genetics Cancer Research
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Statistical Analyses of Next Generation Sequencing Data: An Overview -- Using RNA-seq Data to Detect Differentially Expressed Genes -- Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR -- Analysis of Next Generation Sequencing Data Using Integrated Nested Laplace Approximation (INLA) -- Design of RNA Sequencing Experiments -- Measurement, Summary, and Methodological Variation in RNA-sequencing -- Functional PCA for differential expression testing with RNA-seq data -- Mapping of Expression Quantitative Trait Loci using RNA-seq Data -- The Role of Spike-In Standards in the Normalization of RNA-seq -- Cluster Analysis of RNA-sequencing Data -- Classification of RNA-seq Data -- Isoform Expression Analysis Based on RNA-seq Data -- RNA Isoform Discovery Through Goodness of Fit Diagnostics -- MOSAiCS-HMM: A Model-based Approach for Detecting Regions of Histone Modifications from ChIP-seq Data -- Hierarchical Bayesian Models for ChIP-Seq Data -- Genotype Calling and Haplotype Phasing from Next Generation Sequencing Data.- Analysis of Metagenomic Data -- Detecting Copy

Number Changes and Structural Rearrangements using DNA Sequencing -- Statistical Methods for the Analysis of Next Generation Sequence Data from Paired Tumor-Normal Samples -- Statistical Considerations in the Analysis of Rare Variants.

Sommario/riassunto

Next Generation Sequencing (NGS) is the latest high throughput technology to revolutionize genomic research. NGS generates massive genomic datasets that play a key role in the big data phenomenon that surrounds us today. To extract signals from high-dimensional NGS data and make valid statistical inferences and predictions, novel data analytic and statistical techniques are needed. This book contains 20 chapters written by prominent statisticians working with NGS data. The topics range from basic preprocessing and analysis with NGS data to more complex genomic applications such as copy number variation and isoform expression detection. Research statisticians who want to learn about this growing and exciting area will find this book useful. In addition, many chapters from this book could be included in graduate-level classes in statistical bioinformatics for training future biostatisticians who will be expected to deal with genomic data in basic biomedical research, genomic clinical trials and personalized medicine. About the editors: Somnath Datta is Professor and Vice Chair of Bioinformatics and Biostatistics at the University of Louisville. He is Fellow of the American Statistical Association, Fellow of the Institute of Mathematical Statistics, and Elected Member of the International Statistical Institute. He has contributed to numerous research areas in Statistics, Biostatistics and Bioinformatics. Dan Nettleton is Professor and Laurence H. Baker Endowed Chair of Biological Statistics in the Department of Statistics at Iowa State University. He is Fellow of the American Statistical Association and has published research on a variety of topics in statistics, biology, and bioinformatics.