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Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Front Cover; About the Editor; Contents; Acknowledgments and How to Cite; List of Contributors; Introduction; Part I: RNA-Seq; Chapter 1: The Bench Scientist's Guide to Statistical Analysis of RNA-Seq Data; Chapter 2: Assembly of Non-Unique Insertion Content Using Next-Generation Sequencing; Chapter 3: RSEM: Accurate Transcript Quantification from RNA-Seq Data With or Without a Reference Genome; Part II: Microarray; Chapter 4: A Regression System for Estimation of Errors Introduced by Confocal Imaging into Gene Expression Data in Situ Chapter 5: SPACE: An Algorithm to Predict and Quantify Alternatively Spliced Isoforms Using Microarrays Chapter 6: Link-Based Quantitative Methods to Identify Differentially Coexpressed Genes and Gene Pairs; Chapter 7: Dimension Reduction with Gene Expression Data Using Targeted Variable Importance Measurement; Part III: GWAS; Chapter 8: Genome-Wide Association Study of Stevens-Johnson Syndrome and Toxic Epidermal Necrolysis in Europe; Chapter 9: Genotyping Common and Rare Variation Using Overlapping Pool Sequencing Chapter 10: Learning Genetic Epistasis Using Bayesian Network Scoring Criteria Chapter 11: Combined Analysis of Three Genome-Wide Association Studies on vWF and FVIII Plasma Levels; Part IV: Proteomics;

Chapter 12: Statistical Methods for Quantitative Mass Spectrometry Proteomic Experiments with Labeling; Chapter 13: MRCQuant: An Accurate LC-MS Relative Isotopic Quantification Algorithm on TOF Instruments; Author Notes

Sommario/riassunto

The book introduces bioinformatic and statistical methodology and shows approaches to bias correction and error estimation. It also presents quantitative methods for genome and proteome analysis.
