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Titolo	Science amusante . 3e serie 100 nouvelles experiences // Tom Tit
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Livello bibliografico	Monografia
2. Record Nr.	UNINA9910810575303321
Titolo	Advances in statistical bioinformatics : models and integrative inference for high-throughput data // edited by Kim-Anh Do, The University of Texas M.D. Anderson Cancer Center, Zhaohui Steven Qin, Emory University, Atlanta, GA, Marina Vannucci, Rice University, Houston, TX [[electronic resource]]
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ISBN	1-139-89118-9 1-107-24941-4 1-107-24858-2 1-299-70751-3 1-107-25107-9 1-107-25024-2 1-139-22644-4 1-107-24775-6
Descrizione fisica	1 online resource (xv, 481 pages) : digital, PDF file(s)
Classificazione	MED090000
Disciplina	572.80285
Soggetti	Bioinformatics - Statistical methods Biometry Genetics - Technique

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Note generali	Title from publisher's bibliographic system (viewed on 05 Oct 2015).
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	<p>""Contents""; ""List of Contributors""; ""Preface""; ""1 An Introduction to Next-Generation Biological Platforms""; ""Virginia Mohlere, Wenting Wang, and Ganiraju Manyam""; ""1.1 Introduction""; ""1.2 The Biology of Gene Silencing""; ""1.2.1 DNA Methylation""; ""1.2.2 RNA Interference""; ""1.3 High-Throughput Profiling""; ""1.3.1 Molecular Inversion Probe Arrays""; ""1.3.2 Array Comparative Genomic Hybridization (aCGH)""; ""1.3.3 Genome-Wide Association Studies""; ""1.3.4 Reverse-Phase Protein Array""; ""1.4 Next-Generation Sequencing""; ""1.4.1 Whole-Genome and Whole-Exome Sequencing""; ""1.4.2 ChIP-Seq""; ""1.4.3 RNA-Seq""; ""1.4.4 BS-seq""; ""1.5 NGS Data Management and Analysis""; ""1.6 Platform Integration""; ""Acknowledgments""; ""References""; ""References""; ""2 An Introduction to The Cancer Genome Atlas""; ""Bradley M. Broom and Rehan Akbani""; ""2.1 Introduction""; ""2.2 History and Goals of the TCGA Project""; ""2.3 Sample Collection and Processing""; ""2.3.1 Step 1: Tissue Collection""; ""2.3.2 Step 2: Quality Control and DNA/RNA Extraction""; ""2.3.3 Step 3: Molecular Profiling and Sequencing""; ""2.3.4 Step 4: Data Collection and Public Distribution""; ""2.3.5 Step 5: Data Analysis""; ""2.4 Data Processing, Storage, and Access""; ""2.4.1 TCGA Barcodes and UUIDs""; ""2.4.2 The Data Coordinating Center""; ""2.4.3 Data Access Matrix""; ""2.4.4 Bulk Download""; ""2.4.5 HTTP""; ""2.4.6 CGHub""; ""2.4.7 Sample and Data Relationship Format (SDRF) and Investigation Description Format (IDF) Files""; ""2.4.8 File Format""; ""2.4.9 Version""; ""2.5 Tools for Visualizing and Analyzing TCGA Data""; ""2.5.1 cBio Cancer Genomics Portal""; ""2.5.2 MBatch Portal""; ""2.5.3 Next-Generation Clustered Heat Maps""; ""2.5.4 Regulome Explorer""; ""2.5.5 Integrative Genome Viewer""; ""2.5.6 Cancer Genomics Browser""; ""2.6 Summary""; ""Acknowledgments""; ""References""; ""References""; ""3 DNA Variant Calling in Targeted Sequencing Data""; ""Wenyi Wang, Yu Fan, and Terence P. Speed""; ""3.1 Introduction""; ""3.2 Background""; ""3.2.1 Single-Nucleotide Variation""; ""3.2.2 Long Padlock Probes""; ""3.2.3 Array-Based Resequencing""; ""3.3 Sequence Robust Multiarray Analysis""; ""3.3.1 Quality Control""; ""3.3.2 Variant Calling""; ""3.4 Application of SRMA""; ""3.4.1 Candidate Gene Study for Mitochondrial Diseases""; ""3.4.2 Validation Results""; ""3.4.3 Biological Findings""; ""3.5 Conclusion""; ""Appendix""; ""References""; ""References""; ""4 Statistical Analysis of Mapped Reads from mRNA-Seq Data""; ""Ernest Turro and Alex Lewin""; ""4.1 Background""; ""4.1.1 RNA Biology""; ""4.1.2 RNA Technology""; ""4.2 Mapping and Assembly Strategies""; ""4.2.1 De Novo Assembly of the Transcriptome""; ""4.2.2 Genome-Guided Assembly of the Transcriptome""; ""4.2.3 Alignment to a Reference Transcriptome""; ""4.3 Modeling Expression Levels""; ""4.3.1 Poisson Model for Expression Quantification""; ""4.4 Normalization""; ""4.4.1 RPKM Normalization""</p>
Sommario/riassunto	<p>Providing genome-informed personalized treatment is a goal of modern medicine. Identifying new translational targets in nucleic acid characterizations is an important step toward that goal. The information tsunami produced by such genome-scale investigations is stimulating parallel developments in statistical methodology and</p>

inference, analytical frameworks, and computational tools. Within the context of genomic medicine and with a strong focus on cancer research, this book describes the integration of high-throughput bioinformatics data from multiple platforms to inform our understanding of the functional consequences of genomic alterations. This includes rigorous and scalable methods for simultaneously handling diverse data types such as gene expression array, miRNA, copy number, methylation, and next-generation sequencing data. This material is written for statisticians who are interested in modeling and analyzing high-throughput data. Chapters by experts in the field offer a thorough introduction to the biological and technical principles behind multiplatform high-throughput experimentation.

3. Record Nr.	UNINA9910144463103321
Titolo	Journal of veterinary pharmacology and therapeutics
Pubbl/distr/stampa	[Oxford, England], : Blackwell Science
ISSN	1365-2885
Descrizione fisica	1 online resource
Disciplina	636.089
Soggetti	Veterinary pharmacology Therapeutics Drug Therapy - veterinary Pharmacology - veterinary Therapeutics - veterinary Pharmacologie veterinaire Therapeutique pharmacology veterinary medicine Pharmakologie Tiermedizin Zeitschrift Online-Ressource Traitement medical Medecine veterinaire Farmacologia veterinària Terapèutica veterinària Fulltext Internet Resources.

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periodicals.
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Note generali	Refereed/Peer-reviewed "Official Journal of the American Academy of Veterinary Pharmacology and Therapeutics, the American College of Veterinary Clinical Pharmacology, the Association for Veterinary Clinical Pharmacology and Therapeutics (UK)--and the European Association for Veterinary Pharmacology and Toxicology."
