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Autore	Fusaro, Diego
Titolo	Il nichilismo dell'Unione Europea / Diego Fusaro, Silvio Bolognini
Pubbl/distr/stampa	Roma, : Armando, 2019
ISBN	978-88-6992-592-4
Descrizione fisica	239 p. ; 21 cm
Collana	Metodologia delle scienze umane e sociali
Altri autori (Persone)	Bolognini, Silvio <1952->
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2. Record Nr.	UNINA9910814421103321
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ISBN	9786612690365 9781118211526 1118211529 9781282690363 1282690361 9780470567647 0470567643 9780470567630 0470567635
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Altri autori (Persone)	LeeJae K
Disciplina	570.285
Soggetti	Bioinformatics - Statistical methods Biology - Data processing
Lingua di pubblicazione	Inglese
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Nota di contenuto	STATISTICAL BIOINFORMATICS; CONTENTS; PREFACE; CONTRIBUTORS; 1 ROAD TO STATISTICAL BIOINFORMATICS; 2 PROBABILITY CONCEPTS AND DISTRIBUTIONS FOR ANALYZING LARGE BIOLOGICAL DATA; 3 QUALITY CONTROL OF HIGH-THROUGHPUT BIOLOGICAL DATA; 4 STATISTICAL TESTING AND SIGNIFICANCE FOR LARGE BIOLOGICAL DATA ANALYSIS; 5 CLUSTERING: UNSUPERVISED LEARNING IN LARGE BIOLOGICAL DATA; 6 CLASSIFICATION: SUPERVISED LEARNING WITH HIGH-DIMENSIONAL BIOLOGICAL DATA; 7 MULTIDIMENSIONAL ANALYSIS AND VISUALIZATION ON LARGE BIOMEDICAL DATA; 8 STATISTICAL MODELS, INFERENCE, AND ALGORITHMS FOR LARGE BIOLOGICAL DATA ANALYSIS 9 EXPERIMENTAL DESIGNS ON HIGH-THROUGHPUT BIOLOGICAL EXPERIMENTS 10 STATISTICAL RESAMPLING TECHNIQUES FOR LARGE BIOLOGICAL DATA ANALYSIS; 11 STATISTICAL NETWORK ANALYSIS FOR

BIOLOGICAL SYSTEMS AND PATHWAYS; 12 TRENDS AND STATISTICAL CHALLENGES IN GENOMEWIDE ASSOCIATION STUDIES; 13 R AND BIOCONDUCTOR PACKAGES IN BIOINFORMATICS: TOWARDS SYSTEMS BIOLOGY; INDEX

Sommario/riassunto

This book provides an essential understanding of statistical concepts necessary for the analysis of genomic and proteomic data using computational techniques. The author presents both basic and advanced topics, focusing on those that are relevant to the computational analysis of large data sets in biology. Chapters begin with a description of a statistical concept and a current example from biomedical research, followed by more detailed presentation, discussion of limitations, and problems. The book starts with an introduction to probability and statistics for genome-wide data, and moves into
