1.	Record Nr.	UNINA9910971315803321
	Autore	Eratosthenes
	Titolo	Eratosthenes' Geography / / fragments collected and translated, with commentary and additional material, by Duane W. Roller
	Pubbl/distr/stampa	Princeton, : Princeton University Press, c2010
	ISBN	9786612458774
		9781282458772
		1282458779
		9781400832217
		1400832217
	Edizione	[Core Textbook]
	Descrizione fisica	1 online resource (320 p.)
	Altri autori (Persone)	RollerDuane W
		Strabo
	Disciplina	913
	Soggetti	Geography, Ancient
		Physical geography
	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 and index.
	Nota di contenuto	Frontmatter -- Contents -- Illustrations -- Introduction -- Abbreviations -- Eratosthenes and the History of Geography -- Eratosthenes Geographika -- Book 1 -- Book 2 -- Book 3 -- Summaries and Commentaries -- Commentary to Book 1 -- Commentary to Book 2 -- Commentary to Book 3 -- Gazetteer -- Maps -- Appendices -- Appendix 1. On the Measurement of the Earth -- Appendix 2. Testimonia for the Life of Eratosthenes -- Appendix 3. Lengths of Measurement -- Bibliography -- Index of Passages Cited -- General Index
	Sommario/riassunto	This is the first modern edition and first English translation of one of the earliest and most important works in the history of geography, the third-century Geographika of Eratosthenes. In this work, which for the first time described the geography of the entire inhabited world as it was then known, Eratosthenes of Kyrene (ca. 285-205 BC) invented the discipline of geography as we understand it. A polymath who served as librarian at Alexandria and tutor to the future King Ptolemy IV, Eratosthenes created the terminology of geography, probably including

the word geographia itself. Building on his previous work, in which he determined the size and shape of the earth, Eratosthenes in the Geographika created a grid of parallels and meridians that linked together every place in the world: for the first time one could figure out the relationship and distance between remote localities, such as northwest Africa and the Caspian Sea. The Geographika also identified some four hundred places, more than ever before, from Thoule (probably Iceland) to Taprobane (Sri Lanka), and from well down the coast of Africa to Central Asia. This is the first collation of the more than 150 fragments of the Geographika in more than a century. Each fragment is accompanied by an English translation, a summary, and commentary. Duane W. Roller provides a rich background, including a history of the text and its reception, a biography of Eratosthenes, and a comprehensive account of ancient Greek geographical thought and of Eratosthenes' pioneering contribution to it. This edition also includes maps that show all of the known places named in the Geographika, appendixes, a bibliography, and indexes.

2.	Record Nr.	UNINA9910140840803321
	Autore	Dziuda Darius M
	Titolo	Data mining for genomics and proteomics : analysis of gene and protein expression data / / Darius M. Dzuida
	Pubbl/distr/stampa	Hoboken, N.J., : Wiley, c2010
	ISBN	9786612707575
		9781282707573
		1282707574
		9780470593417
		0470593415
		9780470593400
		0470593407
	Descrizione fisica	1 online resource (348 p.)
	Collana	Wiley Series on Methods and Applications in Data Mining ; ; v.1
	Disciplina	572.8/6
	Soggetti	Genomics - Data processing
		Proteomics - Data processing
		Data mining
	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 and index.
Nota di contenuto	DATA MINING FOR GENOMICS AND PROTEOMICS; CONTENTS; PREFACE; ACKNOWLEDGMENTS; 1 INTRODUCTION; 1.1 Basic Terminology; 1.1.1 The Central Dogma of Molecular Biology; 1.1.2 Genome; 1.1.3 Proteome; 1.1.4 DNA (Deoxyribonucleic Acid); 1.1.5 RNA (Ribonucleic Acid); 1.1.6 mRNA (messenger RNA); 1.1.7 Genetic Code; 1.1.8 Gene; 1.1.9 Gene Expression and the Gene Expression Level; 1.1.10 Protein; 1.2 Overlapping Areas of Research; 1.2.1 Genomics; 1.2.2 Proteomics; 1.2.3 Bioinformatics; 1.2.4 Transcriptomics and Other -omics . . .; 1.2.5 Data Mining; 2 BASIC ANALYSIS OF GENE EXPRESSION MICROARRAY DATA 2.1 Introduction2.2 Microarray Technology; 2.2.1 Spotted Microarrays; 2.2.2 Affymetrix GeneChip(®) Microarrays; 2.2.3 Bead-Based Microarrays; 2.3 Low-Level Preprocessing of Affymetrix Microarrays; 2.3.1 MAS5; 2.3.2 RMA; 2.3.3 GCRMA; 2.3.4 PLIER; 2.4 Public Repositories of Microarray Data; 2.4.1 Microarray Gene Expression Data Society (MGED) Standards; 2.4.2 Public Databases; 2.4.2.1 Gene Expression Omnibus (GEO); 2.4.2.2 ArrayExpress; 2.5 Gene Expression Matrix; 2.5.1 Elements of Gene Expression Microarray Data Analysis; 2.6 Additional Preprocessing, Quality Assessment, and Filtering 2.6.1 Quality Assessment2.6.2 Filtering; 2.7 Basic Exploratory Data Analysis; 2.7.1 t Test; 2.7.1.1 t Test for Equal Variances; 2.7.1.2 t Test for Unequal Variances; 2.7.2 ANOVA F Test; 2.7.3 SAM t Statistic; 2.7.4 Limma; 2.7.5 Adjustment for Multiple Comparisons; 2.7.5.1 Single-Step Bonferroni Procedure; 2.7.5.2 Single-Step Sidak Procedure; 2.7.5.3 Step-Down Holm Procedure; 2.7.5.4 Step-Up Benjamini and Hochberg Procedure; 2.7.5.5 Permutation Based Multiplicity Adjustment; 2.8 Unsupervised Learning (Taxonomy-Related Analysis); 2.8.1 Cluster Analysis 2.8.1.1 Measures of Similarity or Distance2.8.1.2 K-Means Clustering; 2.8.1.3 Hierarchical Clustering; 2.8.1.4 Two-Way Clustering and Related Methods; 2.8.2 Principal Component Analysis; 2.8.3 Self-Organizing Maps; Exercises; 3 BIOMARKER DISCOVERY AND CLASSIFICATION; 3.1 Overview; 3.1.1 Gene Expression Matrix . . . Again; 3.1.2 Biomarker Discovery; 3.1.3 Classification Systems; 3.1.3.1 Parametric and Nonparametric Learning Algorithms; 3.1.3.2 Terms Associated with Common Assumptions Underlying Parametric Learning Algorithms; 3.1.3.3 Visualization of Classification Results 3.1.4 Validation of the Classification Model3.1.4.1 Reclassification; 3.1.4.2 Leave-One-Out and K-Fold Cross-Validation; 3.1.4.3 External and Internal Cross-Validation; 3.1.4.4 Holdout Method of Validation; 3.1.4.5 Ensemble-Based Validation (Using Out-of-Bag Samples); 3.1.4.6 Validation on an Independent Data Set; 3.1.5 Reporting Validation Results; 3.1.5.1 Binary Classifiers; 3.1.5.2 Multiclass Classifiers; 3.1.6 Identifying Biological Processes Underlying the Class Differentiation; 3.2 Feature Selection; 3.2.1 Introduction; 3.2.2 Univariate Versus Multivariate Approaches 3.2.3 Supervised Versus Unsupervised Methods
Sommario/riassunto	Data Mining for Genomics and Proteomics uses pragmatic examples and a complete case study to demonstrate step-by-step how biomedical studies can be used to maximize the chance of extracting new and useful biomedical knowledge from data. It is an excellent resource for students and professionals involved with gene or protein expression data in a variety of settings.