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Nota di contenuto	Analyzing Microarray Gene Expression Data; Contents; Preface; 1 Microarrays in Gene Expression Studies; 1.1 Introduction; 1.2 Background Biology; 1.2.1 Genome, Genotype, and Gene Expression; 1.2.2 Of Wild-Types and Other Alleles; 1.2.3 Aspects of Underlying Biology and Physiochemistry; 1.3 Polymerase Chain Reaction; 1.4 cDNA; 1.4.1 Expressed Sequence Tag; 1.5 Microarray Technology and Application; 1.5.1 History of Microarray Development; 1.5.2 Tools of Microarray Technology; 1.5.3 Limitations of Microarray Technology; 1.5.4 Oligonucleotides versus cDNA Arrays 1.5.5 SAGE: Another Method for Detecting and Measuring Gene Expression Levels1.5.6 Emerging Technologies; 1.6 Sampling of Relevant Research Entities and Public Resources; 2 Cleaning and Normalization; 2.1 Introduction; 2.2 Cleaning Procedures; 2.2.1 Image Processing to Extract Information; 2.2.2 Missing Value Estimation; 2.2.3 Sources of Nonlinearity; 2.3 Normalization and Plotting Procedures for Oligonucleotide Arrays; 2.3.1 Global Approaches for Oligonucleotide Array Data; 2.3.2 Spiked Standard Approaches; 2.3.3 Geometric Mean

	and Linear Regression Normalization for Multiple Arrays 2.3.4 Nonlinear Normalization for Multiple Arrays Using Smooth Curves2.4 Normalization Methods for cDNA Microarray Data; 2.4.1 Single-Array Normalization; 2.4.2 Multiple Slides Normalization; 2.4.3 ANOVA and Related Methods for Normalization; 2.4.4 Mixed-Model Method for Normalization; 2.4.5 SNOMAD; 2.5 Transformations and Replication; 2.5.1 Importance of Replication; 2.5.2 Transformations; 2.6 Analysis of the Alon Data Set; 2.7 Comparison of Normalization Strategies and Discussion; 3 Some Cluster Analysis Methods; 3.1 Introduction; 3.2 Reduction in the Dimension of the Feature Space 3.3 Cluster Analysis3.4 Some Hierarchical Agglomerative Techniques; 3.5 k-Means Clustering; 3.6 Cluster Analysis with No A Priori Metric; 3.7 Clustering via Finite Mixture Models; 3.7.1 Definition; 3.7.2 Advantages of Model-Based Clustering; 3.8 Fitting Mixture Models Via the EM Algorithm; 3.8.1 E-Step; 3.8.2 M-Step; 3.8.3 Choice of Starting Values for the EM Algorithm; 3.9 Clustering Via Normal Mixtures; 3.9.1 Heteroscedastic Components; 3.9.2 Homoscedastic Components; 3.9.3 Spherical Components; 3.9.4 Choice of Root; 3.9.5 Available Software; 3.10 Mixtures of t Distributions 3.11 Mixtures of Factor Analyzers3.12 Choice of Clustering Solution; 3.13 Classification ML Approach; 3.14 Mixture Models for Clinical and Microarray Data; 3.14.1 Unconditional Approach; 3.14.2 Conditional Approach; 3.15 Choice of the Number of Components in a Mixture Model; 3.15.1 Order of a Mixture Model; 3.15.2 Approaches for Assessing Mixture Order; 3.15.3 Bayesian Information Criterion; 3.15.4 Integrated Classification Likelihood Criterion; 3.16 Resampling Approach; 3.17 Other Resampling Approaches for Number of Clusters; 3.17.1 The Gap Statistic 3.17.2 The Clest Method for the Number of Clusters
Sommario/riassunto	A multi-discipline, hands-on guide to microarray analysis of biological processes Analyzing Microarray Gene Expression Data provides a comprehensive review of available methodologies for the analysis of data derived from the latest DNA microarray technologies. Designed for biostatisticians entering the field of microarray analysis as well as biologists seeking to more effectively analyze their own experimental data, the text features a unique interdisciplinary approach and a combined academic and practical perspective that offers readers the most complete and applied coverage of the subject