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	Nota di contenuto	Analysis of Microarray Data; Contents; Preface; List of Contributors; 1 Introduction to DNA Microarrays; 1.1 Introduction; 1.1.1 The Genome is an Information Scaffold; 1.1.2 Gene Expression is Detected by Hybridization; 1.1.2.1 Hybridization is Used to Measure Gene Expression; 1.1.2.2 Microarrays Provide a New Twist to an Old Technique; 1.2 Types of Arrays; 1.2.1 Spotted Microarrays; 1.2.2 Affymetrix GeneChips; 1.2.2.1 Other In Situ Synthesis Platforms; 1.2.2.2 Uses of Microarrays; 1.3 Array Content; 1.3.1 ESTs Are the First View; 1.3.1.1 Probe Design; 1.4 Normalization and Scaling 1.4.1 Be Unbiased, Be Complete1.4.2 Sequence Counts; References; 2 Comparative Analysis of Clustering Methods for Microarray Data; 2.1 Introduction; 2.2 Measuring Distance Between Genes or Clusters; 2.3 Network Models; 2.3.1 Boolean Network; 2.3.2 Coexpression Network; 2.3.3 Bayesian Network; 2.3.4 Co-Occurrence Network; 2.4 Network Constrained Clustering Method; 2.4.1 Extract the Giant Connected Component; 2.4.2 Compute "Network Constrained Distance Matrix"; 2.5 Network Constrained Clustering Results; 2.5.1 Yeast Galactose Metabolism Pathway; 2.5.2 Retinal Gene Expression Data

| Sommario/riassunto | This book is the first to focus on the application of mathematical networks for analyzing microarray data. This method goes well beyond the standard clustering methods traditionally used. From the contents:* Understanding and Preprocessing Microarray Data* Clustering of Microarray Data* Reconstruction of the Yeast Cell Cycle by Partial Correlations of Higher Order* Bilayer Verification Algorithm* Probabilistic Boolean Networks as Models for Gene Regulation* Estimating Transcriptional Regulatory Networks by a Bayesian Network* Analysis of Therapeutic Compound Eff |