1. Record Nr. UNINA9910144107303321

Titolo	Analysis of microarray data : a network-based approach / / edited by Frank Emmert-Streib and Matthias Dehmer
Pubbl/distr/stampa	Weinheim, [Germany] : , : Wiley-VCH Verlag GmbH & Co. KGaA, , 2008 ©2008
ISBN	1-281-94703-2 9786611947033 3-527-62281-0 3-527-62282-9
Descrizione fisica	1 online resource (440 p.)
Disciplina	572.8636
Soggetti	DNA microarrays Electronic books.
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 at the end of each chapters and index.
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
2.5.3 Mouse Segmentation Clock Data2.6 Discussion and Conclusion; References; 3 Finding Verified Edges in Genetic/Gene Networks: Bilayer Verification for Network Recovery in the Presence of Hidden Confounders; 3.1 Introduction: Gene and Genetic Networks; 3.2 Background and Prior Theory; 3.2.1 Motivation; 3.2.2 Bayesian Networks Theory; 3.2.2.1 d-Separation at Colliders; 3.2.2.2 Placing Genetic Tests Within the Bayesian Network Framework; 3.2.3 Learning Network Structure from Observed Conditional Independencies; 3.2.4 Prior Work: The PC Algorithm; 3.2.4.1 PC Algorithm
3.5 Results and Further Application3.5.1 Estimating False-Positive Rates for the v-Structure Test; 3.5.2 Learning an Aortic Lesion Network; 3.5.3 Further Utilizing Networks: Assigning Functional Roles to Genes; 3.5.4 Future Work; References; 4 Computational Inference of Biological Causal Networks - Analysis of Therapeutic Compound Effects; 4.1 Introduction; 4.2 Basic Theory of Bayesian Networks; 4.2.1 Bayesian Scoring Metrics; 4.2.2 Heuristic Search Methods; 4.2.3 Inference Score; 4.3 Methods; 4.3.1 Experimental Design; 4.3.2 Tissue Contamination; 4.3.3 Gene List Prefiltering
4.3.4 Outlier Removal

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