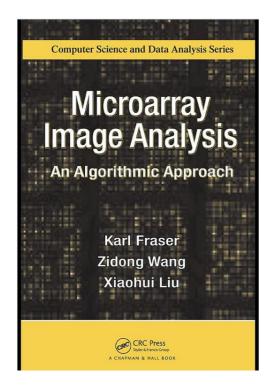


KARL FRASER, ZIDONG WANG, XIAOHU LIU MICROARRAY IMAGE ANALYSIS AN ALGORITHMIC APPROACH



Chapman and Hall/CRC

ISBN-13: 978-1-4200-9153-3 Hardback 335 pages 2010 One of the greatest challenges to utilize the high-throughput potential of DNA microarray technology is the decoupling of the requirements of operator assistance from the analysis stages of the process. In pursuit of such goal, *Microarray Image Analysis: An Algorithmic Approach* proposes an automatic system for microarray image processing, built upon and extended traditional analytical-based methods and custom-designed novel algorithms, to achieve this decoupling.

In the beginning of the book the focus is placed on a new technique that takes advantage of a multiview approach to image analysis. The challenges of applying powerful traditional techniques (e.g. clustering) to full-scale microarray experiments are also addressed. Further are presented and analyzed:

- an effective feature identification approach;
- an innovative technique that renders highly detailed surface models yielding clearer observations to feature regions of interest;
- a new approach to subgrid detection with better performance which could be used in other areas of image analysis;
- a novel technique for the background removal process;
- a useful technique for removing "noise".

The authors also propose an expectation—maximization (EM) algorithm which shows great promise for modeling gene regulatory networks from gene expression time series data on genome-wide scale. The overall benefits of these techniques in the biological and computer sciences are discussed in the final chapter where future research topics are also outlined. The fields of image processing, data analysis, and molecular biology are systematically integrated throughout the text to advance the state of the art in this important area. Despite the fact that the main focus of the book is placed on improving the processes involved in the analysis of microarray image data, the described methods could be applied to a much broader range of problems in the areas of medicine and computer vision analysis.

Table of Contents



Copasetic microarray analysis framework overview	
Summary	
Data Services	53
Introduction Image transformation engine Evaluation	
Summary Structure Extrapolation I	70
Introduction	/>
Pyramidic contextual clustering Evaluation Summary	
Structure Extrapolation II	90
Introduction	
Image layout-master blocks Image structure-meta-blocks Summary	
Feature Identification I	127
Introduction Spatial binding Evaluation of feature identification Evaluation of copasetic microarray analysis framework Summary	
Feature Identification II	153
Background Proposed approach-subgrid detection Experimental results Conclusions	
Chained Fourier Background Reconstruction	189
Introduction Existing techniques A new technique Experiments and results Conclusions	
Graph-Cutting for Improving Microarray Gene Expression Reconstruction	205
Reconstructions Introduction Existing techniques Proposed technique Experiments and results Conclusions	
Stochastic Dynamic Modeling of Short Gene Expression Time Series Data	219
Introduction Stochastic dynamic model for gene expression data An EM algorithm for parameter identification Simulation results Discussions Conclusions and future work	
Conclusions	245
Introduction Achievements Contributions to microarray biology domain Contributions to computer science domain Future research topics	
Appendix A: Microarray Variants	259
Appendix B: Basic Transformations	
Appendix C: Clustering	
Appendix D: A Glance on Mining Gene Expression Data	
Appendix E: Autocorrelation and GHT	
References	281