
Preface

In April 2003, the completion of the Human Genome Project was the capstone to a scientific journey that began decades earlier when Francis Crick and James Watson unraveled the mystery of the human genetic code. The sequencing of the human genome opened the flood gates of ideas and imagination to explore the structure and function of specific genes. Empowered researchers applied the fundamental principles of biology's central dogma to advance areas of scientific investigation ranging from genetics and evolution to molecular medicine, health, and disease.

The rapid advance of science and technology yielded the development of the microarray technique. Deciphering genetic sequences propelled the use of microarrays from a new fad in genome research to a ubiquitous tool in biological investigations. Turning genes on or off by the thousands critically orchestrates everyday biological processes and the amount of data generated from a single microarray experiment can be overwhelming, time-consuming, and tedious. By combining technological advances in microarrays with statistical and bioinformatics software, investigators have become armed with some of the most powerful means of biological problem-solving. Statistical reduction enables researchers to sort through the transcriptome and generate useable lists of significantly-modulated genes highlighting changes that chance alone cannot explain.

The underlying theme of this book is the use and application of microarray technology throughout the life sciences. This compilation of chapters provides an overview of how microarrays can be used to address diverse complex biological questions. In this collection, authors present information on using microarrays to unlock molecular mechanisms and gene expression patterns associated with research areas ranging from biodefense, pathological changes, and monitoring antimicrobial resistance genes to diagnostics, marine biodiversity, and dermal toxicology.

By using microarray technologies and specialized software, gene-expression profiles can provide insight into the development or evaluation of prophylactic and/or therapeutic treatments that target specific molecular pathways or genes. These data can ultimately lead to effective analyses using a molecular-systems biology approach that can feed into translational and predictive research. Due to the abundance of microarray data available in the open scientific literature, researchers can apply statistical approaches to identify biomarkers and perform risk assessments without the need of experimentation. In this book, authors utilized previously published data for the functional prediction and understanding of molecular

processes, the identification of reference genes using meta-analysis, and the development of a phenotypic anchoring model for drug-induced liver injury.

Biomarker-based discovery and risk assessment are important to provide mechanistic insight into factors as such as genetic background, diet, and lifestyle modulate the risk of disease. The continual development and refinement of improved molecular techniques to predict, treat, and prevent disease is critical to improving human health. Researchers must identify key components indicative of individuals or populations that pose an increased risk of infection or disease in order to achieve the goal of highly-individualized medical interventions (e.g., personalized medicine). For example, one chapter identifies an 18-gene signature that differentiates treatment responders and non-responders to interferon therapy. Based on the expression levels of this gene signature, a positive prediction value higher than 96% was observed for accurately predicting whether an HCV patient will or will not respond to interferon therapy. Moreover, another chapter describes the use microarrays to uncover mechanistic details underlying Alzheimer's disease pathology that track to cholesterol and lipid metabolism while highlighting the interactions between cholesterol and amyloid- β peptide.

Although using microarrays for monitoring changes in mRNA transcripts has dominated the application of this cutting-edge tool, other approaches for using microarrays include expression analysis of non-coding RNAs. Both microRNAs and long non-coding RNAs are involved in many biological processes by regulating transcriptional activity and subsequent processes. In this book, three chapters discuss the expression, annotation, and function of microRNAs and long non-coding RNAs to characterize macrophage microvesicle function, cutaneous inflammatory disorders, and elucidate their potential involvement in pathophysiological roles.

Almost every cell type within an organism contains the same genetic information locked up within DNA, but what makes these cells different from one another is based on the number, type, and magnitude of genes that are activated. The transcription of DNA to messenger RNA and subsequent translation into proteins is what leads to the unique phenotype exhibited by each cell, which could ultimately be normal or abnormal. To help differentiate one cell type from another, or differences among tissues, DNA microarrays have advanced the understanding of the genome with respect to structure and function. The implementation of microarrays and companion statistical and informatics tools is continually evolving and helping scientists discover new and exciting aspects of life science that will advance systems biology to a new level of understanding of how biological organisms function and respond to internal and external stimuli as well as provide insight into personalized or predictive medicine.