
Preface

The postgenomic era presents a multitude of challenges for scientists in all areas of science. The information overload from new discoveries in genomics and proteomics highlight how little we really know about the functioning of a cell. The advent of Next-Generation Sequencing technologies promises to make our genetic blueprint available to the common man. The availability of the plethora of biological information has lead to the development of new areas of science and the coining of new “omics” terms including transcriptomics, methylomics, toxicogenomics, pharmacogenomics, metabolomics, lipidomics, and so on. Remarkable research is being conducted to understand the various aspects of human health and how processes like histone modifications, promoter usage, alternative splicing, posttranscriptional, and posttranslational modifications contribute to disease. The advent of systems biology has unified chemists and biochemists alike in the struggle to eradicate or treat human disease.

Microarrays have blossomed into a fast developing and cutting-edge technology that promises to become a major component of personalized medicine. The 1990s witnessed a boom in many areas including genome sequencing, combinatorial chemistry, and computers, all of which have contributed to the development of microarray technology from its infancy into a mature tool. The growing potential of this tool is evident from the number of publications since 1991 when Fodor et al. of Affymax (now Affymetrix) first described the microarray prototype. The number of publications using microarrays in 1990–1999 was approximately 300, while over 8,200 journal articles have been published in the first half of this year alone. The usage of microarrays in experiments designed to identify differential gene expression is well accepted now. Since the seminal work of Pat Brown’s group at Stanford, microarrays became a technology that could be developed by any individual researcher using simple spotting robots. Currently, few laboratories make their own arrays due to the availability of commercial cost-effective solutions that are less prone to variation.

Microarrays have evolved from traditional oligonucleotide arrays for gene expression into tools that have even more fascinating applications. Today, one can find arrays containing not only DNA oligonucleotides but antibodies, carbohydrates, small molecules, and enzymes. The diversity of these applications makes this field exciting and limited only by imagination. This, however, makes it challenging for an inexperienced scientist wishing to enter this arena. I am still surprised by the lack of general information amongst individuals regarding how to design and conduct a microarray experiment. As we get exposed to the concept of “Personalized Medicine”, we find ourselves confounded by the myriad of platforms and applications attributed to microarrays. This book aims at enlightening individuals with all levels of experience about some of the

most common applications of microarrays in drug discovery and development. I hope that this book will serve as a reference for students and scientists alike who would like to enter this exciting field but are a bit intimidated.

I am especially grateful to the many friends, colleagues, and family who encouraged me in this effort.

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