Preface

The genomics research world has moved on since the first volume of *Genomics Protocols* in the Methods in Molecular Biology series was published in 2001. This progression is reflected in the themes of the chapters that adorn the current volume. It is true that there is the same apparently eclectic mixture of subjects as in the former volume. However, undeniably, the emphasis has switched from gene identification to functional genomics and the characterization of genes and gene products.

Although essentially a volume of "wet lab" techniques, in silico approaches also are represented through three chapters addressing the detection of genome sequence variation and the prediction of gene function, respectively.

We make no apologies for including texts that may appear in volumes devoted to other of the "omics." Rather, we feel that the majority of these relative newcomers are derivatives of genomics, and from the perspective of being able to see "the bigger picture," a great value is to be gained from considering these research disciplines collectively.

For some of the specialist techniques, it is difficult to avoid the use of a specific/particular commercial platform or piece of equipment. For these procedures, the authors have focused on the generic issues (e.g., data analysis), which are all too often given inadequate coverage in user manuals. While not wishing to advocate particular systems, by including these topics we acknowledge the importance, and possibly the uniqueness, of the technologies involved.

Through the choice of some of the topics, we tried to remember that not everyone is engaged in investigation of organisms for which an annotated sequenced genome or a high-density genetic map is available. Similarly, lest we forget that not all researchers are affiliated to well-equipped laboratories, Chapter 5 describes a relatively inexpensive and low-tech approach to genetic mapping using microsatellites.

To our minds, the jewel in the crown of the Methods in Molecular Biology series remains the "Notes" section of each chapter. In spite of the complexity of some of the subject matter, the authors have endeavored to ensure that as little technical detail as possible is left to either the reader's imagination or to the extensivity of their organization's library.

The first chapter addresses an issue that all too often is a prerequisite for comprehensive genome analysis: high fidelity whole genome amplification. Chapters 2–4 focus on a spectrum of procedures that are a prelude to genetic linkage analysis (Chapter 5).

The molecular profiling of genomic DNA in a variety of guises is encompassed in Chapters 6–9. Chapters 10–12 are devoted to transcriptional profiling, and focusing on small samples and the use of formalin-fixed archival tissue, deal with two of the thornier issues confronting researchers. The profiling of microRNAs (Chapter 12) is an exciting area of interest in the study of the regulation of gene expression in disease.

The line between proteomics and functional genomics can be a little fuzzy, but Chapters 12–17 describe alternative strategies for protein profiling, while Chapters 18–26 arguably constitute approaches for gene characterization and the identification of protein interaction networks. The volume concludes with a detailed tutorial (Chapter 27) about an exciting genomics technology useful in the elucidation of gene function and with huge potential therapeutic applications.

So there you have it. All that remains is for us to thank a group of redoubtable authors, the series editor, John Walker, and all those involved at Humana Press. We truly hope that you find the book informative and a valuable addition to your laboratory bookshelf.

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