
Preface

The Life Sciences are undergoing more than ever an accelerating evolution currently culminating in the -omics era characterized by the development of a multitude of high-throughput methods that are now getting to be routinely applied in the modern biochemistry lab. While the basic principles of classic analytical methods, such as Northern or Western blot analysis, are still dominating, the individual methods have advanced and continuously morphed into sophisticated techniques, such as expression profiling of whole genomes via DNA microarrays or the use of delicate protein chips to specifically detect thousands of macromolecules simultaneously during one single experiment. Those innovative techniques are capable of delivering tremendous amounts of data accompanied by the need of only trace amounts of samples and at a minimum in both personnel and material costs. The progress in almost every aspect of computer hardware technology obeys Moore's law, i.e., computer performance still grows exponentially at doubling times in the range of months rather than years. In fact, these advances are an indispensable prerequisite to handle data sets typically obtained by today's procedures applied in the field of Functional Genomics.

Now, after almost a decade has passed by since the first edition of this book has been released, the pace in progress of biochemical and biotechnological high-throughput methodologies ultimately requires the release of an updated version. Compared to the first edition, the scope of this book has been extended considerably, now no longer just dealing with DNA microarrays as the pioneering technology that then initiated the establishment of the formerly new field of Functional Genomics. Instead, due to the methodological expansion of Functional Genomics, other high-throughput techniques, for instance those involved in analyzing proteins and metabolites, are also included.

Functional Genomics can be distinguished from Comparative Genomics by its focus on the dynamic aspects of the transcriptome, proteome, and metabolome, respectively. Nevertheless, it is noticeable that in the literature the two disciplines are frequently mentioned in the same breath which prompted us to open this volume with a chapter about Bioinformatics, although with a strong focus on computational tools suitable to make functional predictions. In contrast to most other publications in the field, the following paragraphs are structured with attention to the nature of the biochemical target molecules rather than the different laboratory methods under consideration, i.e., each chapter contains separate discussions about the analysis of DNA, RNA, proteins, and metabolites. Although we are aware that this strategy cannot completely exclude redundancies, we feel that they at least can be reduced to a minimum. Overall, each individual contribution is intended to be self-contained and largely independent from the other chapters of the book. Ideally, each chapter can be seen as a unit of its own which consequently reduces the importance of the order of chapters.

The book is useful for all scientists who plan to establish or extend one of the technologies described here in their own labs. Although short introductions of the basic principles of each procedure are not omitted, the focus of each chapter lies mainly on the practical aspects of each method enabling the reader to easily acquire all the equipment and materials needed

and to successfully perform the experiments autonomously. As often as possible original lab protocols are included, making it easier to reproduce the respective procedures.

Finally, we would like to thank all the contributors for their time, patience, and endurance that undoubtedly was necessary to do such an excellent work. Regarding the reader, we hope that this book will satisfy its intention of being one of the pieces helping him to perform his experiments successfully, which, with respect to everyday lab experience, unfortunately is often an exception rather than the rule in a scientist's real life.

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