
PREFACE

Many of the chapters within this volume were first published almost two decades ago. Since then, these basic algorithms have not changed. However, what has changed is the huge increase in computer speed and ease of use along with the corresponding decrease in the costs. The increase in computer speed has made the use of some algorithms common that were almost never used in biochemistry laboratories two decades ago. During the past two decades, the training of the majority of senior M.D.s and Ph.D.s in clinical or basic disciplines at academic research and medical centers has not kept pace with advanced coursework in mathematics, numerical analysis, statistics, or computer science.

Nevertheless, the use of computers and computational methods has become ubiquitous in biological and biomedical research. One primary reason is the emphasis being placed on computers and computational methods within the National Institutes of Health (NIH) Roadmap. Another factor is the increased level of mathematical and computational sophistication among researchers, particularly among junior scientists, students, journal reviewers and NIH Study Section members. Yet another is the rapid advances in computer hardware and software that make these methods far more accessible to the rank-and-file members of the research community.

There exists a general perception that the applications of computers and computer methods in biological and biomedical research are either basic statistical analysis or the searching of DNA sequence data bases. While these are important applications, they only scratch the surface of the current and potential applications of computers and computer methods in biomedical research. The various chapters within this volume include a wide variety of applications that extend far beyond this limited perception. The chapters within this volume are basically in chronological order of original publication in *Methods in Enzymology* volumes 210, 240, 321, 383, 384, 454, and 467. This chronological order also provides a general progression from basic numerical methods to more specific biochemical and biomedical applications.