

Preface

Bioinformatics, an integral part of post-genomic biology, creates principles and ideas for computational analysis of biological sequences. These ideas facilitate the conversion of the flood of sequence data unleashed by the recent information explosion in biology into a continuous stream of discoveries. Not surprisingly, the new biology of the twenty-first century has attracted the interest of many talented university graduates with various backgrounds. Teaching bioinformatics to such a diverse audience presents a well-known challenge. The approach requiring students to advance their knowledge of computer programming and statistics prior to taking a comprehensive core course in bioinformatics has been accepted by many universities, including the Georgia Institute of Technology, Atlanta, USA.

In 1998, at the start of our graduate program, we selected the then recently published book *Biological Sequence Analysis (BSA)* by Richard Durbin, Anders Krogh, Sean R. Eddy, and Graeme Mitchison as a text for the core course in bioinformatics. Through the years, *BSA*, which describes the ideas of the major bioinformatic algorithms in a remarkably concise and consistent manner, has been widely adopted as a required text for bioinformatics courses at leading universities around the globe. Many problems included in *BSA* as exercises for its readers have been repeatedly used for homeworks and tests. However, the detailed solutions to these problems have not been available. The absence of such a resource was noticed by students and teachers alike.

The goal of this book, *Problems and Solutions in Biological Sequence Analysis* is to close this gap, extend the set of workable problems, and help its readers develop problem-solving skills that are vitally important for conducting successful research in the growing field of bioinformatics. We hope that this book will facilitate understanding of the content of the *BSA* chapters and also will provide an additional perspective for in-depth *BSA* reading by those who might not be able to take a formal bioinformatics course. We have augmented the set of original *BSA* problems with many new problems, primarily those that were offered to the Georgia Tech graduate students.