Preface

In the early 1990s when one of us was teaching his first bioinformatics class, he was not sure that there would be enough students to teach. Although the Smith-Waterman and BLAST algorithms had already been developed they had not become the household names among biologists that they are today. Even the term "bioinformatics" had not yet been coined. DNA arrays were viewed by most as intellectual toys with dubious practical application, except for a handful of enthusiasts who saw a vast potential in the technology. A few bioinformaticians were developing new algorithmic ideas for nonexistent data sets: David Sankoff laid the foundations of genome rearrangement studies at a time when there was practically no gene order data, Michael Waterman and Gary Stormo were developing motif finding algorithms when there were very few promoter samples available, Gene Myers was developing sophisticated fragment assembly tools when no bacterial genome has been assembled yet, and Webb Miller was dreaming about comparing billion-nucleotide-long DNA sequences when the $172,282$-nucleotide Epstein-Barr virus was the longest GenBank entry. GenBank itself just recently made a transition from a series of bound (paper!) volumes to an electronic database on magnetic tape that could be sent to scientists worldwide.

One has to go back to the mid-1980s and early 1990s to fully appreciate the revolution in biology that has taken place in the last decade. However, bioinformatics has affected more than just biology—it has also had a profound impact on the computational sciences. Biology has rapidly become a large source of new algorithmic and statistical problems, and has arguably been the target for more algorithms than any of the other fundamental sciences. This link between computer science and biology has important educational implications that change the way we teach computational ideas to biologists, as well as how applied algorithmics is taught to computer scientists.

For many years computer science was taught to only computer scientists, and only rarely to students from other disciplines. A biology student in an algorithms class would be a surprising and unlikely (though entirely welcome) guest in the early 1990s. But these things change; many biology students now take some sort of Algorithms 101. At the same time, curious computer science students often take Genetics 101 and Bioinformatics 101. Although these students are still relatively rare, keep in mind that the number of bioinformatics classes in the early 1990s was so small as to be considered nonexistent. But that number is not so small now. We envision that undergraduate bioinformatics classes will become a permanent component at every major university. This is a feature, not a bug.

This is an introductory textbook on bioinformatics algorithms and the computational ideas that have driven them through the last twenty years. There are many important probabilistic and statistical techniques that we do not cover, nor do we cover many important research questions that bioinformaticians are currently trying to answer. We deliberately do not cover all areas of computational biology; for example, important topics like protein folding are not even discussed. The very first bioinformatics textbooks were Waterman, 1995 (108), which contains excellent coverage of DNA statistics and Gusfield, 1997 (44) which includes an encyclopedia of string algorithms. Durbin et al., 1998 (31) and Baldi and Brunak, 1997 (7) emphasize Hidden Markov Models and machine learning techniques; Baxevanis and Ouellette, 1998 (10) is an excellent practical guide to bioinformatics; Mount, 2001 (76) excels in showing the connections between biological problems and bioinformatics techniques; and Bourne and Weissig, 2002 (15) focuses on protein bioinformatics. There are also excellent web-based lecture notes for many bioinformatics courses and we learned a lot about the pedagogy of bioinformatics from materials on the World Wide Web by Serafim Batzoglou, Dick Karp, Ron Shamir, Martin Tompa, and others.

Website

We have created an extensive website to accompany this book at

`http://www.bioalgorithms.info`

This website contains a number of features that complement the book. For example, though this book does not contain a glossary, we provide this service, a searchable index, and a set of community message boards, at the above web address. Technically savvy students can also download practical

bioinformatics exercises, sample implementations of the algorithms in this book, and sample data to test them with. Instructors and students may find the prepackaged lecture notes on the website to be especially helpful. It is our hope that this website be used as a repository of information that will help introduce students to the diverse world of bioinformatics.

Acknowledgements

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