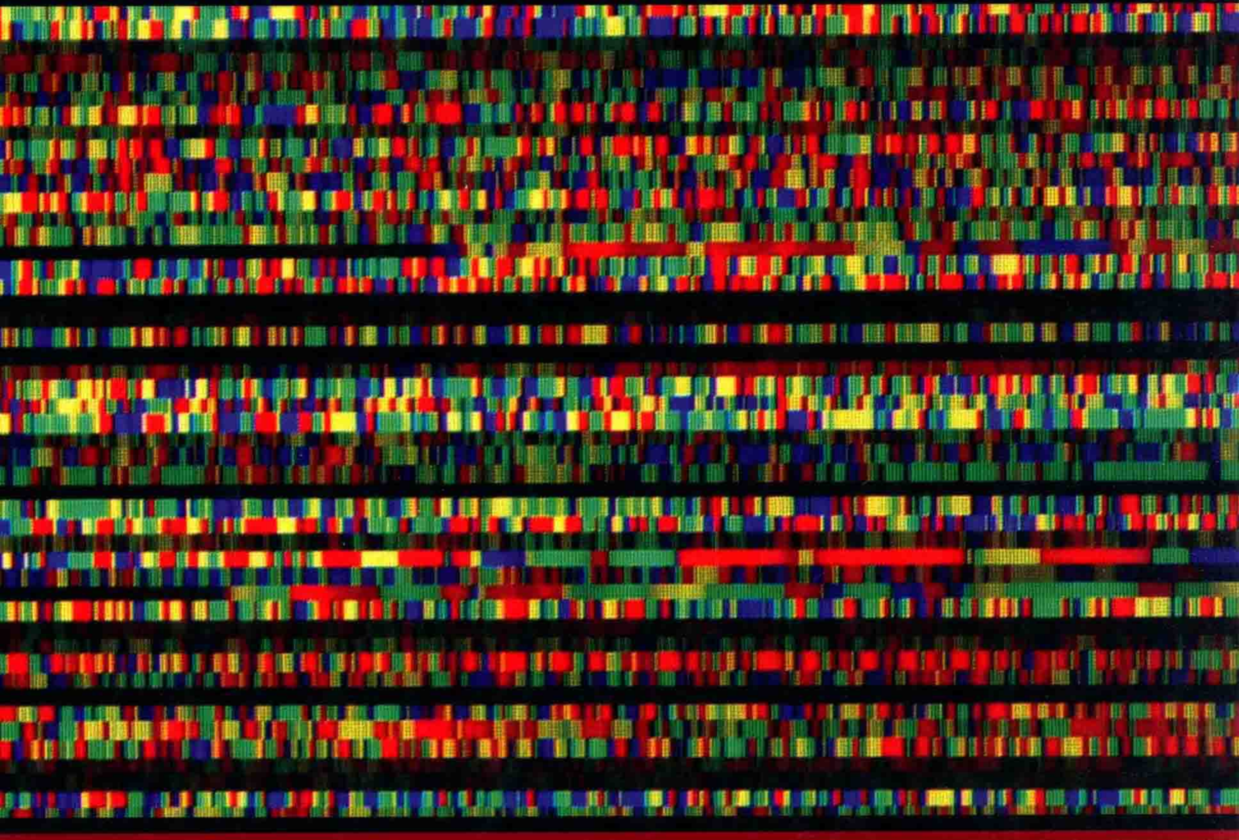
Exploring Bioinformatics

A PROJECT-BASED APPROACH



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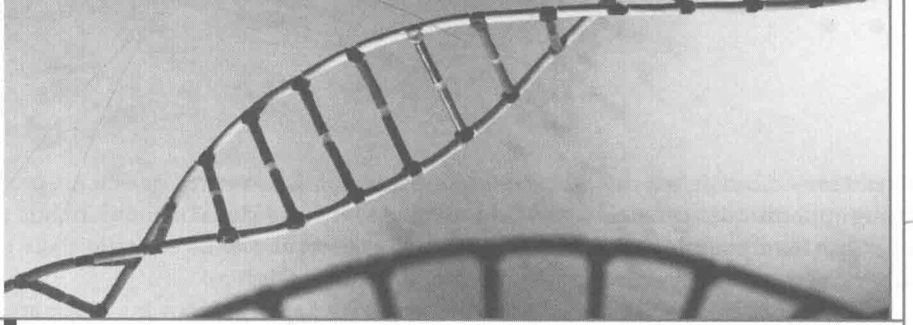

Preface

Why We Wrote This Book

Bioinformatics is a rapidly growing field of increasing importance to both biologists and computer scientists. Although DNA sequence data, and later whole genome sequence data, obtained by molecular geneticists served as the driving force in the rapid development of bioinformatics, molecular biology is far from the only field in which these techniques are now employed. Ecologists, zoologists, botanists, evolutionary biologists, physiologists, developmental biologists, biochemists, and others are using bioinformatics to manipulate DNA and protein data to gain new insights. Bioinformatics has also found a wealth of applications in medicine, pharmacology, agriculture, and many other industries. With so much interest in the use of computers to sift through complex and voluminous biological data, it is a sure bet that biologists trained in computational analysis and computer scientists with a biological background will be in demand for years to come.

We sought to develop a course that would introduce both biologists and computer scientists to bioinformatics. Although we wanted our course to explore key concepts in some depth and to delve into the algorithms that make bioinformatic programs tick, we also wanted to keep it on an introductory level: A first course in bioinformatics for computer science students who have had an introductory course in molecular biology, or for biology or biochemistry majors who have had an introductory programming course. We wanted the course to be hands-on, investigative, and research-rich, exposing students to current and unanswered questions, providing opportunities to tackle real-world problems with the kinds of bioinformatic programs used by actual researchers, and giving them the tools to write their own programs or modify existing ones to meet specific needs.

This book developed from that course. In each chapter, we cover a major area in which bioinformatics provides the means of attacking biological problems of current relevance. The topics are presented as a series of projects where students can learn both biological concepts and computational techniques as they explore questions using data and software freely available on the World Wide Web and then move on to an understanding of the underlying algorithms and finally development of their own code. This book is not intended to be a comprehensive reference on either molecular biology or computer programming; instead, we have endeavored to provide "just enough" instruction in each chapter so that students from both sides of the spectrum can master the ideas they need to investigate bioinformatic solutions to important problems. The exercises and questions found throughout the book are intended not merely to test students' knowledge but to *develop* it, as it is our experience that the best learning takes place when students are actively engaged in finding their own solutions.

This book is adaptable for use in different kinds of courses. We approach our own course from a combination of biological and computational perspectives, and our students learn both the use of web-based tools and Perl programming. A biologist with more limited programming background might choose to have students explore how the algorithms work in the *Guided Project* sections but not expect them to write their own programs; complete Perl programs downloaded from the companion website could be used in a course of this nature to complete many of the exercises (identified by a disk icon) and to see how the algorithms work in practice. A mathematically oriented course might take a similar approach, emphasizing the mathematics underlying the algorithms without concern for their implementation. We also hope that we have provided "just enough" background material that a biologist with a real interest in programming or a computer scientist with a serious interest in biology could use the text effectively even in the absence of strong foundational knowledge in the complementary area.

We welcome your comments and ideas as you explore bioinformatics.

How to Use This Book

The goal of this book is to engage you in learning bioinformatics by actually *using* bioinformatic tools—both existing web-based programs and your own software solutions—to approach real-world problems. This section will help you get acquainted with the layout of the book and the various resources it provides.

The first chapter serves as a general introduction to bioinformatics and its potential, and to the idea of biological problem-solving using computational techniques. Each of the remaining chapters introduces a current biological problem: genetic disease, antibiotic resistance, drug design, and so on. The *Understanding the Problem* sections in each chapter will help you recognize the importance of the problem to today's life scientists and the limitations of traditional techniques in exploring the topic. The next section, *Bioinformatics Solutions*, discusses the value of computational approaches in shedding light on the problem.

With this relatively brief introduction to the problem, two kinds of hands-on projects give you the opportunity to try using and writing relevant bioinformatic tools. First, a *Guided Project* will take you step-by-step through a structured approach to bioinformatic tools and algorithms. This project is divided into two parts: In the *Web Exploration* section, you will encounter data sources and analytical programs commonly used by biological researchers and freely available on the World Wide Web, while the *Programming Project* lets you look "under the hood" as bioinformatic algorithms implemented in the Perl programming language are presented, dissected, and used to explore data. The experience gained from the *Guided Project* will enable you to tackle the *On-Your-Own Project*, where programming concepts relevant to investigating a related but distinct problem are presented, but no actual program code is provided, allowing you to develop your own algorithms or implementations.

This book is deliberately not comprehensive or encyclopedic in its approach; instead, it emphasizes a limited number of key bioinformatic principles and encourages active learning through hands-on exploration. For students with less coursework in biological science, *BioBackground* sections provide additional background for understanding the projects. The programs in this text are written in Perl, an easy-to-use language with excellent text-processing features suitable to the manipulation of DNA and protein data. *Perl: Need to Know* sections throughout the text introduce Perl syntax, commands, and functions, while two appendices assist the less-experienced programmer in mastering the use of this language. In addition, *More to Explore* sections suggest possibilities for further study and *Connections* sections look forward to the future of bioinformatics.

Three kinds of exercises are included in each chapter to allow you to test and apply your knowledge and to provide opportunities for instructors to evaluate their students' performance. *BioConcept Questions* help you check your understanding of the biological ideas underlying the chapter's problem and determine whether you need to use the *BioBackground* sections to fill gaps in your knowledge. *Web Exploration Questions* ask you to develop your skills in using existing bioinformatic tools. *Putting Your Skills into Practice* exercises allow you to write your own Perl code to modify and extend the utility of the programs given in the *Guided Project* and then see how your programs work in dealing with real-world data. You will notice that all of the exercises in each chapter are numbered consecutively (even though there may be two or three groups of exercises) to make it easier for instructors to assign specific exercises from throughout the chapter.

Finally, a companion website, http://biology.jbpub.com/bioinformatics, provides additional resources. All of the code discussed in the *Guided Projects* can be downloaded to eliminate the need for retyping. DNA and protein sequences needed to complete the projects and exercises are also found on the website, as are test data. For instructors, complete solutions to the programming exercises can be downloaded from http://www.jbpub.com/biology/bioinformatics, facilitating use of the software in courses that do not require programming.

Acknowledgments

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Jones and Bartlett Titles in Bioinformatics

Biomedical Informatics: A Data User's Guide
Jules J. Berman

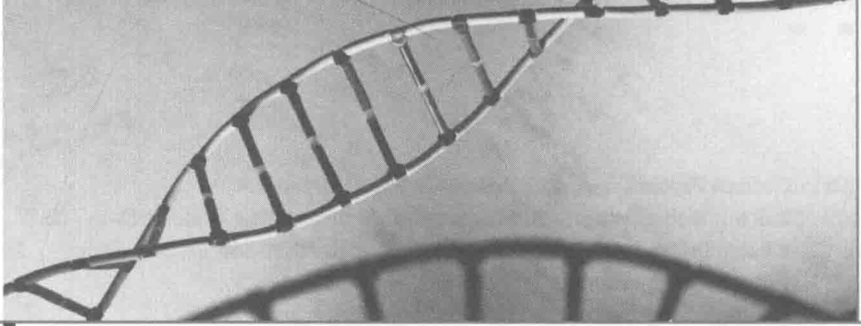
Medical Informatics 20/20: Quality and Electronic Health Records through Collaboration, Open Solutions, and Innovation
Douglas Goldstein, Peter J. Groen, Suniti Ponkshe, and Marc Wine

Perl Programming for Medicine and Biology
Jules J. Berman

Python for Bioinformatics
Jason Kinser

R for Medicine and Biology
Paul D. Lewis

Ruby Programming for Medicine and Biology
Jules J. Berman



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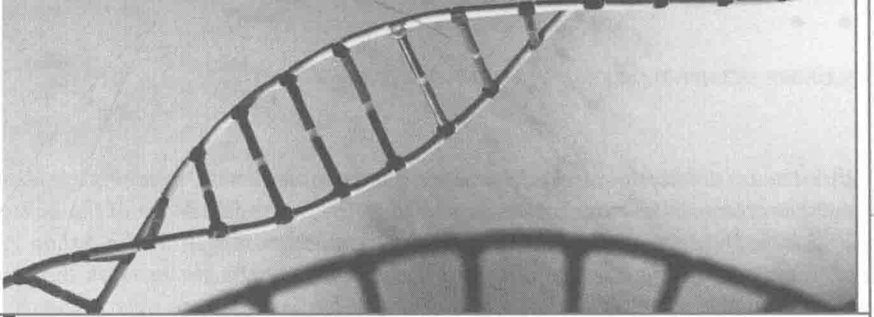

chapter 1

Exploring Bioinformatics

In a small community in western Nova Scotia, researchers discovered a rare genetic disease, now known as Nova Scotia Niemann-Pick disease (NS-NPD). This genetic disorder affects the nervous system and appears most commonly in children. A genealogical path was found connecting all known patients afflicted with this disease to a single seventeenth-century Acadian couple born and raised in western Nova Scotia. A single mutant gene is believed to be responsible for NS-NPD. It is presumed that inbreeding within the community resulted in the high frequency of

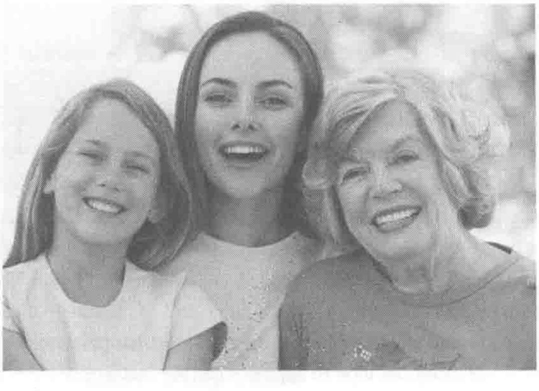

Figure 1.1 • The secrets of long life and health...are they in the genes?

this disease among descendants of the original couple. Today, residents are encouraged to marry outside the community to limit the future incidence of the disease.

Across the ocean in Italy, Stoccareddo, a small town high in the Italian Alps, also has a high rate of inbreeding and has sparked geneticists' interest. But in this case, residents of the town are amazingly healthy. Even though over 97 percent of the residents are closely related, the rate of disease is extremely low and genetic disease is virtually nonexistent. Here, residents are being encouraged to marry inside the community, and researchers are seeking to identify specific genes that contribute to the extraordinary well-being of this population.

What happened over the 800-year history of Stoccareddo that left its modern residents so healthy? What "bad" genes have been eradicated by generations of natural selection? What "good" genes contribute to the startling good health of the community? Could modern technology bring similar benefits to others? And what of NS-NPD? Will the disease gene be "weeded out" over time? What can we do for those who have already inherited the disease?

1.1 Understanding the Problem: The Promise of Bioinformatics

In the late nineteenth century, Austrian monk Gregor Mendel quietly initiated a genetic revolution by providing science with its first tools for understanding how characteristics are inherited. The identification of **DNA** (deoxyribonucleic acid) as the genetic material in 1953 sent the revolution in a new direction, allowing researchers to directly correlate changes in genes with the workings of cells and organisms in health and disease. But the floodgates of genetic information truly opened in the mid-1990s, as large-scale DNA sequencing technology became capable of revealing the complete nucleotide sequence of entire genomes (see Figure 1.2), including the three billion base-pairs that make up the human genome (completed in 2003).

Today, molecular geneticists seeking to extract the secrets that lie within cells are awash in a vast and ever-increasing flood of genetic information. They have uncov-

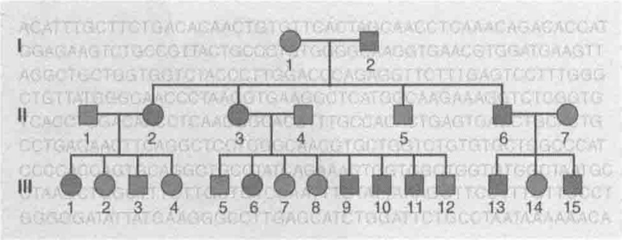

Figure 1.2 • Bioinformatics—a field that has grown out of the information explosion resulting from the use of molecular tools to approach genetic problems.

ered the specific mutations that underlie sickle-cell anemia, cystic fibrosis, Tay-Sachs disease, and a host of other inherited diseases, and they have used that information for new therapeutic strategies. Scientists have developed corn and cotton that make their own insecticides and drugs made from proteins released in the milk of genetically engineered goats. Both the scientific literature and the popular press promise new and exciting innovations and applications, ranging from understanding the physiology of cells and organisms to curing genetic disease, improving food supplies, reversing environmental degradation, and providing individualized medicine. Truly, we live in the age of genetics.

Unfortunately, even with our tremendous technological advances and all the data we have amassed, the discovery process is slow, and many fascinating and important problems will undoubtedly remain unsolved for years to come. Part of the problem is finding ways to get meaningful information from the mountains of data available. Because of the enormity of genetic data, new analytical approaches must be developed in order to uncover new nuggets of information. **Bioinformatics** is the new science at the interface of molecular biology and computer science seeking to develop better ways to explore, analyze, and understand genetic data.

The goal of this book is to introduce several "hot topics" within the young field of bioinformatics and provide experience with key techniques used to investigate questions within those areas. Our project-based approach is intended to engage you in actually using and developing these techniques as you apply them to questions relevant to real-world research. As you work through the problems and exercises in each chapter, you will use existing web-based software, explore how bioinformatic algorithms work, and write your own software solutions in Perl.

What kinds of questions and problems are investigated using bioinformatics? Bioinformatic tools are being used in both basic research and practical applications in fields as diverse as ecology, cancer biology, agriculture, pharmacology, and forensics. Here are just a few examples of biological questions whose solutions will include a key role for computer technology:

- Why don't all tumors of the same type respond to the same chemotherapies? Could we individualize treatment to increase the chances of successful therapy?
- What are the causes of the hundreds of genetic diseases? How do genes influence complex diseases such as diabetes, obesity, heart disease, cancer, and alcoholism? What can we do about these diseases?
- How should we define a species, and how can we determine whether two different organisms belong to the same species?
- In the human genome, how does a surprisingly small set of genes—probably fewer than 25,000—result in the synthesis of hundreds of thousands of proteins? And what functions remain to be discovered for the 99 percent of the genome that apparently does not encode proteins?

- How do bacteria and viruses cause disease, and how can better understanding of their physiology improve prevention and treatment?
- Can DNA evidence be relied upon in convicting—or exonerating—those accused of crimes?
- What is the risk that a child will inherit a genetic disease or susceptibility?
- What are the evolutionary pathways that have led to the development of the diversity of organisms that we see today?
- Are there organisms with genes that we could apply to breaking down oil spills or cleaning up toxic waste?
- How can drug design be improved so that specific drugs can be made to work on specific targets, rather than using a "shotgun" approach?
- What can the genes of bacteria, yeast, flies, worms, plants, and mice tell us about the functions of human genes?

We are able to ask most of these questions because of the advent of molecular biology, which got its start as scientists like Max Perutz and Linus Pauling began to dissect the structure of proteins, while others, including Frederic Griffith, Alfred Hershey, Martha Chase, James Watson, and Francis Crick found that DNA (see Figure 1.3) was the solution to the riddle of the genetic material. Initially, the goal of molecular biology was to understand the workings of genes and how they encode proteins. As the details of those processes became clearer, molecular biologists turned their attention to understanding key biological processes at the molecular level.

Today, the questions asked by molecular biologists span multiple areas of biology. Researchers using molecular biology techniques might actually be working in the field of development, trying to understand how genes are turned on and off in sequence to produce the changes that occur between the egg and the adult organism. Or, they might be comparing DNA sequences to study evolutionary relationships among species. A molecular biologist might work for a biotech company, altering the genetic makeup of a plant to improve its characteristics, or in a clinical setting seeking a permanent cure for a genetic disease. What unites these very different applications of molecular biology is their focus on DNA and the proteins it encodes. In addition, they all face the common problem of dealing with huge

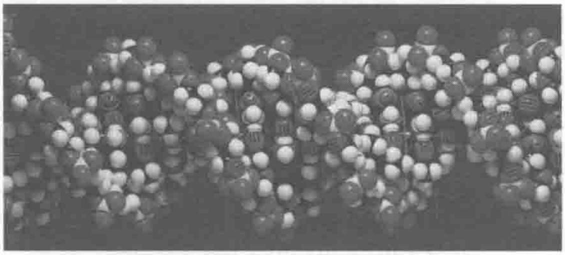

Figure 1.3 • DNA—the genetic material of all living things.