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Included is an integrated package of theoretical modeling and analysis tools, computational modeling techniques, and parameter estimation and model validation methods, with a focus on integrating analytical and computational tools in the modeling of biological processes. Divided into three parts, it covers basic analytical modeling techniques; introduces computational tools used in the modeling of biological problems; and includes various problems from epidemiology, ecology, and physiology. All chapters include realistic biological examples, including many exercises related to biological questions. In addition, 25 open-ended research projects are provided, suitable for students. An accompanying Web site contains solutions and a tutorial for the implementation of the computational modeling techniques. Make sure to price the book competitively with the other options presented, so you have the best chance of selling your book. We provide a list of quotes below. If you decide to sell your book to one of the sites, they will provide you free shipping labels. After you print

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We present a collection of modules under development that can be used in existing mathematics and biology courses, and we address a critical national need to introduce students to mathematical methods beyond the interface of biology with calculus. Based on ongoing research, and designed to use the projectbasedlearning approach, the modules highlight applications of modern discrete mathematics and algebraic statistics to pressing problems in molecular biology. For the majority of projects, calculus is not a required prerequisite and, due to the modest amount of mathematical background needed for some of the modules, the materials can be used for an early introduction to mathematical modeling. At the same time, most modules are connected with topics in linear and abstract algebra, algebraic geometry, and probability, and they can be used as meaningful applied introductions into the relevant advancedlevel mathematics courses. Opensource software is used to facilitate the relevant computations. As a detailed example, we outline a module that focuses on Boolean models of the lac operon network.

INTRODUCTION In the last decade, the field of life sciences has undergone revolutionary changes spanning remarkable discoveries at all levels of biological organization—molecules, cells, tissues, organs, organisms, populations, and communities. A salient trait of these advances is the increased need for statistical, computational, and mathematical modeling methods. Scientific instruments are now, by orders of magnitude, more sensitive, more specific, and more powerful. The amounts of data collected and processed by these newgeneration instruments have increased dramatically, rendering insufficient the traditional methods of statistical data analysis. Nowhere, however, have the problems of amassing huge amounts of data been more clearly demonstrated than in attempts to unravel the secrets of genetic mechanisms.

For example, automated DNA sequencing has given rise to an information explosion, and the challenge now is to extract meaning from all of this sequence information. The quest to better understand temporal and spatial trends in gene expression has led us to search for DNA sequences that have been conserved over time in a large number of species. The existence of such conserved strings in different species suggests that these sequences may perform fundamental functions in the genome and thus be critical to our understanding of life on earth. However, determining candidates for DNA sequences that have been conserved over time across different species is a tremendous task, because the human genome alone is approximately 3 billion base pairs. Comparing across species then requires comparisons of further billions of sequences, over thousands of species. The sheer size of the data sets suggests that appropriate use of mathematical models coupled with statistical methods for data analysis and inference will play an irreplaceable role in contemporary biology. Frequent announcements of the sequencing of additional organisms, such as the rhesus macaque Gibbs and the Rhesus Macaque Genome Sequencing and Analysis Consortium, 2007 and the domestic horse Wade et al., 2009 demonstrate that the complexity of the data sets is continually growing; thus, future advances in molecular biology will need to rely even more heavily on the use of mathematical methods. Similarly, the field of molecular systems biology has emerged as equally mathematically driven Robeva, 2010 . Understanding these interactions will enable greater progress against conditions such as heart disease, cancer, and diabetes.

A recent proposal for a new national initiative toward “the New Biology” identifies health issues as one of four key areas where a systems biology approach and improvements in mathematical and statistical modeling will be prerequisites for progress “Although there are increasing efforts to apply quantitative approaches to biological questions, more must be done to transform biology from its origins as a descriptive science to a predictive science. We will ultimately be limited in our ability to deploy biological systems to solve largescale problems unless we significantly deepen our fundamental understanding of the organizational principles of complex biological systems, a staggeringly difficult challenge. The challenge is to combine the rich but disparate insights of molecular biology into a conceptual framework that better allows us to see the overall structure of molecular and other mechanisms. Mathematical models have proved to be indispensable in this

regard. Preparing students of our educational systems to meet these challenges is consequently a crucial national need. Methods in the algebraic group include elementary discrete mathematics, graph theory, probability, linear algebra, abstract algebra, and polynomial algebra and algebraic geometry. In this discussion, we refer to this selection of noncalculusbased methods as modern discrete mathematics. Particularly notable in this group is the field of algebraic geometry. At its most elementary level, this is a classical subject that captures mathematical patterns and relationships through geometric figures varieties that can be described as sets of common solutions to polynomial equations. ² To emphasize the parallel with linear algebra, which studies solution sets to systems of linear equations, the term polynomial algebra is also used.

Aspects of modern discrete mathematics and algebraic statistics have recently made a significant impact on molecular biology, much as calculusempowered population biology and epidemiology have had in the early 20th century. Examples include finite dynamical systems models of the metabolic network in *Escherichia coli* Samal and Jain, 2008 and the abscisic acid signaling pathway Zhang et al., 2008 , methods from algebraic geometry applied in evolutionary biology to develop new approaches to sequence alignment Pachter and Sturmfels, 2004 , new modeling of viral capsid assembly developed using geometric constraint theory Sitharam and AgbandjeMckenna, 2006 , and algorithms based on algebraic combinatorics used to study RNA secondary structures Apostolico et al., 2009 . We believe the notable absence of modern discrete mathematics from the undergraduate mathematical biology curricula can be attributed primarily to a lack of appropriate materials rather than inaccessibility of the essential underlying mathematical concepts. Indeed, elementary topics in modern discrete mathematics and the underpinnings of algebraic statistics including topics from discrete mathematics, matrix theory, graph theory, linear and polynomial equations, and basic probability and statistics constitute the bulk of general education mathematics courses, whereas more advanced topics i.e., in linear algebra, graph theory, and modern algebra permeate the noncalculusbased math major curriculum. As indicated by the popularity of texts such as “Ideals, Varieties, and Algorithms” Cox et al., 2007 , now in its seventh printing, entire courses in algebraic geometry have become popular at many institutions. One of this papers authors T. H.

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