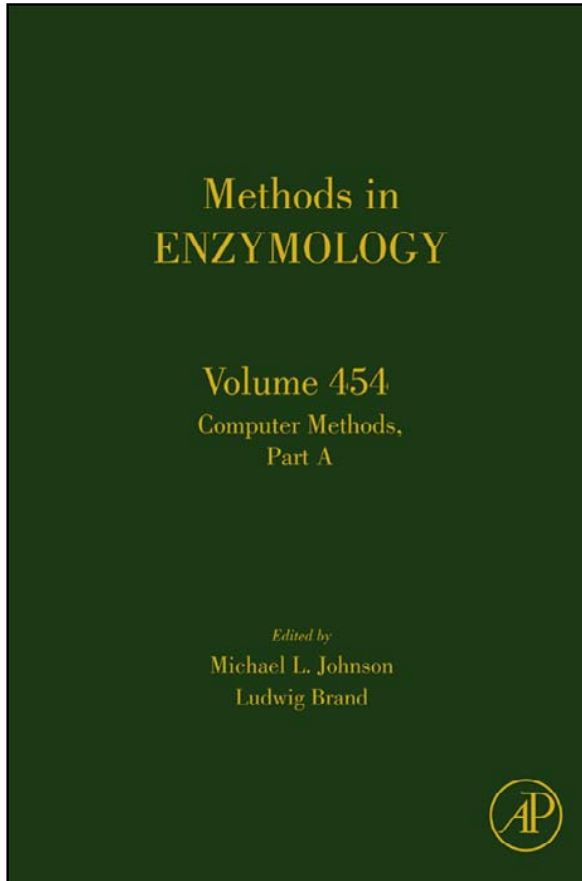


**Provided for non-commercial research and educational use only.
Not for reproduction, distribution or commercial use.**

This chapter was originally published in the book *Methods in Enzymology*, Vol. 454, published by Elsevier, and the attached copy is provided by Elsevier for the author's benefit and for the benefit of the author's institution, for non-commercial research and educational use including without limitation use in instruction at your institution, sending it to specific colleagues who know you, and providing a copy to your institution's administrator.



All other uses, reproduction and distribution, including without limitation commercial reprints, selling or licensing copies or access, or posting on open internet sites, your personal or institution's website or repository, are prohibited. For exceptions, permission may be sought for such use through Elsevier's permissions site at:

<http://www.elsevier.com/locate/permissionusematerial>

From: Raina Robeva, Desegregating Undergraduate Mathematics and Biology—
Interdisciplinary Instruction with Emphasis on Ongoing Biomedical Research.
In Michael L. Johnson and Ludwig Brand editors: *Methods in Enzymology*, Vol. 454,
Burlington: Academic Press, 2009, pp. 305-321.

ISBN: 978-0-12-374552-1

© Copyright 2009 Elsevier Inc.

Academic Press.

DESEGREGATING UNDERGRADUATE MATHEMATICS AND BIOLOGY— INTERDISCIPLINARY INSTRUCTION WITH EMPHASIS ON ONGOING BIOMEDICAL RESEARCH

Raina Robeva

Contents

1. Introduction	306
2. Course Description	309
2.1. Institutional context	309
2.2. Target audience and pedagogy principles	310
2.3. Features of the course	310
2.4. Course structure	311
2.5. Course topics	312
3. Discussion	317
Acknowledgments	320
References	320

Abstract

The remarkable advances in the field of biology in the last decade, specifically in the areas of biochemistry, genetics, genomics, proteomics, and systems biology, have demonstrated how critically important mathematical models and methods are in addressing questions of vital importance for these disciplines. There is little doubt that the need for utilizing and developing mathematical methods for biology research will only grow in the future. The rapidly increasing demand for scientists with appropriate interdisciplinary skills and knowledge, however, is not being reflected in the way undergraduate mathematics and biology courses are structured and taught in most colleges and universities nationwide. While a number of institutions have stepped forward and addressed this need by creating and offering interdisciplinary courses at the juncture of mathematics and biology, there are still many others at which

Department of Mathematical Sciences, Sweet Briar College, Sweet Briar, Virginia

Methods in Enzymology, Volume 454
ISSN 0076-6879, DOI: 10.1016/S0076-6879(08)03812-3

© 2009 Elsevier Inc.
All rights reserved.

there is little, if any, interdisciplinary interaction between the curricula. This chapter describes an interdisciplinary course and a textbook in mathematical biology developed collaboratively by faculty from Sweet Briar College and the University of Virginia School of Medicine. The course and textbook are designed to provide a bridge between the mathematical and biological sciences at the lower undergraduate level. The course is developed for and is being taught in a liberal arts setting at Sweet Briar College, Virginia, but some of the advanced modules are used in a course at the University of Virginia for advanced undergraduate and beginning graduate students. The individual modules are relatively independent and can be used as stand-alone projects in conventional mathematics and biology courses. Except for the introductory material, the course and textbook topics are based on current biomedical research.

1. INTRODUCTION

In the last decade, the field of life sciences has undergone revolutionary changes spanning remarkable discoveries at all levels of biological organization—from molecules, to cells, to tissues, organs, organisms, and populations. 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 new-generation instruments have increased dramatically, rendering insufficient the traditional methods of statistical data analysis. To organize this information and arrive at a better fundamental understanding of life processes, it is imperative that powerful conceptual tools from mathematics be applied to the frontier problems in biology (*BISTI Report, 2000*).

For instance, automated DNA sequencing has given rise to data explosion, and the challenge now is to extract meaningful information from these data. The quest to better understand temporal and spatial trends in gene expression has led to a search for DNA sequences that have been conserved over time in a large number of different species. This is a tremendous task, as the human genome alone is approximately 3 billion base pairs. Comparing across species then requires comparisons of 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 exceptional role in modern biology and demonstrates that future advances in molecular biology will not be possible without the help of mathematics.

The field of molecular systems biology has emerged as equally mathematically driven. Broadly defined, this is a field that examines how “... large number of functionally diverse, and frequently multifunctional, sets of elements interact selectively and non-linearly to produce coherent behavior