

# Bioscene

$$v = \frac{V_{max}[s]}{k_m + [s]}$$

$$S = CAZ$$

$$C_{AB} = \frac{1}{2}(1 - e^{-2X_{AB}})$$

$$\partial_{NS}M_1 / \partial t = W_1 \text{ where } dM = \partial_{NS}M_1 + \partial_{EC}M_1$$

$$\frac{dN_1}{dt} = r_1 N_1 \left( \frac{K_1 - N_1 - \alpha N_2}{K_1} \right)$$

$$\frac{dN_2}{dt} = r_2 N_2 \left( \frac{K_2 - N_2 - \beta N_1}{K_2} \right)$$

$$p = e^{-\mu m}$$

$$g(r, \theta) = \sum_{n=-\infty}^{+\infty} g_n(r) i^n e^{in\theta}$$

$$g_n(r) = \frac{1}{2\pi} \int_0^{2\pi} g(r, \theta) C^{-in\theta} d\theta$$

$$W_k(n) \leq \frac{1}{k^{d/k}} \sum \mu(d) n^{k/d}$$

$$x = (d_{AB} + d_{AC} - d_{BC}) / 2$$

$$y = (d_{AB} - d_{AC} + d_{BC}) / 2$$

$$z = (-d_{AB} + d_{AC} + d_{BC}) / 2$$

$$\frac{dv}{dt} = \frac{-1}{c} [g_{Na}(V)(V - V_{Na}) + g_K(V)(V - V_K) + g_L(V - V_L)]$$

$$\frac{dn}{dt} = \alpha_n(V)(1 - n) - \beta_n(V)n$$

$$\frac{dm}{dt} = \alpha_m(V)(1 - m) - \beta_m(V)m$$

$$\frac{dh}{dt} = \alpha_h(V)(1 - h) - \beta_h(V)h$$

# *Bioscene*

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### Table of Contents

#### *Articles:*

- Integrating Information Technology into Biology Courses .....3  
Buzz Hoagland
- Hydrothermal Vents: More than just a lot of hot water! .....8  
Nancy Sanders
- Ten Equations that Changed Biology:..... 11  
Mathematics in Problem-Solving Biology Curricula  
John R. Jungck

#### *News & Views:*

- AMCBT 41st Annual Meeting at Beloit College  
Preliminary Program .....37  
Call for Nominations .....40
- Echoes from the past... .....41  
Ed Kos, AMCBT Historian
- AMCBT to ACUBE? .....41
- Kimball's Biology Pages on the Web .....41
- Proposed AMCBT Constitution Changes .....42
- Membership Application .....43
- AMCBT on the WEB .....44

Cover Illustration: "Ten Equations that Changed Biology." See Figure 1 on page 12 for a context.

## *Bioscene: Journal of College Biology Teaching*

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Letters to the Editor  
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# Integrating Information Technology into Biology Courses

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*Information technology is successfully integrated into biology courses through a variety of mechanisms. Class e-mail distribution lists are used to answer student questions outside of regular class/laboratory time. The World Wide Web (WWW) is used for posting interactive course syllabi, posting student-generated data, and as a research tool. Ninety eight percent of students surveyed (n = 42) indicated that integrating the Internet and the WWW into four different biology courses was useful, and 74% of respondents believe the WWW should be incorporated into additional courses.*

Key Words: IT, WWW, web pages, cyberspace, e-mail, hypertext, links, browsers

## Introduction

The three most popular letters in the world today are without a doubt WWW. It seems that one can't watch a television program or commercial without those ubiquitous symbols appearing in the epilogue. Newspapers, magazines, and radio programs all advertise their presence in cyberspace. Telephones are becoming obsolete as phone software becomes more available. A few years back it was fashionable to hand out business cards with your name, physical address, telephone number, and fax number. In today's world, those same cards won't leave an impression without a cyber-address (email and homepage). It appears then, that all forms of communication are converging on the WWW, or, at the very least, each desires a presence on the WWW. As biology educators, we need to take advantage of this burgeoning field of Information Technology and integrate it into our courses.

The Internet is a world-wide network of interconnected computers that communicate with each other through various protocols. The simplest information sharing protocol allows exchange of data and text, and the most complicated systems allow transmission of images, video, and sound through a hypertext interface known as the World Wide Web. Hypertext is a format for documents that are accessed on the WWW. Some words, phrases, or graphics in a hypertext document are highlighted or underlined (or both), and these words, phrases, or graphics are hypertext links (links or hyperlinks for short) to other documents. A Web page allows you to use a computer mouse to click on a highlighted word or graphic and link seamlessly with parts of other documents, whether the documents are stored on the same computer or on separate machines in distant places around the world. Web pages are made available by computers running special software called servers. Hypertext files are viewed by users through use of special soft-

ware programs called browsers (e.g., Netscape, Microsoft Explorer). Although the Internet has been in existence since the 1960s, the WWW did not come on-line until 1990 and did not become popular until the National Center for Supercomputing Applications (NCSA) released Mosaic (Web browsing software) in 1993 (Leiner et al, 1997). Since 1993, growth of the WWW has surpassed every other mode of online communications, increasing exponentially with a current doubling time of less than six months. Gray (1996) estimates that approximately 9.5 million computers with Internet addresses existed in January 1996, and that in July 1996 there were 230,000 servers serving web pages to the WWW. Each server typically makes hundreds to hundreds of thousands of Web pages available to browsers of the WWW. Therefore, it is highly probable that there are millions of web pages available at any time (although the exact number will never be known because there is no central registry for Web pages). Finding information in this morass of cyberspace is at best a daunting and frustrating task. Fortunately, there are search engines that facilitate information retrieval, but the nature of these software programs and the WWW does not allow the level of sophisticated searching typically associated with online catalogues at libraries or other Boolean Logic tools used in searching online databases such as Medline® (U.S. National Library of Medicine, 1997). Nonetheless the WWW can be successfully integrated into and used to enrich many different biology courses.

## How can Information Technology be integrated into biology courses?

Electronic mail (e-mail) is a simple, yet effective, communication tool that can be easily adapted for use in any course. I establish electronic distribution lists that allow me to simultaneously send the same message to

all students in a class. This is especially helpful when a student poses a question on Thursday that I can't answer without consulting a reference in my office. Instead of waiting to share the answer with the class five days later on the following Tuesday, I send it to everyone via e-mail within a few hours of when the class ended. Also, many students formulate questions while studying late at night. Instead of telephoning at such late hours, they e-mail questions which I answer the following morning. Our librarians have established a similar service entitled ASKUS, in which students are encouraged to submit questions via e-mail that are answered within 24 hours. I also require students to subscribe to e-mail discussion groups. These discussion groups can be very enlightening, or they can be disastrous. One learns the difference very quickly. Finding discussion groups is relatively easy. Search engines such as Yahoo (Yahoo, 1997) or directories such as LISZT (Southwick, 1997) are good places to start searching for relevant discussion groups.

The WWW is used in my classes for three different purposes: 1) posting interactive syllabi, 2) locating resources, and 3) posting student generated data. I do not provide a copy of the course syllabus on the first day of class, or at any time during the semester. Instead, I make the syllabi available through the Biology Department homepage (Hoagland, 1997a); students are introduced to the WWW and the Internet during the first class. Each syllabus includes the following standard information: meeting times and places, office hours, contact information, course description, assessment, and schedule of laboratory and lecture topics. Additionally, hypertext links allow stu-

- ◆ **The MIT Biology Hypertextbook** (MIT Experimental Study Group, 1996) is a good resource for learning cell and molecular biology, and the Department of Biochemistry & Molecular Biology at the University of Leeds has a terrific tutorial for glycolysis (Maber, 1996).
- ◆ 3-D animations of many cellular metabolic pathways can be accessed through the **Center for Biophysics and Computational Biology at the University of Illinois at Urbana Champaign** (Crofts, 1996).
- ◆ **The National Museum of Natural History at the Smithsonian Institution** maintains a searchable database of all currently recognized species of the world's mammals (Wilson and Reeder, 1993).
- ◆ David and Wayne Madisson (1996) at the University of Arizona have developed the **Tree of Life Website** in which they present the most comprehensive phylogeny available anywhere.
- ◆ **The Human Genome Project Website** (U.S. DOE, 1997) provides access to the human genome database, and **OMIM – Online Mendelian Inheritance in Man –** (NCBI, 1997) is a superb searchable human genetics database.
- ◆ **The U. S. Census Bureau** (U. S. Census Bureau, 1997) provides a searchable database which allows visitors to access current and projected population statistics for the United States and the World, monitor the spread of HIV infection, and obtain related demographic, social, and economic information with the click of a mouse button.

There are also many resources available that provide assistance in developing web pages, including

- ◆ **A Beginner's Guide to HTML** (NCSA, 1996),
- ◆ **Online HTML Tutorial** (Maricopa Center for Learning & Instruction, 1996),
- ◆ **Web Tutorial** (Global SchoolNet Foundation, 1996)

dents to access weekly objective files which include study questions, aids for writing scientific papers, WWW resources, and results of laboratory experiments. Because new ways of understanding traditional biological concepts frequently arise during class discussions and laboratory experiments, I update the study questions each week. I also frequently revise the WWW links on my syllabi because of the dynamic nature of the web. Syllabi for my classes; Genetics I, Biological Concepts, Vertebrate Physiology, Mammalogy, and Biology in Cyberspace are posted.

**Table 1. Responses to surveys administered to biology classes making extensive use of the World Wide Web and electronic mail. (see text for further details)**

Question	Yes	No	NA	Maybe	Blank
1. Did you find the use of the Internet and the World Wide Web useful? -----	41	1			
2. Did you find the use of the Internet and the World Wide Web interesting? -----	40	2			
3. Did you like having the syllabus on the World Wide Web? -----	38	3	1		
4. Did you like having the instructor send you e-mail messages? -----	36	4	2		
5. Did you like using e-mail? -----	36	5	1		
6. Would you like other courses to have their syllabi on the World Wide Web? If so, which ones? -----	31	5	3		3
7. Was any of the information on the Biology homepage helpful to you? If so, please list those resources you found most helpful. -----	27	2	3	3	7
8. Do you intend to take any more biology courses? -----	23	13		6	
9. Did you use e-mail and the World Wide Web before you took this class? -----	18	24			
10. Will you use e-mail and the World Wide Web in the future? -----	41	1			

Searching the WWW can be very time consuming and frustrating, therefore I also maintain a list of resources that are of general interest to biology majors. This list (Hoagland, 1997e) currently contains greater than 300 hyperlinks and is much too extensive to include in this paper. However, brief descriptions of a few sites will serve to demonstrate the value of the WWW as a teaching resource.

#### Student Labs

One of the most valuable uses of the WWW is for posting the results of student experiments. This is especially useful for courses with multiple lab sections because data from each section can be posted on the web at the conclusion of the experiment, and multiple data sets can be pooled for a more statistically rigor-

ous analysis. Additionally, data sets from previous years can be included in analyses or used for comparison. I have found this aspect of integrating the WWW into biology courses one of the most positive for students. For example, for many years students at Westfield State College have conducted classic experiments with onion and broad bean root tips in an effort to obtain a greater understanding of the cell cycle (Hoagland and Doe, 1997). Students use freshly prepared slides to count the numbers of cells in interphase and in each stage of mitosis, and to calculate a mitotic index. Most student generated data yield estimates for a mitotic index approximately 2-3 times greater than published estimates. Their lab reports inevitably attribute this difference to experimenter error. In other words, students conducting scientific experi-

ments which don't yield the "correct" results view themselves as failures. Despite the fact that these students generate hypotheses, design and conduct experiments, analyze data, and then compare those data with published results, if their results differ from those published, they conclude that they failed because they are only students, not scientists. These attitudes change when they compare their data with other student generated data and find no significant differences. Students then begin to view themselves as scientists. Posting student-generated data on the WWW helps biology educators teach students to become scientists. Additional student-generated data sets are available on our Web pages (Hoagland, 1997f).

### Evaluation

In an attempt to determine if students view the integration of the WWW and Internet into biology courses as valuable, I surveyed two primarily non-majors biology courses during the 1996 summer session and two majors biology courses during the fall 1996 (Hoagland, 1997g). Approximately 52% of the respondents were non biology majors enrolled in Environmental Biology (n = 14) and Human Biology (n = 8) during the summer 1996, and the remainder were biology majors in those summer courses (Environmental Biology, n = 1; Human Biology, n = 1) and in a second semester freshman course (Biological Concepts ; n = 13) and Genetics I (n = 5) offered during the fall 1996. I made no attempt to separate non-majors responses from majors responses for this analysis. Despite the fact that 57% of students surveyed had no prior experience with the WWW and the Internet, they enthusiastically endorsed the use of this telecommunications technology in biology courses (Table 1). The few students who did not like using the WWW indicated that the problem was lack of access to adequate computer facilities. Those students who did not like using e-mail identified the lack of word-processing power in the SMTP mail editor as the major problem. The majority of students would also like cybersyllabi for all biology, chemistry, physics, astronomy, psychology, business, finance, and all

other courses. Students reported that the lab results pages, hyperlinks, list of Websites, and search engines were most helpful.

### Why integrate Information Technology into courses?

Since the 1950s science educators have been criticizing the methods of science education in the U. S. (National Society for the Study of Education, 1960). In the intervening years a consensus has developed around the necessity of incorporating scientific inquiry and the process of science into biology and other science courses (AAAS, 1990; Hobson, 1996; Moore, 1994;

**Integrating the WWW into biology courses facilitates achievement of this goal of teaching students how to become scientists by making data available from experiments commonly conducted in undergraduate teaching laboratories. Students can access data for comparison purposes or to increase their own sample size. This can be particularly helpful for small classes where a limited amount of data are generally collected, and when experiments fail to yield meaningful data. When more student-generated data become available on the WWW, more comparisons will be possible.**

NAG, 1990; Nissani, 1989; Roy, 1996; Wilcox and Jensen, 1997; Woods, 1989). For example, my students have collected birth and death data from a Westfield, MA cemetery that are currently available on the Biology Department server (Hoagland, 1996c). When similar data become available from cemeteries in different regions of the U.S. (or the world), students will be able to conduct comparative, open-ended investigations. The WWW then becomes an additional teaching tool that can be used to assist students on their journeys to becoming scientists. Students will also be better prepared for life after college because information technology is becoming increasingly relevant to large sections of society (Resmer, 1997).

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# HYDROTHERMAL VENTS: more than just a lot of hot water!

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*Abstract: The biological problems faced by organisms inhabiting hydrothermal vents can lead to lively discussions in introductory biology. Current research investigations and controversies centered on this unusual habitat are described for those wishing to consider incorporating this topic into their classes or learning more about phenomena first discovered in 1977.*

**Key Words:** hydrothermal vents, introductory biology, habitats, electron transport chain, island biogeography, origin of life.

A few years back, when I had first thought (with some prodding) to write this article, I could safely say to my introductory biology students that hydrothermal vents were an especially exciting topic because they had first been discovered so recently to be within the student's own lifetime. This year, I realized that this approach could no longer work because the majority of my incoming freshman class had a birth year of 1978! This makes them no less exciting, however, and they are still a very active, viable research environment in fields such as biology, chemistry, and geology. Each year, numerous scientific papers, reviews and general articles illustrate new findings about the biology of hydrothermal vent organisms, including descriptions of novel species with each new vent site explored.

What is a hydrothermal vent? Vents occur on the deep sea where continental plates are spreading apart (rift zones and spreading centers) or pushing together. Ambient seawater seeps downward through cracks on the ocean floor, is superheated and transformed by its contact with magma, and is then expelled, sometimes seeping and sometimes with great force, in hydrothermal vent fields. Hydrothermal vents were first discovered in 1977 off the Galapagos Islands by a team of geologists (Cone, 1992). They had been hoping to find temperature anomalies on the ocean floor in areas of continental plate contact; if so, this evidence would lend further support to plate tectonic theory. What was not expected, however, was the dense assemblage of initially bizarre animals that they encountered in regions of higher temperatures. The 1977 expedition paved the way for subsequent biological expeditions to the original site and to dozens of other sites throughout the world's oceans.

You may well ask, "why would she be talking with her introductory biology students (in Missouri) about hydrothermal vents in the first place?" There are, I counter, many ways to use the exciting discoveries from hydrothermal vents to illustrate various points in biology. Comparisons with photosynthesis and the

C4 carbon fixation pathways, and the effects of hydrogen sulphide on the functioning of the electron transport chain are the most obvious ones. Hydrothermal vents and the organisms that dwell there also provide interesting examples of island biogeography, evolution, symbiosis, surviving in "toxic" environments, and the ideas of origin of life on earth. In short, virtually any topic of interest to a biology major can be linked to hydrothermal vents!

When discussing the environment surrounding hydrothermal vent organisms, it is tempting to use terms such as "harsh" and "toxic." In fact, the first thing one must remember is that something that may seem toxic to a human (e.g., micro-molar concentrations of hydrogen sulphide, low partial pressures of oxygen and rapidly fluctuating temperatures) is absolutely essential to the survival of another animal, e.g., a hydrothermal vent tubeworm with bacterial endosymbionts that are sulphide dependent. Humans can detect the odor of hydrogen sulphide at concentrations less than  $0.01 \mu\text{mol l}^{-1}$  and find the odor offensive at concentrations as low as  $0.15 \mu\text{mol l}^{-1}$ . Despite external sulphide concentrations commonly as high as  $300 \mu\text{mol l}^{-1}$ , vent animals including the tubeworms, clams and crabs have oxygen consumption rates comparable to similar species inhabiting non vent deep sea environments.

These questions, and many more, have been addressed by ecological physiologists from around the world, including the work of Jim Childress, Charles Fisher, Horst Felbeck and George Somero and their colleagues.

One way to teach students about the electron transport chain and oxidative phosphorylation is to discuss what might happen if various components of these systems were removed or disabled. Hydrogen sulphide, in addition to being a potent inhibitor of various enzymes and respiratory proteins, binds to the cytochrome c oxidase complex and thereby interferes with the production of ATP. This presents a dilemma

How do these organisms balance the uptake of oxygen and hydrogen sulphide (not known for maintaining their independence when mixed!), both of which are needed by the aerobic endosymbionts? How do animals which have sulphide requiring symbionts keep the sulphide from poisoning their own systems? How do animals without sulphide oxidizing endosymbionts, which still live as scavengers within the hydrothermal vent environment, detoxify the sulphide that they are unable to prevent from crossing their epidermis or respiratory surfaces?

for organisms such as the hydrothermal vent tube worm *Riftia pachyptila*. These tubeworms harbor endosymbiotic chemolithoautotrophic (students are most impressed with this term) sulphide oxidizing bacteria that need hydrogen sulphide as an energy source. They are also obligate aerobes - they utilize oxygen as the terminal electron acceptor. Scientists first wondered if the cytochrome c oxidases in these organisms were somehow different than those of organisms not dwelling in high concentrations of hydrogen sulphide. This proved not to be the case; instead, in endosymbiont containing animals, hydrogen sulphide is bound by the haemoglobin (e.g., *Riftia*) or a separate binding factor (e.g., the vent clams) and transported efficiently to the endosymbionts.

Animals without symbionts, such as the vent crab *Bythograea thermydron*, also do not have cytochrome c oxidase systems that are resistant to sulphide poisoning. In these animals, it would not be desirable, however, to have a sulphide binding factor, because as hemoglobin does for oxygen, the binding factor serves to concentrate the substance it binds. The strategy used by these animals is to detoxify hydrogen sulphide to a less toxic form, e.g., thiosulphate, that can then be excreted. This allows the crabs to maintain aerobic respiration (the electron transport chain using oxygen as the terminal electron acceptor) even approaching  $\mu\text{mol l}^{-1}$  concentrations of hydrogen sulphide. Truly remarkable!

Looking out the window of a submersible, and seeing dense assemblages of bizarre living creatures at depths of 2700 meters and beyond, is truly an awe inspiring experience. For geologist John Corliss, present in the submersible D.S.R.V. *Alvin* on the first dive to a hydrothermal vent site teeming with life, this proved to be a life changing moment. Corliss, along with colleagues John Baross and Sarah Hoffman, a short time later proposed new ideas on the origin of life on earth - where else, but at hydrothermal vents (Corliss, Baross, and Hoffman, 1981). The vent environment is ideal in many respects for the development of life according to some current scientific models for the origin of life on earth. Although there are some

very hot hydrothermal sites, with chimneys blasting out water up to several hundred degrees Celsius, most of the vent fields are more habitable, a comfortable 10 - 30°C. The geological development of hydrothermal vent sites leads to many crevices, caves and overhanging ledges where the water is still and warm. Vent water is heavily laden with inorganic molecules. There is an energy source - hydrogen sulphide. Oceanic hydrothermal vents have been around a long time - as long as the seas and oceans have been in existence. Not that this idea of origin of life at hydrothermal vents is without controversy! Many authors have supported or countered the first publications on this topic. It makes an ideal example for students to examine how scientists go about defending their hypotheses when their ideas are criticized by other scientists with very different ideas.

Hydrothermal vents are interesting examples of island biogeography (MacArthur and Wilson, 1967). How isolated is a hydrothermal vent site? How do sessile organisms colonize new vent habitats? One can ask many questions concerning evolutionary biology in this context as well. Recent articles by Tunnicliffe (1991, 1992, 1996), Lutz (1997), Mullineaux (1995, 1996) and Hart (1997) address these topics in some detail. Each new major hydrothermal vent field explored by scientists yields new species, and sometimes genera, families, orders, classes, and some would argue, phyla, of organisms. These exotic residents have evolved in relative isolation in the depths of the ocean; each major vent field is generally isolated by tens of kilometers or more from their nearest neighbors. Hydrothermal vent sites are dominated by animals from the phyla Annelida, Mollusca and Arthropoda, which is very different from the faunal composition of the surrounding deep sea. The vast majority of hydrothermal vent organisms are endemic - currently about 95% of the species found at hydrothermal vents are known from no other habitat. Intriguing questions concerning larval transport, and colonization of new hydrothermal vent sites are actively pursued avenues of research.

Currently, just twenty years after scientists first viewed a hydrothermal vent site from a submersible port, new and exciting discoveries characterize research in hydrothermal vent biology and related fields. Although it is rare now to find a textbook that proclaims "all life on earth depends upon sunlight," this was the prevailing view just a few short years ago. Many introductory level textbooks now have a photo or two of vents organisms, but video (available commercially) filmed at deep sea hydrothermal vent sites amazes even the most complacent students. Our own, often narrow, perspective of life is challenged by organisms thriving under almost unimaginable conditions. Take a dive with your students!

My own experiences at the hydrothermal vents have certainly shaped my career as a scientist, and my ways of thinking about living things. On the evening prior to every submersible dive, scientists climb inside the submersible for a pre dive checkout. The excitement just at this stage is almost overwhelming for a first time diver. Climbing into the sub in the morning, the sensory stimuli of every kind during the launch phase, the final okay to dive, traveling through water with every shade of blue as you descend, and bioluminescence once the sunlight is no longer detectable to the human eye - these are no less exciting than the first glimpse of the bottom of the ocean. The hydrothermal vent sites were to me the capstone of my dive experiences, I think because there is more animal and bacterial life packed into small spaces than one could hardly imagine. As I sit in Northeast Missouri reflecting on my experiences of another place and time, I appreciate the privileged life I had as a graduate student which allowed me several trips to the bottom of the sea. In my classes I am able to inspire my students with "home movies" and personal stories of my experiences. My respect for life in all its forms has been deepened by these and other hands on adventures, and I share this with my students in whatever ways I can. Whatever our hands on experiences as biologists, our students are ultimately the recipients of our enthusiasm and knowledge. Perhaps one of my Truman students will go on to be part of the next generation of submersible divers!

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# Ten Equations that Changed Biology: Mathematics in Problem-Solving Biology Curricula

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**Abstract:** *Mathematics has played exceptionally important roles throughout the history of biology. Too frequently, these roles have been unappreciated in biology curricula because textbook authors assume that biology students have an inadequate mathematical preparation. This practice: (1) deskills many biology students, (2) is inconsistent with our requirements, (3) misrepresents contemporary biological research, and, hence, (4) underprepares students to read many articles or to contribute to many areas of biology. However, the recent calculus reform movement has empowered thousands of American undergraduate biologists to become proficient in the use of mathematical software packages that could be used to investigate the behavior of many famous mathematical models in biology. But where can they look? There are numerous recent texts in mathematical biology, research journals, web sites, and some advanced biological texts which are replete with numerous models. However, there is a need to identify a succinct list of achievements that represent the power of mathematics in biology. Hence, ten equations and a brief description of their historical importance are presented here in order to draw students' and faculty's attention to a variety of mathematical models that have been intrinsic to many of the significant discoveries in biology in the twentieth century.*

**Key words:** mathematical biology, history of biology, models, equations, evolution, population genetics, medical imaging, phylogenetic trees, genetic maps, allometry, biodiversity, island biogeography, enzyme kinetics, genetic codes, neuron, membrane potential, logistic, predator-prey, mutation, fluctuation test, tests of teleology

Why is mathematics required for biology majors if they never use it throughout their education in biology? How can we generate a problem-solving based curriculum reform in biology if we, professors of biology, do not introduce appropriate mathematical tools which could help them solve problems? Does the beauty, power, historical importance, and utility of mathematics in biological research belong in undergraduate biological curricula? Is this just special pleading from a mathematical biologist in the ever ending struggles for space in undergraduate curricula? I hope not because I sincerely believe that mathematics plays five distinct and important roles in undergraduate biological education: (1) for conceptual understanding and historical appreciation, (2) through simulation and modelling, (3) for visual aesthetics and graphical representation, (4) as intrinsically embedded in tools of analysis, measurement, and data collection, and (5) within the everyday practices and equipment in the laboratory and field. I have briefly elaborated each of these five in a description of the 1997 BioQUEST Curriculum Consortium workshop entitled: "BIOLOGICAL AFTERMATH: What can we learn from contemporary mathematics reform?" (Jungck, 1997). Herein I instantiate the conceptual and historical importance of mathematics in biology by privileging ten equations (Figure 1) that warrant these claims.

I assert that we can help students deal more effectively with the massive explosion in technical information

and with personal/social issues of empowerment by: (1) privileging curricular reform via problem-solving, collaborative learning, critically reflexive, and less-is-more approaches, (2) sharing elegant, robust, scalable, highly visual, and transferable mathematical approaches, (3) employing models that work in several different areas in biology to reduce the ever increasing size of introductory textbooks, and (4) better preparing students to be more responsible researchers and citizens.

Gross (1994) summarized Ellison's<sup>1</sup> survey of the mathematics requirements of many biology departments across the nation:

Given the need for quantitative training, what do current curricula require of students? First, quantitative training is typically isolated in mathematics or statistics courses that are weakly, if at all, coupled to the life science courses in the curriculum. ... on average ... such students are required to take slightly less than two semesters of quantitative courses, with approximately 79% of programs requiring some calculus, 16% requiring some statistics, and 13% requiring some computer science. Fully 10% of the programs either had no requirement for quantitative courses or required only high-school-level quantitative skills.

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<sup>1</sup>anonymous ftp to mhc.mtholyoke.edu in file/pub/ecology/ecomath.csv

**Figure 1. Ten Equations That Changed Biology.**

These equations were selected upon the basis of wide-spread recognition of the value of the models as indicated by their: (1) being cited in common undergraduate biology textbooks, (2) being the subject of biographies of the names associated with these equations, (3) appearance in historical monographs on biology, and/or (4) receipt of public awards such as Nobel prizes and British Knighthood.

**Fisher's "Fundamental Theorem of Natural Selection"**

$$\partial_{NS} M_i / \partial t = W_i, \text{ where } M = \partial_{NS} M_i + \partial_{EC} M_i$$

"The rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time."

**Cormack Computer Assisted Tomography**

$$g(r, \theta) = \sum_{n=-\infty}^{+\infty} g_n(r) i n^\theta$$

where

$$g_n(r) = \frac{1}{2\pi} \int_0^{2\pi} g(r, \theta) C^{-in^\theta} d\theta$$

**Genetic Mapping (The Haldane Function)**

$$C_{AB} = \frac{1}{2} (1 - e^{-2x_{AB}})$$

$C_{AB}$  = recombination fraction between loci A and B  
 $x_{AB}$  = map distance between loci A and B

**Lotka-Volterra Interspecific Competition Logistic Equations**

$$\frac{dN_1}{dt} = r_1 N_1 \left( \frac{K_1 - N_1 - \alpha N_2}{K_1} \right)$$

$$\frac{dN_2}{dt} = r_2 N_2 \left( \frac{K_2 - N_2 - \beta N_1}{K_2} \right)$$

$N_i$  = population size of species  $i$   
 $T$  = time  
 $r_i$  - instantaneous or intrinsic rate of increase  
 $K_i$  = carrying capacity

**Hodgkin-Huxley (Goldman) Equations for Neural Axon Membrane Potential**

$$\frac{dv}{dt} = \frac{-1}{c} [g_{Na}(V)(V - V_{Na}) + g_K(V)(V - V_K) + g_L(V - V_L)]$$

$$\frac{dn}{dt} = \alpha_n(V)(1 - n) - \beta_n(V)n$$

$$\frac{dm}{dt} = \alpha_m(V)(1 - m) - \beta_m(V)m$$

$$\frac{dh}{dt} = \alpha_h(V)(1 - h) - \beta_h(V)h$$

where  $g_{Na} = \bar{g}_{Na} m^3 h$  and

**Micaelis - Menten Equation for Enzyme Kinetics:**

$$V = \frac{V_{max} [s]}{k_m + [s]}$$

**Allometry: E.g., MacArthur-Wilson Theory of Island Biogeography Species-Area Law**

$$S = CA^z$$

**Hypothesis Testing: Luria-Delbrück Fluctuation Test for Mutations in Viruses**

$$p(\text{proportion of zero class}) = e^{-\mu n}$$

$\mu$  = mutation rate  
 $n$  = population size

**Crick - Griffith - Orgel Comma-free Coding Theory for the Adaptor Hypothesis of Genetic Coding**

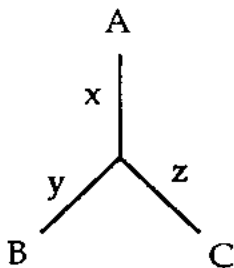
$$W_k(n) \leq \frac{1}{k} \sum_{d|k} \mu(d) n^{k/d}$$

$W_k(n)$  = number of comma-free code  $k$ -letter words with alphabet  $n$   
 $\mu(d)$  = Möbius function  
 summation is extended over all divisors  $d$  of  $k$

**Fitch-Margoliash Little Maximum Parsimony Algorithm for Phylogenetic Tree Construction**

	A	B	C
A	∅	$d_{AB}$	$d_{AC}$
B		∅	$d_{BC}$
C			∅

Distance matrix



$$x = (d_{AB} + d_{AC} - d_{BC}) / 2$$

$$y = (d_{AB} - d_{AC} + d_{BC}) / 2$$

$$z = (-d_{AB} + d_{AC} + d_{BC}) / 2$$

Tree topology and branch lengths

Based on a systematic personal examination of introductory biology textbooks designed for majors, Blystone (personal communication) argues that equations have been replaced by pictures in texts over the past fifty years. Even though Blystone specializes in biological visualization, and, hence, deeply loves good illustrations. Thus, Blystone and Cooper (1996) are currently developing tools for students in biology and statistics to mutually inform one another's investigations of biological images. He wants students to move beyond simply acquiring pictures. This exclusion of equations in textbooks has three unfortunate consequences; namely, a lack of respect for, consistency with, and empowerment of students.

**RESPECT:** First, this exclusion connotes an explicit lack of respect for the intellect and talents of our students. Our students are dealing with the mathematics in their calculus courses as well as in other frequently required courses such as physics. Many students have already illustrated success in high school and college mathematics courses. Almost all biology students come with a variety of computational skills and heuristics for reasoning quantitatively. In a democratic society, can we afford such a deep lack of respect?

**CONSISTENCY:** Second, this condescension leads to deskilling behavior. Instead of building upon the foundation of mathematical thinking developed in other courses, the students learn that professors have not taken their own requirements seriously because these professors are not regularly building upon this foundation and that they can get by even if they let their mathematical skills atrophy. Is this not inconsistent, as well hypocritical?

**EMPOWERMENT:** Third, this hidden curriculum plays into the hands of the "star" system or produces a tracking component that has differential career consequences because as Gross (1994) has reported: the more mathematics background that a biologist has, the better that she or he does economically, on average. A lack of mathematical background deprives students the opportunity to read a rich primary literature without skipping over the mathematics contained therein. One of the most regular comments that I hear from alumnae in graduate school programs in biology is that they end up having to learn a large amount of mathematics in order to be able to comprehend many of the papers that they are assigned to read and discuss. Go to your library and open a variety of biological journals; the diversity and richness of mathematics therein may surprise you. Why shouldn't this literature be accessible to far more of our students?

<sup>1</sup>(<http://www.math.duke.edu/faculty/moore/pcalc.html>)

<sup>3</sup>(<http://alan.sewanee.edu:8080/sc/links.html> (provides 18 links on this project))

<sup>4</sup>(<http://www-cm.math.uiuc.edu/>)

What should we do to begin a transformation? Gross (1996) has explicitly addressed this issue:

#### "Lessons from the Above

It is unrealistic to expect many math faculty to have any strong desire to really learn significant applications of math that students will readily connect to their other course work, though there is a core group who might do this.

So what do we do to enhance quantitative understanding across disciplines? Below is what I say to life science faculty: Who can foster change in the quantitative skill of life science students?

Only you, the biologists can do this!

Two routes:

1. Convince the math faculty that they're letting you down
2. Teach the courses yourself

Note: Math faculty will not take you seriously unless you show them how the quantitative topics you insist that they cover will be used in your own courses!

This means biology courses must become less of a "litany of conclusions," and more an exploration of how and why natural systems came to be as they are.

Unfortunately, this battle must be fought over and over at each institution."

This is a real call to action! I am eager to explore ways in which we biologists can collaborate with our collegial mathematicians in developing the mathematical background of our biology students. We have three particular opportunities at this juncture to undertake a significant reform for greater inclusion of mathematics in biology education.

First, we truly can do "biological aftermath" in terms of curricular reform. The recent successes in mathematical education reform; e.g., Project CALC<sup>2</sup>, the Harvard calculus reform<sup>3</sup>, and Calculus & Mathematica<sup>4</sup>, despite some retrograde recalcitrance (Wilson, 1997), have transformed the mathematical education of many of our students already and is having an impact on more and more institutions at an increasing rate. We should build on these successes. Jim

Cornette at Iowa State University and Fred Adler at the University of Utah both have calculus texts forthcoming that explicitly deal with many biological applications.

Second, several mathematicians and biologists are already collaborating in ventures that we can use as models. For example, as already mentioned, Bob Blystone and Rick Cooper are teaching coordinated sections of statistics and biology and are developing materials for use in both; Sandy Lazarowitz and Jerry Uhl<sup>5</sup> have developed a course entitled BioCalc at the University of Illinois - Champaign-Urbana wherein they have almost completely done away with lectures and have a series of *Mathematica*<sup>TM</sup> notebooks with biologically informed calculus education projects; Lou Gross' group at the University of Tennessee - Knoxville has collected an enormous set of world wide web resources for a quantitatively based biology curriculum; and many mathematical biologists such as Leah Edelstein-Keshet (1988) at the University of British Columbia and John Tyson at Virginia Tech are able to teach courses by themselves that equally treat both biology and mathematics in depth.

Third, the BioQUEST Curriculum Consortium has evaluated, field tested, and distributed (Jungck *et al.*, 1996) over fifty simulations, tools, and texts, many of which enhance a mathematically informed biological problem solving curriculum.

Hence, my main point here is to embrace the efforts of my colleagues by sharing a perspective from my personal vantage as a historian of biology, an evolutionary biologist, and an educator. Based on thirtyfive years of discussion, I believe that many biologists deeply believe that mathematics is irrelevant to biological research. While I was allowed to minor in mathematics as an undergraduate, I was actively discouraged from taking mathematics and computer science courses as a graduate student, both at the masters and doctoral levels at two different institutions. In pretenure years, my research was not viewed as serious by some senior colleagues at three different institutions if I did not maintain a wet lab. Students at five institutions have frequently challenged me as to why they had the peculiar misfortune to have mathematically informed courses in evolution, genetics, developmental biology, biochemistry, cellular and molecular biophysics, and population biology. Often faculty or student friends would say: "Well, yes, mathematics is important in X or Y, but, of course, it doesn't apply to my field Z." On the other hand, each per-

sonal negotiation has catalytically provided an opportunity to seek out examples that they would enjoy, would run counter to their assertions, or as a challenge to develop computer simulations to illustrate the beauty or power of mathematically informed biological perspectives. It is from this personal history that I share some examples which have served me well in such challenging situations.

The most recent motivation for this exercise is twofold. First, in 1995 at the International Society for the History, Philosophy, and Social Studies of Biology meeting at the University of Leuven in Belgium, Evelyn Fox Keller challenged me to come up with examples where informed mathematical thinking was critical to historically important biological research programs. I was deeply bothered because, distinct from the above group of challengers, Professor Keller is a distinguished mathematical biologist (Keller and Segel, 1970; 1971) as well as a major cultural historian and feminist critic of biology. Second, while pondering my discouragement, I began looking at some popular expositions of contemporary and historically important aspects of mathematics on my bookshelves and noted the conspicuous absence of biology. While I could cite exceptions of course, none of them take the point of view of mathematical biologists that biology has contributed much to mathematics as presented by Simon Levin.

Later that year, Michael Guillen (1995), ABC TV's Science Editor for *Good Morning America*, arrived with the most immediate solution to my dilemma with his *Five Equations that Changed the World: The Power and Poetry of Mathematics*. Now I have to say that, while taken by Guillen's choice of equations and his chatty historical introduction to them, on the other hand, his popularization upsets me greatly in terms of my own expectations for expository mathematics. In Guillen's (1983) prior book, *Bridges to Infinity: The Human Side of Mathematics*, he "did it all without subjecting the reader to a single equation (1995)." Why is that "the" human side? Are equations not human constructions? Why are there no references in the current text? Are we to presume that mathematicians are polymaths who are both completely self-sufficient and have an incredible memory? Amongst sources, I am particularly curious whether Guillen had read Harald Fritzsche's (1994) book entitled *An Equation That Changed the World: Newton, Einstein, and the Theory of Relativity* (which had appeared initially in German in 1988 as *Eine Formel verändert die Welt: Newton, Einstein und die Relativitätstheorie*). Have we really accomplished the handshake that we extend if we do not overcome deep suspicions about mathematical formulations? In contrast to Guillen, consider John L. Casti's (1996)

<sup>5</sup>(<http://www.life.uiuc.edu/micro/lazarow.html>)

<sup>6</sup>(<http://www.math.utk.edu/~gross/quant.lifesci.html>)

<sup>7</sup>([gopher://merlot.gdb.org:70/00/Math-In-Biology/math/](http://gopher://merlot.gdb.org:70/00/Math-In-Biology/math/))

recent book, *Five Golden Rules: Great Theories of 20th-Century Mathematics - and Why They Matter* which is full of equations and is also highly readable. However, not only Guillen, but other popularizers of mathematical beauty also completely avoid the use of equations. For example, compare the mathematical richness of D'Arcy Wentworth Thompson's *On Growth and Form* (1917) with a recent popularization by Delta Willis (1995) who wrote *The Sand Dollar and the Slide Rule*. In deep contrast, Sand<sup>8</sup> gives Guillen's (1995) *Five Equations ...* high praise for pedagogical purposes: "Dr. Guillen takes famous equations we all learned in high school science classes and turns them inside out. Slowly, delicately, he explores the history of the experimenter/scientist. Each discovery reaches a crescendo that culminates in examples of how they shaped the modern world. For those who fell asleep in science class this is a refreshing look at the mystery and excitement of discovery." Hence, despite my reservations, I set out to identify equations that have had tremendous impact on biological research and which have been publically acknowledged.

The ten equations presented here were selected upon the basis of wide-spread recognition of the value of the models as indicated by their: (1) being cited in common undergraduate (admittedly sophomore or above levels) biology textbooks, (2) being the subject of biographies of the names associated with these equations, (3) appearance in historical monographs on biology, and/or (4) receipt of public awards such as Nobel prizes and British Knighthood. Why ten, when three authors could write a whole book on one equation or five equations? I believe that in order to convince biologists, one has to show the importance of

mathematics across a variety of subdisciplines in biology to avoid the oft stated claim: "Oh, that may apply to population genetics, but it doesn't apply to my area of biology." Are ten sufficient? Probably not. Partly I respect the reader's endurance. Partly I do not have the temerity nor the intelligence to emulate David Hilbert (1862-1943) who opened the twentieth century (at the International Congress of Mathematics in 1900) by posing twenty-three problems which have been the subject of much mathematical investigation ever since. Nor do I believe that displaying 49 equations in a light hearted manner as Salem, Testard, and Salem's (1992) *The Most Beautiful Mathematical Formulas* would convince my colleagues.

Hence, this short list of equations represents an historical thread of mathematical contribution to fundamental questions of twentieth century biology. Henry Oliver Lancaster (1994) states that: "it could be concluded that mathematics enters into biology as an adjunct to measuring and counting problems, that is, in most cases, as an aid to the technology of, rather than the science of, biology" (p.16). In contrast, in each of my essays I have tried to illustrate scientific, as opposed to mere mechanistic, importance of each historical example and at least one additional opportunity for understanding some social, cultural, political, philosophical, or ideological aspect associated by various interpreters of an equation. In reading them, I ask you to re-ask Steen and Albers's (1981) questions: "What role should applications play in mathematics curricula? Is the traditional division between mathematics and science instruction still valid? How can mathematical topics be related to cultural issues that are relevant to students?"

### I. Fisher's "Fundamental Theorem of Natural Selection"

Sir Ronald A. Fisher along with Sewall Wright and J. B. S. Haldane are usually credited by Anglo-American biologists for synthesizing two, then warring, major disciplines in twentieth century biology: namely, genetics and evolution. This integration is usually referred to as the neo-Darwinian Synthesis. "In 1930 *The Genetical Theory of Natural Selection* represented the most substantial contribution to the synthesis of Mendelism, Darwinism, and biometrics yet published" (Provine, 1971, p.154). Biographies exist for each of the three luminaries. Since population genetics has been called the most successful application of mathematics to biology, there are far too many equations to privilege just one; however, Frisman (1978) states: "One of the most interesting results of the mathematical theory of natural selection is known as Fisher's Fundamental Theorem of Natural Selection." According to Price (1972), Fisher believed that his "Fundamental Theorem" was as important to biology as the second law of thermodynamics was to chemistry. While nearly every population geneticist qualifies the contemporary importance of this equation, Ewens (1979), as a representative of this cautionary group, says: "it so beautifully quantifies in genetic terms the main theme of the Darwinian theory." If controversy is the life-blood of science, students could not appreciate the fullness either of the Mendelian-Darwinian debate nor its resolution without some understanding of the mathematics of population genetic theory in neo-Darwinian syntheses.

<sup>8</sup>(in an electronic book review - ssand@ionet.net)

(In order to make this manuscript cohere as well as possible, references for the non-equation portion of this article are placed conventionally at the end of the article; however, references that relate directly to a particular equation are at the end of each section.)



Equations from Price (1972), who notes the importance of understanding Fisher's theorem as a partial differential equation rather than as an ordinary differential equation:

$$\partial_{NS} M_i / \partial t = W_i \text{ where } dM = \partial_{NS} M_i + \partial_{EC} M_i$$

"The rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time."

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**Relevant WWW sites:**

*General population genetics:*  
<http://darwin.ceh.uvic.ca/people/koop/genetics/popgen.html>  
<http://darwin.eeb.uconn.edu/eeb348/eeb348.html>

A. W. F. Edwards on R. A. Fisher and "fundamental theorem": <http://www.medschl.cam.ac.uk/miu/People/edwards.htm>

Andreas Wagner on importance of Fisher and Wright: <http://peaplant.biology.yale.edu:8001/~waganda/>

Bruce Walsh's "Quantitative Genetics Resources" contains a nice introduction to One- and Two-Locus Theory: <http://marine.geol.sc.edu/BIOL/Courses/BIOL765/Fitness.html>

Maple worksheet on derivation of reproductive value (Fitness and Population Genetics. Theoretical Ecology: BIOL765 Department of Biological Sciences, University of South Carolina, Columbia, SC, 29208): [http://nitro.biosci.arizona.edu/zbook/volume\\_2/chapters/vol2\\_04.html](http://nitro.biosci.arizona.edu/zbook/volume_2/chapters/vol2_04.html)

NaturalSelection - software written by Robert Desharnais: [http://vflylab.calstatela.edu/edesktop/edp\\_apps/natsel/natsel.html](http://vflylab.calstatela.edu/edesktop/edp_apps/natsel/natsel.html)

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Price, Frank and Virginia Vaughan. (1996). "Evolve." *The BioQUEST Library IV*: (The BioQUEST Core Collection): University of Maryland - College Park.

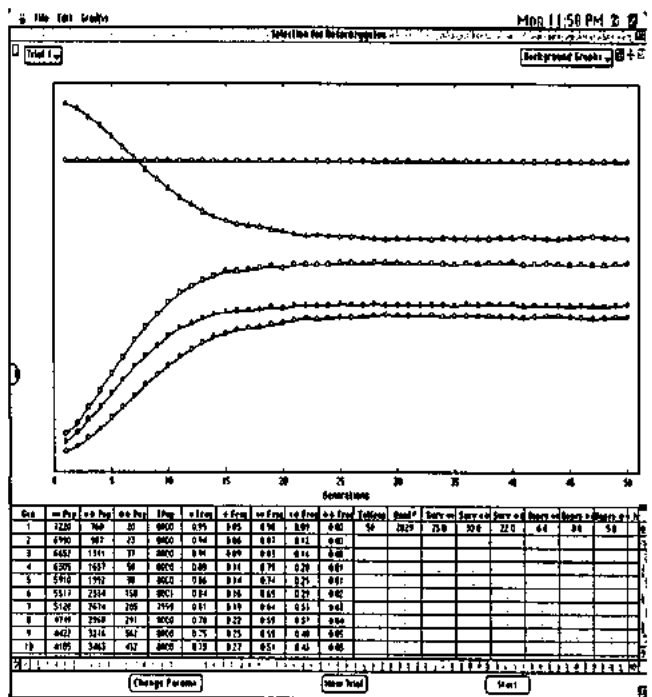


Figure 2. Screen shot of Evolve.

## II. Cormack: Computer Assisted Tomography

Computer Assisted Tomography (CAT), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), and ultrasonography have revolutionized noninvasive visualization in medical practice in just twenty years (Sochurek 1988.). While the developers were largely ignored in their early years (see PBS special in the New Explorers series called "Doctors with X-Ray Vision"), most hospitals are currently considered underequipped without these instruments and/or without physicians educated well in interpreting them. In particular, Raymond V. Damadian (see Schneider 1997) experienced heavy resistance to his innovation of magnetic resonance imaging (MRI). Cormack shared the 1979 Nobel Prize for his design of CAT scanners with a source and sensor across from one another on an apparatus that could be rotated around a patient to visualize a thin slice by sweeping through a region and which could use attenuated X-rays. He solved the traditional phase problem which so plagues other arenas in biological imaging such as in X-ray crystallography of biopolymers. His scanning process looked at small three dimensional points (voxels) which could then be stacked into a full three dimensional image of the portion of the individual being examined. Cormack (1963) was even surprised by the originality of his own insight because: "One would think that this problem would be a standard part of the nineteenth century mathematical repertoire, but the author has found no reference to it in standard works." In 1983, he reviewed the work on Radon's (1917) problem of reconstructing densities from their projections which was not generally known as well as citing his own pleasure in pursuing solutions to this problem. Robert Ledley, another mathematical biology pioneer who published a book in 1965 entitled *Use of Computers in Biology and Medicine*, received the 1997 National Medal of Technology for his development of the automatic computed transverse axial (ACTA) scanner which "revolutionized the fields of radiology and medical imaging and set the standard for all subsequent CT [and MRI and PET] scanners" [announced in *Scientific American*, June 1997]. Shepp (1983) noted the lack of appreciation of such major work not just by biologists, but by mathematicians as well:

The central technology in CT is unquestionably recognized to be mathematics, not only in the medical community but in the physics and engineering areas of CT as well. It is unfortunate that the mathematical community itself has less of an appreciation and understanding of this important application of mathematics. The reason for this is the usual one, that mathematicians are often content to work on questions 'of intrinsic interest', and there are always plenty of these around which do not have to deal with the realities of a real-world problem such as CT" (p. ix) and "... to illustrate the frequent characterization of the mathematician as one who ignores the real world and prefers to be imbedded in axiomatics and idealized abstract models. Nevertheless, the advantages of the mathematical approach, based on a well-defined model, to a real problem are manifold: clarity, computability, elegance, to name a few" (p. 1).

From a personal point of view, I have seen the transformation that these technologies, especially ultrasonography, have had on couples expecting a child. When my son and daughter-in-law brought home the ultrasonography videotape to show grandpa (me) the movie of their developing fetus, I appreciated deeply how this application of mathematics has modified our understanding of and personal interpretation of ethical issues involved in embryogenesis as discussed by feminists considering the new technologies (Sandelowski, 1994).

Equation from Cormack (1963):

$$g(r, \theta) = \sum_{n=-\infty}^{+\infty} g_n(r) i^n$$

where the line integral is

$$g_n(r) = \frac{1}{2\pi} \int_0^{2\pi} g(r, \theta) C^{-in\theta} d\theta$$

"Suppose for now that X-ray absorbancy has a well defined value [g] at each point in the patient's cross section. Then ... the value at a point ... is approximately equal to the line integral between the source and the detector of the X-ray absorbancy of the patient's tissue. ... In order to reconstruct the values of [g] at individual points in the patient's cross section, we need to estimate its line integrals for many different lines L. ... In a modern CT scanner this number is of the order  $10^5$  to  $10^6$  [lines]." (Herman, 1986)

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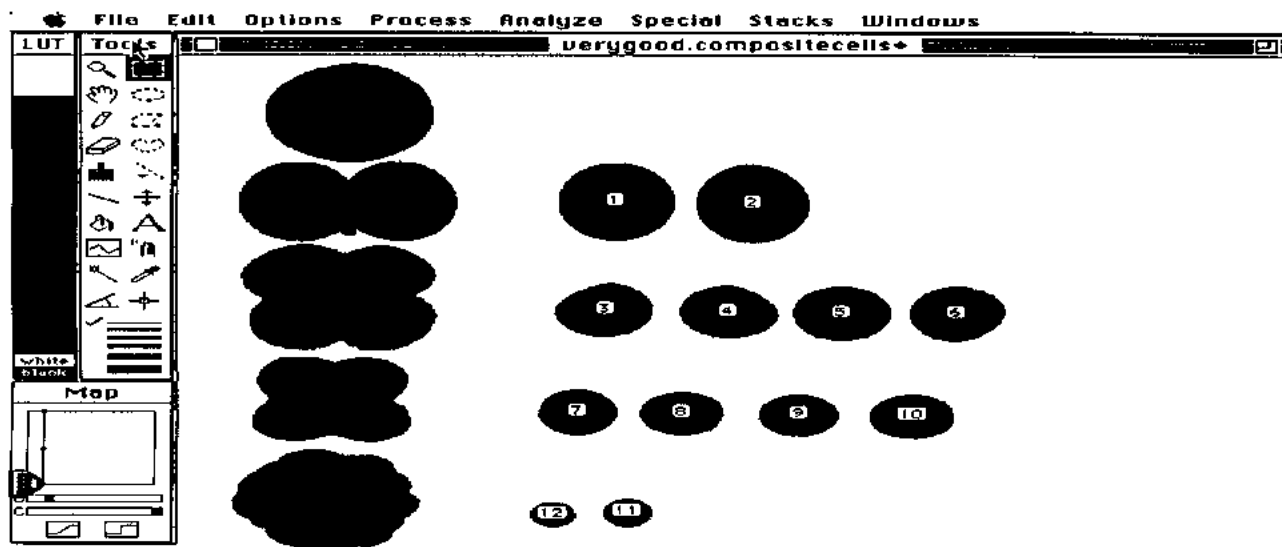


Figure 3. Screen shot of *Image Analysis* (starfish embryos) in *NIH Image*.

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- Relevant web sites:**
- Dale Alvin Walters (1996) has a nice visualization of a CAT set-up: <http://casual1.enci.ucalgary.ca/~dawalter/Cat.html>
- Beth Israel Hospital has an introduction to CAT Scanning for patients to help them prepare for an exam. It also includes photographs of patient in a CAT scanner, and CT scans of a head and kidneys, as well as illustrations of what is going on: <http://www.bih.harvard.edu/radiology/Modalities/CT/CT.html>
- Computed tomography of forest canopies (Dave Vieglais) : <http://ze.ke.kbs.ukans.edu>
- Relevant BioQUEST modules:**
- Blystone, Robert and Richard Cooper. (1996). "Image Analysis." *The BioQUEST Library IV*:(First Review Folder): University of Maryland - College Park.
- Rasband, Wayne. (1996). "NIH Image" *The BioQUEST Library IV*:(Support Materials Archive): University of Maryland - College Park.

### III. Genetic Mapping (The Haldane Function)

Thomas Hunt Morgan won the 1933 Nobel Prize for his "Theory of the Gene" which presented chromosomes as linear maps. Students should be able to easily relate to this achievement because the first genetic map published was calculated by an undergraduate named A. H. Sturtevant in Morgan's lab in 1913. The unit of measurement for genetic distance is named after Morgan. In 1919, J. B. S. Haldane published the first equation for relating the observed % of crossing-over between two loci (recombination rate) with the physical distance between two loci on a chromosome (see Wimsatt (1992) for a history of controversies about several models of linkage). While this equation does not include multiple crossing-overs, interference, synteny, or special biological features associated with particular taxa, it captured several features of the functional relationship between the empirical measurements and the inferred map including a maximal distance of 50 centiMorgans because any longer distance would represent no linkage (Mendel's independent assortment) and the nonlinear form of this correlation. We could see all of contemporary work in genomic analysis: sequencing genomes, restriction maps, contig assemblies, complementation maps, deletion maps, transcription maps, cytogenetic FISH (fluorescent *in situ* hybridization) or chromosome painting, etc. as derivative of this pioneering work. Wimsatt (1992) reviews two approaches which he believes "are indicative of the problems theorists and experimentalists have in talking to each other everywhere, and I suspect that many or most of the reasons are generalizable."

Relationship between recombination frequency and mapping distance (Haldane function):

$$C_{AB} = \frac{1}{2}(1 - e^{-2x_{AB}})$$

$C_{AB}$  = recombination fraction between loci A and B

$x_{AB}$  = map distance between loci A and B

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- Thompson, Elizabeth A. (1986). *Pedigree Analysis in Human Genetics*. The Johns Hopkins University Press: Baltimore, MD.
- Weir, B. S. (1990). *Genetic Data Analysis: Methods for Discrete Population Genetic Data*. Sinauer Associates, Inc.: Sunderland, Massachusetts, p. 210-221.
- Wimsatt, William C. (1992). "Golden generalities and co-opted anomalies: Haldane vs. Muller and the *Drosophila* group on the theory and practice of linkage mapping." In Sahotra Sankar, editor, *The Founders of Evolutionary Genetics*, Kluwer Academic Publishers: Netherlands, p. 107-166.

#### Relevant WWW pages:

MendelWeb (conceived and constructed by Roger B. Blumberg):

<http://www.netspace.org/MendelWeb/>

Microbial Genetics problems (for 2 and 3 point crosses):

<http://www.life.uiuc.edu/micro/316resources/problems/recombination/3factor-crosses/>

Online Mendelian Inheritance in Man:

[http://www.ornl.gov/TechResources/Human\\_Genome/vl.html#omim](http://www.ornl.gov/TechResources/Human_Genome/vl.html#omim)

Mapping sites: Gateways To Other Resources: <http://www.ornl.gov/hgmis/links.html#mapping>

Science Human Linkage Maps:

<http://www.chlc.org/ScienceData.html>

Three relevant historical papers on-line:

Mendel's Paper in English. Experiments in Plant Hybridization (1865):

<http://hermes.astro.washington.edu/mirrors/MendelWeb/Mendel.html>

Morgan, Thomas, H. (1909). What are "factors" in Mendelian explanations? *American Breeders Association Reports*, 5:365-369: <http://www.gdb.org/rjr/history/thm-09.pdf>

Bridges, Calvin B. (1914). Direct proof through non-disjunction that the sex-linked genes of *Drosophila*

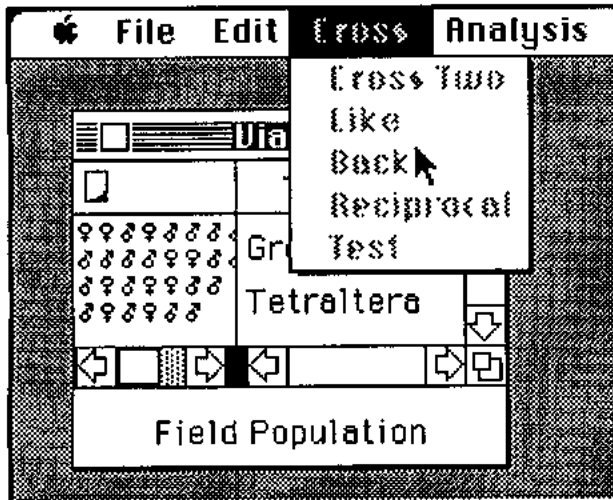


Figure 4. Screen shot of GCK.

are borne on the X-chromosome. *Science, NS vol. XL:107-109*: <http://www.gdb.org/rjr/history/cbb-14.pdf>

**Relevant BioQUEST modules:**

Calley, John N. and John R. Jungck. (1996). "Genetics Construction Kit." *The BioQUEST Library IV*: (The BioQUEST Core Collection): University of Maryland - College Park.  
 Calley, John N. and John R. Jungck. (1996). "Microbial Genetics Construction Kit (GCK)." *The BioQUEST Library IV*: (Candidate Collection): University of Maryland - College Park.

**Other Software:** Map Manager is a program for a Macintosh personal computer which helps analyze the results of genetic mapping experiments using backcrosses, intercrosses, or recombinant inbred (RI) strains. It is a specialized database proplay of information from such mapping experiments, but it also has tools for statistical analysis of the experimental results. Map Manager was created and is maintained by Kenneth F. Manly, Robert Cudmore, Jr, and Greg Kohler in the Department of Molecular and Cellular Biology at Roswell Park Cancer Institute. To contact the developers of Map Manager: [mapmgr@mcbio.med.buffalo.edu](mailto:mapmgr@mcbio.med.buffalo.edu)

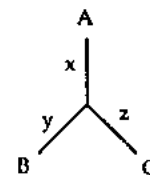
**IV. Fitch-Margoliash Little Maximum Parsimony Algorithm for Phylogenetic Tree Construction**

The availability of amino acid sequences of proteins with similar functions from many different species excited systematicists and geneticists in the mid-1960's. Emile Zuckerkandl and Linus Pauling (1965) are usually credited for the fundamental reasoning behind molecular evolutionary research; namely, proteins and nucleic acids are better molecules for building phylogenetic relationships than are secondary metabolites which do not reflect sequential information transferred between generations. Cavalli-Sforza and Edwards (1967) stated an additive hypothesis for converting distances between molecular sequences into phylogenetic trees. However, the first development of an algorithm that was employed in building a tree of proteins that was fairly congruent with classical taxonomy was widely publicized in Walter Fitch's and Emanuel Margoliash's (1967) analysis of

cytochrome C's. While the combinatorial explosion of topologies ( $\bar{X} = \sum_{i=1}^{n-2} (2i - 5)!$  or over Avogadro's number for just 22 taxa) makes an exhaustive search computationally prohibitive, they circumvented many complications by collapsing nodes after each new sequence was added. By using a known topology, they only had to solve for distances using three equations with three unknowns. Four taxa trees have three different topologies and a series of over-determined equations. So Fitch and Margoliash collapsed the two closest taxa into the tip of a single branch in each iteration and then added each taxon successively. They overcame the problem of the order of entry of taxa by randomizing the order until a particular topology was well supported (such as minimizing total distances over a tree). Since their publication, revolutions in cladistics, resampling statistics (bootstrapping and jackknifing), maximum likelihood techniques, multiple sequence alignment algorithms, and general computer science have led to a proliferation of powerful alternative techniques (Huelsenbeck and Rannala 1997). Nonetheless, the Fitch-Margoliash algorithm is still employed and its historical importance is indelible because of its language of minimal mutational distances, invariant residues, and inferring function from homologous molecular sequence alignments. Furthermore, I agree wholeheartedly with Clegg (1984) when he stated: "Much of what is occurring today (in molecular biology especially evolution) could not have been anticipated by a logical extension of population genetic theory, no matter how inspired."

Distance Matrix	A	B	C
A	∅	$d_{AB}$	$d_{AC}$
B	$d_{AB}$	∅	$d_{BC}$
C	$d_{AC}$	$d_{BC}$	∅

Tree



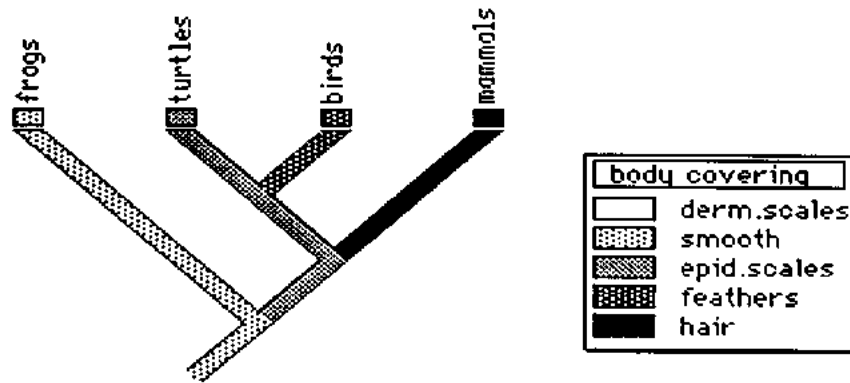


Figure 5. MacClade tree with trace of character states

Equations from Nei (1987), p. 56:

$$x = (d_{AB} + d_{AC} - d_{BC}) / 2$$

$$y = (d_{AB} - d_{AC} + d_{BC}) / 2$$

$$z = (-d_{AB} + d_{AC} + d_{BC}) / 2$$

#### References:

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#### Relevant WWW sites:

David and Wayne Maddison's "Tree of Life" and their MacClade homepage: <http://phylogeny.arizona.edu/tree/phylogeny.html>  
<http://phylogeny.arizona.edu/macclade/macclade.html>

TREEBASE, a searchable data base of phylogenies from various papers. It's in its early days yet so it has almost entirely angiosperm phylogenies in it: <http://phylogeny.harvard.edu/treebase/>

Joe Felsenstein's course syllabus, references, and PHYLIP software:

<http://weber.u.washington.edu/~genetics/courses/genet590/genet590.html>

<http://weber.u.washington.edu/~genetics/courses/genet554/genet554.html>

<http://evolution.genetics.washington.edu/phylip.html>

PAUP homepage: <http://phylogeny.arizona.edu/tree/programs/programs.html#PAUP>

Computational Molecular Evolution: <http://dexter.gnets.ncsu.edu/lab/moleevol.html>

Good site for links on evolution: <http://golgi.harvard.edu/biopages/evolution.html>

#### Relevant BioQUEST modules:

Maddison, Wayne and David Maddison. (1996). *MacClade 2.1* (student use only), *The BioQUEST Library IV*:(Support Materials Archive).

Peterson, Nils S. (1996). "Taxonomic Features Data Manager." *The BioQUEST Library IV*:(Extended Learning Resources).

Brewer, Steve "Phylogenetic Investigator." (1996). *MacClade 2.1* (student use only), *The BioQUEST Library IV*:(First Review Folder).

<http://141.218.91.93/docs/PIGuide/PIguide.html>

## V. Lotka-Volterra Interspecific Competition Logistic Equations

Israel (1985) describes a critically important transition in the way that biology is done: "The 1920's were a period of rapid growth and change in modern biomathematics. ... The first of these was a kind of *invasion* [emphasis his] of biology by mathematics; mathematics was no longer used merely as a technical aid but as a conceptual tool for investigation purposes. It was no longer a question of using a few formulae for carrying out an occasional calculation, but of bringing into action the whole vast array of sophisticated theorems of mathematical analysis." While the notion of exponential population growth has been discussed throughout much of recorded history, most of us credit the Reverend Thomas Malthus for calling attention to the idea of a finite carrying capacity. In other words, exponential ( $N_t = N_0 e^{rt}$ ) models do not adequately mimic the actual growth of species with finite space and nutrients (such as bacteria in a chemostat or flour beetles in a granary) because populations asymptotically approach a maximal equilibrium value. If we increase the complexity by adding biotic factors such as the existence of species which may compete for the same food or exist in some well-recognized co-evolutionary relationship: predator-prey, host-parasite, plant-pollinator, commensalism, mutualism, proto-cooperation, or amensalism, we need a more sophisticated model. In the era discussed by Israel above, Lotka (1925) and Volterra (1931) independently modelled two species interactions with a pair of simultaneous differential equations. While many challenges to the field validity of their assumptions and many modifications have been added to these equations to account for time lags and other complexities, the Lotka-Volterra equations still serve as a cornerstone of much population ecology. Historically, students could also learn much about priority disputes as a part of science through a closer look at this example (Kingsland 1985). An even more fascinating historical twist is that the utilization of these equations have been elaborated with a strong political interpretation (Wilson and Bossert 1971) based on r- and K-selection. Haraway (1997) states these implications thusly: "Careful parents with solid family values versus vermin and weeds: That seems to be the gist of the story in this reading of an equation. ... In the U.S. imperialist imaginary, societies 'down there' relative to the United States, in the warm and sordid regions of the planet, seem to have lots of human beings who act like r-strategists. The colder, more cerebral, less genital climes to the north - if one discounts immigrants of color and other nonprogressive types common in racist imagery - are replete with good K-strategists."

Lotka-Volterra Interspecific Competition Logistic Equations from Hedrick (1984) pp. 231-232.

$$\frac{dN_1}{dt} = r_1 N_1 \left( \frac{K_1 - N_1 - \alpha N_2}{K_1} \right)$$

$$\frac{dN_2}{dt} = r_2 N_2 \left( \frac{K_2 - N_2 - \beta N_1}{K_2} \right)$$

$N_i$  = population size of species  $i$

$T$  = time

$r_i$  - instantaneous or intrinsic rate of increase

$K_i$  = carrying capacity

### References:

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- Kingsland, Sharon. (1985). *Modeling Nature: Episodes in the History of Population Ecology*. University of Chicago Press: Chicago, Illinois.
- Lotka, A. J. (1925). *Elements of Physical Biology*. Williams and Wilkins: Baltimore, Maryland.

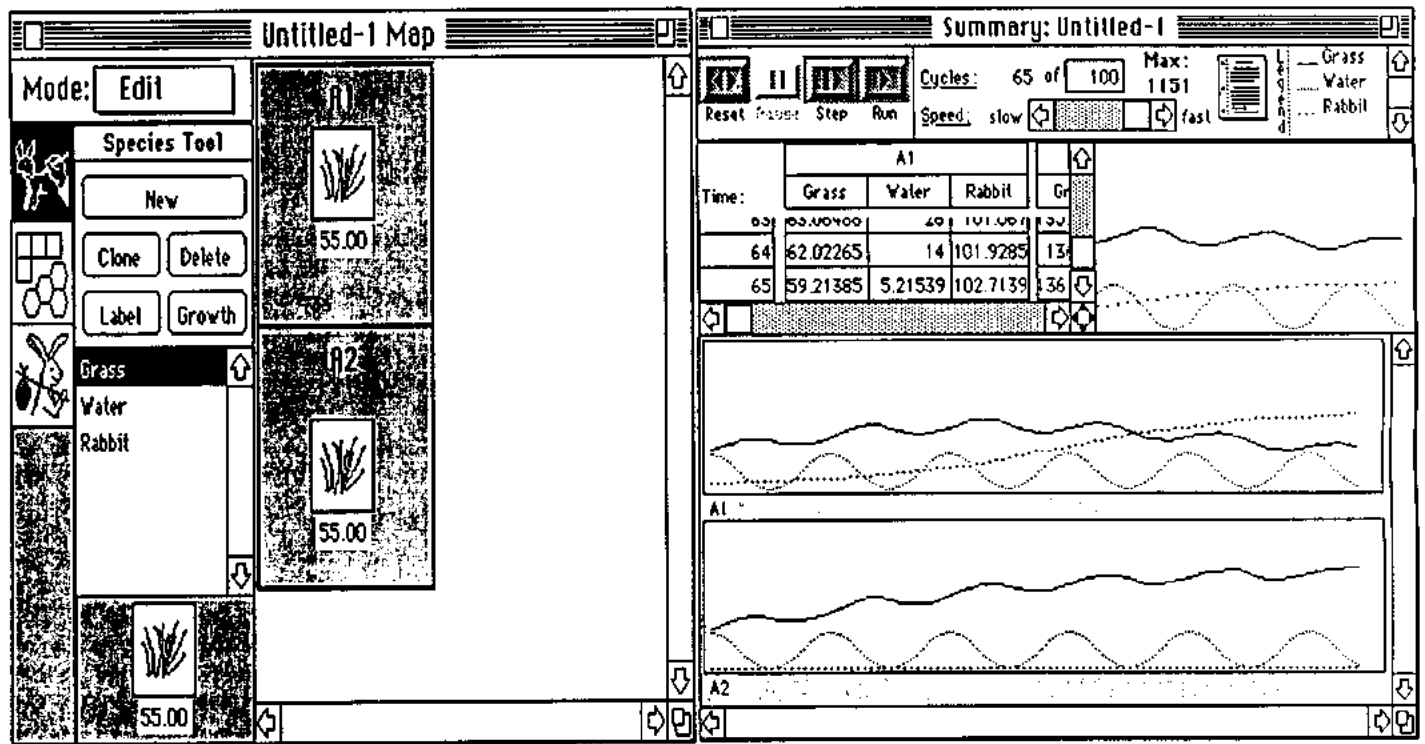


Figure 6. Two windows from Biota.

Swartzman, Gordon L. and Stephen P. Kaluzny. (1987). *Ecological Simulation Primer*. Macmillan: New York, New York.

Thompson, J. M. T. (1979). "An evolution game for a prey-predator ecology." *The Journal of Mathematics and Its Applications* 15:162-167 (July).

Volterra, V. (1931). Variazioni e fluttuazioni del numero d'individui in specie animal conviventi. *Mem. Acad. Lincei*. 2:31-113. Translated as an appendix to Chapman, R. N. (1976). *Animal Ecology*. McGraw-Hill, Inc.: New York, New York.

Wilson, E. O. and W. H. Bossert. (1971). "The Lotka-Volterra equations." "Volterra's principle." "r and K Selection." *A Primer of Population Biology*. Sinauer: Sunderland, Massachusetts, p.129-138, 110-111.

**Relevant WWW sites for Lotka-Volterra Equations and mathematical approaches to solving them:**

Lotka-Volterra Model (Quantitative Population Ecology: Dept. of Entomology, Virginia Tech, Blacksburg, VA):

<http://www.gypsymoth.ento.vt.edu/~sharov/PopEcol/lec10/lotka.html>

Stability in Random Lotka-Volterra Webs:

<http://www.santafe.edu/~tkeitt/papers/foodweb/node3.html>

Applications of Systems of Differential Equations; Predator-Prey Problems; The Lotka-Volterra system (Mathematica): <http://mac205.sjcdcc.ca.us/ODE/7-B-1/7-B-1-ma.html>

The dynamical game. The Lotka - Volterra equations

for taxa: <http://www.iiasa.ac.at/~muellers/these/node29.html>

Mathematical Modelling of Lotka-Volterra Predator-Prey (Department of Mathematics and Statistics University of South Alabama):

<http://www.mathstat.usouthal.edu/~hitt/courses/590/population/population09.html>

Lotka-Volterra Dynamics (Russell K. Standish). EcoLab Documentation. EcoLab is a system that implements an abstract ecology model:

<http://parallel.acsu.unsw.edu.au/rks/docs/ecolab temp/note/node3.html> node3.html

Oscillating Chemical Reactions Simulated by Molecular Dynamics : A particular example: MD simulations of the modified Volterra-Lotka reaction:

<http://virgil.ruc.dk/~kneht/csp/node3.html>

Interactive Text BRE 471/571 - Nonlinear Systems BRE 471/571 - Biosystems Modeling Techniques. Topic: Nonlinear Systems. Cellular Automata: <http://biosys.bre.orst.edu/bre571/mech/nonlin1.ht>

Systems of Differential Equations; Population Dynamics; Two Species Model: [http://spam.maths.adelaide.edu.au/jdenier/dyn\\_mod/](http://spam.maths.adelaide.edu.au/jdenier/dyn_mod/)

Second-order differential equations. Solution to the set of...: [http://dept.physics.upenn.edu/courses/gladney/mathphys/java/sect3/subsection3\\_1\\_5.html](http://dept.physics.upenn.edu/courses/gladney/mathphys/java/sect3/subsection3_1_5.html)

XPP Tutorial: Basic Idea and Introduction. Dynamical systems theory provides the language and the machinery for the analysis ...: <http://www.cnd.mcgill.ca/computing/doc/xpptut/xpptut.html>



An interactive predator-prey model using PERL from Sweden: [http://fisher.teorekol.lu.se/simulation\\_server/](http://fisher.teorekol.lu.se/simulation_server/)  
 Pollination model from the same source: <http://fisher.teorekol.lu.se/cgi-bin/pollination.pl>  
 Chrisitan V. Forst. A general system of high-order differential equations describing... Chaotic Interactions of Self-Replicating RNA.  
<http://www.santafe.edu/sfi/publications/Abstracts/95-10-093abs.html>

**Relevant BioQUEST modules:**

Danbury, Jim, Ben Jones, John Kruper, Eric Nelson, William Sterner, Jeff Schank, Jim Lichtenstein, Joyce Weil, and William Wimsatt. (1996). "Biota." *The BioQUEST Library IV*: (The BioQUEST Core Collection): University of Maryland - College Park.  
 Schank, Jeff and William Wimsatt. (1996) "Modelling Tools: Logistic Growth," *The BioQUEST Library IV*: (Collection Candidates): University of Maryland - College Park.

**VI. Hodgkin-Huxley (Goldman) Equations for Neural Axon Membrane Potential**

Membranes have served to define many biological systems from the boundary condition of closure that separates inside from outside or a biological organism from its environment. Yet these membranes are semi-permeable. This border of exchange mediates communication between a cell and its neighbors, interactions with other species, chemical signals (hormones, neurotransmitters, antigens, drugs, pheromones, etc.) or various physical factors (mechanical, electrical, thermal, etc.). Hence, models that could capture much of the qualitative and quantitative behavior of membrane systems have been an important theme of cell, plant, and animal physiology and biophysics. Given the anthropocentric bias that confers special status toward vertebrate brains, it is not surprising that neural membranes receive even greater attention. Paradoxically an invertebrate model has historically been associated with the most well known model of neural behavior: namely, the Hodgkin-Huxley equations for squid axons' action potentials. The model is used to model mammalian nerves as well as the mechanical responsiveness of some plant membranes. Hodgkin and Huxley won the 1963 Nobel Prize in Physiology and Medicine "for their discoveries concerning the ionic mechanisms involved in excitation and inhibition in the peripheral and central portions of the nerve cell membrane." For students who are interested in model organisms, historical investigation of squid axons would be enormously beneficial.

Equations from Edelstein-Keshet (1988): "The Hodgkin-Huxley equations consist of four coupled ODEs with highly nonlinear terms. For this reason they are quite difficult to understand in an analytic mathematical way."

$$\frac{dv}{dt} = \frac{-1}{c} [g_{Na}(V)(V - V_{Na}) + g_K(V)(V - V_K) + g_L(V - V_L)]$$

$$\frac{dn}{dt} = \alpha_n(V)(1 - n) - \beta_n(V)n$$

$$\frac{dm}{dt} = \alpha_m(V)(1 - m) - \beta_m(V)m$$

$$\frac{dh}{dt} = \alpha_h(V)(1 - h) - \beta_h(V)h$$

where  $g_{Na} = \bar{g}_{Na} m^3 h$  and  $g_K = \bar{g}_K n^4$

"In assessing the Hodgkin-Huxley model, we should keep in mind that all but one of its equations were tailored to fit experimental observations. Part of the surprisingly great success of the model lies in its ability to predict fairly accurately the results of many other observations not used in formulating the equations" (Edelstein-Keshet, 1988). The equations have also been the focus of a great deal of mathematical exploration and competition amongst software developers to tame the complexities of these equations. Furthermore, models were extended to excitable media in two dimensions and applied to cardiac arrhythmias.

**References:**

Aidley, David J. (1989). *The Physiology of Excitable Cells, third edition*. Cambridge University Press: Cambridge, United Kingdom.  
 Cole, K. S. (1972). *Membranes, Ions, and Impulses*. University of California Press: Berkeley, California.  
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 Edelstein-Keshet, Leah. (1988). *Mathematical Models in Biology*. Random House: New York, New York, p. 314-346.

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- Riggs, Douglas Shepard. (1963). *The Mathematical Approach to Physiological Problems*. MIT Press: Cambridge, Massachusetts.

#### Relevant WWW sites:

- Hodgkin and Huxley Equations (equations scanned from original):  
<http://152.3.161.11/neurolab/hhequat.htm>
- A Brief history of Computational Neuroscience (John W. Moore @ Duke Univ. - see wife of Steven E. Fox, Department of Physiology, SUNY Health Science Center at Brooklyn):  
<http://theta.hippo.hscbklyn.edu/fox/Neuron.User.Manual/2/pioneer.html>
- The Hodgkin-Huxley Equations under Voltage Clamp (Yong-Nam Jun @ CalTech):  
<http://www.klab.caltech.edu/~yongjun/cns221/homeworks/haus1/node2.html>
- Models and Math pages (Lance Hahn @ UPenn):  
 Hodgkin-Huxley model:  
[http://retina.anatomy.upenn.edu/~lance/modelmath/hodgkin\\_huxley.html](http://retina.anatomy.upenn.edu/~lance/modelmath/hodgkin_huxley.html)

Software simulation from (Yoram Etzyon @ Department of Physiology Faculty of Health Sciences, Ben Gurion University, POB 653, Beer-Sheva, Israel):  
<http://medic.bgu.ac.il/mededu/software/hh/hh.html>

Hodgkin Huxley Equation (University of Stirling, U.K.): <http://www.students.stir.ac.uk/biology/membpot/hodhux.htm>

#### Relevant BioQUEST modules:

- Bergland, Mark. (1996). "Action Potential Experiments." *The BioQUEST Library IV*: (Extended Learning Resources Folder): University of Maryland - College Park.
- Macey, Robert and John N. Calley. (1996). "Axon." *The BioQUEST Library IV*: (The BioQUEST Core Collection): University of Maryland - College Park.
- Meir, Eli. (1996). "Spike Studio." *The BioQUEST Library IV*: (Support Materials Archive): University of Maryland - College Park.
- Roy, Marc M. (1996). "Real-Time Data Acquisition." *The BioQUEST Library IV*: (First Review Folder): University of Maryland - College Park.

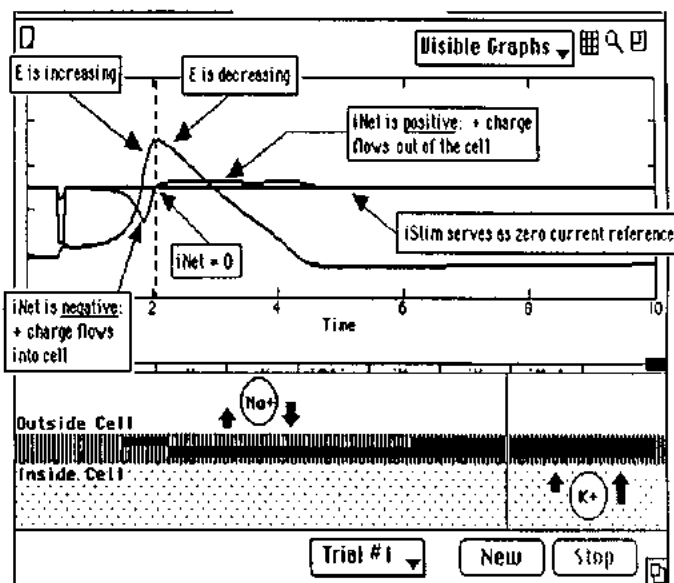


Figure 7. Axon window.

#### VII: Michaelis-Menten Equation for Enzyme Kinetics

Enzyme catalyzed reactions occur so fast that they have often been used as equivalents for life itself such as in the vitalism (Pasteur) - materialism (Büchner) debate of the previous century. In order to understand these rapid reactions, most models have focused on the initial rate of these reactions as a function of substrate concentration. Leonor Michaelis and Maude Leonora Menten (1913) collaborated on developing a basic equation that has served to describe the qualitative behavior of thousands of enzymes, many with only minor modification. Since then, their model has been modified to handle steady state conditions rather than at equilibrium (Briggs-Haldane) and to account for temperature and pH differences. The linear transforms of their equation are also so famous that they too bear their developers' names: Scatchard, Eadie-Hofstee, Wolff-Augustinson, Lineweaver-Burke (usually the worst way to plot one's data despite the popularity of this double reciprocal plot - see Dowd and Riggs 1965), and in other disciplines such as in plant physiology (Classen and Barber 1974.). Since today we could directly do a nonlinear fit to the original Michaelis-Menten equation, there would seem little benefit in

continuing to use these linear transformations especially when they do not robustly test the validity of the underlying assumptions of the kinetic model. Segel (1984) provides a thorough mathematical development of the Michaelis-Menten model. Fantini (1988) describes the French school's approach to regulation which developed exponential versions of the equation to deal with allosterity and feedback inhibition as well as conformational shifts in repressors regulating operons. Cornish-Bowden (1995) has developed software named "Leonora" to celebrate this woman's (Smith 1979) important contribution to quantitative biology.

Michaelis-Menten equation:

$$v = \frac{V_{max}[s]}{k_m + [s]}$$

$v$  = velocity

$V_{max}$  = maximal velocity

$[s]$  = substrate concentration

$k_m$  = kinetic constant

#### References:

Cleland, W. W. (1979). "Statistical analysis of enzyme kinetic data." *Methods in Enzymology* 63:103-138.

Cornish-Bowden, Athel. (1995). *Fundamentals of Enzyme Kinetics*, 2nd edition. Portland Press: London, United Kingdom.

Dowd, J. E. and D. S. Riggs. (1965). "A comparison of estimates of Michaelis-Menten kinetic constants from various linear transformations." *Journal of Biological Chemistry* 240:863.

Fantini, Bernardino. (1988). *Jaques Monod: Pour une éthique de la connaissance*. (Histoire des sciences series). La Decouverte: Paris, France.

Futon, Joseph S. (1972). *Molecules and Life: Historical Essays on the Interplay of Chemistry and Biology*. Wiley-Interscience: New York, New York.

Jack, R. Cecil. (1995). *Basic Biochemical Laboratory Procedures and Computing*.

Laszlo, J. A. (1987). "Determination of stoichiometric association constants by a non-iterative computational method." *Computer Applications in the Biosciences* 3:351-357.

Michaelis, Leonor and Maude Leonora Menten. (1913). "Die Kinetik der Invertinwirkung." *Biochim. Z.* 49: 333-369.

Nimmo, I. A. and G. L. Atkins. (1979). "The statistical analysis of non-normal (real?) data." *Trends in the Biochemical Sciences* 4:236-238.

Rudolph, F. B. and H. J. Fromm. (1979). "Plotting methods for analyzing enzyme rate data." *Methods in Enzymology* 63:138-159.

Segel, Lee A. (1984). *Modeling Dynamic Phenomena in Molecular and Cellular Biology*. Cambridge University Press: Cambridge, U.K.

Smith, D. B. (1979). "The Menten of the Michaelis-Menten equation." *Trends in the Biochemical Sciences* 4: N150.

Washington, Clive, Neena Washington, and Clive Wilson. (1990). *Pharmacokinetic Modelling using Stella on the Apple™Macintosh™*. Ellis Horwood Limited: Chichester, West Sussex, England.

Zierler, K. (1989). "Misuse of nonlinear Scatchard plots." *Trends in the Biochemical Sciences* 14:314-317.

#### Relevant WWW sites:

Mathcad for Computers in Chemistry course at <http://www.pmf.ukim.edu.mk/PMF/Chemistry/wmc-rmm1.html>

Kinetics of Enzymatic Reactions: The Michaelis-Menten Equation: <http://www.pmf.ukim.edu.mk/PMF/Chemistry/wmc-rmm1.html>

Fitting Michaelis-Menten parameters to nutrient uptake data (Mineral Nutrition of Plants, SoilScience/Botany/Horticulture 626, Phillip Barak and Edgar Spalding, Instructors, University of Wisconsin-Madison):

<http://www.soils.wisc.edu/~barak/soilscience626/mm3.htm> (based on: A method for characterizing the relation between nutrient concentration and flux into roots of intact plants. N. Classen and S.A. Barber. (1974.) *Plant Physiol.* 54:564-568.

<http://esg-www.mit.edu:8001/esgbio/eb/kinetics/MandM.html>

<http://oac1.oac.tju.edu/CWIS/OAC/biochemistry/kinetics/HTML/PAGE3A.HTML>

[http://www.chem.ufl.edu/~chapo/gepasipage/gepasi\\_intro.html](http://www.chem.ufl.edu/~chapo/gepasipage/gepasi_intro.html) (metabolic modeling)

<http://www.geotrans.com/bio1d.html> (Anaerobic Biodegradation)

<http://www.micromath.com/pklib2.html> (Micromath: Pharmacokinetics)

<http://www.denison.edu/fipse/chem/sokolik.html> (Maple programs)

<http://www.chem.ualberta.ca/courses/plambeck/p102/p02175.htm>

<http://www.liv.ac.uk/~jse/abouthyp.html> (Windows: Hyperbolic Regression Analysis)

<http://www.engr.umd.edu/~nsw/ench485/lab13.htm> (Chemical Engineering Experiment)

<http://www.biochemtech.uni-halle.de/molmod/subkin.html> (in German - nice graphics)

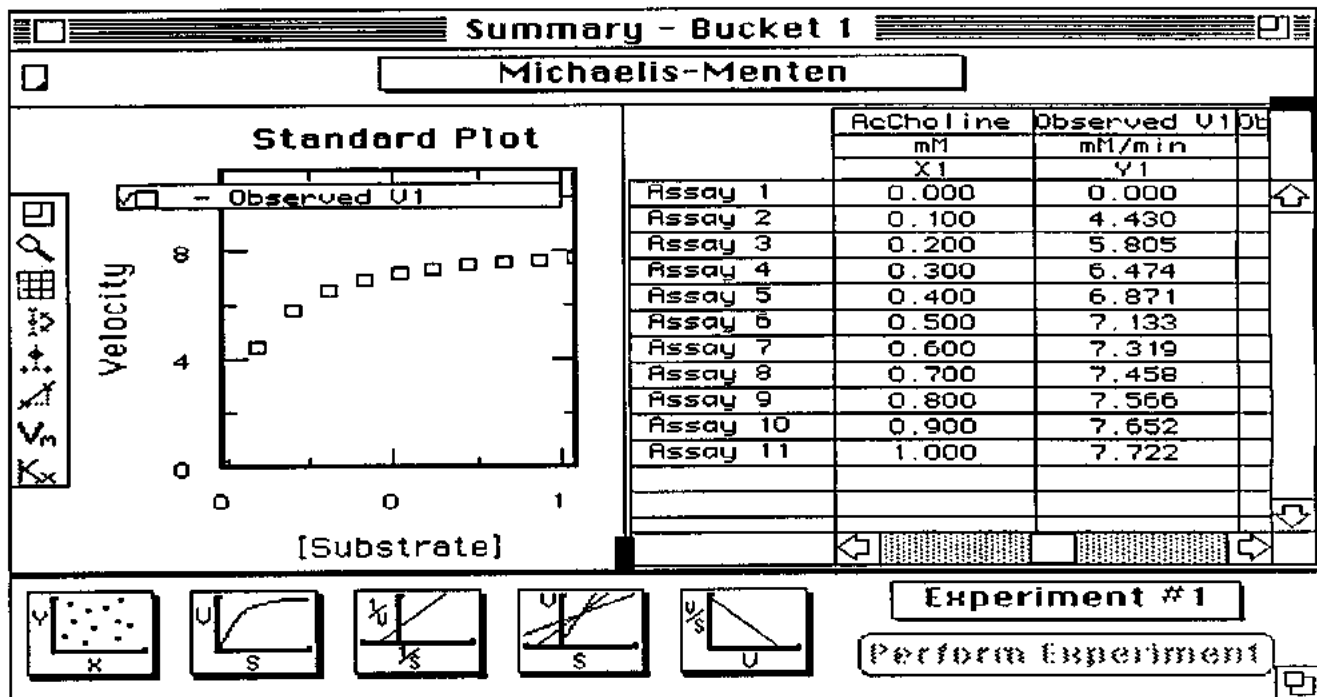


Figure 8. Screen shot of Ratelt!

Pharmacokinetic Software: listing & links:

<http://www.cpb.uokhsc.edu/pkin/soft.html>

Models and Math pages (Lance Hahn @ UPenn):

Michaelis-Menten Function:

<http://retina.anatomy.upenn.edu/~lance/modelmath/michaelis.html>

Relevant BioQUEST modules:

Gilbert, Don. (1996). "Enzyme Kinetics." *The BioQUEST Library IV*:(Support Materials Archive): University of Maryland - College Park.

Place, Allen and Tom Schimdt. (1996) "Ratelt!" *The BioQUEST Library IV*:(Candidate Collection): University of Maryland - College Park.

Other Software: The software package "Lenora" for IBM PC compatible computers is designed expressly for fitting enzyme kinetic data. It is included on a disk in: Athel Cornish-Bowden. (1995). *Analysis of Enzyme Kinetic Data*. Oxford University Press: Oxford, United Kingdom.

### VIII: Allometry: e.g., MacArthur-Wilson Theory of Island Biogeography Species-Area Law

The relationship between size and shape is perhaps the simplest of all equations to have had a major importance in biology and has been commented upon since Galileo, who argued that if you enlarged a mouse to the size of an elephant, it would not have skinny legs like a mouse but stout legs like an elephant to support the mass because mass increased according to the cube of the linear dimensions. D'Arcy Thompson's *On Growth and Form* (1917) and J. B. S. Haldane's (1928) essay *On Being the Right Size* are two of the most famous examples of the biological application of this concept. In the 1930's and 1940's Huxley and others popularized the investigation of allometry in embryonic growth. More recently Niklas (1994) has made an industry of understanding allometric relationships in the biomechanical constraints on plants. Most recently, West, Brown, and Enquist (1997) have developed "a general model for the origin of allometric scaling laws in biology" based on fractal geometry (Williams 1997). However, after the suggestion of Ethel Stanley, I'll stress a different allometric relationship which has received considerable attention as a level above the individual organism, namely, ecology. Robert H. MacArthur and Edward O. Wilson developed a theory of island biogeography in 1967 which simply stated an allometric relationship between the diversity of species that could survive in a region with the size of that region. They plotted this relationship for the disappearance of habitat in various archipelago and the famous recolonization of the Krakatau Islands. Earth First and other environmental activist organizations have widely adopted this hypothesis in their arguments to preserve much larger habitats than the small regions where "charismatic megafauna" are sighted. Even much of the professional biodiversity literature has maintained the theory of island biogeography while modifying it with fractal measures of areas in order to understand the effects of rough edges which may be more conducive to "weedy species" and whether corridors of many small islands (metaphorically understood as well as literally: forests in cattle lands of the Amazon, mountain islands in the sky, meadows surrounded by tilled land, oases in deserts, etc.) work as well as one large region. David Quammen's

*The Song of the Dodo: Island Biogeography in an Age of Extinctions* (1996) is one of the best and most recent popularizations of this theory. While Gilbert (1980) had argued that it was premature to base nature conservation on the theory of island biogeography, Harris (1984) pioneered "the use of this theory as an alternative to current practices of timber harvesting" and won the 1986 Wildlife Society Publication Award for his case study.

Allometry Equation: E.g., MacArthur-Wilson Theory of Island Biogeography Species-Area Law

$$S = CA^z$$

S = species

A = area

C = constant

z = allometric exponent

#### References:

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**Relevant Web Pages:**

Ferdinando Villa, Department of Environmental Sci-

ences, University of Parma, Viale delle Scienze, 43100 Parma, Italy, villa@eagle.bio.unipr.it, also has a nice web write-up on island biogeography: <http://eagle.bio.unipr.it/cv/cv.villa/node10.html>

Galapagos and Island Biogeography web tak:

<http://erasmus.biol.csufresno.edu/isbio.txt>

Bibliography on island biogeography:

<http://erasmus.biol.csufresno.edu/isbib.txt>

**Relevant BioQUEST module:**

Center for Polymer Studies, Boston University. (1996) "Fractal Dimension." *The BioQUEST Library IV: (Candidate Collection)*: University of Maryland - College Park.

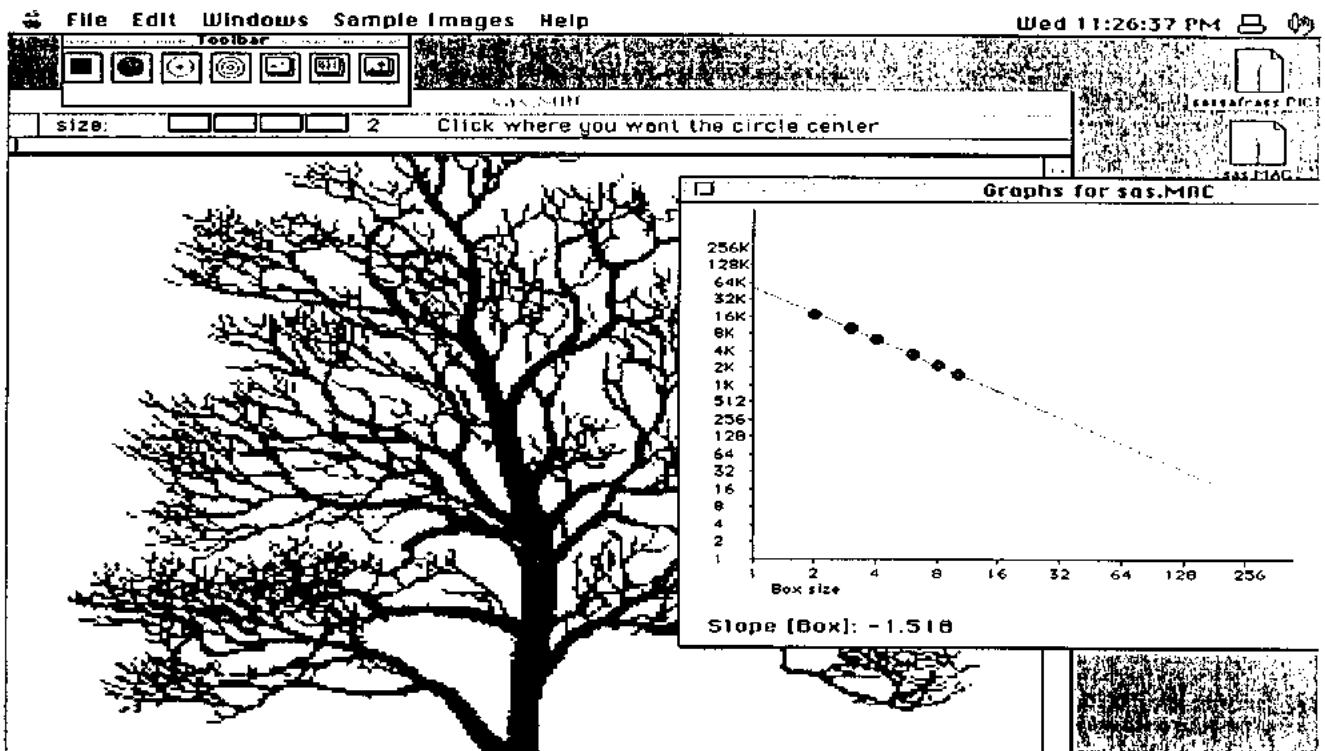


Figure 9. Fractal Dimension of a Tree Image.

**IX: Hypothesis Testing: Luria-Delbrück Fluctuation Test for Mutations in Viruses**

Perhaps no more normative practice of twentieth century biology exists than the notion of hypothesis testing within the context of statistical fiducial levels set ahead of time; e.g., a 5% level or less chance that the results would be expected on the basis of chance alone. While statistics often has an uneasy home in some mathematics departments, most biologists see statistics as one of the most crucial aspects of their students' education. However, when you try to pin biologists down, many are uneasy with statistical tests as the final arbiter of crucial hypotheses unless the chance of a hypothesis being rejected is beyond the level of belief (e.g.  $10^{-20}$ ). In an extended analysis of Fisher's statistical reasoning, Howson and Urbach (1989) conclude:

that one cannot derive scientifically significant conclusions from the type of information which the Fisher and Neyman-Pearson theories regard as adequate. We shall also see that in order to match significance testing with scientific practice, extra principles need to be imported, and that these involve the personal judgment of the experimenter or statistician. Hence, the much-vaunted objectivity of the classical approach is spurious ..." (p. 130).

On the other hand, my personally favorite experiment in twentieth century biology is the Luria-Delbrück Fluctuation Test of teleology in evolutionary biology. It applied the Poisson distribution to rule out Lamarckian premises and to estimate mutation rates quantitatively. Luria and Delbrück shared the 1969 Nobel Prize in Physiology and Medicine. I was delighted to see that the popular general biology textbook author, George Johnson (1996) of Washington University in Saint Louis, also identified it in his list of most significant experiments. In an obituary for Delbrück (*Trends in Biochemical Sciences* May 1981), an anonymous editor reinforced the importance of this classic paper:

“Just as the birth of genetics is considered to have taken place in 1865 upon the appearance of Gregor Mendel’s paper reporting the conclusions he had drawn from his crosses of the garden pea, so the birth of bacterial genetics can be dated as of 1943, when Luria and Delbrück published a joint paper in which they showed that the variants in cultures of phage-resistant variants in cultures of phage-sensitive bacteria represented the selection of spontaneous bacterial mutants. This conclusion was contrary to the then current teachings of bacteriology, which, according to Luria, were ‘the last stronghold of Lamarckism.’ Luria and Delbrück were not the first to study bacterial mutation, any more than Mendel was the first to cross plants for the study of heredity. But with their paper Luria and Delbrück did for bacterial genetics what Mendel had done for general genetics - namely, showed for the first time what kind of experimental arrangements, what kind of data analysis, and, above all, what kind of sophistication was needed for obtaining meaningful and unambiguous results.”

The Luria-Delbrück Fluctuation Test has recently been the subject of further mathematical exploration as well as being under attack by a new round of “neo-neo-Lamarckians” who have argued that mutagenesis can be directed and advantageous for a population under stress. Richardson (1994), Keller (1992), and Sarkar (1991b) provide accounts of the controversy between Darwinists like Lenski, Levin, and Stahl with challengers like Cairns, Shapiro, Rosenberg, and Hall. With stakes the likes of Darwin and Lamarck, this revived controversy is great fun for students to follow and learn why controversy is often considered the lifeblood of science. Also, this example illustrates well how experiments are reinterpreted much later in light of new theories and experiments.

Luria-Delbrück Fluctuation Test Equation for Poisson Process:

$$p \text{ (proportion of zero class)} = e^{-\mu n}$$

$\mu$  = mutation rate  
 $n$  = population size

#### References:

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Stewart, Frank M. (1992). *DataFit (Macintosh software for analyzing Luria-Delbrück fluctuation tests)*. Department of Mathematics, Brown University, Providence, Rhode Island.

Thompson, W. A. (1988). *Point Process Models with Applications to Safety and Reliability*. Chapman and Hall: London. See p. 83: "The Luria-Delbrück Model" and problem set on p. 88.

**Relevant WWW sites:**

Luria and Delbruck/ Benzer/ Poisson:  
<http://www.life.uiuc.edu/micro/316resources/problems/mutations/poisson/>  
 "Important Experiments in Life Science Field"  
[http://life.nthu.edu.tw/~mjhsieh/Biology/experiment/fluct\\_test.html](http://life.nthu.edu.tw/~mjhsieh/Biology/experiment/fluct_test.html)

**References on adaptive mutation:**

[http://helix.biology.mcmaster.ca/4d3/direct\\_mut.html](http://helix.biology.mcmaster.ca/4d3/direct_mut.html)  
 The Poisson Distribution in Biology: ABC '95, a Biological Sciences Web Page, W. R. McClure, wm0p+@andrew.cmu.edu, Department of Biological Sciences, Carnegie Mellon University  
<http://info.bio.cmu.edu/courses/abc/ABC95Poisson/ABC95PoissonPage.html>  
 The Impact of Biology on Mathematics:  
<http://www.gdb.org/Dan/mathbio/1.html>

**Relevant BioQUEST modules:**

Calley, John N., and John R. Jungck. (1996). "Microbial Genetics Construction Kit ( $\mu$ GCK)." *The BioQUEST Library IV*: (Candidate Collection): University of Maryland - College Park.

Hornbach, Daniel. (1996). "Biometrics." *The BioQUEST Library IV*: (Candidate Collection): University of Maryland - College Park.

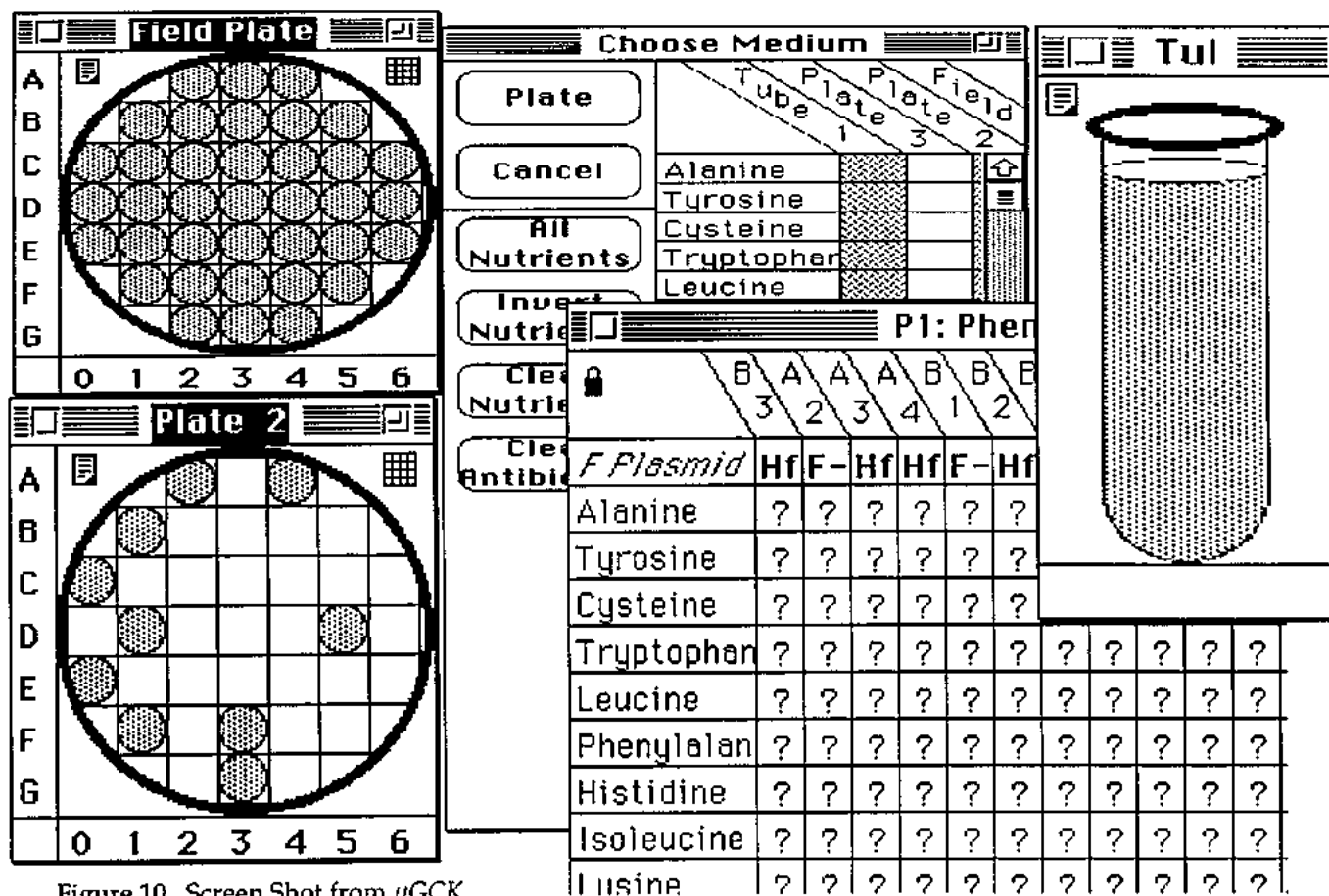


Figure 10. Screen Shot from  $\mu$ GCK.



## X. Genetic Coding: Crick-Griffith-Orgel Comma-free Coding Theory for the Adaptor Hypothesis

One of the greatest ironies of scientific exploration is generating a significant hypothesis based on improper inference or invalid data. For example, Stephen Jay Gould (1996) noted that Charles Darwin's development of the theory of natural selection had made an improper inference:

For those who still cherish the myth that fact alone drives any good theory, I must point out that Darwin, at his key moment of insight - making his analogy from geography to time and evolution - was quite wrong in his example. *Macrauchenia* is not, after all, an ancestor (or even a close relative) of guanacos, but a member of a unique and extinct South American mammalian group, the Litopterna.

This is not only a phenomena of the past century, but our own as well. In their contribution to generating a theory of genetic coding, Crick, Griffith, and Orgel (1957) made a critical mistake of fact: there are not twenty amino acid words (codons) because the maximal number of comma-free code words is twenty because genetic coding does not use a comma-free mechanism; however, for the wrong reasons they predicted that genetic coding is dependent upon an adaptor molecule of nucleic acid that carries an amino acid and is recognized by a three nucleotide site in messenger RNA. We now know this adaptor molecule as transfer RNA and their work ascribed a function to a series of heterogeneous molecules heretofore referred to simply as "soluble RNA." "Poor analogy, good idea." Crick *et al.* (1961) corrected themselves in an important theoretical paper in which they asserted that the standard genetic code is commaless rather than comma-free, has sixty four not twenty codons, is degenerate, starts from a fixed point and then reads a contiguous and continuous sequence. Their second paper explained frameshift as well as point mutations and made suggestions for the elucidation of genetic coding. However, even here, their enthusiasm exceeded reality because they predicted that: "If the coding ratio is 3, as our results suggest, and if the genetic code is the same throughout Nature [sic], then the genetic code may well be solved within a year." Most historians would argue that it took until 1966 before sufficient words were exhaustively scrutinized such that all sixty-four codons were assigned with textbook certainty and we now know that "the genetic code is [NOT] the same throughout Nature." Crick, Griffith, and Orgel (1957) contributed critically to our understanding by generating a hypothesis that enabled us to interpret and design a large number of experiments that was respected even by geneticists and biochemists skeptical of mathematics. Interestingly, both biochemists (Hoagland 1996) and philosophers (Sarkar 1996) have tried to trivialize the role that theory played and in so doing express deep concerns about the expectations of "theory" by both. Personally, I have been concerned with genetic codes as codes for a long time and have shown how Crick, Griffith, and Orgel's (1957) work can be used to understand another problem (Jungck, 1984), namely, the origins of genetic codes, and Shepherd (1981) has developed a pragmatic set of tools based on comma-free codes that are commonly used in nucleic acid sequence analysis packages to predict reading frame.

Equation for comma-free codes:

$$W_k(n) \leq \frac{1}{k} \sum_{d|k} \mu(d) n^{k/d}$$

$W_k(n)$  = number of comma-free  
code k-letter words with alphabet n  
 $\mu(d)$  = Möbius function  
summation is extended over all divisors d of k

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**Relevant WWW sites:**

The Impact of Mathematics on Cellular and Molecular Biology:  
<http://www.gdb.org/Dan/mathbio/2.html>  
*in silico* biology: Computational Molecular Biology and Molecular Bioinformatics (contains many links and bibliographies):  
<http://juno.ucsd.edu/~sjc/thailand.html>  
 Computational Biology in the UW-Madison CS Dept.:  
<http://www.cs.wisc.edu/~shavlik/uwcompbio.html>

**Relevant BioQUEST modules:**

Bergland, Mark. (1996). "DNA Electrophoresis." *The BioQUEST Library IV*: (Extended Learning Resources): University of Maryland - College Park.

Gilbert, Don. (1996). "SeqApp, SeqPup, Dotty Plotter, GelFragSizer, GenBank Search, and LoopDLooP/LoopViewer" *The BioQUEST Library IV*: (Support Materials Archive): University of Maryland - College Park.

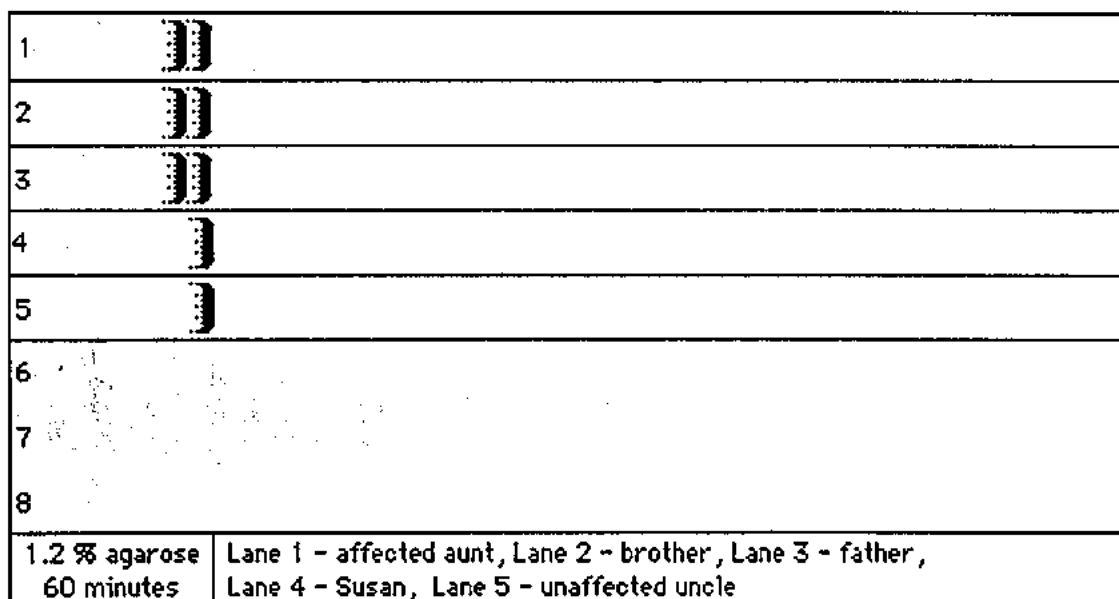


Figure 11. DNA Electrophoresis screen shot.

## Conclusions:

The best aspect of these ten equations in terms of their roles in the foundations of twentieth century biological research is that it was so difficult narrowing the list to ten. If I have made the case for any one of these equations' importance to an area of biology that you teach or an area about which you strongly feel that twenty-first century biology students should know something about, then I hope that you will help us address the need for much more mathematics in general biology education. Not only do I believe that students deserve the respect that this curricular move would make, but I believe that it would be a fun challenge for ourselves in terms of professional and personal growth. Please revisit Steen and Albers's (1981) questions quoted herein on page 15 and see whether you agree that: (1) applications should play a role in mathematics curricula, (2) that the traditional division between mathematics and science instruction is invalid, and (3) that mathematical topics can be related to cultural issues that are relevant to students. If I have not convinced you that these are appropriate responses to their questions, then I urge you to read Simon A. Levin's introduction to the one hundredth volume in the series of books that he has edited on mathematical biology:

Mathematical biology has changed a great deal in the last decade, mainly for the better. Whereas twenty years ago, it was peripheral to many subdisciplines of biology, its success is marked today by ever increasing integration into areas of application. Mathematical biologists, who once found in each other the most eager listeners and constructive critics, now see their work guiding experiments, and shaping the conceptual foundations of almost all areas of biology. Indeed, in some areas, the integration is so complete that there are no clear distinctions between theoretician and experimentalist: every respectable researcher must be a little of each. And in areas where that is not yet true, it will be so within a decade more. (Levin 1994)

As we enter the next century, can we afford to continue to offer biology curricula so distinctly removed from contemporary research practices, from important historical foundations, and cultural issues that all would be so much better informed by greater familiarity with mathematical beauty, utility, and robustness?

## Acknowledgements:

First, I want to thank Evelyn Fox Keller and Chuck Dyke for encouraging me to address these questions. Second, I am deeply appreciative to senior mentorship from Hugo Martinez, Lee Segel, Frank Stewart, and the late Sol Rubinow for helping me develop a career in mathematical biology. Third, I have been extremely fortunate to have had the opportunity to collaborate closely with six mathematicians over my career: Martha (Bertman) O'Kennon now at Albion College, Linda Deneen now at the University of Minnesota - Duluth, Bill Briggs now at the University of Colorado - Boulder, Gus Rabson at Clarkson University (Potsdam, New York), Myron Hood now at Cal Poly in San Louis Obispo, and Paul Campbell, my colleague at Beloit. We have run workshops for faculty, co-authored papers, held regular journal clubs for ourselves and our students, developed algorithms for software development, and shared our ideas for teaching shared students. I have deeply benefitted from each of these interactions. Fourth, I have had many student research collaborators in mathematical biology over the past thirtyone years who have tremendously enriched my life and my work. Fifth, I am indebted to Srebrenka Robic, Vanja Klepac, Ethel Stanley, Teresa Holevas, Patti Soderberg, Frank Price, Kun Zhang, Jeff Schank, Martijn Huygen, John Rosenwald, Virginia Vaughan, Sarah Renish, and Lakmini Weerakoon for their multiple readings, revisions, and reviews of this manuscript. I have incorporated many of their suggestions, but, of course, I didn't take all of their advice and hence have to admit responsibility for the opinions expressed herein. And, finally, I thank all those members of the Association of Midwestern College Biology Teachers who have participated in my annual workshops, lectures, and poster sessions on mathematical biology.

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#### Sources on Mathematics Reform:

Project CALC (Smith and Moore, 1996),

<http://www.math.duke.edu/faculty/moore/pcalc.html>

<http://141.224.128.4/pkal/resources/ptw/duke.html>

<http://www.math.duke.edu/researchd/smith/smith.html>

<http://www.mathsource.com/cgi-bin/MathSource/Applications/Education/Calculus/0202-745>

#### Harvard-Calculus Overview

<http://archives.math.utk.edu/projnext/summaries/harvardCalculus.html>

<http://www.mat.ufrgs.br/~portosil/harvard.html>

<http://alan.sewanee.edu:8080/sc/links.html>  
(provides 18 links on this project)

Lazarowitz and Uhl have developed a course entitled BioCalc at the University of Illinois - Champaign-Urbana wherein they have almost completely done away with lectures and have a series of *Mathematica*<sup>TM</sup> notebooks with biologically informed calculus education projects

<http://www.life.uiuc.edu/micro/lazarow.html>

#### Calculus&Mathematica

<http://www-cm.math.uiuc.edu/>

<http://www-cm.math.uiuc.edu/people/authors/jerry.html>

<http://www.wolfram.com:80/education/colleges/courseware/uhl.html>

Gross' group at the University of Tennessee - Knoxville has collected an enormous set of world wide web resources for a quantitatively based biology curriculum: <http://www.math.utk.edu/~gross/quant.lifesci.html>

The Mathematics Association of America (MAA), led by Wayne Roberts, Project Director, published five volumes (and mailed to every mathematics department in the U.S.!) with copy-able materials for Calculus. These are:

1. A lab book (26 technology-based but platform-independent labs): *Learning by Discovery*, Anita Solow (ed), MAA Notes, volume 27, 1993

2. A book of concept-oriented problems: *Calculus Problems for a New Century*, Robert Fraga (ed), MAA Notes, volume 28, 1993

3. A volume of 18 project-length application based problems from different areas: *Applications of Calculus*, Phil Straffin (ed), MAA Notes, volume 29, 1993

4. A collection of student investigation problems (one page each, and thus shorter than the application problems): *Problems for Student Investigation*, Mike Jackson and John Ramsay (eds), MAA Notes, volume 30, 1993, and

5. A series of readings for Calculus. Resources for Calculus, 5 volume collection: *Readings for Calculus*, Woody Dudley (ed), MAA Notes, volume 31, 1993.

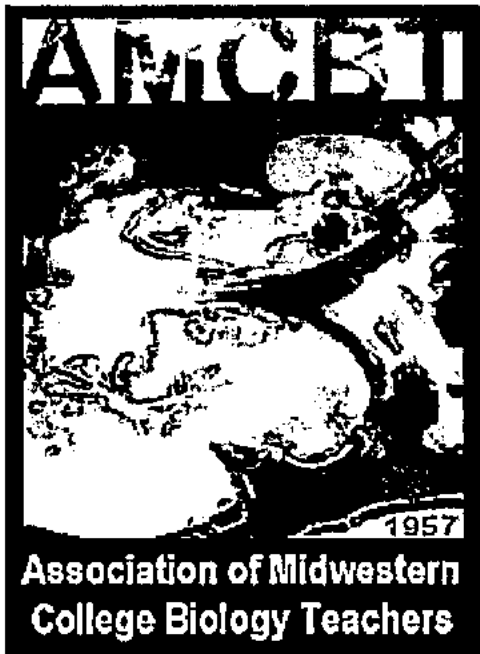
Leitzel, James R. C., and Alan C. Tucker, Editors. (1994). *Assessing Calculus Reform Efforts: A Report to the Community*. Series: MAA Notes. Mathematics Association of America: Providence, RI.

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#### From one of the reviewers

(Jeff Schank - Indiana University):

I just read through the manuscript you sent me, and of course I completely agree with you. The main comment I have is that you have an extremely powerful argument regarding the use of statistics in biology that should be driven home even harder. First, there is virtually no research that can be published these days without the use of statistics, which means choosing one or more statistical models for the data. Every biologist must be able to model, have basic mathematical knowledge of the statistics he or she is using, and understand what assumptions must be satisfied to use the model. Thus, to avoid teaching mathematical ideas in biology is negligent. Second, mathematical modeling in statistics can be just like mathematical modeling biological mechanisms in that one starts with a basic model or linear equation ( $Y = Xb + \text{epsilon}$ ) and then it is elaborated for different experimental designs. Third, by recognizing that using statistics is modeling, I think one can begin to see that there may be other strategies for modeling data (I mean other than standard models in Statistics textbooks) such as doing Monte Carlo simulations. ... Mathematical modeling in teaching is one of the newly emerging threads in the history of modeling in biology.



## AMCBT 41st Annual Meeting

Beloit College  
Beloit, Wisconsin

October 16-18, 1997

*Preliminary Program*

### Constructing Coherent Curricula: Pushing the Boundaries

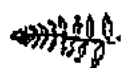
#### Thursday, October 16th

6:00 PM - Registration and Reception  
8:00 PM

Logan Anthropology Museum  
Wright Art Museum

8:00 PM Opening Session  
Welcome for AMCBT  
AMCBT President: *Leona Truchan, Alverno College*  
Program Chair: *Nancy Sanders, Truman State University*  
Local Arrangements Chair: *John Jungck, Beloit College*  
Welcome to Beloit College

Dining Room  
Pearsons Hall



OPENING ADDRESS (Public Welcome to Attend)  
Is There Light in a Black Hole? Fast Plants and Film Cannery  
*Paul Williams, University of Wisconsin-Madison*

9:30 PM Executive Committee Meeting

Cafe Bio  
Chamberlin Hall

9:30 PM - Open Lab: Student facilitators  
11:59 PM  
1. Real Time Data Acquisition  
2. Internet: Web Page Development  
3. Computer Simulations and Tools  
4. Digital Video Microscopy

Chamberlin Hall  
214  
202  
218  
208

#### Friday, October 17th

7:00 AM - Early Registration  
8:00 AM

Foyer  
Pearsons Hall

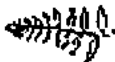
7:00 AM - Buffet Breakfast by Interest Group  
8:00 AM

Dining Room  
Pearsons Hall

8:00 AM - Resources for Curriculum Construction  
8:30 AM

Dining Room  
Pearsons Hall

- 8:30 AM - Continuing Registration  
12:00 PM Cafe Bio  
Chamberlin Hall
- 8:45 AM - **CONCURRENT FIELD TRIP/ WORKSHOP SESSIONS I**  
12:00 PM
1. Sugar River Canoe Trip
  2. Fossil Hunt
  3. Prairie Field Trip /Mini Workshop  
Yaffa Grossman, *Beloit College*
  4. DNA in Introductory Biology  
Karen Klyczek, *UW-River Falls*
  5. Internet and the Curriculum  
Tim Mulkey, *Indiana State University*
  - 6.
- 12:00 PM - Luncheon with Keynote Address  
1:45 PM **KEYNOTE ADDRESS:**  
Jeanne Narum, *Project Kaleidoscope (PKAL)*
- Dining Room  
Pearsons Hall
- ~~Office~~
- 2:00 PM - **CONCURRENT FIELD TRIP/ WORKSHOP SESSIONS II**  
4:00 PM
1. Case Writing I  
Margaret Waterman, *Southeast Missouri State University*
  2. Computerized Lab Practicals  
Harold Wilkinson, *Millikin University*
  3. Case It! Update  
Mark Bergland, *University of Wisconsin - River Falls*  
Karen Klyczek, *University of Wisconsin - River Falls*
  4. Dairyland Seed Tour: Evolutionary Biology in Agriculture  
John R. Jungck, *Beloit College*
  5. Wisconsin Food Tour  
Marion Fass, *Beloit College*
  6. Potential Exhibitor Workshop  
Ed Sachs, *MacLab, ADInstruments*
  - 7.
- 4:00 PM - **Afternoon Break (Refreshments)**  
4:15 PM Cafe Bio  
Chamberlin Hall
- 4:15 PM - **CONCURRENT PAPER SESSIONS I**  
5:00 PM
1. Capstone Courses in Biology  
Dick Wilson and K. Williams, *Rockhurst College*
  2. Visual Learning in the Curriculum  
Ethel Stanley, *Beloit College*
  3. Field Team Investigations: Students Connecting Students by Tours  
Tom Davis, *Loras College*
  4. Ethnobotany of Coastal Native Americans  
Austin Brooks, *Wabash College*
  5. The Role of Computers in a Project Based Biology Curriculum  
Presley Martin, *Hamline College*
  - 6
- 5:00 PM - Writing for *Bioscene*  
5:45 PM **All presenters please attend!**
- Upper Floor  
Pearsons Hall

5:30 PM - 7:00 PM	Posters, Exhibits, and Social	Pearsons Hall
7:00 PM	BANQUET	Pearsons Hall
8:00 PM	BANQUET ADDRESS **TBA**	
9:30 PM - 10:45 PM	Curricular Issues Discussion	Upper Floor Pearsons Hall
9:30 PM - 10:30 PM	Bioscene Editorial Board	Conference Room Pearsons Hall

## Saturday, October 18th

8:00 AM - 9:15 AM	Continental Breakfast	Dining Room Pearsons Hall
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8:30 AM - 10:30 AM	***Open Balloting***	
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### 9:00 AM - CONCURRENT WORKSHOP SESSIONS III

- |          |   |
|----------|---|
| 11:00 AM | 1. Case Writing II<br>Margaret Waterman, <i>Southeast Missouri State University</i>                                       |
|          | 2. ChemLinks<br><i>Beloit College</i>   |
|          | 3. Internet Friendly or Internet Phobic?<br>Uses of the Internet in College Biology<br>Marion Fass, <i>Beloit College</i> |
|          | 4.  |

### 9:00 AM - CONCURRENT PAPER SESSIONS II

- |         |  |
|---------|--|
| 9:45 AM | 1. Freshman in Science Seminar<br>Ed Kos, Dick Wilson, Anita Salem and Jim Dronberger,<br><i>Rockhurst College</i>   |
|         | 2. The Largest Microorganism<br>Austin Brooks, <i>Wabash College</i>   |
|         | 3. Educational Forum I: Building Learning Communities<br>Ann Larson, <i>University of Illinois -Springfield</i><br>Buzz Hoagland, <i>Westfield State College</i> |
|         | 4. CELS: Coalition for Education in the Life Sciences<br>Louise Liao, <i>University of Wisconsin - Madison</i>   |
|         | 5. Student Project Studies<br>Gopal Krishna and Suzanne Martin,<br><i>Moberly Area Community College</i>   |

9:45 AM - 10:15 AM	Morning Break Posters, Exhibits, Refreshments ***Balloting Closes at 10:30 AM***	Pearsons Hall
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### 10:15 AM - CONCURRENT PAPER SESSIONS III

- |          |  |
|----------|--|
| 11:00 AM | 1. Commonalities in Biology<br>Bill Brett, <i>Indiana State University</i> |
|----------|--|



2. Proposal Preparation Seminar for Biology Majors  
Charles Bicak, *University of Nebraska - Kearney*
3. Educational Forum II: What is a Biology Major?  
Leona Truchan, *Alverno College*; Buzz Hoagland, *Westfield State College*  
Bob Wikel, *Doane College*
4. Including Invertebrates  
Bob Wallace, *Ripon College*
- 5.

11:00 AM - Luncheon with Business Meeting Dining Room  
12:30 PM BUSINESS MEETING Pearsons Hall

Presidential Address: Leona Truchan, *Alverno College*

Election Results: Dick Wilson, *Rockhurst College*  
Bioscene: John R. Jungck and Ethel Stanley, *Beloit College*  
Tim Mulkey, *Indiana State University*  
Executive Secretary Report: Marc Roy, *Beloit College*

=====ADJOURNMENT OF REGULAR MEETING=====

12:35 PM - Executive Committee Meeting Conference Room  
1:15 PM Includes newly elected Exec. Comm. members! Pearsons Hall

If you have specific questions about the program, please contact:

Program Chair: Nancy Sanders  
Truman State University  
Kirksville, MO 63501-0828  
nsanders@truman.edu

\*\*\*NOTICE\*\*\*

## Call for Nominations

We are seeking nominations/self nominations for elections to be held at the 1997 AMCBT Annual Meeting. At this meeting we will elect the President-Elect, two Steering Committee members and secretary. Letters of nomination with an attached CV should be sent by July 1, 1996 to:

John Jungck  
Department of Biology  
Beloit College  
700 College Street  
Beloit WI 53511

Email correspondance should be addressed to jungck@beloit.edu

## Echoes from the past.....

At the most recent meeting of the Steering Committee held at Beloit College the weekend of February 22 and 23, which met to outline the fall Annual Meeting program (Beloit College, October 16-18, 1997), I was struck by how certain concerns keep surfacing in AMCBT. The proposed theme for this coming fall's meeting is "Constructing Coherent Curricula: Pushing the Boundaries", and this recalled to mind something Joe Kapler (an Emeritus member from Loras) told me at the meeting last fall at Loras. Back in the fifties, the biology department of Drake University was charged by the State of Iowa to ascertain the biology preparedness of Iowa students wishing to attend medical school. What struck everyone was the variability of preparation and background that these students from different Iowa schools possessed. Led by Leland and Willis Johnson, a group of biology teachers (as recalled both high school and college) met to discuss some sort of standards for biology education---a coherent curriculum. This discussion led to the formation of an association dedicated to the advancement and development of the biology curriculum in Iowa (and eventually other places), the Association of Midwestern Biology Teachers, now AMCBT. We continue to prove the practice of reaffirming our prime directives.

.....Ed Kos, Historian-AMCBT

NOTICE TO ALL VOTING MEMBERS:  
After forty years, a second name change is suggested:

## AMCBT to ACUBE?

At the Steering Committee meeting in Beloit we addressed the issue of renewing our papers filed officially in the state of Iowa because they told us that we needed an official representative for the organization in the state. We elected Tom Davis to serve in this capacity. However, while we were on the discussion of these filed papers, many of us learned for the first time that the papers listed us as AMBT (note: no C). Many university members of the committee felt that if we had to change names officially that they would like to see U (university) in our acronym. After much discussion, the Steering Committee unanimously approved a name change to ACUBE (Association of College and University Biology Educators). Many felt that the name change better reflected the membership of the organization, would be more conducive towards attracting new members, and would be easier to remember. Such an action needs to be announced twice and then voted on at the annual meeting. Hence, this is the first announcement. A near duplicate of this announcement will appear in the July issue. The final announcement will be made prior to voting at the October annual meeting.

The second item for action (besides the constitution changes suggested later in this issue) is the classification of members. Heretofore, we will recognize five types of members: regular, honorary life, graduate student, retired, and sustaining. This simply clarifies a practice that we have been observing for some time.

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## *Announcing Kimball's Biology Pages on the web*

<http://www.ultranet.com/~jkimball/BiologyPages>

Kimball's Biology Pages consist of a list of topics, arranged alphabetically, of biological terms. The terms are mostly from the areas of molecular and cellular biology, although items dealing with environmental and health questions are included as well.

Each item includes a definition, and many are linked to illustrated "mini-essays". The topics have been selected and written to be appropriate for a biology student in the introductory college course.

While this site is still under construction (and will be indefinitely), your students may find it worthwhile to examine it now. Some of the topics now available include: the cell cycle, DNA replication, antigen presentation, endocytosis, histocompatibility molecules, mitosis, meiosis, protein kinesis, transcription, translation, mutations, cellular respiration, photosynthesis, oncogenes, cytogenetics, protein structure, radiation, recombinant DNA, selector genes, transgenic animals.

I hope that you will inform your colleagues of the existence of this site, and I welcome any comments and suggestions that you or they may have. Send them to: [jkimball@ma.ultranet.com](mailto:jkimball@ma.ultranet.com)

# Proposed Constitution Changes

by  
Ann Larson

During the past year the organization has been smoothly shifting the executive secretary's duties and data from Ed Kos at Rockhust to Marc Roy at Beloit. The plan for the transition engendered last year's constitutional changes. In the process, it became apparent that the constitution had last been reviewed in the mid 1980s and that there was a need for it to be generally revisited and updated by recommendations that are presented to the membership. In this issue we present to you the routine changes in language and our reasons for them. In the issue before the fall meeting, they will be presented again in ballot form.

At the executive board meeting a subgroup reviewed the constitution, the bylaws and their appendices. The constitution is in good shape. In the By-laws, the description of the duties and terms of office are not written in a consistent manner and the appendices that present in detail the duties of each office definitely need to be updated. After a full discussion, we recommend to you that the by-laws should indicate that attendance at the meetings is expected, that positions be generally defined and that the terms of office be specified and that the executive board prepare a handbook of more detailed duties that can be updated without going through the process of amending the constitution. Below is the proposed new language of our bylaws. The changes involve: 1. defining the terms of all officers in SECTION 1 by adding the term description of the executive secretary, 2. the expectation of participation, the generalized description of primary duties and the reference to more detailed duties for each office in SECTIONS 4 - 11. Suggested changes are in italics.

## By-Laws

### ARTICLE 1. TERMS & DUTIES OF OFFICERS

SECTION 1. The term of office . . . . . *The executive secretary shall serve for a minimum of three years and a maximum of five years at the discretion of the Steering Committee.*

SECTION 3. The president-elect, *in the absence or at the request of president, shall perform all duties of the president, recommend* ....(rewritten to eliminate the "assumed" he)

SECTION 4. The first vice-president is expected to attend the executive board meetings, be the fall program chair and *fulfill duties as outlined in the Executive Board Handbook.*

SECTION 5. The second vice-president elect is expected to attend the executive board meetings and will be responsible for the program the following year and *fulfill duties as outlined in the Executive Board Handbook.*

SECTION 6. The second vice-president is expected to attend the executive board meetings, serve as the local arrangements at the host institution and *fulfill duties as outlined in the Executive Board Handbook.*

SECTION 7. The secretary is expected to attend the executive board meetings, keep minutes of the Association and Steering Committee and *fulfill duties as outlined in the Executive Board Handbook.*

SECTION 8. The executive secretary is expected to attend the executive board meetings, provide information about the state of the organization and *fulfill duties as outlined in the Executive Board Handbook.* The executive secretary is a non-voting member of the Executive Board.

SECTION 9. The past president is expected to attend the executive board meetings, *evaluate the currency of the constitution and fulfill duties as outlined in the Executive Board Handbook.*

SECTION 11. The association historian shall maintain a permanent archive of Association publications, minutes and other memorabilia. *The historian is a non-voting member of the Executive Board.*

As chair of the constitution committee, I will be contacting past officers to ask for their help in preparing the new handbook and making sure that all of our expectations can continue to be met. We hope to have a draft of the handbook ready for next fall so that past practitioners can edit it at the fall meeting. The Steering Committee would like to approve the handbook at its next spring meeting with the stipulation that it be reviewed every five years.

In addition we will be asking your permission for the Steering Committee to appoint a Web Master to maintain our Web Site as an extension of our authority to appoint a print editor of *Bioscene*. Last years addition of an Association Historian reflects our respect for our past and the addition of an Association Web Master reflects our readiness to participate in the technology of the future.

ASSOCIATION OF MIDWESTERN COLLEGE BIOLOGY TEACHERS

NAME: \_\_\_\_\_ DATE: \_\_\_\_\_  
TITLE: \_\_\_\_\_  
DEPARTMENT: \_\_\_\_\_  
INSTITUTION: \_\_\_\_\_  
STREET ADDRESS: \_\_\_\_\_  
CITY: \_\_\_\_\_ STATE: \_\_\_\_\_ ZIP CODE: \_\_\_\_\_  
ADDRESS PREFERRED FOR MAILING: \_\_\_\_\_  
CITY: \_\_\_\_\_ STATE: \_\_\_\_\_ ZIP CODE: \_\_\_\_\_  
WORK PHONE: \_\_\_\_\_ FAX NUMBER: \_\_\_\_\_  
HOME PHONE: \_\_\_\_\_ EMAIL ADDRESS: \_\_\_\_\_

MAJOR INTERESTS:

- 1. Biology
- 2. Botany
- 3. Zoology
- 4. Microbiology
- 5. Pre-professional
- 6. Teacher Education
- 7. Other \_\_\_\_\_

SUB DISCIPLINES: (Mark as many as apply)

- A. Ecology
- B. Evolution
- C. Physiology
- D. Anatomy
- E. History
- F. Philosophy
- G. Systematics
- H. Molecular
- I. Developmental
- J. Cellular
- K. Genetics
- L. Ethology
- M. Neuroscience
- N. Other \_\_\_\_\_

RESOURCE AREAS:

\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

RESEARCH AREAS:

\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

How did you find out about AMCBT? \_\_\_\_\_

Have you been a member before: \_\_\_\_\_ If so, when? \_\_\_\_\_

PLEASE MAIL  
MEMBERSHIP APPLICATION  
FORM TO:

Marc M. Roy  
Executive Secretary, AMCBT  
AMCBT Central Office  
Department of Biology  
Beloit College  
700 College Street  
Beloit WI 53511

Phone: 608-363-2429—FAX: 608-363-2052 or 2718  
email: roym@beloit.edu

CURRENT DUES ARE \$25.00  
\$15.00 for Graduate Students

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## Welcome to the AMCBT Home Page:

URL: <http://papa.indstate.edu/amcbt>



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Featuring the online AMCBT archive for:

*Bioscene: Journal of College Biology Teaching* (1975 - present)  
*AMCBT Newsletter* (1964 - 1974)  
*AMCBT Proceedings* (1957 - 1972)

Other useful AMCBT information includes:

AMCBT Executive Committee  
Editorial Board of *Bioscene*  
1997 Annual Meeting of the AMCBT  
Searchable Membership Database (coming soon)  
Online Membership Application  
Archive of the AMCBT ListServer  
Scientific Meetings of Interest to Membership  
Position Announcements  
AMCBT in the News

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The Association of Midwestern College Biology Teachers has developed its own list server to facilitate communication between its members. The purpose of the AMCBT mailing list is to provide announcements, information and discussion of a wide variety of topics.

Information mailed to:

[amcbt-l@biology.indstate.edu](mailto:amcbt-l@biology.indstate.edu)

will be sent to all members of the list.

To subscribe/unsubscribe to the list, send email to:

[list-admin@biology.indstate.edu](mailto:list-admin@biology.indstate.edu)

To subscribe, send this message line:

**subscribe amcbt**

To unsubscribe, send this message line:

**unsubscribe amcbt**

If you have any questions about AMCBT-L,  
contact Tim Mulkey at [mulkey@biology.indstate.edu](mailto:mulkey@biology.indstate.edu)