The Quaternion

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What Happened to Calculus Reform?

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Is the calculus reform movement history? Was calculus reform just a passing fad? What happened to all the calculus reform textbooks? Where have all the calculus reform conferences gone? What happened to all the funding for calculus reform? What happened to the listserves dedicated to calculus reform?

In some respects it seems calculus reform is a thing of the past.

Maybe this is because all the calculus educators are all reformed. Maybe there is no need for further calculus reform: everyone who needed to be indoctrinated with the ideas of calculus reform is fully indoctrinated, and teaching by calculus reform methods.

Maybe we have lapsed into pre-reform methods of teaching calculus. Perhaps calculus reform is something the mathematical community has tried, found wanting, and abandoned.

Perhaps we have simply moved on to something else. Modern texts have lots of technological support, from CDs to websites, all for students to work on out of class. Some of this is probably a result of the calculus reform emphasis on technology; some of this is probably fragmentary pieces of distance learning.

So were all the conferences, the money spent, the time and energy expended for naught?

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Computing With Biomolecules

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When people mention mathematical biology, our minds are usually drawn towards mathematical models such as stochastic processes, differential equations and statistical methods that are used to solve problems in genetics, population growth or epidemiology. But recently, a new direction within the intersection of mathematics and biology has been introduced. Few years ago, more precisely, in November of 1994, *Science* published an article authored by Lenard Adleman. The article reported that a small instance of the well known Hamiltonian Path Problem was solved solely by using DNA molecules and techniques from molecular biology. Although the instance solved was tiny, the potential for using DNA molecules for computing opened a field for new ideas in both mathematics and biology. DNA computing, now known as a separate field, energized the scientific minds of many molecular biologists, computer scientists, chemists, mathematicians ... .

It was a question of connecting two very well known facts, one in molecular biology and the other in mathematical recursion theory. Molecular biologists have observed that the complexity of each living being is a result of several simple biological processes (transcription, replication, recombination...) that are guided by the information that is encoded in DNA. This reminded mathematicians of the fact that every computable function can be

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Calculus Reform

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Calculus reform was a package of innovations, giving students the opportunity to work in problem-solving teams, concentrating on the ability to use concepts effectively, encouraging students to reflect on what they are learning, reducing the drudgery of rote computations by having students delegate some of it to machines, ... Much of it was controversial: it seemed to be abandoning some of the classical curriculum while watering down other areas. And yet is appeared to be a program more relevant to what the students needed.

(We say "appeared," because there hasn't been much follow-up to see what has happened to these students.)

It would be interesting to survey mathematics educators to get some answers. Lacking such a survey, we offer our perspective on what the answers would be.

For many mathematics educators at colleges and universities across the nation, calculus reform had little or no impact. This may be particularly true for university faculty where many, many students pass through calculus each year, in class sizes that are too big to try much innovation. Calculus is probably taught as it has been for decades.

At small colleges and community colleges, calculus reform is probably more evident. At these places, an entire class can meet in a computer lab, one instructor is responsible for the entire class, and class size is conducive to innovation.

These statements are probably not universally true, however. This is because the impact of calculus reform is found in the textbooks that are in use today. In fact, many of the books in use today, include to a lesser or greater extent, calculus reform ideas. These include the use of calculators to perform symbolic and numerical calculations. There are writing exercises to encourage students to write and reflect on mathematics. The triad of graphic, symbolic, and numerical presentations is encouraged. There are group exercises and projects for students to work collaboratively on. There are experiments for students to do where they can come to grips with mathematical concepts. Some books even have real-life exercises to show the applicability of calculus.

In this respect calculus reform has had a lasting impact. The new texts may not be particularly written as calculus reform texts, but most texts incorporate calculus reform ideas. But how are these texts used? Educators who attended workshops or forums on calculus reform may more fully incorporate reform ideas into their teaching than those who never paid much attention. Some of us have tried certain new methods, found some work, and found some don't. But the textbooks as a whole contain the ingredients to teach a course with calculus reform ideas.

For those of us who were engaged in the calculus reform movement several years ago, teaching calculus has probably changed. No longer is the lecture the only method of delivering calculus as in the years past. Now we may assemble students into groups on a given day. We may assign a computer project. We may go the computer lab with the class and work on the project together. We may give a writing assignment. If we do lecture, we will make sure to emphasize symbolic, numeric, and graphic representations. We may even use a graphing calculator extensively in class, or even use a CAS. In this way, the calculus reform movement has had a lasting impact.

Biomolecules

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obtained by simple operations (composition and recursion) applied to a basic set of functions (the constant zero function, the "add one" function and the identity function). This observation accounts for the appearance of many theoretical models of DNA computers capable of performing the complex computations of a universal Turing machine, i.e. computations of any electronic computer that we know.

Though there is no lack of theoretical models, the experimental verification of their feasibility is yet to be determined. Only very small instances of computational problems have been solved experimentally. But the investigations and the experiments in progress at several institutions worldwide

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are scientifically significant. They bring together scientists with deep knowledge of many different fields and it is certain that their contributions will elevate both science and technology.

The situation is familiar to mathematicians and computer scientists who work with “Turing machines,” which operate on strings of letters and “accept” words from given languages. Most of the DNA computer models use this linearity (as in strings of letters) as a main metaphor.

The information in a DNA molecule is stored in a sequence of nucleotides, also called bases. The bases are adenine (A), guanine (G), cytosine (C), and thymine (T), and sequences of bases are linked together by phosphodiester bonds into long strands. A relatively short sequence of nucleotides is called *oligo*. A single strand of DNA has also a “beginning” (usually denoted by 5’) and an “end” (denoted by 3’). Hence the molecule is oriented.

The nucleotides also tend to seek their complements (A is complementary to T and C is complementary to G). This is the well known “Watson-Crick (WC) complementarity.” Two single stranded DNA molecules with complementary sequences of nucleotides and opposite orientation join together through hydrogen bonds and form a double stranded molecule which in space appears as a double helix. When double stranded molecules are heated to 95^oC, they disentangle (denature) into single stranded molecules. If single stranded molecules are cooled, they seek their complement and re-anneal into double stranded form. These properties are used by many models of DNA computers. A four letter alphabet can be used $\{A, C, G, T\}$ (in comparison with the boolean alphabet $\{0, 1\}$ of computer models like many Turing Machines) and simple operations on the DNA strings can be performed using a few commercially available enzymes that act on the molecules in different ways.

Adleman solved a special case of the Hamiltonian Path Problem for a directed graph by generating paths using DNA molecules. Recall that a “directed graph” is a collection of points (vertices), with arcs running *from* point *to* point (see Figure 1 below).

The Hamiltonian Path Problem (HPP) asks whether in a given directed graph G there is a path from one vertex (denote it with v_{in}) to another vertex (denote it with v_{out}) that visits every other vertex exactly once. If such path exists then it is called Hamiltonian. For the example in Figure 1, v_{in} is the vertex 0 and v_{out} is the vertex 6. The graph is chosen such that there is at least one Hamiltonian path, given by the sequence of vertices 0,3,4,1,2,5,6.

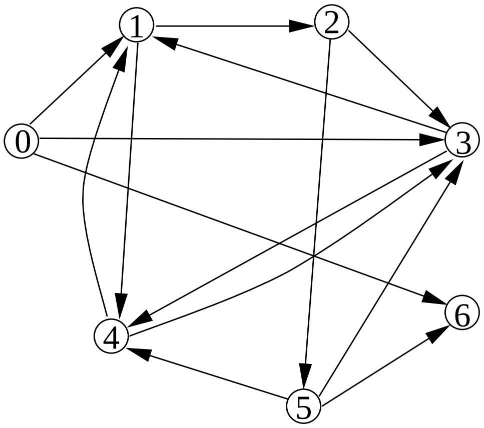

Figure 1: The Adleman’s graph.

Adleman encoded the vertices and the edges of the graph in strands of DNA. Using the WC-complementarity, in a singe mix, the strands are joined together and many new molecules are formed that represent paths in the graph (some of them being the solution of the problem). Afterwards, using several biomolecular techniques, the solution of the problem was extracted from this large mix of molecules representing paths in the graph.

The problem that was chosen for this experiment was a well known so called “NP-complete” problem that is generally “intractable” in the sense that for a relatively modest size of the graph, with any known algorithm, an impractical computer time (years or centuries) is needed for a solution. Adleman’s approach to this problem is not much dif-

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ferent then a brute force search but the use of the "massive parallelism" of DNA made it very novel. A very large number of molecules, 10^{15} or more, can be used in a single reaction and the WC-complementarity assures that in the first step of the algorithm, the sequences representing paths are formed. A very large number of them are formed, such that, if a solution to the problem exists, with a high probability it will be represented within one of the formed sequences. So the immense labor required to solve the problem was taken care of with the massive parallelism — the fact that many molecules were "working" on the problem at once — and the WC-complementarity. In his article, Adleman asserted that if we consider each DNA molecule as a computational devise, DNA based computers can bring potential savings in energy and increase in speed and storage of 10^8 fold. This was certainly one of the reasons for excitement.

Several theoretical models based on the lab protocols used in the Adleman's experiment can be found in the literature. They all use more or less the same set of operations: *merge, separate, detect, amplify*, etc., and it is feasible that they all can be executed by a robotic system. These operations can be even used to break the Data Encryption Standard (DES) code. Approximately one gram of DNA is needed and using robotic arms (assuming each operation to last one minute) breaking DES is estimated to take five days. The most significant advantage in the analysis for breaking DES is that the success is quite likely even with the (at this point unavoidable) large number of errors within the lab protocols.

The big drawback in the Adleman's approach is the need to have a very large pool of initial molecules that have to be generated in order to assure correct solution to the problem. In Figure 1, the graph has only 7 vertices. The first step of the algorithm requires approximately 2^7 distinct molecules to be generated in order to be sure that the solution (if exists) will be present in the mix. Working with over 10^{15} DNA molecules, generating 2^7 distinct molecules does not seem difficult. But for a larger graph, say a modest size of 200 vertices, one needs (as Hartmanis noted) "DNA more than the weight of the Earth". The subsequent studies have concentrated on developing algorithms such that not necessarily all of the potential solutions are constructed at once.

The field of DNA computing has already branched so that other biomolecules such as RNA and liposomes and even cells are considered as potential computational tools. Recently, the chemists at New York University constructed a molecular mechanical device attributed to the properties of B-Z (right-handed and left-handed double helix) transition of DNA. This opens a horizon for design of computational three dimensional DNA objects that can participate in biochemical processes, and at the same time perform controlled mechanical movements.

Much work remains to be done on both experimental and theoretical level. We are at the beginning of a very exiting era. Biomolecular computers are in the stage equivalent to the one that the electronic computers were in mid 30's when Turing introduced the idea of a universal computer, of which the Turing machine is the primeval example. It is impossible to say which one, or whether any of the numerous theoretical models and experimental investigations will emerge as a successful new way of computing, but the knowledge that we acquire along the way will certainly be enormous. This field has become a common platform for exchanging ideas between computer science, mathematics, molecular biology, chemistry ... . Its development is bound to change our ideas and understanding of both, computing and the biological processes in vivo.

Events Calendar

More information about upcoming events will appear at our website,

`http://www.math.usf.edu`,

as the event approaches. So mark the event on your calendar, and plan on taking part.

Professor *F. Alberto Grunbaum* of UC Berkeley will talk about **Mathematics in medical imaging: the present and the future** on Nov. 1, at 7:30 pm, in the University Lecture Hall (ULH).

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The talk will be on the mathematics, physics, and engineering that went into the development of Computerized Tomography (CAT) and other techniques like Magnetic Resonance Imaging (MRI). For more information, consult the Departmental website.

Nagle Lecture Series

Last Fall, Professor A. K. Dewdney of the University of Waterloo gave the Nagle Lecture on "Do Aliens Do Math?" The question is whether extraterrestrials might do mathematics (and science) as we understand it. This question leads to the philosophical question of whether mathematics is about "real" objects (like stars, planets, and automobiles) or about social conventions (like words, customs, and clothing fashions).

A. K. Dewdney is a Professor of Computer Science, and a longtime writer. He conducted the Mathematical Games and Computer Recreations column in the Scientific American, and has written several popular books on mathematics and computer science.

Center for Mathematical Services

The Center for Mathematical Services continues to be involved in outreach and service activities to the area counties served by the University of South Florida.

For the 23rd year, the Center conducted this past summer three programs for gifted and high-ability secondary students. Two programs were for high school students and one program was for middle school students. Faculty from the Departments of Mathematics, Biology, Chemistry, Geology, and Physics, and from the College of Engineering were involved as instructors in the programs. All programs ran for a five-week period and students were on campus each day from 9 AM until 3 PM.

The high school programs were the Mathematics and Engineering Program with 46 students and the Biomedical and Life Science Program with 37 students. Both programs had first and second-year students. Students in the Mathematics and Engineering Program learned number theory, linear algebra, C++ and Maple programming, and various topics from engineering science. Second-year students worked on individual research projects with faculty mentors in physics, mathematics, and engineering. Students in the Biomedical and Life Science Program were instructed in cellular and molecular biology and engaged in "hands - on" laboratory experiences on pre-designated topics each afternoon. Second-year and third-year students obtained research experience by working in the laboratories each day of individual research faculty from the College of Arts and Sciences at USF.

The program for the middle school students was the Mathematics and Science Program. It had 95 students, primarily from Hillsborough County. The students received instruction in HTML and JavaScript computer programming, basic foundations of mathematics, geology, and environmental issues. The environmental portion of the program was accomplished using the facilities and staff of the Museum of Science and Industry.

The Center is planning on conducting similar programs during the summer of 2002.

Information about activities of the Center can be obtained by calling (813) 974-4068.

Faculty News

Two mathematics faculty are leaving USF.

Anton Kaul arrived here last Fall. He received his Ph.D. from Oregon State University, and works in geometric group theory and low-dimensional topology. He is departing to go to Tufts University, and we wish him well on his further adventures.

Ed Saff arrived at USF in 1969, one year after getting a Ph.D. from the University of Maryland. He was tenured in 1974, promoted to Professor in 1976, and then to Distinguished Research Professor (now University Professor) in 1986. He is one of the world leaders in approximation theory, and he also does work in potential theory, complex analysis, and numerical analysis. He is the longstanding editor-in-chief of *Constructive Approximation*, one of the world's most influential mathematics

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journals, and Director of the USF Institute for Constructive Mathematics. He has had ten doctoral students, produced seventeen books (monographs, texts and anthologies), and nearly two hundred papers. In addition to other service, he sits on the editorial boards of two journals and a book series, and he has been Director of the USF Center for Mathematical Services. He is going to Vanderbilt University, and we wish him well on his further adventures.

We welcome the arrival of three new faculty.

Brian Curtin works in algebraic combinatorics, in particular Bose-Mesner and planar algebras, emphasizing graph theory, self-duality, and spin models. He received his Ph.D. from the University of Wisconsin, Madison, in 1996. Since then he has been a postdoctoral fellow in Japan and, under NSF auspices, at UC Berkeley. We welcome him to USF.

Wenxiu Ma works in differential equations, mathematical physics, and symbolic computation. He received his his Ph.D. from the Academia Sinica (Beijing), in China, in 1990. Since then he has worked in several positions in China, Europe, and North America, and he has accumulated a number of honors on the way. He will be arriving for the Spring semester, and we welcome him to USF.

Saralees Nadarajah is a statistician who works in distribution theory, experimental design, extreme value theory and environmental modeling, numerical analysis for branching processes, sampling theory, and simulation techniques. He received his Ph.D. from the University of Sheffield, in the United Kingdom, in 1994. Since then he has worked in England (especially at the Universities of Sheffield and Plymouth), with brief interludes at California and New Zealand. We welcome him to USF.

Other News

Ken Pothoven and **Fred Zerla** organized th 34th Meeting of the Florida Section of the Mathematics Association of America, which met jointly with the Florida Two-Year College Mathematics Association (FTYCMA) at Florida Gulf Coast University last March. There were two workshops, a plenary talk by Barry Cipra, and 37 contributed talks.

The 7th annual meeting on DNA Based Computers was held here at USF this June. This conference on “biomolecular computing” draws together molecular biology, chemistry, computer science, and mathematics. The invited plenary speakers were from UC Berkeley, Yale, Georgia Tech and Brown University. Topics covered included the structure of DNA, constructing DNA-based computers, molecular-level behavior of DNA computation, applications, and related issues. The main organizer was **Natasha Jonoska**.

The conference was preceded by a day of tutorials. The conference had four invited plenary speakers were from UC Berkeley, Yale, Georgia Tech and Brown University, and 27 additional presentations. About 100 people attended the conference.

Student News

We congratulate the students who received the Bachelor’s degree in Mathematics this past year.

In Summer, 2000: Toby Mitchell Clark; Nairouz El Geioushi; David Michael Hill; Sara Elizabeth Kinzel; Cynthia Lee Lozano; David Michael Odum; David Mathew Rosenberg (summa cum laude); Stephen Michael Searce.

In Fall, 2000: Patricia Laura Henjum (cum laude); Amy Priscilla Yarbrough.

In Spring, 2001: Ismael Dario Aldama-Apodaca; Thomas Dean Bronson; Rhonda Sue Riddle Carswell; Brian Douglas Cupp; Joseph Edward Farrell; Ayodele Genevieve Gilpin; Suzanne Heather Gosch (summa cum laude); Janine Marie Mattson; Michael Sean McBride (magna cum laude); Patrick Allen McClain; Chad J. Smudde (magna cum laude); Paul A. Tanner; Kevin P. Wagner (summa cum laude); Victoria Pace Wood (magna cum laude); Cheryl Ann Scilex (INM).

We congratulate the students who received the Master’s degree in Mathematics this past year: Louis Camara; Zhao Chen; Edgardo Cureg; Stephen Drier; Ann Gauntlett; David Kephart; Kalpana Mahalingham; Deborah Nelson, thesis:

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Beans and Pots (advisor: McColm); Jost Thais, thesis: Newton's Method of Cubic Polynomials (advisor: Oberste-Vorth); Kevin Wagner.

And we congratulate the students who received the Ph.D. in mathematics this past year: David Benko, *Approximation by Weighted Polynomials* (advisor: Vilmos Totik); Ming Dai, *Identification of the Parameters of a Multivariate Normal Distribution by the Distribution of Maximum* (advisor: Arun Mukherjea); Daniel Jelsovsky, *Quandle Cohomology and State-sum Invariants of Knots* (advisor: Masahico Saito); Victor Maymeskul, *On Some Problems in Complex and Multivariate Approximation and Interpolation* (advisor: Ed Saff); Henry Roberts, *Predicting The Performance of Software VIA The Power Law Process* (advisor: Chris Tsokos); George Yanev, *Statistical modeling of Epidemic Disease Propagation via Branching Processes and Bayesian Inference* (advisor: Chris Tsokos).

Student Clubs

A9+, the Mathematics Honor Society, and the USF Student Chapter of the MAA again combined to present a varied program for mathematics students. The year began with the traditional A9+ Presidential Address as *Kathleen Mierau*, Chapter President for the second year, discussed "Trends in the Distribution of Wealth and other Applications of Calculus to Economics." To continue our tradition of introducing new Mathematics faculty members to our members, the guest speaker at our second meeting was Dr. Mohamed Elhamdadi, who discussed some interests from his graduate days in a talk on "A Certain Set of Functional Equations." To help our students prepare for life after graduation, Larry English of the USF Career Center told about things we can do now to ease the transition in "Pre-graduation Opportunities for Mathematics People." *Victoria Wood*, senior mathematics major at USF, discussed other opportunities for undergraduates when she told of her participation in the Summer Undergraduate Research Institute at Miami of Ohio in the summer of 2000. The clubs participated in *Fantastic Friday*, a program for prospective students, and Honors Week Patio when we told USF students about ourselves. **Pi Mu Epsilon** also hosted approximately 300 students and teachers from county public highs schools at the Spring Hillsborough County Math Bowl in the Special Events Center. *Cynthia Gomez Martin*, President of the USF Student Chapter of the MAA, told of her work in "Statistical Analysis using Statistical Analysis Software (SAS)." *Bonnie Bussman Peters* discussed her experiences as an actuary. Bonnie, who graduated from USF with a double major in Mathematics and Physics then returned to obtain a Masters in Physics, is an actuary for the Aegon Group. She spoke to us last year and, this year, her company asked her to return to try to persuade USF students to consider a career in Actuarial Science.

This year saw a surplus of riches as Pi Mu Epsilon selected two seniors as Outstanding Scholars for the year. *Aaron Anderson*, the first of our mathematical co-valedictorians, told of his honors project, "Aspects of the Mean Value Theorem." The second of the pair, *Suzanne Gosch*, presented her honors thesis, "Gender Differences in Education (with an emphasis toward mathematics)." The year closed with the Pi Mu Epsilon Induction Banquet celebrating our Coral & Jade (35th) Anniversary as a chapter. Twelve students were welcomed into Pi Mu Epsilon for the year: James P.S. Ascher, Nathan N. Chau, Brian Douglas Cupp, Adam William Francis, James Hearl, Samuel A. Gibson, Kimberly M. Janowiak, Karol Mason McIntosh, Ryan C. Parrish, Wendy A. Pogoda, George W. Stewart, Yousef Yassin Turshani. Dr. Brian Space of the Department of Chemistry told of some interesting things he encountered in his work in "Quantum Shape Shifters: The Collision of Mathematics, Chemistry, and Reality." And *Ryan C. Parrish* won the Mathematics Scholarship this year.