



Courant Institute of Mathematical Sciences

Newly Established Peter D. Lax and Charles M. Newman Fellowships

The first recipients, for the 2008-09 academic year, were announced recently.



The Peter D. Lax Fellowship has been established by a generous gift from the Peter and Anneli Lax Foundation to support exceptional students. **Miranda Holmes**, who is advised by Oliver Buhler, has been named the first recipient. Miranda's background in mathematics and physics is highly relevant for her interdisciplinary research on internal wave breaking in the deep ocean; such wave breaking is crucial for ocean circulation and climate evolution.

Miranda also has a longstanding interest in outreach activities, epitomized by her founding cSplash, a now annual one-day festival of Mathematics and Computer Science classes held at the Courant Institute.



The Charles M. Newman Fellowship has been established through a generous gift from Marshall and Marilyn Butler in honor of Chuck Newman's mathematical achievements. The Fellowship--given to an outstanding Courant student--was awarded for the first time this year to **Felix Krahmer**, who is advised by Percy Deift and Sinan Gunturk. His thesis project concerns the asymptotic theory of coarse quantization, and draws on harmonic analysis, and the theory of orthogonal polynomials. He too has been an energetic contributor to the broader life of the Courant Institute, having been a co-organizer of the Graduate Student and Postdoc Seminar, and also involved in the running of cSplash.

Faculty Awards and Distinctions



Bud Mishra and Amir Pnueli named ACM Fellows. Mishra for his "contributions to symbolic computation and computational biology" and Pnueli for his seminal work introducing temporal logic into computing science and the development of the temporal methodology for the specification, verification, and synthesis of reactive systems.



Bob Kohn receives the Keith Medal Research Prize. Kohn has received the Prize for his co-authorship of the paper "A compactness result in the gradient theory of phase transitions." The paper "presents a proof of a result in the calculus of variations" and is described as "a model of elegance and clarity."



Chuck Newman elected into Brazilian Academy of Sciences. Its primary objective is to contribute to "the advancement of science and technology, education and the social well being of the country." Newman's work in recent years on highly disordered models, on a novel metastate approach and on flaws in Parisi's replica-symmetry-breaking approach has re-energized the study of Edwards-Anderson spin glasses.



John Rinzel receives an Aisenstadt Chair. Rinzel received the Andre-Aisenstadt Chair during the theme semester (Fall, 2007) on Applied Dynamical Systems at the Center for Research Mathematics at McGill University. Rinzel was recognized for his research over the past decades in several areas of mathematical neuroscience. Rinzel's Aisensteadt lecture, "Dynamics of Visual Perception," was on alterations of perception when one views some ambiguous scenes, such as the Necker cube.



Zvi Kadem named IEEE Fellow for developing algorithms and systems that create a high-performance reliable parallel machine (a virtual "perfect" parallel computer) using a distributed collection of potentially unreliable computers (unreliable due to crashes, slowdowns, etc.).



AMS Elections for Sylvain Cappell. Cappell has chaired various national committees for the AMS and has been involved in helping plan its various mathematical research, outreach and educational activities. He was elected by the membership to its Council and subsequently by the Council to the Executive Committee of the AMS. Cappell has also been reelected by acclamation to a second term as Chair of NYU's Faculty Senators Council.



Amir Pnueli Receives ACM Software System Award along with other developers of the "Statemate Software Development System," a system completed twenty years ago which is now being recognized. The tool "enables designers to specify, then test and execute the required interactions among system elements, allowing costly errors to be detected early in the design process."

Inside This Issue:	
Mike Shelley.....	2
Puzzle.....	2
Charles Peskin.....	3
Donor List.....	4
Shasha and Bonneau....	5
Student Prize Winners..	6
Spring Events.....	6

Mike Shelley: A Very Fluid Individual

By M.L. Ball

Every seven years or so, Professor Mike Shelley changes fields to keep himself excited about something new. Currently a Professor of Mathematics and Neural Science, the Lilian and George Lyttle Professor of Applied Mathematics, and Co-Director of NYU's Applied Mathematics Laboratory, what excites him now are problems involving complex fluids, in particular biofluid dynamics.

"My interest these days lies in biofluids, things that move around in fluids, and fluids that move themselves," explains Shelley. "Right now I'm trying to understand the dynamics of active suspensions, which are fluids filled with particles that move around. Bacterial baths are an example.

"Basically, bacteria swim around in the fluid, and in so doing press against each other through the fluid. When there are millions of bacteria doing this, pushing at each other through fluid, the fluid can organize the whole motion. It has been observed in experiments that this creates large-scale vortices and jets that mix the fluid together across large scales. Perhaps this is one way that groups of organisms stay alive, as a result of their joint action which mixes nutrients through the whole population.

"My current work aims to turn this system of fluid mixing into mathematical problems, and to describe mathematically how such a system evolves over time. And we have done this, by studying the behavior of detailed models of swimmers, and also deriving what are called kinetic theories that describe these systems as a complex continuum fluid."

Of particular interest to Prof. Shelley is how the swimmers influence these large-scale mixing flows. "It turns out that our models say that the way in which an organism locomotes itself determines whether a large-scale mixing flow is occurring," he explains. "An organism that locomotes by pushing from behind rather than pulling from the front works better, similar to rear-wheel drive."

According to Shelley, the field of biophysics is very active right now. "There is a lot of experimentation going on," he

says, "lots of data analysis using sophisticated video imaging, which is what you need for modeling."

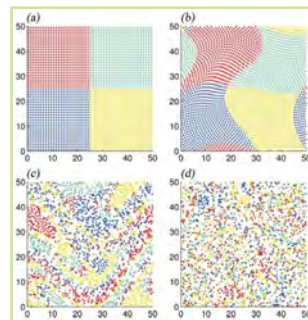
Going beyond the lab and the computer, a possible real-world application of Shelley's current work is bioremediation. "In ground water, contamination occurs when water is trapped in rock or soil. Chemical plumes move into porous rock and enter drinking water," he explains. "Bacteria can eat contaminants and convert them or contain them. Certainly population behaviors are important for understanding how well this works in practice."

Prof. Shelley's other area of research concerns the new technology of microfluidics, which concerns the motion of fluids in small volumes and in complicated spaces. Again, mixing has attracted his attention. "I'm looking at how fluids can move independently into a chamber, and then be mixed together."

"There are two ways to get a reagent and a sample to mix" Shelley adds. "The first is diffusion. Think of putting a drop of dye into a bowl of water. The dye will eventually spread itself evenly throughout the fluid but it's a slow process.

"The other method is to mix the two agents together mechanically. One interesting way to do this is via an active suspension. Penn State researchers have fabricated motile nanorods, which are bimetallic rods put into a chemical bath. The rods react with the fluid they're in, which causes them to locomote as if they're bacteria. So perhaps these rods can mix the whole thing up.

As someone who likes ebb and flow in his professional life rather than a static existence, it makes perfect sense that what now holds Mike Shelley's attention are fluids, locomotion, and movement – much like life itself.



Initially segregated regions of colored particles, moved passively by the flow generated by the locomotors, are mixed together.

From Saintillan & Shelley 2008.

Spring/Summer Puzzle – Protein Chime

By Dennis Shasha, Professor of Computer Science

In the 1950s Jacques Monod and Francois Jacob of the Pasteur Institute showed that certain regulator proteins in *E. Coli* bacteria can repress the production of other proteins. For this puzzle, let's write $X \Rightarrow Y$ to mean that protein X represses protein Y . If X goes up (that is, the protein appears), then Y will go down (the protein disappears) after a short time (say, one second). If X goes down and no other repressor for Y is up, then Y will go up one second after X goes down.

Now consider three proteins A , B and C such that $A \Rightarrow B \Rightarrow C \Rightarrow A$.

If A goes up, B goes down one second later. After another second, C goes up, and after one more second A goes back down. Then the pattern continues: B up, C down, A up, B down and so on. We call this a circuit of proteins: A , B and C periodically appear and disappear, acting like a biochemical clock. Researchers Michael Elowitz and his advisor Stanislas Leibler from Princeton have actually constructed such a clock. They used an odd number of proteins in each circuit because any even-numbered circuit could be stable: half the proteins would stay up all the time and half would stay down.

To start a circuit cycling predictably it can be forced. In the above example you might choose to force B up for 3 seconds. One second after the forcing begins, C would go down; 2 seconds after, A goes up. But B would go down only after 4 seconds, i.e. one second after the forcing of B ends. Thereafter the circuit cycles in the normal way: C goes up after 5 seconds, A goes down after 6 seconds, B up after 7 seconds, etc.

(i) Your task is to create a "protein chime" that will ring every 70 seconds. There are eight circuits, labeled A through H , each containing three, five, seven, or nine proteins (shown below). Proteins in different circuits have no effect on each other. But one protein in each circuit represses T , the special chiming protein that rings when it goes up. If any of these eight repressor proteins (labeled $A1$ through $H1$) goes up, T will go down one second later. And T will not go back up until one second after all eight of the repressor proteins are down. You may choose to include or exclude any of these circuits.

To ring the T chime every 70 seconds, you will need only four of the eight circuits. (The excluded circuits have no effect on T .) Your challenge is to determine which circuits to activate and how to start each one: which protein in each circuit must be forced up and for how long? You may force a protein for up to 15 seconds; after that, the chime must operate on its own.

(ii) For each k , $1 \leq k \leq 70$, create a chime that rings at times $t = k \bmod 70$. There may be an initial period in which there is no chime ring. Again, you may use only 4 circuits.

Circuit A: $A1 \Rightarrow A2 \Rightarrow A3 \Rightarrow A1$

Circuit B: $B1 \Rightarrow B2 \Rightarrow B3 \Rightarrow B1$

Circuit C: $C1 \Rightarrow C2 \Rightarrow C3 \Rightarrow C4 \Rightarrow C5 \Rightarrow C1$

Circuit D: $D1 \Rightarrow D2 \Rightarrow D3 \Rightarrow D4 \Rightarrow D5 \Rightarrow D1$

Circuit E: $E1 \Rightarrow E2 \Rightarrow E3 \Rightarrow E4 \Rightarrow E5 \Rightarrow E6 \Rightarrow E7 \Rightarrow E1$

Circuit F: $F1 \Rightarrow F2 \Rightarrow F3 \Rightarrow F4 \Rightarrow F5 \Rightarrow F6 \Rightarrow F7 \Rightarrow F1$

Circuit G: $G1 \Rightarrow G2 \Rightarrow G3 \Rightarrow G4 \Rightarrow G5 \Rightarrow G6 \Rightarrow G7 \Rightarrow G8 \Rightarrow G9 \Rightarrow G1$

Circuit H: $H1 \Rightarrow H2 \Rightarrow H3 \Rightarrow H4 \Rightarrow H5 \Rightarrow H6 \Rightarrow H7 \Rightarrow H8 \Rightarrow H9 \Rightarrow H1$

$A1 \Rightarrow T; B1 \Rightarrow T; C1 \Rightarrow T; D1 \Rightarrow T; E1 \Rightarrow T; F1 \Rightarrow T; G1 \Rightarrow T; H1 \Rightarrow T$

For the solution, email courant.alumni@nyu.edu

Charles Peskin: At the Heart of Major Advances

By M.L. Ball

It's been quite a few years since Professor Charles Peskin visited the 14th Street meat market, bought a beef heart, and brought it into his mathematics cardiology class to dissect it.

But after 35 years at the Courant Institute, the heart and all its intricate functions, known and unknown, still fascinate him. Along with Professor David McQueen and post-doc Boyce Griffith, plus graduate student Paul Hand, Professor Peskin heads up Courant's team of experts working on the heart.

According to Professor Peskin, "The latest thing we've done – actually David McQueen is the main person who did this – is to construct an anatomically correct heart model based on real data, namely computed from tomography scans. I developed a theory of how the fibers of the heart ought to be laid out and it compares well with the heart's true anatomy. We've just completed it but only in the anatomical sense; that is, we still have to endow it with the right physiological properties and get it to beat."

David McQueen adds, "When we started out, we expected it to take a couple of months, but it turned out to be trickier than we thought. We had previously constructed a model heart in which muscle layers in the heart wall were represented in a highly idealized way as the surfaces of cones. The muscle fibers, geodesics on these surfaces, are very well behaved and presented relatively few surprises. Our new model heart uses surfaces which come from actual measurements on a person. These surfaces are much less smooth than the cones we were familiar with, and getting geodesics to cover them in a reasonable way took a little longer than we expected."

What's most exciting about this development is its application in the field of cardiology, which has enormous potential. "Sometime in the future," Professor McQueen explains, "we'll have a model that can be customizable to a particular person. So when a person gets an MRI scan, we would then construct a model of that person's heart and adjust it so that it acts like it has the same disease. We'd make interventions in the model so that we could go back to the physician and show him what we think will happen after a particular treatment. So this will be vital input in helping a physician or surgeon decide what to do."

Another recent accomplishment is largely the work of Boyce Griffith, one of Professor Peskin's former students and now a post-doc, supported by the American Heart Association. "He's done a lot of important things, so my recent progress is really his recent progress," Peskin explains. "One of these is making adaptive computational methods. Previously, we used a uniform grid for the computations, so the fluid was represented in the computer using a uniform 3-d grid. The problem with this kind of grid is that if you have to refine it for more resolution, it

gets very expensive in a hurry. One strategy is to do local refinement, to refine the grid where you need to, which is called adaptive mesh refinement. This is one of the things Griffith is doing."

Capitalizing on connections within the Courant Institute, Professor Peskin is using the style of adaptive mesh refinement invented by Marsha Berger, a Professor of Computer Science at Courant. "She invented the basic methodology that we're adapting to the heart," he says.

Professor Peskin's other recent advance (also with Griffith) is in the physiological realm, specifically the electrophysiology of the heart. He explains that in the right atrium is a region called the pacemaker, which has spontaneous electrical activity. All by themselves, these cells generate waves of activity like a clock generates ticks, telling the heart to contract and then relax. "What we're doing now is modeling that electrical activity, which allows us to create a more complete model of the heart – not only anatomically and mechanically complete but also electrically complete. We're working closely on this with Dr. Glenn

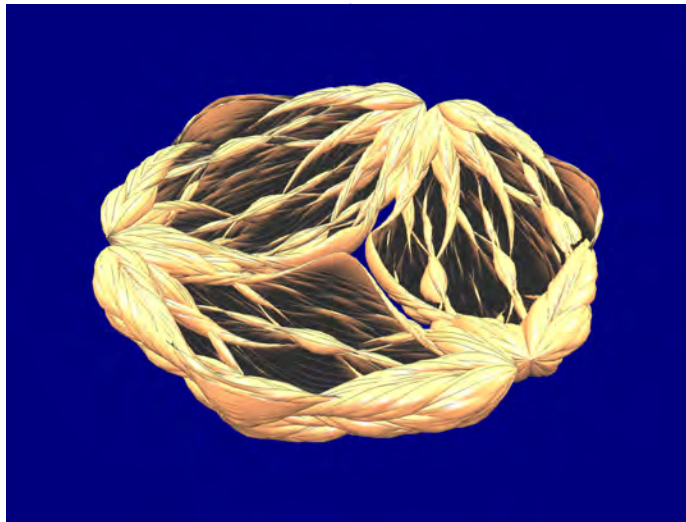
Fishman, the head of Cardiology at NYU Medical Center."

Particularly pleasing to Professor Peskin is the fact that "the way we do the mechanics is a method I originally introduced years ago in my Ph.D. thesis, called the immersed boundary method which deals with fibers in fluid. A combined electrical and mechanical computation is under development now, and they are both based on the immersed boundary method. So it's being used now for more and more things, which makes me very happy," he says with a broad grin.

Not bad for someone who doesn't even have a math degree; his is in physiology. Professor Peskin is grateful to Courant's math community for taking him in when he was just starting out, and for appreciating his work from the beginning. "No other math department would have hired me," he confesses. "It really is remarkable."

Asked for his thoughts on Courant, he answers without hesitation, "It's the best. Especially from this point of view, we're the best in the world. No question. Because we're serious about the applications, whether it's climate change, weather prediction, plasma physics, fluid mechanics, materials science, nanotechnology, electromagnetics, neuroscience, genomics, systems biology, biomolecular motors, insect flight, medical imaging, or heart physiology, to name just some of what goes on here on any given day."

He continues, "This is a remarkable place, encapsulated in the name: Mathematical Sciences. It's not the Courant Institute of Mathematics; there's a point to that name, which takes a broad view of math as blending into the sciences. That's an extremely valuable feature of this place that needs to be preserved."



The figure shows the numerical solution of a partial differential equation for the mechanical equilibrium of the closed valve. The complexity of the computed solution is a consequence of a singularity located at the center of the valve, where its three leaflets meet. If this singularity is not mollified, the model valve has a fractal dimension of about 2.2, as determined by Julie Stern who used a recursive box-counting procedure.

Computer model of the aortic valve, by David M. McQueen and Charles S. Peskin.

The Courant Institute recognizes with gratitude the following alumni, faculty, and friends who have made gifts for Academic Year 2007-2008:

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			above.

The Power of Two: Shasha and Bonneau

By M.L. Ball

Dennis Shasha, Professor of Computer Science, and Rich Bonneau, joint Assistant Professor of Computer Science and Biology, have joined forces to unlock the secrets of protein docking. According to Dennis, “Docking is the problem of determining how proteins physically connect. It can be one protein embracing another copy of itself or two different proteins embracing one another. Given two protein forms that aren’t embracing, what we’re trying to figure out is how they’re going to change their shape and where they’re going to touch.

“People in the group that Rich comes from (the so-called Rosetta commons) have built a docking program which can answer this problem but it’s very expensive computationally. So the question is, can one do this much faster? We don’t have an answer yet but we’ve gotten some promising preliminary results with protein ‘speed dating.’ The idea here is that maybe we can create candidate dock positions and evaluate them quickly. There are many, many possible embraces – billions probably – so we’d like to create 100 possible near-embraces and then evaluate them rapidly. If one of them is right, we can vastly cut down on the time it would take to figure out what the best docking will look like.”

Rich illuminated some of the groundbreaking applications their research could generate. “If with speed dating you could quickly create confident models of how things are going to interact, then you could do things like examine an interaction, snip out part of it, redesign it on the computer, and make it into a drug. Eventually, this might become a way of diagnosing or treating some disease which was initiated by this interaction.”

When one speaks with them, it’s striking how warmly they speak of each other. Rich says he met Dennis several years ago when he came to NYU to speak on protein folding.

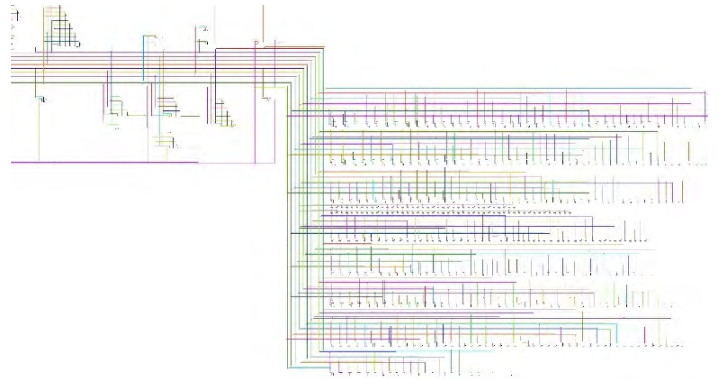
Dennis explained, “To a large extent Rich has solved this problem in the sense that he can predict how proteins will fold, based on pattern matching. Other people would like to predict based on pure physics but pattern matching works really well. This was a huge breakthrough, and he was only a second-year graduate student.”

Rich added, “Dennis was one of the nicest people I interviewed with, and he convinced me there was a lot of potential for collaboration here at NYU. So he was one of the people instrumental in bringing me to Courant.”

In true collaborative fashion, both Dennis and Rich agreed that Courant is “an awesome place.” Dennis said, “The fact that computer science is so physically close to the biology labs is very important. Also, it’s key that Courant is in New York because a lot of people come through here very easily, from across the country and around the world.”

Although a large part of their time is spent working together, both Dennis and Rich have accomplished amazing things alone. For five years, Dennis has been introducing computer science to the realm of biology, specifically plant biology, working with Gloria Coruzzi, Chair of NYU’s Biology Department. He helps her design experiments and then determines further experiments to design based on the results.

And although relatively young, Rich caught the world’s attention with his work on complete characterization on an extremeophilic archaea, which appears as the cover story of the December 28th edition of the journal *Cell* and is the subject of a recent *Wired* article. Rich explained, “My team was one of the first to do a functional genomics project on



Part of the circuit diagram for *Halobacterium* (a halophilic archaea). Colored lines indicate regulatory influences of transcription factors and environmental parameters on the rate of each gene or cluster of genes in this organism. Each gene or cluster of genes is represented as a horizontal line with a large arrow indicating the output (or rate of synthesis of that gene). The lines leading into the gene are the regulatory influences, which are modeled as an ordinary differential equation. This picture represents a subset of the ~500 ODEs that make up our global model of this organism's regulatory circuit (500 equations with 1,500 couplings). So the mess at the top left is a network with cycles and complex behaviors (the interesting part of the circuit) and the lower right is the read out (cell processes that do not directly control the levels of other genes, do not have transcription factors in their gene clusters: levels of metabolic enzymes, cell wall proteins, DNA repair, etc.)

the archaea; it is important to explore this domain of life.

It’s really similar to what Dennis is doing with Gloria except it’s on a different system; from a computational perspective, there are a lot of similarities in terms of the methods. You measure the genes going up and down and then have to reconstruct how they’re connected in a causal network, but it’s much harder to do in plants than in bacteria.

“This is because it’s hard to see what a single plant cell is doing; separating the cells from each other adds a whole other layer to the experiment that adds time and money, and you have to be very, very skilled in order to do it properly.” He added, “Cells have really complex networks and reactions, and this system hasn’t been designed, it’s evolved. Even the simplest organisms on the planet have evolved really advanced interconnected networks where, if you put a bunch of things in, they rattle around and produce some output. With systems biology, we can reconstruct some of that decision network. That’s the aim of what we’re doing now – we want to make this less of a black box.”

Dennis likened the goal of their research to how one can figure out the function of an electronic circuit. “You can probe it, measure the current and the voltage, and at any point, adjust the inputs, learn what the circuit does, and adjust its output. We would like to be at that stage for biology. We’re far from that because first of all, the measurements are hard to make; electronic circuits tend to be more discrete because typically the represented values are ones and zeros, so you don’t need to get the exact voltages. Cell biology depends on continuous values, so even small differences in one place could cause a large difference in another and we might not be able to measure the first causal small difference. But that would be the goal.

“And what would that give us? In the case of plants, it could allow people to grow plants that require less fertilizer or less water. Bacteria could be engineered to perform bioremediation or synthesis of complex molecules, such as drugs. In the end mankind relies on living systems for carrying out countless processes ... so these sorts of general methods will support a great many applications.

“We love these kinds of problems because they are important, multiple technologies are arising concurrently that give us the means to solve them, and we love the challenge.”

2008 Courant Institute Student Prizes

This year’s ceremony, held April 18th, recognized 15 students. Congratulations to the winners:

Henning Biermann Award – Ameet Talwalkar
Sandra Bleistein Prize –

Lyubov Chumakova and Raia Hadsell

Hollis Cooley Prize – Sinziana Picu

Janet Fabri Prize – Michael Freedman

Kurt O. Friedrichs Prize – Martin Raphan

Harold Grad Memorial Prize –

Yotam Gingold and Felix Krahmer

Moses A. Greenfield Research Award –

Fred Laliberté and Samuel Stechmann

Wilhelm Magnus Memorial Prize –

Emmanuel Schertzer and Atilla Yilmaz

Bella Manel Prize – Miranda Holmes

Matthew Smosna Prize –

Tadashi Hirata and Farhan Shamsi

Spring ‘08 Events at the Courant Institute

This March, Professor Jon Kleinberg of Cornell University gave the Courant Lectures on the interdisciplinary issue of social and information networks, with special attention to privacy, information flow, and power imbalances in economic exchange and social interaction more generally.

The AMS held its Spring 2008 special session in honor of Sylvain Cappell’s sixtieth birthday, and focused on “Singularities in Geometry and Topology.” The event was funded in part through a generous gift from Dr. Henry Laufer. Frank Hoppensteadt’s seventieth birthday was celebrated with a conference on “Dynamical Systems in Biology,” and was funded in part through a generous gift from The Swartz Foundation.

The 5th IACR Theory of Cryptography Conference met to explore “the paradigms, approaches and techniques used to conceptualize, define and provide solutions to natural cryptographic problems.”

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