

THURSDAY
SEPTEMBER 22, 2005

Scaife Hall Auditorium
Room 125

4:00 PM
Refreshments—3:30 PM



CLAIRE TOMLIN

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Claire J. Tomlin is an Associate Professor in the Department of Electrical Engineering and Computer Sciences at the University of California at Berkeley, and an Associate Professor in the Department of Aeronautics and Astronautics at Stanford University. She received a Ph.D. in Electrical Engineering from the University of California at Berkeley in 1998, joined Stanford in September 1998 as a Terman Assistant Professor, and received tenure at Stanford in November 2004. In July 2005, she joined Berkeley as an Associate Professor. She received the M.Sc. from Imperial College, London, in 1993, and the B.A.Sc. from the University of Waterloo, Canada, in 1992, both in Electrical Engineering. She has held visiting research positions at NASA Ames, Honeywell Labs, and the University of British Columbia. Claire Tomlin is a recipient of the Eckman Award of the American Automatic Control Council (2003), MIT Technology Review's Top 100 Young Innovators Award (2003), the AIAA Outstanding Teacher Award (2001), an NSF Career Award (1999), and the Bernard Friedman Memorial Prize in Applied Mathematics (1998). Her research interests are in control systems, specifically hybrid control theory, and she works on air traffic control automation, flight management system analysis and design, and modeling and analysis of biological cell networks.

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For more information:
<http://www.ece.cmu.edu/seminar>

USING MATHEMATICAL MODELING TO HELP DECODE BIOLOGICAL CIRCUITS

In this talk, methods that we have designed to analyze and help to identify certain protein regulatory networks will be presented. Hybrid automata are a suitable modeling framework, as the protein concentration dynamics inside each cell are modeled using linear differential equations; inputs activate or deactivate these continuous dynamics through discrete switches, which themselves are controlled by protein concentrations reaching given thresholds. We present an iterative refinement algorithm for computing discrete abstractions of a class of symbolic hybrid automata, and we apply this algorithm to a model of multiple cell Delta-Notch protein signaling. The results are analyzed to show that novel, non-intuitive, and biologically interesting properties can be deduced from the computation, thus demonstrating that mathematical modeling which extrapolates from existing information and underlying principles can be successful in increasing understanding of some biological systems. However, more often, only incomplete abstracted hypotheses exist to explain observed complex patterning and functions in cellular regulatory networks.

We conclude with our recent results in developing a mathematical model for Planar Cell Polarity signaling in fly wings, explicitly demonstrating that the model can explain the complex behaviors of the system. This is joint work with Keith Amonlirdviman and Ronojoy Ghosh, and Professor Jeff Axelrod of the Stanford University School of Medicine.