



Biomathematics Career Initiative

State University of New York, College at Geneseo



Tony Macula, Gregg Hartvigsen, Wendy Pogozeleski, Chris Leary

The Undergraduate Biomathematical Research Career Initiative at SUNY Geneseo supports the continuing research and curricular commitment of sixteen students across two related research programs. The project builds upon current strengths of the undergraduate program at Geneseo and the expertise of the four co-PI's. We have a large number of students that have already participated in the program directly (see panel on right) as well as many others who have participated in various biomathematics activities (e.g., travel to local and regional meetings). Most notably we have been able to dramatically increase the number of students conducting research at the intersection of the two fields.

The two major research areas (DNA hybridization technologies and network analysis in ecological and epidemiological systems) are fields that share several characteristics that make them ideal for a UMB proposal. They are both active fields at the cutting edge of research. The amount of work being done in these areas is large and there are many important questions that are both accessible and exciting to undergraduates. Although the program is young our it has resulted in students gaining employment and graduate school placements in the field of biomathematics. We also currently have several first-year students who have been identified early and, because of this program, are working toward dual-majoring in mathematics and biology.

Publications

Wendy K. Pogozeleski, Matthew P. Bernard, Salvatore F. Priore, and Anthony J. Macula, Experimental validation of DNA sequences for DNA computing: Use of a SYBR green I assay, DNA 11, Springer Lecture Notes in Computer Science, to appear.

Christina Callear, Niels Hanson, G. Hartvigsen, A. Macula, Group testing to annihilate complexes, submitted, Journal Statistical Planning and Inference Special Issue on Metaheuristics, Combinatorial Optimization and Design of Experiments.

Hartvigsen, G., J.M. Dresch, A.L. Zielinski, A.J. Macula, and C.C. Leary. Network structure, population size, and vaccination strategy and effort interact to affect the dynamics of influenza epidemics. Accepted, pending revisions, to Journal of Theoretical Biology.

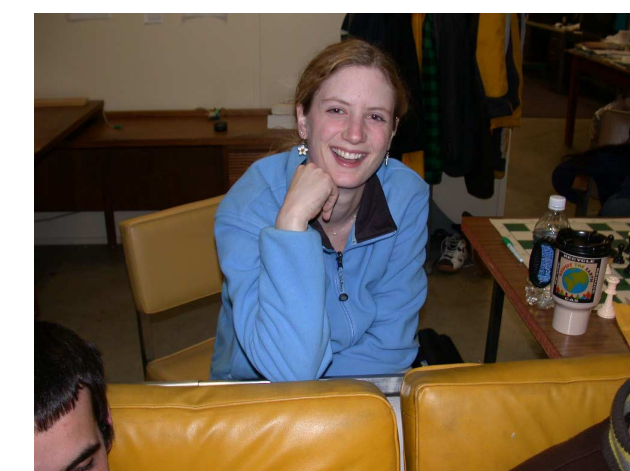
Dresch, J.M., N. Hansen, G. Hartvigsen, C. Leary, and A. Macula. Component Averages in Circulant-like Graphs. In review at Bulletin of the Institute for Combinatorics.

Conferences Participated in by Students in the Biomathematics Program:

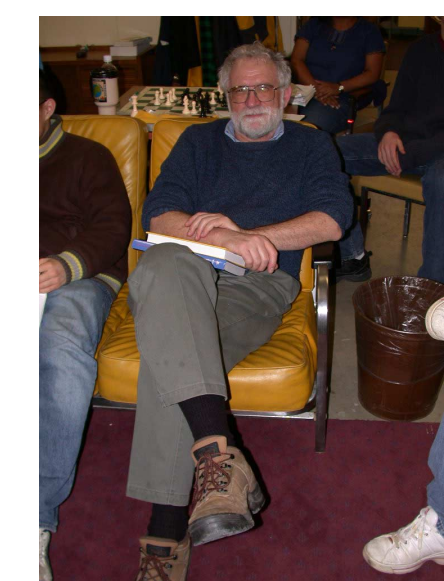
- 2005 Society of Mathematical Biology, Tubingen, Germany
- 2005 Ecological Society of America, Montreal, Canada
- 2005 Hudson River Undergraduate Math Conference, Williams College
- 2005 DIMACS Workshop on Biomolecular Networks, Rutgers University
- 2005 DNA 11, University of Western Ontario
- 2006 Nebraska Women's Math Conference
- 2006 DIMACS Workshop on Epidemiology and Evolution of Influenza
- 2006 Hudson River Undergraduate Math Conference, Westfield State College

Outreach

- 2005 DNA Word Conference
- 2005 Summer Workshop on Modeling Disease Dynamics
- 2006 MAA Seaway Section Session on Biomathematical Applications
- 2006 Macula visits Corning Community College with two of their former students, Mathias Youngs and Lauren Wood (and local UBM participants), to talk about biomath.
- 2006 Geneseo Regional Undergraduate Conference on Biomathematics.



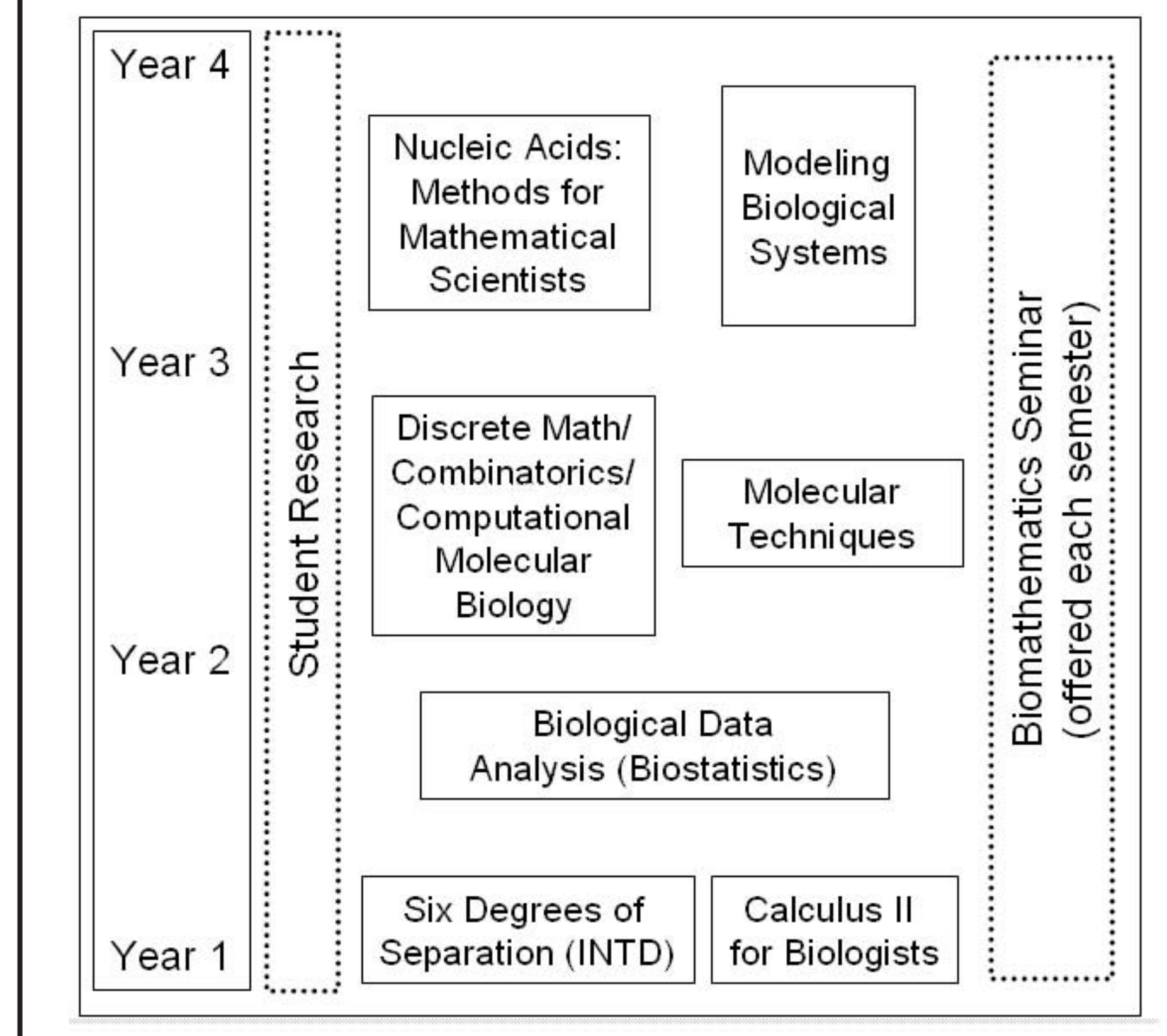
Kate Huggler



Gary Towsley



Undergraduate Curriculum in Biomathematics



Christina Callear, Jackie Dresch, Cynthia Stallard and Elizabeth Darrow.

Eighth Annual
Nebraska Conference for
Undergraduate Women
in Mathematics
February 3-5, 2006



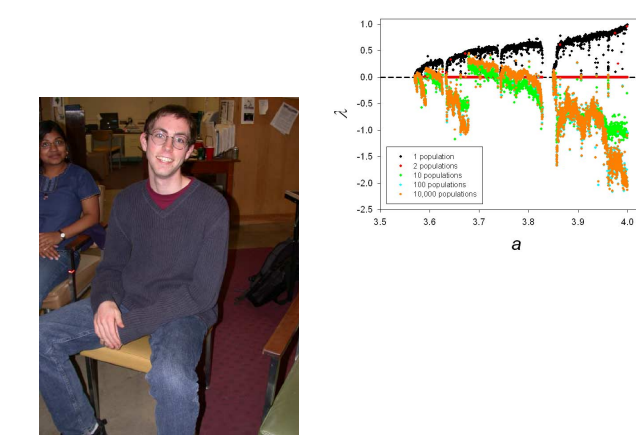
Cynthia Stallard and Tony Macula

Trip to the Hudson River Undergraduate Mathematics Conference, April 2005.

Undergraduate Student Researchers

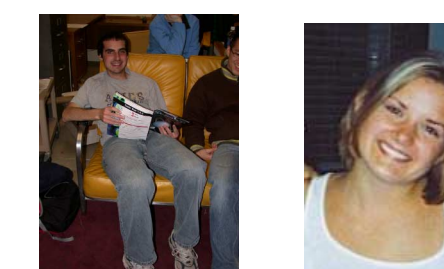
- Amy Zielinski ('06), Modeling vaccination protocols in influenza for hosts in small-world and scale-free networks. [College Honors Student]
- Andrew McCarthy ('06), Modeling the dynamics of influenza evolution in response to changing partial-immunity functions.
- Arunima Ray ('09), Modeling the emergence of cooperation on a lattice.
- Brian Kaplan ('05), DNA Code Web Interface
- Brian Wight ('07), DNA Code Web Interface
- Chelesea Schiano ('07), DNA code testing.
- Christina Callear ('07), Group Testing to Annihilate Regular Families
- Colin Kremer ('08), Modeling the ensemble dynamics of chaotic subpopulations.
- Cynthia Stallard ('06), Maple Computational Molecular Biology Programming
- Dan Fitzgerald ('07), Analyzing the spread of cooperation in a small-world network model.
- Dan Marcus ('06), Modeling the spread of influenza across meta-cities.
- Dave Quinzi ('07), DNA code web programming
- Elizabeth Darrow ('08), Fitting Thermodynamic Data
- Garrett Jones ('07), DNA Hybridization Alignment and Assembly Simulator and Visualizer
- Jacqueline Dresch ('06), Modeling vaccination protocols in influenza for hosts in small-world and scale-free networks.
- Jamie Romeiser ('05), Quantitative analysis of the movement of green sea turtles from nesting to feeding grounds.
- Joseph Kane ('09), Modeling cooperation on a small-world network.
- Kate Huggler ('08), Modeling HIV dynamics within human hosts.
- Katie Button ('04), Modeling cross-immunity in influenza for hosts in small-world and scale-free networks.
- Kayla Nimmo ('06), DNA code testing.
- Kevin Pinto ('06), Comparing HA evolution in a small-world network model of influenza dynamics to real data.
- Lauren Wood ('06), DNA code testing.
- Mark Chynoweth ('06), Matching theory and data in home range estimates for animals.
- Mathias Young ('05), Optimization of group testing for critical vertices in a graph
- Mathias Young ('05), Group Testing to Annihilate Edges.
- Matt Bernard ('06), DNA code testing.
- Mehmood Sheik ('09), Exploring modeling biological systems.
- Michelle Amsler ('05), Modeling cross-immunity in influenza for hosts in small-world and scale-free networks.
- Morgan Bishop ('05), DNA Code Generating Programs
- Niels Hanson ('05), Group Testing to Annihilate Edges.
- Olukemi Jaiyesimi ('08), Exploring modeling biological systems.
- Sal Prior ('06), DNA code testing.
- Sarah Olscamp ('06), Modeling the spread of SARS in a small-world network.
- Shuya Kyu ('06), Modeling the network structure of evolving food-webs.

Quasi-chaotic dynamics in are found in the average behavior of ensembles of chaotic subpopulations



Colin Kremer

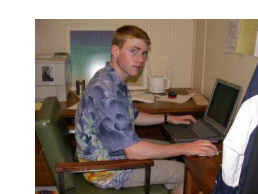
Stopping influenza epidemics on small-world networks



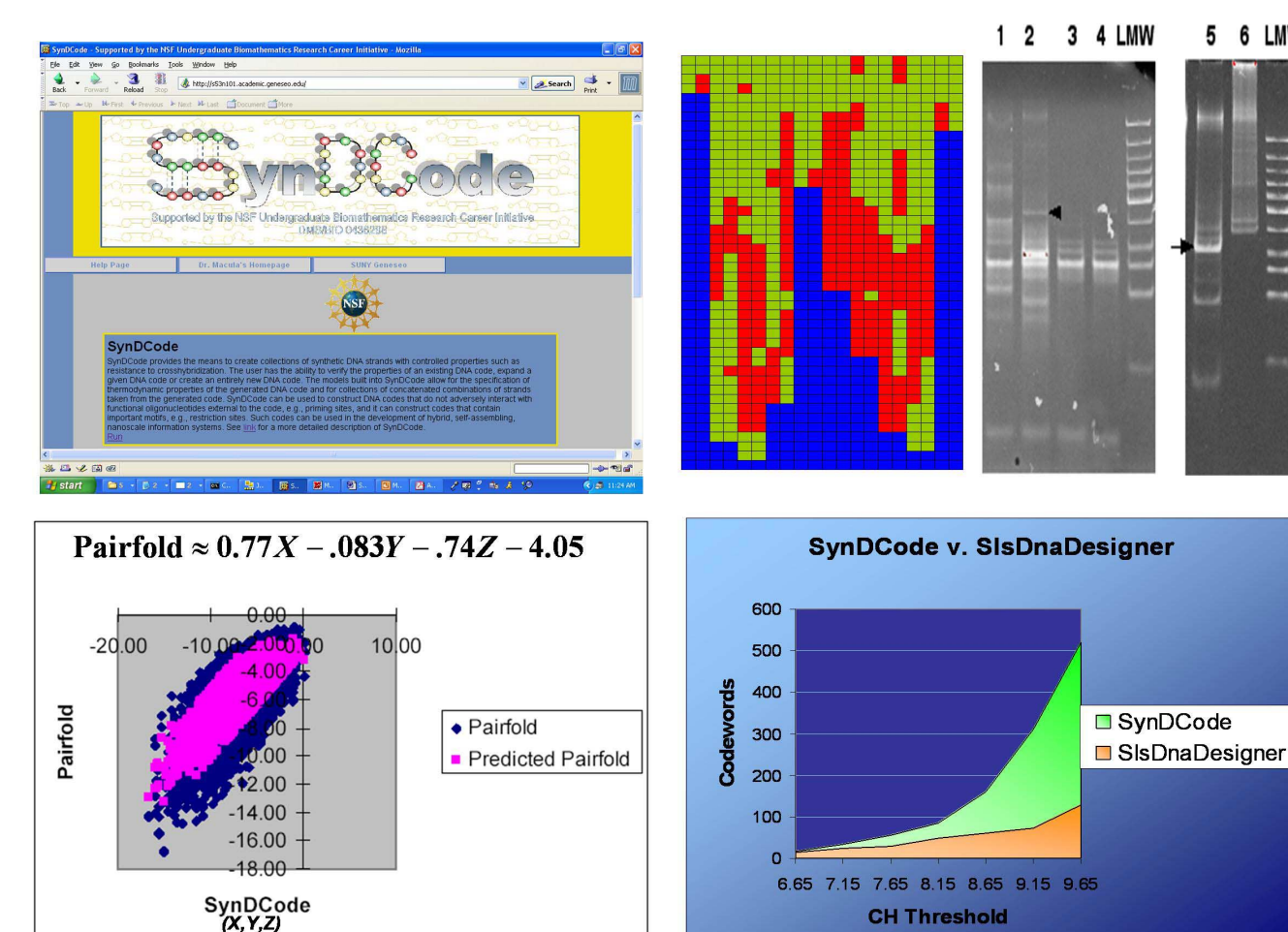
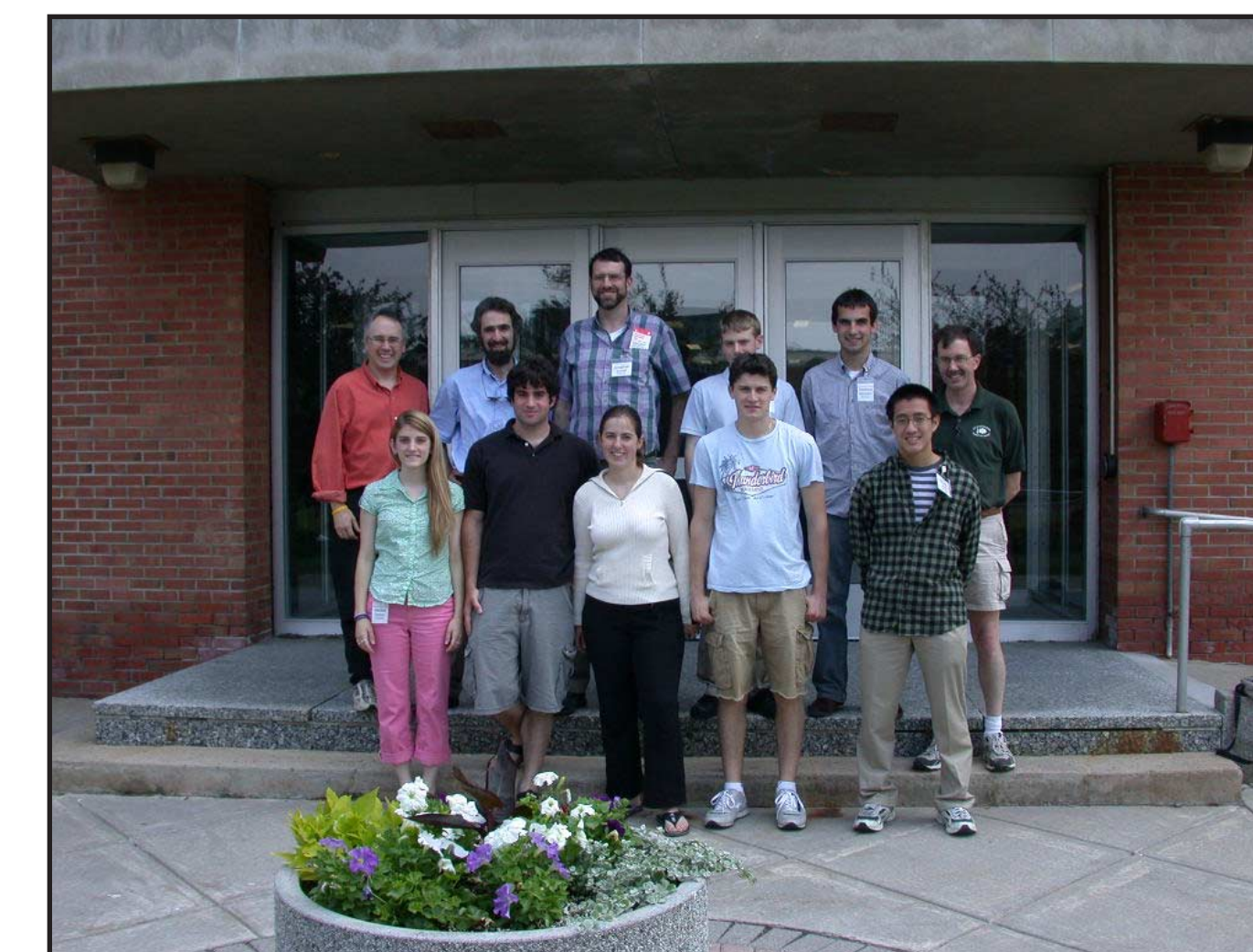
Quantifying the structure and evolution of interactive species in food webs.



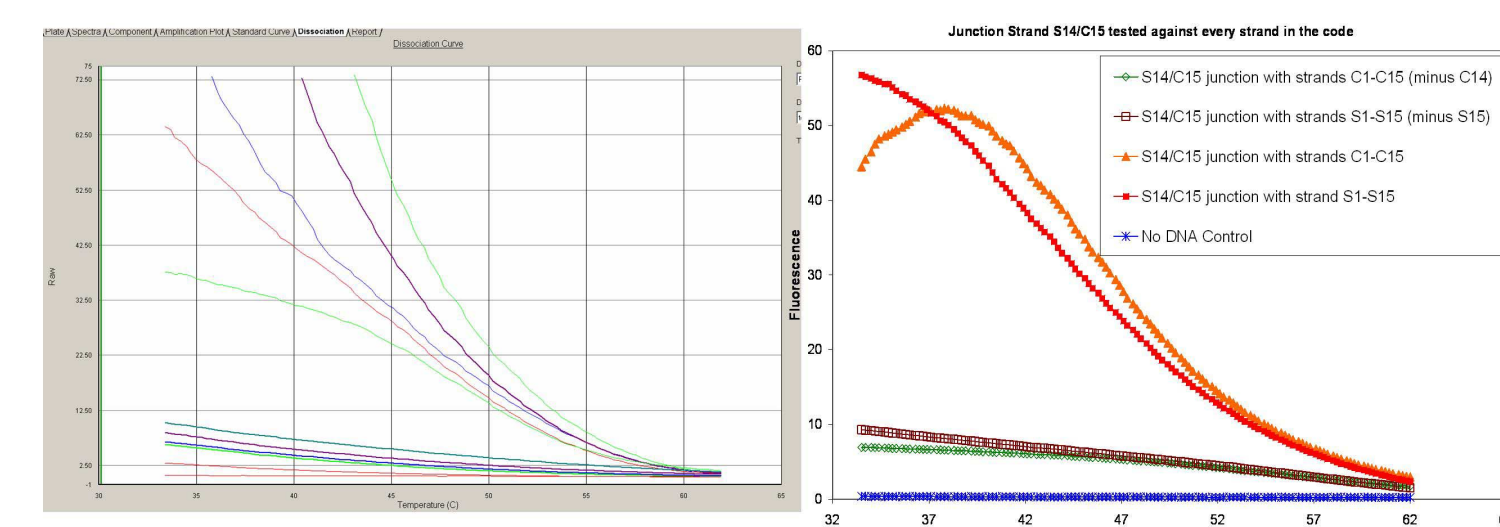
Global cooperation emerges on small-world networks.



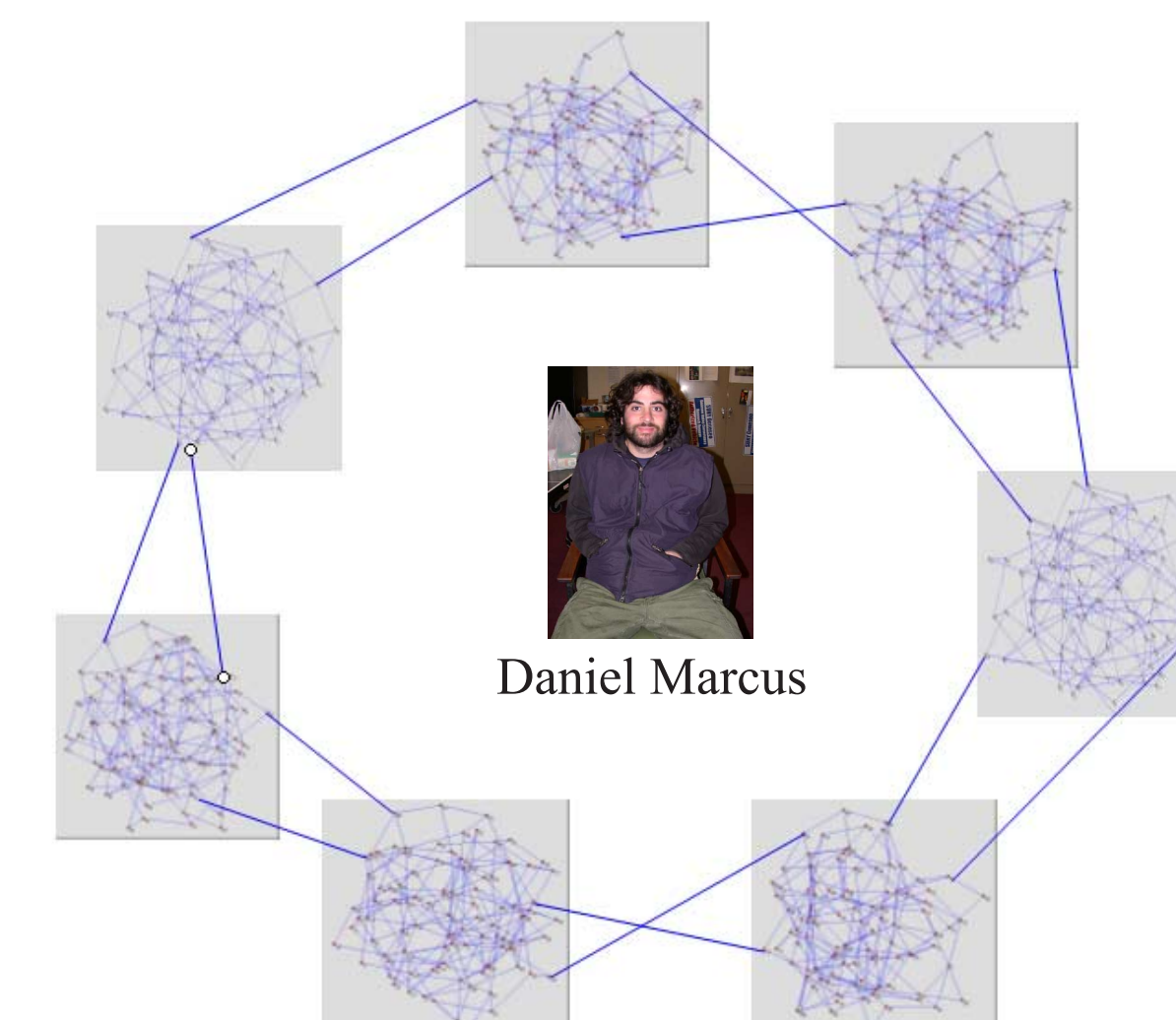
Biomathematical Explorations. Focus Workshop on spatial processes and epidemic modeling. June 2005.



DNA Code Design and Optimization in Vitro and Sicillo: Students: Morgan Bishop (math), Jackie Dresch (math), Sal Priore (biochem/math), Matt Bernard (BioChem), Dave Quinzi (math), Brian Wight (biochem/biophysics), Garrett Jones (math), Chelsea Schiano (biochem), Brian Kaplan (math). Faculty: A. Macula (math), W. Pogozeleski (biochem)



Unexpected crosshybridized DNA duplexes hinder nanostructure formation and performance. Pooling DNA with Sybr Green reveals the presence of crosshybridized DNA. Algorithmic pooling construction and decoding is critical to the elimination of bad sequences. Students: Niels Hanson (math), Christina Callear (math), Lauren Wood (bio), Kayla Nimmo (bio). Faculty: A. Macula (math), W. Pogozeleski (biochem), Ruel Mcknight (biochem)



Daniel Marcus

Spread of influenza on small-world networks among cities

Acknowledgements

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