



# BEACON

An NSF Center for the Study of  
Evolution in Action

# BEACON

## Congress

August 16-19, 2014

BEACON Headquarters  
567 Wilson Road  
Michigan State University  
East Lansing, MI 48824  
(517) 884-2555



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**Saturday, August 16**

**Student/Postdoc Retreat Day**

**Location:**

Plant & Soil Sciences Building, room 1200

1066 Bogue St

East Lansing, MI 48824

\*Across Wilson Road from BEACON headquarters

9:00-10:30	Breakfast & Don't just create a teaching philosophy, create an inclusive philosophy (Judi Brown-Clarke, Ph.D.)
10:30-11:00	Break
11:00-12:30	Academia, Industry, and Government: Pursuing Science in the Modern US (Terran Lane, Ph.D.)
12:30-1:30	Lunch
1:30-2:30	Open Questions in Machine Learning, Complexity, and Evolution (Terran Lane, Ph.D.)
2:30-3:00	Break
3:00-4:30	Round Table: Avoiding burnout and staying motivated
4:30-5:00	Break
5:00	Dinner at Nancy Moore Park

## Sunday, August 17

8:00-9:00	Breakfast served in atrium	Executive Committee meeting
9:00-10:00	Plenary Session: Erik Goodman, "State of BEACON Address" (BPS 1410)	
10:00-10:30	Break	

	BPS 1410	BPS 1425	BPS 1400	Conference		
10:30-12:00	<b>Contributed Talks: Mutation, Selection &amp; Speciation (Moderator: Jeffrey Conner)</b>	<b>Sandbox:</b> Synthetic Biology & Evolution (Leandra Brettner)	<b>Tutorial:</b> Harnessing social media for science outreach and professional networking (Randal Olson)	Diversity Steering Committee Meeting		
10:30-10:45	Jeffrey Conner: Maintenance of a conserved trait: natural and artificial selection on stamen lengths in wild radish					
10:45-11:00	Jimmy Woodward: Effects of competition and microbial symbiosis on plant phenotype in a polyploid <i>Trifolium</i> community					
11:00-11:15	Annat Haber: Breaking the mold: the effects of mutations on phenotypic covariation in the fruit fly wing					
11:15-11:30	Jason Keagy: Male competition fitness landscape predicts both forward and reverse speciation					
11:30-12:00	Discussion/Break					
	BPS ATRIUM	BPS 1410				
12:00-12:45	Lunch					
12:45-1:30		<b>BEACON Faculty Affiliate Candidate, José Ponciano:</b> Parameter identifiability and the structure of variability in ecological and evolutionary time series				
	BPS ATRIUM	BPS 1425				
1:30-2:15	<b>POSTER SESSION A (Odd-Numbered Posters)</b>	<b>Sandbox:</b> Host-microbial coevolutionary models: Is a synthesis possible? (Kevin Theis)				
2:15-3:00						
3:00-3:30	Break					

### Color Codes:

Plenary	Break/Meal	Contributed Talk: 12 minutes plus 3 minutes for questions	Tutorial: a how-to session. Come ready to learn and ask questions!	Sandbox: interactive sessions to stimulate new collaborations, ideas & discussion	Committee meeting: not open to general membership	Responsible Conduct of Research: sign in and get RCR credit!
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## Sunday, August 17 continued

	BPS 1410	BPS 1425	BPS 1400
3:30-5:00	<b>Contributed Talks: Teaching Evolution &amp; Genetics (Moderator: Alita Burmeister)</b>		
3:30-3:45	Alita Burmeister: Assessing student perceptions & explanations of microbial evolution		
3:45-4:00	Emily Weigel: Genetic variation as a pivotal point in genetics-to-evolution course sequences		
4:00-4:15	Wendy Johnson: The effects of Avida-ED on students' explanations of evolution		
4:15-4:30	Jared Moore: Evolve-A-Robot: An evolutionary robotics environment in the web browser		
4:30-4:45	Allison Walker: Speculative fiction: Literature raises questions about the ethicality of genetic research		
4:45-5:00	Discussion/Break		
5:30-7:30	Dinner in the BPS Penthouse		

**Color Codes:**

Plenary	Break/Meal	Contributed Talk: 12 minutes plus 3 minutes for questions	Tutorial: a how-to session. Come ready to learn and ask questions!	Sandbox: interactive sessions to stimulate new collaborations, ideas & discussion	Committee meeting: not open to general membership	Responsible Conduct of Research: sign in and get RCR credit!
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## Monday, August 18

8:00-9:00	Breakfast served in atrium	Executive Comm Mtg
9:00-10:00	Plenary Session: Lee Spector, "Evolution of Expressive Programs: Principles, Products, and Prospects" (BPS 1410)	
10:00-10:30	Break	

	BPS 1410	BPS 1420	BEACON Seminar
10:30-12:00	<b>Contributed Talks: Communication, Cooperation, &amp; Intelligence (Moderator: Eric Bruger)</b>		
10:30-10:45	Eric Bruger: Quorum sensing promotes the maintenance of public goods production in experimental populations of <i>Vibrio harveyi</i>		
10:45-11:00	Randal Olson: Exploring the evolution of a trade-off between vigilance and foraging in group-living organisms		
11:00-11:15	Chris Adami: What games are these hyenas playing? Unraveling the selective pressures shaping dominance hierarchies		
11:15-11:30	Lyndon Jordan: Transfer of information through hierarchical social systems		
11:30-11:45	Aditya Rawal: Evolution of communication in mate selection		
11:45-12:00	Padmini Rajagopalan: The evolution of general intelligence		
	BPS ATRIUM	BPS 1410	
12:00-12:45			
12:45-1:30	Lunch		<b>BEACON Faculty Affiliate Candidate, Laura Grabowski:</b> Brilliance, Bit by Bit: Evolving Artificial Intelligence
	BPS ATRIUM	BEACON Seminar Room	
1:30-2:15	<b>POSTER SESSION B (Even-Numbered Posters)</b>		
2:15-3:00			<b>Tutorial:</b> Markov Network Brains (Cliff Bohm & Jory Schossau)
3:00-3:30	Break		

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Plenary	Break/Meal	Contributed Talk: 12 minutes plus 3 minutes for questions	Tutorial: a how-to session. Come ready to learn and ask questions!	Sandbox: interactive sessions to stimulate new collaborations, ideas & discussion	Committee meeting: not open to general membership	Responsible Conduct of Research: sign in and get RCR credit!
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## Monday, August 18 continued

	BPS 1410	BEACON 1420	BEACON Seminar
3:30-5:00	<b>Contributed Talks: Synthetic Biology &amp; Evolutionary Applications (Moderator: Travis Hagey)</b>		
3:30-3:45	Travis Hagey: Using FEA simulations to investigate the gecko adhesive system		
3:45-4:00	Joseph Graves, Jr.: Evolution of metallic/metallic oxide nanoparticle resistance in bacteria		
4:00-4:15	Christopher Marx: Efficient use of a horizontally-transferred pathway for dichloromethane catabolism requires post-transfer refinement of the host		
4:15-4:30	Chris Takahashi: A low cost, customizable turbidostat for use in synthetic circuit characterization and evolution		
4:30-5:00	Discussion/Break		
5:00-6:00	Break & transportation		
6:00-8:00	Dinner at Patriarche Park		

### Color Codes:

Plenary	Break/Meal	Contributed Talk: 12 minutes plus 3 minutes for questions	Tutorial: a how-to session. Come ready to learn and ask questions!	Sandbox: interactive sessions to stimulate new collaborations, ideas & discussion	Committee meeting: not open to general membership	Responsible Conduct of Research: sign in and get RCR credit!
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## Tuesday, August 19

8:00-9:00	Breakfast served in atrium	Education Comm Mtg
9:00-10:00	Plenary Session: Ross Nehm, "The contextual nature of evolutionary reasoning: implications for teaching, learning, and assessment" (BPS 1410)	
10:00-10:30	Break	

	BPS 1410	BPS 1420	BEACON Seminar	BEACON Conference		
10:30-12:00	<b>Contributed Talks: Molecular Evolution (Moderator: Michael Wiser)</b>	<b>Sandbox:</b> Evolution of Intelligence (Fred Dyer, Chris Adami, Charles Ofria, & Rob Pennock)	<b>Increase Your Broader Impacts with Data Nuggets!</b> (Elizabeth Schultheis & Melissa Kjelvik)	BEACON Administrative Meeting		
10:30-10:45	Michael Wiser: Evolutionary dynamics over large time scales					
10:45-11:00	Jacob Clifford: Context-dependent selection of binding sites on DNA by cooperating proteins using a statistical theory					
11:00-11:15	Amir Shahmoradi: Predicting evolutionary site variability from structure in viral proteins: buriedness, packing, flexibility, and design					
11:15-11:30	Caroline Turner: Evolution of elemental composition in <i>E. coli</i> under carbon and nitrogen limitation					
11:30-11:45	Dakota Derryberry: Self-similarity of doubly-sequenced GBM samples in The Cancer Genome Atlas					
11:45-12:00	Discussion/Break					
	<b>BPS ATRIUM</b>	<b>BEACON Conference Room</b>				
12:00-1:30	Lunch in the atrium	<b>Lunch discussion topic:</b> BEACON's Disability Action Plan (Judi Brown Clarke)				

### Color Codes:

Plenary	Break/Meal	Contributed Talk: 12 minutes plus 3 minutes for questions	Tutorial: a how-to session. Come ready to learn and ask questions!	Sandbox: interactive sessions to stimulate new collaborations, ideas & discussion	Committee meeting: not open to general membership	Responsible Conduct of Research: sign in and get RCR credit!
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## Tuesday, August 19 continued

	BPS 1415	BPS 1420	BEACON Seminar Room
1:30-3:00	<b>Sandbox:</b> Priorities in Evolution Education (Louise Mead)	<b>Sandbox:</b> Increasing the Impact of Evolutionary Computation (Brian Goldman)	<b>Increase Your Broader Impacts with Data Nuggets! (continued)</b> (Elizabeth Schultheis & Melissa Kjelvik)
3:00-3:30	Break		
	<b>BPS 1410</b>		
3:30-5:00	Plenary Sandbox: Grand Challenges in Evolution in Action		
5:00-6:00	Break & Transportation		
6:00-8:00	Dinner at Rob Pennock's house		

### Color Codes:

Plenary	Break/Meal	Contributed Talk: 12 minutes plus 3 minutes for questions	Tutorial: a how-to session. Come ready to learn and ask questions!	Sandbox: interactive sessions to stimulate new collaborations, ideas & discussion	Committee meeting: not open to general membership	Responsible Conduct of Research: sign in and get RCR credit!
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## POSTER SESSIONS

This year presentations will be divided up into two sessions to decrease traffic and give participants more time to interact. Presenters with odd-numbered posters should plan to stand by their poster during session A, while those with even-numbered posters should be present during session B. Please keep all posters up for both days.

**Poster Session A, Sunday August 17, 1:00-3:00 pm – Odd numbers, highlighted in YELLOW**

**Poster Session B, Monday August 18, 1:00-3:00 pm – Even numbers, highlighted in BLUE**

Poster	Authors (Presenter in bold)	Title
<b>Coupling genomic processes to phenotypic variation</b>		
1	<b>Glenney, Carrie</b> ; Kerr, Benjamin	The evolution of killer proteins
2	<b>Conlin, Peter</b> ; Kerr, Benjamin; Ratcliff, William	Fitness decoupling during the evolutionary transition to multicellularity
3	<b>Chapman, Samuel</b> ; KC, Dukka; Adami, Chris; Wilke, Claus; Knoester, David	Protein contact map prediction using the evolution of Markov networks
4	<b>Hanson, Noah</b> ; Payen, Celia; Dunham Maitreya	Tracking the genetic factors of <i>Saccharomyces cerevisiae</i> strains under the selective pressures of the beer brewing process
5	Feng, Colin; Lim, Sujung; Vrana, Marc; Zane, Grant; Wall, Judy; <b>Hillesland, Kristina</b>	Is specialization for mutualism beneficial? Investigating why a sulfate-reducer lost its defining metabolic feature
6	<b>Perez, Samuel</b> ; Conner, Jeffrey; Schemske, Douglas	Patterns and mechanism of a nonfunctional trait loss
7	<b>O'Donnell, Daniel R.</b> ; Parigi, Abhijna; Fish, Jordan A.; Dworkin, Ian; Wagner, Aaron P.	The roles of standing genetic variation and evolutionary history in determining the evolvability of anti-predator strategies
8	<b>Harris Rayna M</b> ; Dijkstra Peter D; Hofmann Hans A	Comparative analysis of pro-opiomelanocortin gene families reveals complex structural and regulatory evolution
<b>Evolution of Complex Behaviors</b>		
9	<b>Mirmomeni, Masoud</b> ; Hintze, Arend; Strauss, Eli; Adami, Chris	The "Collective Hunting Game": A new game to study all or nothing behavior in animals
10	<b>Emily G. Weigel</b> ; Jenny Boughman	Short-term density exposure affects male reproductive success in threespine stickleback ( <i>Gasterosteus aculeatus</i> )
11	<b>Martinez, Jonatan</b> ; Keagy, Jason; Doolittle, Katie; Boughman, Janette W.	Genetic basis of female mate discrimination in recently diverged species of threespine sticklebacks
12	<b>Young, Rebecca L.</b> ; O'Connell, Lauren A.; Kar, Ranjeet D.; Hofmann, Hans A.	Convergent evolution of the monogamous brain: Deep homology uncovered by comparative transcriptomics
<b>Experimental Evolution in the lab and in silico</b>		
13	<b>Schossau, Jory</b> ; Adami, Chris	Toward the measure of a brain
14	<b>Blount, ZD</b> ; Weatherspoon, KM; Rowles, MO; Quandt, EM; Lenski, RE	Genetics of ecological specialization and incipient speciation in an experimental population of <i>E. coli</i>
15	<b>Leon, Dacia</b> ; Quandt, Erik; Blount, Zachary; Ellington, Andrew; Georgiou, George; Barrick, Jeffrey	Understanding the mechanistic basis of mutations potentiating the evolution of citrate utilization in the LTEE
16	<b>Ward, Nathan</b> ; Jackson, Julius; Goodman, Erik	Simulating evolution of gene organization in bacteria
17	<b>Cunningham, Quincy</b> ; Nonga, Herve; Campbell, Adero; Tajkarimi, Mehrdad; Graves, Joseph L.	Minimum inhibitory concentration of silver nanoparticles in evolved silver-resistant <i>Escherichia coli</i> K12 MG1655.
18	<b>Tajkarimi, Mehrad</b> ; Cunningham, Quincy; Campbell, Adero; Nonga, Herve; Harrison, Scott, H.; Graves, Joseph L.	The cell wall of experimentally evolved silver nanoparticle resistant bacteria: Surface biophysical properties
19	<b>Riazi, Siavash</b> ; Rojas Echenique, José; Marx, Christopher	Predicting and testing the strength of selection and epistatic interactions throughout a metabolic pathway in <i>Methylobacterium extorquens</i> PA1
20	<b>Pogachar, Jamie</b> ; Payen, Celia; Ong, Giang; Brewer, Bonnie; Dunham, Maitreya	Stability of a large amplification in <i>Saccharomyces cerevisiae</i>
21	<b>Suarez, Gabriel</b> ; Barrick, Jeffrey	Simpler and more reliable synthetic biology with <i>Acinetobacter baylyi</i> ADP1
22	<b>Miyagi, Michael</b> ; Adami, Christoph; Gupta, Aditi	Why is genome length negatively correlated with mutation rate?
23	<b>Sweet, Tyler</b> ; Kohn, Cory; Williams, Barry L.	Exploring the impact of missing data on phylogenetic accuracy using experimental phylogenetics with Avida

Poster	Authors (Presenter in bold)	Title
<b><i>Evolution of Communities &amp; Collective Dynamics</i></b>		
24	<b>Vaeilli PM</b> ; Theis KR; Coddington EJ; Eisthen HL	Microbial origins and physiological consequences of tetrodotoxin toxicity in the rough-skinned newt ( <i>Taricha granulosa</i> )
25	<b>Zhbannikov, Ilya Y.</b> ; Williams, Janet E.; Foster, James A.	MetAmp: a novel approach to clustering analysis of microbial community structures using multiple genomic fingerprints
26	<b>Estrela, Sylvie</b> ; Morris, Jeff; Lenski, Richard; Klavins, Erik; Kerr, Ben	Microbial interdependencies through loss of complementary metabolic functions
27	<b>Green, Robin</b> ; Pineda, Jose; Shou, Wenyng	Emergence of novel dependencies in evolving populations
28	<b>Klausmeier, Christopher A.</b>	Eco-evolutionary modeling with adaptive dynamics and Mathematica
<b><i>Evolutionary algorithms, robotics, and other applications</i></b>		
29	<b>Gaur, Abhinav</b>	TBA
30	<b>Moradi Kordmahalleh, Mina</b> ; Gorji Sefidmazgi, Mohammad; Homaifar, Abdollah	Gene regulatory network based on a novel evolvable partially connected artificial neural network
31	<b>Goldman, Brian W.</b> ; Punch, William F.	Parameter-less population pyramid
32	<b>Burks, Armand</b> ; Punch, Bill	Genetic diversity methods for improving genetic programming
33	<b>Clark, Anthony J.</b> ; Tan, Xiabo; McKinley, Philip K.	On-board evolution of a model-free adaptive controller for a robotic fish
34	<b>Liang, Jason</b> ; Miikkulainen, Risto	Metaevolution: Evolving parameters for evolutionary algorithms
35	<b>Moore, Jared M.</b> ; McKinley, Philip K.	Evolving joint-level control with digital muscles
36	<b>DeVault, Travis</b> ; Pokharel, Jayandra; Soule, Terence; Heckendorf, Robert	Distributed evolution of navigation in autonomous ground robots
37	<b>Payson, Charles</b> ; Moore, Jared; Clark, Anthony; McKinley, Philip	3D evolutionary robotics on the web: EVOLVE-A-ROBOT
38	<b>Mahjourian, Reza</b> ; Miikkulainen, Risto	Robotic control through neuroevolution



## ABSTRACTS

## **SPECIAL LUNCHTIME EVENTS**

### **“Tables of Content” Lunch Discussions (Sunday, Monday, & Tuesday, 12:00-1:30; Various Locations)**

Tables will be organized around attendee-suggested topics -- especially topics that we haven't had a chance to talk about during a session. We will have a sign-up board where you can write a topic down for a table. Here's your chance to network, explore new ideas, find potential collaborators, and make new friends.

### **Lunch Discussion: BEACON’s Disability Action Plan (Tuesday, 12:00-1:30; BEACON Conference Room)**

BEACON is establishing itself as a best-practice model for increasing diversity in STEM education; and as a result, our Consortium is enriched and enhanced. In order to sustain these benefits, BEACON needs to strategically recruit and support inclusive participation. Many individuals with disabilities underreport their status due to a feeling of vulnerability and/or potential bias. The “face” of scientists rarely displays researchers with disabilities, and this perceived exclusion robs science/technology of a diverse and robust capacity. Despite these challenges, BEACON’s 2.7% participant rate of individuals with disabilities surpasses the national norms of 1.1%. The goal of this discussion session is to design a webpage which provides a repository of techniques/skills for teaching different learning styles, strategies to create adaptive labs and research equipment, alternative ways for field research and data collection, creative ways for scientific communication, and video vignettes of BEACONites overcoming disabilities.

## **Plenary Sessions**

*All Plenary Sessions will take place in BPS 1410.*

**Sunday, August 17, 9:00-10:00**

**Erik Goodman, BEACON Director**  
**"The State of BEACON Address"**

Erik Goodman will provide an overview of what's been happening in BEACON over the past year, and what to look forward to in the next year.

**Monday, August 18, 9:00-10:00**

**Lee Spector, Professor of Computer Science, School of Cognitive Science, Hampshire College**  
**"Evolution of Expressive Programs: Principles, Products, and Prospects"**



Algorithms modeled on biological evolution can be applied to populations of computer programs and also to populations of program-driven digital organisms. Some of the resulting program evolution systems can solve difficult computational problems, and some can serve as objects of study in our quest to understand general principles of evolution. One factor that contributes to the behavior and power of a program evolution system is the language in which it allows evolving programs to be expressed. In this talk I will show how the use of expressive program representations, along with insights from biology concerning the nature of variation and selection, can enhance the power and utility of program evolution systems. I will discuss applications ranging from software engineering to bioinformatics, and

describe some of the ways in which these systems might help us to better understand biological processes.

**Tuesday, August 19, 9:00-10:00**

**Ross Nehm, Associate Professor, Ecology & Evolution, Stony Brook University;**  
**Member of BEACON's External Advisory Committee**  
**"The contextual nature of evolutionary reasoning:**  
**Implications for teaching, learning, and assessment"**



Recent studies of evolutionary reasoning across age groups (elementary, high school students), nations (China, Germany, Indonesia, and the USA), and expertise levels (undergraduates, practicing scientists) have revealed new insights about how humans think about evolutionary change. This talk will summarize these empirical findings, and discuss their implications for biology teaching, learning, and assessment.

## **BEACON Faculty Affiliate Candidate Talks**

BPS 1410

**Sunday, August 17, 12:45-1:30. José Ponciano, University of Florida: “Parameter identifiability and the structure of variability in ecological and evolutionary time series.”** “The enormous usefulness of mathematics in the natural sciences is something bordering on the mysterious and there is no rational explanation for it.” Eugene Wigner, the physicist and author of the essay quoted above, famously pointed out that just because a single piece of mathematics can be found in two different systems does not mean that the two systems are related to each other. But as another physicist said (S.J. Gates), “it’s fun to think about these things!” The purpose of this talk is to purportedly commit such intellectual debauchery in the context of stochastic population dynamics models for ecological and evolutionary time series. In the process, I will explain under which conditions, how, and why mathematics and in particular stochastic processes and statistical methods, can help us achieve a better understanding of fundamental questions pertaining the variance in the trends of ecological and evolutionary time series.

**Monday, August 18, 12:45-1:30. Laura Grabowski, University of Texas-Pan American. “Brilliance, Bit by Bit: Evolving Artificial Intelligence.”** The natural world boasts a multitude of solutions to the problem of intelligence. Evolution discovered a wide variety of remarkable and clever mechanisms that allow even the simplest organisms to survive and flourish in changing environments. Humans' attempts at creating artificial intelligence (AI) have, so far, not fared as well. Despite the widespread success of AI in applications such as games, pattern recognition, and controllers, the early promise of AI to build human-like intelligence remains unfulfilled. I will discuss how I am applying digital evolution to address questions in Biology and applying the results back to computer science. Specifically, I am working to understand how evolution produces the building blocks of intelligent behaviors, and exploring how we may leverage these techniques to solve computational problems. I will present an overview of my research results in two key areas: 1) evolving memory use, and 2) evolving increasingly complex behavior.

## Sandbox Sessions, Tutorials, & Workshops

Sunday, August 17

**10:30-12:00, BPS 1425. Sandbox: Synthetic Biology & Evolution (Leandra Brettner).** The past decade or so has been witness to the rise of a new syndicate between biology and engineering. Inspired by the parallels between living systems and modern computational devices, researchers in the field of synthetic biology seek to treat genetic material like programmable software with the protein dictated inner workings of the cell as the corresponding hardware. Given our ever increasing perspective on life's seemingly boundless capabilities, the limits of engineered organisms could potentially be hindered only by our own imaginations. In this Sandbox Session, we will focus the discussion around the two central themes of evolution and synthetic biology:

1. Decreasing or controlling evolvability to develop more reliable synthetic systems.

Unfortunately, and for a variety of reasons, synthetic genetic systems are particularly prone to evolutionary instability. Evolutionary pressures are highly influential on the expenditure of metabolic resources. Because novel genetic programs often provide little to no benefit to the organism, cells that lose all or part of the synthetic function can often outcompete those that retain the intact circuit. This is one of the problems that has slowed the progress of synthetic biology as a field and could potentially be greatly improved by looking at system design through evolutionary lenses.

2. Using synthetic biology as a hacking instrument to address evolutionary questions.

The new technologies developed and driven by the ascent of synthetic biology provide a fresh new toolbox with which to probe the tenets of evolution. By more or less allowing for the construction of biological systems from the bottom-up, researchers now have unprecedented control over the behaviors and functions of interest. To date, synthetic biologists have expanded the genetic code, unveiled the noise in protein expression, engineered novel altruistic and mutualistic microbial populations, and more. Despite these accomplishments, there is still a vast landscape of possibilities to explore.

**10:30-12:00, BPS 1400. Tutorial: Harnessing social media for science outreach and professional networking (Randal Olson).** In the past decade, social media has grown from a playground for angst teenagers into a tool that pervades nearly everyone's lives. In fact, almost 3/4 of all internet-using adults in the U.S. now use social media in some form or another in their daily lives. It's no surprise, then, that social media has become a fertile ground for science outreach to the public and professional networking among scientists. This hands-on tutorial will walk you through three major social media platforms (Twitter, blogging on WordPress, and reddit) and show you how they are best used for science outreach and professional networking. Make sure to bring your laptop; we will be signing up for and using these services during the tutorial.

**1:30-3:00, BPS 1425. Sandbox: Host-microbial coevolutionary models: Is a synthesis possible? (Kevin Theis).** Given the ubiquity and generational persistence of functionally integrated host-microbial partnerships, classical views of animal and plant evolution are dissatisfying. There are a handful of broadly circulating evolutionary concepts that claim to account for the complexity of these interkingdom partnerships (e.g. extended phenotype, niche construction, hologenomics, epigenetics, multi-level selection), but proponents of each appear to be talking past one another. Can we identify a core set of premises that unite these concepts, and craft a contemporary host-microbial coevolutionary synthesis?

**3:30-5:00, BPS 1425. Sandbox: Major Evolutionary Transitions (in Action) (Ben Kerr, Charles Ofria, & Will Ratcliff).** A major transition in evolution occurs when multiple units at one level in the biological hierarchy form an integrated reproducing higher-level unit. Major transitions have led to the origin of the chromosome (as a linked set of genes), the eukaryotic cell (as a prokaryotic association), multicellularity (as a collective of related cells) and the eusocial colony (as a reproductively differentiated group of individuals), just to name a few examples. In essence, a major transition involves the origin of a new biological individual, or, alternatively, a new level in the biological hierarchy. Why and how such transitions have occurred in different taxa, and at different scales, constitute some of the most exciting and important questions in the study of evolution. In this Sandbox Session, we will briefly review core concepts and share some recent experimental approaches exploring transitions in real time with microbes and digital organisms. We will then focus group discussion on open questions and future challenges

regarding the major transitions in evolution. In particular, we seek to explore what issues researchers are trying to understand about evolutionary transitions, and how these advances in our understanding could be applied in different areas, such as bioremediation or algorithm development.

**3:30-5:00, BPS 1400. Tutorial: Evolutionary Bilevel Optimization (Kalyanmoy Deb).** Many practical problem-solving tasks involve multiple hierarchical search processes, requiring one search and optimization task to solve another lower-level search and optimization problem in a nested manner. In their simplicity, these problems are known as "Bilevel optimization" problems, in which there are two levels of optimization tasks. A solution at the upper level is feasible if the corresponding lower level variable vector is optimal for the lower level optimization problem. Problems in economics and business involving company CEOs and department heads or governmental decision makers and NGOs are standard bilevel optimization problems. In engineering, optimal control problems, structural design problems, transportation problems and other hierarchical problems fall into this category. Hierarchical games having multi-level controls are better posed as bilevel problems. These problems are also known as Stackelberg games in the operations research and computer science community. In this tutorial, we shall introduce principles of the emerging topics on bilevel optimization for single and multiple objectives and discuss the challenges in solving such problems. A number of immediate and future research ideas on evolutionary bilevel optimization (EBO) will be highlighted. More information about Evolutionary Bilevel Optimization can be found from the recently created website <http://www.bilevel.org>.

### Monday, August 18

**BPS 1415. Sandbox: Bringing Evolution in Action to the Public (Jory Weintraub & Will Ratcliff).** Jory Weintraub (Assistant Director, Education and Outreach at NESCent) and Will Ratcliff (Assistant Professor at Georgia Tech, and SSE Huxley Awardee) will present some models for effective communication and outreach, to include programs with which BEACON faculty, graduate students and postdocs can participate and ideas for how to develop strong collaborations with educators. Following their presentations we will have time to discuss current and future outreach efforts across BEACON. Please bring all ideas and projects to share! Louise Mead will moderate.

**10:30-12:00, BEACON Seminar Room. Scientific Virtues Toolbox Session (Rob Pennock & Michael O'Rourke).** What are the scientific character virtues and how do they relate to responsible conduct of research? These workshop/discussions can be used to help fulfill NSF's annual RCR requirement. First timers will discuss curiosity and the goals of science. Those who attended last year will do new modules on honesty and courage.

**1:30-3:00, BEACON Seminar Room. Tutorial: Markov Network Brains (Cliff Bohm & Jory Schossau).** A Markov Network Brain is an evolvable digital decision-maker. They can be used to perform decision tasks, such as performing simple math operations and controlling robotic or virtual agents. In BEACON they've been successfully used to study evolutionary processes, evolution of cognitive structures, and evolutionary game theory. Markov Network Brains are composed of brain states and logic gates that operate on those states. The logic used in these brains is similar to that used on circuit boards, composed of simple boolean logic, such as AND, OR, and NOT. Connected in both series and parallel, these evolvable logic functions compose a decision network, which can encode any computable logic. Markov Network Brains are encoded via a string of characters, groups of which represent logic components and connections between components. The character string representing the genetic material encoding a Markov Network Brain can be mutated by any number of methods such as point mutations, recombination, duplications, and deletions. We will introduce Markov Network Brains, and provide hands-on examples to get you comfortable running and modifying your own Markov Network Brains. **This will be a hands-on session; bringing your computer is recommended but not required.**

**3:30-5:00, BPS 1415. Sandbox: Evolution-In-Action Software and the Web (Charles Ofria, Jared Moore, Luis Zaman & Tony Clark).** Web development, now of central importance in the corporate world, has been making significant inroads into academia. Most journals are now online, many data repositories now exist, new collaboration apps are becoming more prevalent, MOOCs and other online learning options

are abundant, and powerful new development tools are allowing scientists to make high-performance research software dramatically more accessible. In this sandbox session, we will discuss web-based research and education tools that currently exist, those that are under development, and those that we would like to see exist. Additionally, we will talk about tools to facilitate the development of new web applications, but focusing only on high-level utility, not low-level details of how to use those tools. Feel free to come with demos of web applications that you are working on, or suggestions for existing web-based tools that you think others might find useful. And, of course, bring ideas for web tools that you would like to see created!

**3:30-5:00, BEACON Seminar Room. Scientific Virtues Toolbox Session (Rob Pennock & Michael O'Rourke).** What are the scientific character virtues and how do they relate to responsible conduct of research? These workshop/discussions can be used to help fulfill NSF's annual RCR requirement. First timers will discuss curiosity and the goals of science. Those who attended last year will do new modules on honesty and courage.

### Tuesday, August 19

**10:30-12:00, BPS 1420. Sandbox: Evolution of Intelligence (Fred Dyer, Chris Adami, Charles Ofria, & Rob Pennock).** Intelligence is one of the most complex biological capacities; understanding its evolutionary origins is of fundamental interest both to biologists, who want to understand how it was produced and how it works, and to computer scientists who want to reconstruct this powerful capability in artificial systems. The overwhelming complexity of brains (particularly in humans) has been a primary obstacle to 'top-down' analyses of natural brain functions and design of artificially intelligent machines. However, evolution provides a 'bottom-up' perspective for understanding intelligence.

For this sandbox, we adopt Kamil's broad definition of intelligence as "those processes by which organisms obtain and retain information about their environments, and use that information to make behavioral decisions." We plan to discuss topics related to selective pressures that promote the initial evolution of intelligent behaviors (including information acquisition, storage, processing, and use in adaptive behavior), how more powerful cognitive processes can be produced, and how to construct artificial systems that can replicate these dynamics, ultimately to produce applied intelligent solutions to real-world problems. In particular, we plan to explore how the evolution of intelligence can be best studied in biological organism (in both the field and the laboratory), as well as what systems and experiments are likely to have the most success in the computational realm (in digital organisms, artificial neural networks, or Markov Network Brains, to name a few).

**10:30-12:00, 1:30-3:00, BEACON Seminar Room. Workshop: Increase Your Broader Impacts with Data Nuggets! (Elizabeth Schultheis & Melissa Kjelvik).** Do you need to increase broader impacts for your research? Want to further develop your communication skills? Come to our hands-on workshop at BEACON Congress and create a Data Nugget based on your research!

Data Nuggets are short worksheets that emphasize developing quantitative skills for K-16 students. They are based on recent and ongoing research, bringing cutting edge research into the classroom and helping scientists share their work with broad audiences. The standard format of each Nugget provides a brief background to a researcher and their study system along with a dataset from their research. Students are then challenged to answer a scientific question, using the dataset to support their claim, and are guided through the construction of graphs to facilitate data interpretation.

We are currently seeking to add to our collection of Data Nuggets to increase the diversity of topics covered and showcase science done all over the country. See examples of Data Nuggets and learn more about our project at <http://datanuggets.org>. During the workshop we will walk you through our template and help you identify a proper dataset, scientific question, and hypothesis for students of many ages. In order to finish a Nugget within the allotted time, participants must come to the workshop with a dataset already selected. \*NOTE: This is a 3-hour workshop – you will need to attend both sessions.

**1:30-3:00, BPS 1415. Sandbox: Priorities in Evolution Education (Louise Mead).** Next Generation Science Standards place evolution as one of four core concepts, and new "science practices" stress inquiry and defending claims using evidence. However, a recent report suggests intermediate levels of

understanding of science and evolution and low levels of evolution acceptance among America's educators of prospective teachers. How can BEACON take a lead in developing materials and training teachers to meet this next generation of STEM education? Is there a place for BEACON education in influencing change in undergraduate courses as well? Let's identify a plan of action and develop clear goals for addressing these issues.

**1:30-3:00, BPS 1420. Sandbox: Increasing the Impact of Evolutionary Computation (Brian Goldman).** From improving scientific practices to better meeting the desires of industry, this group discussion will focus on how to make Evolutionary Computation reach its full potential.

**3:30-5:00, BPS 1410. Plenary Sandbox: Grand Challenges in Evolution in Action (Charles Ofria).** As part of BEACON's mission in advancing the role of Evolution in Action in science, education, and broader society, we plan to identify a set of major goals for the field over the next decade. These "grand challenges" will be intended to provide focal points for collaborative efforts, excite the general public, and provide exciting funding opportunities for potential sponsors. For this sandbox session, we will discuss suggestions for grand challenges generated at many of the other sessions this congress, including ad hoc discussion groups that wish to propose one.

Grand challenges should consist of goals that will notably advance the state of the art, and that we expect will take about 10 years to accomplish (i.e., somewhere between five and 20 years). An effective challenge must be sufficiently well defined that its completion should be clear and relatively non-contentious to experts in the area. At the same time, grand challenges should be general enough in scope that a variety of researchers and educators in BEACON will benefit from the challenge being completed. For this session, suggested grand challenges should be kept succinct, ideally under 50 words. We will plan to spend at least five minutes discussing each suggestion (depending on the total number), followed by broader discussion of the future role of these challenges in BEACON. In addition to producing an initial set of grand challenge candidates from this session, we also plan to assemble a position paper reviewing many of the challenges proposed and arguing for their importance.

## **Contributed Talks**

*All Contributed Talks will take place in BPS 1410. Presenter is underlined.*

**Sunday, August 17**

### **Mutation, Selection, & Speciation, 10:30-12:00**

**10:30 Jeffrey K. Conner, Anne M. Royer, Zhigang Zhao, Vanessa A. Koelling, Keith Karoly: Maintenance of a conserved trait: natural and artificial selection on stamen lengths in wild radish.**  
Tetradynamy, the presence of four long and two short stamens within each flower, is a diagnostic trait of the mustard family Brassicaceae, but the reasons for the maintenance of this trait across most of the 3700+ species in the family are unknown. Previous functional studies of pollen removal and selection through male fitness (seed siring success) suggested that the short stamens function to reduce per-visit pollen removal, which increases male fitness under high pollinator visitation rates (Conner et al. 2003 *Evolution*). To further test this hypothesis, we expanded the phenotypic variance of the difference in stamen heights through artificial selection, and measured selection on this trait across multiple days that naturally varied in pollinator visitation rate.

**10:45 Ken Zellig, Carissa Zielinski, Jimmy Woodward, Maren Friesen, Sharon Strauss: Effects of competition and microbial symbiosis on plant phenotype in a polyspecific *Trifolium* community.**  
*Trifolium* (clover) is an extremely diverse legume genus, with over 240 species characterized. The dynamics of *Trifolium* speciation and ecological niche maintenance are not well understood. The Bodega Marine Reserve field site, administered by the University of California, Davis, hosts 8 native *Trifolium* species and several exotic species. The exceptional species richness of this habitat provides a singular opportunity to investigate how plants maintain ecological niche. As a nodulating legume, *Trifolium* also enables us to study the effect of a major mutualism on speciation and niche maintenance; we hypothesize that the symbiosis with *Rhizobium* bacteria plays a major role in niche construction. To probe the effects of competition on plant phenotype and mutualistic behavior, we have grown over 1000 plants from 3 species in a variety of competitive environments, using sterile field soil and microbial treatments comprising bacterial, fungal, and mixed inoculations. We are currently gathering plant phenotype data, including basic plant fitness, *Rhizobium* colonization data, and root architecture data. We report here preliminary results on the effects of conspecific and congener competition in a greenhouse experiment. This experiment, while itself large in scale, will be the first in a series of competition experiments to investigate niche maintenance in *Trifolium*; future experiments will use transcriptomics to elucidate further niche divergence between species, and study in more detail the effect of symbiotic partner choice on niche maintenance.

**11:00 Annat Haber, Will Pitchers, Ian Dworkin: Breaking the mold: the effects of mutations on phenotypic covariation in the fruit fly wing.** The study of character covariation can yield important insights into the interplay between genetic architecture and selection in determining evolutionary trajectories. However, the implication of covariation for evolution depends on its stability relative to the evolution of the population mean. In order to better understand the potential of covariation to change due to segregating variation or fixation of alleles, we used 12 mutant strains of *Drosophila melanogaster*, as well as 12 inbred strains derived from natural populations. All mutant strains were backcrossed into the Samarkand wild type (Sam). All mutations were associated with either the EGFR or TGF- $\beta$  pathways, known to affect adult wing shape. All individuals within a genotype are genetically identical, and therefore their covariance matrix reflects environmental factors only. We extracted 48 landmarks and semi-landmarks from the wing, and superimposed them using Procrustes superimposition. In addition, we used LORY, a recently developed method for evaluating local shape variables as the determinant of the Jacobian matrix of local deformations. This method translates the multidimensionality of the Procrustes coordinates into a multivariate dataset that is amenable to conventional multivariate analyses and therefore more suitable for quantifying covariation. We calculated the covariance matrix and mean shape for each genotype and estimated their differences in terms of total variance, matrix eccentricity, matrix pattern, and mean shape. Mutants that differed more from Sam in their mean shape also had a greater total variance among individuals, suggesting an association between shape change and the level of

phenotypic decanalization. Most mutations do not alter the eccentricity of the matrix, and there is no relationship between shape changes and eccentricity. Differences in covariance pattern, measured as differences in average response to random skewers, correlate positively with shape differences. However, comparing shape space with covariance space indicates that shape changes faster than covariance, suggesting an upper bound on the mutability of covariance. These results suggest a complex non-linear relationship between development and phenotypic variation, and indicate that different aspects of the covariation structure can change independently from each other. In addition, mutation effects do not cluster based on their targeted pathway, suggesting complex pleiotropic interactions that are not yet understood in this system.

**11:15 Jason Keagy, Lilliana Lettieri, Janette W. Boughman: Male competition fitness landscape predicts both forward and reverse speciation.** The effect of sexual selection on speciation is unclear. Male competition's effect on speciation is especially overlooked, despite its direct effect on male reproductive success. Speciation through male competition might occur if disruptive selection from negative frequency dependent selection generated two fitness peaks. However, extant species often occupy small regions of phenotypic space near fitness peaks and thus cannot be used to effectively explore the entire fitness landscape for peaks and valleys. We used a lab-generated F2 hybrid population of two species specialized on different ecological niches, "benthic" and "limnetic" threespine sticklebacks, to estimate the male competition fitness landscape – the multivariate relationship between male phenotypic traits and male ability to build and defend nests. We found an axis of disruptive selection with two fitness peaks corresponding to the multidimensional phenotypes of limnetic and benthic sticklebacks. Although individuals corresponding to these multidimensional phenotypes were not common, rareness per se did not predict fitness, instead suggesting that particular phenotypic combinations are important in male competition. In addition, we found several nonlinear axes of selection that would select for unique combinations of traits, i.e., hybrids. These axes predict one or more additional peaks on the fitness landscape that can explain the multidimensional phenotypic distribution currently observed in a case of reverse speciation after anthropogenic disturbance. Taken together, these results show that the male competition fitness landscape has remarkable predictive power for the multivariate phenotypic distributions of populations evolving both forward and backwards in the dynamic process of speciation.

#### **Teaching Evolution & Genetics, 3:30-4:30**

**3:30 Alita Burmeister, Richard Lenski, James Smith: Assessing student perceptions & explanations of microbial evolution.** Evolution is a core concept for biological literacy at the undergraduate level. However, evolution is often overlooked in microbiology classrooms. Evolution instruction especially lags in laboratory-based courses where the inertia is strong due to efforts involved in revising curricula. We used a theme of antibiotic resistance and evolutionary applications in an upper-level undergraduate microbial genetics laboratory course with the goals of (1) increasing students' ability to explain the details of evolutionary microbial genetics and (2) increasing students' acceptance and value of microbial evolution. We presented core concepts and applications of microbial evolution during the course's weekly lecture. One half of the class also completed a three-week *E. coli* evolution experiment ("treatment" group) while the other half completed only the traditional exercises ("control" group). We assessed the effectiveness of these activities using pre and post attitude surveys and open-ended content questions about microbial variation, inheritance, and selection. Students in both groups highly accepted and valued microbial evolution at the beginning of the semester and had slight but nonsignificant positive attitude gains at the end of the semester. Surprisingly, scores on the content questions did not improve by the end of the semester for either group. We attribute this in part to a lack of grade-based incentives and students' seemingly less earnest attempts on the post assessment. Of greater interest to microbial evolution curricula and assessment, we also observed the potential for traditional microbiological instruction to inadvertently reinforce misconceptions and confound definitions of the key terms "variation" and "selection." To develop suggestions for teachers to avoid these issues, we continue to investigate subdiscipline-specific definitions and language use. This study highlights the persistent need for microbial evolution education tools.

**3:45 Emily Weigel, Louise Mead, Terry McElhinny: Genetic variation as a pivotal point in genetics-to-evolution course sequences.** Evolutionary processes, while integral to biology, are often misunderstood. These deep, variable misconceptions stem frequently from students' first encounters with evolutionary terms, thus we need to understand what information (and misinformation) students obtain from courses preceding Evolution. This is particularly important with respect to Genetics courses, as they often serve as a prerequisite introduction to the fundamental genetics underlying evolution. This study (1) quantified the extent to which students who have taken Genetics retain and apply information to concepts in Evolution; (2) evaluated why specific fundamental concepts show differences between these courses; and (3) compared results from these courses for performance related to key genetics concepts as they relate to evolution. A 16-question assessment was created from the Genetics Assessment literature (GLAI, GeDI and the Genetics Assessment For Core Understanding) and course textbooks. Questions were multiple choice, agree/disagree, and fill-in-the-blank formats, spanned Bloom levels, and concerned previously-documented misconceptions. This assessment was administered at three timepoints: at the end of Genetics (to establish a knowledge baseline), beginning of Evolution (to determine what information has been lost since taking Genetics,) and end of Evolution (to determine with what information students leave the course sequence). Overall and individual item performance were compared using repeated measures mixed models. We found that undergraduate students harbor a number of genetics misconceptions, of which understanding genetic drift appears most pivotal. This research provides possible advantages of a Genetics-to-Evolution course sequence and a better understanding of how timing may influence the integration of material across areas of Biology.

**4:00 Wendy Johnson: The effects of Avida-ED on students' explanations of evolution.** Students' difficulties learning about evolution are well documented in the literature. In addition, recent reform efforts such as Vision and Change and The Next Generation Science Standards emphasize the need to engage students in scientific practices such as asking questions, planning and carrying out investigations, analyzing and interpreting data, and constructing explanations. Instructors face many challenges in teaching evolution in these ways because it is difficult to observe in typical classroom and laboratory settings. As students learn fundamental evolutionary concepts, the explanations they develop are often mixtures of both scientifically accurate ideas as well as scientifically incorrect intuitive reasoning. Educational researchers and curriculum developers are working to identify more effective ways of teaching evolutionary concepts that help students develop both content knowledge and scientific reasoning skills. Avida-ED digital evolution software is one such method; it allows students to observe evolution in a digital environment and to develop and test hypotheses about the processes. Previous work has demonstrated that the use of Avida-ED significantly improves students' understanding of basic evolutionary processes. Current work seeks to compare student learning in two sections of an undergraduate introductory biology course: one that included Avida-ED activities versus one that did not. Preliminary analysis of students' written explanations suggests that those who used Avida-ED developed a more scientifically accurate understanding. The results of this study inform Avida-ED curriculum development and future classroom implementation as well as further support the hypothesis that Avida-ED is more effective for teaching evolutionary concepts than traditional teaching methods alone.

**4:15 Jared Moore: Evolve-A-Robot: An evolutionary robotics environment in the web browser.** Web-based applications are highly accessible to users, providing rich, interactive content while eliminating the need to install software locally. Previous online evolutionary demonstrations (PicBreeder, Endless Forms, and BoxCar2D) have successfully demonstrated concepts to a broad audience. However, evolutionary robotics (ER) has faced challenges in this domain as web-based technologies have not been amenable to 3D physics simulations. Traditionally, physics-based simulations require a local installation and a high degree of user knowledge to configure an environment, but the emergence of Javascript-based physics engines enables complex simulations to be executed in web browsers. These developments create opportunities for ER research to reach new audiences by increasing accessibility eliminating the need to download and install software. In this talk, we introduce the Evolve-a-Robot website, an online tool for evolutionary robotics researchers as well as K-12 students and the general public. Through the use of modern web technologies (WebGL, ThreeJS, and PhysiJS), we have created a completely browser-based implementation of an ER environment. Users explore the evolutionary process by interacting with different parameters of a genetic algorithm and observe the effect of changes immediately in the evolved simulated robots.

**4:30 Allison Walker: Speculative fiction: Literature raises questions about the ethicality of genetic research.** Margaret Atwood, Canadian author of over 40 works of fiction, nonfiction, and poetry, coined the term "speculative fiction" to describe her most recent and thrilling work to date, the MaddAddam Trilogy, a dystopic vision of a future that is "eerily plausible," drawn from current headlines and cutting edge research being conducted in labs around the globe and in our very own backyards. Literary Darwinists and scholars in the emerging field of neurohumanities continue to collect evidence of the biological and psychological effects of language, noting that readers of fiction (as opposed to nonreaders and readers of nonfiction) are more empathetic toward their fellow humans. Literature is therefore a vital addition to any educational curriculum. Exposing students to literature such as Atwood's encourages creative and critical thinking as the characters in the story (and the students themselves) are forced to grapple with big questions of biomedical ethics, politics, and ecology. Atwood's trilogy infuses science fiction with real and accurate science, encouraging readers to speculate about our shared evolutionary past and the future of genetic research.

**Monday, August 18**

**Communication, Cooperation, & Intelligence, 10:30-12:00**

**10:30 Eric Bruger, Chris Waters: Quorum sensing promotes the maintenance of public goods production in experimental populations of *Vibrio harveyi*.** Information exchange, such as by signaling, has been proposed to have an important role in promoting some cooperative behaviors. Quorum sensing (QS) is a form of chemical communication performed by many bacteria in response to both biotic and abiotic environmental cues. In the marine bacterium, *Vibrio harveyi*, a significant fraction of the genome is regulated by QS, including a number of genes encoding exoproduct public goods that are potentially exploitable by non-producing defectors. Thus, this QS system is situated in control of cooperative behaviors, which commonly provide a quandary for evolutionary biology to explain. Typically, alternative conditions such as high relatedness or spatial structure are provided to explain the persistence of cooperation. Interestingly, we have found that, for this bacterium, even in a well-mixed environment cooperative protease production is sustained in cells that have a functioning QS system, while in all cases defectors cheat on and dominate a constitutive QS strain. These results were found in both competitions with lab generated defector mutants and in the presence of defectors that arose in experimentally evolved populations. Briefly, we find that 1) *V. harveyi* QS allows for facultative cooperation which a) provides a potential stabilizing mechanism for cooperative behaviors such as protease production by minimizing cheating and b) potentially leads to cheating on cells that overproduce public goods, and 2) the extent of QS activity that cooperative cells perform also appears to be under selection during experimental evolution.

**10:45 Randal S. Olson, Patrick B. Haley, Fred C. Dyer, Christoph Adami: Exploring the evolution of a trade-off between vigilance and foraging in group-living organisms.** Despite the fact that grouping behavior has been actively studied for over a century, the relative importance of the numerous proposed benefits of grouping remain unclear. Here, we use a digital model of evolving prey under simulated predation to directly explore the evolution of cooperative foraging behavior according to one such benefit, the "many eyes" hypothesis. According to this hypothesis, collective vigilance allows large groups of prey to detect predators more efficiently by making alarm calls and communicating the presence of predators to each other, thereby allowing individuals within the group to spend more time foraging. However, the question remains: Is the benefit of collective vigilance sufficient to outweigh the significant costs of grouping and select for cooperative foraging behavior? In this talk, I will demonstrate how group genetic relatedness and prey reproductive strategy play a major role in the evolution of cooperative foraging behavior.

**11:00 Chris Adami, Masoud Mirmomeni, Arend Hintze, Eli Strauss, Kay Holekamp: What games are these hyenas playing? Unraveling the selective pressures shaping dominance hierarchies.** Hyena societies are organized according to a linear dominance hierarchy, where the dominant female gets first access to a kill, while subdominant members (in particular males) are the ones that actually do the hunting. The strict hierarchical structure is extremely unfair to the lower ranking members of a clan,

which brings up the question: how can such a social structure be evolutionarily stable? I argue that we should be using the tools of evolutionary game theory to investigate this question, and study a number of different game forms towards answering the question: "What games are these hyena playing, and why do they continue to do so?"

**11:15 Lyndon Jordan, Sean Maguire, Randy Olson, Chris Adami, Hans Hofmann: Transfer of information through hierarchical social systems.** Here I will discuss how seeding information at specific nodes of an animal social network influences the flow of information through those systems. In hierarchical social systems, such as those found in human and animal societies, as well as in digital and corporate systems, information may not flow equally among nodes. This may be due to specific behavioural interactions along those networks that either facilitate or inhibit information exchange. Here I show that seeding information at the most behaviourally dominant network node (the dominant male) does not produce the fastest acquisition of group information. Rather, subordinate males in the network, traditionally thought to occupy unimportant network positions, are the most effective agents of information transfer within their social groups. Taking these empirical data, I then discuss ways in which biological networks and *in silico* evolution can be used to help construct optimal network designs for information flow.

**11:30 Aditya Rawal, Jenny Boughman, Risto Miikkulainen: Evolution of communication in mate selection.** A computational study is conducted to evaluate the hypothesis that mate selection is the evolutionary origin of communication. A population of neural networks is evolved for two cooperative tasks - mate selection and prey capture. Simple codes developed for mate selection serve as an effective stepping stone for prey capture but not vice versa. Mate selection followed by an additional prey capture task is also easier to evolve than both together from the beginning. This result suggests that mate selection may be a first step in the evolution of general communication systems in nature.

**11:45 Padmini Rajagopalan, Kay E. Holekamp, Risto Miikkulainen: The evolution of general intelligence.** When studying different species in the wild, field biologists can see enormous variation in their behaviors and learning abilities. For example, spotted hyenas and baboons share the same habitat and have similar levels of complexity in their social interactions, but differ widely in how specific vs. general their behaviors are. This paper analyzes two potential factors that lead to this difference: the density of connections in the brain, and the number of generations in prolonged evolution (i.e. after a solution has been found). Using neuroevolution, network structures with different connectivities were evaluated in recognizing digits and their mirror images. These experiments show that general intelligence, i.e. recognition of previously unseen examples, increases with increase in connectivity, up to a point. General intelligence also increases with the number of generations in prolonged evolution, even when performance no longer improves in the known examples. This outcome suggests that general intelligence depends on specific anatomical and environmental factors. The results from this paper can be used to gain insight into differences in animal behaviors, as well as a guideline for constructing complex general behaviors in artificial agents such as video game bots and physical robots.

### **Synthetic Biology & Evolutionary Applications, 3:30-4:30**

**3:30 Travis Hagey: Using FEA simulations to investigate the gecko adhesive system.** With over 1400 species, gecko lizards can be found using arboreal, terrestrial, and rocky microhabitats with the assistance of their adhesive toe pads. Gecko adhesive pads are composed of modified ventral scales called scanners, each containing millions of microscopic hair-like structures called setae (Russell, 1972). Working in unison, setae cling to a substrate using van der Waals interactions to produce strong frictional and adhesive forces, enough to support many times a gecko's bodyweight (Autumn et al., 2002; Hagey et al., 2014). To properly function, gecko setae are subject to multiple requirements, including self-cleaning, resisting clinging together, and performing on wet and dry irregular surfaces (Hansen and Autumn, 2005; Huber et al., 2007; Pugno and Lepore, 2008; Russell and Johnson, 2007; Stark et al. 2012, Vanhooydonck et al., 2005). Geckos must also efficiently detach their feet during locomotion (Hagey et al., 2014; Gravish et al., 2008). All of these requirements likely dictate gecko adhesive morphology, yet we find morphology to be highly variable within and between species with setal length varying 10-fold

across species (Peattie, 2007; Ruibal and Ernst, 1965; Hagey et al., 2014) and nearly four-fold within individuals (Johnson and Russell 2009). Previous studies have used mathematical models to investigate setal mechanics with limited success likely due to intra-individual variation (Hagey et al. 2014). As a result, we will use micro computed-tomography to build 3D reconstructions of the gecko adhesive system (see Dunlop et al., 2011). These reconstructions will be used to conduct finite element simulations, digitally replicating setal behavior during attachment and detachment. With this approach, we can investigate the causal relationships between setal morphology and performance. These new techniques will allow us to build upon previous biomechanical models of gecko adhesion while incorporating aspects of variation never previously included. This project also highlights how interdisciplinary approaches can be used to strengthen our understanding of animal biomechanics, patterns of evolution and adaptation, and synthetic adhesives.

**3:45 Joseph Graves, Jr., Mehrdad Tajkarimi, Quincy Cunningham, Adero Campbell, Herve Nonga, Scott H. Harrison, Jeffrey Barrick, Richard Lenski: Evolution of metallic/metallic oxide nanoparticle resistance in bacteria.** Metallic/metallic oxide nanoparticles are being deployed as antimicrobials in surgical gowns, surgical gauze, and medical implants. They are lethal to a wide variety of bacteria that are resistant to traditional antibiotics because they impact multiple physiological systems; therefore it is thought that bacteria cannot readily evolve resistance to them. This assumption persists despite the fact that silver and other heavy metal resistance elements are already widely circulating in nature. My laboratory has utilized experimental laboratory evolution to produce silver nanoparticle (AgNP) resistant bacteria. This was achieved within 100 generations via exposure to 10nm citrate-coated AgNPs. *Escherichia coli* strain K12-MG1655 was chosen for this experiment because it does not harbor any of the known chromosomal or plasmid borne silver resistance elements (sil.) This study reports the increase in bacterial growth and minimum inhibitory concentration of AgNP resistant bacteria (T1 – T5) compared to their controls (C1 – C5.) In our first assays of AgNP resistance the (T1 – T5) populations showed greater resistance at concentrations of 100 – 2000 µg/L of bulk AgNO<sub>3</sub>; 50 – 2000 µg/L 10nm citrate-coated; and 2,000 -- 6,000 µg/l of 40nm citrate-coated AgNPs relative to controls at generation 300. Similar results were obtained with PVP-coated NPs. The treatment and control bacteria were resequenced at generations 100, 150, and 200 and compared to the ancestral strain. This analysis showed the rapid sweep of three putative silver nanoparticle resistance mutations to fixation in the treatment populations (in genes cusS, rpoB, and purL). The cusS gene encodes a membrane transporter protein that is involved in sensing copper (a heavy metal), rpoB has been associated with increased antibiotic resistance, and purL is involved in purine synthesis. These data indicate that relatively “naïve” bacteria can rapidly evolve resistance to AgNPs and that the genomic basis of such resistance is relatively simple. This result must be taken into account especially as new metallic/metallic oxide applications as antimicrobials are being deployed without consideration of the ability of bacteria to evolve resistance.

**4:00 Joshua K. Michener, Aline A. Camargo Neves, Stéphane Vuilleumier, Françoise Bringel, Christopher J. Marx:** Efficient use of a horizontally-transferred pathway for dichloromethane catabolism requires post-transfer refinement of the host. The horizontal transfer of genetic material is an important process in microbial evolution. When microbes acquire new abilities through horizontal gene transfer, the genes and pathways must function under conditions with which they did not coevolve. As a result, newly-acquired genes may place stresses on the host that the host is unprepared to accommodate. Productive use of the new ability, then, will depend on further evolutionary refinement of the recombinant strain. We used laboratory evolution to recapitulate this process of transfer and refinement, demonstrating that effective use of a horizontally-transferred pathway for dichloromethane degradation requires one of several mutations to the bacterial host that increase chloride efflux. We then applied this knowledge to identify the refining mutations present in two dichloromethane-degrading strains, *Methylobacterium extorquens* DM4 and DM17. Finally, we showed that imitating the refinement process using a synthetic mobile genetic element that carries both the degradation pathway and a highly-expressed chloride exporter can produce effective dichloromethane degradation in a wide range of *Methylobacterium* environmental isolates. Our results demonstrate the importance of post-transfer refinement in horizontal gene transfer, with potential applications in bioremediation, synthetic biology, and metabolic engineering.

**4:15 Chris N. Takahashi, Aaron W. Miller, Felix Ekniss, Maitreya J. Dunham, Eric Klavins: A low cost, customizable turbidostat for use in synthetic circuit characterization and evolution.**

Chemostats have proven to be extremely valuable tools for microbial evolution. However, chemostats only allow experimenters to probe cells under the condition of nutrient limitation, which represents just a cross section of continuous culture's full potential. The turbidostat was conceived to fill this experimental void enabling experiments in nutrient rich conditions very close to the washout point of a chemostat. Unfortunately, due to high costs and the technical challenges posed by building a turbidostat, experiments requiring turbidostats and similarly complex devices are rarely performed. Additionally, continuous culture designs that are more complex than the chemostat can vary wildly due to specific experimental needs, which contributes their limited utility.

We have developed an inexpensive, miniature, multiplexed, modular turbidostat. Our turbidostat incorporates 3D printable valves and pumps, alongside a modular culture chamber that enables rapid redesign of chambers as need. So far, derived designs include light induction systems for studying light sensitive inducers and a chamber with built in fluorometer. The control software is written in Python with user programmable modules that enable the user to expand capabilities beyond following a single setpoint, such as dynamically varying cell density and control of multiple media sources. Ultimately, we aim to create a rich community of users that contribute unique designs to the project, creating a repository of designs to choose from enabling a rich variety of experimental conditions to choose from.

**Tuesday, August 18**

**Molecular Evolution, 10:30-11:30**

**10:30 Michael Wiser, Noah Ribeck, Rich Lenski:** Evolutionary dynamics over large time scales. Experimental evolution allows us to study evolutionary dynamics as they unfold. The Long Term Evolution Experiment (LTEE) consists of 12 populations of the bacteria *E. coli* which have been evolving in parallel for 26 years, more than 50,000 generations. Here we discuss changes in fitness within the LTEE, both in terms of mean fitness and variance in fitness, and compare empirical results to theoretical expectations. We also compare these results to those from experiments within Avida tracking smaller populations for even larger numbers of generations. Our findings underscore the open-ended nature of the evolutionary process.

**10:45 Jacob Clifford:** Context-dependent selection of binding sites on DNA by cooperating proteins using a statistical theory. Generalizing the formalism of Berg and von Hippel who postulated that evolution selected sites to maintain a specific binding energy, we hypothesize that evolution shapes DNA binding energy as a function of the co-occurring binding sites in the flanking sequence of a site. We extracted from the literature Drosophila Dorsal DNA binding sites active in the Dorsal Ventral developmental network, and classified them based on their cis-distance from Twist in order to test the hypothesis that the co-occurring Dorsal sites with Twist sites are physically different from the Dorsal sites that are not co-occurring with Twist. We find that Dorsal sites that co-occur with Twist are different from the population average Dorsal sites both in sequence composition and information content. Furthermore we show how sensitive our hypothesis is to variations of the Twist motif and the threshold spacer distance between Dorsal and Twist sites.

**11:00 Amir Shahmoradi, Dariya K. Sydykova, Stephanie J. Spielman, Eleisha L. Jackson, Eric T. Dawson, Austin G. Meyer, Claus O.Wilke:** Predicting evolutionary site variability from structure in viral proteins: buriedness, packing, flexibility, and design. Recent works have shown that protein structure can predict site-specific evolutionary sequence variation. In particular, sites that are buried or have many contacts with other sites in a structure have been shown to evolve more slowly, on average, than surface sites with few contacts. Here, we present a comprehensive study of the extent to which numerous structural properties can predict sequence variation. The quantities we considered include buriedness measured solvent accessibility, packing density, structural flexibility (as measured by B factors, root-mean-square fluctuations, and variation in dihedral angles), and variability in designed structures. We obtained structural flexibility measures both from molecular dynamics simulations performed on 9 non-homologous viral protein structures and from variation in homologous variants of those proteins, where available. We obtained measures of variability in designed structures from flexible-backbone design in the Rosetta software. We found that most of the structural properties correlate with

site variation in the majority of structures, though the correlations are generally weak (correlation coefficients of 0.1 to 0.4). Moreover, we found that buriedness and packing density were better predictors of evolutionary variation than was structural flexibility. Finally, variability in designed structures was a weaker predictor of evolutionary variability than was buriedness or packing density, but it was comparable in its predictive power to the best structural flexibility measures. We conclude that simple measures of buriedness and packing density are better predictors of evolutionary variation than are more complicated predictors obtained from dynamic simulations, ensembles of homologous structures, or computational protein design.

**11:15 Caroline Turner, Richard Lenski: Evolution of elemental composition in *E. coli* under carbon and nitrogen limitation.** At the broadest level, organisms can be viewed as a collection of chemical elements in various ratios. These ratios vary between organisms. While this variation in elemental composition is known to have important ecological consequences, little is known about how it changes over evolutionary time. In previous work, we demonstrated that *E. coli* evolved higher nitrogen and phosphorus content and increased carbon use efficiency after 50,000 generations of evolution under carbon limited, high nitrogen and phosphorus conditions. However, this experiment did not differentiate between adaptation to carbon limitation and adaptation to other experimental conditions such as growth in batch culture and in a well-mixed environment. To isolate the effect of nutrient limitation, we further evolved clones from the original 50,000 generation experiment under either carbon limited or nitrogen limited conditions for 1,000 generations. Nitrogen limited evolved populations exhibited dramatic increases in fitness and, unexpectedly, an increase in nitrogen content.

**11:30 Dakota Derryberry, Matt C. Cowperthwaite, Claus O. Wilke: Self-similarity of doubly-sequenced GBM samples in The Cancer Genome Atlas.** Glioblastoma multiforme (GBM) is the most common and deadly primary brain tumor. Since the advent of next-gen sequencing, research efforts have focused on (i) identifying all the mutations common in GBMs, and (ii) identifying specific, targeted therapies. This research, much of which has been done with The Cancer Genome Atlas (TCGA) sequence data, does assume that we are getting a complete and accurate genetic portrait of the tumor with only one sample. We test that assumption by comparing 68 TCGA samples that were sequenced twice. Within samples and between sequencing runs, we find some significant differences.