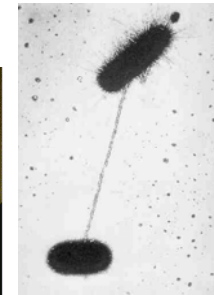


*Department of Ecology and Evolutionary Biology  
Yale University  
Faculty Research Interests*



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**Suzanne H. Alonzo** [suzanne.alonzo@yale.edu](mailto:suzanne.alonzo@yale.edu)  
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***Behavioral and evolutionary ecology, combining theory and empirical research.***

I am currently working on a variety of theoretical and empirical projects concerned with understanding the role of reproductive resources, conflict between the sexes and the existence of alternative reproductive behaviors on sexual selection and male and female reproductive behavior.

In the tessellated darter (a small fish found in most CT streams), we are studying female mate choice, male parental behavior and differences among populations in reproductive behavior. In the ocellated wrasse (found in the Mediterranean, I work in Corsica), I am using behavioral observations and genetic paternity analyses to understand male mating success, female choice among males and the effect of conflict over parental care on male and female behavior. I am also working with my postdoc, Bernard Brennan, on some theory of the evolution of male and female alternative reproductive tactics and some additional theory on the importance of life history strategies for management of exploited (fish and krill) species.

*Ocellatus* head



**Leo Buss** [leo.buss@yale.edu](mailto:leo.buss@yale.edu)  
<http://www.yale.edu/eeb/buss/index.htm>

***Biology of Hydractinia. Conceptual foundations of organismal/evolutionary biology.***

My lab studies:

- Colonial animal form, principally in cnidarians and ascidians, principally by the use of videomicroscopy and mathematical modelling.
- Invertebrate allorecognition (the capacity to recognize and react to conspecifics based on cell-cell contact), using techniques of classical and molecular genetics.
- Lower Metazoan comparative genomics, with a whole genome project on placozoans, EST projects on placozoans and ctenophore and mt genome projects on all major lower metazoangroups.

*Hydractinia* sp.



**Michael Donoghue** [Michael.donoghue@yale.edu](mailto:Michael.donoghue@yale.edu)  
<http://www.phylodiversity.net/donoghue/>  
*Plant evolution and systematics. Phylogenetics theory.*

Research in the Donoghue lab is focused on understanding the Tree of Life. In particular, we are working on the phylogeny of plants (and sometimes fungi). Mostly, this involves comparing gene sequences, but our aim is often to understand the evolution and development of morphological characteristics. Another major area of interest is in historical biogeography and the assembly of plant communities through time. Our main focus has been on understanding the dynamics of plant movement around the Northern Hemisphere during the Tertiary.

So, I would certainly encourage any students who might have an interest in the following areas to come and speak with me about research opportunities, summer work, etc.: plants, fungi, phylogeny, molecular evolution, plant morphological characters, and biogeography.

Order Dipsacales



**Jacques Gauthier (Geology & Geophysics)** [jacques.gauthier@yale.edu](mailto:jacques.gauthier@yale.edu)  
<http://earth.geology.yale.edu/people/moreinfo.cgi?netid=jg256>  
*Vertebrate paleontology. Systematics. Lizard evolution.*

I have students working on the anatomy, phylogeny and evolution of turtles, pterosaurs, lizards, crocodylians & birds and of course their diverse extinct relatives. I also have students considering problems in ecology (species/area curves in fossil record; global warming [“as seen through the eyes” of mammals and reptiles]) and geochemistry (using stable isotopes to tell what extinct animals were eating and what habitats they lived in, etc.). We always have room for volunteers, especially in fossil prep lab, and some support for research via the Peabody.



**Kealoha Freidenburg, Lecturer** [Kealoha.Freidenburg@yale.edu](mailto:Kealoha.Freidenburg@yale.edu)  
<http://www.yale.edu/eeb/people/index.htm>  
*Behavioral ecology and population ecology of aquatic vertebrates.*

As an ecologist, I am very broadly interested in the factors regulating species distributions and abundances. My research takes place in freshwater habitats and very specifically focuses on amphibian communities. There are two main branches of my research. First, I have been studying how forest canopy cover can influence amphibian communities. The amount of light reaching a pond surface dramatically changes the character of that pond and this in turn affects resident amphibian species and is responsible for performance differences (e.g., growth, development, time to metamorphosis) within a species (wood frogs, *Rana sylvatica*). The other part of my research has centered on trying to understand the impact of disease on amphibian populations, particularly in reference to urbanization.

Tadpole of *Rana sylvatica*



**Marta Wells, Lecturer** [marta.wells@yale.edu](mailto:marta.wells@yale.edu)  
<http://www.yale.edu/eeb/wells/index.htm>

*Role of mating signals in reproductive isolation. Behavior and molecular evolution of green lacewings.*

I am interested in understanding the role of mating signals in reproductive isolation among cryptic species of insects. Green lacewings of the order Neuroptera, provide a good system in which to study the role of courtship songs in reproductive isolation and at evolutionary changes in song features among closely related species. A combination of playback experiments, laboratory hybridization, electrophoretic and mitochondrial DNA studies has shown that many species of green lacewings are really groups of cryptic sibling biological species previously unknown. The temporal features of the courtship song (volley duration and interval) seem to be very important features to elicit duetting responses in females. Currently at the University of Connecticut, we are designing female choice experiments to try to understand what features of the male songs are preferred by females. In addition we are looking at aggressive behavior among males.

*Chrysoperla plorabunda*



## Research Scientists and Lecturers

**Gisella Caccone, Senior Research Scientist** [adalgisa.caccone@yale.edu](mailto:adalgisa.caccone@yale.edu)  
<http://130.132.86.97/labwebsite/Cacconelab.html>

**Molecular evolution. Conservation genetics. Director, ECOSAVE Conservation Genetics Laboratory**

Research in our laboratory includes several longstanding projects as well as work by undergraduates, graduate students and post-docs joining the laboratory to get training, collect preliminary data for grant proposals, and complete research contributing to senior projects, Master's theses or PhD dissertations. Some of the projects are: a) We have continued our ongoing work on understanding the evolutionary forces shaping the patterns of intra and inter-islands differentiation in Galapagos tortoises. b) In iguanas, we have compared the genetic make-up of samples before and after a severe oil-spill in 2001 to evaluate the impact of human induced stress (>60% mortality in the populations affected by the spill) on patterns and levels of genetic diversity. c) This year we started a molecular assay on blood and tissue samples of saltwater crocodile, *Crocodylus porosus*, indigenous to the Republic of Palau. The objectives of these studies are to determine: 1. If the Palauan crocodile population is composed of one or more separate species. 2. If the population reflects the genetic influence of crocodylian species other than *Crocodylus porosus*. d) We continue our work on understanding patterns of genetic and ecological diversification between and within populations of the main vector of malaria in Africa, the mosquitoes of the *Anopheles gambiae* complex.

Galapagos tortoise



**Mary Beth Decker, Research Scientist,** [Marybeth.decker@yale.edu](mailto:Marybeth.decker@yale.edu)  
<http://www.yale.edu/decker/>

I am interested in how oceanographic processes and climatic conditions affect the distribution, abundance and behavior of marine predators and their prey and how these processes affect trophic structure of coastal ecosystems. My current research involves the use of statistical models to examine long-term biological and physical data sets. Specifically, I am examining the factors that control jellyfish populations in the Bering Sea and Chesapeake Bay. For example, what are the linkages between temperature, salinity, current flow and prey availability and jellyfish temporal and spatial patterns? Jellyfish have the potential to control the flow of energy and nutrients through the food web due to their seasonally high abundance and their extremely high consumption rates. Thus, by determining the factors that influence the distribution and abundance of jellyfish, the impacts of these predators on ecosystems and economies could be predicted.

*Chrysaora quinquecirrha*

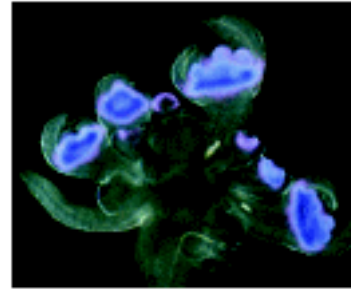


**Vivian Irish (MCDB)** [vivian.irish@yale.edu](mailto:vivian.irish@yale.edu)  
<http://pantheon.yale.edu/~vi5/>

**Plant development. Evolutionary developmental biology**

The Irish lab focuses on dissecting floral development in the model system *Arabidopsis* and comparative approaches to studying floral development from a variety of angiosperm species. Ongoing projects include characterizing evolutionary shifts in developmental control genes involved in flower development in tomato and poppies, as well as a project involved in examining the underlying genetic changes associated with different fruit morphologies in the Solanaceae (which includes tomato, tobacco, pepper, Petunia, eggplant).

Expression of the homeotic APETALA3 gene in *Arabidopsis* flowers



**Antonia Monteiro** [antonia.monteiro@yale.edu](mailto:antonia.monteiro@yale.edu)  
<http://www.arachnology.org/monteiro/>

The Monteiro lab seeks to understand the evolution and development of butterfly wing patterns. Research in the lab addresses both the ultimate selective factors that favor particular wing patterns, as well as the proximate mechanisms that generate those patterns. We combine tools from ethology, population genetics, phylogenetics, and developmental biology to dissect the molecular basis of intra and interspecific variation in developmental mechanisms generating color patterns, and the selective reasons why species display their particular color patterns. Our main model organisms are African satyrid butterflies in the genus *Bicyclus*, but we also dabble into pattern development of other butterflies and moths.

*Bicyclus anynana*

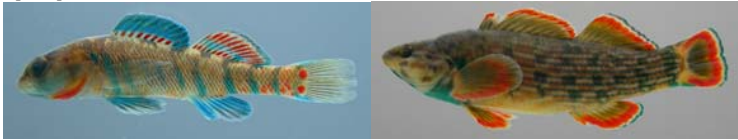


Thomas Near [Thomas.near@yale.edu](mailto:Thomas.near@yale.edu)

Our lab studies the evolutionary biology of fishes by retracing how species are related to one another. We primarily use DNA sequence data to reconstruct the evolutionary relationships of species that is represented through branching diagrams, or phylogenies. The molecular inferred phylogenies can be calibrated using fossil information to provide estimates of divergence times. Once divergence time estimates are available, then we can calculate speciation rates. With these tools we can ask questions that address both the pattern and process of evolutionary diversification.

In addition to Antarctica, our main field sites are in the beautiful areas of the Appalachian and Ozark Mountains of Tennessee, Kentucky, Georgia, Alabama, Missouri, and Arkansas. We offer many different opportunities to gain research experience and contribute to the growing and exciting field of evolutionary biology. Students in our lab are exposed to methods of field collection, curatorial practices in natural history museum collections, molecular biology, and methods of phylogenetic and genomic analysis.

<put species names here>



David Post [david.post@yale.edu](mailto:david.post@yale.edu)  
[http://www.yale.edu/post\\_lab/index.html](http://www.yale.edu/post_lab/index.html)

**Aquatic ecology. Influence of population processes on community structure. Food webs.**

The Post Lab studies food web interactions in a variety of aquatic and terrestrial ecosystems. Central questions include a) the effects of contemporary (rapid) evolution on ecological interactions, b) factors determining food web structure and dynamics, c) the impacts of changes in food web structure on ecosystem characteristics such as primary production and biodiversity, and d) the role of landscape structure and spatial linkages in mediating local interactions among species. We typically combine experimental and comparative methods with techniques ranging from population genetics to stable isotopes to address these questions under natural field conditions. Much of our research revolves around the influence of landlocked and anadromous alewives (a herring like fish) on lake and stream ecosystems in Connecticut. Anadromous alewives are an essential marine resource and a species of concern in New England. Our research on alewife has direct implications for the conservation and restoration of this important fish species, and for the conservation and management of freshwater ecosystems.

*Alosa pseudoharengus*

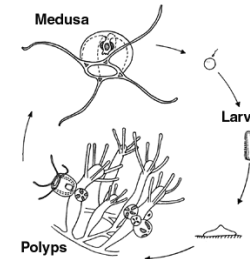


J. Rimas Vaisnys (Electrical Engineering) [juozas.vaisnys@yale.edu](mailto:juozas.vaisnys@yale.edu)  
<http://www.yale.edu/eeb/vaisnys/index.htm>  
**Dynamics of biological systems.**

My research centers on ecological and evolutionary processes, on the behavior of dynamical systems, and on the physics of computation. Specific systems of study have ranged from phage to hominids.

I am interested in the behavior of real systems and in using observational and theoretical techniques most appropriate to a given situation. Most recently, I have been applying techniques drawn from probability theory and statistics, discrete and computational mathematics, linear algebra, and differential equations.

*Podocoryne carnea*



Günter Wagner [gunter.wagner@yale.edu](mailto:gunter.wagner@yale.edu)  
<http://pantheon.yale.edu/%7Egwpwagner/index.html>  
**Evolutionary theory. Evolution of development. Mathematical biology.**

Recent advances in both developmental genetics and complex systems theory are fundamentally changing how we think about the evolution of organisms. The research interests pursued in the Wagner lab can be roughly divided in two groups:

1. Empirical work that relates to the developmental evolution of morphological characters; and,
2. Conceptual and mathematical work on the theory of evolution.

The common denominator of these two directions is the evolution of complex characters. Morphological characters are not the only complex characters worth considering but they are the paradigm of and the best understood examples of complex characters. Currently the most promising empirical approach to the evolution of complex characters is to study the genes that influence their development (e.g., the evolution of Hox genes) as well as to study the evolution of the developmental process itself. The goal is to obtain a mechanistic understanding of issues like "What is Homology", and "How did new characters arise in evolution (Novelty)".

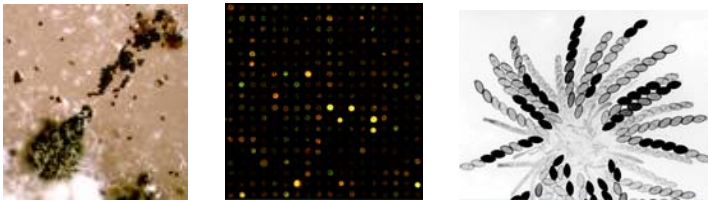
*Chalcides chalcides*



Jeffrey Townsend [Jeffrey.townsend@yale.edu](mailto:Jeffrey.townsend@yale.edu)  
<http://www.yale.edu/townsend/joinus.html>  
*Comparative and functional evolutionary genomics*

Members of the Townsend lab work to integrate mathematical, computational, and molecular biological tools to explain evolutionary processes. Experimentally, all projects in our lab are currently on the population genetics, interspecies fertility, development and functional genomics of The model fungi *Saccharomyces* (wine yeast) and *Neurospora* (bread mold). In particular, we are taking a systems biological approach (including mathematical modeling, simulation, and functional genomic experiments) to reveal the evolutionary biology of aging and LA dsRNA virus infection in *Saccharomyces*. With *Neurospora*, we are using microarrays to understand the development of fungal fruiting bodies and the evolution of species barriers to hybridization at the molecular level. Bioinformatic, computational, and theoretical projects ongoing range from examining the evolutionary impact of horizontal gene transfer on prokaryotes to the evolution of quantitative traits in multicellular organisms to phylogenetic informativeness of molecular sequence data, and there is plenty of flexibility about subject, topic, and approach.

*Perithecium and ejected spores of Neurospora crassa*



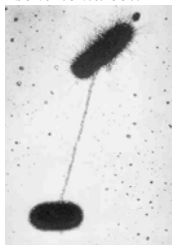
Paul Turner [paul.turner@yale.edu](mailto:paul.turner@yale.edu)  
<http://www.yale.edu/turner/home/index.htm>

*Experimental evolution in viruses, host-parasite interactions, evolution of sex.*

Microbes allow experiments on the order of hundreds (or even thousands) of generations, providing a uniquely powerful way to study evolution in action. The Turner lab uses RNA viruses, DNA viruses, and bacteria as model systems to test evolutionary and ecological theory, especially questions regarding the evolution of genetic exchange (sex), virus ecology and evolution, host-parasite interactions, and the evolution of infectious disease. We employ many approaches, including population genetics, genomics, molecular biology and mathematical modeling.

There are many exciting possibilities for undergraduate research in the Turner lab. For example, the viruses that we study have biology similar to pathogens such as Influenza Virus and West Nile Virus, but are capable only of infecting bacteria or tissue-culture cells. Therefore, we can safely harness microbes to examine key questions. What molecular changes occur as a virus emerges on a novel host species? How can we predict which pathogens are most likely to shift onto humans? Why do pathogens evolve resistance to drugs, and which biological mechanisms foster this evolution? How do ecological interactions among microbes, such as competition, predation, and parasitism, shape the formation of microbial populations and communities? Can we use evolutionary biology thinking to better design anti-viral and anti-bacterial therapies?

*Escherichia coli*



Jeffrey Powell [jeffrey.powell@yale.edu](mailto:jeffrey.powell@yale.edu)  
<http://130.132.86.97/labwebsite/main2.html>  
*Population genetics of Drosophila. Conservation genetics.*

**Mosquito genetics and evolution:** Our major ongoing work concerns the molecular evolution of genes involved in innate immunity of mosquitoes and their relationship to the ability to transmit malaria. Using an evolutionary approach, we hope to identify those insect immunity genes that specifically control the ability to transmit the most deadly form of malaria, that caused by *Plasmodium falciparum*.

**Drosophila codon usage:** The major new work involves the analysis of codon usage bias among the 12 species of Drosophila for which whole genome sequences are available. This provides a heretofore unprecedented rich data base for a set of species that have a well established phylogeny. Thus we can follow the evolution of changes in codon usage and infer the forces that account for codon usage bias.

**Galapagos giant tortoises:** Much of our ongoing efforts on this project concerns analysis of extinct populations of tortoises to supplement our large data set of extant populations in order to gain a better understanding of the history of these magnificent creatures. This involves extraction of DNA from museum specimens collected within the last 200 years.

*Anopheles gambiae*



Richard O. Prum [richard.prum@yale.edu](mailto:richard.prum@yale.edu)  
<http://www.eeb.yale.edu/prum/research.htm>  
*Evolutionary ornithology.*

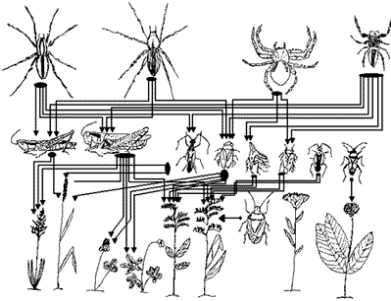
We are working on various research projects on the structure, function, development, phylogeny, and evolution of birds. Current projects include feather development, avian vision, the physics and evolution of structural coloration, morphology of the syrinx (the vocal organ) of birds, and DNA sequencing for population genetics, conservation, and phylogeny reconstruction. We are located next to the Yale Peabody Museum ornithology collections. So, it is also possible to conduct other research using the museums specimens.

*Lyrebird, Menura novaehollandiae*



**Oswald Schmitz (Forestry)** [oswald.schmitz@yale.edu](mailto:oswald.schmitz@yale.edu)  
<http://www.cbc.yale.edu/people/schmitz/>  
**Community ecology. Plant-herbivore interactions.**

We study the dynamics and structure of terrestrial food webs. We focus on plant-herbivore interactions and how they are mediated by carnivores and soil-nutrient levels, both at the level of herbivore foraging ecology and plant-herbivore population dynamics. We develop mathematical theories of plant-herbivore interactions and test these theories through field experiments. We deal with a variety of ecosystems and herbivore species, ranging from deer and snowshoe hare in northern Canada to insects in Connecticut old fields. Current research focuses on: 1. The role of soil nutrients and large mammalian herbivores in limiting forest regeneration after clear-cutting. 2. Herbivore behavioral responses to predators. 3. The dynamics of ecological food chains and food webs comprised of grassland plants and insects.



**Melinda Smith** [melinda.smith@yale.edu](mailto:melinda.smith@yale.edu)  
<http://www.eeb.yale.edu/smith/research.htm>  
**Community ecology, biodiversity and ecosystem functioning.**

We study how changes on species diversity impacts community and ecosystem dynamics, the impacts of global changes, (climate change, species invasions, altered biogeochemical cycles and land use change) on grassland plant communities, and linkages between genes, species and ecosystems. Ongoing projects are: 1. Comparative research on the effects of fire and herbivory on grasslands in North America and South Africa. 2. Impacts of changing climate on grassland ecosystems. 3. Linking genomics to ecosystem responses to climate changes. 4. Effects of multiple resource limitations on diversity and ecosystem functioning.

Grassland



**David Skelly (Forestry)** [david.skelly@yale.edu](mailto:david.skelly@yale.edu)  
<http://www.cbc.yale.edu/people/skelly/>  
**Population and community ecology. Regulation of amphibian populations.**

Our lab is following two primary lines of research. The first one examines how changes in thermal environment lead to rapid evolutionary responses. This work has relevance for understanding impacts of climate change. The second line of research is examining how human altered environments might promote disease and developmental deformities. Both research projects are focused on amphibians and employ a combination of field and laboratory techniques.

*Rana pipiens*



**Stephen Stearns** [stephen.stearns@yale.edu](mailto:stephen.stearns@yale.edu)  
<http://www.yale.edu/eeb/stearns/index.htm>  
**Life history evolution.**

We are investigating the effect of food quality and predation on *Daphnia* life history, including growth rate and reproductive output, by quantifying a set of visible traits produced by the interaction between the genotype and a range of environmental conditions (reaction norms). Predictions based on laboratory results will be tested in the field, providing an opportunity to relate nutrition to predation in a natural environment. Our research addresses the importance of food quality, predation, and genotypic variation on species interactions in the lake ecosystem.

The broader objective of the project is a more complete understanding of the complexity of the aquatic ecosystem. By incorporating chemical, physiological, and molecular approaches to understand ecosystem dynamics, the impact of human-induced environmental change, particularly the eutrophication of lakes via phosphorus enrichment, can be predicted at the molecular, individual, and food web levels. Given the growing stress on the lake environment worldwide, an increased understanding of the consequences of anthropogenic modification of freshwater ecosystems is vitally important.

*Daphnia sp.*

