Department of Ecology and Evolutionary Biology
Yale University
Faculty Research Interests
2011-2012








OML 122D **(ph) 432-3837**
165 Prospect Street **(fx) 432-2374**

www.eeb.yale.edu

Suzanne H. Alonzo ***suzanne.alonzo@yale.edu***
http://www.yale.edu/eeb/alonzo/index.htm

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. In my lab, we are also using mathematical theory to examine a wide variety of questions on the evolution and ecology of reproduction.

A parental male *Symphodus ocellatus* (photo credit: Daniel Bay)

Leo Buss ***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 hydroids, principally by the use of videomicroscopy and mathematical modeling
- Invertebrate allorecognition (the capacity to recognize and react to conspecifics based on cell-cell contact), using techniques of classical and molecular genetics
- Biology of placozoans, including the T*richoplax* genome project

Hydractinia sp.

Michael Donoghue ***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.

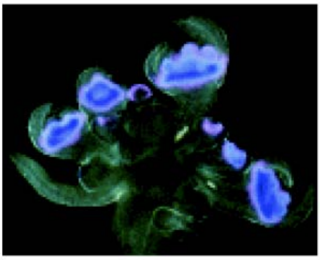
So, I would certainly encourage any students who might have an interest in the following areas to come and speak with me about research opportunities, summer work, etc.: plants, fungi, phylogeny, molecular evolution, plant morphological characters, and biogeography.

Order Dipsacales

Vivian Irish (MCDB) ***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).

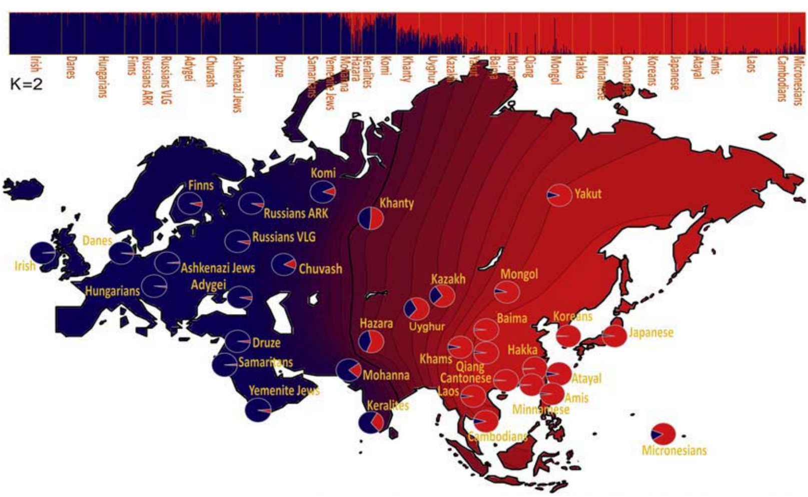
Expression of the homeotic APETALA3 gene in *Arabidopsis* flowers



Kenneth Kidd (Genetics, Psychiatry) ***Kenneth.kidd@yale.edu***
http://info.med.yale.edu/genetics/kkidd http://alfred.med.yale.edu

Human evolution, human diversity.
Our lab explores human diversity and how it relates to our understanding of personalized medicine (e.g., pharmacogenomics), overt phenotype (e.g., skin color), and recent human evolution using DNA polymorphism data we are collecting on over 3000 individuals from populations worldwide. The data contribute to understanding the origins of human diversity, including evidence of recent natural selection in some part of the world. For example, variation in genes for alcohol metabolizing enzymes indicates that natural selection in East Asia cause the high frequency of the variants causing the fIushing reaction. Our accumulated data on thousands of polymorphisms on thousands of individuals from dozens of populations are now being used to investigate many different research questions. Our recent publications, accessible from the lab's web site, illustrate many of those. Our bioinformatics interests are illustrated by ALFRED, the ALlele FREquency Database, which is accessed from around the world thousands of time a month.

A multi-locus cline across Eurasia.



Walter Jetz. ***walter.jetz@yale.edu***
http://www.yale.edu/jetz/wj_index.html

Section of Ecology, Behavior & Evolution.
Humans are currently causing distressing levels of biodiversity loss. My work in ecology, biogeography, and conservation seeks to understand the patterns and underlying processes of the geographic distribution of biodiversity and its potential clashes with environmental change. This research cuts across scales that range from home ranges of single individuals in a landscape to geographic ranges of thousands of species worldwide.

Antònia Monteiro ***antònia.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 developmental biology, population genetics, phylogenetics, and behavioral ecology, to dissect the molecular basis of 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 are now also interested in studying most butterfly and moth wing patterns. Students that join the lab develop their own research projects or participate in ongoing projects that involve fieldwork, behavioral work, and molecular or developmental biology.

Bicyclus anynana

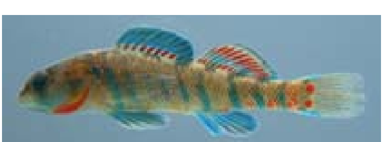
Nancy Moran ***nancy.moran@yale.edu***
http://eebweb.arizona.edu/faculty/moran/

Symbiosis, Genomics, Evolution, Insects, Bacteria, Bees.
Animals and plants interact with microbial symbionts that play diverse roles, from nutritional to defensive. These ““unseen” interactions play a large role in governing ecological processes in nature, and only now are the tools available to illuminate them. Microbial symbionts can be facultative or obligate for the hosts. Many symbionts cannot be cultured in the laboratory, but new technologies allow us to decipher their roles. We use these methods to study the evolutionary genomics of insect-microbe associations and the consequences of associations for both hosts and symbionts. In the course of this work, we have discovered the smallest known cellular genomes, as well as complex systems in which bacteriophage of symbionts protect the insect host against natural enemies. Particular research systems include aphids and their symbionts, and honey bees and their gut microbiota.
Often, students joining the lab initially help with an existing project, and then define their own independent project. Research topics involve bacterial or insect genomics, functional studies of insect-bacterial associations, microscopy, bioinformatics, or some combination.

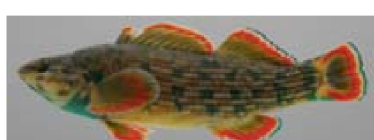
Thomas Near ***thomas.near@yale.edu***
http://www.yale.edu/eeb/near

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.

Etheostoma uniporum



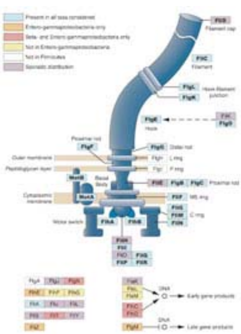
Nothonotus rufilineatum

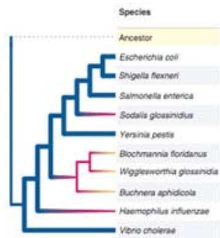


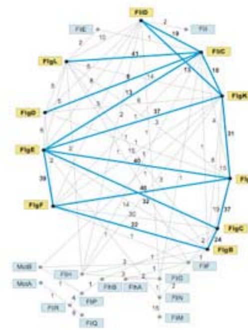
Howard Ochman *howard.ochman@yale.edu*
http://www.yale.edu/ochman/

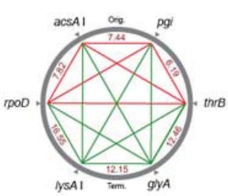
Genome Evolution. Bacterial Diversity.

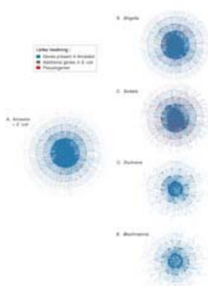
Bacteria are the most ancient and diverse lifeforms, and are present in virtually every environment. Due to their small and gene-rich genomes and the ease in which that can be experimentally manipulated, bacteria have traditionally been among the best-characterized organisms on the planet. In my laboratory, we investigate the following questions concerning bacterial evolution: (1) How do new and complex traits originate in bacterial genomes; (2) What processes drive the evolution of bacterial communities, and how do bacterial species interact with one another and with other organisms.

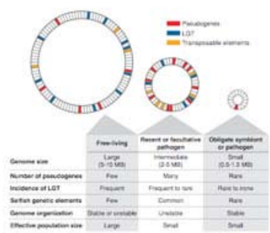












David Post ***david.post@yale.edu***
http://www.yale.edu/post_lab/index.html

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.

Annika Walters installing experimental low flow diversion

Young of the year alewives *Alosa pseudoharengus*

Erika Schielke *with* largemouth bass

Richard O. Prum ***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*

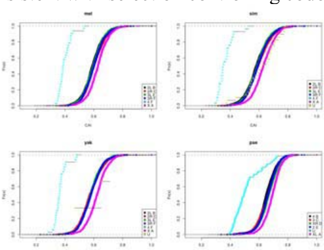
Jeffrey Powell ***jeffrey.powell@yale.edu***
http://www.yale.edu/powell/

Population genetics of Drosophila. Conservation genetics.

Molecular evolution and population genetics of *Drosophila* and mosquitoes.

Drosophila: Our main ongoing interest is to understand codon usage. Why are some codons preferred over others when they code for the same amino acid (synonymous)? We have developed an *in vivo* assay method to measure the effects of codon usage on transcription and translation using plasmid transfection of Drosophila tissue culture cells. To date, we have been unable to detect any effect of codon usage on transcription, while translational effects are substantial, sometimes up to a five-fold difference in level of protein expression. Development of this system opens the first opportunity to experimentally test several theories of the evolution of codon usage in a multicellular eukaryote.

Genes on different Drosophila chromosome arms ("elements") vary in level of codon usage bias. The blue set of points is the non-recombining F element ("dot" in most species). Bright pink is the X chromosome. The Y-axis is the frequency of use of the optimal codon, so the graphs for four different species indicate that the non-recombining F element has the least level of use of optimal codons, whereas the X has the most, consistent with selection controlling codon usage.

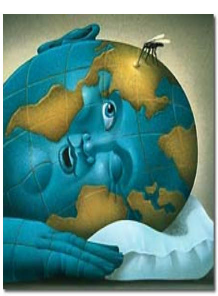


Mosquitoes: Our main focus presently is on *Aedes aegypti* and *Ae. albopictus,* two important vectors of viral diseases such as dengue fever. We have been using molecular population genetics to understand the genetic diversity of these widespread species as well as the history of their spread, some of it ongoing. This offers the exciting prospect of comparative studies of the genetics of invasiveness. We are using established methods (e.g., microsatellites) as well as developing new "next generation" sequencing technologies to delve into the molecular population genetics of these vectors in great detail, as well as providing the tools for studies of genetic control of virus transmission.

Invasion Biology and Epidemiology

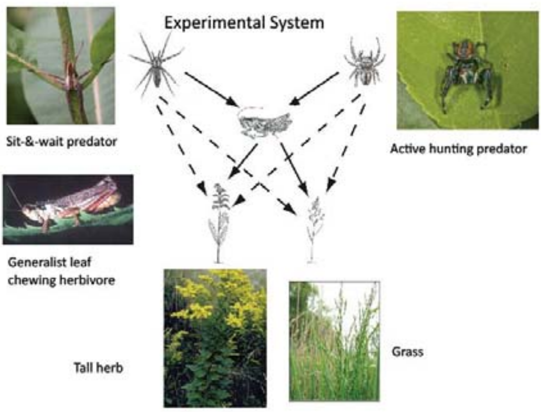
Invasion biology has largely not intersected with that of medical entomology, despite many historical examples of human-aided dispersal of disease vectors."

L. Philip Lounibos



Oswald Schmitz (Forestry and Environmental Studies) ***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 and linkages with ecosystem process. We develop ways to predict how phenotypically plastic responses of herbivores to fear from predators with different hunting modalities. We explore how such phenotypic plasticity determines herbivore selection of plants with different balances of carbon and nitrogen based nutrients and hence the nature of trophic structure and the flux of carbon and nitrogen through the ecosystem. We develop mathematical theories of trophic interactions and test these theories through field experiments. We work in a variety of ecosystems including tiger and deer dominated woodlands in India, jaguar and rodent dominated forests in Panama, and spider and grasshopper dominated meadows in Connecticut.



David Skelly (Forestry and Environmental Studies) ***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.

Hemispherical

Ambystoma maculatum

Melinda Smith ***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 impact 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.

Tall grass prairie in Kansas

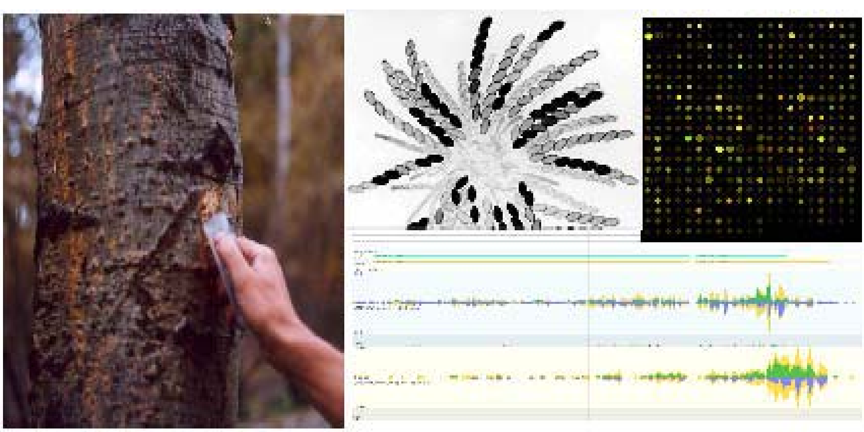
Stephen Stearns ***stephen.stearns@yale.edu***
http://www.yale.edu/eeb/stearns/index.htm

Life history evolution. Evolutionary medicine.
We are using the data gathered in the 3-generation Framingham Heart Study to answer these questions: Is natural selection operating on that contemporary human population? Do early-life components of fitness trade off with late life components of fitness? Can we use the genetic data gathered in the study – the genomes of many of the individuals in the second and third generations are marked by SNPs at 550,000 locations – to help resolve the paradox of the missing heritability by looking at epistatic interactions? Is there genetic evidence for meiotic drive? We are preparing to ask similar questions in other long-term data sets, starting with the long-term MRC study of villages in The Gambia.

Jeffrey Townsend ***jeffrey.townsend@yale.edu***
http://www.yale.edu/townsend/joinus.html

Comparative and functional evolutionary genomics.
The Townsend lab works at the interface of high-throughput experiment and probabilistic mathematical modeling and to explain evolutionary processes. Opportunities in the lab range from learningexperiences in laboratory methods to independent research in theoretical and computational biology.Theoretical work includes the use of computer simulation and analysis to better understand phylogenetics, evolutionary history, molecular evolutionary and population genetic processes.Computationally, experience programming in C/C++, Perl/CGI, SQL, Linux/Irix, HTML and Java is highly desirable. Experimental work in the Townsend Lab includes organismal culturing, microscopy, and molecular techniques including genome-wide DNA microarray analysis, often using the highly tractable baker's yeast *Saccharomyces cerevisiae* or the fireburn fungus *Neurospora crassa*. We encourage students with an interest in careers in science to design and carry out projects of their own or to become collaborators on current projects in the lab in areas that match their interests. We welcome students who are interested in the further development of their laboratory skills, as well as students who prefer to take on greater responsibility, taking a lead in data collection and/or analysis, and following projects through to publication. The lab has a history of publication with undergraduates as contributing authors.

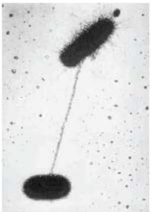
Ascus, microarray, and Neurospora crassa in nature.



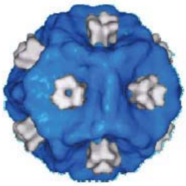
Paul Turner ***paul.turner@yale.edu***
http://www.yale.edu/turner/home/index.htm

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?

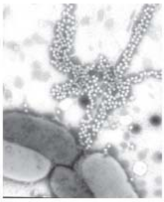
Escherichia coli



Protein Shell of virus phi-6



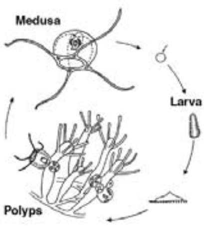
Viruses attached to bacteria



J. Rimas Vaisnys (Electrical Engineering) ***juozas.vaisnys@yale.edu***
http://www.yale.edu/eeb/vaisnys/index.htm

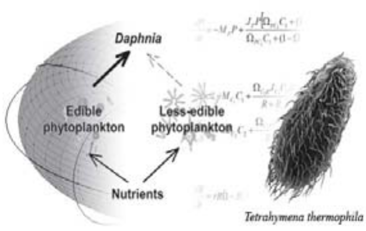
Dynamics of biological systems.
My research centers on ecological and evolutionary processes, on the behavior of dynamical systems, and on the physics of computation. Specific systems of study have ranged from phage to hominids. I am interested in the behavior of real systems and in using observational 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



David Vasseur, ***david.vasseur@yale.edu***
http://www.yale.edu/eeb/vasseur/index.htm

Environmental variation, population and community ecology, ecological theory.
I am interested in understanding how fluctuations in environmental conditions (e.g. temperature) influence many quantitative characteristics of populations and communities, from population variability to ecosystem biodiversity. Within this conceptual theme my research falls into three overlapping areas: i) the causes and consequences of spatial population synchrony; ii) understanding how the indirect effects of environmental fluctuations propagate through food webs; and iii) the influence of spatial and temporal scale on the expression of environmental fluctuations in population dynamics. To address questions in these areas I employ a combination of mathematical modeling, data analysis, and laboratory microcosm experiments using freshwater ciliates. The ciliophora are a wonderfully diverse phylum from which multi-trophic food webs can be assembled and tracked for many generations over a relatively short time.



Günter Wagner ***gunter.wagner@yale.edu***
http://pantheon.yale.edu/%7Egpwagner/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

Research Scientists, Visiting Faculty and Lecturers

Gisella Caccone, Senior Research Scientist ***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 2001to 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 have a started a project on the evolutionary genetics of tsetse flies (Glossina fuscipes), its parasites (Trypanosma brucei and others), and its symbionts (Wolbachia, Sodalis, Wigglesworthia) in Eastern Africa (Uganda, mostly). The project aims at understanding patterns of spatial and temporal structuring of these three different players with the goal of helping control sleeping sickness through an understanding of the population biology of vector, parasites, and symbionts. The project is in collaboration with Serap Aksoy and Alison Galvani from EPH. 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.

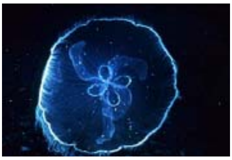
Galapagos Tortoise

Mary Beth Decker, Research Scientist, ***marybeth.decker@yale.edu***
http://www.yale.edu/decker/

Evidence is accumulating that gelatinous zooplankton populations have recently increased in size in some regions of the world. Factors including ocean warming, overfishing, eutrophication, and species introductions are thought to enhance jellyfish populations and jellyfish have been suggested as key indicator species of changing climate conditions. Jellyfish populations are opportunistic, responding quickly to environmental changes, both by increasing production rates of young jellyfish from the benthic polyp stage, and by increased feeding, growth, and reproduction of medusae in favorable conditions. My research examines how climate-induced changes in ocean biotic and abiotic conditions can cause variations in jellyfish populations by affecting their reproduction, survival, and growth. I am looking for undergraduate researchers to help collect jellyfish from the field and to help examine growth of jellyfish under various environmental conditions in the lab.

Chrysaora quinquecirrha, east coast sea nettle

Aurelia aureta, moon jelly fish



Marta Wells, Senior Lecturer ***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