Greetings from Walter Hall, where we have had a very busy fall. Last winter the EEB faculty wrote a self-study, a self-evaluation and planning exercise that happens about every decade. This fall we underwent internal and external reviews based on our self-study. The whole process has been simultaneously exhausting and invigorating, since it was a lot of work, but it brought the EEB faculty together to talk about the past, present and future and realize how happy we all are to be here.

We have recently landed two institutional training grants that will help build our graduate program and strengthen our partnership with the Marine Biological Laboratory. David Rand led a successful effort to land an NSF IGERT entitled “Reverse ecology: Computational Integration of Genomics, Organisms and Environments” that includes faculty from EEB, computer science, applied math, molecular and cellular biology and MBL to focus on the application of next-generation sequencing in ecology and evolutionary biology. Chris Neill, the new director of the Brown/MBL Institutional Partnership and our newest EEB faculty member, led the successful effort to fund an NSF PIRE grant entitled “Land Use, Ecosystem Services and the Fate of Marginal Lands in a Globalized World”, which will involve faculty and graduate students from MBL, sociology and EEB. Good work, David and Chris!

Congratulations to Kelly Benoit Bird (’98) a 2010 recipient of a MacArthur Award. Kelly is currently on the faculty at Oregon State University continuing her work on marine mammal acoustical communication. Congratulations also to Kate Smith for receiving the Exceptional Early Career Contribution to the Field of EcoHealth Award by the International Association for Ecology and Health. Congratulations are also in order for the new cohort of EEB Faculty F1s, Henry Oconee Edwards Dunn, Eva Rose Leslie Rich, and Alexander William Smith Sax.

New to EEB in 2010!

Kathryn Amatangelo:
Postdoc from University of Wisconsin-Madison, Sax Lab

Pascal Antoine-Christin:
Postdoc from University of Lausanne, Edwards Lab

Ryan Carney:
Graduate student from Yale University, Gatesy Lab

David Chatelet:
Postdoc from University of Tennessee, Edwards Lab

Marcy Cockrell:
Research Assistant, Leslie Lab

Tyler Coverdale
Research Assistant, Bertness Lab

Alexandre Fournier-Level:
Postdoc from University of Montpellier, Schmitt Lab

Francisco Borja Figueirido:
Postdoc from University of Malaga, Janis Lab

Laura Garrison:
Graduate Student from San Francisco State University, Edwards Lab

Stephen Goldsmith:
Postdoc from Ohio State University, Porder Lab

Amber Hardison:
Postdoc from Virginia Institute of Marine Science, Rich Lab

Angela Horner:
Postdoc from Ohio University, Roberts Lab

Heinke Jäeger:
Postdoc from Technische Universität Berlin, Porder Lab

Catherine Luría:
Graduate Student from Virginia Commonwealth University, Rich Lab

James Mossman:
Post Doc from University of Sheffield, Rand Lab

Rachel (Chelsea) Nagy:
Graduate Student From Auburn University, Porder Lab

Sohini Ramachandran:
Assistant Professor

Reena Sellamuthu:
Post Doc from Tamilnadu Agricultural University, Schmitt Lab

Stephen Smith:
Post Doc from Yale University, Dunn Lab

Pamela (Lauren) Szathmary:
Graduate Student from University of South Carolina, Bertness Lab

Sophia Tintori:
Research Assistant, Dunn Lab

Jonathan Wang:
Research Assistant, Schmitt Lab

Lei Zhu:
Post doc from Stony Brook University, Rand Lab
I am particularly interested in what we can learn about human history using genetic data. Some questions I study are: what were and continue to be barriers to migration since the modern human expansion out of Africa? Did sex-biased migration generally accompany colonization events in our history? Do different linguistic characteristics between populations accompany/affect genetic differentiation between those same populations? How can we use populations with strong founder events, like the Finnish or Amish, to effectively map genetic diseases? Can genetic variation explain the different incidence of various common diseases across ethnicities? As the study of life, biology has always encompassed a huge array of both questions and techniques to answer those questions. Biologists now accumulate data in such quantities that statistical and computational approaches increasingly yield important insights in our research. This is true in all areas of biology, but especially so in genomics, where technological advances have made DNA sequencing faster and cheaper than we could have once imagined. I started my dissertation analyzing 400 microsatellite markers in 1000 humans sampled from across the globe; four years later, we analyzed 650,000 single nucleotide polymorphisms in the same individuals. As I write this, the whole genomes of 50 of those individuals have been sequenced during the fall semester of 2010 via an effort at Stanford University.

I began graduate school at Stanford with a bachelor’s degree in applied mathematics, just as the reference sequence of the human genome was published. In conjunction with this huge event, efforts began to assess the genetic similarities and differences among globally-distributed individuals: namely, the Human Genome Diversity Panel (1000 two-generation-indigenous individuals) and the International HapMap Project (initially 270 individuals from Africa, East Asia, and descendents of Europeans; now over 1000 globally-distributed individuals) were both initiated and provided much of the data the human population geneticists have studied in the last decade.

I am interested in using datasets like these to infer aspects of human demographic history (specifically, quantifying the order and timing of population divergences, effective population size changes, and migration events) because these inferences provide us with a refined null model with which to study natural selection and how it has been shaping our genome. While an understanding of gene function is required to truly conclude a gene is under selection, looking for patterns in DNA sequences that strongly deviate from those we expect to see in the absence of selection under a particular demographic model gives us a sense of the types of signatures selection might leave on the genome.

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I am currently particularly interested in the X chromosome as a vehicle for studying selection, due to the exposure of deleterious recessive alleles to selection in males. One technique to study selection is using exome sequencing data (direct resequencing of the 20,000 genes in the human genome), and assessing how the distributions of synonymous and amino-acid changing mutations differ, assuming synonymous changes are not constrained by purifying selection and therefore reflect demographic signatures compared to the amino-acid changing mutations, which reflect the relative contribution of selective effects.

As the daughter of two statisticians, I grew up with a Lamarckian love of math problems and then was drawn to human population genetics as a field that brings together math, statistics, programming, archaeology, anthropology, and cultural history to understand the processes that produce and maintain human genetic variation. Before arriving in Providence, I was a postdoc at Harvard in the Society of Fellows, studying coalescent theory and the evolutionary forces that alter gene genealogies. I am delighted to now be a faculty member in Brown’s EEB department and Center for Computational Molecular Biology. It is exciting to be surrounded by such a stellar group of biologists, while also having access to applied math and computer science colleagues through the Center. I look forward to teaching Brown undergraduates and graduate students in the classroom and my lab, sharing with them the quantitative theoretical frameworks that can help inform their approaches to the scientific work they do.
Leslie lab member and Brown-MBL PhD student Sarah Corman was awarded the National Park Service’s George Melendez Wright Climate Change Fellowship this summer, to support her regional studies of productivity and phenology of the salt marsh foundation species Spartina alterniflora. The goals of this student fellowship program are to support new and innovative research on climate change impacts to protected areas and to increase the use of scientific knowledge toward resource management.

Nicolai Konow participated as "Scientist talent" in the recording of a feature-length documentary for National Geographic Television. This show, tentatively called "Speed Kills", is about the structure, function and biomechanics of fast-feeding predators in the open ocean. They basically spent a whole lot of time on closed-circuit rebreathers filming large and toothy fishes attacking their prey, using three submersible high-speed video cameras. The show is tentatively slated for world premiere in Feb 2011 - so, please watch out for it!

Sam Poore, MD,PhD ’04 has been on the move since packing up his Walter Hall office and heading west in September, 2004. A five-year residency in reconstructive surgery at the University of Wisconsin, Madison, kept him either in the operating room or at the bench well below the horizon most of the time, and sightings were rare. With his wife Hannah and two children, Anabelle 8 and Silas 5; Sam settled into a neighborhood not far from Lake Monona that provided bicycle access to the University Hospital. While a full-time surgical student himself during this period, Sam made time to mentor others and for each of three years was awarded the Resident Teaching Award by the medical students in appreciation of his efforts. Earning the Chief Resident appointment from 2008-09, Sam oversaw the day-to-day scheduling of several busy operating rooms while still managing to keep his hand in a research project directed at pediatric hand surgery and operating room safety. In July 2009, Sam began a one-year Fellowship at the Bernard O’Brien Institute of Microsurgery in Melbourne, Australia. The ideal of the Institute is to facilitate laboratory developed advances in tissue engineering and regenerative medicine into clinically successful therapies while providing clinical training in reconstructive microsurgery. Sam is busy managing a research program focused on the cultivation and manipulation of stem cells derived from human adipose tissue in addition to his surgical duties 2 - 3 days each week. The therapeutic goal is the rapid cultivation of tissue from stem cells for patients suffering from breast cancer, cardiac disease, and severe burns. But all is not work. Sam’s family is enjoying full emersion into the Australian culture and landscape with frequent excursions to the beach and outback, picnic basket and binoculars in hand. In September Sam will return to the University of Wisconsin, Madison to begin his tenure as Assistant Professor of Surgery in the Division of Plastic and Reconstructive Surgery. Well done Sam and the best of luck!

Johanna Schmitt has been elected as a fellow of the American Academy of Arts and Sciences (Induction ceremony Oct. 9, 2010)

Kate Smith - AWARD - Recipient of the 2010 Exceptional Early Career Contribution to the Field of Ecohealth Award from the International Association for Ecology and Health.

An EEB team ran the Cape Cod Marathon Relay race again on Halloween Day Oct 31st.

Since our den mother, Carol Casper, has retired (see May newsletter) (We miss you, Carol!), we are fortunate that Shannon Silva has moved over from Morphology to become our new department manager. Both Adella Francis and Trina Pappadia have also received promotions, Adella to Financial/Grants Coordinator and Trina to Graduate Program Coordinator, respectively. Congratulations to all! And, as of December 20, we will have a new administrative assistant, Amy Lanoie. Do drop by Walter Hall 101 to welcome Amy to EEB.

Friday afternoon get-togethers have become state-of-the-art affairs this semester, thanks to the efforts of Matt Heard and Robert Kambic. Far from sticking to the standard pizza and beer theme that stretches back into the early years of EEB, Matt and Robert have time and again come up with novel ways of celebrating that week’s end, complete to the demolition of one turkey on a memorable Friday in late November. Way to go, Matt and Robert!
Muscles are fascinating. Nearly every animal movement involves some sort of muscle contraction. Muscles contract to move your body regardless of whether you are locomoting (running, jumping, climbing on trees), eating (peeling a fruit, chewing, swallowing), singing, or even getting stressed before your doctor’s appointment (high blood pressure results from smooth muscle contractions in the walls of your arteries). With very few exceptions, animal movements are actuated by muscle and thus are governed by its abilities.

One aspect of muscle performance that I’ve been exploring for my thesis, the so-called “length-tension relationship,” is the fact that a muscle is not capable of producing the same amount of force under all conditions. A muscle produces its maximum force over a small range of motion, often called “the plateau region.” When the muscle is stretched beyond or shortened below this range, maximum force decreases. This fundamental limitation of muscle performance is a result of muscle’s molecular makeup and should therefore be true of muscles used for anything. The length-tension relationship has been well studied in the context of locomotion, but rarely in feeding. Imagine a hypothetical animal that has evolved a separate set of jaws in its throat. Weird to think about, I know, but bear with me. Some fish (minnows and carp are my favorites here) have fundamentally changed the use of their backmost gill arch for more efficient feeding. All respiratory function of this gill has been lost (the other, more forward gills thankfully work fine), and the gill has grown teeth by the same hox genes that create your teeth. Some minnows, like the 70-cm black carp that live in our lab at the moment, are snail-eaters, and their “pharyngeal jaws” have developed molar-like teeth specifically for crushing hard-shelled invertebrates. Black carp, then, should have the same troubles with extra large snails as our hypothetical animal had with extra large nuts.

So what have we here: performance that is highly relevant ecologically but extremely difficult to study (the back of the throat is occluded by gills, bones, and pharyngeal mucosa). How do we deal with it? I’ve dealt with it through performance trials using ceramic tubes and by monitoring that performance using XROMM imaging.

Together with an undergraduate, Eric LoPresti (now a graduate working as a technician in Argentina), I developed a method of controlling and varying the size and strength of food items. We took four different sizes of ceramic tubes and filled them with food, and our fish have been happy to crack them open. We coated each size of tube with one or more layers of polyurethane to increase its strength. Then we fed these tubes to our fish and offered progressively stronger tubes until the fish were unable to crush them anymore, establishing a maximum possible performance at each size. After a summer of feeding trials, we have discovered, as we might expect, that our fish have consistently lower maximum performance at large food sizes.

The second phase of this work has involved using x-ray videos to reconstruct actual bone movements (www.xromm.org has all the details on this intriguing technique), and thus muscle lengths. Using a transducer and electrically stimulating the muscle, we can measure force production with changes in muscle length. This work is still in development, but we hope that it will continue to shed light on how each of the jaw-closing muscles contributes to overall jaw performance.
2010 Fall Seminars

Brown Bag Seminars
Talks that catch up on research and work within the department.

9/17 Catherine Luria, Graduate Student.
Factors influencing the abundance, community composition, and activity state of bacterioplankton from the tidal freshwater James River.

9/24 Nick Gidmark, Graduate Student.
An histological exploration of the Cyprinidae and global warming.

10/1 Kathryn Amatangelo, Postdoctoral Research Associate.
Shifts in plant traits and communities over a half century in Wisconsin upland forests.

10/8 Heinke Jaeger, Postdoctoral Research Associate.
Testing mechanisms of species invasion in Galápagos: role of resource competition and species traits.

10/15 Rachel Nagy, Graduate Student.
Effects of land use/cover on ecosystem carbon storage in Apalachicola, FL.

10/22 Attila Bergou, Postdoctoral Research Associate.
Engineering falling with style: bat flight maneuvers.

10/29 Angela Horner, Postdoctoral Research Associate.
Crouched locomotion in mammals: the effects of habitat and aging.

11/5 Nicolai Konow, Postdoctoral Research Associate.
Muscular control of animal movement.

11/12 James Mossman, Postdoctoral Research Associate.
The role of mitochondrial genetic variation on sperm function.

11/19 Alexandre Fournier-Level, Postdoctoral Research Associate.
The Map of adaptation in Arabidopsis thaliana.

12/3 Amber Hardison, Postdoctoral Research Associate.
Carbon and nitrogen cycling within the sediment microbial community.

Monday Colloquia
A more formal colloquium that features speakers outside of the University.

9/13 Rick Ostfeld, Cary Institute of Ecosystem Studies.
Biodiversity loss and the rise of emerging infectious diseases.

9/20 M. Deane Bowers, University of Colorado, Boulder.
Eating and being eaten: The ecology and evolution of caterpillar chemical defense.

9/27 Peter Girguis, Harvard University.
Peering into the lives of microbes: Insights into microbial hydrocarbon cycling and extracellular electron transfer in the deep sea.

10/4 John Stachowicz, University of California, Davis.
Consequences of species and genetic diversity for marine communities.

10/18 Steven Allison, University of California, Irvine.
Linking ecosystem processes with microbial evolution and physiological adaptation.

10/25 Theodore Fleming, University of Miami.
The pollination of Sonoran Desert columnar cacti.

11/1 Brenna Henn, Stanford University.
Evolutionary history of African hunter-gatherers inferred from genomic data.

11/8 John Doebley, University of Wisconsin.
The evolution of plant form: an example from maize.

11/15 Stephen Deban, University of South Florida.
Cold-blooded snipers: ectotherms.

11/22 Douglas Schemske, Michigan State University.
Ecological genetics of geographic adaptation in Arabidopsis thaliana.

11/29 Hugh Ducklow, The Ecosystems Center, MBL.
Palmer LTER: Process studies in a rapidly changing polar marine ecosystem.
In the Greenhouse

By Fred Jackson

Aside from the long wait before renovations of the research greenhouse begin, activity is still apparent at the Plant Environmental Center.

Students Andrew Migneault ’11 and Maddie Brown ’10, frequent visitors and plant enthusiasts, apparently became bored with the conservatory and have taken it upon themselves to design a new layout for it. The conservatory is a 1,800 ft² greenhouse, open to the public and used extensively by art and biology classes. Presently, most plants in the conservatory are displayed according to families, with one display of South American medicinal plants. Projected new exhibits include Chinese medicinal plants, fragrant/oil plants, carnivorous plants, unusual plants, and economic plants. New signs and self-guided tours are also in the works with this project.

Laura Garrison, a new graduate student in the Edwards lab, is starting a project in the research greenhouse. As a pilot project for her dissertation work, she will be growing 50 species of grasses, chosen to represent as many as possible of the transitions between C3 and C4 photosynthesis in the grasses. Laura will take measurements of leaf gas exchange, heavy isotope composition, and other physiological traits, with particular emphasis on traits relevant to the global carbon cycle. The data will be analyzed in a phylogenetic framework to determine whether variation among species is better explained by shared evolutionary history or by photosynthetic type. In addition to being a pilot dissertation project, the plants will also serve as an alternative project for the laboratory section of Plant Ecophysiology in the spring; students will measure photosynthetic rate, daily water potentials, and stomatal conductance, and use the plants to understand the physiological differences between photosynthetic types. Laura, welcome to the greenhouse!

New book from EEB

Steven Haddock and Casey Dunn have written a most useful book, Practical Computing for Biologists (Sinauer), launched on November 1st. Some of you may recall an early incarnation of these materials from the graduate seminar.

The funky cover design of a microcontroller board cum shorebird suggests from a distance that the authors have designed a user-friendly book. Its raison d’être is to apprise scientists, especially biologists, of methods that make it feasible (i.e., possible) to handle large data sets economically and efficiently, making use of materials freely available on the web. It’s explicitly not a book on programming, but an effort to present a range of tools and a variety of applications to ease the way of those less confident, and in the process build up courage to handle more complex problems. In this regard, the book serves a most useful purpose, for most of us really don’t know the extent of the resources available in the computer in front of us or of the freeware available on the web. Although much of the current attention over monstrous data sets concerns the genomics explosion, biologists have many other large-scale computing needs (phylogenetics, ecosystem analysis, etc.) – and our needs will only accelerate.

The book consists of 22 chapters, which cover a broad span of subjects, from setting up to command lines, Python programming (the language adopted in this book), and working with pixel images. Chapters begin with a brief statement about the information to follow and end with a bulleted summary listing the specific points you will have learned, other words of wisdom (“Moving Forward”) and recommended reading. Colored symbols in the margins identify tips, potential pitfalls, and notations of where Windows and Linux differ from the OS 10 used here.

Although the text focuses on Mac OS X, it provides parallel instructions for Windows and Linux where needed, making it useful for all. It can be used as a self-guiding primer, as well as a classroom text. After the first three sections, one can move about the text as desired to sample the following riches.

This is a living project, with a website (http://practicalcomputing.org) that provides information posted by contributors and the opportunity to ask questions when stumped. One can imagine that user groups will evolve from this website. When I checked out the site, I found that these interactions had already begun to take place. For instance, it contained a discussion about merging PDF files in Snow Leopard and a post on reading files from different platforms in Python. Certainly there should soon be more to come.


Haddock SHD & CW Dunn. 2010. Practical computing for biologists. Sinauer Assoc. (see review on p. 6).


Rand DM, DM Weinreich, D Lerman, D Folk & GW Gilchrist. 2010. Three selections are better than one: clinal variation of thermal QTL from independent selection experiments in Drosophila. Evolution 64:2921-2934.


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