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Growing Knowledge and Know-how

Conference Abstracts



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POSTER SESSION 1

P1001

A Metagenome Analysis of an Extreme Microbial Symbiosis

Cary, S.C., University of Delaware, Murray, A.E., Feldman, B., Garcia, J., Luther, G., Gao, G., Kaplar, M., Zhang, J., Ghadiri, A., and Campbell, B.J.,

Alvinella pompejana colonizes the sides of black smoker chimneys along the East Pacific Rise. A diverse, yet phylogenetically constrained, epsilon Proteobacterial community is associated with its dorsal surface. By placing the genome biocomplexity of this community directly into an environmental context we will resolve the ecological role and inter-relationships of this microbial/invertebrate association. Our central hypothesis maintains that under the intense constraints imposed by the geochemical environment the episymbiotic consortia employ a congruous basic metabolic strategy (core or consensus metabolism). To test this hypothesis, we generated small insert, metagenomic shotgun libraries of the bacterial symbionts. We currently have sequenced over 55,000 clones of the proposed 500,000 reactions. We designed and are implementing an Oracle relational database to move the raw sequences through an annotation pipeline which will perform nucleotide and protein BLASTs, ORF finding, and gene finding utilities. These results will also be assigned metabolic pathways and functional categories based on comparison to known COGs and pFAMs. These data will be searchable through a web-based platform allowing statistical analysis and the elucidation and testing of the core metabolism. Our international Biocomplexity team consists of experts in microbial ecology (Cary, Campbell, Feldman), bioinformatics (Gao and Garcia-Frias), geochemistry (Luther), microarray analysis (Murray) and protein thermal adaptation (Daniel). Preliminary sequence analysis has revealed the prevalence and expression of a rare microbial carbon fixation pathway (reverse TCA cycle) and the ability of the episymbiont community to actively reduce nitrate. Already these data have allowed us to form a preliminary 'core' metabolic model that will be tested via RNA microarray and proteomic profiling of the community in our upcoming Extreme 2003 cruise.

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P1002

NSF Biocomplexity: Analysis of Factors Determining the Ecological Function and Resilience of Microbial Communities

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The major objective of this project is to develop an ecological model for the food web of a simple acid mine drainage (AMD) biofilm community. The community nominally comprises three bacterial and three archaeal members according to 16S rRNA-based methods and the primary energy producing reaction sustaining the community is iron oxidation. Our intended approach is to replicate the community in a purpose-built bioreactor and to induce environmental perturbations, such as changes in pH and temperature, to determine physiological responses of member species at the genomic level using microarrays. Finally, experimental data will be mathematically modeled.

A prototype bioreactor and eight second generation Teflon (for inert properties at low pH) flow bed reactors have been constructed and installed in a constant temperature and humidity environment. The bioreactors can be monitored at multiple points along the flow bed and controlled for pH, temperature, humidity, and some solution chemistry.

Shotgun libraries prepared from a biofilm sample collected from the Richmond Mine at Iron Mountain near Redding, CA, have been sequenced, assembled and automatically annotated. Significant fractions of five microbial genomes could be reconstructed from the shotgun data ranging from 10x coverage (*Leptospirillum* group II, *Ferroplasma* type II) to 3x coverage (*Leptospirillum* group III, *Ferroplasma* type I, and “*G-plasma*”), confirming the extreme simplicity of the community structure. However, PCR-based methods indicate the presence of numerous rare genome variants of the dominant types that are not represented in the shotgun libraries.

Annotation of the bacterial *Leptospirillum* group II genome supports its predicted role as a primary producer in the biofilm, supplying fixed C and N to the rest of the community. Similarly, annotation of the archaeal genomes is consistent with a predicted scavenger-type lifestyle for the archaea, which appear particularly adept at processing amino acids for carbon and energy. The annotated sequence will be used for microarray design for a *Ferroplasma* isolate and a subset of functionally important community genome genes.

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P1003

BE-IDEA: Large-Scale Wireless Sensor Networks for *In Situ* Observation of Ecosystem Processes
George Koch, Northern Arizona University, Paul Flikkema, Northern Arizona University, James Clark, Duke University, Bruce Hungate, Northern Arizona University

Progress in an array of technologies – including microelectronic sensing and computation, wireless communication, and the self-assembly of autonomous devices into cooperative networks – has inspired the vision of wireless sensor networks. While networks of intelligent agents transparently embedded into our physical environment could advance human welfare in a number of domains, any successful wireless sensor network must be carefully optimized for its application. One of the most compelling of these applications is dense spatio-temporal sensing of environments to enable better understanding of environmental and ecosystem processes across multiple scales. Our goals are to (i) complete the development of wireless environmental sensor network technology, (ii) make significant progress in understanding the maintenance of biodiversity and in measuring ecosystem properties by applying this technology to three field projects, (iii) build awareness of the benefits of the technology to society, and (iv) improve collaboration between engineering and the sciences. This interdisciplinary collaboration will impact several research areas, including observation systems and cyber-infrastructure, biodiversity and ecosystem dynamics, biogeochemical cycles, and the interaction of experiments and models.

The instrumentation development component of this project builds on a successful seed effort in which we have constructed a small proof-of-concept wireless environmental sensing network. We will build a “distributed instrument”---a prototype network comprising hundreds of palm-sized wireless sensors. In anticipation of this prototype development, we have paid careful attention to ensuring that our networking technology will scale up to thousands of sensors, providing dense coverage at landscape scales.

The prototype network technology will be deployed to enable a new degree of data quality in three diverse field studies. First, we will probe the role of the role of fine-scale environmental phenomena in the maintenance of ecosystem diversity in two Eastern US forests. The second experiment maps the complexity of microclimates and their effects on biodiversity in the crowns of the coastal redwoods of California. And in the third field study, we will determine the effects of scale on eddy covariance measurements of ecosystem energy balance in Northern Arizona. The results of these studies will have global implications for biological diversity and ecosystem function.

This project will have broad impacts in the following ways: it will 1) convey the scientific advances made possible by this research to students, the public, land managers, and policy makers through hands-on activities, an interactive cd-rom, and a website; 2) educate students from under-represented groups and across biological and engineering disciplines, broadening cultural perspectives in the sciences; and 3) disseminate knowledge of wireless sensor networks to an interdisciplinary and international group of researchers through workshops.

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P1004

Biocomplexity of Aquatic Microbial Systems: Relating Diversity of Microorganisms to Ecosystem Function

Bess Ward, Princeton University

Microbial biogeochemical cycling of the elements regulates a dynamic environment in which the cycles of different elements are linked through the physiology of microorganisms. The microbial world contains immense diversity and complexity at every level including high genetic diversity among different organisms apparently engaged in the same biogeochemical function within single communities and great variability in the species composition of different communities that apparently perform equally well. We are investigating relationships between complexity in microbial communities and biogeochemical function at a range of scales from eutrophic to oligotrophic conditions of the inland waters of Chesapeake Bay to the Sargasso Sea.

At the end of the third year of our project we have developed new methods to quantify microbial community composition and diversity using macro- and microarrays for functional genes (e.g., nifH, nirS, amoA); archived hundreds of DNA/RNA samples with extensive spatial and temporal coverage and begun to analyze them with the new methods; discovered and described unprecedented diversity in functional genes for N cycle enzymes; documented spatial and temporal trends in N transformations in the sediments and water column of the Bay.

The large sequence datasets acquired in this work are being used to investigate the structure of microbial communities and the extent of diversity in functional guilds (e.g., nitrogen fixers, denitrifiers). The species abundance curves for nifH, nirS and amoA appear to exhibit a log normal distribution, as is commonly found in larger organisms. Quantitative comparisons among stations on the basis of diversity and N transformation rates reveal complex relationships, as expected!

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P1005

Biocomplexity: Bio-Feedback Basis of Self Organization in Planktonic Ecosystems using Phaeocystis as a Model Complex Adaptive Ecosystem

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Motivation: The phytoplankton genus *Phaeocystis* produces prodigious blooms of gelatinous colonies, releases copious amounts of the greenhouse gas DMS, and significantly alters material flows among trophic levels and export from the upper ocean. The life cycle form in which it occurs determines

whether primary production flows through the traditional "great fisheries" food chain or the more regenerative microbial food web.

Objective: Our central question is: how do, chemical, biological, and self-organizational mechanisms interact with life-cycle transformations of *Phaeocystis* to mediate ecosystemic patterns of trophic structure, biodiversity, and energy flow? The approach includes a series of laboratory, mesocosm, and field studies constrained and advised by ecosystem model simulations, to deconvolve the bio-feedbacks between the complex adaptive behavior exhibited by *Phaeocystis* and that of the physical, chemical, and biological components of the surrounding ecosystem.

Challenges: 1) A five-year project inherently spans the time frame for changes in status and attendant motility of participants, especially students and postdocs. Maintaining continuity in the project team is a constant focus. 2) Models of biocomplexity such as being developed here are nontraditional: their success is highly dependent upon successful feedback and mutual understanding among empiricists and modellers. 3) Field studies of biocomplexity in planktonic ecosystems with their inherently dynamic behavior operating at very short time scales (hours-days) require a combination of excellent planning and fortuitous events.

Outcomes: Eight papers have been presented at national meetings, two have been accepted for publication, three more are being finalized, and several others are being written. The papers in press include "Observations on Colony Formation by the Cosmopolitan Phytoplankton Genus *Phaeocystis*", and "Molecular Detection of Algal Prey in Copepod Guts and Faecal Pellets".

URL: <http://www.skio.peachnet.edu/research/veritylab/biocomp/>

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P1006

Biocomplexity: Common Mycorrhizal Networks -- Active or Passive Channels? Interacting Roles of Mycorrhizal Fungi, Soil Resources and Plants in Carbon and Nutrient Transfers

Darlene Southworth, Southern Oregon University, Caroline Bledsoe, William Horwath, David Rizzo, Robert Zasoski, University of California-Davis, Michael Allen, University of California-Riverside

The goals of the project are to determine the spatial and temporal distributions of soil resources that interact with mycorrhizal fungi and plant roots to form common mycorrhizal networks (CMNs) belowground. The central hypothesis is that magnitude and direction of carbon and nutrient flows in CMNs are not determined wholly by plants or by fungi. Instead, exchange of materials is determined by interactions between plants mycorrhizal fungi and soil resources—resources whose availability changes in complex ways in space and time. We have shown transfer of water and nutrients among plants in the greenhouse and in the field. The link between functional biodiversity and biocomplexity has emerged as our biggest challenge. We continue to investigate mycorrhizal diversity and function. We have demonstrated hydraulic lift, temporal heterogeneity (seasonal growth of roots and fungal inocula), spatial heterogeneity (limited species overlap among trees), transfer via a variety of mechanisms (direct hyphal transfer, secretion and re-uptake), site variability (diverse tree species, distance to nearest neighbor oak), and roles for animals. A major role for CMNs may be sharing of limited soil resources, a concept that influences how we perceive belowground processes and ecological interactions. Diversity of fungi and their ability to acquire limited resources may be more important than sharing resources. Research activities among the three institutions has been well coordinated with frequent consultations, semi-annual meetings, exchange of students, ideas, and methods, inclusion of mycorrhiza researchers beyond the grantees, and organization of symposia at national and international meetings.

<http://fungus.ucdavis.edu>

<http://www.sou.edu/BIOLOGY/biocomplex/main.htm>

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P1007

Biocomplexity: the Emergence of Ecosystem Patterns

Simon Levin, Princeton University, Stephen Pacala, Ignacio Rodriguez-Iturbe, Francois Morel, Lars Hedin, Daniel Sigman. Postdocs: Tanguy Daufresne, Irakli Loladze, Megan McGroddy, Rebecca Robinson-Graham, Princeton University, Princeton, NJ 08544

Abstract: At the level of ecosystems, macroscopic processes such as nutrient cycles, nutrient limitation, hydrological dynamics, resiliency, stability, and structural diversity emerge from the complex interplay of myriad biotic and abiotic elements. This project seeks to understand what mechanisms, at the level of the interactions between organisms and their environments, sustain those processes. The existence of macroscopic patterns at regional scale is relevant both for basic questions on how biocomplexity emerges above the level of organisms and species, and for applied questions about sustainability and management of ecological systems. Our approach combines empirical and theoretical work to attempt to answer these questions.

Among empirical results we identified strong patterns C:N:P ratios in forest ecosystems on global and regional scales. The variation in these ratios is similar to that expressed by Redfield type ratios in particulate matter in the ocean. Addressing the roles of nutrients with an eco-physiological model, we showed that selection leads to specific C:N:P ratios in algae and that the value of the ratios shift depending on the temporal constancy of resource supply. Among other results, we showed that the outcome of plant competition depends on the budget of nutrients at the ecosystem level. We improved our understanding of global oceanic N budget by identifying the dominant source of N loss through measurements of concentration and isotopic composition of nutrients. Our next step is to combine these results to build up an integrative understanding of how interactions between local selection and ecosystem processes lead to the emergence of ecosystem nutrient patterns.

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P1008

BIOCOMPLEXITY -- INCUBATION ACTIVITY: Origins of Biocomplexity: Colonization and Succession of Microbial Communities in a Dynamic Geochemical Environment

S.C. Cary, University of Delaware, (Co- PI's): P.A. O'Day and J.R. Holloway, Arizona State University

One of the fundamental challenges of biocomplexity is to understand how biological systems establish and evolve in relation to changing physical and chemical environments. Although it is recognized that biological and abiotic physiochemical processes must be linked, quantitative descriptions of complex physical, chemical, and biological feedbacks, and thus predictive capability, are lacking. This incubation activity initiated a collaborative program to develop new methods of young chimney recovery and to integrate microbiological and geochemical studies of abiotic-biotic transitions at seafloor diffuse-flow vents. During two cruises with the *DSV Alvin*, (Oct.-Nov. '01 and '02) to 9°50'N East Pacific Rise, we developed and tested new microcosms for recovering microorganisms and fragile young chimney samples with the *Alvin* submersible. The microcosms were designed to present a pristine, *abiotic* environment into the fluid stream in an effort to detect microorganisms capable of colonizing newly forming or sterilized minerals surfaces in a short time (24-96 hours). Using these devices, we have recovered several pioneer microbial communities from diffuse-flow vents. Phylogenetic analysis showed that some communities were dominated by a high diversity of unique *Nanoarchaeotal* sequences (and their crenarchaea host, *Ignicoccus*) that are closely related to the archaeal symbiont *Nanoarchaeum equitans*, the first member identified from the new phylum "Nanoarchaeota". The results to date suggest that these

groups are prevalent in deep-sea hydrothermal systems. However, these organisms and the other members of the pioneer community are so poorly known that we have no knowledge of their ability to colonize new microhabitats, their range of diversity within pioneering consortia, nor the modes of succession to mature microbial communities.

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P1009

Complex Interactions among Policies, People, and Panda Habitat in the Wolong Nature Reserve Landscape

Jianguo (Jack) Liu, Michigan State University

Collaborators: Sandra Batie, Richard Groop, Zai Liang, Angela Mertig, Zhiyun Ouyang, Jianguo Qi, Hemin Zhang

Postdoctoral Fellow/Doctoral Students: Li An, Scott Bearer, Xiaodong Chen, Guangming He, Clinton Jenkins, Marc Linderman

Student interns: Kim Borland, Jason Egeler, Gan Tan, Eunice Yu

Many studies have found that policies can significantly shape human activities and biodiversity, but most of those studies have focused on a single policy at a time and ignored the interactive effects among various policies. In Wolong Nature Reserve (southwestern China) for the endangered giant pandas, human population size has been rapidly increasing to more than 4000 people in approximately 1000 households and panda habitat continued to be lost since the reserve was established in 1975. To protect panda habitat, the Chinese government is implementing three policies: eco-hydropower plant program, natural forest conservation program, and grain-to-green program. The objectives of this project are to: (1) assess the interactions among the three policies and local residents; (2) evaluate the interrelationships between local residents and panda habitat; (3) examine the need for and feasibility of policy modification and improvement; and (4) model and simulate multi-scale interactions among policies, people, and panda habitat across space and time. The methods include field observations, interviews with stakeholders, geographical information systems, remote sensing, global positioning systems, statistical tools, systems modeling and simulation, and advanced visualization techniques. In addition to addressing many fundamental ecological and socioeconomic questions, the research will be tightly integrated with the education of students from elementary school to graduate school, as well as outreach to various stakeholders from local to international levels. The project has significant implications for biocomplexity theory, methodology, and application. So far, a number of papers have been in review or published (including one cover story in NATURE and two publications in SCIENCE). There has been countless world-wide media reports about the findings. Further data collection and analysis efforts are under way. (<http://www.fw.msu.edu/people/liu/>)

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P1010

Biocomplexity of Introduced Avian Diseases in Hawaii

David C. Duffy, University of Hawaii, Manoa

With the necessity that each vector mosquito must successfully bite an appropriate host twice, malaria would appear a disease with an easily broken transmission cycle; however, the malarias, both human and animal, have resisted medical control, even though they were among the first diseases to be understood epidemiologically. Simple parasite-host studies appear unable to capture the behavior of malaria in the

wild. This project uses an avian malaria in the Hawaiian Islands to study the malaria system at levels ranging from the genetics of the disease, its vector and its hosts, to the response of hosts to infection, the effect of seasonality on host and vector populations, through to the effect of landscape patterns and anthropogenic change on disease cycles.

The native forest birds of Hawaii had apparently no resistance to malaria when it was introduced into the islands sometime in the last century. In response, these species disappeared from the lowlands and became confined to the higher elevations of mountains, above the reach of malaria-bearing mosquitoes. While our work is still ongoing, it suggests that at least some of the species have acquired some form of resistance to malaria and they are now present in the lowlands where they are able to survive and breed, even under intense exposure to malaria. Preliminary work suggests that native bird species with the least degree of genetic dispersal have the greatest degree of resistance, perhaps because they are exposed to strong local selection, while less philopatric birds may dilute selection, delaying the development of resistance.

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P1011

Development of Methods Linking Genomic and Ecological Responses in a Freshwater Sentinel Species

Joshua W. Hamilton Ph.D., Dartmouth College, Carol L. Folt Ph.D., Dartmouth College

We are developing the aquatic crustacean, *Daphnia pulex*, as a model sentinel species for linking genomic level and ecological studies in aquatic systems, using the toxic metals mercury and cadmium as model environmental stressors. *Daphnia* is an ideal candidate given its pivotal ecological role, widespread natural distribution, extensive characterization, ease of use in the field and lab, and its extensive characterization. We are developing a suite of genomic tools for use in characterizing the physiological, demographic, and adaptive responses in naive and metal pre-conditioned populations. The anticipated benefits will be to provide tools for rapid, sensitive and specific assessment of environmental effects in natural systems and to provide biomarkers of exposure and effects that are applicable to other organisms and exposures. In our first year we have primarily focused on: developing, sequencing and cataloging both an expressed cDNA and a BAC genomic library for *Daphnia pulex*; developing and validating glass slide based cDNA arrays for *Daphnia* that can be used for differential expression studies; and performing dose-response, time course and life table analyses. Our challenges included assembling and coordinating a new interdisciplinary working team from three different institutions and formulating a common set of criteria for our experiments. These early discussions and challenges greatly focused and strengthened our working group and reinforced to us the benefits and synergy possible with truly interdisciplinary research. Our early interactions and successes within this collaborative group have led in turn to the recent formation of a larger international consortium focused on *Daphnia* genomics. See <http://daphnia.cgb.indiana.edu/> for more information.

Grant supported by NSF: DEB 02-21837

P1012

Dynamics of an Invasive Non-Native Species and its Biological, Physical, and Human Impacts: *Spartina alterniflora* on the Pacific Coast

Alan Hastings, University of California, Davis

Spartina alterniflora is a salt marsh cordgrass, native to the Atlantic and Gulf coasts of the United States, that is invading Pacific estuaries. Our focus has been on two sites, San Francisco Bay where *S. alterniflora* interacts with the native species *S. foliosa*, and Willapa Bay, Washington, where *S. alterniflora* is invading mudflats that have no native vascular plants. The final product will be a truly integrated study of the dynamics of an invasive species, including a core mathematical/conceptual model, physical and biological feedbacks, and a careful, justified study of impacts on non-commercial human values. Our Willapa Bay work emphasizes the importance of evolution (life history traits malleable over 100 years) for understanding the invasion. We have documented the mechanism for an Allee effect and examined the impact on the rate of spread using models. Our work with aerial photographs will soon provide detailed demographic information at a scale and relationship to the environment not achieved before for an invasive species. We have demonstrated theoretically and empirically the role of indirect effects through 'ecological engineering' (an example of the use of our core model) and the importance of wrack (dead plant material) for affecting other species. In San Francisco Bay, we have demonstrated effects on bird species and have shown the long term and long lasting effect of *S. alterniflora* on the invertebrate community. Our work on the economic aspects, which depended on the preliminary biological work, is just getting underway. Major challenges have been logistical, rather than scientific. Further information is at <http://two.ucdavis.edu/spartina>

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P1013

Early Bird: A Collaborative Project to Resolve the Deep Nodes of Avian Phylogeny *Michael J. Braun, National Museum of Natural History, Smithsonian Institution*

Early Bird is a large-scale, cooperative effort among five institutions in the U.S., one in Scotland and two in Australia to determine the evolutionary relationships among all major groups of birds. The immediate results of this project will be to provide a detailed, comprehensive and robust "family tree" for birds, and to facilitate the use of that tree to organize and interpret the vast amounts of other information already available about birds. The project will generate large amounts of DNA sequence data for all major avian lineages from a series of carefully selected genes. These data will be integrated with existing and new morphological and fossil data to bring all relevant evidence to bear on the problem. Extensive analysis of the evidence will be conducted with the rapidly expanding suite of computational tools available for the inference of relationships, divergence times and evolutionary patterns. The data will be made accessible to other researchers in an online database with tools for analysis and export, and to the general public through a website with background information on the importance of evolutionary relationships, progress reports on the project, and interactive educational tools with which interested persons can explore the data themselves.

The impact of this project on science and society will be far reaching. Birds are among the most prominent and engaging creatures in most ecosystems worldwide. They have been the subject of an extraordinary number and diversity of scientific studies that figure largely in our understanding of the natural world and humanity's place in it. Their position high in many food chains together with their great mobility makes them sensitive indicators of environmental quality, and monitoring of bird populations is

widely used to set conservation and management priorities. Their powers of flight, physical beauty and captivating behaviors amaze and inspire us, and birds provide tremendous amounts of recreation for serious hunters and birders, as well as millions of backyard birdwatchers each year. All of these human interactions with birds will be enriched by a better understanding of avian evolutionary history and genetic diversity, which Early Bird will provide.

Grant supported by NSF: EF 02-28675, 02-28682, 02-28617, 02-28688

P1014

Exploring the Human-Environmental Interactions Causing Bush Encroachment

Andrew Hudak, University of Idaho

Our objective was to establish relationships between alternative land use practices, fire frequency and woody canopy cover across a semi-arid savanna landscape straddling the Botswana-South African border. The 250 000 ha study area contains three land use zones that have differed in fire management. (1) Madikwe Game Reserve (MGR) in South Africa, where many fires have been prescribed since 1993, (2) South African farms, where only occasional fires have occurred, and (3) Botswana, where fires have been excluded. Fire occurrence and woody plant canopy cover were mapped from independent satellite datasets. Landsat images were used to map fire occurrences from 1972-2000; these were then assembled for the periods 1972-1989, 1990-2000 and 1972-2000 for assessing fire frequency. SPOT Panchromatic images were used to map woody canopy cover in 1990 and 2001, using image texture as an indicator of woody canopy cover. Results showed that as fire frequency increased, image texture decreased, demonstrating an inverse relationship between fire frequency and woody canopy cover in this semi-arid savanna. Once current field collection of woody canopy cover data is complete, woody cover increases (bush encroachment) and decreases (bush thinning) will be quantified and mapped in relation to historic fires, soil type, and land use. This information will then be used to inform a simple model of fire management effects on bush density. The model will be spreadsheet-based and therefore accessible to land users to assist in making ecologically sound management decisions.

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P1015

Factors Affecting, and Impact of, Diazotrophic Microorganisms in the Western Equatorial Atlantic Ocean

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We are examining plankton dynamics in the western Equatorial Atlantic Ocean (WEQAT). This is a complex but understudied ecosystem of global importance. Our study centers on diazotrophic (N₂ fixing) microorganisms as keystone species in these nitrogen depleted systems. Geological, physical, biological,

chemical and even social factors all have a major influence on the population biology and activity of diazotrophs in the WEQAT. Diazotrophs in turn have a major effect on other phytoplankton and trophic levels through input of fixed nitrogen (N).

We are using a combination of both observations and models to help us address a fundamental issue in biocomplexity. Specifically we are interested in understanding how external forcings control the structure of the local populations and how a global ecosystem property (i.e. ecosystem productivity at regional scales in the WEQAT) is influenced by these populations and their N inputs, through the nonlinear interactions of such populations with the plankton ecosystem at large and the local abiotic forcings. The Amazon River affects the region physically by changing salinity and thereby water column stratification and stability, and geochemically by introducing iron and silicate which can then biologically stimulate the growth of diatoms some of which contain the N₂ fixing endosymbiont *Richelia intracellularis*. The area also receives significant seasonal atmospheric inputs of iron in dust from the Sahel region of Africa, which can promote the growth of the important N₂ fixing cyanobacterium *Trichodesmium*. This atmospheric iron source is directly deposited on the surface waters where biological activity is greatest. For *Trichodesmium*, the physical environment (e.g. high wind speed) can also inhibit activity and the formation of blooms. Diazotrophs may be affected by land use practices in the Amazon Basin and the African Sahel, and N₂ fixed by marine plankton can stimulate primary productivity and fishery yields.

Results from three major expeditions in the region are forthcoming and appear largely to confirm our initial hypotheses. The WEQAT region ecosystem changed seasonally and systematically in response to both changes in micro and macronutrients introduced by the aeolian dust deposition and the rivers, as well as physical factors such as surface wind speeds and mixed layer depths. The winter diazotrophic population was almost all *Trichodesmium* while during the summer, the WEQAT was covered by large regions of fresher water (salinity <34 pss) that were dominated by diatoms containing endosymbiotic diazotrophic cyanobacteria. The fate of carbon and nitrogen fixed by these two distinctly different communities followed different pathways – *Trichodesmium* populations appear to release recently fixed nitrogen near the surface which is then available to other phytoplankton, while the diatom populations sink out of the surface water column, contributing directly to the drawdown of carbon. Significant dissolved inorganic carbon drawdown is associated with this biological activity in the summer compared to the winter.

These data have been used to help us develop and validate a coupled, 3-dimensional pelagic food web model that includes an explicit, dynamic representation of N₂-fixation, and incorporates many of the complex physical, chemical and biological interactions that characterize the WEQAT region. This model has, among other things, shown that physical forcing variability determines temporal and spatial patterns in N₂-fixation, and that this N₂-fixation has a strong influence on food web structure and patterns of productivity and export, which has been confirmed by remote sensing observations.

Our research is significantly advancing our understanding of the interaction between physical and biogeochemical processes in an important area the world's oceans, and identifying how these interactions regulate variability in marine ecosystem productivity.

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P1016

Human Ecodynamics in the Hawaiian Ecosystem, from 1200-200 yr B. P

Patrick V. Kirch, University of California, Berkeley

As the Polynesians radiated across the Pacific Ocean, they encountered very different environments – and altered them substantially. Those environments in turn catalyzed cultural changes in Polynesian societies. Our research team, which includes archeologists, ecologists, soil scientists, demographers and paleobotanists, addresses human – environment interactions in the Hawaiian Islands prior to European contact, focusing on two dryland areas, Kahikinui on Maui and Kohala on Hawaii. We evaluate: 1) the spatio-temporal nature of agricultural development, as it linked to biogeochemical gradients; 2) patterns of demographic change, and how these linked to resource use and agricultural intensification; 3) the emergence of socio-cultural complexity, including formal control hierarchies and pronounced disparities in access to resources, and 4) the dynamic effects of a growing human population and evolving culture on its natural resource base, including soil fertility, upland forests, and other biotic resources. Our information is collected and analyzed in a GIS framework, in a way that supports hierarchical modeling of the complex human environment interactions that shaped Hawaiian land and culture.

Our results to date suggest that Polynesian farmers colonized the Kahikinui area relatively late, and that hierarchical control over a relatively undifferentiated agricultural system was imposed more or less rapidly in the 1500s. In contrast, results from the Kohala region suggest a progressive intensification of agriculture in a narrow zone of sufficient rainfall and surprisingly high soil fertility. We speculate that proximity to marine resources and to intensive wetland agricultural systems in Kohala contributed to this difference in agricultural (and probably social and cultural) development.

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P1017

Development of the Human Species and Its Adaptation to the Environment

Morris Goodman, Wayne State University

We held a conference that defined the multi-disciplinary research needed to elucidate human origins. The conference was a three part interdisciplinary workshop. The first part focused on how comparative primate genomic data can be used to decipher the genetic basis of being human. The second part focused on the organismal and cultural-social levels of human evolution in the milieu of challenges from the earth's evolving physical and biological environment. The third part focused on how system-level methodology and computer modeling can investigate the complex interactions that result from responses to environmental challenges via feedback loops connecting the molecular-genetic to the organismal and cultural-social levels of organization.

We arrived at an improved conception of human origins being an holistic process, as well as the avenues to pursue in order to explore the interconnection between the three major levels (genomic, organismal phenotypic, and cultural social). Findings achieved through the three sessions enabled several project collaborators and conference participants to submit successful NSF grants in the area of human origins.

Results from this conference helped to promote the identification of sequencing the chimpanzee genome as a high priority within the National Institutes of Health. Analyses from a sample of genes determined a 0.6% nonsynonymous (*i.e.* functionally important) and 1.6% synonymous (*i.e.* selectively neutral)

difference between humans and chimpanzees. These results implicate Darwinian selection in the divergence of humans and chimpanzees, and serve as a model for genome-wide identification of the important changes that shaped being human. Identified gaps in our knowledge highlighted the need for sequencing other nonhuman primate genomes. The conference proceedings are posted at <http://www.uchicago.edu/aff/mwc-amacad/biocomplexity/>.

Grant supported by NSF: BCS 00-83721

P1018

Restoring Biocomplexity into Agroecosystems as the Basis of Sustainability: A Planning Grant to Link Ecological and Human Networks in Headwater Watersheds Benjamin Stinner, Ohio State University

*Richard Moore, Charles Goebel, Deborah Stinner and Robin Taylor,
Agroecosystems Management Program, Ohio State University*

During the past three years, our multidisciplinary team has been developing an approach to agroecosystem restoration that integrates the complex interactions between natural and social capital for restoration of ecological function to the Sugar Creek Watershed, a highly impaired aquatic system in northeast Ohio. The overall objectives of this project are to: 1) bench-mark the social, physical, and ecological features of the headwater tributaries that most directly relate to understanding the linkages between managed terrestrial and aquatic systems; 2) create increased awareness of watershed ecology, and motivate farmers and others to adopt management practices that improve water quality; and 3) restore biodiversity and ecosystem function on a tributary by tributary basis of whole landscapes, including both agricultural and non-agricultural areas. This planning grant process focuses on: 1) engaging additional investigators with expertise in key areas; 2) developing the necessary experiments and data sets on which to build a full proposal; and 3) expanding an education component that ultimately will integrate student participation into the project, and further link researchers, farmers and students in a co-learning process. In the long-term, we will be evaluating the impact of restored and unrestored headwaters on downstream areas, and will be modeling impacts at sub-basin and larger scale levels. Our long-term plans for education include training for K-12 teachers so that the students and teachers can observe changes in their watershed as they occur. We will seek substantial input from the local farming communities and other stakeholders towards building educational programs around the headwaters concepts and landscape-level experiments as examples of biocomplexity issues.

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P1019

Scaling of Biodiversity: Physical and Biological Foundations of Ecological Principles

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Underlying the diversity of life and the complexity of ecology is order that reflects the operation of fundamental physical and biological processes. Scaling relationships are emergent quantitative features of biodiversity. Some of them appear to be universal, occurring in virtually all taxa of organisms and kinds of environments. They are patterns of structure or dynamics that are self-similar or fractal-like over many orders of magnitude that can be described mathematically by power functions. They allow extrapolation and prediction over a wide range of scales and they offer clues to underlying mechanisms that powerfully constrain biodiversity. To understand these mechanisms we use mathematical models and empirical measurements to elucidate the physical and biological principles that determine how the life history, abundance, distribution, and species richness of organisms scale with body size, space, and time. To accomplish this large-scale multidisciplinary research, our program emphasizes four important forms of interpersonal interactions i) collaborations among physicists, mathematicians, geologists/hydrologists, biologists, and ecologists; ii) interactions and visits with scientists from around the world; iii) cooperation between the University of New Mexico, the Santa Fe Institute, and Los Alamos National Laboratory; and iv) interdisciplinary training for graduate students and postdocs. Here we show five examples of how our interdisciplinary scientific approach results in further understanding of the mechanisms underlying the scaling of five important emergent quantitative features of biodiversity: biomass production, fertility, population density, species richness and landscape complexity.

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P1020

Sequencing Methodology for Large *Bacillus Cereus* Group Plasmids

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The *Bacillus cereus* group of organisms includes the human pathogen, *Bacillus anthracis*, the insect pathogen, *Bacillus thuringiensis*, and the opportunistic pathogen *Bacillus cereus* as well as the non-pathogenic *B. mycoides* and *B. weihenstephanensis*. For the most part these organisms are indistinguishable by 16S rRNA sequences and much of the variability in this group lies within the species-specific plasmids. *B. anthracis* requires two large virulence factor encoding plasmids, pXO1 (~187 kb) and pXO2 (~95 kb), to cause human infection, the *B. thuringiensis* Bt toxin is also plasmid encoded and the *B. cereus* plasmids encode niche specific factors. The comparison of these plasmid sequences to identify specific factors for organism survival in each niche is our goal. Due to physical constraints of plasmid isolation among this group such as large plasmid size, low plasmid copy number and ineffective lysis of the Gram-positive cell wall isolation of these plasmids has been problematic. The current genome sequencing projects have employed a brute force approach to sequencing these plasmids. We have examined the sequencing progress of the plasmid in comparison to the whole genome and determined that a large number of sequence reads are required to produce a relatively complete plasmid sequence, however with standard closure technology the plasmid could be closed much quicker than the genome. Additionally, if the plasmid content of a genomic DNA preparation could be enriched by a factor of 10 the number of sequences required would decrease to < 10000 sequence reads, corresponding to less than a 2X genomic coverage. Efficient plasmid isolation will aid in the sequencing and comparisons of these diverse plasmid sequences.

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P1021

The Bahamas Biocomplexity Project

Daniel R. Brumbaugh, American Museum of Natural History. *Coupled natural and human dynamics in coral reef ecosystems: The effect of marine reserve network design and implementation on fisheries, biodiversity, and humans.*

Concern over the degradation of coral reef ecosystems has risen sharply in recent decades as human activities such as overfishing, pollution, and habitat disturbance increasingly alter the goods and services associated with reef ecosystems. As a consequence, marine reserves – marine protected areas (MPAs) that restrict direct extractive activities – have become a paradigm for managing assorted threats to coral reefs, particularly those relating to overfishing of reef-based fisheries. Although marine reserves and other MPAs have received limited attention from social scientists, the study of various social concerns (such as resource uses, cultural and economic values, governance and management modes, etc.) still requires integration with research on natural dynamics in and around MPAs. Furthermore, both social and biological factors require integration with oceanographic dynamics in order to understand how sets of MPAs may behave as ecologically connected networks. In particular, we must determine which MPA system scenarios, when considered in the context of physical, biological, and social dynamics, allow for the sustainability of reef ecosystems.

Because the Commonwealth of The Bahamas is currently expanding its small set of MPAs into a full, archipelago-wide network of marine reserves, this country serves as the project's study system. By working to integrate theory and data on circulation, population, habitat, and socioeconomic patterns and processes, the Bahamas Biocomplexity Project is addressing major questions about the design of MPA networks. Results will provide researchers, educators, and decision-makers with new analytical tools for understanding complex network dynamics, as well as important empirical data for the planning and evaluation of new MPAs.

Grant supported by NSF: OCE 01-19976

P1022

The Evolution and Radiation of Eucaryotic Phytoplankton Taxa (EREuPT)

Oscar Schofield, Rutgers University

Unlike terrestrial ecosystems, marine photoautotrophs are dominated by few species that are taxonomically diverse. Since the end-Permian extinction the dominant eukaryotic phytoplankton organisms contain plastids derived from the “red” line of the ancestral cyanobacterium. In the Paleozoic oceans however, fossil evidence suggest that the “green” line was dominant. The rise of the eukaryotic red line begins in the Triassic and early Jurassic, due to dinoflagellates and coccolithophorids. This was followed by the diatoms, which grew in prominence during the Cenozoic. We are focused on understanding the origins and environmental conditions that led to the selection, radiation, and present dominance of the major eukaryotic phytoplankton taxa. Plastid genomes in both the red and green lineages suggest that while all algal plastids retain a core set of genes, red plastids retain genes that confer more capacity to autonomously express proteins regulating photosynthesis. We hypothesize gene losses in the green plastid reduced its portability for subsequent symbiotic associations. This reduced plastid portability may have limited subsequent evolutionary advances in the green lineage while providing a competitive advantage to the red lineage. Phylogenetic differences in macronutrient stoichiometries reflect ancestral pre-symbiotic host cell phenotypes, while trace element composition primarily reflects differences in the acquired plastids. Although the average trace element composition of the ensemble of

phytoplankton is correlated with that of Earth's crust, compositional differences between the two plastid superfamilies suggest that changes in ocean redox state have influenced the evolution and selection of eukaryotic phytoplankton.

Grant supported by NSF: OCE 00-84032

P1023

Homeostasis and Degradation in Fragile, Tropical Agroecosystems

Alice N. Pell, Cornell University

When both people and their natural environment operate “at the margin”, as frequently occurs on small farms in Kenya and elsewhere in the developing world, small changes in the natural resource base often have large effects on people's lives. Conversely, modest changes in human activities may significantly affect ecosystem functioning. Our project's goal is to measure, understand and model the interlinked biophysical and socioeconomic processes characteristic of small farms in Kenya. We have collected data from 268 farms in three sites on soil chemistry and biology, crop and livestock production, socioeconomic conditions, land use, labor allocation and investment patterns. The effects of cultivation on soil fertility have been examined by sampling soils that have been cultivated from 1 to more than 100 years. Considerable effort has been expended to determine how social and biophysical aspects of the agro-ecosystem might be linked in a dynamic model to explore the relationships between farmers' perceptions of their options and biophysical and economic processes. Baseline soil data indicate that the site with better market access has soils that contain more soil organic carbon, phosphorus and nitrogen. Longitudinal data indicate higher rates of farmer-reported and measured soil degradation and the importance of off-farm earnings to investment in agricultural intensification and soil nutrient amendments in the site with poorer market access. Our third research site, Baringo, in the Rift Valley experienced serious floods in late 2002 and early 2003 which deposited up to 20 cm of silt, making changes in soil fertility and crop productivity difficult to monitor. <http://label.econ.cornell.edu/>

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P1024

Risk Assessment of Nonindigenous Species

B. Leung, University of Notre Dame, D. Lodge, Gary Lamberti, Jeff Feder, Greg Dwyer, Mark Lewis, Jay Shogren, and Kristin Shrader-Frechette

The science and policy of invasive species are extremely timely and important environmental and economic topics. Invasive species are increasing rapidly worldwide, are one of the top causes of global biodiversity loss and environmental change, and are economically expensive (e.g., they are estimated to cost the US alone as much as \$137 billion/yr). More rigorous and comprehensive risk analysis frameworks for nonindigenous species are urgently needed so that prevention and control strategies can be targeted appropriately. The objectives of the incubation project were 1) to develop a bio-economic modeling framework for nonindigenous species risk analysis; and 2) begin a Laurentian Great Lakes-related application of the risk analysis. Our integrated framework of ecology and economics provides needed quantitative decision frameworks for invasive species management. The model identifies optimal allocation of resources to prevention versus control, acceptable invasion risks, and consequences of invasion to optimal investments (e.g., labor and capital). We apply the model to zebra mussels, and show that society could benefit by spending up to \$324,000 USD/yr to prevent invasions into a single lake with

a power plant. In contrast, the US Fish & Wildlife Service spent \$825,000 in FY2001 to manage *all* aquatic invaders for *all* US lakes. Thus, greater investment in prevention is warranted.

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P1025

Comparative Chloroplast Genomics of Seed Plants

Robert K. Jansen, University of Texas at Austin

Chloroplast genomes of seed plants are highly conserved in their size, gene content, and gene order. Knowledge of the architecture of chloroplast DNA in seed plants is based on the complete sequences for 17 taxa and gene-mapping studies of hundreds of others. In most cases, when changes in genome structure have been identified, the differences can be explained by a small number of events, including inversions, gene duplications, gene deletions, and expansion and contraction of the inverted repeat. Some notable exceptions have been documented in conifers, non-photosynthetic plants, and the angiosperm families Campanulaceae, Fabaceae, Geraniaceae, and Lobeliaceae. Our research group is performing a comparative study of seed plant chloroplast genomes, which involves sequencing plastid genomes of 55 taxa representing all of the major lineages of seed plants, with more intensive sampling in groups with highly rearranged genomes. During the first two years we have completed sequencing or have nearly complete drafts for 10 plastid genomes and an additional 12 genomes are in various stages of progress. We have also developed an annotation program and we have designed and tested several new computational methods for using whole genomes for phylogeny reconstruction. Most of the focus on the project so far has been on the highly rearranged chloroplast genomes of the angiosperm families Campanulaceae and Geraniaceae. The complete sequences of the *Trachelium* (Campanulaceae) and *Pelargonium* (Geraniaceae) chloroplast genomes have identified numerous repeated sequences that are associated with extensive changes in gene order and they suggest that transposition may also be responsible for several genomic rearrangements in *Trachelium*.

Grant supported by NSF: DEB 01-20709

P1026

Biocomplexity: Mathematical and Biological Modeling of Eukaryotic Chemotaxis

Pablo A. Iglesias, Electrical and Computer Engineering, The Johns Hopkins University

The ability to sense the direction of external chemical sources and respond by polarizing and migrating toward chemoattractants or away from chemorepellants – a process known as *chemotaxis* – is crucial for proper functioning of single cell organisms, such as bacteria and amoebae, as well as multi-cellular systems. In fact, chemotaxis occurs to some extent in almost every cell type at some time during its development. It is a major component of the inflammatory and wound-healing responses, the mammalian reproductive systems (spermatozoa), the development of the nervous system as well as tumor metastasis. Despite of recent advances in the understanding of the biochemistry regulating chemotaxis in eukaryotic cells knowledge of the signaling network is far from complete. The research proposed integrates experimental research on the biochemical aspects governing chemotaxis in the slime mold *D. discoideum* with theoretical developments from control engineering and dynamical systems theory. Our goal is to develop high-fidelity models of the regulatory network controlling eukaryotic chemotaxis and to test them and validate them experimentally.

We have presented a model in which the cellular response directing chemotaxis is regulated by the balance between a fast, local excitation signal and a slower, global inhibitor. The model can explain adaptation to spatially inhomogeneous stimuli as well as spatial sensing when in a chemotactic gradient. We have shown that a substrate supply-based positive feedback acting through small G-proteins can explain the amplified response seen in cells. The model makes distinctive predictions that differentiate it from other published models. Moreover, some of these predictions have now been tested experimentally.

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P1027

Evolution and Ecology of Perturbed Interactions—Modeling Disequilibria in Time and Space **Claudia Neuhauser, University of Minnesota**

Perturbations of biological communities, exemplified by habitat loss and the invasion of novel taxa are well documented. Economic development, new technologies, and population pressure have escalated the scale, frequency, and severity of such perturbations. As a result, evolutionary and ecological dynamics may be driven so far from their equilibria that the linear approximations used for understanding and predicting consequences of subtle perturbations are inappropriate and probably misleading.

Our investigations center on four focal species and specific organisms associated with them (Corn borer and *Bt* and non-*Bt* corn, *Echinacea* and other prairie plants and their pollinators, Corn smut and corn, Rhizobia associated with common bean). In each case, community dynamics are subject to genetic and ecological processes that act at similar time scales. Combining empirical studies and theoretical models, we demonstrate the necessity to integrate genetic and ecological processes to gain a full understanding of community dynamics across different spatial and temporal scales.

The major insights in the *Echinacea* study has been that (1) fragmentation reduces allelic diversity at the incompatibility allele, which accelerates extinction of small populations (the extinction vortex), and (2) habitat reduction leads to an excess of heterozygosity at neutral loci (the inbreeding paradox of self-incompatible plants). The corn borer and *Bt* corn study focuses on spatial design questions to delay the onset of evolution of resistance of the European corn borer to *Bt* corn subjected to predation. In both the corn smut and the Rhizobia study, the focus is on explaining the high genetic diversity and the observed spatial patterns of a mutualist (Rhizobia) and antagonist (corn smut) in a system that has undergone habitat expansion (beans and corn).

Web page: <http://www.entomology.umn.edu/CCG/>

Review paper: C. Neuhauser et al. (2003) Community Genetics: Expanding the Synthesis of Ecology and Genetics. *Ecology* 84: 545-558.

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P1028

Experimental Study Of Adaptation To The Edge Of Chaos And Critical Scaling In The Self-Adjusting Peroxidase-Oxidase Reaction

Alfred W. Hubler, University of Illinois At Urbana-Champaign, Alex Scheeline, University Of Illinois At Urbana-Champaign

Self-adjusting systems are ubiquitous in nature. Previous studies of adaptive behavior have shown that adaptive systems will evolve over time to states that are weakly chaotic, known as the edge of chaos. These studies typically use a genetic algorithm to implement adaptation. It is conjectured that most self-adjusting dynamical systems that initially have chaotic behavior will also adapt toward the edge of chaos. A model for self-adjusting dynamical systems is introduced which treats the control parameters as slowly varying, rather than constant. The dynamics of these parameters is assumed to be governed by some low-pass filtered feedback from the dynamical variables of the system. We present studies of very simple systems with adaptation, including the self-adjusting Bernoulli shift map. Further we present a progress report on both numerical simulations and experimental data from a chemical and a biological system: the peroxidase-oxidase oscillator and a thin section of horseradish root tissue suspended in a reactor. If our preliminary findings can be confirmed, this will represent the first experimental evidence for adaptation to the edge of chaos in naturally occurring systems.

[1] Paul Melby, Nicholas Weber, Alfred Hubler, *Robustness of Adaptation in Controlled Self-Adjusting Chaotic Systems*, Fluctuation and Noise Letters, 2, L285-L292 (2003).

[2] See also: <http://www.ccsr.uiuc.edu/biocomplexity/>

Grant supported by NSF: PHY 00-83457

P1029

Bacterial and Computational Experiments to Identify General Principles that Govern the Evolution of Complexity

Richard Lenski, Michigan State, Margaret Riley, Yale University, Chris Adami, Caltec

Overall Mission/Objective: We define biocomplexity as the web of interactions among genes, organisms, and environments. The overall mission of our research is to investigate factors that influence the evolution of biocomplexity. We perform experiments with two different systems, bacterial and digital. In both systems, populations evolve for thousands of generations in defined environments, and the resulting genomic and functional changes are analyzed.

Outcomes: Some recent highlights of our research include:

- Step-by-step analysis of all the mutations leading to the evolution of a complex new function in populations of digital organisms (2003, *Nature* 423:139-144). Extensive press coverage, including NSF press release and selection of two figures for NSF project on communicating science to the public.
- Whole-genome expression arrays demonstrate parallel evolution in bacteria, including first-ever use of such data to trace back to an unknown mutation (2003, *PNAS* 100:1072-1077).
- Sequencing 36 random genomic regions in 12 long-term bacterial populations was completed ahead of schedule (2003, *J Mol Evol* 56:498-508), and has now shifted to candidate genes.
- Latest version of Avida software allows diverse communities of digital organisms to become established on multiple resources, enabling research over an evolutionary timescale on the relationship between productivity and diversity.

- To complement the above work, a 2000-generation experiment with bacteria was completed, and is now being analyzed, that examines adaptation to multiple resources.

Motivation for new approach: Our approach to studying biocomplexity has three motivations. First, biocomplexity on Earth today was generated via evolution. Understanding biocomplexity should benefit from an evolutionary perspective. Second, evolution is a dynamic process, not an end-result. Systems that permit the investigation of evolution in action, including the effects of manipulations, offer a powerful means to study the emergence of biocomplexity. Third, general principles are found by looking at multiple systems, including those different from familiar systems. We employ two very different systems – bacterial and digital – and compare results whenever possible.

Challenges/Problems: One challenge has been keeping up with the many lines of research. This has been addressed by several meetings of PIs and members of their teams. A second challenge has been developing a version of the digital-life software for educational use. Progress has been made on a new user interface, and we extended our collaboration to include Robert Pennock, an expert on the philosophy of science and the teaching of evolution.

URLs to Project Material:

<http://dllab.caltech.edu/> [information on the research with digital organisms]

<http://myxo.css.msu.edu/ecoli/> [information on the long-term *E. coli* evolution experiment]

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P1030

Functional Genomics: Interactions Among Ecology, Population Biology and Gene Expression

Douglas L. Crawford¹, **University of Miami**, David Duvernell², Southern Illinois University, R.T. Kneib³, University of Georgia, Bernard B. Rees⁴, University of New Orleans, Winn, Richard N³, University of Georgia

The goals of the Fundulus Genome Enable Science research are to determine how landscape complexity within a local region and along the steep thermal cline affect genome-wide patterns of gene expression. We propose that landscape structure affects population size, individual growth rates, longevity, migration rates, and genetic structure of populations. We intend to measure these ecological and population variables and explore their relationships to patterns of gene expression. Genetic crosses of field-collected populations, and laboratory acclimation of their progeny, will allow us determine if physiological induction or heritable genetic differences are responsible for the differences in gene expression.

One of the innovations is to quantify Genome-wide patterns of mRNA expression with the use of *F. heteroclitus* microarrays (functional genomics). Because variation in mRNA must be translated into changes in protein concentration to produce a phenotypic change, microarray experiments will be complemented by high-throughput analyses of protein expression (proteomics). It is our contention that variation in gene expression is one of the important adaptive mechanisms and thus, we expect to find significant differences in gene expression associated with differences in landscape and thermal ecology. This research will determine the evolutionary importance of variation in gene expression.

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P1031

Modeling Bronze Age Settlement Systems in a Dynamic Environment

T. J. Wilkinson, The Oriental Institute

The research will examine why third and fourth millennium BC cities in the irrigated zone of southern Mesopotamia grew to a greater size and complexity than those in the rain-fed north. We propose to apply concepts of complex adaptive systems to test the hypothesis that systems of early cities co-evolved in an intimate relationship with their environment, primarily by means of aggregation through time of smaller fundamental units (households). Local rules that determine the subsistence practices of the peasant householder therefore developed through time into more complex land use strategies and social mechanisms that culminated in the emergence of complex settlement hierarchies, the patterns of which show little resemblance to the patterning of the original small scale communities. As larger systems of settlements and more complex exchange and administrative mechanisms developed, parts of the agricultural systems became less sustainable through time. Settlement-land use systems will, therefore, be modeled from small social elements (the household) to much larger entities such as networks of interacting cities. Agent based modeling provides the key to this initiative by allowing for a wide range of choices and trajectories to contribute to the outcome of the modeling exercise. Simulation will employ an advanced object based framework (DIAS and FACET) designed by the Decision and Information Sciences (DIS) Division of Argonne National Laboratory. The DIAS framework allows a range of simulation models and other applications to work together to address a complex modeling problem. It will incorporate climate (GCM), weather (MM5), hydrological and agricultural (EPIC / SWAT), and demographic models plus agent-based models of social behavior. Input data and test data will be derived from the large corpus of landscape and epigraphic data housed within the Oriental Institute and elsewhere.

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P1032

Regulation of metal bioavailability in floodplain continuum by carbon and sulfur cycling

Shiping Deng, Oklahoma State University, Domy C. Adriano, Andrew C. Chang, Marianne Guerin, Steve Harper, Brian Jackson, Andrew Neal, and Mabelle Wilson
University of Georgia, University of California, Riverside and Oklahoma State University
Collaborators: Attila Anton, Zoltan Gyoti, Jozsef Konya, Noemi Nagy, Tamas Nemeth, Christopher Romanek, John Seaman, and Jozsef Szabo

The PIs propose to evaluate the spatial variability of contaminants, microbial activity and community structure (in a floodplain setting) at a variety of scales, from landscape (>km) to micron-scale within soil/sediment cores. The intent is to demonstrate the relationship between soil microbial activity and in situ concentrations of heavy metals (Pb, Zn, Cu, Cd and As), both in solution and bound to solid phases. The objective is to assess, across the floodplain continuum, whether metal dynamics are regulated by the interaction of microbial communities with nutrients (C and S). Estimates of variability in biogeochemical measurements will be used as input into a stochastic model framework, coupled to a hybrid empirical-mechanistic model of metal bioavailability to plants. The hybrid model will be made spatially-explicit via a GIS-based soil database. A Hungarian floodplain, the Tisza River Basin floodplain, will be the field sampling research. This project involves the participation of three academic institutions in the U.S. (University of Georgia, University of California, Riverside and Oklahoma State University) in collaboration with the Hungarian Academy of Science and Debrecen University.

Grant supported by NSF: INT 01-21402

P1033

Deep arthropod phylogeny from 100 targeted nuclear coding-region sequences

Cliff Cunningham, Duke University, Department of Biology, Jerry Regier, Jeff Shultz, Joel Martin and Jeff Thorne

Our overall objective is to obtain a robust phylogenetic tree for the higher level relationships of the major arthropod lineages. As with higher level mammal relationships, prior efforts involving morphology, ribosomal, and whole mitochondrial sequences have led to conflicting -- and in many cases clearly wrong -- conclusions. We were inspired by the remarkable consensus achieved in mammal phylogeny when two independent groups each sequenced 30kb of nuclear protein coding genes. We have assembled and made available on the web a list of 5000 single copy "strict orthologs" between *Drosophila* and *Homo* as a basis for designing primers to amplify 100 nuclear protein coding regions. So far we have found 40 primer pairs that work across a wide range of arthropods. We have developed a successful teaching module incorporating Arthropod phylogeny, and are developing Bayesian methods to estimate divergence times from molecular phylogenies.

<http://www.biology.duke.edu/cunningham/DeepArthropod.html>

Grant supported by NSF: DEB 01-20635

P1034

Agrarian Landscapes in Transition: A Cross-Scale Approach

Margaret C. Nelson, Arizona State University, Charles L. Redman, Ann P. Kinzig, David R. Foster, Myron P Gutmann, Peter M. Kareiva

This interdisciplinary, cross-site project is tracing the effects of the introduction, spread, and abandonment of agriculture at six LTER sites. Many conceptualizations of agrarian transformations assume a simple linear model—change driven by present-day economic, demographic, and technological conditions. This project incorporates a more integrated and long-term view: land-use change affecting landscapes, altered landscapes affecting ecological processes, and both influencing the ways humans monitor and respond to their surroundings, engendering further cycles of change. This study will identify and quantify the ways in which these integrated cycles differ across cultures, biogeographic regions, and time. Analytical approaches include structural-equation modeling, analysis of spatial and causal effects, and cross-site comparisons of case studies. As a practical test, project approaches and insights will be examined in the context of conservation planning at The Nature Conservancy.

This investigation will demonstrate the importance of social-science information and approaches in ecosystem investigations. Second, this project will develop general theories on how socio-ecological legacies, and lags in the recognition of and response to change, vary across space and time. Third, the project expects to show that humans act not only to disturb ecosystems, but also to monitor ecosystem values and maintain stability. Fourth, project results will provide information of use to policy makers by using an approach that explicitly relates socio-ecological processes to varying levels of political organization. Fifth, cross-scale data collection and analyses are expected to demonstrate that some patterns of human-ecological interactions are surprisingly long term, vary across space and time, and are non-linear.

Grant supported by NSF: DEB 02-16560

P1035

Biocomplexity: Emergence of cooperation from human-environmental interactions

J. Stephen Lansing, University of Arizona & Santa Fe Institute

Some results of this project will be featured in Program 3 of “The Sacred Balance”, an NSF-funded television documentary to be broadcast on PBS September 17 2003.

Some results:

- SAIL (“Simulated Agents in Love”), an adaptive agent model designed to help read history and social structure from the genome. Anthropologists and historians are interested in questions about the stability and change of human social structures involving time scales and population sizes that have received comparatively little attention from population geneticists. SAIL simulates patterns of gene flow that are affected by kinship and migration patterns. Pseudo-genetic information and pedigrees are tracked as populations grow, marry, migrate and intermarry. SAIL thus provides a tool to interpret genetic data on patterns of relatedness for both male and female lineages.
- Y chromosome data on 551 Balinese suggests that the prehistoric colonization of Bali was far more complex than predicted by current models of the Austronesian expansion. This conclusion is also supported by our analysis of ancient DNA.
- Using SAIL as well as contemporary ecological and kinship data, we are developing new models to analyze the formation and historical spread of cooperative farmer’s associations on the landscape of Bali.
- Nutrient flow studies showed that current fertilizer policies cause needless damage to terrestrial ecology and that damage extends to coral reefs.
- Comparative analysis of mechanisms conferring robustness in Bali and Borneo ecosystems led to a conference and book

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P1036

Deep 6: Resolving Insect Ordinal Relationships

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Insects are the most diverse extant group of organisms and probably the most successful lineage of life ever to exist. Over a million species have been described distributed between 30 orders which vary widely in body form, life history and ecology. The distinctiveness of the insect orders has long been recognized and many are readily apparent to all: beetles (Coleoptera), flies (Diptera), wasps (Hymenoptera), fleas (Siphonaptera) etc. Despite their long recognition and extensive efforts to elucidate their evolution the inter-relationships of the insect orders is still poorly understood. Deep 6 aims to recover the evolutionary tree of the insects and describe how the great diversity of insect orders came to

be. This goal is being addressed by 3 complementary approaches: extensive sampling, genomic analysis and intensive computing solutions. Even the largest studies of insect evolution have only sampled 120 species to stand proxy for over a million, we aim to sample 2500 species spread evenly amongst the insect families to get a more representative study group. With the expansion of DNA sequencing technology analysis of genomic evolution has become possible, we are sequencing the mitochondrial genomes of 200 species to gain an appreciation of the utility of this data source in understanding insect evolution. Computational analysis has long been a weak point in evolutionary studies with methods of data analysis lagging behind biologist's ability to generate data, we aim to improve the current methods of analysis and their implementation such that they are more efficient and more available to scientists at all institutions.

Grant Supported by NSF: DEB 01-20718

P1037

Form Gene Expression to Multicellular Development In Dictyostelium

Loling Song, Cornell University

This project details an integrated, multiscale and multidisciplinary approach towards characterizing and understanding the development of Dictyostelium discoideum, from gene expression to morphology and multicellular organization. The basic underlying premise is that the time is ripe for the concerted application of quantitative methods, both experimental and theoretical, to a central problem of modern biology, namely how one can form an integrated picture of an organism that connects genetic information to behavioral response. For a variety of reasons, Dictyostelium is the logical system in which to tackle this challenge.

The research project has three components: First, DNA microarray techniques combined with the knowledge of hundreds of well-characterized mutants will be used to acquire a large body of gene expression data relevant to Dictyostelium development. Second, a new generation of experiments, focusing on the cell response to external signals that coordinate multicellular development, will be devised and carried out. Finally, computational simulations will be used to tie together the different pieces, e.g., genetic networks with protein networks, protein networks with cellular response, and cellular response with multi-cellular morphogenesis. To accomplish these tasks, a high quality, interdisciplinary team of scientists has been assembled at the interface of biology, physics, and computation.

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P1038

Marine Viromics: The Interaction of Viral Genomes with the Marine Environment

Anca Segall, San Diego State University

John Paul*, Forest Rohwer, Anabel Miranda, Yuqiu Xu, Nathan Authement, *Amy Long, *Shannon Williams. San Diego State University and *University of South Florida

The roughly 10:1 ratio of viruses to bacterial cells found in almost all environments indicates that viruses profoundly shape bacterial populations. Two basic "flavors" of bacterial viruses, known as phage, exist: lytic and temperate. While lytic viruses are classical obligate parasites that almost always kill their hosts, temperate viruses can choose between the lytic lifestyle and the establishment of lysogeny. During lysogeny, the phage expresses only proteins (generally a repressor and little else) to prevent expression of any proteins that would contribute to lysis. However, the prophage can return to the lytic lifestyle when triggered by specific signals. In the cases of many model phage, the prophage-lysogen relationship is

indefinite, unless disturbed by damage to the host cell's DNA. The overall goal of our Biocomplexity project is to characterize prophage-host relationships in several marine systems, and investigate environmental cues that destabilize the lysogenic lifestyle and lead to lysis of the host. To this end, we are sequencing several genomes of induced prophages, and using bioinformatics analyses to identify several genes important for the lysis-lysogeny decision. Once these genes are identified, we will be testing their control of the switch from lysogeny to lysis in vitro and will develop a mathematical model to describe these events. The ultimate goal is to use the information gained to follow the lysogeny-to-lysis decision in the environment, and understand the influence of this decision for bacterial populations. We have completed the sequence of two phages (the *Listonella pelagia* and *Staph. saprophyticus* phages) and are completing the genome of a third phage from a *Bacillus pumilis* marine isolate. We have found physiological conditions in which the *S. saprophyticus* phage is induced, and will use the genomic information to design macroarrays to detect gene expression changes in these conditions. This and other data will be presented at the meeting. Our genomic data can be accessed at http://www.segall-lab.com/phage_sequences.htm

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POSTER SESSION 2

P2001

Atmospheric Deposition, Transport, Transformations and Bioavailability of Mercury across a Northern Forest Landscape

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Widespread contamination of mercury in remote aquatic environments due to atmospheric deposition and consequent high concentrations in aquatic biota, suggest that there is an acute need to improve understanding of the mechanisms of mercury transport and transformations in lake/watershed ecosystems. Atmospheric deposition of mercury to forest ecosystems is enhanced by processes within the canopy. Mercury entering the forest floor largely via throughfall and litterfall may be a factor of two or more greater than wet deposition. Following deposition, mercury undergoes a series of complex pathways and transformations, which interconnect with other element cycles, and ultimately control the supply of methyl mercury to aquatic biota. Important, but poorly understood mechanisms of Hg transport and transformations include: mineralization of litter mercury inputs, binding of mercury and methyl mercury in forest soils, wetlands and sediments, conversion of ionic mercury to methyl mercury and/or volatile elemental mercury, and the bioavailability of methyl mercury to aquatic biota.

The overarching hypothesis for this proposed research is: Canopy processes enhance atmospheric mercury deposition to northern forest ecosystems. Following deposition, the transport and transformations of mercury and ultimately the supply of methyl Hg to aquatic biota is controlled by the pathway of deposition, redox-controlled microbial transformations and landscape characteristics (e.g., vegetation, wetlands, surface waters).

This study will be conducted in the Adirondack region of New York, an acid-sensitive forested area with high concentrations of mercury in fish relative to other lake districts in eastern North America. The specific objectives of this study are to:

1. To quantify the inputs, transformations and losses of mercury species in an upland northern hardwood forest.
2. To determine conditions controlling the complexation, immobilization and net methylation of mercury.
3. To assess the fate, transport and bioavailability of atmospheric mercury deposition across the Adirondack landscape.

To accomplish our research objectives and test the hypotheses, we propose an integrated program of field and laboratory research. We will conduct detailed plot-level field studies examining pathways of mercury deposition to the forest floor, and the subsequent transport and fate of atmospherically deposited mercury. These studies will be conducted at the Huntington Forest, in Newcomb, NY. We will instrument a previously studied plot and conduct detailed measurements of mercury exchange with the forest floor. Laboratory experiments will be used to determine binding of ionic mercury and methyl mercury with dissolved and soil organic matter. Biotic controls on methylation/demethylation will also be evaluated in the laboratory under a range of terminal electron acceptors, and molecular techniques will be used to identify communities of methylating bacteria. To investigate how well our understanding of mercury dynamics can be applied across the Adirondacks, we will conduct field measurements of atmospheric deposition, soil Hg species, and Hg species in lake water and aquatic biota in eight watersheds. The water column and sediment mercury deposition have been previously been studied in the lakes of these eight watersheds. We will supplement these observations with a comprehensive sampling of the biotic assemblages. The process-oriented Mercury in Adirondack Wetlands Lakes and Terrestrial Systems model will be a critical tool in this project. Results from the field plot study and the laboratory studies

will be used to improve formulations of important processes affecting mercury deposition, fate, transport, transformations and bioavailability in northern forest ecosystems.

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P2002

Biocomplexity of Frost-Boil Ecosystems: Self-organization across the Arctic Bioclimate Gradient

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Frost boils are small barren or sparsely vegetated circular patches that develop in the Arctic through processes of frost heave. They appear to be particularly sensitive to differences in climate. Frost-boil morphology varies dramatically across the Arctic bioclimate gradient due to complex interactions between the physical and biological elements of the system (frost heave, soil properties, vegetation). A differential frost-heave (DFH) model describes the physical processes involved in the self-organization of frost boils. A vegetation succession model (ArcVeg) describes how vegetation responds to differences in climate and disturbance regimes. Currently, a conceptual model shows how the strength of the various interactions between the physical and biological components of the system differ under different climate regimes. A major goal is to link the physical and biological models to help explain how frost heave, in concert with the vegetation, responds to differences in climate and disturbance regimes.

Starting in 2002, a team of researchers from the US and Canada began studying frost-boil ecosystems at a network of 11 study sites along a transect from Happy Valley, Alaska to Ellef Ringnes Island, Canada and two sites in Russia. The interdisciplinary project has five major components: Climate and Permafrost, Soils and Biogeochemical Cycling, Vegetation, Ecosystem Modeling, and Education (See abstract by Gould and Walker regarding integrating Frost-Boil Biocomplexity Science and Education). Vegetation, active layer and snow depth have been mapped in 18 10x10-m grids. Climate stations, soil-heave monitoring and detailed soils descriptions and analysis has been conducted at all the research grids.

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P2003

Biocomplexity: Oceanic Nitrogen Fixation and Global Climate

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Oceanic nitrogen fixation has recently been identified as a significant part of the oceanic nitrogen (N) cycle and the balance of nitrogen fixation and denitrification may directly influence the sequestration of atmospheric CO₂ in the oceans. Accumulating evidence indicates that iron (Fe) availability may be a key

controlling factor for nitrogen fixation. The primary pathway of Fe delivery to the upper oceans is through dust deposition, a climate dependent process. Nitrogen fixers may therefore be directly involved in global feedbacks with the climate system and these feedbacks may also exhibit complex dynamics on many different time-scales.

The hypothesized feedback mechanism has the following component parts. The rate of N₂ fixation in the world's oceans can have an impact on the concentration of the greenhouse gas, carbon dioxide (CO₂), in the atmosphere on time-scales of decades (variability in surface biogeochemistry) to millennia (changes in the total NO₃⁻ stock from the balance of N₂ fixation and denitrification). CO₂ concentrations in the atmosphere influence the climate. The climate system, in turn, can influence the rate of N₂ fixation in the oceans by controlling the supply of Fe on dust and by influencing ocean circulation. Humans also have a direct role in this cycle by our influence on agriculture at the margins of deserts and our effect on atmospheric CO₂.

We are studying each of the components of this system and testing their hypothesized feedback processes in a set of models. The fieldwork has just finished and involved a mix of ocean observations, direct experiments on mesocosm scales and the collection and analysis of sediment cores to probe the past earth history. We used initial model runs to help guide the field program. One key early question, the extent to which changes in nitrogen fixation will draw CO₂ out of the atmosphere and into the oceans shows that the ocean-atmosphere system (as modeled) is quite sensitive to the balance between nitrogen fixation and denitrification. Because of the interaction of the various parts of this system, simple models of this feedback cycle exhibit complex behaviors on a variety of time-scales.

Project URL: <http://wrigley.usc.edu/bc/>

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P2004

Biocomplexity: Feedbacks between Ecosystems and the Climate System

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The overall goal of our research program is to characterize and quantify the feedback mechanisms between terrestrial ecosystems, the climatic system, and air pollution involving cycles of water, energy, and relevant chemical species (See Figure). To address this goal we are developing and using coupled models that include: (1) dynamic and linked terrestrial hydrology and ecology, (2) comprehensive coupled physical climate (three-dimensional atmosphere and ocean), and (3) atmospheric chemistry (gaseous and aqueous phase chemical processes). The integrated models represent the major complex biological systems on Earth and span the scales from local to global.

With the new coupled models we are beginning to quantify the combined effects of air pollution (O₃, NO₃, SO₄[□]), and climate change on the productivity and distribution of vegetation globally. We also are making progress on determining how changes in land ecosystems, caused by pollution and climate change, can feedback to climate through changes in albedo, carbon storage, and trace gas exchange rates. As the impact of multiple stressors acting simultaneously on forest production are determined, their roles in amplifying or damping regional disparities are being elucidated. Toward these ends we have improved our Terrestrial Ecosystem Model and Atmospheric Chemistry Models to facilitate their interaction. We have also further developed our 3D Ocean Circulation Model to incorporate biogeochemical cycles and

our 3D Atmospheric Intermediate Model can now be coupled to it for interactive studies. We also adapt the NCAR CCM for selected atmospheric chemistry studies. Our work should provide significant information for understanding how our future global environment will evolve under the joint effects of growing world population, changing technological and agricultural practices, and economic development.

We argue that uncertainties in most of the relevant feedback processes are large. Therefore, to understand the above interactions we have begun comprehensive studies of the sensitivity of our conclusions to critical input assumptions, and calculations of the probability distributions of critical output variables. We address this through the use of multiple (ensemble) simulations, of flexible models, and of powerful (probabilistic collocation) methods to compute uncertainties.

There are significant educational byproducts of this research designed to effectively communicate results to students, fellow researchers, journalists, industry and environmental policy-makers. We also expect to make contributions to general methodologies to study and numerically simulate very complex and interactive spatially and temporally resolved phenomena using distributed memory computers.

Some of our research has already appeared in multiple papers in JGR, Tellus, GRL, Climatic Change, GBC, J. Veg. Sci. and other journals and several papers are under review.

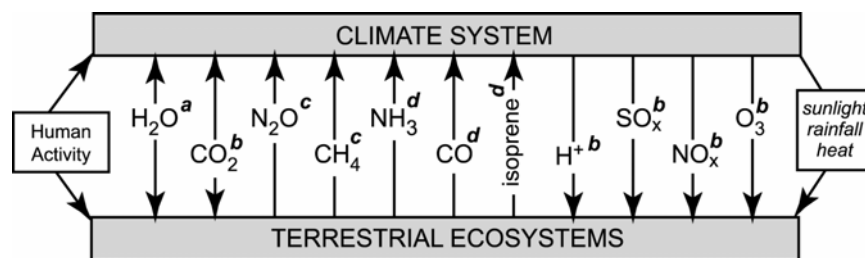


Figure. Schematic focusing on feedbacks between the climate system and land ecosystems emphasizing exchanges of trace gases and aerosols important in climatic and biosphere processes. The influences of human activity (trace gas emissions, land-use change, *etc.*) are being specified using results from the MIT IGSM and other studies. The superscripts *a* (well studied) to *d* (few studies) represent qualitatively the current state of knowledge of these various chemical flows and their effects.

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P2005

Biogeochemical processes and community dynamics in gas hydrate systems of the Gulf of Mexico
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The Gulf of Mexico has abundant gas hydrates and oil/gas seeps. The overarching goal of this project was to understand the geochemical and microbial processes involved in the cycling of carbon and sulfur in Gulf of Mexico gas hydrate systems. Our approach was an integration of molecular DNA, lipid

biochemistry, stable isotopes, and organic/inorganic geochemistry. The following summarizes our current understanding of the biocomplexity in the gas hydrate systems in the Gulf of Mexico:

1. 16S rDNA and functional genes indicate the presence of diverse Bacteria and Archaea. Bacterial and archaeal community composition is more similar within sites than between sites.
 2. Lipid biomarkers and stable carbon isotopes suggest that anaerobic methane oxidation is mediated by consortia of sulfate-reducing bacteria and Archaea.
 3. Geochemical measurements and modelling indicate that microbial oxidation of non-methane hydrocarbons dominate over methane oxidation in driving carbonate precipitation, which is coupled to enhanced sulfate reduction.
 4. Abundance of archaeal biomarkers and stable isotope signatures are similar to those of the Mediterranean mud volcanoes but are distinct from those of the Hydrate Ridge or Cascadia Ridge, suggesting variations in microbial communities, methane oxidation kinetics, and carbon sources among the different geological settings.
- Future research will strengthen the integration of geochemistry and microbiology to determine the underlying mechanisms for species diversity and functions in the gas hydrate systems. We will also substantiate our modeling effort to better evaluate specific microbial processes mediating hydrocarbon oxidation and carbonate precipitation in the hydrate systems, which contribute to the overall oceanic carbon sinks.

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P2006

Biogeochemistry of Fe(III) and Sulfate Reduction in Extreme Acidic Environments

Richard F. Yuretich, University of Massachusetts at Amherst

Acid waters rich in iron and sulfate can support a wide variety of microorganisms that catalyze the oxidation-reduction reactions of these bioactive elements, exemplified by acid-mine drainage (AMD). A large amount of research has focused on the processes of AMD generation, but the biogeochemistry of natural attenuation is relatively unknown. The principal goals of this project are to carefully examine the processes of Fe(III) and SO_4^{2-} reduction in a representative AMD site through field studies, modeling, and laboratory experiments, and to quantify the roles of acidophilic and acid-tolerant anaerobic microorganisms. K12 teachers are part of the research teams and the effects of research experiences on their higher-level understanding of science will be evaluated.

The field site at Davis Mine, an abandoned pyrite mine in rural Rowe Massachusetts has been established. In April, 2003, we drilled nine multi-level monitoring wells along the outflow to document the hydrogeology and to examine the three-dimensional distribution of major and trace elements in the groundwater. The volume of surface water reaching nearby Davis Mine Brook is being monitored via a weir. Preliminary data indicate a restricted lens of impacted groundwater that moves rapidly through the mine tailings and shallow bedrock fractures, but is contained by ambient groundwater from uncontaminated recharge areas. We will use the data to develop well-constrained flow and geochemical models. Soil samples collected from the drilled wells are being used to provide inoculums for cultivating bacteria and identifying DNA. Two high-school teachers are collaborating as full partners in the project, engaged in the seminars, working in the laboratories and completing research projects.

We were motivated to take this multi-disciplinary approach by the apparent dynamic equilibrium that has restricted the extent of the AMD in this area, and by some initial evidence that sulfate reduction is

occurring at the fringes of the site. If bacterially-catalyzed reduction is present, we can document the conditions that may stimulate it so that it may be used as an alternative to extensive and invasive engineering efforts for AMD remediation.

Project web site: <http://www.umass.edu/biocomplexity/>

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P2007

Biosphere-atmosphere fluxes of CO₂ at Scales from Ecosystem to Continent

Paul Moorcroft, Harvard University, Steven C. Wofsy, J.W. Munger & David Hollinger Co-investigators: Bruce C. Daube, Christoph Gerbig, John C. Lin & Cassandra Volpe Horii

Concerns over recent and future changes in atmospheric CO₂ concentrations and climate make it critically important to improve our understanding of where, why, and at what rates terrestrial ecosystems remove CO₂ from, or release CO₂ to, the atmosphere. This requires linking process-level biological knowledge, typically obtained from individual plants or ecosystems over short time scales, with observations and models that characterize the large spatial domain and long time scales of regional and global concern. We are addressing this issue by obtaining comprehensive observations and using archived data for spatial(local to regional) and temporal (hourly to decadal) scales, and by developing an integrated ecosystem-atmosphere model that captures both slow and fast ecosystem processes and is thus capable of assimilating biological knowledge with diverse atmospheric and ecological data. The integrated model will be optimized using constraints from atmospheric and biospheric data, obtained using aircraft and ground measurements in the project, to link quantitatively emergent properties of the terrestrial biosphere-atmosphere system with the underlying fundamental biological and physical processes. In particular, the optimized model will yield quantitative information on the environmental dependencies of photosynthesis, plant respiration, mortality and decomposition and other factors that is consistent with both short and long-term dynamics of terrestrial carbon fluxes at regional scales. In doing so, the optimized model will yield improved predictions of future changes in the carbon cycle in response to environmental changes, such as climate and pollution, or human forcing such as harvesting and land use change.

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P2008

Biotic and Abiotic Controls on the Emergence of Terraced Carbonate Mineralization

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The goal of this project is to determine whether terraced carbonate deposits arise as a result of microbial interactions with the hot spring physical and chemical environment. The ability to distinguish ancient and modern geological features that are biologically influenced, from those that are purely abiotic in origin, advances our understanding of the timing and pattern of bacterial evolution and provides a tool to identify microbial life in the fossil record. This interdisciplinary effort involves: 1) in situ crystallization experiments; 2) correlating calcite crystal growth form, distribution and chemistry with microbial diversity and metabolic activity; and 3) quantitative modeling of carbonate terrace formation using stochastic differential equations.

As a first step in determining microbe-carbonate associations, we have sampled eleven different crystal features within a travertine system at Mammoth Hot Springs, Yellowstone National Park. Centimeter-scale crystalline growth forms are composed of 10 to 50 micron aragonite needles arranged in dendritic, radial, and arcuate patterns. Denaturing gradient gel electrophoresis (DGGE) analysis of PCR-amplified 16S rRNA gene fragments was used to determine the diversity and frequency of bacterial phylotypes within and between these unique crystalline deposits. Features with phylotypes representing aquificales-like organisms in high-temperature facies, were easily distinguished from features in high to middle temperature facies by the dominance of B-proteobacteria. Phototrophic eukaryotes gradually appeared in select features within the pond, proximal and distal slope facies. Scale-invariance of the travertine terraces is being tested with pond measurements derived from photogrammetric analyses in addition to controlled laboratory experiments of the hot springs to develop a comprehensive picture of the physical setting that these microbe-carbonate associations thrive.

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P2009

Complex Molecular to Global Interactions and Feedbacks in the Marine DMS Cycle

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With participation of B Huebert, University of Hawaii

Ocean ecosystems are part of a complex geophysical-biogeochemical web that transforms matter and energy and sets the conditions for life on the surface of the Earth. Communication and feedback between different parts of this web are mediated to a significant degree by the exchange of radiatively important, biogenic trace gases. One such feedback involves marine plankton, the volatile sulfur compound dimethylsulfide (DMS), and global climate. In this feedback, DMS produced by marine phytoplankton and the food web enters the troposphere and is oxidized there to sulfate particles, which influence cloud albedo and, consequently, climate. Large-scale climate change, in turn, affects phytoplankton abundance and food web processes in the oceans and thereby closes the feedback loop.

The strength-and even the sign-of this feedback loop is still unresolved, largely because of the exceedingly complex network of biogeochemical and ecological processes that affect the concentration (and hence emission) of DMS. For instance, we now understand that it is not only algal species composition but also food web dynamics that are of paramount importance to the DMS cycle. Fascinating new interactions in this cycle are still being discovered with some regularity, but mechanistic and prognostic mathematical models of this system have yet to incorporate many of these developments. Furthermore, there have been no field studies in which all of the relevant rates and concentrations in the marine DMS cycle have simultaneously been measured, nor have complex interactions or measurements been included for important geophysical or chemical parameters (e.g., light, Fe, water column physics), hampering the ability of models to accurately map spatial and temporal variations in surface DMS concentrations. Specifically, we propose to: 1) Measure and model all known relevant fluxes of concentrations of DMS and related species during intensive field studies in two ocean biomes: a subtropical gyre and the Southern Ocean; 2) Develop a global marine DMS model built upon the proposed field measurements and other existing measurements and models; and 3) Use such a model to evaluate the potential for feedbacks between climate and the marine DMS cycle.

We suggest that the DMS biogeochemical system represents a tractable research subject that can aid in understanding the complexities involved in biosphere-geosphere regulation at the regional and global scales. We also argue that the DMS system serves as an excellent, research-accessible model for food-web dependent biogeochemical processes. Because dimethylsulfonio- propionate (DMSP), the precursor of DMS, is intimately connected to virtually all levels of the food web, and because DMSP itself contributes significantly to the carbon (and hence energy) flow in the ocean, our investigation of the complex controls on the DMS/DMSP cycle should shed light on the critical factors influencing the ecological distributions of organisms in the sea and the biogeochemical cycles of major nutrient elements (C, N, P, S, Fe). By advancing the knowledge of DMS/DMSP biogeochemistry we will not only allow better predictions of the local, regional and global scale responses to anticipated shifts of climate, but also gain valuable insights into the connections within the biogeochemical-geophysical web that sustains life on Earth.

This project will involve the broader community by including undergraduate and graduate students in the laboratory and field research, mentoring and furthering the professional development of a postdoctoral modeler and 2 K-12 TEA teachers (in the successful OPP program, in which the PI has been involved: tea.rice.edu/tea_rosenberger_frontpage.html), and creating an interactive web page within the Bigelow web site in accordance with Maine's Learning Results criteria, similar to ongoing projects (www.bigelow.org/shipmates). In addition, each of the 10 participating investigators will formalize on-going interactions with regional K-12 schools by creating and using a shared presentation.

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P2010

Consequences of Greenhouse Warming For Biocomplexity and Biogeochemical Cycles: A Multidisciplinary Case Study Across The Paleocene-Eocene Boundary

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Approximately 55 million years ago, the Earth experienced a rapid and extreme episode of global warming that was the product of an unusually massive release of carbon into the ocean-atmosphere system. This event, known as the Paleocene-Eocene Thermal Maximum (PETM; a.k.a. LPTM), had far reaching and significant impacts on global marine and terrestrial ecosystems that ranged from mass extinction of deep sea foraminifera to dispersal and subsequent radiation of mammals. The combination of these climatic and biotic perturbations, initiated dramatic changes in the planet's biogeochemical cycles that eventually worked to restore equilibrium to the carbon cycle. However, the recovery process took over 150,000 years, and some changes were irreversible. Questions arise concerning the nature of the feedbacks between the biota and the environment during this event, particularly the biogeochemical couplings.

A multi-institutional interdisciplinary program was initiated just over a year ago to investigate the effects of this unique climatic event on the global biosphere and coupled biogeochemical cycles of carbon and nutrients. Building on a foundation of existing work, this project is utilizing an array of models to determine the coupling of inorganic and organic chemical processes, and to evaluate the relative contributions of these processes in sequestering excess carbon, both on short and long-time scales. These models are being constrained and tested with empirical data from both marine and terrestrial systems. Here we present results of one model developed at UCSC that was designed to evaluate soil carbon isotope records in terms of changes in plant productivity, soil respiration rates, and atmospheric pCO₂,

with the aim of identifying transient features of the terrestrial carbon cycle and environment characterizing this climate event. The empirical data to test this model were generated from analyses of soil nodules collected in the Bighorn Basin. The primary results indicate an increase in terrestrial primary productivity during the thermal maximum. In this way, the terrestrial biosphere may have served as a transient sink for excess carbon released to the atmosphere.

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P2011

Ecosystem Response to Elevated Arsenic Concentrations

Thomas Pichler, University of South Florida

The shallow-water submarine hot springs near Ambitle Island, Papua New Guinea afford an ideal opportunity to investigate the response of benthic diversity, activity, and biogeochemistry of microorganisms, foraminifera, and infaunal invertebrates to arsenic. The aim of the proposed research is to sample and analyze vent fluid, seawater, and sediment on Ambitle Island from sites of high and low As concentrations over a 4-year period. Analyses will include an extensive suite of inorganic aqueous species, isotopes and dissolved organic carbon from pore fluids and the water column. In addition, microbial, foraminiferan, meiofaunal, and macrofaunal invertebrate diversities and community structures will be investigated in the sediments using morphological, isotopic and PCR-based molecular methods. The goal of this study seeks to answer seven first-order questions with respect to As cycling in the hydrothermal system at Ambitle Island:

- What is the source for the As and what conditions lead to its accumulation in the sediment?
- Is the As in Tutum Bay sediments available for biological processes?
- How diverse are the microbial community structures at the sites, and how do these correlate with variations in chemical composition, especially As levels?
- What are the growth characteristics of As-tolerant or As-metabolizing mesophiles and thermophiles in Tutum Bay, and how to geochemical energy sources constrain their activity?
- What effect do elevated As values have on taxonomic diversity of benthic fauna in Tutum Bay sediments?
- What are the major geochemical and biotic differences between the dry and wet season?
- Can we mathematically describe and predict benthic diversities relative to As concentrations in Tutum Bay?

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P2012

Forward and Inverse Modeling of CO₂ and ¹³CO₂ in the NCAR CCSM

Neil S. Suits Colorado State University, Scott Denning, Ian T. Baker, Peter E. Thornton and John B. Miller

This is a three-year research program to study the exchanges of CO₂ and ¹³CO₂ between the atmosphere, ocean, and terrestrial biosphere, and the processes that govern them. Spatial and temporal variations of these two tracers in the atmosphere contain information about the sources and sinks of CO₂. The stable isotope ratio of carbon can be used to partition a total flux into terrestrial and marine components, reducing uncertainties in regional monthly fluxes calculated by inversion of tracer transport models. Stable isotope code already developed in the Simple Biosphere Model (SiB2) will be ported into the

Community Climate System Model (CCSM) and combined with a parameterization of the carbon cycle and $\delta^{13}\text{C}$ in the ocean, allowing prediction of spatial, seasonal, and interannual variations in fractionation and disequilibrium at the air-sea interface and from terrestrial ecosystems. Inversion of observed patterns in atmospheric CO_2 concentrations to estimate surface fluxes is ill-conditioned because response patterns in the current network are not unique. Consequently, we will develop new inversion methods that make better use of the ^{13}C constraints, including variations in both discrimination and isotopic disequilibrium between the atmosphere and terrestrial ecosystems. We will attempt to use these variations to extract information from the observations about the effects of environmental forcing on physiological stress and turnover of organic matter. Finally, we will perform an inversion of the past 20 years of atmospheric CO_2 and ^{13}C data to estimate regional monthly fluxes, isotopic exchanges, and the processes that control them.

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P2013

High Precision $^{13}\text{CO}_2/^{12}\text{CO}_2$ Ratio Measurements Using an Optical Fiber Based Difference Frequency Generation Laser Source

***David J. Carlson, NCAR,** Alan Fried,¹ Dirk Richter,¹ Jim Walega,¹ Frank Tittel,² Chad Roller,² Bruce Vaughn³, and Jim White³*

Scientists from the National Center for Atmospheric Research,¹ Rice University,² and the University of Colorado³ along with Educational and Outreach participants from two local high schools have carried out a comprehensive system design for a portable high precision spectrometer for in-field CO_2 isotopic ratio measurements. Our design covers: 1) spectroscopic calculations for optimal sampling to minimize systematic errors associated with differential temperature, pressure, and relative humidity between sampling and reference arms; 2) inlet system design and testing strategies to minimize isotopic fractionation and other systematic error sources; 3) optical system design, including sampling cell, difference frequency generation laser source development, and transfer optics; and 4) development and testing of data acquisition hardware and data reduction fitting algorithms. We have started construction and testing of the optical and mechanical system components. The figure below showing our optical system coupled to the sampling cell illustrates the innovative design and the novel use of fiber optic components. Our poster will include a discussion of several education and outreach activities intended to help and encourage high school teachers and students begin to explore current issues in carbon cycle research and current laser-based detection technologies.

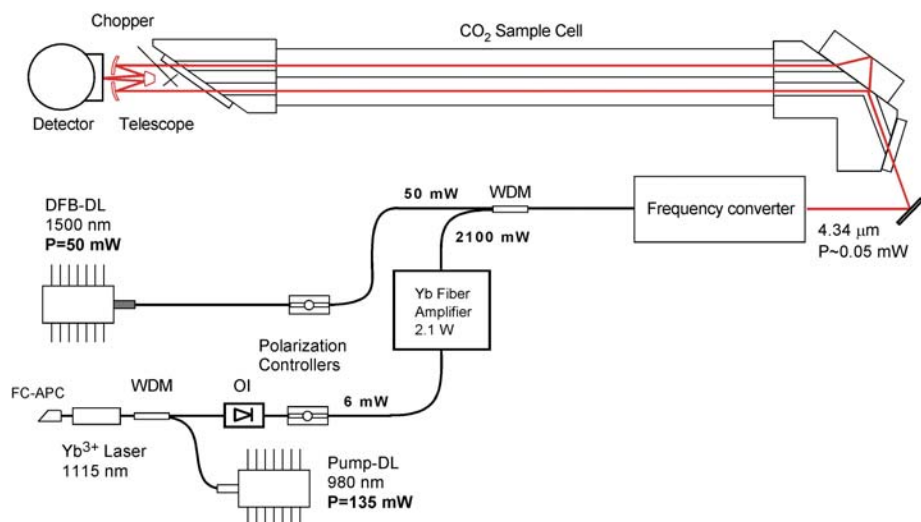


Figure 1: Schematic of mid-IR difference frequency generation laser source, sampling cells, and detection system.

Grant supported by NSF: ATM 02-15702

P2014

Impact of agroecosystem management on coupled biogeochemical cycles and on ecosystem services valued

Laurie E. Drinkwater, Cornell University

This exploratory project will use meta-analysis linked to modeling to provide a synthesis of the extensive literature published on carbon (C) and nitrogen (N) cycling processes in agricultural systems. This quantitative approach to understanding complex, non-linear interactions will help predict the impact of changes in management practices on primary productivity, yields and global biogeochemical cycles. We will investigate the potential for increased coupling of C and N cycles to reduce N losses from managed ecosystems and improve N and C balances over the long term. These reductions in surplus N in agricultural fields will impact humans via the quantity and quality of both marketable outputs and non-marketable services such as reductions in nitrate leaching and runoff. The project will make significant contributions to our fundamental understanding of interactions between ecosystem management and ecosystem function in terms of coupled biogeochemical cycles. Evaluating the management factors that optimize resilience of agroecosystems while minimizing riskiness will be a major goal of the proposed work. The study will also examine potential socially-valued effects that could emerge from changes in management in alternative agroecosystems. Triple-balance sheet accounting (economic, social and environmental) will be used to compare contrasting scenario analyses of watershed level impacts, and policy implications will be documented and published.

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P2015

NITROGEN AND IRON METABOLISM BY BACTERIAL COMMUNITIES IN ACIDIFIED STREAMS

JoAnn Silverstein, University of Colorado, Boulder, Jennifer Baeseman¹, Ben Heavener¹, Richard Smith² *¹Dept. of Civil, Environ., and Arch. Engineering, Univ. Colorado, Boulder¹ U.S. Geological Survey, Boulder, Colorado*

Acid mine drainage (AMD) contaminates between 8,000 to 16,000 km of streams in public lands in the West and more than 7,000 km of streams in the Eastern U.S. Nitrogen cycling in these acidic, metal-laden streams may be disrupted based on observations that denitrification is inhibited under low pH conditions. In addition, bacterial iron metabolism, especially iron respiration, is expected due to the abundance of iron in AMD, and may affect nitrate metabolism as well - negatively, by inducing competition for substrate or positively, by inducing conditions that enhance denitrification such as anoxia. Denitrification and iron respiration in streams (sediment and water) impacted by AMD was studied in three streams to determine the role of pH and source of acidity, seasonality, and electron acceptor (NO_3^- and Fe^{3+}) availability. Nitrate and/or ferric iron was added to laboratory microcosms containing sediment and water samples from each of: a stream draining an abandoned mine, a naturally acidic stream (no mine drainage), and a pristine circum-neutral stream. pH ranged from 2.6 to 4.91. Complete conversion of nitrate to nitrogen gas was observed in sediments from all sites. Furthermore, the pH of the microcosms after denitrification increased 0.23 to 1.49 pH units, depending on the site. Iron reduction (increase in ferrous iron) was observed in all biotic samples as well, and did not appear to be affected by denitrification. Phylogenetic studies of the sediment microbial communities in the sampled streams are underway. Initial results show significantly greater diversity in the circum-neutral stream than in the AMD-impacted streams.

Grant Supported by NSF: BES 02-21880

P2016

Land-Water Interactions at the Catchment Scale: Linking Biogeochemistry and Hydrology

Marc Stieglitz, lamont Dohert earth Obs. Of Columbia University

The study of integrated biogeochemical cycles is challenging due to the numerous processes and linkages that govern the dynamics of individual element cycles. For example, the movement of materials such as carbon (C) and nitrogen (N) within patches on the landscape and from land to water is governed by physical drivers of climate and hydrological flow, the processes of biological production and decomposition, and the chemical reactions that transform materials into either more or less reactive components in the system. This land-water movement of materials, especially C and nutrients, critically controls how both terrestrial and aquatic ecosystems function, and on how they interact with each other and with the atmosphere.

The focus of our recently funded NSF Biocomplexity project has been on understanding the initiation of hillslope hydrologic connectivity, that is, the condition by which once unconnected regions on the hillslope are linked via subsurface water flow, and the subsequent implications that this has for the downslope transport of nutrients and the spatial patterns of ecosystem productivity along the toposequence. Our research at various catchments tells us that for much of the year nutrient flushing takes place when the ridges and valleys are unconnected; that is, in many catchments the hydrologic connectivity among the hillslope communities is most pronounced during the spring snowmelt, but is more sporadic in the summer and depends on antecedent conditions and storm activity. Summertime transpiration reinforces this tendency toward a hydrological disconnect between upper slopes and the

midslope-riparian zones. Consequently, growing season nutrient flushing occurs mostly in near-stream riparian zones.

Our NSF Biocomplexity project has been designed to model, validate, and refine these ideas about hydrologic connectivity and its relationship to nutrient fluxes and productivity. Our focus site is the Innvait Creek catchment near the Toolik Lake Arctic LTER station, located in the foothills of the Brooks Range, in Northern Alaska. The project involves researchers at the University of Michigan, the University of California, and The Marine Biological Laboratory. Research will use existing, state-of-the-art models of hydrology and biogeochemistry and improve them with field studies of critical processes of plant production, microbial decomposition, and production rates of dissolved substances in soil waters. It is our intention that these models will be linked to determine how soil moisture, spatial connectivity, and the timing of meteorological drivers impact C-N cycling and catchment export. Model simulations will be used to explore how disturbances (increased nutrients, storms) propagate across the landscape.

Publications and URL

J. Shaman, J. McNamara, G.W. Kling, V. Engel, J. Shanley, An Approach to Understanding Hydrologic Connectivity on the Hillslope and the Implications for Nutrient Transport, accepted at Global Biogeochemical Cycles.

Rastetter E.B., Kwiatkowski B.L., Séverine Le Dizès, Hobbie, J.E., The Role of Down-Slope Water and Nutrient Fluxes in the Response of Arctic Hill Slopes to Climate Change, accepted at Global Biogeochemical Cycles

<http://www.ldeo.columbia.edu/~marc/> (see “For More Information” hyperlink)

Grant supported by NSF: ATM 02-21835

P2017

Coupled Biogeochemical Cycles of Carbon and Nitrogen in a Subglacial Volcanic Crater Lake **Eric Gaidos, University of Hawaii**

We have discovered an active microbial community in a subglacial lake within the Grímsvötn volcanic caldera, Iceland. We used a hot water drill to penetrate the 300 meter ice shelf and retrieved lake water and volcanic tephra sediments. We also acquired samples of borehole water before and after penetration to the lake, overlying glacial ice and snow, and water from a nearby subaerial geothermal lake for comparative analyses. Lake water is at the freezing point, fresh (TDS = 190 mg L⁻¹) and oxic. Cell counts in the lake water are 2 × 10⁴ ml⁻¹ whereas those in tephra sediments are relatively high (4 × 10⁷ g⁻¹). Plate counts showed a high abundance of cold-adapted cultivable organisms in the lake water, but not in the borehole water or ice. Denaturing gradient gel electrophoresis (DGGE) of 16S rRNA gene fragments amplified from genomic DNA extracted from Grímsvötn samples indicate that the lake community is distinct from the assemblages of organisms in borehole water (before penetration to the lake) and the overlying ice and snow. Sequencing of selected DGGE bands revealed that many sequences are highly similar to known psychrophilic organisms or cloned environmental DNA from other cold environments. Significant uptake of ¹⁴C-labeled bicarbonate in dark incubations of lake and tephra samples indicated the presence of autotrophs. Acetylene reduction assays for nitrogen fixation showed significant activity by diazotrophs. However, neither the specific carbon nor nitrogen fixation activity exhibited by our samples appears sufficient by themselves to explain the estimated concentrations of organic carbon and total nitrogen in the lake.

Grant supported by NSF: EAR 01-20435

P2018

Regulation of the Hydrologic and C Cycles by Native Shrubs in Soils of Sub-Saharan Africa

Richard P. Dick Oregon State University, *A. Badiane M. Sene M. Khouma, S. Ndiaye Institut Sénégalais de Recherches Agricoles, Senegal*

Desertification and degradation of soils in Sub-Saharan Africa is serious and likely reducing agricultural productivity, and there is interest in storing C in soils of these landscapes. Assessing soil degradation and C sequestration potential is spatially and temporally complex in this semiarid landscape. We have identified a largely unrecognized component of the semi-arid Sahel; woody shrubs (*Piliostigma reticulatum* and *Guiera senegalensis*) that voluntarily regrow in farmers' fields after the summer cropping season, which appear to be more important than trees or organic inputs such as animal manures in regulating C inputs/sequestration and hydrologic processes. Under current management, farmers cut and burn the shrub biomass each spring that may not be the most effective way of managing this organic residue. Also, we theorized that these shrubs might do "hydraulic lift" of water from wet sub soils to the dry surface. This could drive rhizosphere processes in "dry" soil such as nutrient mineralization/C cycling and possibly provide small amounts of water to shallow rooting crops. Our overall goal is to determine the unrecognized role of shrubs as key determinants in sequestration of C, water relations, and soil degradation mitigation in the semiarid ecosystem of Senegal that is representative of much of Sub-Saharan Africa. The approach includes: (1) rapid participatory surveys of rural communities; (2) landscape spatial analysis of shrubs; (3) detailed studies of how shrubs control C/N/P cycling, soil microbiology, and soil physical properties; (4) studies of water relations of shrubs and soils; and (5) modeling C cycling relative to shrub management over decadal periods.

Grant supported by NSF : EAR 01-20732

P2019

The Biocomplexity of Mangroves

Ilka C. Feller, Smithsonian Environmental Research Center

www.mangroves.si.edu

Mangroves ecosystems are complex adaptive systems. As such, it is important to realize that intersystem differences rarely can be explained on the basis of one or a few simple mechanisms. Rather, differences almost always must be explicated in terms of differences in context. The objective here is to demonstrate how system-level differences can be understood in terms of context.

The mangrove ecosystems of Twin Cays, Belize exhibit significant functional differences. Feller and McKee have demonstrated how three mangrove ecotopes on Twin Cays respond disparately to nutrient additions. The system that *fringes* the open waters respond positively to nitrogen enrichment, but not to additions of phosphorus. By contrast, the community of *dwarf* trees distant from the sloughs respond dramatically to extra P, but are indifferent to added N. A *transitional* ecotone exhibits mixed response to exogenous nutrient loads. No simple explanation for these dynamics has been found in terms of simple mechanisms.

Project investigators have chosen to regard the nutrient process involved in tree growth as elements embedded in a larger matrix of trophic interactions. Most of the project activities are, therefore, oriented to the construction of 18 trophic flow networks quantifying the transfers of carbon, nitrogen and phosphorus among ca. 50 ecosystem components in each habitat during the rainy and dry seasons. Ulanowicz and Baird have demonstrated how the sensitivities of a system-level property called the

ascendency reveal all the bottlenecks in nutrient processing. Thus, the plan is to subject all of the estimated networks to this sensitivity analysis in the hopes of highlighting exactly which are the processes limiting whole-ecosystem functioning in each habitat.

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P2020

The Jasper Ridge Global Change Experiment: Biocomplexity in Ecosystem Responses to Long-Term Environmental Changes

Chris B. Field, Carnegie Institute

This research utilizes annual grassland as a model system to test 4 hypotheses concerning the regulation of the cycles of carbon, nitrogen, and water in response to global change. Specifically, we will explore the mechanisms through which (1) plant physiology and species dynamics alter cycles of C, N, and H₂O, (2) levels and dynamics of C, N, and H₂O regulate plant species composition, (3) microorganisms control short-term and long-term N availability, and (4) plant chemical composition regulates structure and function of the soil microbial community. Together, these 4 hypotheses dissect the complex web of feedbacks linking biogeochemical cycles and ecological dynamics. The research builds on the infrastructure and ongoing operations of the Jasper Ridge Global Change Experiment (JRGCE), a multi-factor, ecosystem-scale manipulation that includes two levels of temperature, two of CO₂, two of N deposition, and two of precipitation, with single-factor manipulations as well as all of the possible 2-way, 3-way, and 4-way combinations.

With a team that includes biogeochemists, ecophysiologicalists, population biologists, and microbial ecologists, the project explores interactions between biogeochemical cycles and species dynamics across a range of time scales. Results to date range from unexpected dynamics in the hydrologic cycle, where warming causes an increase in late-season soil moisture, to the carbon cycle, where elevated CO₂ has inconsistent effects on net primary production. Several of the most dramatic responses are driven by treatment effects on the timing of resource availability. Using molecular techniques, we find that simulated global changes lead to striking shifts in the composition of the soil microbial community.

Grant supported by NSF: EAR 02-21838

P2021

Biocomplexity: the Roles of Resources, Competition, and Predation in Microbial Degradation of Organic Matter

Gary L. Taghon, Rutgers University

Bacteria play crucial roles in cycling of elements and thus the functioning of the biosphere. We know a great deal about the metabolic diversity of bacteria, and the pathways of the reactions they perform. Outside of simple laboratory systems, however, we cannot predict with any certainty the rates at which bacteria grow, metabolize, and mineralize organic matter. This project is about understanding, at a mechanistic and thus quantitative level, what affects the activity of bacteria in nature. While initially the problem seems straightforward, we believe its solution has been elusive because there are complex processes involved. This complexity exists over several levels of biological organization (individual, population, community), and in the microscale spatial heterogeneity of the environments in which bacteria function.

Our ultimate goal is to develop, and test, a model that will predict the rates of organic matter cycling in natural systems. Such a model must include the physical and chemical factors controlling the availability

of resources (reactants) to bacteria, interactions (potentially competitive) among different bacterial populations, and interactions among bacteria and their predators. Our approach centers on a tight coupling between modeling and empiricism, since it is our belief that models and experiments lead to new, useful knowledge only when there is a steady interaction. The model we are developing considers both “bottom up” (e.g., resource availability) and “top down” (e.g., predation) controls on bacterial activity.

Grant supported by NSF: OCE 01-20453

P2022

An Autonomous Genosensor for Environmental Water Quality Monitoring

John H. Paul, University of South Florida, David Fries, Matthew Smith, Erica Casper, and Andrew Farmer. University of South Florida

The deterioration of water quality, particularly in the coastal zone, has become a global issue. Understanding the processes which may compromise the quality of surface water, groundwater, and the coastal ocean are important for public health, ecological, economic, and, since September 11th, national security reasons. Surface and groundwater quality can rapidly deteriorate in response to rainfall resulting from episodic events or global climatic oscillations. We intend to develop an Autonomous Microbial Genosensor to detect microbial water quality indicators, based upon target mRNA amplification and detection. Our point of departure is the enteroviral group of viruses, for which we have ample experience in detection through traditional molecular technologies. We have developed a molecular beacon-based amplification assay that successfully detects a wide range of enteroviruses. A sensor module consisting of a blue LED, IR heater, and fluorescence detector has been built and successfully tested. A fluidic manifold is under construction. Current design options are based upon RNA extraction in columns linked to individual amplification cells in the sensor module. A challenge/problem is the front-end sample processing for enteroviruses in Tampa Bay, which may require ~100-1000 L for successful viral detection. Therefore, we may switch target organisms from Enteroviruses to the Florida Red Tide organism, *Karenia brevis*, the detection of which would only require filtration of 10-100 ml. Once developed, sensors will be integrated into existing platforms of the Coastal Ocean Prediction System (COPS) in Tampa Bay that provides nowcast data of existing hydrodynamic conditions. The broader impacts of these projects included a hands-on lab session in the Oceanography Camp for Girls in July 2003 and module in the USF Center for Oceanographic Education Excellence (COSEE) program. The project URL is: http://www.marine.usf.edu/~bwawrik/genosensor_.html

Grant supported by NSF: BES 02-16305

P2023

Disposable and Reusable Textile Materials in Healthcare Facilities-A MUSES Study

Gang Sun, University of California, Davis, Susan Kaiser, Margaret Rucker

This project involves multidisciplinary research on materials uses, new technologies and environmental impact of medical use textiles, which include surgical gowns, gloves, drapes, wraps, sheets, covers, and facemasks. Medical use textiles are composed of two major competing textile materials-disposable and reusable fabrics that serve primarily to impede the transmission of pathogens in healthcare facilities. The competition between the two materials in medical applications is very heated with gains and losses of market share based on concerns about materials uses, environmental impacts, and development of new technologies. Our goals as researchers was to provide an unbiased evaluation of these materials from several perspectives, including: 1) Environmental concerns of use and disposal of disposable and reusable

textiles; 2) Regulations from EPA and other government agencies on selection of two textile materials; 3) Economic consequences of selecting two materials, (analysis of both purchasing and maintenance costs of reusable textiles versus disposables without consideration of environmental impact); 4) Perceptions of disposable versus reusable textiles among healthcare workers and hospital purchasing agents; 5) Desired properties of medical use textiles (need for antibacterial functions on textile products as well as other important functional properties for textiles in healthcare facilities). We have conducted surveys of hospital administrators and infection control professionals. The findings are very important and have raised many new questions for future studies. The results of the research are discussed in the poster.

Grant supported by NSF: DMI 02-23987

P2024

Automated Submersible Flow Cytometry for Characterizing Coastal Phytoplankton Assemblages ***Alexi Shalapyonok, Woods Hole Oceanographic Institute***

Robert J. Olson, Heidi M. Sosik, In Situ Measurement of Marine Microbes to Investigate Mechanisms of Community Structure Regulation

Our understanding of the dynamics of phytoplankton communities has been limited by the space and time scales associated with traditional monitoring approaches. To overcome some of these limitations, we have developed a submersible flow cytometer (FlowCytobot) designed for extended autonomous monitoring of phytoplankton abundance, cell size, and pigmentation of particles as small as 1 μm phytoplankton cells. We have deployed FlowCytobot at two cabled coastal observatories, the LEO-15 site off New Jersey and the Martha's Vineyard Coastal Observatory off Massachusetts, and have produced automated data processing techniques to create hourly-resolved time series of cell abundance and cell size for various groups of phytoplankton. Measurements reveal distinct populations of *Synechococcus* and cryptophytes as well as an assemblage of other pico- and nano-phytoplankton of mixed taxonomy. For certain cell groups, such as *Synechococcus*, we have also developed a modeling approach for estimating population growth rates from diel changes in cell size distributions. FlowCytobot is currently moored on the seafloor 3 km south of Martha's Vineyard where it has operated continuously since May 2003. Water from 5 m depth is constantly pumped through the instrument, and samples are drawn by a robotic syringe pump every 5 minutes. Current phytoplankton signatures and details of operation can be seen in real time at <ftp://128.128.205.35> (user: guest, password: guest).

Grant supported by NSF: OCE 01-19915

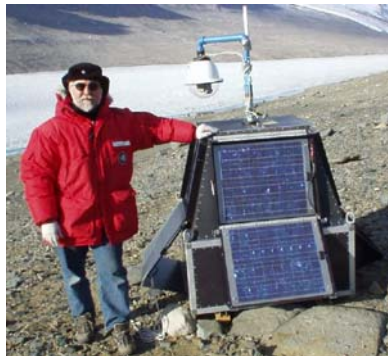
P2025

Solar/Wind Powered Instrumentation Module Development for Polar Environmental Research ***Tony Hansen, Magee Scientific Company, Berkeley, CA***

TonyHansen@mageesci.com; www.mageesci.com/Antarctic

This project is developing instrumentation modules to support a generalized 'payload' of scientific equipment in a powered, warm enclosure with radio data communications. The internal space can accommodate instrumentation, data acquisition and communications to support any form of sensor- or observation-based research. The acronym '*Taisu*' represents **T**ransportable **A**utonomous **I**nstrumentation **S**upport **U**nit. In the first field season of this project, two solar-powered *Taisus* with environmental research instrumentation payloads and wireless Internet-connected steerable live cameras were successfully deployed in the McMurdo Dry Valleys. They were pre-configured at the main base in

McMurdo; transported by helicopter and set down on the ground; the solar panels were unfolded, and the units were operational in a few minutes.



'Large' *Taisu* with live steerable webcam at Lake Bonney, McMurdo Dry Valleys, Antarctica. Communications by '802.11' wireless.

These units have space for two 19-inch racks of equipment, but are large and heavy. For deployment in the 2003/04 Antarctic field season, we are developing a smaller version containing a standard datalogger connected to an 'Iridium' modem for data transmission.



'Mini' *Taisu* under development for testing in 2003/04 Antarctic season: datalogger, Iridium modem. 15 kg. max

This project is supporting the development of the hardware specifically for generalized scientific use: when tested and proven, these and similar units will be offered to the research community.

Granted Supported by NSF: DBI 01-19793

P2026

Development and Test of Biospectral Logger in Lake Tahoe

Nathan Bramall, University of California, Berkeley, Ryan Bay, and Buford Price, University of California, Physics Department

The search for microbial life in the polar ice and snow of Antarctica and Greenland has been a slow and laborious process prone to many problems such as sample contamination. In order to rapidly detect microbial life *in situ* in these environments, we developed a borehole logging tool, the Biospectral Logger (BSL), which searches for the autofluorescence of ubiquitous biomolecules found in microorganisms. Its initial design used an excitation wavelength of 370 nm and seven channels of fluorescence detectors at wavelengths from 424 nm to 496 nm. We report on the development and test of our BSL in Lake Tahoe, where it recorded chlorophyll fluorescence, peaking at a depth of ~57 m, and NADH fluorescence that increased with depth, qualitatively consistent with an increase of bacterial counts in water samples with depth.

Although the original application to logging deep boreholes such as GISP2 and Siple Dome is complicated by the background fluorescence of organic borehole fluids, the BSL is well suited for microbial exploration in dry boreholes and polar oceans. We have designed a miniaturized version that can be used in 4-cm-diameter boreholes in deep mines, and ultimately in Martian permafrost. Its sensitivity will be sufficient to detect microbial concentrations down to ~ 1 cell/cm³ in media with relatively low background fluorescence.

Grant supported by NSF: OPP 01-19988

P2027

BIOCOMPLEXITY: Development of Instrumentation for Measurement of Biosphere-Atmosphere Fluxes of Carbon and Nitrogen.

Peter Curtis, Ohio State University, Brian Lamb, Washington State University, Hal Westberg, Washington State University, Alex Guenther, NCAR, Paul Shepson, Purdue University, George Mount, Washington State University (co-PIs)

Abstract: The biosphere/atmosphere exchange of CO₂, biogenic volatile organic compounds, nitrogen containing species, and other atmospheric constituents is a focal point for our understanding of complex feedback mechanisms between the atmosphere and the biosphere. However, current methods for measuring the exchange of gases and aerosols between the biosphere and atmosphere are limited to a few cases where fast instrumentation allows the use of eddy covariance methods or other less accurate methods are employed.

Our overall goals are to develop robust, flexible, and modular biosphere/atmosphere flux measurement systems for tower-based and airborne platforms, test these systems, and ensure transfer of the technology to the biosphere/atmosphere community.

Our research objectives include:

- a) development of disjunct eddy covariance (DEC) and accumulation (DEA) flux units for installation on tower and airborne platforms;
- b) development of a light aircraft flux facility with capabilities for micrometeorological and selected gas flux measurements;
- c) development of tower- and aircraft-based disjunct eddy covariance sampling system using fourier transform spectroscopy to measure CO₂ isotope ratios;
- d) testing of airborne DEC/DEA flux systems for measurement of stable carbon isotopes, BVOC and deposition of nitrogen species; and
- e) transfer our technology to the user community and develop the light aircraft flux facility as a user facility.

We are entering year three of our four year grant period and have made significant progress on objectives a), b) and c). We plan a large-scale field deployment of our tower and airborne DEC and DEA systems in 2004.

Grant supported by NSF: ATM 01-19995

P2028

Development of a Instrument for *in situ* Measurement of Microbial Enzyme Activities in Aquatic Ecosystems

J. W. Ammerman, Rutgers University, R. J. Chant, and G. Klinkhammer, Rutgers and Oregon State Universities

Microbial cell-surface enzymes are important agents of polymer hydrolysis in aquatic environments and indicators of the state of microbial carbon, nitrogen, or phosphorus nutrition. However, like most other microbial metabolic rate measurements in aquatic environments, enzyme activity measurements have usually been limited to manual assays with discrete water samples. An instrument for continuous underway measurements of microbial enzyme activities using high-sensitivity fluorescent substrates has recently been developed. With this instrument enzyme activities can be mapped in much the same way that temperature, salinity, phytoplankton fluorescence, and other parameters are mapped from a research ship while underway. However, this system is limited to horizontal mapping of water samples continuously pumped from the surface and requires frequent operator intervention. Under a new NSF Biocomplexity (IDEA) grant, we will take the next much larger step. This step is the remote *in situ* measurement of microbial enzyme activities at ocean observatories. The research and education team includes a microbial ecologist (J. Ammerman), a geochemist (G. Klinkhammer), a coastal physical oceanographer and modeler (R. Chant), and an education specialist (E. Simms). The goal of this project is to develop a remotely operated instrument for measurement of microbial enzyme activities and to deploy it at the Rutgers University LEO-15 Observatory for periods of weeks to months.

Grant supported by NSF: DBI 02-16154

P2029

Biocomplexity in the High Arctic

J. Welker, Colorado State University, R. Sletten, B. Hallet, J. Schimel, H. Steltzer, B. Hagadorn, P. Sullivan, J. Howarth.

We are quantify the coupling of the carbon and water cycles and the interacting physical, chemical and biological (PCB) processes that control C exchange between cold, dry terrestrial ecosystems and the atmosphere. We are focusing on cold, dry ecosystems because: (1) understanding of carbon and water interrelationships and net C exchange is only rudimentary for this extreme environment, making it impossible to predict the vulnerability of this ecosystem to the expected anthropogenically-exacerbated warming; (2) these tundra systems are sufficiently simple allowing the quantification of all key components and the development of a system behavior conceptual model and (3) the vital role of unfrozen water in this cold, dry environment underlies the importance of thresholds (e.g. 0°C is a distinct threshold for water availability) and highly nonlinear interactions between PCB processes. Our discoveries will contribute to the understanding and the quantification of global carbon and water cycling, as well as to the understanding of extreme habitats on Earth, and possibly on other cold, dry planetary bodies. We are committed to the educational facets and broader implications of our research and thus, we will be offering a field course at our main study that will include U. S. and international students.

Grant supported by NSF: OPP 02-21606

P2030

Linking ecology, genetics and epidemiology of *Vibrio cholerae*: a genomic approach

Deborah A. Chiavelli, PI: Ronald K. Taylor¹; co-PIs; Deborah A. Chiavelli^{1,2}, Kathryn L. Cottingham², and Anwarul Huq³

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3. University of Maryland Biotechnology Institute, Baltimore, Maryland, USA

Vibrio cholerae is both the causative agent of the infectious disease, cholera, and a common planktonic bacterium in aquatic ecosystems all over the world. Seasonal outbreaks of cholera coincide with freshwater plankton blooms, and *V. cholerae* is often found attached to zooplankton and phytoplankton surfaces. Attachment is hypothesized to enhance survival, growth, and transmission to human hosts, and is of ecological importance via its impact on bacterial productivity. Interactions between attachment and environmental factors, such as free nutrient levels, temperature, and pH have not been well studied. With a fully sequenced and well-studied genome, microarray technology can be used to observe *V. cholerae* gene expression in varying environmental conditions, and to link these responses to both heterotrophic bacterial dynamics in aquatic ecosystems and cholera epidemiology in human populations that utilize these ecosystems.

We have observed effects of aquatic nutrients of *V. cholerae* genes regulating attachment, metabolism, uptake, protein synthesis, and pathogenicity. Current laboratory projects include monitoring genetic responses to long and short-term bacterial starvation, and comparison of attached and unattached gene expression. Field work in Bangladesh includes ongoing monitoring of physicochemical conditions, plankton communities, and bacterial populations in ponds with contrasting levels of human use, and observing seasonal patterns of *V. cholerae* gene expression in these same ponds.

Obstacles have included effective communication across disciplines and among institutions, as well as numerous technical and analytical challenges involved in the use of microarrays. We have learned a great deal while overcoming these difficulties, and remain confident that our approach will yield many exciting and useful discoveries in the fields of aquatic ecology, bacterial genetics, and cholera pathogenicity and epidemiology.

Grant supported by NSF: OCE 01-20677

POSTER SESSION 3

P3001

A Temporal Perspective on Biocomplexity in the Aleutian Islands

Dennis O'Rourke PI—University of Utah, Dixie West, Kansas University

The Aleutian Islands represent a model ecosystem to track human-environment interactions over the past 10,000 years. This Incubation Grant provided support for two workshops to focus on ecological change and human impacts during the Holocene in the Aleutian Islands. The first workshop, held in Anchorage, AK in October 2001, was attended by 12 researchers representing anthropology, archaeology; genetics, sea mammal biology and ecology, geophysics, data base management, and Aleut cultural heritage and health. This workshop sought to identify existing databases on Aleutian biodiversity and ecological change, and key investigators with the research orientation and skills required to conduct future collaborative research to assess human impacts and ecological change over the past 10,000 years in the archipelago. The second workshop met in June 2002 in Salt Lake City, UT with 22 participants, many of whom had been identified as representing critical areas of expertise in the first workshop. This two-day workshop explored new research areas needed to assess Aleutian ecological change and concomitant human impacts, and challenges in providing a more precise temporal framework for Holocene environmental change in the islands. The original goals of the incubation project were generally met during the workshops, and resulted in a research collaboration among a number of participants. The final product is a collaborative project investigating temporal change in the Aleutian ecosystem that will be submitted to the Biocomplexity in the Environment program in the next cycle.

Grant Supported by NSF: BCS 01-19759

P3002

Biocomplexity in the Pacific Northwest: Salmon, Climate, and Hydrologic Variability

Abbott, Mark B. (PI), University of Pittsburgh, Dan Nelson, University of Pittsburgh

Population growth in the Pacific Northwest of the United States has led to increased dependence on dwindling water resources, and increased vulnerability to climate related phenomena such as droughts or storm activity. Ecosystem response to climate change has only been observed over the relatively short instrumental climate record, making the identification of long-term climate trends and ecosystem responses impossible. Because lake sediments are deposited annually and record information about the environment in which they formed, they serve as an excellent tool for extending the observational record. This allows for greater understanding of the magnitude and extent of past changes, the identification of cycles and trends, and more detailed knowledge of the nature of ecosystem response to environmental change.

By collecting sediment records from a variety of lakes in Washington State, we aim to document temperature and humidity changes from the last 12,000 years. Interpretations of other environmental changes and responses will incorporate these data so that a more holistic understanding of the thresholds and feedbacks present in the ecosystem may be gained. Sediment cores from larger lakes will be used to reconstruct the magnitude of past Salmon runs for comparison with the environmental record so that correlations may be drawn between the two. The components of this study will lead to a more detailed understanding of the ecosystem as a whole in order to anticipate responses to predicted climate changes, as well as outline the importance of biodiversity in adjusting to these changes.

Grant supported by NSF: ATM 02-21804

P3003

Neighborhood Ecosystems: Human – Climate Interactions in a Desert Metropolis

S. Harlan, Arizona State University, A. Brazel, L. Larsen, W. Stefanov, Arizona State University

In urban ecosystems, which are fragmented corresponding to patterns of organized social life, the concept “neighborhood ecosystem” anchors both ecological and sociological questions about the causes and consequences of human – environment interactions. This project is developing a framework and evidence to show that inequalities in neighborhood capital, comprised of economic, human, social, and natural capital within small areas, determines exposure of human and biological communities to climate stress and their vulnerability to risks of climate change. Results, combining an array of data sources at several geographic scales for the Phoenix, AZ metropolitan area, trace a relationship between inequality in neighborhood capital and high temperatures: 1) negative correlations between surface temperature and SAVI, as well as surface temperature and household income, across census tracts and neighborhoods; 2) less vegetated landscaping in poor neighborhoods (inhabited by Hispanics in the urban core) than in richer neighborhoods on the desert fringe and urban core; 3) distinct spatial temperature variations among neighborhoods and large amounts of microclimate variation within neighborhoods that may be explained by land cover; 4) people in poor neighborhoods are more vulnerable to summer heat. Challenges of interdisciplinary work are reconciling the temporal and spatial scales of remotely sensed data, biogeophysical character of the neighborhoods, air temperature records, and social surveys; and developing parallel measures of vulnerability and resilience in human and biological communities. Some social survey results from this project are at <http://www.asu.edu/clas/sociology/PASS.html>.

Grant supported by NSF: SES 02-16281

P3004

The Sand Hills Biocomplexity Project

D.A. Wedin, University of Nebraska

F.E. Harvey, D. B. Loope, and G. M. Henebry (<http://sandhills-biocomplexity.unl.edu>)

Today, the 58,000 km² Nebraska Sand Hills are stable and covered by native grassland interspersed with wetlands and lakes. This landscape’s stability affects not only hundreds of cattle ranches, but also the recharge of much of the High Plains Aquifer. The starting point for the Sand Hills Biocomplexity project was the recent observation by UNL geoscientists that many of these dunes were destabilized (lost their grass cover) and became active as recently as 900 years ago. How do short- and long-term climate change interact with ecological, hydrological and bioatmospheric processes to destabilize this massive sand dune system, or, on the other hand, restabilize large areas of moving sand? What role do the numerous interdunal wetlands and lakes of the region play in stabilizing this system? An interdisciplinary team of 15 scientists received a BE-CBC grant in 2003 to tackle these questions. The project has three main components: 1) geological and paleoecological studies will reconstruct Sand Hills climate and dynamics during the late Holocene; 2) a large-scale manipulative experiment will examine the effects of grassland destabilization on the coupled budgets of energy and water that drive both ground-water recharge and canopy-atmosphere interactions; 3) mesoscale climate modeling of the coupled climate – vegetation – hydrologic system will test whether the processes and feedbacks that we hypothesize

govern the stability of the Sand Hills can account for patterns observed in both the geologic and satellite-based record.

Grant supported by NSF: DEB 00-84075

P3005

Understanding Interannual NEE Variability in a Tropical Rain Forest Using Constrained Estimates of Carbon Exchange

Steven F. Oberbauer, Florida International University.

Strengths of the eddy covariance technique are its focus on net ecosystem C exchange and the relatively large forest footprint measured. It has become clear, however, that major issues need to be addressed with respect to eddy covariance measurements, particularly in tropical rain forests. A fundamental limitation is the prevalence of still-air conditions at night (>90% of nights), preventing accurate assessment of nighttime ecosystem respiration by this technique in these forests. To evaluate the validity of the eddy covariance estimates of net ecosystem C exchange (NEE) in terms of their sign, magnitude, and climatic variation, eddy flux studies need to be compared to on-site ground measurements of the key processes in forest C cycling. Because of the large within-landscape spatial variation in tropical forest structure and function (200+ tree species, for example), spatial stratification and replication are needed to scale up plot-based estimates to the landscape level.

In a research program at La Selva, Costa Rica, we are directly addressing these challenges to move toward assessment of tropical forest carbon flux and how it is likely to respond to on-going climate change. We are comparing independent estimates of whole-forest photosynthesis, autotrophic and total ecosystem respiration, and NEE obtained by direct and indirect approaches: 1) Highly-replicated direct measurement of forest structure and function across the landscape; 2) Process-based modeling of daytime uptake and NEE based on these ground data; 3) Intensive cross-comparison of these data and model results with a 3-yr eddy covariance dataset over strongly contrasting climatic conditions, including the 1997/98 mega-ENSO.

Grant supported by NSF: ATM 02-23284

P3006

Biocomplexity and the Environment: Response of host and symbiont genomes to environmental stress and its ecological consequences

Katrina Mangin (Co-PI), University of Arizona

Overall Mission: Results will add to understanding of how symbiotic interactions and genomic plasticity determine population responses to climate changes and geographic distributions of organisms. A research-based course for secondary teachers will incorporate modern molecular technology to examine gene expression of hosts and symbionts under environmental stress and will link results to basic concepts in ecology and evolutionary biology, enabling these teachers to bring a synthetic view of modern biology to their classrooms.

Outcomes: (start date is 12/2003).

Motivation: This multidisciplinary team will assess how genomic responses of host and symbionts jointly determine tolerances and how these sensitivities link with other ecological pressures to determine population persistence and geographic distributions. The focus is on the genetic constraints on heat tolerance and how these constraints affect host densities and

distributions in natural and human-influenced habitats. Proposed experiments exploit the genomic resources now available for the aphid *Acyrtosiphon pisum* and for its multiple bacterial symbionts, a model symbiotic system. Responses will be examined using gene microarray and quantitative PCR. Lab and field experiments will address how complex patterns of heat sensitivity and parasite resistance determine population dynamics. Results will be used to construct predictive models of population performance under different climate conditions.

Challenges: The primary challenge is to link molecular level responses of complex organisms to observed ecological patterns. In addition, a major challenge is to guide high school teachers in developing an appreciation of research approaches and technology for addressing multiple levels of biological processes. Finally, we will need to facilitate communication among scientists with expertise spanning bioinformatics, molecular biology and genomics, organismal biology, ecology, and mathematical modeling, plus an expert in research-based science education.

Grant supported by NSF: EF 03-13737

P3007

A Genome Wide Approach to the Study of Coral Symbiosis

Mónica Medina, Joint Genome Institute

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Symbiotic interactions are common and important in a wide variety of biological communities. Among the more complex symbiosis is the mutualism between benthic marine invertebrates, especially cnidarians, and photosynthetic dinoflagellates in the genus *Symbiodinium*. In this mutualism, the algae are intracellular symbionts of their cnidarian hosts. The symbiosis between scleractinian corals and *Symbiodinium* is highly susceptible to changes in environmental factors (e.g. seawater temperature, light levels). Global warming has affected coral reefs worldwide leading to a disruption of these symbioses (coral bleaching) and subsequently resulting in widespread coral mortality. Little is known about the molecular basis for the establishment and maintenance of this important biological relationship. We will use microarray expression profiling developed from EST data to identify genes involved in the *Montastraea faveolata-Symbiodinium* symbiosis on Caribbean reefs. Sequencing of BAC clones containing putative symbiosis genes will help us understand how these genes are regulated in both host and symbiont. This research will be the first attempt to look at an important mutualistic relationship using a genome wide analysis of gene expression. Gaining a better understanding of host-symbiont relationships in coral reef ecosystems can have implications for atmospheric and ocean sciences, conservation biology and the study and diagnosis of microbial diseases in corals.

Grant supported by NSF: OCE 03-13708

P3008

Biocomplexity in mediterranean climate watersheds

Adina M. Merenlender, UC Berkeley

Interaction among humans and ecosystem components, referred to as *biocomplexity*, is at its zenith in mediterranean climate watersheds where the supply of fresh water is uncertain. River systems in these watersheds are characterized by significant temporal and spatial variability. To meet the increasing demand for water, management of these systems occurs at multiple scales and reduces variability, resulting in lower ecological resilience. Crises arise when natural and human system resilience is low and biotic diversity or water security is at risk. This recently occurred in the Klamath basin where water allocation was argued in terms of environment versus agriculture, or as an Endangered Species Act issue. In fact, the institutional capacity to create relationships that achieve equity in water scarce times was entirely missing, resulting in decreased system resilience.

The focus of this research is on finding optimum relations at different scales between social and ecological organization that decreases risk and increases resilience to both human and natural systems. Ultimately, we want to develop a decision support tool that will examine the impacts of various policy and restoration scenarios to avoid system collapse and determine pathways of recovery.

Research on the following topics is being proposed to meet our objectives.

- 1) The extent to which particular biophysical conditions are necessary for river system resilience.
- 2) The impacts of water management systems across multiple scales on both the resilience of the biophysical system and the risks to security of supply for humans.
- 3) The impacts of present and potential future restoration policies at these different scales.

Grant supported by NSF: BCS 01-19992

P3009

Development of a Biocomplexity Research Program in an Urban Salt Marsh

Levandowsky, Michael, Pace University

The purpose of this planning grant was to bring together a group of scientists from several universities, to develop a proposal to NSF's Biocomplexity program, to explore the biocomplexity of an urban salt marsh, the New Jersey Meadowlands. We held 2 workshops and collected preliminary data, leading eventually to a full-scale proposal, which was not funded.

We investigated 3 approaches to defining biocomplexity in microbial communities (bacteria, protists and meiofauna) in 3 adjacent intertidal sediments in the Hackensack Meadowlands, NJ. Replicate surface sediment samples were taken in March and June from: a mudflat, a stand of *Phragmites australis* and a stand of *Spartina alterniflora*, all at the same tidal level, within 10 meters of each other. Bacteria were analyzed using epifluorescence microscopy, diversity of 16S rRNA genes and phospholipid fatty acids extracted from replicate aliquots. Gymnamoebae and other protists were analyzed by cultural assays of 10 mg aliquots and classified as morphospecies by microscopic examination of living cells. Meiofauna were extracted from preserved, stained 10 gram aliquots by sieving and identified to the level of phylum or class. ²¹⁰Pb data from cores indicate the *Spartina* site has been accumulating sediment at an unsustainable rate in recent years,

while the other 2 sites appear to have been subject to erosion or other physical disturbance. They were readily distinguishable on the basis of bacterial and meiofaunal data, as were the winter and summer samples. We analyzed protistan data using 3 approaches to the concept of biocomplexity: (1) a box fractal dimension; (2) a graph theoretic measure of connectivity; (3) a measure derived from information theory, comparing conditional entropies of bipartitions with entropy of the full data set. In particular, the graph theoretic approach yielded “small world” distributions, indicating highly nonrandom, distinct levels of organization or complexity (in the sense of connectivity) in the protistan populations of the 3 microhabitats.

These data have been presented in a poster at the 2003 meeting of the American Society of Microbiologists and the East Coast Protozoology meeting. A manuscript is being prepared for publication in a refereed journal.

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P3010

Land/Ocean Biogeochemical Observatory for Nutrient and Carbon Cycling

Kenneth Johnson, MBARI, Steve Monismith, Stanford, Adina Paytan, Stanford, Marc Los Huertos, UCSC, Kerstin Wasson, ESNERR

Studies of complex, biogeochemical processes in oceans, lakes and rivers are often hindered by a lack of sensor systems that can be deployed for long-term, continuous observations. This is particularly true for chemical sensors. While a variety of chemical sensor systems have been demonstrated, there are few that can operate unattended for long periods (>3 months) in aquatic systems. We have been funded by the BE/IDEA program to develop and refine a variety of chemical sensor systems for extended endurance, autonomous observations. The operation of these instruments will be verified by deploying them in an experimental Land/Ocean Biogeochemical Observatory (LOBO) in the Elkhorn Slough National Estuarine Research Reserve (ESNERR) at the head of Monterey Bay, CA. LOBO will be an array of moorings equipped with autonomous chemical and physical sensors and water samplers that will be operated in near real-time while linked to the Internet through a wireless Local Area Network. The initial operation of the observatory system will be demonstrated with two nitrate sensor systems, which we have developed, that can operate for 3 to 4 month periods without intervention. These sensors will be augmented with additional detection systems for phosphate, silicate, ammonia, iron, pH and CO₂ that are in various stages of development. A coupled hydrodynamic model of Elkhorn Slough will allow us to calculate mass balances and source and sink terms for chemical cycling.

Grant Supported by NSF: ECS 03-08070

P3011

Marine Viromics: The Interaction of Viral Genomes with the Marine Environment

John H. Paul, University of South Florida

Lauren McDaniel, Shannon Williamson, College of Marine Science, University of South Florida, Anca Segall and Forest Rohwer, San Diego State University

Marine viruses (principally bacteriophages) are the most abundant form of life on our planet. Through their lytic activities, viruses modulate carbon flow through marine microbial food webs and catalyze the collapse of many algal blooms. Through their lysogenic activities, viruses confer immunity to superinfection and cause conversion to a diverse array of phenotypes. The majority

of marine bacteria in culture produce some type of virus-like particles (VLP's), indicating that the occurrence of lysogeny (or pseudolysogeny) is widespread. We have initiated the field of *Marine Viromics*, which we define as the interaction of viral genomes with the marine environment. In this program, genomes for temperate viruses infective for marine bacteria and cyanobacteria will be sequenced and analyzed. By studying the interaction of environmental factors with the expression of viral genes in culture, we hope to determine how temperate phage switch between lytic and lysogenic infection in the marine environment. Genomes for the vibriophage $\phi 16$, ϕ HSIC (a pseudotemperate phage) and ϕ RS7 (a temperate phage) have recently been closed and two more phage genomes are in progress. Bioinformatic analyses are being used to guide further molecular studies of the lifestyle of these phages in the marine environment and their effects on bacterial populations. The program is a partnership between San Diego State University and the University of South Florida. The broader impacts of our research include educational outreach in the form of "hands on" undergraduate workshops at SDSU and participation in Oceanography Camp for Girls and Project Oceanography at USF. The societal impacts of our research stem from the fact that nearly every incidence of bacterial pathogenesis is the result of expression of prophage-encoded virulence genes. Our research will yield fundamental information on the biocomplexity environmental-viral genome interactions as well as predictions of viral response to environmental change. The project URLs are:

www.marine.usf.edu/~bwawrik/Viromics/viromics.html and www.rohan.sdsu.edu/~segurita/vp16

Grant supported by NSF: OCE 02-21763

P3012

Physical, Biological, and Human Interactions Shaping the Ecosystems of Freshwater Bays And Lagoons

Mark, Bain, Cornell University

Our hypothesis is that hydraulic residence time is a key variable defining whether ecosystems are self-organized or dominated by external influences. Our study systems are freshwater bays and lagoons along the New York coast of Lake Ontario, including associated watersheds, wetlands, and human settlements. Results from the first two years of research have demonstrated substantial variation among our study systems for most physicochemical, biological, and human properties. Evidence for both internal self-organization and external forcing have been obtained. Data recently analyzed has shown that we did not understand prominent aspects of system structure so detecting internal self-organization is not uniformly established. Biological responses to external forcing are clear in some systems, and an unanticipated form of external system forcing has emerged. Much of our data collection effort has shifted from season-long repeated measurements to short-term and intense event monitoring for addressing increased externally driven change. New challenges have developed from differently paced progress among disciplines, balancing disciplinary interests with whole study integration, maintaining current understanding of developments across disciplines, and managing effort allocations among study group, discipline, and project level activities. Our project has attracted wide interest by government agencies and conservation groups, and we have added considerable additional funding for developing applied aspects of the research. Our project web site is well developed and it is the major mechanism for communications, data sharing, and progress reporting. The site is at <http://ontario.cfe.cornell.edu/>

Grant supported by NSF: OCE 00-83625

P3013

Modeling Bronze Age Settlement Systems in a Dynamic Environment

John H. Christiansen, Argonne National Laboratory

Settlement Systems Within a Dynamic Environment and Economy: Contrasting Northern and Southern Mesopotamian City Regions

The research will examine why third and fourth millennium BC cities in the irrigated zone of southern Mesopotamia grew to a greater size and complexity than those in the rain-fed north. We propose to apply concepts of complex adaptive systems to test the hypothesis that systems of early cities co-evolved in an intimate relationship with their environment, primarily by means of aggregation through time of smaller fundamental units (households). Local rules that determine the subsistence practices of the peasant householder therefore developed through time into more complex land use strategies and social mechanisms that culminated in the emergence of complex settlement hierarchies, the patterns of which show little resemblance to the patterning of the original small scale communities. As larger systems of settlements and more complex exchange and administrative mechanisms developed, parts of the agricultural systems became less sustainable through time. Settlement-land use systems will, therefore, be modeled from small social elements (the household) to much larger entities such as networks of interacting cities. Agent based modeling provides the key to this initiative by allowing for a wide range of choices and trajectories to contribute to the outcome of the modeling exercise. Simulation will employ an advanced object based framework (DIAS and FACET) designed by the Decision and Information Sciences (DIS) Division of Argonne National Laboratory. The DIAS framework allows a range of simulation models and other applications to work together to address a complex modeling problem. It will incorporate climate (GCM), weather (MM5), hydrological and agricultural (EPIC / SWAT), and demographic models plus agent-based models of social behavior. Input data and test data will be derived from the large corpus of landscape and epigraphic data housed within the Oriental Institute and elsewhere.

Grant supported by NSF: BCS 02-16548

P3014

Urban Wetlands: Sustaining Multiple Functions

Santelmann, Mary, Oregon State University

Our project mission was to provide an opportunity for leaders in research on urban wetlands to summarize and synthesize the state of our knowledge of wetlands and their functions in the urban landscape at a conference and workshop on urban wetlands, and to identify key directions for future research. Specific objectives were to conduct a conference on urban wetlands where leaders in research on urban wetlands could present their work, stimulate discussion, and identify key directions for future research. We also worked to build an interdisciplinary team and develop a proposal addressing these research needs, including active participation by graduate students and inviting participation by educators. Among the outcomes of our 12-month grant have been the conference “Urban Wetlands, Sustaining Multiple Functions”, held in Portland, OR on May 20-21, 2002. Five publications by conference participants submitted to Wetlands, focusing on the state of our knowledge of urban wetlands specifically with reference to the multiple functions desired of wetlands in urban systems. Three have been accepted with revisions requested, and two are still in review. A project web site is being maintained at:

<http://www.cwest.oregonstate.edu/wetlands/>

We have been successful in building partnerships with colleagues at Portland State University, public agencies, and organizations concerned with urban ecosystem research in the Portland OR region. A consortium of these individuals and organizations has combined efforts to promote urban ecosystem research. The project-related web site for the Urban Ecosystem Research Consortium is found at: <http://www.esr.pdx.edu/uerc/>

Grant supported by NSF: DEB 01-19783

P3015

An Integrated Analysis of Regional Land-Climate Interactions

David Campbell, Michigan State University,

Jeff Andresen, Marianne Huebner, David Lusch, Jennifer Olson, Jiaguo Qi, Michigan State University; Bryan Pijanowski, Purdue University.

The intensity and spatial reach of contemporary human alterations of the Earth's land surface are unprecedented. Land use and land cover change (LULCC) are among the most significant human influences. Climate change is expected to significantly affect people and ecosystems as well. While research has focused on global climate modeling and socioeconomic drivers of land use change, inadequate attention has been given to the question: *What is the magnitude and nature of the interaction between land use and climate change at regional and local scales?*

Our international multi-disciplinary team includes social, ecological, atmospheric, remote sensing and statistical scientists. This project will be one of the first to “complete the loop” between climate and land use change. It will address how land use changes affect climate change as well as how climate variability affects land use change. Our team will characterize a regional climate-land system by quantifying and modeling agricultural and rangeland systems, the socioeconomic and biophysical determinants of land use change, the physical properties of land cover, and regional climate dynamics. East Africa, with its variety of ecosystems, wide range of tropical climatic conditions, areas of rapid land use change, and a population vulnerable to climatic variability, is the location of the research.

Anticipated broader impacts include: A direct link to grade school education through inclusion of project findings in MSU courses for education majors and in-service teachers; participation of underrepresented groups through recruitment of research assistants; and capacity building of young and mid-career African scientists and policy makers.

Grant Supported by NSF: BCS 03-08420

P3016

Workshop to Enhance Interdisciplinary Interactions among Recent PhD Recipients Weiler, C. Susan, Whitman College

<http://marcus.whitman.edu/~weilercs/biocomplexity/>

October 3 – 6, 2003

Wrigley Marine Science Center, Catalina Island, California

C. Susan Weiler, Whitman College

Ronald B. Mitchell, University of Oregon

Anthony F. Michaels, Wrigley Institute for Environmental Studies

After years of specialization, today's graduates are often transported to an environment that requires connections between distant disciplines and a network of colleagues from divergent backgrounds. The historic divide between the physical/natural and social sciences must often be bridged as well. And, work must often be placed in a context relevant to and understandable by managers and policy makers. While PhD institutions are evolving to meet the needs of interdisciplinary graduates, some issues transcend institutional boundaries. How can we prepare recent graduates to address these challenges? During the 2-day workshop, participants will consider existing leadership programs, identify specific needs of recent Ph.D. grads engaged in interdisciplinary work, and develop possible solutions in the context of a Capstone Program that can be disseminated via electronic resources or implemented in the context of a week-long meeting.

The Workshop will take both a top-down and bottom-up approach, involving established professionals and recent graduates. Overviews of existing training programs will be presented. In addition, each participant has been asked to propose at least one element they think should be included either as a web-based resource or as part of a 1-week training program/symposium. Participants will break into working groups to craft a 'model' program and reconvene to discuss results make overall recommendations. A final report will be published on the Workshop website.

Grant Supported by NSF: DEB 01-19960

P3017

A Conceptual Model of Biocomplexity

Stephen J. Klaine¹, Clemson University

Alan R. Johnson¹, Billy J. Barfield², Daniel E. Storm² and Scott R. Templeton¹, John Hayes¹, William Focht², John Morse¹, Mark Schlautman¹, Jeffery Allen¹, Jonathan Yoder³, William Fisher², Christine Mosley², Della Baker¹, Marty Matlock⁴, Catherine Mobley¹

1 –Clemson University, Clemson, SC, 29634.

2 –Oklahoma State University, Stillwater, OK, 74078.

3 – Washington State University

4 – University of Arkansas

The objective of this biocomplexity incubator grant was to assemble and integrate a group of natural and social scientists to address issues regarding sustainable natural resource management. Further, this group proposed to develop and refine a semi-quantitative model that illustrated the relationship of these disciplines in biocomplexity. Biocomplexity refers to the dynamic web of often surprising interrelationships that arise when components of the global ecosystem-- biological, physical, chemical, and the human dimension--interact. The model posits the poli-

socio-economic basis of land use; environmental consequences of changes in land use; impacts on natural capital; and, consequential changes to society from the change in natural capital. Finally, the role of education and states of knowledge in providing feedback between changes in natural capital and different poli-socio-economic conditions is emphasized.

Several outcomes have evolved from this work. First, an interdisciplinary working group has been formed to conduct research and education on biocomplexity issues. Second, this group has integrated biocomplexity concepts into interdisciplinary graduate education. The motive for this came from the major challenge facing the group: communication. Scientists classically trained in an individual discipline have difficulty communicating with other disciplines. In addition, these scientists may also have difficulty appreciating the additional points of view expressed by the other disciplines. We believe that integration of these concepts into graduate education and providing multi-disciplinary experiences for graduate students will reduce these difficulties for future interdisciplinary groups.

The third outcome of this project has been the integration of this conceptual model into existing watershed projects. The original goal of the Changing Land Use and the Environment (CLUE) project was to develop the cause and effect relationships between land development and water quality. By incorporating the ECOPLEX model into this project, we have integrated social scientists into the research group and have endeavored to impact stakeholders and decision-makers within the watershed.

Grant supported my NSF: DEB 01-19422

P3018

Biocomplexity: Marine Benthic Population Dynamics

Jesús Pineda, Woods Hole Oceanographic Institution

Hal Caswell, Claudio DiBacco, Petra Klepac, Michael Neubert, Andrew R. Solow, Victoria Starczak, Fabián Tapia, Manuel López, Alejandro Parés-Sierra. Dep. de Oceanografía Física, Cicese, Ensenada, BC Mexico, Alberto Scotti. Dept. Marine Sciences, Univ. of North Carolina, Chapel Hill, NC, Jeremiah N. Jarrett. Dept. Biol. Sciences, Central Connecticut State Univ., New Britain, CT

The processes that govern the population dynamics of nearshore benthic species -larval production and transport, larval settlement, local disturbance, predation, competition for space, etc. are each complex. For example, larval settlement depends not only upon nearshore larval abundance, but also the availability of free substrate, larval behavior, and small-scale hydrodynamics. Each of these processes is nonlinear, and has been studied separately. But because each one is complex and operates at a different temporal and spatial scale, little progress has been made in coupling them together. Furthermore, the phenomenology spans across several disciplines, from larval biology to hydrodynamics.

We address this problem with a research program (**NO-HYPE**, Nearshore/Offshore **HY**drodynamics and **P**opulation **E**cology) that identifies the key phenomena in benthic population dynamics, and then couples them together. This approach is helping us address significant problems such as regional (10's km) variability in population density of benthic invertebrates. For example, we are addressing how the interaction of nearshore hydrodynamics, physical transport, larval behavior, and adult abundance possibly create a positive feedback

process involved in maintaining extreme variability in along-shore invertebrate settlement and population density. Observational studies in Alta and Baja California and New England are underway, and the comparative study of these dissimilar systems is revealing a preponderance of different processes. The challenges of our research program includes integration of a wide range of scales, and various research disciplines and philosophies.

URL: <http://www.whoi.edu/science/B/biocomplexity/>

Grant supported by NSF: OCE 00-83976

P3019

BE/CHN: Urban trace-gas emissions study (UTES): Interactions among canopy processes, anthropogenic emissions, and social institutions in the Salt Lake Valley, Utah

Diane E. Pataki, University of Utah

The objective of this study is to quantify the functioning of the urban “airshed” with an emphasis on the interactions between urban land cover and atmospheric trace gases. Carbon dioxide, water vapor, and Volatile Organic Compounds (VOC’s) are important constituents of climate and air quality that are affected by both human activities and natural processes. We have assembled an interdisciplinary team to quantify emissions of these gases and the variety of processes that affect their distribution and transport in the urban airshed of Salt Lake City and its surrounding valley. These results are being applied to a systems dynamics model in conjunction with stakeholders in government and non-profit sectors in order to develop a tool for examining the impacts of future urban development and climate change on local air quality and greenhouse gas emissions.

Outcomes – In our first year we worked closely with stakeholders to better define goals and testable hypotheses that are of interest to local decision-makers. In line with the agreed upon objectives, we have chosen three study sites representing pre-urban (agricultural) land cover, a residential neighborhood built within the last decade, and an older, mixed use residential neighborhood with a mature urban forest canopy. Atmospheric monitoring of CO₂ fluxes, energy balance, isotopic tracers, VOC’s, and aerosols will begin at these sites this fall, for comparison with criteria pollutant data. The results of these experiments will be incorporated into our systems model. The core of the urban development model “SprawlSim” has been completed and is available for public use on our website (URL below).

Motivation for a new approach - Interactions between urban environments and the atmosphere are of growing importance in the study of the global carbon cycle, the hydrologic cycle, and local to regional air quality. Urban land cover is expanding more rapidly than the rate of population growth, yet the linkages between the drivers of urbanization, ecological processes, and atmospheric composition are poorly understood. We propose a multi-disciplinary, collaborative approach for improving our understanding of the complexity of the urban airshed and engaging decision-makers in systems dynamics modeling of the outcomes of alternative airshed management policies.

Challenges/Problems - We have experienced the variety of challenges described by previous interdisciplinary teams of this kind, including communication and consensus among disparate groups of natural scientists, social scientists, and decision-makers. To facilitate this process, the dynamics of the participant interactions are being recorded and studied by a subset of project participants. In addition, a somewhat unanticipated challenge has been the difficulty of obtaining permission to establish study sites in an urban environment where a variety of regulations apply.

We have been fortunate to establish relationships with community partners that are allowing us to construct research towers at their facilities.

Site URL: <http://www.slvoirshed.utah.edu>

Grant supported by NSF: ATM 02-15768

P3020

Building an International Interdisciplinary Community on Urbanization and the Environment

Richard C. Rockwell, University of Connecticut

My aim in the Biocomplexity program application was to create an international community of researchers to study the complex nexus of cities and the environment in an interdisciplinary manner. The actual task turned out to be slightly different: first, I had to produce the researchers themselves, because very few people are in fact doing this kind of interdisciplinary work, although many applaud it. This required capacity building on a large scale. I cooperated with the International Secretariat for the Global Change System for Analysis, Research, and Training (START) in submitting a major proposal to the David and Lucile Packard Foundation, which provided funding for three major three-week capacity-building workshops, the second of which was on the topic of my BE proposal. In other words, the NSF incubation funding has leveraged a very large grant to START, and with this grant we have a real shot at creating the community that is needed.

The "Urbanization, Emissions, and the Global Carbon Cycle" Institute was held in August, 2002 at the National Center for Atmospheric Research in Boulder, CO. My co-organizer was Dr. Robert Harriss, Director of NCAR's Economic and Societal Impacts Group. The Institute had 19 participants, mostly from developing countries, whose expenses were paid in full. The employing organization of each participant pledged to continue to pay the person's salary and to set aside research time (20% minimum) for the person when he or she returns home. Each participant wrote a research proposal while in residence at the Institute and received intensive critique from organizers, faculty, and peers. It is expected that every participant will get a seed grant averaging about \$15,000, plus a modern laptop computer with essential software, including STELLA modeling software. Each participant will be assigned two mentors, one on location and one likely to be in the developed world. Participants will be brought back together in two years to report their results to each other and to a larger audience. The poster provides the schedule of events during the three weeks and lists the participants.

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P3021

Coupled Human/Ecosystems over Long Periods: Mesa Verde Region Prehispanic Ecodynamics

Timothy A. Kohler, Department of Anthropology, Washington State University (with three co-PIs at other institutions)

This project seeks to understand the long-term interaction of humans, their culture(s) and their environment in southwestern Colorado, USA, from A.D. 600-1300. The research employs agent-based simulation to examine various models for how farmers locate themselves and use resources on this landscape. Further, the simulation examines the exchange of agricultural goods among households, and whether exchange causes households to aggregate into villages in certain times and places, and disperse into smaller settlements during other times. Finally, the simulation examines why this area is depopulated in the late A.D. 1200s. Households in this model act in a virtual environment where the elevation, soil type, temperature, vegetation, potential agricultural production, and precipitation vary over an 1800-sq-km study area.

The simulation is possible because high-resolution archaeological and environmental records are available for the study area during this period, including an inventory of thousands of archaeological sites, tree-ring records, and estimates of available surface water and ground water. Estimates of agricultural production change annually according to climatic inputs reconstructed from tree-ring records, and possibly in response to landscape degradation due to farming as well. Over longer periods, the same factors affect the availability of surface water and ground water, and changes in the location and availability of water will also be incorporated into the simulation. Population size and the location of settlement on the landscape vary according to the experiences of the households during the period under investigation, and population flows from and to other areas.

In its final form, the simulation will employ cultural algorithms (variants of genetic algorithms) through which households may optimize their landscape and resource use with respect to other households with whom they exchange corn and compete for agricultural land. These algorithms will also be used to simulate selection of farming strategies, including those that use surface water for irrigation. In this way, the simulation will be used to determine how exchange of agricultural goods, competition for land, and changing farming strategies affected household movement and formation of villages. The behavior of households in all variants of the simulation will be compared against a database for archaeological sites in the study area that specifies their location, size, function, and period of occupation, allowing an assessment of how well each variant fits the archaeological record.

Outcomes - This work contributes to understanding changing land-use strategies in small-scale farming societies experiencing significant climate change and population growth. It also contributes to understanding the evolution of economic systems and population aggregation in such societies. In particular, the study is clarifying the factors that resulted in village formation and the depopulation in one of the most famous archaeological areas in the world: the Mesa Verde region. In addition, the research will develop tools to make the future examination of such systems more effective. The groundwater model will help to predict what might happen to groundwater supplies in this area as climate changes in the future. Basic archaeological research undertaken by Crow Canyon Archaeological Center, Cortez, Colorado, in 2002 and 2003 with support from this grant has greatly improved our knowledge of the sizes, layouts, and

chronologies for the largest sites in our study area. Finally, by clarifying the relationships between climate, culture, and behavior in this area, this research will be useful in unraveling the complexities of coupled human and natural systems in other areas.

Motivation for new approach - Although the causes of village formation and the abandonment of this region in the late A.D. 1200s are problems that have been addressed many times before, previous approaches have not been able to take into account the interaction among human degradation of the landscape, population levels, changing climates, and the changing distribution of resources on the landscape in response to both human action and climate change. The agent-based modeling approaches we are developing allow us to understand each of these processes not in isolation, but in the context of the other processes that are likely to have affected the success of agriculturalists on this landscape.

URL to Project Material: See <http://www.wsu.edu/~village/> for details on the current status of this project, activities to date, and papers/publications in progress. Final products will start to appear in 2005 and several interim products are now available, or will become available shortly.

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P3022

Biocomplexity: Integrating Models of Natural and Human Dynamics in Forest Landscapes

Acevedo M., University of North Texas

Callicott B., Gunter P., Ji M., Kennedy J., LaPoint T., Mauldin D., Mikler M., Monticino M., (University of North Texas), Kellert S. (Yale University), Harcombe P. (Rice University), Ablan M., Davila J., Ramirez H., Torres A. (Universidad de Los Andes), Rosales J., Delgado L., Castellanos H., Mansuti, A. (Universidad Nacional de Guayana).

Although it is recognized that most ecosystems are subject to extensive human influence, the impact that natural systems and their integrity have on human behavior is less readily acknowledged. This project studies what conditions of human-natural system interactions lead to long-term sustainability of forest ecosystems and how these conditions vary across scales- from a stand to landscape and across cultures (Texas-Venezuela). One major force affecting forested landscapes in Texas is the spread of urban development. While in Venezuela, deforestation for agricultural use is the primary contributor to fragmentation of forest reserves. Land use change is a common denominator in these systems. This work focuses on the complex interactions between human decisions - private choices and public policies - and ecosystems. In particular, we study how the environmental consequences of these decisions may then influence human values and subsequent decisions. The interactions between human stakeholders are simulated using multi-agent models that act on forest landscape models in the form of land use change, and receive feedback about the effects of these actions through ecological habitat metrics and hydrological response. We present results from two sites, one in a riparian area of the Dallas-Fort Worth region and another in the Caparo Forest Reserve in Venezuela. Also, we describe preliminary work to extend these models to portions of the Big Thicket in SE Texas and the Imataca Forest Reserve in Venezuela.

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P3023

Modeling Interactions among Urban Development, Land Cover Change, and Bird Diversity ***Marina Alberti, University of Washington***

The objective of our project is to develop an integrated model of urban development and land-cover change in the central Puget Sound region that can interface with models representing a large set of ecosystem processes. The focus of our project is on linking urban development to bird diversity through land cover change modeling as a test case for an integrated modeling approach. Instead of separately simulating urban growth and its impacts on habitat for birds, this project is developing a framework to simulate metropolitan areas as they evolve through the dynamic interactions between urban development and ecological processes and link them through a spatially explicit representation of the urban landscape. We build on the UrbanSim model, a dynamic microsimulation model of household and business location, and real estate development, and link it to a land cover model, consisting of a set of spatially explicit multinomial logit models of site-based land cover transitions. This project aims to provide local and regional agencies with tools to assess land transformation and human-induced stresses under alternative policy scenarios. Currently we have developed a prototype model to predict land cover change in the Puget Sound Region and are integrating this component into the larger UrbanSim simulation model. We have developed a protocol for land cover classification and change analysis for 2-3 year time steps from 1985 to 2000. Classification of the multiple-year landsat images is underway to further refine our land cover change model. The UrbanSim software has successfully be rewritten in Java and is now running version 2.2. Field work to support the bird habitat modeling has concluded another successful field season and development of bird models will begin this year. Integrating three highly complex models is perhaps the greatest challenge of this project. We have developed a series of options for model integration of our three modeling efforts into a seamless, integrated model.

More information about our project can be found at www.urbaneco.washington.edu and www.urbansim.org or by contacting the PI at malberti@u.washington.edu

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P3024

Multilevel Cycles, Models, and Scenarios for Iron Alloying Elements

Thomas E. Graedel, Yale University, Daniel B. Mueller, Timothy Considine, Robert B. Gordon, and Reid J. Lifset, Yale University and Pennsylvania State University

In the nineteenth and twentieth centuries, steel has formed the framework around which we have built our modern civilizations. Steel is a major component of automobiles, ships, airplanes, bridges, high-rise buildings, appliances, and machines. A variety of alloys of iron or coatings on iron, involving a dozen other elements, give the steel specific properties such as strength, ductility, and corrosion resistance.

Despite their strategic and ecological importance, there is little knowledge about the anthropogenic cycles of steel and its associated elements. An understanding of these cycles is a prerequisite for sustainable resource use, because only an appropriate picture of national and global stocks and flows would allow governments, industries, and consumers to anticipate future problems and opportunities, and to plan and coordinate actions that they may wish to take.

In this research project, we will characterize the cycles of iron and of the elements involved in coated and stainless steels. Simultaneously, we will develop a material flow model and an economic model to analyze the linkages and dependencies in those elemental cycles. The project is built around five methodological pillars: (1) Dynamic material flow analysis; (2) Economic analysis; (3) A multi-cycle approach; (4) A multi-level approach; (5) Scenarios of possible futures.

This work builds on previous metal cycle development for copper and zinc. The project for iron and its associated elements was begun in September, 2003, and will continue until September, 2007.

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P3025

Biocomplexity, Scale, and Fragmentation: Implications for Arid Land Ecosystems

Thompson Hobbs, Colorado State University, Katherine Galvin, Randy Boone, Roy Behnke, Robin Reid, Carol Kervin, Andrew Ash, Philip Thorton, Michael Coughenour

Biological complexity in arid and semi-arid lands (ASALs) arises from spatially-linked ecological states and processes. Herbivores, humans, and other agents integrate distinct spatial units by moving among them. Ecosystems are simplified by breaking up interdependent spatial units into separate entities, compartmentalizing ecosystems into isolated sub-units. The result is a reduction in the scale over which complex interactions among environment, large herbivores and human management take place. Ecosystem fragmentation and the reduction of biocomplexity interferes with ecosystem function and reduces system capacity to support ecological communities, social structures and economic activities. As a result, many of the world's ASAL ecosystems are dysfunctional to varying degrees.

Our goal is to demonstrate the importance of complexity and costs of fragmentation at sites around the world by linking ecological and socio-economic research, and in the process, create an international network of scientists addressing these issues. Our global objectives are:

- 1) Develop a framework for analyzing and describing ecosystem spatial complexity and its role in grazed ecosystem function and sustainability..
- 2) Determine the effects of real fragmentation experiments on herbivores, ecosystems, enterprises and people, and use model-simulated fragmentation/consolidation experiments to identify options for ecological and economic sustainability.
- 3) Characterize patterns of ecosystem fragmentation as they exist under different environmental, political and economic systems.

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P3026

Biocomplex Dimensions of Industrial Ecology: Sectorial Trade-offs in the Use, Disposal, and Environmental Impacts of Toxic Metals

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In February 2003, the California Departments of Toxic Substances Control, Environmental Protection Agency, and the Integrated Waste Management Board established legislation (22-CCR-66273), which permanently classified Cathode Ray Tubes, and consumer electronic devices (e.g. cell phones) as “Universal Waste”. This legislation effectively banned these products from landfills because of their lead (Pb) content. Although Pb used in the electronics industry accounts for < 4.2% of the total used in the U.S. (1.7 million tons in 2002), an increasing proportion of Pb in landfill leachate is from defunct electronics. In contrast, Pb used in storage batteries accounts for 87.5% of total Pb, but there is policy for battery recovery and recycling, which prevents environmental impacts. The 2000 Toxic Release Inventory shows that electronics industries accounted for 0.57% of total emissions of Pb nationwide. The targeting of Pb in electronics is controversial because they contain other metals such as mercury and copper, and brominated fire retardants, which may pose comparable threats to the environment and public health. However, international attention is focused on Pb because the national health care costs attributable to Pb poisoning exceeds \$43 billion annually, and no comparable data exists for other metals. The situation calls for a comprehensive U.S. policy that takes into consideration, materials science, manufacturing costs, end-of-life options (recycling, land-filling, incineration, exportation), and ecosystem/public health effects. The goal of our multidisciplinary research project is to identify and test key components of a policy decision framework that informs analytical models of trade-offs among various sectors concerned with the environmental fate of hazardous metals.

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P3027

The Industrial Ecology of Particulate Materials

Tim Considine, Pennsylvania State University, Frank DeNapoli, Michael Lanagan, Holly Lewis, V. Daniel Guide, Barry Scheetz, Michael Silsbee, and Erin Snyder

This project develops decision support tools for evaluating the technical, economic, and environmental trade-offs associated with alternative product and process design options involving particulate materials. Materials generally have their largest impact on the environment during their particulate stage when they are the most labile. Particulate materials are manufactured from both virgin and recycled materials involving consolidation of individual particles with energy into monolithic structures.

Our focus is on four broad classes of particulate materials: cements, powder metals, ferroelectric and dielectric materials, and pharmaceuticals. The focus on particulate materials is beneficial because many engineering issues are similar while scale and unit values are quite different.

The proposed research has two phases. The first phase involves material flow analysis (MFA) that identifies and estimates sources and sinks for these materials and their associated environmental impacts. The second phase involves the development of design tools in

conjunction with in-depth cases studies of design-for-the-environment strategies available in each sector. The models or design tools will be developed to suit the unique features of each industry and the constraints imposed by limited information.

The intellectual merit of this research is the development of a paradigm for integrating complex scientific, engineering, economic, and logistical information into decision models that identify the trade-offs and uncertainties associated with design strategies for improving the environment. The societal benefit of this research is the development of practical design tools for industry and society that will assist in the discovery and adoption of sustainable technology and business practices.

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P3028

Towards Sustainable Materials Use for Drinking Water Infrastructure Virginia Tech

Andrea M. Dietrich, Virginia Tech

Marc Edwards, GV Loganathan, Dietmar Glindemann, Civil and Environmental Engineering; Susan Duncan, Food Science and Technology; Sharon Dwyer, Institute for Community Health; Darrell Bosch Agricultural and Applied Economics; Tamim Younos, Water Resources Research Center, Anne Camper, Civil and Environmental Engineering, anne_c@erc.montana.edu, Montana State University.

Sustainable materials for drinking water support the health, safety, and security of societies worldwide. In the United States, our declining public infrastructure loses 10-32% of potable water resource to corrosion at an estimated cost of \$22 billion per year for the public infrastructure and nearly twice that for private infrastructure. Consumers are familiar with infrastructure materials problems including discolored water, tastes and odors, pin-hole leaks, pipe replacement, water damage costs, and gastrointestinal upset. When confronted with plumbing problems, consumers must face stresses, costs, and uncertainties to make important decisions regarding materials selection. Often, technical guidance is lacking because causes of corrosion are poorly understood by scientists, engineers, and consumers. Society must develop the science necessary to protect our investment in plumbing materials while also meeting USEPA regulations. This will have implications for selection of new plumbing in new building, altering treatment practices, and re-plumbing existing systems anywhere that water is treated, distributed, and consumed. Our interdisciplinary study of materials for drinking water infrastructure is designed to solve some of these problems. Because all problems with materials use in drinking water infrastructure are inextricably interwoven, three phases of work are defined based on organizational necessity including: 1) Biochemistry of Materials Degradation and Water Quality, 2) Aesthetics and Analytical Chemistry of Corroded Materials, and 3) Economics, Health and Perception in Consumer Decision-making. The anticipated results of the work include: 1) an understanding of how changes in disinfectant type and removal of natural organic matter (in response to current EPA regulations) will alter materials performance, water quality, biological stability and aesthetics, 2) fundamental understanding of chemical and sensory measurement of copper and plastic materials interaction with water, and 3) gaining consumer input on home plumbing and its failures, and development of tools of use to policy makers and citizens to make informed decisions.

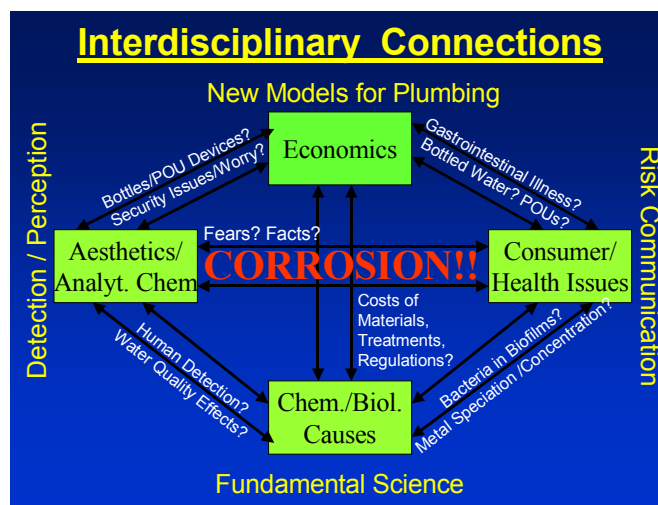


Figure 1: Diagram illustrating synergy between disciplines and connections to interdisciplinary research for advancing the science and public understanding of corrosion and its impacts on drinking water.

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P3029

Understanding Biocomplexity: Developing Methods of Defining Sustainable Uses for Agricultural Products

Robert P. Anex, Iowa State University, Reid Lifset, Andrew M. Wood, Yale University and University of Oklahoma

The use of biomass for energy and bio-based products is often touted as a means of achieving greater sustainability. However, this is by no means a universal view.

The transition to greater renewable raw material use demands a systematic understanding of impacts on the long-term sustainability of the complex environmental system that comprises the agricultural and social systems, use and depletion of fossil resources, and the natural environment.

This MUSES planning project is aimed at developing the people, skills and tools needed for understanding the system-wide sustainability of bio-based products. This is being accomplished by developing a consensus-based methodological framework, building an interdisciplinary team, and developing international networks for research, education, and dissemination of results.

Consensus Workshop

A two-day international workshop was held in June 2003 to review the state-of-knowledge of the impacts of bio-based materials and work to build a consensus regarding appropriate assessment methods.

Workshop reports have appeared in recent issues of the International Society for Industrial Ecology Newsletter and the International Journal of Life Cycle Assessment (see:

http://www.scientificjournals.com/sj/db/pdf/lca/8/lca8_313_314.pdf).

Case Study

The team has developed a framework for analysis of the environmental-social-industrial system comprising the bio-based material life cycle. The assessment framework is being further developed through case study of a bio-based polyester derived from bacterial fermentation of corn-derived dextrose.

Teaching Module

Working with a team from the *Authentic Teaching Alliance (ATA)* consisting of two ATA Fellows and a secondary chemistry teacher we have created an authentic teaching activity module on bio-based material chemistry. This module was used in a high school chemistry course during spring 2003.

The *ATA* is a project of the University of Oklahoma, sponsored by the NSF Graduate Teaching Fellows in K-12 Education Program. For more information, please see:

<http://www.coe.ou.edu/ata/>

URL to project materials: <http://www.ou.edu/spp/biobased>

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P3030

Integrated Life Cycle Design Framework for Sustainable Concrete Infrastructure Materials and Systems

Gregory A. Keoleian, University of Michigan

Global production of concrete drives huge flows of material between natural and human systems. The sheer magnitude of this material flow, which exceeds 12 billion tons each year, causes significant societal impacts. For example, concrete-based infrastructure projects require major investments of public capital, trigger enormous greenhouse gas emissions from cement production, and lead to construction-related traffic congestion resulting in pollution and lost productivity. These broad economic, environmental, and social consequences have largely been ignored in materials R&D. Development and application of new materials has focused almost exclusively on the interplay between material microstructure, physical properties, processing, and performance. This is a considerable shortcoming, particularly as new materials are sought to supplement or replace concrete given its inherent brittleness and limited durability.

A novel framework for sustainable design that integrates microstructure tailoring with life cycle analysis based on environmental, social, and economic indicators is being developed to address this shortcoming. This work encompasses multi-scale boundaries ranging from nanometers to kilometers, and multi-disciplinary perspectives including civil and materials engineering, geology, environmental health sciences, industrial ecology, environmental economics, and public policy. The research focuses on the development and application of a new class of materials known as engineered cementitious composites (ECC). Its aim is to enhance the sustainability of bridge, road and pipe infrastructure using ECC. Among the issues being explored are the impacts on sustainability performance of concrete replacement with ECC, material sourcing alternatives (e.g., superquarries vs. smaller mines), and location of infrastructure projects (e.g., urban vs. rural, and U.S. vs. China).

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P3031

Project SLUCE: Spatial Land Use Change and Ecological Effects

Daniel G. Brown (PI)

Joan Nassauer (co-PI), and Scott E. Page (co-PI), and 7 others
NSF Biocomplexity, Coupled Human and Natural Systems

Our project focuses on the development of agent-based models of land-use change at the urban-rural fringe, and their subsequent use in evaluating the ecological consequences of these changes and potential for interventions to reduce negative impacts. (1) We have started by building simple models of urban land-use change and evaluating the dynamics in conjunction with simple analytical models of the processes of change. (2) We are taking advantage of a survey of residents conducted in 2001, to evaluate the distribution of location preferences within the residential population. This analysis, along with new choice experiments, is helping us to populate the agent-based model with realistic agents. (3) We are compiling land-use and land-cover histories for about 13 townships within Southeastern Michigan, 1950-2000, based on archived plat maps and aerial photographs. These data are being analyzed to provide information for more detailed models that will link land-use change to land-cover change. (4) We are also using these data, and others, to develop validation methods for the agent-based models. One method attempts to recognize variability in agent-based simulations and account for the uncertainty associated with model outcomes, especially that resulting from stochastic elements of the model and path dependence. (5) We have run simulations to evaluate the influence of a greenbelt on the timing of sprawl around a developing urban center and the influences of zoning. We will develop further experiments, based on our models to evaluate alternative approaches to land-use policy that affect landscape ecological function. (6) We are developing new coursework at the University of Michigan, including several graduate and undergraduate students in the project, and developing instructional models that will be placed on the world-wide web and available for instruction about agent-based modeling concepts as well as land-use dynamics.

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