

Half day symposium „Theoretical Evolutionary Ecosystems Ecology“

Thursday 4 February

Eawag Centre for Ecology, Evolution & Biogeochemistry,
Kastanienbaum,

Seeheim lecture room (video conference to Dübendorf, room fc-c24)

8:15 Dr. Carlos Melian

Eco-Evo Dynamics in Networks: From Genomes to Radiations and Ecosystems

9:00 Dr. Axel Rossberg

Universal power-law diet partitioning by marine fish and squid: Implications for complexity-diversity relations

9:45 refreshments

10:00 Dr. Claudia Acquisti

Molecular evolution in natural ecosystems: from biological stoichiometry to comparative genomics

10:45 Dr. Russell Naisbit

Phylogenetic structure in the organization of natural communities

Abstracts

Carlos Melian

National Center for Ecological Analysis and Synthesis, Santa Barbara, CA

Eco-Evo Dynamics in Networks: From Genomes to Radiations and Ecosystems

We now have unprecedented means of collecting data at several chemical, physical, biological levels and spatial scales. We have relatively cheap and accessible computer power to store this data. There is, however, a general sense that understanding only a fraction of these data together has lagged far behind its accumulation. Biology needs a theoretical basis linking several levels and scales to unify these data in a coherent -- flexible -- and integrative framework. In the present talk I aim to discuss: (1) my approach with focus on the challenges -- and the trade-offs -- theoretical ecology and evolutionary biology are facing to analyze these massive data sets in such a flexible and integrative framework; (2) examples of nearly-neutral models of eco-evolutionary dynamics in networks to understand radiations and biodiversity (for example Darwin's finches and cichlids), and (3) my future research directions with emphasis on how scientific cooperation triggers creative ways of linking multiple data sets and theory in a flexible framework.

Axel Rossberg

Queens University, Belfast, Northern Ireland, UK

Universal power-law diet partitioning by marine fish and squid: Implications for complexity-diversity relations

One question that has emerged from the complexity-diversity-stability debate is how the number of predator-prey links relates to the number of species in community food webs. For simple dynamical food-web models, the link density, i.e., the ratio of links to species, is bounded from above as the number of species increases; but empirical data rather suggest it increases without bounds. I will present new upper bounds on link density in large marine communities, with emphasis on fish, squid, and their diets. Using a novel statistical technique that avoids several known sources of bias, these bounds were determined from diet tables of six communities ranging from the South China Sea to the Bering Sea and spanning a factor five in species richness. Bounds are expressed in terms of the diet partitioning function (DPF, Rossberg et al., *J. Theor. Biol.* 243:261--272, 2006), that is, the average number of resources contributing more than a threshold fraction to a consumer's diet. All observed DPF are compatible with a functional form closely related to a power law, and fitted power-law exponents are independent of species richness at the empirical accuracy. The general power-law form of DPF, but not the universal exponent, can be understood from a simple statistical model. Constancy of the power-law exponent implies, among others, for any given diet-fraction threshold a universal upper bound on link density across the oceans. Power-law DPF explain the broad variation in link densities reported for aquatic systems in the literature. They also suggest that an overhaul of the questions and hypothesis underlying the complexity-diversity-stability debate might be in place.

Claudia Acquisti^{1, 2}

1 Center for Evolutionary Functional Genomics, The Biodesign Institute, Arizona State University

2 Ecology, Evolution, and Environmental Sciences, School of Life Sciences, Arizona State University

Molecular evolution in natural ecosystems: from biological stoichiometry to comparative genomics

In most ecosystems primary production is commonly limited by nitrogen (N) and phosphorus (P), elements that are essential components of nucleotides and amino acids. Here we focus on the role of N-limitation in the evolution of genomes, transcriptomes and proteomes in multicellular autotrophs and heterotrophs, using the N-content of molecular sequences as a marker to trace connections between the genomes and the ecophysiology of the organisms. We show that the N-content of the transcriptome is significantly higher in animal than in plant model organisms. Consistent with the predictions of natural selection for N-conservation, the transcriptomes and proteomes of crop species have higher N-content than those of undomesticated plants, likely due to a relaxation of natural selection by the extensive use of N-rich fertilizers. By examining the elemental composition of major functional classes of proteins involved in metabolic processes, we have found that ecophysiological selection for N-conservation specifically targets the proteins involved in the catabolic apparatus, which are highly expressed in response to nutrient limitation. These results directly link gene sequences with the ecosystem context within which biota evolve, and suggest a pivotal role of the availability of nitrogen in affecting evolutionary change.

Russell Naisbit^{1, 2}

1 University of Fribourg Switzerland

2 University of Neuchâtel Switzerland

Phylogenetic structure in the organization of natural communities

Evolutionary history clearly plays a role in determining trophic interactions in nature, but it is only recently that phylogeny has begun to be incorporated into models seeking to explain the organization of natural communities. Most work has instead focussed on body size as the principal determinant of who eats whom. I will present analyses demonstrating a phylogenetic signal in the structure of individual food webs, and in the general relationship between the body masses of predators and their prey. Both results highlight the need to include macro-evolutionary patterns in ecological models of community structure.