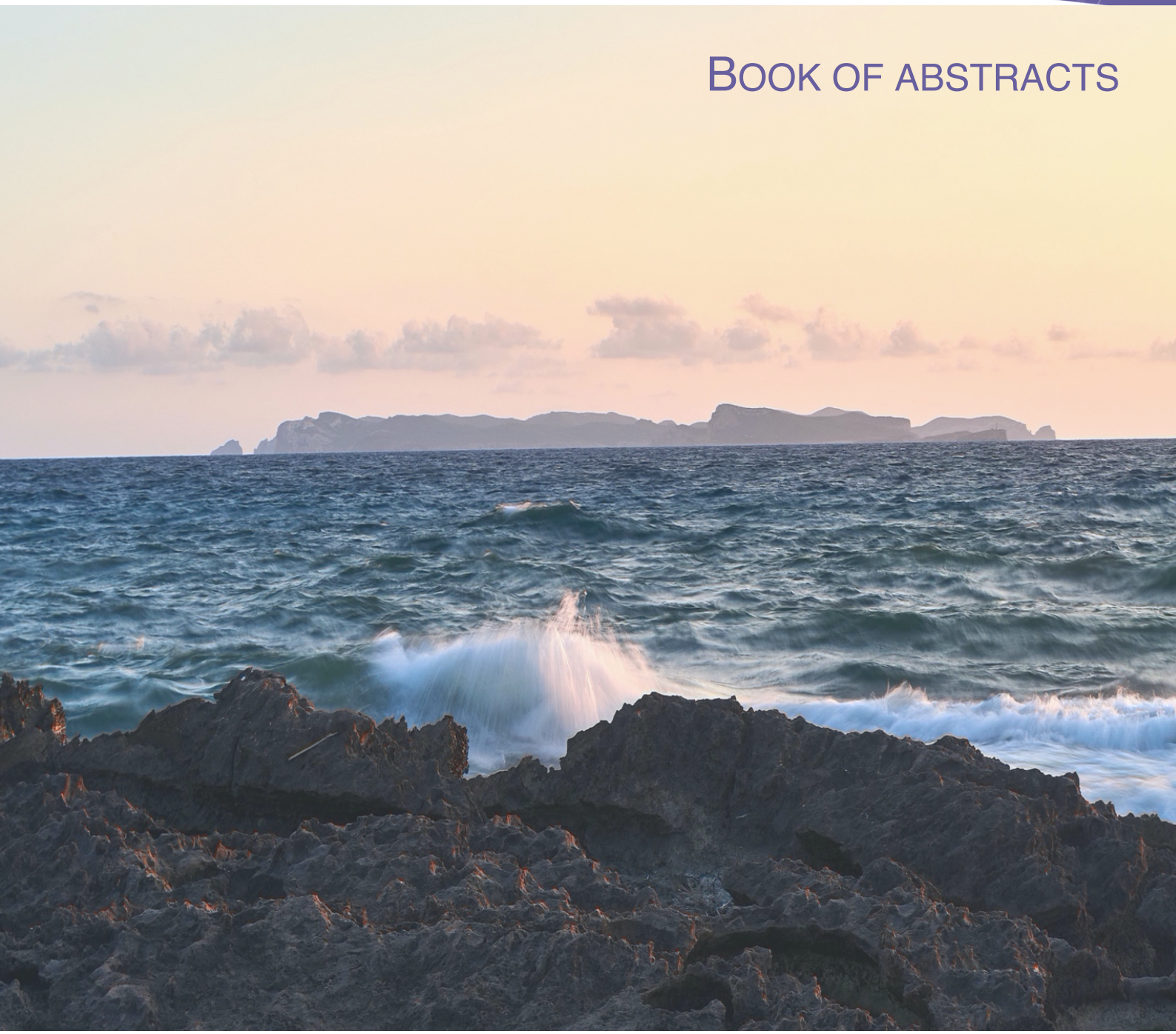
V Symposium on Ecological Networks 2021

10 -12 November 2021

Universitat de les Illes Balears



BOOK OF ABSTRACTS

Palma de Mallorca, Illes Balears, Spain

ORGANIZING COMITTEE

ANNA TRAVESET (Chair)
Institut Mediterrani d'Estudis Avançats (CSIC-UIB)

VÍCTOR M. EGUÍLUZ (Chair)
Instituto de Física Interdisciplinar y Sistemas Complejos (CSIC-UIB)

ISABEL DONOSO
Institut Mediterrani d'Estudis Avançats (CSIC-UIB)

JUAN FERNÁNDEZ
Instituto de Física Interdisciplinar y Sistemas Complejos (CSIC-UIB)

SANDRA HERVÍAS-PAREJO
Institut Mediterrani d'Estudis Avançats (CSIC-UIB)

AMPARO LÁZARO
Institut Mediterrani d'Estudis Avançats (CSIC-UIB)

JORGE P. RODRÍGUEZ
Institut Mediterrani d'Estudis Avançats (CSIC-UIB)

SPONSORED BY

GOIB CONSELLERIA FONS EUROPEUS, UNIVERSITAT I CULTUR DIRECCIÓ GENERAL POLÍTICA UNIVERSITÀ I RECERCA

Universitat de les Illes Balears



MERCEDES PASCUAL
University of Chicago - USA

From eco-evolutionary assembly to network structure and back in a hyper-diverse host-pathogen system

A major alternative to neutral assembly of diverse ecological communities invokes specific interactions that result in negative-frequency dependent competition and niche formation. Identifying "macroscopic" patterns that can allow us to infer important underlying processes of eco-evolutionary assembly remains a challenge for theory, especially for systems where diversity is vast. The network structure of diversity can contribute key information to address this problem. I provide an example at another level of organization, that of strain variation within a pathogen population, based on the hyper-diverse malaria parasite P. falciparum in high-transmission regions. Pathogens compete for hosts in a frequency-dependent manner as these acquire specific immune memory against their variable surface antigens. Networks describing patterns of limiting similarity can help us identify the importance of such non-neutral process. Implications for pathogen persistence and responses to perturbations are discussed, as well as similar questions in other ecological systems.



YAMIR MORENO
Universidad de Zaragoza - Spain

On the influence of competition and mutualism on the biodiversity of mutualistic ecosystems

Relations among species in ecosystems can be represented by complex networks where both negative (competition) and positive (mutualism) interactions are concurrently present. Recently, it has been shown that many ecosystems can be cast into mutualistic networks. However, the role of competitive and mutualistic relations on the species' biodiversity is not fully understood. Here, we discuss a framework based on the concept of multilayer networks, which naturally accounts for both mutualism and competition. Hence, we abandon the mean-field hypothesis and show, through a dynamical population model and numerical simulations, that there is an intricate relation between competition and mutualism. Specifically, we show that when all interactions are taken into account, mutualism does not have the same consequences on the evolution of specialist and generalist species. This leads to a non-trivial profile of biodiversity in the parameter space of competition and mutualism. We also identify what are the topological determinants of the system's dynamics. Our findings emphasize how the simultaneous consideration of positive and negative interactions can contribute to our understanding of the delicate trade-offs between topology and biodiversity in ecosystems and call for a reconsideration of previous findings regarding the structural and dynamical stability of mutualistic systems.



SHAI PILOSOF

Ben-Gurion University of the Negev - Israel

Ecological multilayer networks in the microbial world

Microbial ecology has seen a surge in the use of network theory in the past decade. However, the analysis of multiple dimensions such as variation in space or interconnected networks has been limited. In this talk I will demonstrate how the use of multilayer networks can generate new hypotheses regarding the processes underlying community assembly, assuming that structure is a signature for eco-evolutionary processes. In the first example we use sequences-similarity networks to identify potential pathways of gene transmission across interconnected rumen plasmidomes. In the second, we analyze a metacommunity of the rumen microbiome to disentangle the potential role of local (within-community) vs global processes in determining microbe co-occurrence. These two very different examples jointly provide complementary angles for the untapped potential of the application of multilayer networks in microbial ecology.



CARLOS MELIÁN

EAWAG - Swiss Federal Institute of Aquatic Science and Technology - Switzerland

Diversification and biodiversity dynamics on eco-evolutionary networks

Most theoretical, experimental and empirical studies have shown that speciation, diversification and biodiversity patterns involve many complex processes at different biological levels and spatial scales. Yet, connecting speciation to diversification and biodiversity patterns remain at a very incipient stage. This is mostly because the many constraints to build theory and experiments connecting the ecological and evolutionary processes occurring at fine spatiotemporal scales to the macroevolutionary patterns of biodiversity. In the first part of the talk, I will introduce the challenges to connect theory, experiments and data to unify diversification to biodiversity patterns. In the second part, I aim to join simple and testable with complex and realistic models of eco-evolutionary networks as a way to connect the ecological and evolutionary forces shaping biodiversity patterns. Specifically, I will discuss landscape genetics and ecological models connecting demographic stochasticity with speciation taking into account mating and interaction networks to map diversification and biodiversity patterns. Finally, I will discuss how the interplay between ecological and evolutionary processes occurring in networks might help to decipher the biogeography of hot and cold spots in rapidly changing scapes.



ANNA EKLÖF
Linköping University - Sweden

Structural properties in ecological networks - what level of detail do we need for understanding their functioning?

As ecologists we often argue that data is in short supply. We are also well aware of that we by default never capture the full complexity of the ecosystems we are analyzing. Still, the amount of data we have access to is excessive. Also, data on ecological networks are becoming increasingly detailed and new methods will continue this positive development. However, analyzing ecological networks which contain thousands of species, and thousands of interactions, can quickly get overly complex. This raises the question on how much detail we need and to what extent and with which methods simplifications can be done. Usage of different community detection techniques is one approach to identify large-scale patterns of how species interact. In this talk I will address how different community detections methods are used in ecological networks and their ecological relevance. In particular, if and how can these approaches be used for understanding functioning. Is the devil in the details?

SCHEDULE

	WEDNESDAY 10	THURSDAY 11	FRIDAY 12
8:00 - 8:40	REGISTRATION		
8:40 - 9:00	WELCOME		
9:00 - 10:00	**MERCEDES PASCUAL** From eco-evolutionary assembly to network structure and back in a hyper-diverse host-pathogen system	**SHAI PILOSOF** Ecological multilayer networks in the microbial world	**ANNA EKLÖF** Structural properties in ecological networks - what level of detail do we need for understanding their functioning?
10:00 - 10:20	THEORETICAL AND MODELLING APPROACHES **Kate Pereira Maia** The hierarchical organisation of ecological networks	METHODOLOGICAL APPROACHES **Emilio Hernandez-Garcia** Lagrangian flow networks, connectivity and betweenness of marine populations	ANTHROPOGENIC IMPACTS ON NETWORKS **Ana Carolina Antunes** Disentangling the importance of vertebrate food webs to deliver key ecosystem services across Europe
10:20 - 10:40	**Violeta Calleaja Solanas** Structural predictors for species survival in ecological networks	**Chris Terry** Finding missing links in ecological networks - and what to do about them	**Cecilia Andreazzi** Forest loss affects the organization of host-parasite interactions in the Brazilian Atlantic forest
10:40 - 11:00	**Meghdad Saeedian** Effect of delay on the resilience and stability patterns in Lotka-Volterra ecological dynamics	**Fredric Windsor** Identifying plant mixes for multiple ecosystem service provision using ecological networks	**Jan Hrcek** Impact of warming on *Drosophila* -parasitoid networks: bridging gap between field and laboratory ecology
11:00 - 11:30	COFFEE BREAK	COFFEE BREAK	COFFEE BREAK
11:30 - 11:50	**Dominique Gravel** Are real food webs optimized for stability?	**Lucía López López** Understanding the drivers behind trophic rewiring	**Ana Filipa Palmeirim** On the emerging properties of species-habitat networks in fragmented landscapes: a multi-taxa analysis
11:50 - 12:10	**Aniello Lampo** Hybrid structural arrangements mediate stability and feasibility in mutualistic networks	**Maximillian Tercel** The problem of omnivory: trophic networks and DNA metabarcoding	**Carmelo Gómez Martínez** Pollinator richness, pollination networks and diet adjustment along local and landscape gradients of resource diversity
12:10 - 12:30	**Oskar Rennstam Rubbmark** How behavioral choice influences the resilience and stability of ecological networks	EMPIRICAL STUDIES (NON-ANTHROPOGENIC IMPACTS) **Daniel García** Ecological networks as a tool for identifying key species in feedback ecosystem services	**Alba Costa** The role of exotic species in island plant-frugivore networks
12:30 - 12:50	**Camille Carpentier** Reinterpreting the link-species relationship connects community structure and various robustness measures	**Camille DeSisto** Drivers and consequences of structure in lemur-plant networks	**Moisan Louis** Identifying spatial pathways in a Arctic food web through a global migration network
12:50 - 13:10	**Dolores Ruiz-Lupión** Simulating the effect of spatial structure on the persistence of a relatively complex food web	**Jorge Isla** Drivers of individual-based, antagonistic interaction networks in plant-expansion	FLASH TALKS
13:10 - 13:30	**Bideault Azenor** Latitudinal variation and warming impacts in fish food web dynamics	**Juan Pedro González-Varo** Incorporating functional information into the links of ecological networks	
	LUNCH TIME	LUNCH TIME	
15:00 - 16:00	**YAMIR MORENO** On the influence of competition and mutualism on the biodiversity of mutualistic ecosystems	**CARLOS MELIÁN** Diversification and biodiversity dynamics on eco-evolutionary networks	
16:00 - 16:20	**Eva Llabres** Modelling spatial interactions among seagrasses	**Jörg Albrecht** Herbivore specialization tracks host plant diversity during the Cenozoic	
16:20 - 16:40	**Nuria Galiana Ibáñez** The spatial scaling of ecological networks across the globe	**Julie Garrison** Temporal and spatial changes in benthic invertebrate trophic networks along a salinity gradient	
16:40 - 17:10	COFFEE BREAK	COFFEE BREAK	
17:10 - 17:30	**Juan Fernández-Gracia** Ocean microbiome ecological dynamics model from longitudinal abundance data	**Aina Pons Salom** The architecture of the social network correlates with the gut microbiome similarity in marine fish	
17:30 - 17:50	**Jacob O'Sullivan** The emergent macroecology of Lotka-Volterra metacommunities: networks of ecological networks	**Jordan Cuff** Evidence toward in-field life-history-dependent nutrient-specific foraging	
17:50 - 18:10	**Tuan Pham** Predicting collapse of adaptive networked systems without knowing the network	**Melanie Thierry** Multiple parasitoid species enhance top-down control, but parasitoid performance is context-dependent	
18:10 - 18:30		**Talya Hackett** Landscapes of multiple habitats support greater community function	
20:00		SYMPOSIUM DINNER	

LIST OF ORAL COMMUNICATIONS

Wednesday 10th November

08:00 **Registration**

08:40 **Welcome**

THEORETICAL AND MODELLING APPROACHES

09:00 **Keynote: From eco-evolutionary assembly to network structure and back in a hyper-diverse host-pathogen system** - Mercedes Pascual

10:00 The hierarchical organisation of ecological networks - Kate Pereira Maia

10:20 Structural predictors for species survival in ecological networks - Violeta Calleaja Solanas

10:40 Effect of delay on the resilience and stability patterns in Lotka-Volterra ecological dynamics - Meghdad Saeedian

11:00 **Coffee break**

11:30 Are real food webs optimized for stability? - Dominique Gravel

11:50 Hybrid Structural Arrangements Mediate Stability and Feasibility in Mutualistic Networks - Aniello Lampo

12:10 How behavioral choice influences the resilience and stability of ecological networks - Oskar Rennstam Rubbmark

12:30 Reinterpreting the link-species relationship connects community structure and various robustness measures - Camille Carpentier

12:50 Simulating the effect of spatial structure on the persistence of a relatively complex food web - Dolores Ruiz-Lupión

13:10 Latitudinal variation and warming impacts in fish food web dynamics - Bideault Azenor

13:30 **Lunch time**

15:00 **Keynote: On the influence of competition and mutualism on the biodiversity of mutualistic ecosystems** - Yamir Moreno

16:00 Modelling spatial interactions among seagrasses - Eva Llabres

16:20 The spatial scaling of ecological networks across the globe - Nuria Galiana Ibáñez

16:40 **Coffee break**

17:10 Ocean microbiome ecological dynamics model from longitudinal abundance data - Juan Fernández-Gracia

17:30 The emergent macroecology of Lotka-Volterra metacommunities: Networks of ecological networks - Jacob O'Sullivan

17:50 Predicting collapse of adaptive networked systems without knowing the network - Tuan Pham

Thursday 11th November

METHODOLOGICAL APPROACHES

09:00 **Keynote: Ecological multilayer networks in the microbial world** - Shai Pilosof

10:00 Lagrangian flow networks, connectivity and betweenness of marine populations - Emilio Hernández-Garcia

10:20 Finding missing links in ecological networks - and what to do about them - Chris Terry

10:40 Identifying plant mixes for multiple ecosystem service provision using ecological networks - Fredric Windsor

11:00 **Coffee break**

11:30 Understanding the drivers behind trophic rewiring - Lucía López López

11:50 The problem of omnivory: trophic networks and DNA metabarcoding - Maximillian Tercel

EMPIRICAL STUDIES [NON-ANTHROPOGENIC IMPACTS]

12:10 Ecological networks as a tool for identifying key species in feedback ecosystem services - Daniel García

12:30 Drivers and consequences of structure in lemur-plant networks - Camille DeSisto

12:50 Drivers of individual-based, antagonistic interaction networks in plant-expansion - Jorge Isla

13:10 Incorporating functional information into the links of ecological networks - Juan Pedro González-Varo

13:30 **Lunch time**

15:00 **Keynote: Diversification and biodiversity dynamics on eco-evolutionary networks** - Carlos Melián

16:00 Herbivore specialization tracks host plant diversity during the Cenozoic - Jörg Albrecht

16:20 Temporal and spatial changes in benthic invertebrate trophic networks along a salinity gradient - Julie Garrison

16:40 **Coffee break**

17:10 The architecture of the social network correlates with the gut microbiome similarity in marine fish - Aina Pons Salom

17:30 Evidence toward in-field life-history-dependent nutrient-specific foraging - Jordan Cuff

17:50 Multiple parasitoid species enhance top-down control, but parasitoid performance is context-dependent - Melanie Thierry

18:10 Landscapes of multiple habitats support greater community function - Talya Hackett

20:00 **SYMPOSIUM DINNER**

Friday 12 November

ANTHROPOGENIC IMPACTS ON NETWORKS

09:00 **Keynote: Structural properties in ecological networks - what level of detail do we need for understanding their functioning?** - Anna Eklöf

10:00 Disentangling the importance of vertebrate food webs to deliver key ecosystem services across Europe - Ana Carolina Antunes

10:20 Forest loss affects the organization of host-parasite interactions in the Brazilian Atlantic forest - Cecilia Andreazzi

10:40 Impact of warming on Drosophila-parasitoid networks: bridging gap between field and laboratory ecology - Jan Hrcek

11:00 **Coffee break**

11:30 On the emerging properties of species-habitat networks in fragmented landscapes: a multi-taxa analysis - Ana Filipa Palmeirim

11:50 Pollinator richness, pollination networks and diet adjustment along local and landscape gradients of resource diversity - Carmelo Gómez Martínez

12:10 The role of exotic species in island plant-frugivore networks - Alba Costa

12:30 Identifying spatial pathways in an Arctic food web through a global migration network - Moisan Louis

FLASH TALKS

12:50 Regional and community stability of ecological spatial networks - Javier Jarillo Díaz

12:55 Tradeoffs in sampling completeness in multitrophic networks in agroecosystems - Juan Pablo Gregoire

13:00 Bird-insect predation patterns: combining networks and metabarcoding - Luis Silva

13:05 Effect of fertilization on food web and community structure dynamics at a high temporal resolution - Pedro Leote

13:10 Impact of plant age and genotype on xylem microbial network associations in cultivated olive trees - Manuel Anguita-Maeso

13:15 Range overlap as a potential factor of parasite centrality in a sharing network - Ana Paula Lula Costa

13:20 Structural patterns in animal social networks - Bárbara J. Seaman

13:25 **Closing remarks**

- ORAL COMMUNICATIONS -



© Estefanía Pereira

The hierarchical organisation of ecological networks

Kate Pereira Maia[1*], Paulo R. Guimarães Jr[1]

(1) University of Sao Paulo

*kate.maia@usp.br

Ecological networks are organised into modules, groups of tightly connected species, which have been proposed to represent coevolutionary units. Nevertheless, other types of group structures emerge at higher and lower network scales. Above modules, ecological networks are organised into components, isolated groups of interacting species which can be further divided in two sectors with the loss of a minimum set of specific interactions. Below modules, motifs – small repeated structural units of species and interactions – emerge. Like modules, such group structures could contain the spread of coevolutionary effects between species, challenging the role of modules as ecological networks' coevolutionary units. Here, we investigate whether the structure of ecological networks is organised hierarchically, i.e., whether groups at higher network scales are composed of groups at lower scales. We then investigate whether such hierarchical structure dams the spread of coevolutionary effects between species and, if so, at which network level. We do so, combining 376 empirical mutualistic and antagonistic networks of eight interaction types, structural network analysis and a coevolutionary matrix which contains information on the coevolutionary effects between species through direct and indirect network paths.

Structural predictors for species survival in ecological networks

Violeta Calleaja Solanas[1*], Emilio Hernandez-Garcia[1], Sandro Meloni[1]

(1) IFISC (UIB-CSIC)

* violeta@ifisc.uib-csic.es

Understanding the characteristics that promote ecosystems' resilience is crucial to explain and protect biodiversity. Environmental factors may alter the interaction of species interactions, which adds another travail to the study of the effect of the structure of the ecological network on the dynamics. Here, we study the structural features of the network that prevent the ecosystem for extinctions cascades when the interaction strength is varied. We have found that a high eigenvector centrality is a key factor for survival in mutualistic networks. This result reinforces the importance of the species' neighbors' identity and the existence of positive feed-backs that prevent ecosystem collapse. On the contrary, this panorama changes with competitive interactions. In that case, the species that go extinct by extinctions cascades are determined not by their low eigenvector centrality but by a high degree. When both competitive and mutualistic interactions are taken into account, the behavior is much richer. In that case the ecosystem is more resilience, delaying the collapse of the network to higher values of the interaction strength. The eigenvector centrality cannot fully predict species fate, and other individual properties as mutualistic/competitive interaction rate is also an important factor. Monitoring the eigenvalue centrality opens the door to the discovery of other important factors to prevent ecosystems' collapse.

Effect of delay on the resilience and stability patterns in Lotka-Volterra ecological dynamics

Meghdad Saeedian[*1], Emanuele Pigani[1], Amos Maritan[1], Samir Suweis[1], Sandro Azaele[1]

(1) Dipartimento di Fisica 'G. Galilei', Universita di Padova, Via Marzolo 8, 35131 Padova, ItalyUniversité de Sherbrooke

* meghdad.saeedian@gmail.com

Understanding conditions of feasibility and asymptotic stability in ecological systems is a major challenge in theoretical ecology. The seminal work of May in 1972 and recent developments based on the theory of random matrix has shown the existence of emergent universal patterns of both stability and feasibility in ecological dynamics, which not depends on many of the models' details. However, few studies have investigated the role of delayed effects of mutualistic or antagonistic on the stability of interacting species dynamics. In this work, we study the discrete delay effect on Generalized Lotka-Volterra population dynamics of several interacting species in closed ecological environments. First, we investigate the relation between feasibility and stability of the modelled ecological community in the absence of delay. We then show how, by increasing the time delay, there is a transition in the stability phases of the population dynamics: from an equilibrium state to a stable non-stationary phase. We also find an upper-lower bound for the population of species in the stable non-stationary regime. Finally, we investigate a sufficient condition for global asymptotic stability of both feasible and non-feasible equilibrium states, derived from a proper Lyapunov function.

Are real food webs optimized for stability?

Dominique Gravel

Université de Sherbrooke

dominique.gravel@usherbrooke.ca

By travelling thousands of kilometres, migratory species maintain exchanges of energy, nutrients, toxins and parasites between distant ecosystems. Migratory species also influence communities along the way through interactions such as herbivory, pollination and predation. Considering the heterogeneity of global changes across the globe, it is essential to understand the spatial structure of migration networks so we could eventually address the spreading of perturbations. Our objectives were to i) propose a network framework to define multi-species migration patterns at a community scale and ii) illustrate the structure of a multi-species migration network with the non-breeding areas of each species connected to a High-Arctic tundra site, focusing on Bylot Island as a case study. We identified 3 short distance and 28 long distance migratory species in the food web. We develop criteria to select the most appropriate range data for each species and then refine general range maps based on flyway and wintering habitat type. We use a bipartite network approach with species and non-breeding range to represent and describe the structure of the migration network. We show that migratory species of Bylot Island are distributed in different habitats across several continents (Americas, Africa and Europe) during the non-breeding season. We also find modules of species using similar regions and habitats of the globe during the non-breeding season. The detection of species grouping during non-breeding season allows us to identify the pathways of perturbations across the globe to an Arctic food web.

Hybrid structural arrangements mediate stability and feasibility in mutualistic networks

Aniello Lampo[1*], María J. Palazzi[2], Javier Borge-Holthoefer[2], Albert Solé-Ribalta[2]

(1) Universitat Rovira i Virgili; (2) Universitat Oberta de Catalunya

* alampo@uoc.edu

One of the largest debates in theoretical ecology concerns the emergence of structural patterns in interaction networks of biota. In addition to methodological problems, such as pattern identification, an important challenge regards the relationship between candidate architectures and the resulting dynamical behavior. In the case of mutualistic communities, the issue revolves mostly around two structural arrangements, nestedness and modularity, and two necessary requirements for ecological persistence: feasibility and stability. The former, defined as the probability to avoid extinctions, is strongly related to nestedness, while the latter is enhanced by modularity. Community persistence would require the two properties, and thus the coexistence of both nestedness and modularity, but this is problematic because of their antagonistic relationship. In this context, our work addresses the role of the interaction architecture in the maintenance of stability and feasibility, introducing the idea of hybrid architectural configurations. Specifically, we examine in-block nested networks, compound by weakly interlinked blocks with internal nested organization, and prove that they grant a balanced trade-off between stability and feasibility. Remarkably, we analyze a large amount of empirical communities and find that a relevant fraction of them exhibits a significant in-block nested character. We elaborate on the implications of these results, arguing that they provide new insights about the key properties ruling community assembly.

How behavioral choice influences the resilience and stability of ecological networks

Oskar Rennstam Rubbmark[1*], Daniela Sint[1], Michael Traugott[1]

(1) Department of Zoology, University of Innsbruck, Austria

* oskar.rubbmark@uibk.ac.at

We are still trying to identify the key mechanism that allow ecosystems to be stable. Not the least because making empirical observations to confirm theoretical work so far have been difficult. However, it is likely that a considerable amount of the selection that occur in ecosystems is occurring in a behaviorally adaptable trait space. Not only is this behavioral sorting empirically observable, but because behavior allow animals niches to be flexible the destabilizing effects of competition could be negated by the ability to temporarily step out of competitive dynamics when conditions are adverse. Consider for example that an individual that make a “choice” could prioritize either adjusting its foraging behavior to the resources available or to avoid negative encounters, and that species experiencing strong competition are likely to constrain their niches and/or use alternative “less optimal” resources. This means that assessing how choices are made will allow us to show if species interactions are in phases of top-down (competition regulated) or bottom-up (resource regulated) control. Following this rationale, we here show how combining molecular-derived trophic data with food web ecology allowed us to measure such a shift between top-down and bottom-up control of biological control in real world predator prey networks. Furthermore, we also provide an argument for why the relative ability of species to adapt and focus on their optimal niches has a clear link to both ecological stability and the response and recovery components of resilience.

Reinterpreting the link-species relationship connects community structure and various robustness measures

Camille Carpentier

Research Unit in Environmental and Evolutionary Biology; Institute of Life, Earth and the Environment; Namur Institute of Complex Systems - University of Namur, Belgium

camille.carpentier@unamur.be

For 50 years, ecologists have examined how an ecosystem's structure determines its capacity to cope with disturbances. This structure can be characterised by various properties such as the number of species and the number of interactions between them. The relationship between these structural properties has been studied extensively, as well as their influence on an ecosystems' ability to cope with species removal (robustness). However, how these properties are mathematically interconnected remains elusive. Here, we identify a single parameter b that formally connects the number of species, the number of links and the robustness of ecological network facing random removals. To do so, we reinterpret the link-species relationship as a network-specific property and mathematically demonstrate how the parameter shaping this relationship allows one to predict various robustness measures such as the fraction of species to remove to lose a given proportion of species, the extinction slope or the extinction area. Analysis of 435 empirical networks through *in silico* extinction experiments confirmed these results. Furthermore, we show that our results, derived in an ecological context, should be extensible to scale-free networks in general, as they rely on networks degree distribution. Taken together, our results elucidate the intricate relationships between network structure and robustness in community networks.

Simulating the effect of spatial structure on the persistence of a relatively complex food web

Dolores Ruiz-Lupión[1*], Gabriel Barrionuevo[2], Leocadio G. Casado[2], José María Gómez[3,] Jordi Moya-Laraño[3]

(1) Laboratory of Arid Zones and Global Change, Department of Ecology, Multidisciplinary Institute for Environmental Studies "Ramón Margalef" (IMEM). San Vicente del Raspeig, Alicante, Spain; (2) Supercomputing and Algorithms (SAL) Group, Computer Department of the University of Almería, UAL, Almería, Spain; (3) Department of Functional and Evolutionary Ecology, EEZACSIC, Almería, Spain.

* loli.ruizlupion@gmail.com

One of the principal challenges in ecology is to understand the long-term persistence and stability of complex food webs across space and time. To study this, we used the multi-trophic spatially explicit Next-Generation Individual-Based Model WEAVER 2.0, by conducting in silico experiments. We simulated the ecological dynamics of a relatively complex beech forest leaf-litter food web composed of: 1 cannibalistic predator, 4 omnivorous species, 5 fungivorous species and 3 syntopic fungi species as basal resources. In this system the water is heterogeneously distributed in resource-rich "islands" at the micro-scale level, consisting in dry patches intermingled with wet patches located underneath plants, rocks, trunks or at the "pieds de mont", where nutrients accumulate. Our objective was to evaluate the ability of predators to couple the global ecological dynamics when the spatial structure is altered, for which we ran simulations with/without predators. We tested the effect of the distance among islands on food web persistence, simulating seven equidistant islands of equal size and productivity, with one central island and the other six forming a hexagon around it. These mimicked wet patches in the forest floor where fungi could grow, while the surrounding space was too dry and individuals only used it to move among islands. Finally, to evaluate the influence of a micro-ecological corridor, we decreased the productivity of the central island while maintaining the global productivity constant. With our simulations we hope to understand how predators can contribute to minimize the effects of habitat fragmentation.

Latitudinal variation and warming impacts in fish food web dynamics

Bideault Azenor[1*], Matthieu Barbier[2], Arnaud Sentis[3], Michel Loreau[4], Gravel Dominique[1]

(1) Université de Sherbrooke; (2) Plant Health Institute Montpellier; (3) Institut national de recherche pour l'agriculture, l'alimentation et l'environnement; (4) Station d'Écologie Théorique et Experimentale

* azenor.bideault@usherbrooke.ca

Understanding the effects of both the latitudinal temperature gradient and climate warming on food web dynamics is crucial to explain the distribution of biodiversity and to predict its changes due to global change. Using a modeling approach coupled to a dataset of fish food webs at the global scale, we explore the latitudinal variation and the warming impacts in food web dynamical properties. We focus on the effect of species interactions, and explore variation in three food web properties. Our results suggest that bottom-up control, temporal variability of biomass and collectivity, a metric describing the importance of indirect interactions in the network, decrease with latitude. We investigate how different variables varying with latitude such as temperature, species richness, productivity or food web structure drive these latitudinal variations. We find that trophic control is mainly affected by species richness and variability by body mass, whilst collectivity is mainly driven by species richness and temperature. Second, we investigate how a 2 degrees warming affects trophic control, variability and collectivity as well as community and species biomasses. Community properties are moderately affected by warming. Warming however strongly affects individual species in the food webs, inducing both increases and decreases in species biomass but no important changes in total community biomass. This result indicates that changes in species interactions due to warming could have more important consequences at the species level than at the community level. Our study gives a better understanding of the drivers of latitudinal variation in community dynamics.

Modelling spatial interactions among seagrasses

Eva Llabres

IFISC (UIB-CSIC)

llabres.ll@gmail.com

Seagrasses are a key element in the Mediterranean Sea, and the drastic demise of its population in the last decades has worrying implications for marine ecosystems. Spatial models based on clonal networks provide us with a mathematical framework to study dynamical processes and emergent collective behaviour in seagrass meadows. These models are crucial to predict the response of seagrasses to different global warming scenarios, to analyze the resilience of existing seagrass patterns, and to optimize replantation techniques. In this talk, we propose a spatial model based on clonal growth rules that includes interactions among different species of seagrasses. We present a theoretical analysis of the model applying it to the specific case of the seagrass-seaweed interaction between *Cymodocea nodosa* and *Caulerpa prolifera*. Our simulations successfully reproduce field observations of shoot densities in mixed meadows in the Alfacs Bay. Besides, the proposed model allows us to investigate the possible underlying mechanisms that mediate the interaction among the plants.

The spatial scaling of ecological networks across the globe

Nuria Galiana Ibáñez

Institut de Ciència i Tecnologia Ambientals, Universitat Autònoma de Barcelona, Barcelona, Spain.

galiana.nuria@gmail.com

Larger geographical areas contain more species–an observation raised to a law in ecology. Less explored is whether biodiversity changes are accompanied by a modification of interaction networks. We use data from 32 spatial interaction networks from different ecosystems to analyse how network structure changes with area. We find that basic community structure descriptors increase with area following a power-law. Yet, the distribution of links per species varies little with area, indicating that the fundamental organization of interactions within networks is conserved. Our null model analyses suggest that the spatial scaling of network structure is determined by factors beyond species richness and the number of links. We demonstrate that biodiversity–area relationships can be extended from species counts to higher levels of network complexity. Therefore, the consequences of anthropogenic habitat destruction may extend from species loss to wider simplification of natural communities.

Ocean microbiome ecological dynamics model from longitudinal abundance data

Juan Fernández-Gracia[1*], Somaye Sheykhali[1], Xabier Irigoien[2], Carlos M. Duarte[3], Víctor M. Eguíluz[1]

(1) IFISC (UIB-CSIC); (2) AZTI; (3) KAUST

* juanf@ifisc.uib-csic.es

Microorganisms like bacteria, archaea and eukaryotes coexist in large and complex ecosystems. Actually, microbial communities form the largest and more diverse ecosystems on the planet. The interactions among their individuals are diverse, encompassing mutualism, commensalism, or competition. Measuring these interactions in direction and strength at a large scale is a challenging process that requires a combination of data analysis and modeling. Furthermore, the dynamic nature of the abundances of different species of microorganisms cannot be ignored to present a sound theory on microbial interactions. Here we use experimental data that reported the OTU abundance every day for a period of 20 days. These data on OTU abundances are fitted to a growth model that contains a local term, and an interaction term. The fitted model reveals thus the intrinsic growth rates of singles OTUs and the interaction network among OTUs. This interaction network contains both positive and negative ties, reflecting the synergetic or antagonistic nature of the interactions. We performed statistical significance analysis to detect relevant interactions. Finally, we show the interactions as a multilayer signed and weighted network with two layers, where Eukaryotes sit on one of the layers and Prokaryotes on the other. Furthermore, we apply several network tools to assess different properties of the network. Our approach offers a comprehensive view on microbial communities' organizations from a dynamical perspective fusing modelling strategies and data analysis.

The emergent macroecology of Lotka-Volterra metacommunities: Networks of ecological networks

Jacob O'Sullivan

Queen Mary, University of London

j.osullivan@qmul.ac.uk

A metacommunity can be understood as a network of local communities dynamically coupled via dispersal between sites. At the site scale, community composition and diversity structure are emergent properties of local interaction networks embedded in heterogeneous environments. At the regional scale, spatio-temporal patterns in biodiversity emerge as a result of between site differences in composition. Recent advances in the theory of metacommunities have shown that even simple ecological models, when embedded in a spatially explicit and environmentally heterogeneous landscape, can self-organise to produce a variety of empirically observed patterns in spatial and temporal macroecology, as a result of this interplay between local and regional scale emergent properties. These key patterns include the species abundance, and range size distributions, occupancy-frequency distributions and the accumulation of diversity in space and time, jointly described as the Species-Time-Area-Relation. Here I show how these patterns fit into and expand upon a broader theory of ecology that describes the system-scale signatures of 'ecological structural instability', a phenomenon known to intrinsically regulate key diversity properties in ecological models. I also discuss how these insights can inform both our fundamental understanding of landscape-scale ecology, but also our predictions of the response of such systems to perturbation, in particular habitat destruction.

Predicting collapse of adaptive networked systems without knowing the network

Tuan Pham[1*], Leonhard Horstmeyer[2], Jan Korbel[1], Stefan Thurner[1,3]

(1) Medical University of Vienna and Complexity Science Hub Vienna; (2) Complexity Science Hub Vienna; (3) Santa Fe Institute

* physicsidea@gmail.com

The collapse of ecosystems, the extinction of species or the breakdown of banking networks usually hinges on topological properties of the underlying interaction networks, such as the existence of self-sustaining feedback cycles. Such collapses can be understood as a massive change of the network topology, usually accompanied by the extinction of a macroscopic fraction of nodes and links. It is often related to the breakdown of the last relevant directed catalytic cycle within a dynamical system. Without structural information it seems impossible to say whether the network is in the vicinity of a critical state of an impending collapse. We show that for a large class of dynamical systems with coupled node-link coevolutionary dynamics, a temporal network with a single directed cycle can exhibit a "quantization effect" of the node state vector. This phenomenon is derived as a direct consequence of a corollary of the Perron–Frobenius theorem and is used as an indicator of collapse in many complex systems. The proposed early warning signal captures their structural instability without relying on structural information. We illustrate the validity of the approach in a transparent model of co-evolutionary ecosystems and show this quantization in systems of species evolution, epidemiology, and population dynamics.

Lagrangian flow networks, connectivity and betweenness of marine populations

Emilio Hernandez-Garcia[1*], Enrico Ser-Giacomi[2], Vincent Rossi[3], Cristobal Lopez[1]

(1) IFISC (CSIC-UIB); (2) Dept. of Earth, Atmospheric and Planetary Sciences, MIT, Cambridge, USA; (3) Mediterranean Institute of Oceanography, Marseille, France.

* emilio@ifisc.uib-csic.es

Ocean currents impact on marine ecosystems in a variety of ways, highlighting the importance of processes occurring at the physics/biology interface. In particular, marine flows drive large-scale larval dispersal, with consequences for the demography, biogeography and even management of marine populations. The Lagrangian Flow Network methodology integrates the information obtained from the trajectories of a large number of virtual tracers transported by ocean currents into a network in which nodes are small marine regions and link strength encodes the amount of flow or of larvae between them. With this tool, several questions related to marine connectivity and population structure can be addressed. For example, marine provinces and coherent subpopulations can be identified with available network community detection algorithms, which have implications in the design of marine reserves and of fisheries assessment units. Biological information, such as the quality of different sites for spawning and for settlement can also be incorporated in the formalism. We apply these methodologies to the circulation simulated in the upper layers of the Mediterranean Sea, with emphasis on larval dispersal of species of commercial and ecological interest, such as the European hake. A quantity typically characterizing connectivity in networks, betweenness, can also be evaluated from a purely dynamical-systems point of view.

Finding missing links in ecological networks - and what to do about them

Chris Terry

Queen Mary University of London

c.terry@qmul.ac.uk

Ecological interaction networks are often severely under-sampled, missing both species and links between them. These absences may lead to inaccurate estimates of key network properties but are challenging to address. I examine how a variety of statistical models can be used to give moderate improvements to the estimates of a variety of network metrics by identifying the relative likelihood that each unobserved link is in fact a false negative. Using both a large database of empirical networks and a set of simulated networks, I show that the relative performance of individual models depends on the underlying network structure, but that consistently good results can be gained from using consensus models that combine multiple sub-models. Looking to the future, while there is likely some room for further incremental improvement in estimating the probability of missing links, the potential accuracy of such methods is intrinsically limited and it is not reasonable to expect the problem of missing links to ever be fully solved. Despite this, I argue that these tools (wrapped in an R package) are sufficiently advanced that focus can and should shift towards use in providing robustness checks for analyses of potentially undersampled networks. However, considerable caution is necessary to avoid introducing damaging circularities and biases.

Identifying plant mixes for multiple ecosystem service provision using ecological networks

Fredric Windsor[1*], Julia Tavella[2], Débora C. Rother[3], Rafael L. G. Raimundo[4], Mariano Devoto[2], Paulo R. Guimarães Jr[3], Darren M. Evans[1]

(1) Newcastle University; (2) U. de Buenos Aires; (3) U. de São Paulo; (4) U. Federal da Paraíba

* fredric.windsor@newcastle.ac.uk

Managing agricultural environments in a way that maximises the provision of multiple ecosystem services is a significant challenge. Advances in network ecology provide a way forward, providing a way to incorporate mutualistic and antagonistic interactions. Here, we present an approach to identify mixes of non-crop plant species that provide multiple ecosystem services whilst minimising disservices. Genetic algorithms were applied to the Norwood Farm ecological network – a comprehensive dataset of antagonistic and mutualistic species-interactions on an organic farm in the United Kingdom. We aimed to show how network analyses can be used to select plants supporting a high diversity of insect pollinators and parasitoids of insect pests, but low herbivore diversity. Further to this, we wanted to understand the trade-offs in ecosystem service provision associated with conventional management practices that focus on individual ecosystem services. We show that multilayer network analyses can be used to identify mixes of plant species that maximise pollination and parasitism, whilst minimising herbivory. Trade-offs were apparent with several plant species associated with both positive and negative (herbivores) functional groups. As a result, optimal plant species mixes for individual ecosystem services were different from the multilayer mix. Our findings show that plant mixes designed solely for maximising pollination are not optimal for other ecosystem services and disservices. This avenue of predictive network ecology has the potential to enhance agricultural management, supporting high levels of biodiversity and food production by manipulating ecological networks in specific ways.

Understanding the drivers behind trophic rewiring

Lucía López López[1*], Manuel Hidalgo[1], Nina Larissa Arroyo[2], Jose Miguel García Rebollo[3], Daniel Iglesias[2], Isabel Muñoz[3], Renaud de Stephanis[2], Eva Velasco[4], Izaskun Preciado[2]

(1) Oceanographic Centre of the Balearic Islands (IEO, CSIC); (2) Oceanographic Centre of Santander (IEO, CSIC); (3) Oceanographic Centre of Cádiz (IEO, CSIC); (4) Oceanographic Centre of Vigo (IEO, CSIC)

* lucia.lopez@ieo.es

Characterising the network of trophic interactions in complex biological communities is one of the grand challenges of community and ecosystem ecology. These networks are commonly constructed based on the potential interactions among consumer and resource species pairs, however, empirical studies evidence that feeding interactions do not always take place whenever a potential consumer and resource species co-occur. Here, we make use of an extensive time series of empirically determined feeding interactions among marine demersal predators and their prey. The data stem from annual oceanographic surveys between 1990 and 2020, whose primary objective is to evaluate the status of the demersal ecosystem in the Southern Bay of Biscay. Our main aim was to investigate the drivers affecting the different occurrence of realised and potential trophic interactions, respectively. To this end, we recorded, for each sampling point and year, all the potential feeding interactions based on species co-occurrences, and the realised interactions based on the empirical data. We explored the resulting patterns using binomial GAMs with a wide set of explanatory variables such as the consumer-resource body size ratio, the consumer and resource abundances and the abundance and relative size of alternative prey. Our results indicate that prey abundance on its own is a poor predictor for realised feeding interactions. Our results also provide essential information on how to produce more realistic trophic networks in the absence of empirical dietary information and avoid unrealistic assumptions that may impact network analyses.

The problem of omnivory: trophic networks and DNA metabarcoding

Maximillian Tercel

Cardiff University

tercelm@cardiff.ac.uk

Dietary analysis using DNA metabarcoding is a powerful tool that is increasingly being used to further our knowledge of highly complex trophic networks but is not without limitations. Omnivores, the most generalist of consumers, pose unique challenges when using such methods because they may interact with a huge number of other nodes. Here, we provide the rationale to understand the problems associated with analysing the complex diets of omnivores. By reviewing existing metabarcoding studies of omnivorous diet, and constructing hypothetical scenarios arising from each, we outline that great caution is required when interpreting sequencing data in such cases. In essence, the problems of accidental consumption and secondary ingestion may be significant sources of error when investigating omnivorous diets and could lead to inaccurate understanding of the trophic network. The integration of multiple high throughput sequencing markers increases the taxonomic breadth of taxa detected but we reveal how some detections may be misleading. Disentangling which taxa have been deliberately or accidentally consumed by the focal omnivore is challenging and can falsely emphasise those that were not intentionally consumed, obscuring biologically meaningful interactions. Although we suggest ways to disentangle these issues, we urge that the results of such analyses should be interpreted with caution and all possible scenarios for the presence of biota within omnivores given due consideration.

Ecological networks as a tool for identifying key species in feedback ecosystem services

Daniel García[1*], Juan Carlos Illera[1], Marcos Miñarro[2], Gemma Palomar[3], Beatriz Rumeu[4], Juan Pedro González-Varo[4]

(1) Universidad de Oviedo; (2) Servicio Regional de Investigación y Desarrollo Agroalimentario de Asturias SERIDA; (3) Jagiellonian University; (4) Universidad de Cádiz

* danielgarcia@uniovi.es

Biodiversity crisis has overcome the scene of endangered habitats and rare species to perform in anthropogenic landscapes inhabited by common species, otherwise crucial for ecosystem functioning. Developing conservation strategies requires thus new theoretical paradigms, like the link between biodiversity and ecosystem services, and new tools for assessing species roles on ecosystem functions, such as ecological networks. Here, we focus on avian assemblages in apple orchards and their surrounding hedgerows in Asturias, to identify key species in two feedback ecosystem services: pest control and seed dispersal. For one year, we monitored bird, fruit and arthropod assemblages, and mist-netted one thousand birds. We registered the occurrence of seeds of fleshy-fruited species on bird regurgitations and droppings, and identified arthropod species on bird faecal samples through DNA metabarcoding. We built interaction matrices between 31 species of apple pest arthropods and 22 insectivorous birds, as well as between 9 frugivorous birds and 18 fleshy-fruited plants. From the multilayer network, we identified bird species highly connected to both pest arthropods and fleshy-fruited plants. Abundance was a clear predictor of the central role of bird species in the network connecting pest control and seed dispersal. Our results suggest that common bird species are pivotal for maintaining ecosystem services feedbacks in temperate agroecosystems, encouraging to consider them as conservation targets irrespective of their population status.

Drivers and consequences of structure in lemur-plant networks

Camille DeSisto[1*], James Herrera[1]

(1) Duke University

* Camille.desisto@duke.edu

Species interactions are fundamental evolutionary and ecological processes, such that loss of plant-animal interactions may drive changes in ecosystem structure and function. Plant and animal traits, as well as phylogenetic effects, affect the likelihood of interactions and drive community tolerance to perturbations. Tolerance is particularly important on Madagascar, where the plants and primates are concomitantly endemic and threatened with extinction. We combined mutualistic and antagonistic interactions of lemurs (55 species) and their food plants (590 genera) to generate ecological networks. We analyzed the effects of phenotypes and phylogeny on the probability of interactions using Exponential Random Graph Models. We then simulated lemur and plant extinction to analyze structure and robustness to secondary extinctions. Larger, frugivorous lemurs with faster life history and living in arid habitats have a higher probability of interactions in the network, given all other variables. Endangered lemurs are especially highly connected. Plants with higher wood densities are more likely to interact with different lemur species, and more closely related plants are more likely to interact with the same lemur species. Networks are more robust to plant than lemur extinctions; the loss of lemurs quickly erodes interactions with plants, more so than vice versa. The robustness of the network to secondary extinctions decreases when Endangered and Critically Endangered lemurs are removed, but the effects are not significantly different from random extinctions. The results reveal that the tolerance to perturbations of plant-lemur networks is threatened by the loss of lemurs, with critical implications for future ecosystem functions.

Drivers of individual-based, antagonistic interaction networks in plant-expansion

Jorge Isla[1*], Miguel Jácome-Flores[2], Daniel Pareja[3], Pedro Jordano[1]

(1) Estación Biológica de Doñana, CSIC; (2) Centro del Cambio Global y Sustentabilidad, Villahermosa, Tabasco, México; (3) Departamento de Biología Vegetal y Ecología, Universidad de Sevilla

* jorge.isla@ebd.csic.es

Ecological interactions are a fundamental component of ecosystem complexity due to their diversity and number of species involved. Species-level network analyses often collapse a significant part of that complexity by ignoring the biological characteristics and the ecological context of the individuals actually interacting. To address the ecological drivers of individual-based interaction networks we focused on the pre-dispersal antagonistic assemblage of *Juniperus phoenicea* subsp. *turbinata* within a plant-expansion process, along a colonization gradient in Doñana National Park. The relative influence of individual traits and landscape settings on network structure was evaluated with Exponential Random Graph Models. Individual-based networks were highly diversified, including invertebrates, birds and mammals. The composition of the species assemblage was similar among stands, yet interactions with avian fruit/seed predators increased at the colonization front stand, where the pressure from invertebrates and rodents was lower. ERGM models showed that both intrinsic traits of plants and extrinsic attributes determine the structure of the interaction networks by affecting the animal preferences. Changes in the prevalence and relative strength of interactions with invertebrates and vertebrates re-shape the interaction networks and explain the structural differences between the individual-based networks along the colonizations gradient. Our results highlight the importance of individual-based approaches to understand how variation of interaction outcomes fuels functional processes affecting plant expansion.

Incorporating functional information into the links of ecological networks

Juan Pedro González-Varo

Universidad de Cádiz

juanpe.varo@uca.es

Ecological networks often include species interactions that entail both trophic and functional outcomes. The most outstanding examples are plant-animal mutualisms where animals feed on nutritive rewards produced by the plants while plants typically obtain a function performed by the animals (e.g., pollination, protection against herbivores or seed dispersal). However, there is an extensive body of literature showing that some pairwise interactions do not result in mutualistic function but, instead, they can result in purely antagonistic outcomes like seed predation. Moreover, the way in which different animal species perform a mutualistic function can vary enormously in relation to multiple ecological features of interest (e.g., within- vs among-population pollination or seed dispersal). In this talk, I will present two studies where we used natural history information to incorporate functional outcomes into the links of ecological networks. The first study shows how information on fruit-handling behaviour can be used to classify the occurrence of the seed-dispersal function in the links of plant-frugivore networks. The second study shows how, by combining information on plant phenology and bird migration, the links of seed-dispersal networks can be partitioned according to the potential for long-distance seed dispersal towards cooler latitudes, a critical functional component for helping plants to track climate change.

Herbivore specialization tracks host plant diversity during the Cenozoic

Jörg Albrecht[1*], Torsten Wappler[2], Susanne A. Fritz[1], Matthias Schleuning[1]

(1) Senckenberg Biodiversity and Climate Research Centre (SBiK-F); (2) Natural History Department, Hessisches Landesmuseum Darmstadt

* joerg.albrecht@senckenberg.de

Resource specialization has been proposed as a key determinant of coevolution, species coexistence and biodiversity. The higher species diversity at lower latitudes has often been attributed to the higher specialization of biotic interactions in tropical regions. Theories of adaptive radiation and coevolution predict a negative relationship between the diversity of available resources and the resource specialization of consumers. Thus, for herbivorous insects, it has been hypothesized that lower latitudes might harbor more specialized herbivores because of the diversity of host plants. However, it remains unknown whether this relationship persisted throughout earth's history. Here we close this gap by reconstructing plant-herbivore networks based on traces of insect damage on more than 46,000 fossil leaves from 27 sites covering the entire Cenozoic era. We show that herbivore specialization closely tracked changes in host plant richness, while host plant richness closely followed trends in paleoclimatic conditions: That is, higher temperatures were associated with increased host plant richness, which in turn lead to reduced niche breadth and increased niche partitioning among herbivores. Our results suggest that the relationships between climate, host plant diversity and herbivore specialization that are observed today along latitudinal gradients have shaped plant-herbivore interactions throughout the past 65 million years.

Temporal and spatial changes in benthic invertebrate trophic networks along a salinity gradient

Julie Garrison[1*], Marie Nordström[2], Jan Albertsson[3], Francisco J.A. Nascimento[1]

(1) Stockholm University, (2) Åbo Akademi University; (3) Umeå University

* julie.garrison@su.se

Species interactions underlie all ecosystem functions and are important for understanding ecosystem changes. Representing one type of species interaction, trophic networks are constructed from biodiversity monitoring data and known trophic links to understand how ecosystems have changed over time. The Baltic Sea is subject to high anthropogenic pressures, and its low species diversity makes it an ideal candidate for understanding how pressures change food webs. In this study, we used benthic monitoring data from 20 years from the Swedish coast of the Baltic Sea and Skagerrak to investigate changes in benthic invertebrate trophic interactions. We constructed food webs and calculated fundamental food web metrics that we compared over space and time. Our results show that the west coast of Sweden (Skagerrak) suffered a reduction in benthic invertebrate biodiversity by 40% between the 1980's and 2010's, and that the number of links, linkage diversity, generality of predators, and vulnerability of prey have been significantly reduced. However, connectance has not significantly changed in the Skagerrak. The other basins (Bothnian Sea, Baltic Proper and Bornholm Basin) do not show any consistent significant trends in any food web metrics investigated, demonstrating resilience at a lower species diversity. The decreased complexity of the Skagerrak food webs indicates vulnerability to further perturbations and pressures should be limited as much as possible to ensure continued ecosystem functions.

The architecture of the social network correlates with the gut microbiome similarity in marine fish

Aina Pons Salom[1*], Eneko Aspillaga Cuevas[1], Ignacio A. Catalán[1], Ramon Rosselló-Mora[1], Tomeu Viver[1], Robert Arlinghaus[2,3], Martina Martorell-Barceló[1], Margarida Barceló Serra[1], Josep Alós[1]

(1) Mediterranean Institute for Advanced Studies (IMEDEA, CSIC-UIB); (2) Department of Biology and Ecology of Fishes, Leibniz Institute of Freshwater Ecology and Inland Fisheries, Berlin; (3) Division of Integrative Fisheries Management, Faculty of Life Sciences, Humboldt-Universität zu Berlin.

* apons@imedea.uib-csic.es

The connection between an individual's microbiome and its social behaviour is still a poorly studied topic. Here, we have first reconstructed the social network of a marine fish using a high-quality positioning data-set composed of 7,930 one-day long trajectories corresponding to 153 females and 79 males. We have determined the social network for the entire tracking period and found a classical harem-like social structure composed of one male and several females, where males actively defended their territories. Subsequently, a sample of the social network was captured, and the operational phylogenetic units' (OPUs) diversity of their gut microbiome was quantified using the analysis of 16S rRNA gene amplicons by high throughput next generation sequencing. We have found that the associations from the social network analysis have a strong relationship with the Bray-Curtis dissimilarity matrix of the gut microbiome. Thus, a pair of microbiome samples from different individuals in the same harem were more similar than a pair from another harem. This finding constitutes one of the first empirical demonstrations that social contact imposed by the architecture of the social network may provide a key transmission pathway for gut symbionts that shapes gut microbiota, even in aquatic animals. This work underlines the potential of high-resolution tracking and guts microbiome similarity to study how important are social interactions in determining the gut microbiome composition in natural populations.

Evidence toward in-field life-history-dependent nutrient-specific foraging

Jordan Cuff[1*], Maximillian PTG Tercel[2], Ian P Vaughan[2], Lorna E Drake[2], Shawn M Wilder[3], James R Bell[4], Carsten T Muller[2], Pablo Orozco-terWengel[2], William OC Symondson[2]

(1) Newcastle University; (2) Cardiff University; (3) Oklahoma State University; (4) Rothamsted Research

* jordancuff@gmail.com

Nutrients are a fundamental driver of interspecific interactions, but are rarely studied in the context of empirical ecological networks in the field. Nutrient-specific foraging is the ecological theory that generalist consumers may be capable of selecting food resources based on their macronutrient content, which has yet to be demonstrated in the field. High-throughput sequencing technology allows prey to be identified from DNA in predator gut samples and compared with prey availability in the field, to reveal the mechanisms underlying prey choice, including theories such as nutrient-specific foraging. Here we measured the macronutrient content of prey in the field and showed that the diet of spiders deviates in nutrient content from the communities in which they forage. Through a novel nutrient-based taxonomy and null modelling, we revealed how macronutrient content is a significant factor in prey choice. Our results highlight the importance of all three macronutrients (carbohydrates, lipids and proteins) in predator foraging choices. This evidence for nutrient-specific foraging under field conditions can refine predictions surrounding trophic interactions, with important implications for predicting trophic networks, biocontrol outcomes in agriculture, and conservation management.

Multiple parasitoid species enhance top-down control, but parasitoid performance is context-dependent

Melanie Thierry[1*], Nicholas A. Pardikes[2], Miguel G. Ximénez-Embún[3], Jan Hrček[3]

(1) University of South Bohemia, Faculty of Science, České Budějovice, Czech Republic; (2) University of Nevada, Reno, USA; (3) Institute of Entomology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czech Republic;

* melanie.thierry34@gmail.com

Ecological communities are composed of a multitude of interacting species, forming complex networks of interactions. Current global changes are altering community composition and we thus need to understand if the mechanisms structuring species interactions are consistent across different species compositions. However, it is challenging to explore which aspects of species interactions are primarily driven by community structure and which by species identity. Here we compared the outcome of host-parasitoid interactions across four community modules that are common in host-parasitoid communities with a laboratory experiment using a pool of three Drosophila host and three larval parasitoid species, resulting in nine different species assemblages. Our results show general patterns of community structure for host-parasitoid interactions. Multiple parasitoid species enhanced host suppression without general antagonistic effects between parasitoid species. Presence of an alternative host species had no general effects on host suppression nor on parasitoid performance, therefore showing no evidence of indirect interactions between host species nor any host switching behavior. However, effects of community structure on parasitoid performance were species-specific and dependent on the identity of co-occurring species. Consequently, our findings highlight the importance of both the structure of the community and its species composition for the outcome of interactions.

Landscapes of multiple habitats support greater community function

Talya Hackett[1*], Alix M. C. Sauve[2], Kate P. Maia[3], Daniel Montoya[2], Jane Memmott[2]

(1) University of Oxford; (2) University of Bristol; (3) University of São Paulo

* Talya.Hackett@zoo.ox.ac.uk

Conservation, restoration, and land management are increasingly applied at the landscape scale. However, because ecological network data tend to be habitat specific and focused on a few guilds, exactly how habitats combine to affect community structure, stability and function remains poorly understood. Using multi-guild species interaction data collected at sites with one, two or three habitats, along with a field experiment and a null modelling approach, we show that multi-habitat landscapes support more even insect species communities and interactions as well as more complementary interactions and more-consistent robustness. This translates to improved pollination success and consistency at sites with more habitats, and emergent network properties not explained by summing the component habitat webs. Linking landscape composition, through community structure, to ecosystem function, highlights the mechanisms by which multiple contiguous habitats can support ecosystem services.

ANTHROPOGENIC IMPACTS ON NETWORKS

Disentangling the importance of vertebrate food webs to deliver key ecosystem services across Europe

Ana Carolina Antunes[1,2]

(1) German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; (2) Friedrich-Schiller-University Jena

ana_carolina.antunes@idiv.de

In a scenario of continuous climate and land-use change, loss of biodiversity is expected to affect the functioning of ecosystems and the ability of natural systems to deliver ecosystem services. Yet, there is no clear mechanistic understanding on the relationship between biodiversity and ecosystem functioning for multitrophic, vertebrate communities. In this study, we use local species occurrences to generate local food webs across Europe. Using metabolic theory, we evaluate the energy fluxes between consumers and resources in each local vertebrate food web, and directly relate these fluxes to specific ecosystem functions and services provided by terrestrial vertebrates. Pixel-based distributions of the vertebrate food web across Europe provide quantitative estimates of ecosystem services at a resolution of 1km. Changes in food-web structure caused by changes in species occurrences modify all fluxes in the food web via direct and indirect effects. In that way, we mapped and investigated key functions developed by terrestrial vertebrates across Europe. Therefore, we can better understand the effects of anthropogenic drivers such as climate and land use on the ecosystem functions and services. We also demonstrate the importance of maintaining food webs' structure to avoid the loss of ecosystem services. The development of an up-to-date scenario on the distribution of biodiversity and ecosystem services across Europe is an essential step to identify conservation priority areas, as well as conservation options to be discussed with stakeholders.

Forest loss affects the organization of host-parasite interactions in the Brazilian Atlantic Forest

Cecilia Andreazzi[1*], Mariana Moraes Vidal[2], Leandro Reverberi Tambosi[3]

(1) Center for Functional Ecology, University of Coimbra; (2) Instituto Oswaldo Cruz (IOC/Fiocruz); (3) Universidade Federal do ABC

* ci.andreazzi@gmail.com

Understanding how deforestation-driven changes in species composition affect parasite-host interaction networks and if the reconfiguration of interactions amplifies or dilutes the risk of disease emergence is a current challenge. We investigated how small mammal communities and their potential interactions with parasites are assembled according to landscape structure across 210 landscapes in the Brazilian Atlantic Forest. We calculated the ranges of forest cover for the occurrence of each species and categorized them as forest specialists and disturbance-adapted species. This allowed us to define a sequence of host extinction events and the introduction of new species in communities according to increasing levels of forest loss. For each of the 69 small mammal species in those landscapes, we searched the literature for interactions with virus, bacteria, protozoa, fungi and helminth parasites. This resulted in a parasite-host metaweb with 300 parasites and 665 interactions, including 29 zoonotic pathogens. We simulated the local interaction networks based on the metaweb, evaluating how forest loss leads to changes in the organization of potential host-parasite networks. Network connectance and nestedness tended to increase in deforested landscapes, while modularity was not associated with forest cover. We found a peak in small mammal species richness when the landscape reaches 60% of forest cover, and a peak of potential parasites when forest cover is reduced to 20% of the landscape. Thus, landscapes with relatively low forest cover harbor a small number of mammal species but with higher potential to host many parasites, indicating an important zoonotic potential in these communities.

Impact of warming on Drosophila-parasitoid networks: bridging gap between field and laboratory ecology

Jan Hrcek[1*], Chia-Hua Lue[1], Nicholas A. Pardikes[1]

(1) Biology Centre, Czech Academy of Sciences

* janhrcek@gmail.com

There is a strong split in biology between field and laboratory research. In my talk I show how we use a Drosophila-parasitoid network module to bridge the gap between complex reality in nature and mechanistic understanding achievable with laboratory experiments. To do this, I use an example of studying the response of ecological networks to warming predicted with climate change. We first studied Drosophila-parasitoid networks in the field in tropical rainforest of Australia. We found that parasitism rate in nature increases towards low elevations. We then took the component species of this network to laboratory to conduct experiments. We found that parasitoids do best at temperatures similar to low elevation temperatures in the field, but that further increase in temperature leads to marked decline in parasitoid performance. In a second experiment we asked whether community context can reduce negative impacts of warming on timing of species interactions. We found that presence of alternative host can lead to better parasitoid persistence. Therefore, efficiency of biological control by parasitoids is at risk due to climate change, but we can partly offset this negative effect by encouraging presence of alternative hosts.

On the emerging properties of species-habitat networks in fragmented landscapes: a multi-taxa analysis

Ana Filipa Palmeirim[1*], Carine Emer[2], Maíra Benchimol[3], Danielle Storck-Tonon[4], Anderson S. Bueno[5], Carlos A. Peres[6]

(1) CIBIO-InBIO, Universidade do Porto, Campus de Vairão, Vairão, Portugal; (2) Laboratório de Interação Planta-Animal, Departamento de Botânica, Universidade Federal de Pernambuco; (3) Laboratório de Ecologia Aplicada à Conservação, Universidade Estadual de Santa Cruz, Ilhéus; (4) Programa de Pós-Graduação em Ambiente e Sistemas de Produção Agrícola - PPGASP, Universidade do Estado de Mato Grosso, Rod. MT 358 km 7, Jardim Aeroporto, Tangará da Serra, MT, CEP:78300.000, Brazil; (5) Instituto Federal de Educação, Ciência e Tecnologia Farroupilha, Júlio de Castilhos, RS, Brazil; (6) School of Environmental Sciences, University of East Anglia, UK

* anafilipapalmeirim@gmail.com

Habitat loss and fragmentation poses a pervasive driver of biodiversity decline worldwide. Yet, little is known about the community-level processes occurring at the scale of whole fragmented landscapes. To address this gap, we examined species-habitat networks of eight biological forest groups – mid-large mammals, non-volant small mammals, lizards, understorey birds, frogs, dung-beetles, orchid bees and trees – surveyed across 22 insular fragments and three continuous forest sites, located within and nearby a hydroelectric reservoir in central Amazonia. Species-habitat networks were characterized by both low connectance and modularity, and high nestedness. Networks' robustness was extremely low for most groups, yet to a lesser extent for orchid bees. From the habitat perspective, large islands and continuous forests disproportionately contributed more to network structure, whereas from the species perspective, body size was the most often trait structuring the landscape network. Our results alert for the functionality disruption of species-habitat networks in insular fragmented forest landscapes.

Pollinator richness, pollination networks and diet adjustment along local and landscape gradients of resource diversity

Carmelo Gómez Martínez

Mediterranean Institute for Advanced Studies (IMEDEA, CSIC-UIB)

cgomez@imedea.uib-csic.es

Global changes in ecosystems lead to the homogenization of landscapes and communities, affecting the availability of habitats and resources that pollinators need. Resource diversity at both local and landscape scales might affect pollinator communities and their pollination interactions in natural communities within agricultural landscapes. Understanding how pollinators and their interactions vary along resource diversity gradients may help to determine their capability to adapt to current diversity loss related to global change. We used data on 20 plant-pollinator communities along gradients of local and landscape diversity to understand how the diversity of resources at different scales affected wild pollinator abundance and richness, the structure of plant-pollinator networks, and pollinator diet breadth and species' specialization in networks. We show that resource diversity at local and landscape scales are significant predictors of the abundance and richness of wild pollinators, the structure of their pollination interactions and their diet breadth and specialization. Flower-rich habitats held richer and more abundant wild pollinator communities. Both landscape and local diversity increased modularity and functional complementarity in pollination networks. Although wild pollinators widened their taxonomic and functional diets as flower richness increased, neutral processes were less common in flower-rich habitats, increasing species specialization in the networks. Interestingly, landscape influenced overall network metrics at larger scale than species and group-level metrics. This study highlights the importance of including different scales to understand the effects of global change on pollination service through changes in resource diversity.

The role of exotic species in island plant-frugivore networks

Alba Costa[1*], Ruben Heleno[2], Christopher N. Kaiser-Bunbury[1]

(1) University of Exeter; (2) University of Coimbra

* ac920@exeter.ac.uk

Seed dispersal by vertebrates is a pivotal ecosystem function highly threatened by the introduction of invasive exotic species. Species interaction networks are particularly well positioned to disentangle the community level consequences of such introductions on the dispersal of native seeds. However, our knowledge on tropical seed dispersal is based mainly on ecological networks collected in the Neotropics. Here we present data on fruit and frugivore abundance and phenology and seed dispersal interaction networks on eight inselberg plant communities with different invasion levels in the island of Mahé, Seychelles. The completeness and taxonomic resolution of the networks was maximised by combining four different sampling methods: direct frugivory observations, camera trapping, identification of seeds in faecal samples, and dispersers identification based on DNA barcoding. We compare the fruiting phenology of native and introduced plants and explore whether the seed dispersal network structure varies between the peak of the fruiting season and off-peak. We found that native and exotic plant species exhibited a similar fruiting phenology, with exotic plants potentially diverting seed dispersal services from natives. Seed dispersal networks were relatively small, and the functional role of frugivores was consistent during the entire year, with native frugivores dispersing more species, more frequently and for longer periods. Native seed dispersers were also more selective and presented a higher species strength than introduced ones. We show that exotic plants are likely to negatively affect the seed dispersal of native species and highlight the importance of native frugivores for the conservation of native forests in Seychelles.

Identifying spatial pathways in a Arctic food web through a global migration network

Moisan Louis[1*], Gravel Dominique[2], Don-Jean Léandri-Breton[3], Jean-François Lamarre[4], Joël Bêty[1]

(1) University of Québec at Rimouski; (2) University of Sherbrooke; (3) University McGill; (4) Polar Knowledge Canada

* Louis.Moisan@uqar.ca

By travelling thousands of kilometres, migratory species maintain exchanges of energy, nutrients, toxins and parasites between distant ecosystems. Migratory species also influence communities along the way through interactions such as herbivory, pollination and predation. Considering the heterogeneity of global changes across the globe, it is essential to understand the spatial structure of migration networks so we could eventually address the spreading of perturbations. Our objectives were to i) propose a network framework to define multi-species migration patterns at a community scale and ii) illustrate the structure of a multi-species migration network with the non-breeding areas of each species connected to a High-Arctic tundra site, focusing on Bylot Island as a case study. We identified 3 short distance and 28 long distance migratory species in the food web. We develop criteria to select the most appropriate range data for each species and then refine general range maps based on flyway and wintering habitat type. We use a bipartite network approach with species and non-breeding range to represent and describe the structure of the migration network. We show that migratory species of Bylot Island are distributed in different habitats across several continents (Americas, Africa and Europe) during the non-breeding season. We also find modules of species using similar regions and habitats of the globe during the non-breeding season. The detection of species grouping during non-breeding season allows us to identify the pathways of perturbations across the globe to an Arctic food web.

- FLASH TALKS -



© Estefanía Pereira

Regional and community stability of ecological spatial networks

Javier Jarillo[1*], Francisco J. Cao-García[2], Frederik De Laender[1]

(1) Research Unit of Environmental and Evolutionary Biology, Namur Institute of Complex Systems, and Institute of Life, Earth, and the Environment, University of Namur, Belgium; (2) Departamento de Estructura de la Materia, Física Térmica y Electrónica, Universidad Complutense de Madrid, Spain. Instituto Madrileño de Estudios Avanzados en Nanociencia, IMDEA Nanociencia, Spain

* javier.jarillodiaz@unamur.be

The spatial structure in landscapes can modify the stability of meta-communities. Stability can be characterized regionally, representing the complete spatial network, or for each of the local patches; moreover, it can also be characterized at species level, or for the whole community. Furthermore, stability can be defined in multiple ways, including resistance, resilience (rate of return after the perturbation), or invariability (inverse of the amplitude of the biomass fluctuations caused by environmental stochastic perturbations). Here, our aim is to analyze the scale-dependence of different stability estimates in spatial and ecological networks. More specifically, we ask how spatial scale (regional vs. local) and ecological scale (community vs. species) influence stability properties. We find that, for spatially heterogeneous perturbations in meta-populations, the regional resilience is just the arithmetic mean of the local resiliencies, weighted by the local abundances. Moreover, the regional resistance is obtained to be also the mean of local resistances, but employing the harmonic instead of the arithmetic mean. Analogous results hold for the community estimates. Hence, we can consider that both resilience and resistance are "scale-free" properties of ecological and spatial networks, in the sense that the network estimates are just some average of the estimates at the sub-units. However, this does not hold for invariability, from which we see that generally the regional and community invariabilities are greater than the local and species invariabilities. These results indicate that different stability components can scale differently with spatial or ecological scale.

Tradeoffs in sampling completeness in multitrophic networks in agroecosystems

Juan Pablo Gregoire[1*], Julia Tavella[1], Mariano Devoto[1,2]

(1) University of Buenos Aires, Faculty of Agronomy; (2) CONICET

* gregoire@agro.uba.ar

Multitrophic ecological networks provide a tool to simultaneously assess natural pest control and pollination in agroecosystems. However, the detection of interactions in the field may be limited by the complexity of the community, the type of interaction considered, and the sampling effort invested. This study aims to: assess the incidence of intrinsic (type of interaction) and local (species richness) factors on the sampling completeness of multitrophic networks in agroecosystems; (2) develop criteria to distribute sampling effort to simultaneously study different types of interactions. We sampled plant-pollinator, plant-herbivore and herbivore-parasitoid interactions in twenty field margins in the Pampean region of Argentina. We identified factors that influence two Chao-based completeness indicators. While a network-level indicator was affected by species richness and interaction type, a species-level indicator (which gave more weight to generalist species) was only affected by species richness. Most notably, distributing sampling effort evenly among interaction types resulted in large differences in sampling completeness between the three types of networks. Our study highlights the importance of balancing sampling effort among multiple interaction types to achieve comparable levels of sampling completeness when building multitrophic networks.

Bird-insect predation patterns: combining networks and metabarcoding

Luis Silva

CIBIO-InBIO, Research Center in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal

lfpascoals@gmail.com

Due to the rapid changes occurring around the world, there is an urgent need to understand biodiversity, not only in terms of species composition but also on how species interact with each other. Among researchers, for several years now, it is unanimous that combining network analysis and metabarcoding techniques will provide a higher understanding of species interactions at several levels and simultaneously provide a deeper knowledge of several ecosystem services. Metabarcoding methodologies allow a much higher taxonomic resolution to identify species in complex mixtures of organisms, often with only vestiges of the taxa. Nonetheless the number of studies combining these two methods are very few and are mostly related with pollen dispersal studies and herbivory. The use of metabarcoding is becoming common in dietary studies of insectivorous animals but these are often focused in a single or limited number of species. This is somewhat surprising, because insectivorous animals can play important ecosystem services, as pest control, which have been gaining public visibility and recognition. In this study we studied the diet of two bird communities in eucalypt plantations and evaluate their interaction patterns. We also found that bird communities are eating several exotic insect pests, including exotic eucalypt pests that spread with eucalypt plantations. Overall, our results highlight the power of joining DNA metabarcoding and ecological networks, by providing highly resolved networks with hundreds of interactions, that would otherwise be impossible to detect.

Effect of fertilization on food web and community structure dynamics at a high temporal resolution

Pedro Leote[1*], Oskar Rennstam Rubbmark[1], Michael Traugott[1]

(1) University of Innsbruck, Department of Zoology, Applied Animal Ecology group

* pedro.leote@uibk.ac.at

Biological control is a natural alternative to agricultural pesticides. However, the mechanisms that regulate the reliability of this ecosystem service are still poorly understood. Not the least because pest are not always in present in fields, and could be seen as ephemeral resources that the predator community needs to adapt to exploit. Therefore, it is likely that biological control is temporarily regulated, and to assess this regulation studies spanning an entire growth season are needed. Furthermore, because species adapt their niches to avoid stronger competitors it is also likely that behavioural interactions among predators are driving the reliability of biological control. The intensity of competition for prey will alter the redundancy within the predator community, such that when competition is lower, redundancy increases and species' niches can overlap more, making biological control more effective and resilient. To show how biological control is regulated over time and by predator interactions, we therefore assessed which time points during the season were critical for the maintenance and reliability of biological control. This was done by conducting a study in summer barley fields naturally infested with aphids. By applying manure to part of the fields, competition was artificially alleviated by increasing resource abundance evenly from a basal level to both pest and alternative prey. Community and food web structures were later compared between fertilized and unfertilized treatments throughout the entire cereal growth season using species abundances and molecularly-derived dietary data of several thousand individual predators.

Impact of plant age and genotype on xylem microbial network associations in cultivated olive trees

Manuel Anguita-Maeso[1*], Carmen Haro[1], Luca Testi[1], Angjelina Belaj[2], Juan A. Navas-Cortés[1], Blanca B. Landa[1]

(1) Institute for Sustainable Agriculture, Spanish National Research Council (IAS-CSIC), Córdoba, Spain; (2) Centro de Investigación y Formación Agraria de Alameda del Obispo, Instituto de Investigación y Formación Agraria y Pesquera (IFAPA), Córdoba, Spain

* manguita@ias.csic.es

Understanding microbial associations through co-occurrence network analysis is a very effective tool to detect patterns of copresence and mutual exclusion among members of the plant-associated microbiome. By using 16S and ITS rRNA metagenomics sequencing, we studied the associations of bacterial and fungal communities present in xylem sap of plantlets and adult olive trees of 'Picual', 'Arbequina', 'Arbosana', 'Frantoio' and 'Hojiblanca' olive varieties. Results based on the analysis of amplicon sequence variant and network assembly analysis showed distinct microbial association behaviors according to olive plant age and genotype. Thus, *Pseudomonas*, *Bosea* and *Meiothermus* showed the highest positive associations in the xylem of adult trees whereas *Azospirillium*, *Rhizobium* and *Brevundimonas* showed the greatest positive interactions in olive plantlets. Furthermore, MCODE method identified clusters of highly interconnected regions for each olive genotype, where *Alternaria* and *Phaeococcomyces* genera were unique to 'Arbequina'; *Rhizobium*, *Bradyrhizobium* and *Brevibacillus* were exclusive to 'Arbosana'; *Gardnerella* and *Rathayibacter* to 'Frantoio'; *Acinetobacter* and *Micrococcus* to 'Hojiblanca' and *Arthrobacter*, *Lawsonella*, *Massilia*, *Sphingopyxis*, *Thermaerobacter* and *Variovorax* to 'Picual'. Interestingly, *Pseudomonas* and *Anoxybacillus* were positioned at the network cores obtained when data were analyzed by plant age and plant genotype, respectively. Network association analysis has revealed new knowledge regarding specific microbial associations occurring among olive genotypes at different plant age, offering the identification of keystone xylem-inhabiting microbial species that may result determinant for olive growth and health.

Range overlap as a potential factor of parasite centrality in a sharing network

Ana Paula Lula Costa[1*], André Andrian Padial[1]

(1) Federal University of Paraná

* anapaulalula@gmail.com

Hosts links by parasitism highlight possible transmission paths across space. Host switching is first influenced by local factors, but its establishment and success depend on the frequency and opportunities of transmission events. *Prochilodus* evolutionary history resulted in well-distributed genera in South America. The species *Prochilodus lineatus* has a diverse well-known metazoan parasite community. We create a fish-parasite sharing network between *P. lineatus* parasite fauna and fishes that share at least one parasite species with it throughout South America Basins. Our goal is to analyze what factors underline parasite sharing between host species. Here, we analyzed the relation between range overlap and host connectivity through parasite sharing. We constructed sharing networks with the presence/absence data of each fishes in South America's main Basins. We used host degree centrality as a parasite sharing measure and parasite betweenness centrality (BC) as a host connectivity measure in each network. Our preliminary analyses showed that there was no relation between host DC and range overlap, in contrast, we had a significant difference with BC and range overlap ($p = 0.017$). Our results show that higher parasite centrality was related to the range overlap, but not parasite sharing with *P. lineatus*. Parasites with higher BC are better host connectors in the network. So, although basins in which *P. lineatus* is present did not have a significant difference of higher parasite sharing, fishes in these basins seem to be better connected throughout the parasite fauna. Further analyses with host traits and phylogeny will be made.

Structural patterns in animal social networks

Bárbara Seaman[1*], Pablo A. Marquet[1,2,3]

(1) Pontificia Universidad Católica de Chile; (2) Instituto de Ecología y Biodiversidad (IEB); (3) Santa Fe Institute

* b.seaman.e@gmail.com

The development of tracking technologies has boosted the study of animal societies in the last decade and has made it possible to investigate behavioral repertoires and interaction network structures in a wide variety of taxa. However, so far there are few studies that synthesize the knowledge generated on social networks in animals. Given that social networks are not random and that functions such as the efficient flow of information are key to group survival, we expect that there are large scale trends in the structure of animal social networks that allow us to account for regularities associated with functionality. On the other hand, in different types of biological networks, patterns related to their size are known. According to the literature, such relationships could be associated with the robustness and explorability of networks, however it is not known whether animal interaction networks adhere to these patterns. In our work, we conducted a literature review of around 300 ASN articles, from which we collected information on taxa, interaction types, and sampling methodologies to identify general trends in the study of animal social networks. For those networks with available data, we performed statistical analyses of network structural properties such as density, modularity and clustering. The main results indicate that ASNs present structural patterns similar to those observed in other biological networks, which suggest the existence of universal properties linked to information flow in complex biological networks.

- POSTERS -



© Estefanía Pereira

The hidden role of multi-trophic interactions in driving diversity-productivity relationships

Georg Albert

German Centre for Integrative Biodiversity Research (iDiv)

Georg.Albert@idiv.de

Resource-use complementarity of producer species is often invoked to explain their generally positive diversity-productivity relationships. Additionally, multi-trophic interactions that link processes across trophic levels have received increasing attention as a possible key driver. Given that both are integral to natural ecosystems, their interactive effect should be evident but has remained hidden. We address this issue by analysing diversity-productivity relationships in a simulation experiment of producer communities nested within complex food-webs, manipulating resource-use complementarity and multi-trophic animal richness. We show that these two mechanisms interactively create diverse communities of complementary producer species. This shapes diversity-productivity relationships such that their joint contribution generally exceeds their individual effects. Specifically, multi-trophic interactions in animal-rich ecosystems facilitate producer coexistence by preventing competitive exclusion despite overlaps in resource-use, which increases the realized complementarity. The interdependence of food-webs and producer complementarity in creating biodiversity-productivity relationships highlights the importance to adopt a multi-trophic perspective on biodiversity-ecosystem functioning relationships.

A network perspective on the vectoring of human disease

Ben Bellekom

University of Oxford

ben.bellekom@zoo.ox.ac.uk

Blood-sucking insects are important vectors of disease, with biting Diptera alone transmitting diseases that cause an estimated 700 000 human deaths a year. Insect vectors also bite nonhuman hosts, linking them into host-biting networks. While the major vectors of prominent diseases, such as malaria, yellow fever, dengue, and Zika, are intensively studied, there has been limited focus on the wider interactions of biting insects with nonhuman hosts. Drawing on network analysis and visualisation approaches from food-web ecology, we discuss the value of a network perspective for understanding host–insect–disease interactions, with a focus on Diptera vectors. Potential applications include highlighting pathways of disease transmission, highlighting reservoirs of infection, and identifying emerging and previously unrecognised vectors.

Stability of ecosystem functioning in food webs in response to warming and eutrophication

Jerome Eschenbrenner[1*], Elisa Thebault[1]

(1) CNRS

* jerome.eschenbrenner@sorbonne-universite.fr

While ecosystems are facing rising anthropic perturbations, theoretical models remain focused on either systems of low complexity, or measurements of stability that do not incorporate perturbations explicitly. Here, we present results on an allometric food web model, in which we explicitly modelled warming and eutrophication, while tackling the multidimensionality of stability in response to perturbation. We show that the functioning of the primary producer and the animal communities respond differently to the two perturbations, with total animal biomass being more affected by warming, while the biomass of primary producers is more impacted by nutrient enrichment. The results also show that the presence of inedible plants, resulting from the perturbations, greatly affect the overall ecosystem response as it creates a "trophic cul-de-sac". Our findings deviate from previous predictions on interactive effects of warming and enrichment in predator-prey models, highlighting the importance of considering complex food webs, explicit perturbations and the different communities in the study of ecosystem stability.

Inferring leader-follower behavior from presence data

Juan Fernández-Gracia[1*], Jorge P. Rodríguez[2], Víctor M. Eguíluz[1]

(1) IFISC (CSIC-UIB); (2) IMEDEA (CSIC-UIB)

* juanf@ifisc.uib-csic.es

Social interactions are ubiquitous in groups of animals, including humans. These interactions might be of different nature, for example, competitive, mutualistic, or kinship; and their global structure is naturally studied with the tools of complex network theory. Traditionally, it has been challenging to examine social interactions in the marine environment given the difficulties associated with data collection, however, developments in acoustic telemetry technologies now present a novel way to remotely examine such behaviour. Here, we propose a method to extract leader-follower networks from presence data collected by a single acoustic receiver at a specific location. The method is based on the Kolmogorov-Smirnov distance between the distribution of lag times between the consecutive presence of an individual followed by the presence of another and its conjugate distribution. We apply it to detection data collected for acoustically tagged reef manta rays by a single acoustic receiver positioned at a frequently visited site. We find, in agreement with biological and ecological insights, that (i) female reef mantas follow more males than expected; (ii) male reef manta rays follow fewer females than expected, but with a stronger association to certain individuals; (iii) reef manta rays follow each other with a weaker association than larger individuals do, while the rest of the reported interactions between individuals appear to be random.

Structure of the demersal food web in Western Mediterranean Sea

Lucía López-López[1*], Marina Sanz-Martín[1], Marta Sáinz-Bariain[2], Marina Zamanillo[1], Encarnación García[3], Miguel Vivas[3], Antonio Esteban[3], Manuel Hidalgo[1]

(1) Oceanographic Centre of the Balearic Islands (IEO, CSIC); (2) Oceanographic Centre of Santander (IEO, CSIC); (3) Oceanographic Centre of Murcia (IEO, CSIC)

* lucia.lopez@ieo.es

Binary networks based on feeding interactions are considered the most straightforward method to characterise the structure of complex ecological communities. These basic structural models, however, are still lacking for most natural systems, hampering the understanding of the structural consequences of environmental and anthropogenic stressors at the ecosystem level. Here, we performed a bibliographic review on the feeding habits of the most abundant and recurrent 200 demersal species in the Mediterranean coasts of the Iberian Peninsula, and their main prey. Our study, based on over 100 articles describing the species' trophic ecology, identified more than 5000 feeding links at high taxonomic resolution (mostly species level), which we used to construct a binary network for the Western Mediterranean Sea. We characterised this meta-web using a set of network indicators, identifying the main modules of densely connected species within the metaweb, and discussing their ecological implications. Our bibliographic research also pointed out the high heterogeneity found in the metrics used for describing feeding interactions, which may prevent the integration development of flow networks and future meta-analyses. Thus, we propose a series of recommendations that we deem essential when reporting results in trophic ecology studies in high diverse systems such as the Mediterranean Sea.

Post-release monitoring shows no non-target effects of a biocontrol agent against an invasive plant

Francisco A. López-Núñez[1*], Ruben Heleno[1], Hélia Marchante[1,2], Elizabete Marchante[1]

(1) Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Portugal; (2) Escola Superior Agrária, Instituto Politécnico de Coimbra, Portugal

* lnfran85@gmail.com

Post-release monitoring is essential to evaluate the direct and indirect, target and non-target effects of biocontrol agents. However, rigorous monitoring is still commonly absent or inaccurate. Here, based on a comparative before-after experimental design, we implemented an interaction networks approach to fully unravel the effectiveness, potential impacts and underlying ecological processes during invasive plant management in Europe after the release of a Southern hemisphere BCA. In 2015, the bud-galling wasp Trichilogaster acaciaelongifoliae was released in Portugal to manage the invasive species Acacia longifolia. The detailed assessment of pre-release interactions networks between plants, galling insects, their parasitoids and inquilines forecasted potential indirect impacts on native communities via shared parasitoids (i.e., apparent competition). Four-years after release, the BCA has spread along more than 150 km of the Portuguese littoral and its population has grown exponentially after adjusting to the northern hemisphere conditions, reaching more than 20000 galls counted in 2020. Despite such tremendous growth, we could not detect any significant non-target effects either directly (non-target hosts) or indirectly (apparent competition) on the native communities. We have also not detected any significant changes on network structure after BCA release. So far, these results are highly encouraging since the BCA has fully established, with yet undetected non-target effects. The effectiveness of the BCA to control A. longifolia and to restore invaded communities will require continued detailed monitoring.

Wide road verges have a critical role in the conservation of plant-pollinator networks in intensively managed agroecosystems

Marcos Monasterolo[1,2*], Mariano Devoto[1,3], Santiago Poggio[4]

(1) Universidad de Buenos Aires, Facultad de Agronomía, Cátedra de Botánica General, Buenos Aires, Argentina; (2) Centro de Investigaciones y Transferencia de Catamarca (CITCA), CONICET-UNCA. San Fernando del Valle de Catamarca, Argentina; (3) Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET); (4) IFEVA, Universidad de Buenos Aires, CONICET. Facultad de Agronomía, Departamento de Producción Vegetal, Buenos Aires, Argentina

* marcosmonasterolom@gmail.com

Landscape fragmentation and agricultural practices can affect plant-pollinator communities that linear landscape elements host in agroecosystems. To assess the role of road verges in sustaining plant-pollinator networks, we studied twenty portions of road verges in two consecutive field seasons (2014-2015) in the Argentine Pampas. We considered the features of road verges at three different scales of observation: width of the road verges (patch scale), adjacent field use (community scale), and landscape heterogeneity (landscape scale). We assessed the influence of these features on plant-pollinator networks. Species composition between road verges was similar and unique interactions were rare; accordingly, plant-pollination networks were robust and relatively stable to anthropic disturbances. Verge width, a patch scale feature, was the most influential, as wider verges had higher interaction richness and generality of flower visitors. At landscape scale, the evenness of interactions decreased with higher landscape diversity. Our study shows that the conservation of road verges helps to sustain complex and functional plant-pollination networks in intensively managed agroecosystems.

The role of indirect effects in coevolution: from mutualism to antagonism

Fernando Pedraza Perez[1*], Hanlun Liu[1,2], Klementyna A. Gawecka[1], Jordi Bascompte[1]

(1) Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland; (2) Department of Ecology, State Key Laboratory of Biocontrol, School of Life Sciences, Sun Yat-sen University, Guangzhou, China

* fernando.pedraza@ieu.uzh.ch

Species interactions have evolved from antagonistic to mutualistic and back several times throughout life's history. Yet, it is unclear how changes in the type of interaction between species alter the coevolutionary dynamics of entire communities. This is a pressing matter, as transitions from mutualisms to antagonisms may be becoming more common with human-induced global change. Here, we combine network ecology and evolutionary theory to simulate how shifts in interaction types alter the coevolution of empirical communities. We show that as mutualistic networks shift to antagonistic, the contribution of indirect effects to coevolution reduces, meaning that the selection imposed by direct partners begins to outweigh that imposed by indirect partners. This is associated with mutualistic communities losing their tight integration of traits and increasing their rate of adaptation. Furthermore, we highlight that the alterations to the coevolutionary dynamics of mutualistic communities are more pronounced if specialist consumers are the first species to switch to antagonism. The extent to which global change alters the direction and speed of coevolution, will therefore depend on which species are most affected by it.

Network-based analysis reveals differences in plant assembly between the native and the invaded ranges

Laura del Rio-Hortega[1*], Irene Martín-Forés[1], Isabel Castro[2], Jose Manuel de Miguel[1], Belén Acosta-Gallo[1]

(1) Dpto. Biodiversidad, Ecología y Evolución. Facultad de CC. Biológicas. Universidad Complutense de Madrid, España (Spain); (2) Department of Ecology, Autónoma University of Madrid, Madrid, Spain

* lriohort@ucm.es

Annual grasslands of the Mediterranean-climate regions provide an excellent scenario to study the assembly after a historic unidirectional introduction of species, from the Mediterranean Basin to the Mediterranean-climate region of South America. Here, we aimed to compare the assemblage and interactions of naturalized species with the rest of the species in the plant community in both the native and the invaded (i.e., Chile) ranges. In order to achieve this objective, we carried out a co-occurrence and network analyses, with a novel approach. Our results suggested that the native and invaded range differ in the community structure, specifically, naturalized species displayed more significant interactions and key role within the community than they do in the native range. This methodology allows to improve the knowledge on how the naturalization process affects the community assembly and identify the key species in the community assembly.

Landscape configurations and trophic structures interactively drive species-area relationships in meta-food-webs

Remo Ryser[1*], Myriam Hirt[1]

(1) German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

* remo.ryser@idiv.de

Spatial and trophic processes simultaneously shape biodiversity in nature, but they are addressed by mostly independent ecological theories. The theory of island biogeography and related theories predict higher species richness with increasing area across islands or habitat patches. In contrast, food web theory explores the effects of traits and network structure on coexistence within local communities. Exactly how landscape configurations interact with food-web dynamics in regulating metacommunities has remained unclear. We explore these interacting effects in a meta-food-web model and show that when habitat patches are interconnected by dispersal, more species can persist on smaller islands than predicted by the classical island biogeography model. When patch sizes are distributed in an autocorrelated way in the landscape, this effect flattens the slope of the species-area relationship. However, when landscapes have random patch-size distributions, the slope of the species-area relationships can even become negative, indicating that small patches harbor higher diversity than larger ones. These relationships are further affected by the structure of trophic networks. This highlights the importance of simultaneously considering landscape configuration and trophic network structure to understand drivers of species-area relationships in metacommunities.

Potential for coexistence in stage-structured populations

Marco Saltini[1*], Claus Rueffler[1]

(1) Uppsala University

* marco.saltini@ebc.uu.se

Most eukaryotic organisms undergo significant changes of size during their lifetime. Therefore, ontogenetic niche shift, i.e., the change of the ecological interactions of an organism with its environment resulting from ontogenetic development, is a ubiquitous feature in biological communities. Hence, it is surprising that the life cycle complexity resulting from ontogenetic niche shifts have traditionally been overlooked by ecologists interested in studying the ecological and the evolutionary coexistence of diverse species in biological communities. We employ analytical theory and computer simulations to assess the effect of complex life cycles on the origin and maintenance of biological diversity. We show that, while on the one hand complex life cycles promote species coexistence in large networks with inter-specific competition for shared resource, on the other hand this coexistence is hardly obtained through adaptive speciation mechanisms.

Population dynamics and competition in seagrass meadows in a global warming scenario

Tomas Sintes Olives

IFISC (UIB-CSIC)

tomas@ifisc.uib-csic.es

Temperature anomalies in the coastal water are expected to be intensified in the next years due to the global climate change. Temperature elevation has been observed to strongly affect the ecosystems of seagrass meadows worldwide, decreasing the shoot density, biomass and leaf productivity. This effect will be particularly relevant in the Mediterranean Sea in which seagrasses and seaweeds (*C. prolifera*) compete. The different response to the thermal stress by the different species will alter the growth dynamics, their spatial distribution and, consequently, the ecosystemic functionality. In this study we present an individual based model able to develop complex spatial networks from the application of elementary clonal growth rules. We monitor the change in the seagrass demography, the emergence of collective behavior, and evaluate the resilience of these ecosystems in the Mediterranean, when the growth parameters (i.e., the shoot mortality and branching rates) and the interaction among species are triggered by the raise of the sea water temperature.

Application of eDNA metabarcoding for assessing mangrove ecological restoration

Pilar Suárez[1*], Darren O'Connell[2], Darren M. Evans[1]

(1) Newcastle University; (2) University College Dublin

* nmdps@newcastle.ac.uk

Mangrove ecosystems provide a broad range of ecological benefits and ecosystem services. They are recognized as a nursery habitat for many fish species and play a critical role in carbon storage. Despite their importance and worldwide restoration efforts, it's still one of the most degraded and endangered ecosystems. Thus, mangrove restoration assessment is urgently needed to ensure effective practices that maintain healthy communities. Environmental DNA metabarcoding is a practical ecological tool for monitoring biodiversity and community structure, but its application to restoration projects is limited. Here, we investigate the utility of eDNA metabarcoding to assess the mangrove restoration outcome on community structure and species-interaction networks. We compare three replicated restoration treatments in two mangrove sites in North Sulawesi, Indonesia: Monoculture Reforestation, Mixed species Regeneration and Natural Forest as the reference system. Water samples were collected in 36 sampling quadrants during the dry season; they were later filtered through Sterivex cartridges and preserved for DNA extraction. Metabarcoding assays targeting the mitochondrial COI and 12s genes will be applied to the extracted eDNA. We expect that eDNA metabarcoding detects patterns of community between treatments despite tides and water movement. We also expect the mixed regenerated community should more closely resemble the natural forest, in terms of biodiversity and ecological interactions, than would be the case with the monoculture restoration. The results of this study will provide evidence to guide future mangrove restoration efforts and facilitate decision-making.

Modelling the effect of herbicide application on plant-pollinator networks in agroecosystems

Julia Tavella[1*], Marcos Monasterolo[1,2,] Tania P. Palacios[1,3], Débora C. Rother[4], Fredric M. Windsor[5], Paulo R. Guimarães Jr[4], Darren M. Evans[5], Mariano Devoto[1,6]

(1) Universidad de Buenos Aires, Facultad de Agronomía, Cátedra de Botánica General. Buenos Aires, Argentina; (2) Centro de Investigaciones y Transferencia de Catamarca (CITCA), CONICET-UNCA, San Fernando del Valle de Catamarca, Argentina; (3) Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina; (4) Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo, Brazil; (5) School of Natural and Environmental Sciences, Agriculture Building, Newcastle University, UK; (6) Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina

* juliatavella@gmail.com

The maintenance of natural or semi-natural vegetation on field margins, in the form of hedgerows or flower strips, is essential for the conservation of biodiversity and its emerging ecosystem services in agroecosystems. In regions of intensive agricultural production, herbicides are widely used to control the spontaneous vegetation of cropped fields and their margins. Plant responses to herbicides range from vulnerable to tolerant, and may even develop resistance. As a result, herbicide application triggers changes in the structure and dynamics of plant communities in field margins. These changes may affect non-target organisms associated with them. We present the outline of a study that will explore how herbicide application affects plant communities in agroecosystems and, indirectly, the pollinators that depend on them. We will link an herbicide-plant network with a plant-pollinator network in the crop margins of agroecosystems in the intensively-cropped Pampean region of Argentina. We will analyze changes in a plant-pollinator network structure by simulating herbicide-induced changes in the plant community of field margins and their knock-on effect on pollinators. We will consider contrasting scenarios of herbicide application, herbicide characteristics (site of action), plant traits, and the rewiring of interactions in plant-pollination networks. The information generated will help to develop an "ecological thinking" in the management programs of weeds, which is critical to ensure the sustainability of agricultural production.

Epigenetic response to climatic stress in two related grasses: *Festuca amethystina* L. and *Festuca tatrae* (Czakó) Degen

Przemysław P. Tomczyk[1*], Marcin Kiedrzyński[1], Ewa Forma[2], Katarzyna M. Zielińska[3], Edyta Kiedrzyńska[4, 5]

* przemyslaw.tomczyk@biol.uni.lodz.pl

(1) Department of Biogeography, Paleoecology and Nature Conservation, Faculty of Biology and Environmental Protection, University of Lodz, Lodz, Poland; (2) Department of Cytobiochemistry, Faculty of Biology and Environmental Protection, University of Lodz, Lodz, Poland; (3) Department of Geobotany and Plant Ecology, Faculty of Biology and Environmental Protection, University of Lodz, Lodz, Poland; (4) European Regional Centre for Ecohydrology of the Polish Academy of Sciences, Lodz, Poland; (5) UNESCO Chair on Ecohydrology and Applied Ecology, Faculty of Biology and Environmental Protection, University of Lodz, Lodz, Poland

Protecting ecosystem stability and supporting sustainable agriculture are two challenges that require a lot of knowledge of plant adaptations under climate change (including their epigenetic response to stress conditions). The presented study concerns the epigenetics of Festuca grasses, plants important for both: ecosystem stability and agriculture. It examines the level of global DNA methylation under stress and favorable conditions of two closely-related species, *Festuca amethystina* L. (2x and 4x) and *F. tatrae* (Czakó) Degen (2x), in a common garden experiment (the plants originated from different climates and habitats). An exponential relationship was observed between global DNA methylation level and insolation 24 hours before sampling. Higher air temperature, higher insolation, and lower air humidity induced greater DNA methylation. In most cases, tetraploids had higher mean DNA methylation than diploids. We discovered that each species and cytotype had unique DNA methylation and thus individual epigenetic pattern of stress response. It was showed that climatic provenance of the examined plants appeared to modify the overall global DNA methylation level rather than independently shape it. We also analyzed the influence of mycorrhiza fungus on grasses under drought stress conditions, in particular, how these biotic interactions, considered as ecological networks, can shape stress resistance of the examined set of species and cytotypes.

Effects of increasing wild deer densities on plant-pollinator communities and interaction networks

Daycy Noimy Valladares Pérez[1*], Carlos Hernádez-Castellano[2,3], Juan A. Calleja[4], Emmanuel Serrano Ferrón[5]

(1) Facultat de Biociències, Universitat Autònoma de Barcelona; (2) CREAF; (3) Univ. Autònoma de Barcelona, E08193 Cerdanyola del Vallès, Spain; (4) Departamento de Biología (Unidad de Botánica), Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Universidad Autónoma de Madrid; (5) Wildlife Ecology & Healt Group (WE&H), Servei d'Ecopatologia de Fauna Salvatge (SEFaS), Departament de Medicina i Cirurgia Animals, Universitat Autònoma de Barcelona

* dnvalpe@gmail.com

Large herbivores, such as deer, are key components of most Mediterranean ecosystems. To our knowledge, effects of large herbivores on interaction networks remains unexplored. We conducted a study in which we experimentally modified deer density constructing three different scenarios, thereafter treatments. A control treatment with no deer; a low-density treatment simulating natural densities; and a high-density treatment simulating overpopulations. Vegetation of the plots were dominated by *Cistus ladanifer*, *Rosmarinus officinalis*, *Cistus populifolius* and *Thymus mastichina* (thereafter focal plants). In each treatment we established transects in which we evaluated browsing degrees and number of flowers of each flowering plant. We also conducted plant-pollinator surveys. Browsing degrees differed between treatments. *C. populifolius* and *T. mastichina* were affected by browsing but only in the high-density treatment. Plant community composition changed in the high-density treatment, mainly by the extirpation of several herbaceous plants. Moreover, *C. populifolius* and *T. mastichina* showed reduced number of flowers per individual in the high-density treatment.

Pollinator composition paralleled plant community composition patterns, being simplified in the high-density treatment. Network vulnerability of *C. ladanifer* and *T. mastichina* and interaction richness of the network was reduced in the high-density treatment. Number of network modules was unaffected by deer density, but module composition changed dramatically. These results demonstrate that deer populations can affect plant-pollinator interaction networks. However, negative effects seem to occur only at high densities, and our results suggests that, in this scenario, damage on some eco-evolutionary dynamics might be irreparable.

Multiple specialised fisheries in food web networks: how do they influence themselves and each other?

Alexandra Werner[1*], Benoit Gauzens[1], Ulrich Brose[1]

(1) FSU Jena

* alexandra.werner@idiv.de

Effective ecosystem-based management of marine resources requires an improved understanding of how disturbances via fishing spread through a food web. As many types of fisheries exist in parallel, administrators are moving towards developing multi-species management plans, yet theoretical investigations from an ecological view are rare. Building upon previous results, I propose a bioenergetics food web model coupled with multi-species fisheries to explicitly include humans and their feedback effects on biodiversity and ecosystem functioning in marine fish communities. Testing combinations of different trophic level harvesting would allow for a greater understanding of complex feedback loops from trophic interactions driven by humans and the economy, leading to improved ecosystem-based management plans.

Impacts of spatio-temporal heterogeneity and invasive species on ant communities and their trophic networks

Yazmin Zurapiti[1*], Evan Economo[1], Masako Ogasawara[1], Takuma Yoshida[1], Masashi Yoshimura[1]

(1) Okinawa Institute of Science and Technology

* yazmin.zurita@oist.jp

The web of interactions within an ecological community are inherently complex and highly dynamic, with the potential to change in magnitude and/or direction in response to environmental factors including seasonality, land use or invasive species. With the accelerated rate of change in global climate and land cover, it is critical to better understand how environmental stressors such as land use and invasive species affect community composition, species abundances, and species interactions. However, most network analysis of trophic interactions across space make use of taxa of the same trophic level; examples of how multiple trophic levels change across environmental gradients are scarce. This is particularly challenging for generalist and omnivorous taxa, as both prey and predator are members of the same taxa. Using the trophic interactions of ants (Hymenoptera: Formicidae) in Okinawa, Japan, as a study system, we are applying a self-develop DNA metabarcoding protocol to determine the diet of ecologically important ants that are distributed island-wide. We will evaluate the impacts of land cover and invasive species on across-taxon associations using multilevel network analysis. We expect mild association shifts due to land cover change and interference of invasive species as seapare factors, nevertheless, we expect a strong interactive effect between both, land cover and invasive species, which would present drastic rearrangements in ant trophic networks.