EcoNet 2025

VII Symposium on Ecological Networks (EcoNet2025)

The Stephenson Building, Newcastle University

3-5th September 2025

Welcome

The School of Natural and Environmental Sciences at Newcastle University, UK are delighted to be hosting the VII Symposium on Ecological Networks. This year our broad theme is *'Network Ecology in the Anthropocene'* and is intended to bring together biologists, theoretical physicists, computational and social scientists who work on network theory or use it as an approach to understand the structure and functioning of biological communities. As always, we believe that the symposium will be an excellent opportunity to share cutting-edge methodologies and new results and serve as a platform to develop joint projects in the future.

Plenary Speakers

Professor Jane Memmott, OBE, FRS, University of Bristol

People & pollinators in a network context

People and pollinators are clearly linked in that pollinators facilitate the production many food crops, along with medicines, construction materials, biofuels and also have a role in human culture. While we are very good at capturing the links between plants and pollinators, explicitly capturing the links between people and pollinators is rather more challenging. In this talk I will present the data from a project that quantifies the links between pollinators and key micronutrients in people's diets in the Himalayas. This data is then used to predict the impact of ongoing pollinator declines and pollinator conservation measures on farmer health and farming income. I will then look back more generally at networks and consider some of the assumptions we use when making plant-pollinator networks (reasons to be careful) and end by considering some new approaches that could be implemented looking forward (reasons to be cheerful!).

Dr. Blanca Arroyo-Correa, Estación Biológica de Doñana (EBD-CSIC)

Bridging scales in mutualistic networks: from individuals to community assembly

Understanding how ecological patterns emerge across scales remains one of the central challenges in ecology. Many of the macroscale patterns we observe, such as species distributions or interaction networks, are ultimately driven by mechanisms operating at the level of individual organisms. Mutualistic networks, such as those involving plants and their pollinators or seed dispersers, offer an ideal context for exploring this scaling question. These systems exhibit relatively consistent structures at large scales, yet they are built from locally context-dependent interactions among individuals that collectively shape community assembly and disassembly.

Drawing on recent advances in empirical data collection, mathematical modeling, and data–theory integration, I will highlight how fine-scale processes, such as those related to individual traits, behaviors, and spatial configurations, cascade upward to influence emergent network structure and dynamics in mutualistic communities. I will show how within-population heterogeneity, beyond species-level measures, can affect network architecture and function, shape species roles and community stability, and promote biodiversity.

Bridging the gap between microscale processes and macroscale patterns, from individuals to communities and beyond, requires fostering dialogue across levels of organization and integrating niche and network theories into a more unified framework. I will discuss how advancing this perspective calls for both methodological and conceptual shifts. This approach moves us toward a more mechanistic and predictive understanding of ecological networks and their responses to global change, thereby enhancing our ability to design conservation strategies grounded in real-world ecological mechanisms.

Professor Paulo Guimarães, Universidade de São Paulo (USP)

Indirect effects in ecological networks: consequences for evolution, ecology and ecosystem services

Indirect effects are one of the main consequences of being part of a network. In ecological systems, a myriad of effects can propagate across networks, shaping evolutionary processes, ecological dynamics, and the ecosystem services that benefit humankind. In this talk, we will explore how network structure influences the outcomes of indirect effects. We begin by examining a fundamental law of network architecture—the giant component transition—which leads to two distinct structural patterns in ecological networks. These patterns, in turn, may either hinder or facilitate the emergence of indirect effects. Next, using mutualistic systems as case studies, we investigate some evolutionary and ecological consequences of indirect effects that dissipate as they travel along network pathways. While dissipative indirect effects are likely common in ecological systems, there is a particularly important exception: abrupt ecosystem changes driven by amplifying indirect effects, leading to the collapse of key ecosystem services. We examine these dynamics by modelling how human-driven erosion of plant–frugivore networks threatens a variety of ecosystem services provided by tropical palms. Despite the qualitative differences between dissipative and amplifying indirect effects—which demand different modelling approaches—we show that the consequences of indirect effects are ultimately shaped by the same three structural patterns: the hierarchical organization of cohesive species groups, the small-world phenomenon, and the proliferation of long pathways connecting species within the network.

Dr. Talya Hackett, University of Leeds

Species interactions across boundaries: from mosquitoes to landscapes

Conservation, restoration, land management and applied questions about ecological consequences to change are increasingly applied at landscape-scales and across multiple taxa. Yet, for practical reasons, empirical interaction data are still rarely collected at this level. Thus, while we know that species and interactions spill over between habitats and interact across foraging guilds, the true cross-boundary dependencies are still poorly understood. Spanning from mosquitoes to landscapes, I will present research highlighting how network ecology at these broad scales affects our understanding of communities and the ecosystem services they provide; identifying species roles across a mosaic of habitats; examining the effects of habitat diversity on the structure, robustness and function of the community; predicting how an ecosystem might respond to targeted mosquito species population suppression; and present planned future research on the potential value of unseen aquatic-terrestrial “blue-greenways” for connectivity, ecosystem service provision and landscape-level restoration.

Schedule

Wednesday 3rd September

09:00	Registration (*speakers to upload talks*)	Stephenson Building Foyer
09:45 – 10:10	Welcome	
10:10 – 10:45	**Plenary**: Prof. Jane Memmott, University of Bristol, UK	People & pollinators in a network context
	Theme: Drivers of Environmental Change	
10:45 – 11:00	Violeta Calleja Solanas, Doñana Biological Station, CSIC, Spain	Drivers of biodiversity loss under an ever-changing world
11:00 – 11:15	Sebastián Montoya-Bustamante, Agroscope, Zurich, Switzerland	Artificial light at night reshapes the temporal structure of plant-pollinator multilayer networks

11:15 – 11:30	Sara Beatriz Mendes, Consejo Superior de Investigaciones Científicas (CSIC), Spain	The urbanisation of seed dispersal networks
11:30 – 12:00	***Coffee break***	***Main foyer***
12:00 – 12:15	Alba Costa, Mediterranean Institute for Advanced Studies (IMEDEA, UIB-CSIC), Mallorca, Spain	Anthropogenic disturbance and species’ roles on insular seed dispersal networks
12:15 – 12:30	Beatrice Dale, Northumbria University, UK	Trees and Bees: Incorporating trees into plant-pollinator networks
12:30 – 12:45	Bruno Melati, Eawag - Swiss Federal Institute for Aquatic Research and Technology/USP	Interaction Costs Drive Critical Transitions in Mutualisms: Insights from Boolean Network Models
12:45 – 14:00	***Lunch (Poster Session 1)***	***Main foyer***
Theme: Concepts and Theory		
14:00 – 14:35	**Plenary**: Dr. Blanca Arroyo-Correa, Estación Biológica de Doñana (EBD-CSIC), Spain	Bridging scales in mutualistic networks: from individuals to community assembly
14:35 – 14:50	Jorge Eduardo Castro Cruces, Queen Mary University of London, UK	Predicting ecosystem re-assembly using machine learning
14:50 – 15:05	Siim-Kaarel Sepp, Netherlands Institute of Ecology	Dark interactions: quantifying biotic decoupling in plant-associated communities under range expansion
15:05 – 15:20	Shai Pilosof, Ben Gurion University of the Negev. Israel	Inductive link prediction facilitates the discovery of missing links and enables cross-community inference in ecological networks
15:20 – 15:35	Nerea Montes Pérez, Estacion Biologica de Doñana CSIC, Spain	A comprehensive probabilistic metaweb of plant-pollinator interactions across EU
15:35 – 16:20	***Tea break***	***Main foyer***
Theme: People and Nature		
16:20 – 16:35	Anna Eklöf, Linköping University, Sweden	Ecosystem Vulnerability in the Barents Sea: A Network Approach to Threat Interactions and Ecosystem Service Loss
16:35 – 16:50	Anna Stanworth, University of Southampton, UK	Assessing the robustness and resilience of subsistence ecosystem services using a socioecological network
16:50 – 17:05	Giovanni Bianco, Senckenberg Biodiversity and Climate Research Center (BiK-F), Germany	Traits, abundance, interactions: the path from species to Nature’s Contributions to People
17:05 – 17:15	Wrap-up	
17:15 – 18:00	*Speed Reviews, Meet-ups and Networking*	
18:00	Drinks Reception sponsored by the British Ecological Society’s *Journal of Animal Ecology*	Great North Museum: Hancock *(please gather on the steps of the museum for a group photograph)*
19:00	Symposium Dinner	Great North Museum: Hancock *(a bar is available)*

Thursday 4th September

09:30 – 10:05	**Plenary**: Prof. Paulo Guimarães, Universidade de São Paulo (USP)	Indirect effects in ecological networks: consequences for evolution, ecology and ecosystem services

Theme: Ecological Evolutionary Networks

10:05 – 10:20	Marilia Palumbo Gaiarsa, University of California, Merced, USA	From Foraging to Fitness: The Role of Individual Behavior in Shaping Ecological Networks
10:20 – 10:35	Gabriella Lima Tabet Cruz, Departamento de Biodiversidad, Ecología y Evolución, Universidad Complutense de Madrid, Spain	Functional structure and evolutionary signal of immune and virulence profiles of host-bacteria networks
10:35 – 10:50	Pamela Cristina Santana, Lund University, Sweden	Connecting evolutionary dynamics and network structure under anthropogenic change
10:50 – 11:30	***Coffee***	***Main foyer***

Theme: Climate Warming

11:30 – 11:45	Brandon Samuel Whitley, Natural History Museum of Denmark, University of Copenhagen	Tundra in Bloom: Pollination Network Properties Across (Southwestern) Greenland
11:45 – 12:00	Pablo Augusto Poleto Antiqueira, University of Essex, UK	Substructural reorganisation of food webs under warming increases energy flux and mitigates against ecological instability
12:00 – 12:15	Laura Turnbull, University of Durham, UK	The Role of Connectivity in Driving Grassland-Shrubland Regime Shifts
12:15 – 12:30	Eoin O'Gorman, University of Essex, UK	Warming thickens soil arthropod food webs by amplifying intraguild predation
12:30 – 14:00	***Lunch (Poster Session 2)***	***Main foyer***

Theme: Nature recovery

14:00 – 14:15	Xingfeng Si, East China Normal University, China	The structure and dynamics of plant-frugivore mutualistic networks in fragmented habitats
14:15 – 14:30	Klementyna Gawecka, UK Centre for Ecology & Hydrology, UK	The roles of space and food web complexity in mediating ecological recovery
14:30 – 14:45	Daniela Pinto Coelho, Universidade de São Paulo, Brazil	Seasonal variations in habitat use by the globally endangered Lear's Macaw: using the network approach to unravel spatial patterns and identify key-areas in a seasonally dry tropical forest
14:45 – 15:00	Zelin Chen, University of Essex, UK	Benthic biodiversity and food web recovery after decommissioning of oil and gas infrastructure
15:00 – 15:15	Lennart Gries, Senckenberg Biodiversity and Climate Research Centre, Germany	Drivers of trophic population specialization in mammalian carnivores
15:15 – 15:30	Ruben Heleno, Centre for Functional Ecology, University of Coimbra, Portugal	The European Seed Dispersal Network: Who, What and How
15:30 – 16:10	***Tea break***	***Main foyer***

16:10 – 16:45	**Plenary**: Dr. Talya Hackett, University of Leeds, UK	Species interactions across boundaries: from mosquitoes to landscapes
16:45 – 17:00	Final words and student prizes	
17:00	Close	

Friday 5th September

Bamburgh Castle trip (*for those who have purchased tickets*)

09:00 Gather at the Stephenson Building foyer

09:30 Depart by coach from Claremont Road (opposite Great North Museum: Hancock)

10:30 Arrive Bamburgh Castle, tour and walk on beach (time permitting)

13:30 Depart

14:30 Arrive Newcastle University, Afternoon tea served in the Armstrong Building Reception Rooms.

Organising Committee

Darren Evans, Katherine Baldock, Jordan Cuff, Madeleine Fabusova & Shai Pilosof

British Ecological Society Special Feature

Network Ecology in the Anthropocene

We invite submissions for a cross-journal special feature exploring Network Ecology in the Anthropocene

This Special Feature, spanning all seven BES journals, will examine state-of-the-art developments in network ecology in order to understand, manage and predict the impacts of human activity on species-interactions at a range of scales and across biomes. This will involve theoretical and empirical approaches, and explore the consequences of the variety of human impact on network complexity, structure and resilience.

Authors are invited to submit proposals for papers on topics that include (but are not limited to):

- Network structures across levels of organisation, scaling relationships
- Coevolutionary responses to environmental change
- Biomonitoring and network derived metrics
- Network construction methods, inference and applications
- Habitat conversion, fragmentation and degradation
- Agricultural intensification
- Mass extinctions
- How network ecology can inform ecological/environmental management
- Restoration
- Urban ecology and ecological networks
- Multilayer networks
- Spatio-temporal network dynamics
- Socio-ecological networks
- Changes in network ecology over time

For more information, go to https://besjournals.onlinelibrary.wiley.com/hub/call-for-proposals/network-ecology-in-the-anthropocene

Call for Proposals Closes 28 September 2025. There is a ‘Speed Review’ session at 17:15 on 3rd September to discuss your ideas with journal Editors.

Theme: Drivers of Environmental Change

Drivers of biodiversity loss under an ever-changing world

Violeta Calleja-Solanas, Ignasi Bartomeus, Oscar Godoy
Doñana Biological Station, CSIC, Spain

Species interactions are key to maintaining biodiversity. However, how these interactions change over space and time as a result of varying environmental conditions has seldom been explored. This fact limits our understanding of the drivers maintaining biodiversity. Here, we explore two independent long-term (> 8 yr) datasets subjected to the same regime -annual plant grasslands and wild bee assemblages in shrublands- describing changes in species abundance across multiple locations. We found that both systems respond similarly to changes in their main environmental driver (rainfall) despite their disparate evolutionary backgrounds. Specifically, while rainfall variability promotes more diverse communities, a sustained drought over the years would lead to a marked biodiversity loss. Despite the observed spatial context dependency, the structural stability of most of the observed communities is maintained throughout the studied years, but we identify clear winners and losers of drought. The main mechanisms driving the communities are a combination of species-specific changes in their reproduction rates, an increase in the variability of interspecific interactions, and a reduction in the strength of self-limiting effects. These results are obtained through our novel framework that considers the time-varying nature of species interactions. Adding this dynamical aspect to interaction networks has proven crucial for understanding the mosaic that shapes community composition and, consequently, for understanding the effects of harsh climatic conditions on biodiversity loss.

Artificial light at night reshapes the temporal structure of plant-pollinator multilayer networks

Sebastián Montoya-Bustamante[1], Casper J. van der Kooi[2], Vincent Grognuz[1,3], Colin Fontaine[4], Eva Knop[1,3]

[1]Agroscope, Reckenholzstrasse 191, 8046 Zurich, Switzerland; [2]Groningen Institute for Evolutionary Life Sciences, University of Groningen, Groningen NL-9747AG, The Netherland; [3]Department of Evolutionary Biology and Environmental Studies, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland; [4]Centre d'Ecologie et des Sciences de la Conservation (UMR 7204), Muséum National d'Histoire Naturelle, CNRS, Sorbone Université, Paris, France

Artificial light at night (ALAN) is an escalating ecological threat, disrupting the natural diel dynamics that have shaped species interactions. Although species-specific responses to ALAN are increasingly documented, its broader effects on the temporal organization of ecological communities remain poorly understood. In particular, we lack a mechanistic understanding of why certain species are more vulnerable to ALAN and how these vulnerabilities scale up to affect network structure and stability. A major barrier to this understanding is our limited knowledge of how ecological communities are naturally structured across the diel cycle—the "assembly rules" that govern interactions over day and night. In this study, we examine whether plant-pollinator networks are structured across the diel cycle and whether this temporal structure is associated to specific floral traits, such as visual cues and floral complexity. We then assess how ALAN alters this structure and explore the resulting implications for network stability. Our findings show that plant-pollinator networks are indeed temporally structured, with floral traits influencing this organization at multiple scales (overall network vs. diel layers). While the overall temporal structure is primarily associated with floral complexity, plant height, and flower abundance, specific diel layers (morning, afternoon, night) are more strongly associated to colour-related visual cues. ALAN, however, disrupts this temporal structuring and its relationship with these visual cues. As a consequence, plants with traits that are advantageous at night become more vulnerable, as these traits may become maladaptive under artificial lighting. This disruption extends beyond isolated diel layers, affecting the stability of the entire diel cycle. Our results demonstrate that ALAN not only illuminates the night—it rewrites the rules of diel assembly, reshapes interaction patterns, and threatens the stability of ecological communities. Understanding these dynamics is crucial for predicting and mitigating the broader ecological impacts of light pollution.

The urbanisation of seed dispersal networks

Sara Beatriz Mendes[1], Jens Mogens Olesen[2]; Manuel Nogales[1]; Patricia Marrero[1]; Javier Romero[1]; Concepción Nieves[1]; Ruben Heleno[3]

[1]Island Ecology and Evolution Research Group, Institute of Natural Products and Agrobiology (IPNA-CSIC), Spain; [2]Department of Biology, Aarhus University, Denmark; [3]Centre for Functional Ecology, Associate Laboratory TERRA, Department of Life Sciences, University of Coimbra, Portugal.

Rapid urban expansion is affecting the composition of wild communities and creating novel ecosystems worldwide. Seed dispersal is key for ecosystem persistence, particularly in fragmented landscapes. However, generalisations regarding the impacts of urbanisation are still difficult due to the lack of studies encompassing the urban matrix. We examined the seed dispersal networks in natural forests and urban areas in Tenerife Island to explore the effects of urbanisation on seed dispersal. For one year, we observed frugivory events and identified seeds in animal faeces in natural forests and urban areas of the island. We identified 150 interactions between 83 plant and 18 animal species in the forest and 89 interactions between 41 plant and 9 animal species in urban areas. The urban matrix supported half the species richness of fleshy-fruited plants and frugivorous animals relative to the forest. Urbanisation simplified seed dispersal networks, reducing interaction diversity. Novel interactions dominated the urban seed dispersal network, with non-native plants being highly used by native frugivores, accounting for 61% of the interactions (vs. 15% in the forest). Eight frugivore species (42% of the frugivores) likely maintained the functional connectivity between these habitats, potentially facilitating the spread of non-native species from urban areas (where non-native species are more common) into the forests due to their generalist and flexible diets. Six frugivorous species (32%) completely avoided urban areas, which acted as barriers to dispersal, likely hindering the dispersal of many plants across urban landscapes. Our results underscore the importance of promoting the use of native plants as ornamentals, enhancing habitat connectivity between forests and urban areas, and preventing the introduction of non-native fleshy-fruited plants. Ultimately, these findings underscore the importance of sustainable urban planning and active stakeholder engagement to protect the seed dispersal service.

Anthropogenic disturbance and species' roles on insular seed dispersal networks

Alba Costa[1], Sandra Hervías-Parejo[1,2], Manuel Nogales[4], Christopher Kaiser-Bunbury[3], Anna Traveset[1]

[1]Mediterranean Institute for Advanced Studies (IMEDEA, UIB-CSIC), Mallorca, Balearic Islands, Spain; [2]Centre for Functional Ecology (CFE), TERRA Associate Laboratory, Department of Life Sciences, University of Coimbra, Coimbra, Portugal; [3]Centre for Ecology and Conservation, Faculty of Environment, Science and Economy, University of Exeter, Penryn, UK; [4]Institute of Natural Products and Agrobiology (IPNA-CSIC), Tenerife, Canary Islands, Spain

Seed dispersal interaction networks are fundamental to ecosystem functioning, facilitating plant regeneration and contributing to biodiversity maintenance. However, their architecture can be reshaped by anthropogenic pressures such as invasive species introductions and habitat changes. In this study, we conducted a comparative analysis of seed dispersal interactions on two ancient Afrotropical continental fragment islands characterized by distinct disturbance histories; one under long-term conservation, the other heavily modified by human activity. To investigate how species roles may vary between these contrasting contexts, we employed a multi-method framework integrating modularity analysis, centrality metrics, and motif-based approaches. Our results revealed pronounced differences in network structure between islands. The more disturbed island, marked by a higher prevalence of invasive species and greater human impact (e.g. larger population and infrastructure), exhibited a more generalized and complex interaction network with lower structural cohesion. In contrast, the less disturbed island supported a more compartmentalized structure, with interactions dominated by specialists. Species occurring on both islands exhibited context-dependent shifts in their functional roles, underscoring both the plasticity and potential vulnerability of their contributions in changing environments. These findings highlight the importance of incorporating both species identity and network architecture into conservation planning, and demonstrate the value of combining diverse analytical approaches to fully capture ecological change and guide effective management strategies.

Trees and Bees: Incorporating trees into plant-pollinator networks.

Beatrice Dale[1], Matthew Pound[1], Darren Evans[2], Mark Goddard[1], Rinke Vinkenoog[1], Jordan Cuff[2], Katherine Baldock[1]

[1]Department of Geography and Environmental Sciences, Northumbria University, Newcastle upon Tyne, UK; [2]School of Natural and Environmental Sciences, Newcastle University, Newcastle upon Tyne, UK

Insect pollinators provide a crucial ecosystem service but are under threat, with declines reported across all key groups. Land-use change is one of the primary drivers of declines, and urbanisation – a major form of land use change – can reduce native forage, intensify urban heat island effects, and fragment habitats. Previous studies of plant-pollinator networks in urban landscapes have shown that some land uses can provide important forage sources for pollinators. However, most studies limit sampling to flora accessible from ground-level due to the logistical challenges of sampling in trees. The role of urban tree floral resources for pollinators therefore remains a significant knowledge gap. We addressed two questions: 1) How does the inclusion of canopy-level data affect plant-pollinator network structure? 2) How does flower visitation vary between tree and ground level flora? We collected data on flower-visitor interactions at ground level and in tree canopies in an urban park in Newcastle upon Tyne, UK. We first integrated the data to create visitation networks for the entire park and then used neutral foraging null models to investigate pollinator foraging preferences in relation to the availability of resources in the landscape. We compared network metrics with and without canopy data included and explored the importance of different tree species for different pollinator taxa. Integrating flower-visitor interaction data collected from herbaceous plants and trees provides a more comprehensive view of plant-pollinator interactions in a landscape and enables the assessment of the role of trees at different seasonal times. These findings can be used to inform urban greening and pollinator conservation strategies, providing evidence to support planting approaches in order to provide continuous forage sources and support diverse urban pollinator communities.

Interaction Costs Drive Critical Transitions in Mutualisms: Insights from Boolean Network Models

Bruno Melati

Eawag - Swiss Federal Institute for Aquatic Research and Technology / Instituto Biológico - Universidade de São

Mutualistic outcomes depend on both benefits and costs. For instance, the physiological costs to produce nectar could be higher than the benefit offered by the partner. When costs exceed benefits, mutualists become exploiters and mutualism turns antagonistic. Thus, rising costs, e.g., from climate change, can turn mutualists into exploiters. Yet, mutualistic networks may remain stable despite many exploiters, especially when partner benefits act as public goods flowing through the system. But, beyond a threshold, these benefits become insufficient, mutualists turn antagonistic, and exploiters dominate the community. This threshold is known as phase transition — the point at which a small increase in interaction costs leads to a global, qualitative shift in the network's state, from mutualistic to antagonistic. I developed a Boolean network model to investigate the transition phase from mutualistic to exploiter-dominated states due to increased costs and assess how network structure influences the critical transition point. Boolean models offer a powerful approach to explore complex system dynamics and emergent behaviour. To parametrize the model, I used real networks from mutualistic systems. Results showed a second order (gradual) transition phase with his critical point occurring when mutualism costs increase by 60 to 70% from the original costs imposed by the interaction. At this critical point, generalist mutualism, as seed dispersal, is initially more robust: transition occurs when mutualism costs rise to ~70%, and ~75% of species remain mutualists. In contrast, specialized systems, like myrmecophytic, have a critic point at lower mutualistic costs (~60%), with only ~50% remaining mutualists. This suggests that although generalist systems are more resilient early on, tolerating higher costs to become exploiters, they tolerate fewer exploiters before systemic collapse. Due to the high modular structure, specialized mutualisms experience faster initial change of species state, changing from mutualist to exploiter, but can buffer the spread of exploiters within modules. In contrast, generalist mutualisms tend to form highly connected, nested networks that delay critic point but, once infiltrated by exploiters, lack compartmentalization and collapse rapidly. Overall, while mutualistic networks are generally robust to increasing mutualism costs, their tolerance to exploiters—and timing of collapse—strongly depends on network architecture.

Theme: Concepts and Theory

Predicting ecosystem re-assembly using machine learning

Jorge E. Castro and Athen H. Ma

Department of Computer Science, School of Electronic Engineering and Computer Science, Queen Mary University of London, UK.

The effects of climate change are intensifying globally, driven by severe weather events that have resulted in the decline of numerous species. It is imperative to obtain precise insights into the threats posed to our ecosystems, enabling us to effectively manage and potentially alleviate further environmental deterioration in the future. Ecological interconnectedness plays a crucial role in anticipating responses to climate change, as the decline of a single species can cascade through the network, impacting the populations of its predators or prey as species adapt to shifting environmental conditions. Fortunately for us, this project endeavours to enhance our comprehension of how Global Environmental Change (GEC) disrupts ecological networks and redefines community organization. Leveraging machine learning techniques, we aim to unravel the structural and re-assembly principles governing ecosystems under stress. By employing advanced graph data science, we will decode topological characteristics and forecast species adaptation and rewiring in response to climate change. Our model will pioneer a predictive framework to anticipate ecosystem-level responses, providing evidence-based guidance for conservation interventions. Furthermore, this research contributes to the burgeoning field of ecoinformatics by offering novel methodologies for deciphering vast ecological datasets. Through these endeavours, we strive to empower stakeholders with tools to navigate the complexities of ecosystem resilience in the face of environmental change. In conclusion, this research outlines a comprehensive plan to predict new links and ecosystem re-assembly using machine learning techniques. The findings from this research will contribute significantly to the field of Ecology and Machine Learning, providing valuable insights into community organization and resilience in the face of biodiversity loss.

Dark interactions: quantifying biotic decoupling in plant-associated communities under range expansion

Siim-Kaarel Sepp[1], Koen Verhoeven[1], Wim H. van der Putten[1,2]

[1]Department of Terrestrial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands; [2]Laboratory of Nematology, Wageningen University, Wageningen, The Netherlands

Rapid global warming is accelerating species range shifts toward higher latitudes and altitudes, a natural process now occurring at an unprecedented rate. On the one hand, shifting ranges allow communities to withstand changing climates. However, the accelerated movement amplifies the differences in colonisation abilities among different organism groups, creating a critical mismatch between community components, which can disrupt established community assembly mechanisms and lead to ecological disorder. Here, we investigate how plant range expansion impacts the assembly of multitrophic plant-associated communities across a European latitudinal transect (Mediterranean to the Netherlands). We compare native plants to range expanders, distinguishing those with and without native congeneric relatives. Our dataset comprises diverse belowground (prokaryotes, fungi, nematodes) and aboveground (herbivorous insects) organism groups, providing a comprehensive view of community assembly. Acknowledging the challenge of inferring true interactions from species associations, which often confounds network analyses, we employ joint species distribution modelling to isolate residual biotic associations within and among these plant-associated communities from those driven by abiotic and spatial drivers. We introduce the concept of “dark interactions” (unrealised edges), combining insights from community ecology and tools from network ecology to quantify the decoupling of biotic components within these communities in response to plant range expansion. This approach allows us to move beyond network characteristics to infer changes in assembly patterns and system stability at the community scale. By conservatively translating network ecological outputs to community-level processes, this study offers vital insights into the impacts of anthropogenic warming on biodiversity.

Inductive link prediction facilitates the discovery of missing links and enables cross-community inference in ecological networks

Shai Pilosof[1], Barry Biton[1], Rami Puzis[2]

[1]Department of Life Sciences, Ben-Gurion University of the Negev, Beer-Sheva, Israel, [2]Department of Software and Information Systems Engineering, Ben-Gurion University of the Negev, Beer-Sheva, Israel

Predicting species interactions (links) within ecological networks is crucial for advancing our understanding of ecosystem functioning and responses of communities to environmental changes. Transductive link prediction models are often used but are constrained by sparse, incomplete data and are limited to single networks. We addressed these issues using an inductive link prediction (ILP) approach to predict interactions within and between ecological networks by pooling data across communities and applying transfer learning. We evaluated the performance of our ILP model on 538 networks across four community types: plant–seed disperser, plant–pollinator, host–parasite and plant–herbivore, and found that it achieved higher precision and F1 scores than transductive models. However, cross-community prediction efficacy varied, with better performance when plant–seed disperser and host–parasite networks were used as training and test sets, compared with when plant–pollinator and plant–herbivore networks were used. Finally, leveraging the generalizability of ILP, we developed a pretrained model that ecologists could readily use to make instant predictions for their networks. This highlights the potential of ILP to improve prediction of ecological interactions, enabling generalization across diverse ecological contexts and bridging critical data gaps.

A comprehensive probabilistic metaweb of plant-pollinator interactions across EU

Nerea Montes Pérez and Ignasi Bartomeus

Estacion Biologica de Doñana CSIC, Spain

As global change progresses, improving the ability to predict shifts of species and their interactions is essential. However, relying solely on local interaction network data might not be sufficient to predict future shifts caused by climate change or anthropogenic factors. This is particularly alarming for key organisms like plants and their pollinators, where we might be able to create species distribution models, but predicting shifts in local interaction networks remains challenging. This study aims to provide the first probabilistic metaweb for plant-pollinator interactions at the European level, enabling the study of potential shifts in local networks using only species lists. We employed an imputation model to create a probability matrix for plant-pollinator interactions at the European level, using 1.372 plants and 2.148 pollinators from the EuPPollNet dataset. The model integrates linear filtering (LF) and singular value decomposition (SVD) to detect false negatives and capture the network's low-rank structure. Additionally, biotic data such as phylogeny, traits, phenology, and distribution were incorporated to predict interactions

for species with no prior records, covering 95% of all European pollinators. The model's predictions can be adjusted based on network characteristics like connectance, degree, or a hybrid approach. Link prediction for biogeographical regions showed great performance, predicting 20% new links on average with 0.8 predictive power (AUC). This study provides the first probabilistic metaweb for European plant-pollinator interaction networks, offering a valuable tool for exploring how local networks may change under future scenarios.

Theme: People and Nature

Ecosystem Vulnerability in the Barents Sea: A Network Approach to Threat Interactions and Ecosystem Service Loss

Anna Eklöf and Johanna Sollén

Linköping University, Sweden

The Barents Sea is an ecologically and economically significant Arctic marine region facing escalating anthropogenic threats such as climate change, overfishing, and pollution. In this work we employ Bayesian network modeling to assess how multiple interacting threats affect species in the Barents Sea food web and, consequently, the ecosystem services they underpin. Using a literature-based approach, threats were identified and quantified via a modified IUCN scoring method to generate extinction probabilities for the 233 taxa in the food web. These probabilities were used to simulate primary and secondary extinctions and assess ecosystem service vulnerability. The results reveal that secondary extinctions substantially increase overall species loss compared to direct effects alone, particularly when higher-trophic or structurally important taxa are affected. Ecosystem services showed variable sensitivities: food provisioning was relatively robust, while habitat provisioning and CO? sequestration were more vulnerable, especially under climate-driven threats such as ocean warming and acidification. The shape of the biodiversity–service response function significantly influenced outcomes, with strong concave relationships amplifying service losses at early stages of biodiversity decline. We also simulated a threat network, which revealed how indirect drivers such as ice loss and infrastructure development intensify downstream threats, leading to compounding impacts on ecosystem services. These results emphasize the importance of accounting for food web structure and threat interactions in vulnerability assessments. The Bayesian framework proved effective for scenario testing, offering valuable insights for ecosystem-based management in Arctic regions under rapid environmental change.

Theme: Ecological Evolutionary Networks

From Foraging to Fitness: The Role of Individual Behavior in Shaping Ecological Networks

Marilia Palumbo Gaiarsa

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A key challenge in ecology is to understand the underlying processes that give rise to broader patterns in ecological communities, particularly those reflected in network structure. While research at the community and population level has shown that specific ecological patterns can enhance robustness, resilience, and long-term species persistence, these patterns ultimately emerge from individual-level behaviors—especially how individuals use different resources. Yet, it remains unclear how individual-level variation in interaction patterns scales up to shape network structure and, via individual fitness, population persistence. In this talk, I will share results from a controlled greenhouse experiment that links variation in plant–pollinator interaction patterns to individual fitness, providing rare empirical evidence for the relationship between network structure and population-level outcomes. Using a combination of pollen DNA metabarcoding and Raspberry Pi cameras to track foraging behavior, we reveal strong individual-level specialization in pollinators and show how variation in flower nutritional quality shapes both network structure and reproductive output. Integrating individual foraging behavior into ecological networks is essential if we are to understand the responses of pollinator communities, ultimately driven by their behavioral choices about where and when to forage, to extinction drivers in the Anthropocene.

Functional structure and evolutionary signal of immune and virulence profiles of host-bacteria networks

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Functional and molecular traits, such as those related to host immunity and pathogen virulence, play a key role in shaping host-parasite dynamics. This study explores a rarely examined functional network structure that integrates phylogenetic, immunogenetic, and virulence data, and sheds light on host susceptibility and bacterial infectivity. We compiled innate immune profiles from wild mammal hosts across 11 taxonomic orders, including biological processes associated with innate immunity genes and protein classes/families related to bacterial infection. These profiles were combined with virulence factors of zoonotic bacteria (e.g., ?-haemolysin, type IV pili, secretion systems, capsules) and their functional mechanisms (e.g., motility, adhesion, invasion, immune modulation) to assess how trait combinations shape host-bacteria network patterns. Whereas host-bacteria network included all identified bacterial species associated with each host, the bacteria-host network was restricted to bacterial species for which virulence trait information was available. Analysis of the bipartite networks revealed a lack of modularity and high overlap in the host-bacteria and host-immune factor networks, but a well-defined modular structure emerged in the bacteria-virulence factor and bacteria-host networks. The phylogenetic signal in virulence traits, measured using Fritz and Purvis' D index, and the strong match between bacterial modules by hosts and virulence factors, assessed with Cramer's V test, suggest that bacterial associations reflect more conserved and specialised patterns than host immune components. Taxon-specific analyses showed limited immune factor conservation, restricted to few elements per host order. These patterns indicate that immunological diversity is more homogeneous among mammals, likely resulting from the adaptive and widespread distribution of the analysed innate immune factors. In contrast, bacterial virulence traits formed distinct functional modules aligned with host sharing, suggesting ecological and functional coherence among bacteria infecting similar hosts. This asymmetry may reflect divergent evolutionary pressures: bacterial traits linked to host manipulation are subject to constraints that favour specificity, whereas host immune systems evolve more flexibly in response to diverse pathogens. By identifying evolutionary and functional patterns in host resistance and bacterial infectivity, this work contributes to our understanding of the eco-evolutionary dynamics of zoonotic transmission.

Connecting evolutionary dynamics and network structure under anthropogenic change

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One of the most pressing challenges in an era of rapid environmental change is understanding how species' positions within ecological networks influence their evolutionary potential and the persistence of interactions. As communities are continually reshaped, the loss of species interactions often poses a greater threat to ecosystem function than species extinctions alone. We build on over a decade of research on the interactions between woodland star plants (Lithophragma bolanderi, Saxifragaceae) and their specialized pollinators, Greya moths (Prodoxidae). Here, we investigated how pollination networks vary across four L. bolanderi populations in California's Sierra Nevada Forest, each exposed to distinct geographical, ecological, and anthropogenic pressures, including agricultural intensification. We conducted fieldwork during two flowering seasons (March–June, 2023 and 2025), monitoring pollinator visitation, measuring nine floral traits per flower, and collecting fruit capsules to assess female fitness via seed production and detect moth oviposition. We also recorded the plant community and pollinator presence and frequency, including invasive honeybees (Apis mellifera). Two populations are dominated by Greya moths, while the others are primarily visited by solitary bees (Andrena spp.) and beeflies (Bombyliidae). Our findings reveal that traits mediating interactions with Greya moths are diverging from those mediating interactions with co-pollinators, with specialization asymmetry varying geographically. Populations with the specialist pollinator exhibit higher evolvability but less flexibility, suggesting a more canalized yet potentially faster evolutionary response. In contrast, populations increasingly visited by generalist pollinators show lower evolvability, and may be more susceptible to stochastic selection, network instability, and vulnerability to invasions. Finally, we link these patterns to landscape context, showing that agricultural expansion and invasive pollinators increase the risk of interaction breakdown depending on local trait compositions. These findings suggest that anthropogenic pressures reshape not only community structure but also evolutionary trajectories. By integrating ecological network analysis with evolutionary dynamics, this work emphasizes that conservation strategies must consider the architecture of species interactions—not just species richness—to sustain ecosystem resilience and adaptive capacity in the Anthropocene.

Theme: Climate Warming

Tundra in Bloom: Pollination Network Properties Across (Southwestern) Greenland

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The Arctic region is at the front edge of the climate change crisis, with wide-scale changes occurring to its ecosystems, reshaping community compositions and biotic interactions. In this extreme environment, where pollen resources are limited and where the growing season length and timespan is stochastic, understanding the way in which plants and pollinators are interacting can shed important insights on the impacts of a changing climate. Greenland represents an ideal system in which to study these networks, for it contains all Arctic bioclimate zones and offers a natural latitudinal cline off which to sample networks. These qualities make it an optimal proxy for generating broad insights into the structure and properties of Arctic plant-pollinator networks in a changing environment. Our work has focussed on sampling pollinators along the Southwestern coast of Greenland, where we have applied DNA metabarcoding to the pollen found on individual pollinator's bodies to characterise plant visitation network structure across an ~1000 km latitudinal gradient, sampling among representative habitats at each site. We will present our initial insights into the properties of Arctic pollination interaction networks, where we expect to see a commonality of generalist pollinators maintained throughout all sites and latitudes, and where the harshness of the Arctic environment is expected to result in high levels of nestedness among all networks. Moreover, we will present our initial results concerning how individual members of a given species are interacting when compared to the average level of generalisation for their species or higher taxonomic order as a whole. We predict more specialised, resource-limitation driven interactions among individuals with increasing latitude, but decreased network modularity due to overall species generalisation. By interpreting the properties of these Arctic interaction networks, we will shed critical light onto their susceptibility to the diverse disturbances expected in an increasingly changing Arctic climate.

Substructural reorganisation of food webs under warming increases energy flux and mitigates against ecological instability

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Species interactions are fundamental to ecosystem functioning and stability, yet how they respond to climate warming at the substructural level within food webs remains unclear. We investigated how temperature affects the core–periphery organisation of food webs, and how changes in this substructure mediate impacts on ecosystem functioning (energy flux) and stability (robustness) across a natural stream temperature gradient in Iceland (5–25?°C). The relative size of the food web core, the subset of highly connected species, remains consistent across the temperature gradient. However, warming drives significant turnover in both the identity and abundance of core species, indicating that elevated temperatures restructure species' functional roles without altering overall core size. These internal shifts have profound ecological consequences. Warming consistently reduces food web connectance, weakening the network's resistance to secondary extinctions. Yet, the reorganisation of core species under warmer conditions enhances total energy flux and partially offsets this destabilising effect, improving robustness to species loss. Extinction simulations further reveal that food webs are disproportionately sensitive to the loss of core taxa, underscoring their critical role in maintaining ecological stability. Together, our results demonstrate that climate warming can destabilise food webs by simplifying interaction networks, but that substructural reorganisation, particularly within the core, can buffer some of these negative impacts. This compensatory mechanism underscores the significance of internal network architecture in shaping ecosystem responses to environmental change. We advocate for a shift beyond traditional whole-network metrics to include food web substructure as a key lens through which to assess climate vulnerability. Maintaining the functional integrity of core species may be essential to preserving biodiversity and sustaining ecosystem functioning and stability in a warming world.

The Role of Connectivity in Driving Grassland-Shrubland Regime Shifts

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This study explores the role of connectivity in regime shifts from grassland to shrubland under the stresses of prolonged drought and overgrazing, phenomena increasingly prevalent in dryland ecosystems globally. By integrating network theory with numerical modelling, we assess how structural (network topology) and functional connectivity (network dynamics) influence resource distribution across landscapes, facilitating regime shifts. Our findings highlight how drought intensifies disruptions in connectivity, promoting significant vegetation shifts and altering ecosystem resilience. The study also explores the impact of wind and grazing management on connectivity patterns, demonstrating that wind significantly reshapes resource flows across landscapes, while adaptive grazing strategies can mitigate the adverse effects of these shifts. This comprehensive analysis not only underscores the importance of connectivity in understanding and managing vegetation regime shifts but also supports the integration of connectivity metrics into policy frameworks to enhance the resilience and sustainability of dryland ecosystems globally.

Warming thickens soil arthropod food webs by amplifying intraguild predation

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Warming is predicted to simplify ecological networks by increasing the metabolic demands of consumers and channelling energy through fewer, stronger pathways. Empirical tests of this hypothesis in natural systems are rare, though we previously showed a reduction in connectance and mean trophic level of food webs along a stream temperature gradient in the Hengill geothermal valley, Iceland. Here, we quantify food web structure along a soil temperature gradient in the same system using a combination of gut content analysis, feeding trials, and literature research. Surprisingly, we find that connectance and mean food chain length increase with soil temperature, in direct contrast to the aquatic system. Consumers become closer in size to their resources as soil temperature increases, leading to more intraguild predation and fewer apex predators. Thus, increasing temperature and metabolic demands amplify the generalist feeding behaviour of terrestrial arthropod consumers and their ability to tackle similarly sized prey. This response may be less likely in highly size-structured aquatic systems, where predators are largely constrained to feed on much smaller prey, resulting in contrasting temperature effects on food web structure across these different ecosystem types.

Theme: Nature recovery

The structure and dynamics of plant-frugivore mutualistic networks in fragmented habitats

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Species interaction is a key component of biodiversity, as plant and animal species are entangled in nature. However, monitoring species interactions on a large scale is challenging, especially for plant-bird frugivore mutualistic interactions because frugivore foraging behaviour generally occurs in the trees. We developed a camera trap sampling method to monitor plant-bird frugivore interactions simultaneously and continuously during the whole mature fruiting periods on 22 subtropical forested islands and six nearly mainland sites in the region of Thousand Island Lake, China since June 2019. We obtained ca. seven million photos and videos from more than 300 camera traps. We systematically reviewed the first three-year data and identified a total of 17572 independent interaction events, including 39 bird species and 31 fleshy-fruited plant species. We analysed this high-resolution data of plant-frugivore networks, and found large islands supported higher species richness of plants and birds and their interaction richness. Small islands had more connected, less modular, and more nested networks that consisted mainly of small-bodied birds and abundant plants. Common bird species with small body size and high mobility dominate frugivory interactions, potentially serving as crucial mobile links between fragments via seed transfer. By analysing an invasive plant of American pokeweed (Phytolacca americana) in this frugivore network, we found American pokeweed

interacted mainly with local core birds (generalists), indicating that generalist native frugivores with high dispersal potential may accelerate plant invasion in fragmented landscapes. From the temporal scale, migratory birds accounted for 14% of all interactions. Small islands hosted 43% of migratory interactions, highlighting the importance as stopover sites for migratory birds, while large islands supported more frugivore richness but lower migratory proportions, acting as refugia for residents. These findings challenge area-centric conservation priorities by revealing the complementary roles of small and large islands, and advocate enhancing habitat connectivity to sustain seed dispersal and ecosystem resilience in fragmented landscapes. At the end of this talk, I will also quickly introduce our extensive studies of pollination network, oak-rodent seed-dispersal network, and ant-aphid-plant multilayer networks in the same island system.

The roles of space and food web complexity in mediating ecological recovery

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Ecosystem restoration is widely recognised as a key strategy for addressing the global biodiversity loss and climate crises. However, ensuring the long-term sustainability of restoration efforts requires guiding the recovery of complex ecological systems with many interdependent species at a landscape scale. This requires a deep understanding of how species interact with each other and with the surrounding landscape. Due to the complexities of these processes, our understanding of recovery trajectories remains limited. Here, we combine modelling and experimental approaches to study the landscape-scale recovery of species embedded in communities. We represent ecological communities as species interaction networks and landscapes as networks of patches and dispersal pathways. This allows us to capture and disentangle spatial and biotic drivers of recovery. Specifically, we investigate how recovery trajectories are affected by (1) spatial configuration – the number and location of introduced communities, and (2) food web complexity. We assess recovery at both local (habitat patch) and global (landscape) scales. First, using a parameterised metacommunity model, we simulate the dynamics of 15 insect communities varying in food web complexity on a landscape composed of 50 habitat patches. Second, we test the model predictions experimentally using three of the simulated communities in a landscape with five patches. We find that the number and spatial placement of communities affect the colonisation of empty habitat patches, but does not influence population recovery in patches where communities are introduced. Food web complexity reduces the recovery of lower trophic levels. However, this negative effect may be partially mitigated at higher levels of food web complexity. Our results demonstrate that the joint consideration of spatial configuration and species interactions could enhance the effectiveness of restoration actions.

Seasonal variations in habitat use by the globally endangered Lear's Macaw: using the network approach to unravel spatial patterns and identify key-areas in a seasonally dry tropical forest

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Habitat characteristics are constantly changing, resulting in dynamics in resource availability and spatial distribution of populations, especially in markedly seasonal environments, such as the Caatinga dry forest, an endemic and threatened Brazilian biome. Because species respond differently to habitat changes, it is essential to understand how the impacts of conversion of the natural environment into anthropogenic areas affect the habitat use of wild populations. We use the complex networks approach to evaluate the effects of seasonal variations in habitat use, identify key-areas and characterize their land use for GPS-tracked Lear's Macaws (*Anodorhynchus leari*), a specialist frugivorous species, critically endangered, and endemic to the Caatinga. GPS tags were deployed on 11 fledglings in four breeding nuclei at the species single population at Raso da Catarina region, between 2017 and 2023. By assessing the structure of spatial networks, where each node represents a 10 km2 habitat patch and the links represent the movement of individuals between patches, we used network-level metrics (size, degree distribution, connectivity, and modularity) to investigate the influence of climatic seasonality (dry vs. wet seasons) on habitat use and node-level metrics (weight, self-loop, degree and betweenness centrality) to identify key-areas. Seasonality influenced habitat use, indicating greater exploration of the environment in the dry season (85 nodes), with a heterogeneous distribution of links between nodes, implying lower connectivity (0.06) and higher modularity (0.13). On the other hand, there was less exploration of the environment in the rainy season (56 nodes), with a more homogeneous distribution of links between nodes, resulting in higher connectivity (0.09) and lower modularity (0.1). Seasonality also affected the choice of key-areas, indicating variation between the dry and rainy seasons in the most frequented areas, as well as in the areas most important for the flow of individuals between habitat patches, connecting populations. In the next steps, we will characterize the land use in key-areas in order to identify possible threats. In this way, we hope to contribute to conservation actions for the species in the region.

Benthic biodiversity and food web recovery after decommissioning of oil and gas infrastructure

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There is a global increase in the decommissioning of offshore oil and gas (O&G) infrastructure at the end of its operating lifetime. However, there is strikingly limited empirical evidence for the environmental and ecological impacts of decommissioning. Here, we investigate the benthic biodiversity and food web properties of structures sampled in the short term (<1 year; scenario 1), medium term (1-5 years; scenario 2), and long term (>5 years; scenario 3) after decommissioning. We found reduced species richness and simplified food webs in scenario 1, followed by the first signs of recovery in scenario 2, with a slightly higher proportion of intermediate species and density of food web connections. Food webs recovered further in scenario 3, with a much greater density of interactions, but also more links and longer food chains, whilst a reduction in generality and connectance indicated an increased prevalence of specialist species. Our findings demonstrate disturbance risks associated with the decommissioning process in the short term, but a positive recovery trajectory over longer timescales. We highlight the importance of industry collecting more extensive and long-term data at multiple time points and covering different decommissioning types, establishing a standardised data workflow for integrating with available monitoring efforts, and improving stakeholder participation and data accessibility to support an environmentally sound decommissioning process.

Drivers of trophic population specialization in mammalian carnivores

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Global change disrupts trophic networks through biodiversity loss and environmental modification. Species' resilience to such disturbances is often linked to their niche width. The niche variation hypothesis (NVH) posits that generalist populations comprise more specialized individuals, a pattern supported by decades of experimental evidence. However, the extent to which populations within a species differ in specialization remains poorly understood. The potential drivers of this population-level trophic specialization, such as species-specific resource-acquisition capabilities, foraging strategies, geographic variation in resource availability, and phylogenetic relatedness, are largely unexplored. To address this gap, we compiled a population-level diet database from the literature, focusing on terrestrial consumers in three Carnivoran families, and analyzed resource-type use across populations of 60 species. On average, populations used 70% of their species-level trophic niche, and species with broader niches exhibited narrower relative population niche widths. Population-level trophic specialization was primarily driven by metabolic rate, brain size, and home range size, while environmental factors, body mass, and range size had no significant effect. Our findings suggest that generalist species consist of differently specialized populations, while specialists exhibit consistent resource use across their populations, extending the NVH to the population level. Species traits fundamentally shape their trophic adaptability, with high metabolic rates, cognitive capacity and mobility enabling populations to more consistently realize their species niche. Because populations of generalist species only exploit a subset of their total niche, they may be more susceptible to environmental change than previously assumed. This variation in trophic niches may be crucial for understanding species' resilience under global change.

The European Seed Dispersal Network: Who, What and How

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Seed dispersal is a critical ecosystem function, particularly when plants need to move across highly fragmented landscapes like the European ones. However, many groups of animals disperse many types of seeds in many different ways. As most studies on seed dispersal usually focus on a single group of animals or on a specific seed dispersal mechanism (e.g. frugivory), it is hard to have an overall picture of the European seed dispersal network. Here, we analysed a quantitative Europe-wide multi-guild seed dispersal network assembled from published records. The dataset includes 11394 unique interactions between 1901 plant species and 447 animal species (birds, mammals, reptiles and invertebrates) via four dispersal mechanisms (endozoochory, epizoochory, synzoochory, myrmecochory). We then identify global patterns and the topological roles of each animal guild, chiefly specialization, degree and species strength. This revealed that endozoochory by birds and mammals encompasses 90% of plant-animal interaction records. Birds and mammals are equally important for endozoochory, but the diversity of bird dispersers is greater. Surprisingly, fleshy-fruited plants comprise only 15% of all plant species dispersed by animals but are dispersed by more species and via more specialized interactions than plants with dry fruits. Different animal clades tend to disperse plant species via different mechanisms. Epizoochory is almost exclusively carried out by mammals, with a negligible role of birds, insects and reptiles. Synzoochory is performed chiefly by ants (myrmecochory), followed by birds and to a lower degree by mammals. Assigned seed dispersal syndromes based on plant traits had a significant but relatively moderate predictive power over observed dispersal mechanisms, as animals disperse many more species than inferred from classic trait-based approaches – including plants with abiotic syndromes (23-30%) and unspecialized plants (41%).

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