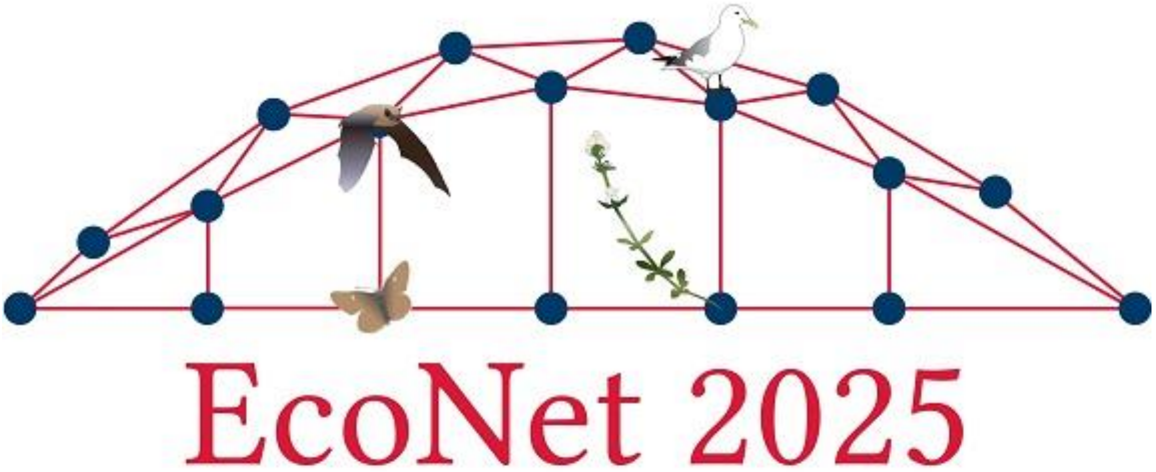

VII Symposium on Ecological Networks (EcoNet 2025)

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.

Poster Sessions

In addition to the plenary speaker talks and thematic sessions, we will be hosting two poster sessions, and this programme brings you the abstracts of those presenting. The two sessions will be held on **Wednesday 3rd September 12.45-14.00** and on **Thursday 4th September 12.30-14.00**, both in the main venue foyer.

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-theanthropocene

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.

Abstracts

Poster session 1: Wednesday 3rd Sep 12.45-14.00

Tracking community change via Network Coherence

Alexandre Fuster Calvo[1], Gracielle T. Higino[2], Katherine Hebert[3], Dominique Caron[3], Francis Banville[4], Pablo Silva[5], François Massol[6], Laura Pollock[3], Guillaume Blanchet[1], Christine Parent[7], Luigi Maiorano[8], Wilfried Thuiller[9], Paulo R. Guimarães Jr[10], Dominique Gravel[1]*

*[1]University of Sherbrooke, [2]University of British Columbia, [3]McGill University, [4]University of Montreal, [5]Federal University of Goias, [6]University Paris Cite, CNRS, [7]University of Idaho, [8]University of Rome, [9]University Grenoble Alpes, CNRS, [10]University of Sao Paulo, *presenting author*

Understanding how ecological communities respond to environmental change remains a key challenge for biodiversity monitoring. To characterize such responses, we need tools that capture how coherently species respond across a community, and to predict their consequences, we must account for ecological interactions. We introduce Ecological Network Coherence (ENC), a concept describing shared responses - whether in abundance, distribution, traits, or environmental sensitivity - among interacting species. We formalize ENC mathematically, explore its dynamics through simulations, and apply it to time series and occurrence data. ENC distributions reveal signals of instability and reorganization and identify species that amplify or buffer variability. ENC offers a general, data-driven foundation for network-based indicators of biodiversity change.

A Century of Ecological Interactions in Svalbard: Revisiting the Network Blueprint

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Communities are shaped not just by species, but by the interactions among them. Describing them as networks highlights the need to monitor changes in both species (nodes) and their interactions (links). The Arctic is a hotspot of environmental change,

as demonstrated by various monitoring programs north of the Polar Circle. As these programs primarily focus on detecting shifts in biodiversity and phenology, the functional dynamics of Arctic systems remain comparatively understudied. Actual species interactions have been investigated less frequently and their current research coverage exhibit considerable temporal and spatial heterogeneity.

Numerous efforts have aimed to synthesize existing knowledge into conceptual frameworks, including for well-studied regions like Svalbard. However, these often overlook interaction strength, likely due to the varied and inconsistent ways it is measured across and within taxa over time and space. Here, we aim to review, standardize, and integrate existing data on interaction strengths to develop an conceptual model of the Svalbard ecological network. We propose the first blueprint of a multilayered, weighted meta-web for the region, which can serve as a new canonical schematic. While still in beta, it represents a significant step forward in understanding the ecological dynamics of the Arctic realm and provides a much-needed baseline for future studies.

Network structure modulates evolutionary dynamics in resource competition networks

Augusto N. Carvalho[*1] and Paulo R. Guimarães Jr. [1]*

*[1]. Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo, 05508-090 São Paulo, Brasil, *presenting author*

Competition for limited resources is an important phenomenon limiting species abundance and promoting niche variation across evolutionary timescales. We have a solid body of empirical and theoretical work exploring how simple, pair-wise competitive interactions affect trait evolution. Because competitors rarely interact with resources in isolation, since species are often inserted in complex networks of interactions, a fundamental problem to solve is how competition shapes trait evolution in a multispecies context. Here, we integrated network theory with a trait-based evolutionary model to investigate how competition and network structure affects trait evolution in resource–sharing networks. By using simple theoretical networks, we described how traits and trait matching between species and resources evolve in response to competition. Specifically, we analyzed the role of network structure ¬— connectance, centrality and centralization — to the evolutionary dynamics. Our results show that trait shifts and trait mismatching due to competition were positively correlated with the importance of the shared resource as a selective pressure to the consumers. Species centrality and network centralization significantly influenced trait evolution, whereas the impact of connectance was weaker. Notably, core species in star–shaped networks experienced the greatest trait shifts under competition but

showed smaller trait mismatches due to their ability to fall back on a subset of their resources. Similar patterns were not observed in linear networks. These results highlight the potential role of network structure to the competitive evolutionary dynamics. We hypothesize that the invasion by supergeneralists will strongly impact peripheral species that interact with more isolated resources in the trait–space, due to propagation of competitive effects through the network.

A low-cost portable method for ground vegetation structural assessment using the iPhone 15 Pro lidar scanner

Broghan Mareighd Erland[*1], Rachel Gaulton[2], Jordan P. Cuff[1]*

*[1]Newcastle University, [2] Fera Science, *presenting author*

Introduction:
Tree in-field systems have the potential to increase biodiversity and the connectivity between species-rich grasslands and woodlands, but they remain poorly characterized. Increasingly, vegetation structural diversity is being recognized as a critical metric for predicting biodiversity. Remote sensing methods provide non-destructive and time efficient ways of measuring structure. In optimal foraging theory, habitat quality provides key insights into invertebrate behaviour and interactions, but the metrics underpinning quality, such as structure, have traditionally been insidious to quantify in these contexts. By ascertaining these data and relating them to interaction networks, it is possible to determine how structure dictates ecosystem services and functioning, and thus the value of discrete habitats in complex landscapes. The use of lidar found in the iPhone Pro models numbered 12 and above for scanning trees has recently emerged in the forestry sector; however, little has been done to facilitate the use for capturing ground vegetation structural data.

Aims:
This work examines the potential of iPhone lidar scanning to estimate the 3D structure of ground vegetation. The low-cost and portability of the iPhone Pro models open methods to researchers with limited funds, limited access to other scanning equipment, and/or limited by how remote a field site may be.

Methods:
Over 30 plots in either a 5m by 2m, or 10m by 2m rectangles were scanned using an iPhone 15 Pro Lidar across several tree in-field systems across the United Kingdom: silvoarable (Wakelyns Farm, Suffolk), silvopastoral (Glensaugh Farm, Laurencekirk), woodpasture (Hepple Estate, Northumberland), woodmeadow (Three Hagges Woodmeadow, Yorkshire), and a roadside biodiversity strip (North Tyneside). A quadrat

was then randomly placed within the grid, scanned, and then intensive vertical structure, cover, and species validation data was collected. Coinciding near-ground and unmanned aerial vehicle imaging data (e.g. Zeb Horizon, DJI Phantom 4 MS, DJI Mini Pro 3) were obtained.

Results:
Preliminary comparisons to the vegetation validation data indicate a high degree of congruence. The methods for extracting meaningful metrics from the iPhone data to link to foraging ecology are being developed with a final field campaign underway to validate methods.

Benefit Accrual: Quantifying the non-linear relationship between pollinator visits and seed production

Christopher R Anderson[1], Lester Squier[2], Fernanda Valdovinos[2], Mark Novak[3], Matthew Smith[4], James D Crall[5], Berry J Brosi[1]*

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Pollinator populations are declining worldwide with uncertain downstream impacts to the plants that they pollinate. Most flowering plants require an insect pollinator to reproduce, receiving many visits from many distinct pollinator species before setting fruit. Given that pollinator populations are declining in the Anthropocene and visitation rates are changing, how will seed production change? Linear relationships between pollinator visits and seed production (as is often assumed in theoretical population models) would result in commensurate decreases or increases in seed set from pollinator declines, whereas saturating benefits (more biologically realistic given finite ovule numbers per flower) would result in little change to seed sets until a critical inflection point has been crossed. Despite some preliminary work in this space, the relationship between individual flower pollinator visits and seeds produced remains challenging to quantify. To characterize the benefit that plants accrue through pollinator visits in wild populations of wildflowers we used a novel camera-trap system coupled with neural net based object-detection algorithms to collect information on the full set of pollinator visits to individual flowers. We then counted resulting seed sets and fit mechanistic models of benefit accrual. While we are still collecting and analyzing data, preliminary results show support for a saturating benefit accrual functional form with some limited evidence for "over-visitation" costs, i.e. a point at which additional visits actually decrease seed set. Understanding the functional form of pollinator benefit accrual relationships could help predict impacts of ongoing pollinator declines in the Anthropocene. Additionally, different functional forms may have distinct stability

implications for plant-pollinator networks that should inform theoretical network models.

Response and recovery dynamics of trophic interactions after multiple disturbances

Daniel Montoya, Ana Burón-Ugarte, Lucille Chrétien & RECODYN team*

*Basque Centre for Climate Change (BC3), *presenting author*

The sheer number of arthropod species place them as a key constituent of trophic interactions and therefore, arthropods greatly contribute to ecosystem functions. Changes in land-use pose a large threat to arthropod diversity, and their vulnerability to warming also threatens ecosystem stability and the ability to recover after perturbation. The difficulty to predict global change alteration of food webs emerges notably from the distinct responses each network component and property can have when combining different types of disturbances. This work aims at: (i) unravelling how such factors affect plant-herbivore-carnivore networks and what are the underlying processes that govern shifts in interactions, and (ii) monitoring the recovery patterns of these communities under global change scenarios. The factors we study are threefold: tilling, warming, and dispersal limitation (i.e. fragmentation), which we apply in twelve connected pairs of enclosures following a semi-factorial design. The enclosures are located in an experimental grassland that we study from 2023 through 2025. Plants are monitored 10 times a year to collect four variables: plant species and corresponding dry biomass, phenology, and feeding damages. Arthropods and molluscs are trapped four times a year to record species, functional groups, abundance, and body length as a fitness proxy. This contribution will present the experiment and preliminary results showing that the occurrence and strength of herbivory decreased within three months following tilling, although warming and fragmentation mitigated this effect. Further analysis of the 2024 data will assess changes in communities of plants, herbivores, and carnivores, identify and quantify shifts in trophic networks, and evaluate their capacity to resist and recover under multifactorial disturbance. Results will provide background information necessary to anticipate global change-driven repercussions on herbivory and better target adaptation measures.

From species to individuals: revealing consistent interaction roles in plant-focused mutualistic networks

*Elena Quintero *[1], Blanca Arroyo-Correa [2], Jorge Isla[2], Francisco Rodriguez-Sánchez [1], Pedro Jordano [1,2]*

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The study of mutualistic interactions among species has received considerable attention over the past 30 years. However, less is known about the structure of individual interaction configurations within species. Recently, individual-based networks have begun to garner more attention, as they represent the fundamental scale at which ecological interactions are assembled and at with natural selection operates. The overarching goal of this study is to investigate the role played by individuals in the assembly of complex ecological networks of species interactions, determining their structuring and functioning. We compiled 44 empirical individual-based networks on plant-animal seed dispersal mutualism, encompassing 995 plant individuals across 28 species from different regions worldwide. We compare the structure of individual-based networks to that of species-based networks and by extending the niche concept to interaction assemblages, we explore levels of individual plant specialisation. We examine how individual variation influences network structure and how plant individuals “explore” the interaction niche of the population. For our analysis, we developed a novel Bayesian framework, implemented in the open-source R package Bayesian Networks, to account for sampling effort variation and uncertainty derived from monitoring ecological interaction. This confidence-based approach improves the reliability of ecological network analyses by mitigating methodological biases from uneven sampling effort.

Both individual-based and species-based networks exhibited high variability in network properties, leading to a lack of marked structural and topological differences between them. Our results reveal low to medium specialisation, with European populations exhibiting higher generality compared to American and Asian populations. Within populations, frugivores’ interaction allocation among plant individuals was highly heterogeneous, with one to three frugivorous species dominating interactions in most populations. Regardless of plant species or geographical region, plant individuals displayed similar interaction profiles across populations, with only a few individuals playing a central role and exhibiting high diversity in the interaction assemblage. Our results emphasise the importance of downscaling from species-based to individual-based networks to understand the structuring of any given ecological community and provide an empirical basis for the extension of niche theory to complex interaction networks.

Interaction nestedness mediates network assembly and affects resulting diversity in host-parasitoid microcosms

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Understanding how diversity is maintained in ecological networks is one of the key questions in ecology. Network structure is thought to have strong effects but disentangling trait-based and species identity-based effects from structural effects is often hard. Here we used sensitivity data to simulate small networks based on known interactions in our Drosophila-parasitoid system. From this data, we chose species assemblages from a defined pool of species with strong differences in predicted nestedness and modularity to build experimentally and observe in a microcosm setup. Our results show that species richness is lower for networks with a higher predicted nestedness after two months. Additionally, variability in species composition was already lower for networks with a higher predicted nestedness after one month. These results suggest that the constrains added by the highly nested original structure influenced the network assembly. Stronger constraints lead to similar responses and reduces the possibilities for networks to respond to changes such as species loss or interaction rewiring.

Ecosystem size mitigates the impacts of extreme rainfall on food web structure and energy flux

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Climate change is expected to intensify rainfall variability, with significant consequences for freshwater food webs and the energy fluxing through them. However, empirical evidence remains scarce, particularly at broad geographic scales. Here, we conducted a multi-site coordinated experiment across Central and South America (18°N to 29°S) to investigate how ecosystem size and extreme rainfall influence food web structure and energy flux in 210 natural freshwater microcosms (tank bromeliads). Using piecewise structural equation modelling with multigroup analysis, we found that increased rainfall amount directly reduced total energy flux by disrupting both decomposition and predation energy channels, while rainfall frequency had no significant effects. In contrast, energy fluxes increased both directly and indirectly with ecosystem size due to food web thickening (which reflects increased complexity through generalist consumers with many links) in larger bromeliads. Food web thickening enhanced energy fluxes across all trophic pathways, whereas food web simplification had specific effects via predation-related energy flux. The influence of both food web dimensions on energy flux varied across sites, highlighting the context-dependent nature of these processes. Our findings reveal that while climate change directly disrupts ecosystem functioning, ecosystem size mitigated climate-driven disturbances through both direct and food web-mediated effects across macroecological scales.

The forest within the forest: restoration of Galapagos host-epiphyte networks

Paula Feldmann[12], Alejandro E. Mieles[3], Anna Traveset[3], Heinke Jägger[4], Isabel Donoso[56]*

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Ecosystem restoration is increasingly implemented as a key strategy to reduce biodiversity loss. Epiphytes form an important fraction of tropical forest biodiversity, and although they are structurally dependent on host plants and vulnerable to deforestation their recovery under restoration has been seldom evaluated. Here, we assessed the effect of restoration through invasive plant removal (Rubus niveus and Cestrum auriculatum) on host-epiphyte interactions in the endemic and endangered Scalesia

Forest on Santa Cruz Island (Galapagos). We evaluated the differences in the structure of host-epiphyte interaction networks and in epiphyte diversity between invaded plots and plots under restoration (11 years of management) and identify the main drivers as well as the key host species for sustaining this diversity. Fieldwork was conducted in 20 paired 10 m x 10 m plots (10 of each treatment). While overall network descriptors showed no significant differences between treatments, restored plots supported significantly higher epiphyte richness. Increased epiphyte richness per host was strongly explained by greater moss cover and larger host tree diameter, both key facilitators of epiphyte colonization. Both were significantly higher in plots undergoing restoration, suggesting that restoration enhances the availability of suitable hosts. Notably, Scalesia pedunculata, the endemic, threatened and (formerly) dominant tree species, emerged as a keystone host with exceptionally high species strength and degree, underscoring its critical ecological role. However, the lack of S. pedunculata regeneration in invaded plots highlights an increasing threat to long-term epiphyte persistence and network stability, mostly due to the low support of the invasive species R. niveus and C. auriculatum to epiphytes. Our findings demonstrate that restoration can enhance epiphyte richness and habitat suitability by promoting structurally suitable native hosts. Furthermore, they emphasize the importance of evaluating key biotic interactions for planning and monitoring restoration programs. This study is the first to evaluate the effects of restoration on epiphyte–host interaction networks, offering valuable insights for forest conservation and the design of effective restoration strategies.

The development of ecological systems along paths of least resistance

Jie Deng[*1,2], *Otto X. Cordero*[2], *Tadashi Fukami*[3], *Simon A. Levin*[4], *Robert M. Pringle*[4], *Ricard Sole*[5], *Serguei Saavedra*[2]

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A long-standing question in biology is whether there are common principles that characterize the development of ecological systems, defined as the appearance of a group of taxa, regardless of organismal diversity or environmental context. Classic ecological theory holds that these systems develop through a sequenced, orderly process that generally proceeds from fast-growing to slow-growing taxa and is shaped by life-history trade-offs. However, it is also possible that this developmental order simply represents the path of least environmental resistance for the survival of the component species, and is thus favored by probability alone.

Here, we use theory and data to show that the progression from fast- to slow-growing

taxa is the most likely developmental path for diverse systems when local taxon interactions self-organize in response to environmental resistance. First, we demonstrate theoretically that sequenced development is more likely than simultaneous development, at least until the number of iterations becomes so large as to be ecologically implausible. We then show that greater diversity of taxa and life histories increases the likelihood of a sequenced order from fast- to slow-growing taxa.

Using published data from microbial, plant, and animal systems, we show empirical evidence that the developmental order of ecological systems follows paths of least environmental resistance. The ability of simple principles to explain consistent trends in the developmental order of diverse ecological systems paves the way for a deeper understanding of the collective features of life.

Predicting maintenance of mobile genetic elements using species abundance distributions

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Microbial systems are among the most plentiful and diverse systems on the planet and span essentially all scales of life, from a single human gut to the global climate. These systems are incredibly robust and adaptive, a feat which undoubtedly underlies their ubiquity. Yet, the mechanisms underlying their resilience are not yet understood. One possible mechanism could be horizontal gene transfer, a process by which mobile genetic elements (MGEs) can spread through microbial populations. These MGEs can provide their hosts with beneficial genes, such as resistance to antibiotics, however as they typically impose some cost on their host they should, in theory, be dynamically removed from the population in the absence of positive selection. This has led to a "paradox", as theoretical models that predict MGE extinction without positive selection contradict empirical measurements that indicate that MGEs are plentiful. As such, identifying additional mechanisms that underlie their maintenance is key to studying potential effects on diversity and stability of microbial systems.

Here, we focus on network-related mechanisms that may facilitate maintenance in the absence of positive selection. In particular, we focus on ecological and infection networks. We show theoretically that these two networks are sufficient to predict MGE maintenance accurately. In fact, it turns out we only need their statistical properties to predict probabilities of MGE maintenance in model systems. In turn, we use these predictions to propose novel mechanisms of maintenance. One such mechanism is that ecologically dominant species --- i.e., those with high abundances --- can act as sources of infection for less abundant species, leading to MGE maintenance. Additionally, we show that ecological networks are in principle only needed to predict species abundance distributions, which can simply be measured directly instead. This point is critical: while inferring interaction networks remains notoriously difficult, measuring (relative) species abundances is comparatively easy thanks to current sequencing techniques. Our work thus further increases the value of abundance distributions, as they offer insight not only into universal (macro)ecological patterns but also into the spread and maintenance of MGEs.

Dissimilarity analysis based on diffusion maps

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Compositional measurements from species assemblages define a high dimensional dataspace in which the data can form complex structures, termed manifolds. Comparing assemblages in this dataspace is difficult because the data is often sparse relative to its dimensionality and the complex structure of the manifold introduces bias and error in measurements of distance. Additionally, ecologically relevant measures of compositional dissimilarity are often formulated in terms of species overlap, reaching a maximum value when two assemblages share no species in common. This can hinder our ability to quantify patterns of compositional variation at large spatial scales where complete species turnover may occur multiple times. We demonstrate the application of diffusion maps, a manifold learning method, to find and characterize manifolds in high-dimensional compositional data. Diffusion maps consider the data as a network in the dataspace where data points-in this case vectors of species abundances-represent nodes that are connected by weighted links defined by some measure of dissimilarity between them. Crucially, data points are connected only if they are sufficiently similar, thereby avoiding the difficulties associated with comparing very different species assemblages. By considering the notion of a diffusion process on this network, diffusion maps embed the data in reduced dimensions in which the Euclidean distance between data points approximates the distance between them along the manifold. This is especially useful when species turnover is high, as it provides a way to measure meaningful distances between assemblages even when they harbor disjoint sets of species. We anticipate diffusion maps will therefore be particularly useful for characterizing community change over large spatial and temporal scales.

Habitats and hubs: what factors shape the microbial communities found on pollinators?

Jordan Twombly Ellis[*1], Alyssa R. Cirtwill[2], Emilie Ellis[3], Tomas Roslin[3,4], Helena Wirta[1,5]*

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As pollinators travel between plants, they are exposed to the microbes on the flowers they visit. These, together with microbes from the environment, the conspecifics, and their nests, form the microbiota on the pollinators. These microbes can be beneficial, detrimental or commensal to the pollinators and the plants. However, the factors that structure pollinators' microbial communities are not yet clear. While habitat likely affects the set of microbes that are locally available, the plants that insects visit could shape their microbiota within a habitat. As insects travel between plants, they transfer microbes between them such that insects visiting similar sets of plants might acquire more similar microbial communities. Further, the microbes themselves impact the formation of the microbial community, by changing the conditions and by the interactions between the microbes. Here, we compare the effects of habitat, plant use, and microbe-microbe cooccurrence on the microbial communities on foraging pollinators collected in forest and field habitats in Central Finland in June 2023. We performed DNA metabarcoding on the microbes as well as on the pollen found on pollinator surfaces to identify the contact pollinators had with plants and microbes. We then used unipartite projection networks to identify plant genera that act as "hubs" or "connectors" and therefore may be especially likely to collect microbes present on many plants within the habitat. Similarly, we identify bacterial "hubs" and "connectors", to see how such microbial taxa impact the community composition. We will test whether habitat, pollinator order, visited plant hub or connector genera, or inclusion of bacterial hub or connector genera explain the microbial community composition of pollinators. Preliminarily, we find that habitat has very little impact on the microbes present, though it does affect the plants pollinators visited. This could mean that microbes on pollinators come only in part from the flowers visited, or that the flowers they visit do not have distinct microbiomes.

How common are nonassortative interactions between communities in ecological networks?

Lachlan Burton[1], Pablo Antiqueira[2], Eoin O'Gorman[2], Yujie Zeng[1], Vito Latora[3,4,5], Athen Ma[1]*

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Community detection is by now a powerful tool in every network ecologist's toolbox for understanding the organisation and function of complex foodwebs. Understanding the modular organization of food web networks is fundamental to questions concerning ecosystem stability, energy flow, and resilience. This problem has been considered with a variety of approaches, most commonly using so-called 'descriptive' computational methods that target mesocale structures with specific relationships between group members, such as 'assortative' and 'core-periphery'. More recent work in network science has demonstrated the advantage of 'inferential' methods which can learn the relevant structures directly from the data, revealing that the interaction patterns between network communities can be, and typically are, significantly more exotic. This raises questions about the role of these previously unstudied structures in ecological networks. I will present the results of applying such methods to a large set of empirical food webs, and discuss the interpretation and relevance of our findings to network ecology.

Linking Plant-Pollinator Network Structure to Parasite Prevalence Bees Across Natural and Managed Landscapes

Lauren Ponisio[1], Rose McDonand[1], Nicole Martinez Llaurador[1], Jesse Fan Brown[1]*

*[1]University of Oregon, *presenting author*

Understanding how ecological network structure influences disease dynamics is critical for pollinator conservation. We examined how plant-pollinator network properties shape parasite prevalence across bee communities in contrasting landscapes. Using parasite screenings for seven common bee parasites (Apicystis spp., Ascosphaera spp., Nosema bombi, Nosema ceranae, Crithidia bombi, C. expoeki, and other Crithidia spp.), we sampled pollinator communities at two natural high-elevation meadows (Cascades Mountains, Oregon; Madrean Sky Islands, Southwestern

US) and two intensively managed sites (California sunflower fields; Oregon harvested forests). Focusing on three bee groups (Bombus, Melissodes, and Apis), we tested how whole-network structure (nestedness, connectance, and H2) relates to community-level parasite prevalence and how species-level network centrality (degree, betweenness, centrality) and reciprocal specialization (d') predict parasite infection risk. We found that greater nestedness and higher H2 were strongly associated with increased Crithidia prevalence across Bombus communities. At the species level, bumble bees with higher d' values also showed increased Crithidia infection rates. In contrast, network structure had limited effects on parasite prevalence in Melissodes and Apis, and for other parasite taxa. Our results suggest that plant-pollinator network structure plays a key role in mediating Crithidia dynamics in native bumble bees, but these effects are not universal across bee taxa or parasite groups.

Incorporating seed dispersal kernels in plant-frugivore networks

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Seed dispersal by animals is prevalent in the Atlantic Forest where the majority of trees disperse offspring through plant-frugivore mutualisms. However, fragmentation and defaunation have driven the loss of many large frugivore species and have potentially affected seed dispersal services, reducing the seed dispersal of large-seed species and long distance events of most plant species. Here, our main aim is to understand the potential consequences of these networks to seed dispersal distances. To do so, we utilised plant-frugivore networks from fragments across the Atlantic Forest, to estimate probabilities of seed dispersal distances using a model parametrised with empirical data on short distance movement. Plant-frugivore networks are combined with seed dispersal traits for plants and frugivores (specifically birds). Forbidden links were identified by comparing the morphologies of fruits and seeds to the gape width of birds, and removed where seed ingestion was theoretically unable to occur. Seed dispersal kernels were produced by scaling the mean distances a bird moved after feeding to body mass with linear regression. Movement patterns and home range size are known to be linked with body size for birds. Therefore, this scaling relationship was used with an exponential decay model to estimate the probability of dispersal over distance. This decay model computes seed dispersal kernels for a species, and weights interactions with the probability of seed dispersal at a given distance. Each fragment's network was analysed for nestedness and modularity; 12 out of the 28 separate networks had significant nestedness (NODF) values for the interaction matrix or its components, and

9 networks had significant modularity. The general differences in structures that arose from weighting events per distance probabilities were analysed: weighted networks had a significant increase in modularity, and significant decrease in nestedness. Removing forbidden links may generate notable differences between the organisation of plant-frugivore interaction networks, and networks weighted for seed dispersal distances. Our analysis indicates that when considering dispersal distances, plant-frugivore networks are characterised by the presence of groups of highly interacting species, indicating seed dispersal services are dependent on the connectivity of species and variable importance of different seed dispersers at different distances

Symbionts as hidden actors in ecological communities

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Microbial symbionts are ubiquitous components of ecological systems, but their functions are rarely integrated into the analysis of ecological networks. Insects, in particular, have developed highly specialised relationships with microbial partners—including obligate and facultative endosymbionts—that can profoundly alter the physiology, behaviour, and ecological interactions of the host. These symbiont-mediated effects can propagate through ecosystems, modifying the intensity, direction, or even existence of interactions between macroorganisms.

We argue that ecological network theory provides a powerful framework for capturing and quantifying the hidden influence of symbionts on community structure and dynamics. Symbionts can be modelled either as explicit nodes within host–symbiont–environment networks or as functional traits of host nodes, depending on the ecological question and system. This approach allows for the application of tools such as indirect interaction analysis, community detection, stochastic coextinction simulations, and multilayer network models to assess effects at the system level.

By integrating these network tools with empirical data, we can uncover how symbionts affect properties such as clustering, stability, and robustness in host communities—insights that remain inaccessible using standard observational or experimental techniques. Incorporating symbionts into network models thus not only reveals their ecological importance, but also opens the door to a deeper, mechanistic understanding of community functioning under both natural and disturbed conditions.

Exploring plant–root-associated fungal interactions across small islands from tropical and temperate archipelagos

Marta Correia[1], Susana Rodríguez-Echeverría[2], José Antonio Morillo[3], Sandra Hervías-Parejo[1], Ruben Heleno[2], Manuel Nogales[4], Anna Traveset[1].*

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Rhizosphere fungi are essential for plant survival and ecosystem functioning, yet the processes shaping plant–fungal association networks remain poorly understood. In this study, we examine plant–fungal networks across five small islands from distinct archipelagos, two in the tropical zona and three in the temperate zona, overing ~150 plant species and three main root-associated fungal groups: mycorrhizal, saprotrophic, and pathogenic fungi. These islands vary in climate, size, origin (oceanic and continental), offering a valuable framework to investigate plant–fungal interactions. Root-associated fungal communities are known to be influenced by soil nitrogen, mean annual precipitation, and plant diversity. Accordingly, we hypothesize that biotic factors—such as plant diversity and phylogeny—and abiotic characteristics will shape the structure of plant–fungal networks, particularly in terms of specialization and modularity. Our results reveal clear differences among fungal guilds in their interactions with plants. Saprotrophic fungi emerge as the most diverse group and dominate network interactions, underscoring their central role in driving overall network complexity. Although less diverse, pathogenic fungi exhibit the highest connectivity with plants, suggesting generalist and opportunistic strategies. Mycorrhizal fungi interact with a wide range of plants but form fewer connections per fungal taxon, reflecting more specialized roles within the networks. We further explored plant–fungal interactions at the island level to assess how network structure varies with island characteristics. Preliminary results indicate that plant–fungi networks differ markedly across islands. Some islands (e.g., Na Redona, Balearic Islands) exhibit higher specialization and modularity, while others (e.g., Daphne, Galápagos) display more generalist and nested interaction patterns. These differences suggest that local environmental conditions and the composition of fungal functional groups are key drivers of network architecture. Together, these preliminary findings offer promising insights into the mechanisms shaping plant–fungal interactions and their potential role in sustaining biodiversity

under global change.

Friend, Foe or Freeloader: Using molecular methods and community science to investigate the ecological outcomes of a potential arachnid-plant commensalism

Rosy Christopher[*1], *Beatrice Dale*[2], *Dr Fredric Windsor*[3], *Dr Darren Evans*[1], *and Dr Jordan Cuff*[1]

[1]*Newcastle University,* [2]*Northumbria University, and* [3]*Cardiff University, *presenting author*

Non-trophic interactions contribute significantly to ecosystem functioning and may be positive, neutral or negative for either of the interacting parties. Commensalisms are interactions in which one party, the commensal, is benefiting from the interaction, and the other party, the host, is neutrally affected. Despite significantly impacting ecosystem functioning and service provision, commensalisms are scarcely incorporated into wider studies of ecological networks. Flower crab spiders (*Misumena vatia*) use flower heads as platforms from which to predate flower visitors attracted by the rewards offered by the flower. We can predict the outcome to the flower visitor, but how does this impact the flower, if at all?

Using a combination of spider dietary metabarcoding to detect trophic interactions, surface eDNA from flowers to detect recent visitors and nectar macronutrient analysis to determine nutrient provision, ecological and nutritional networks will be constructed. Alongside community science data and public records of spider-flower-prey interactions, we are investigating the nature, diversity and drivers of the potentially commensal interactions between flower crab spiders and their flowers, and the implications of and for their prey. Using this model system, we will determine the ecological outcomes of commensalisms, approaches for their integration into wider ecological networks and their implications for ecosystem service provision.

The environmental dependence of ecological interaction networks

Bastien Parisy[1], *Alyssa R. Cirtwill*[2,] *and Tomas Roslin*[*1,3]

[1]*University of Helsinki, Finland,* [2] *Carex EcoLogics, Bracebridge, Canada,* [3]*Swedish University of Agricultural Sciences (SLU, Sweden), *presenting author*

Interactions between species are often assumed to occur whenever species pairs co-occur, allowing us to reconstruct local ecological networks from a deterministic “metaweb”. Thus, a species’ set of metaweb interactions defines its Eltonian niche – the biotic conditions under which it can exist. However, both species and interactions will also have Grinnellian niches, reflecting relationships between probability of occurrence and environmental conditions. We use a set of our empirically-characterized networks to show that both species and link occurrence are stochastic, with probabilities conditional on the environment. This insight improves our ability to model observed variation in network structures. We argue that future research should incorporate environmental impacts on both species and links, thus merging the Grinnellian and the Eltonian niche concept. At the same time, species co-occurrence should not be taken as a sufficient criterion for inferring a link, and work based on inferring local networks from species occurrence alone had better be abandoned.

Plant-pollinator interaction rewiring boosts community survival

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In an idealized world, species forming an ecological community would interact predictably. Theory suggests that the observed structures of these interaction networks can maximize the probability of survival. Unfortunately, the real world is more messy. Whether an interaction is realized within a set of plants and pollinators depends on multiple processes. Some obvious ones are the affinity of species to interact, but the probability of species encounter over space and time is also determinant. Such probability depends on the demographic responses of species to the environment, their environmental constraints (e.g. phenological overlap), and animals' ability to choose with whom to interact to maximize their fitness. Indeed, although these factors produce considerable year-to-year changes in species interactions within plant-pollinator communities, their consequences for the community persistence are unknown, making unclear if this interaction turnover is a driver or a passenger of inter-annual changes in species populations. Here, we characterize year-to-year variation in plant-pollinator interactions using a unique dataset of 8 years on 12 sites and assess for each community their structural stability, a robust theoretical measure describing species persistence. We show that interaction rewiring within the species core consistently boosts community survival compared to random rewiring scenarios. Shifts in population abundances and phenological activities of the core species emerge as critical drivers of this process. While observed networks are not fully optimized, the observed adaptive rewiring enhances species persistence, buffering plant-pollinator networks against environmental challenges.

Poster session 2: Thursday 4th Sep 12.30-14:00

Effects of Natural Vegetation Cover and Fragmentation on Host-parasite Eco-evolutionary Dynamics

Ana Paula L. Costa[1], Klementyna Gawecka[2,3], Paulo Sérgio D'Andrea[1], Gisele R. Winck[1], Cecilia S. de Andreazzi[1,4]*

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The transformation of natural landscapes is a major driver of biodiversity loss and the degradation of ecosystem services, including disease regulation. Despite the evidence linking the loss and fragmentation of natural vegetation cover to an increased risk of zoonotic diseases, a comprehensive understanding of how these factors influence host-parasite eco-evolutionary dynamics remains lacking. From a spatial perspective, the coevolution of parasite infection traits and host defenses generates geographic mosaics in the strength of their interactions, which the landscape's configuration may shape. We investigate how different aspects of host-parasite eco-evolutionary dynamics respond to changes in landscape configuration, specifically in terms of the amount and fragmentation level of natural habitats. Specifically, we aimed to answer the following questions: (1) How does landscape configuration affect ecological and evolutionary outcomes? (2) What are the main drivers of the ecological and evolutionary outcomes? We fitted a metacommunity model with the coevolution of ecological networks, using a metanetwork of mammals, viruses, and bacteria recorded in the Atlantic Forest Biome as input. Host species recorded occurrence frequencies in natural areas were used as the probability of colonization and extinction in forest core, edge, and disturbed patches. We created 12 distinct landscapes, featuring three levels of fragmentation and four proportions of forest cover. The host-parasite metanetwork included 51 mammal species and 103 infectious agents. We measured the strength of the interactions, the ratio between the parasite's local degree and its regional network degree, local network structure, and beta diversity of interactions within and between landscapes. Our results show that landscapes with higher forest cover and a medium to low level of fragmentation have a more homogeneous interaction distribution over habitat types, which diminishes the effect of co-evolution. Whereas, highly degraded landscapes reduce the disease regulation service of core habitats, increasing the risk of zoonotic transmission and different coevolutionary trajectories in edge and disturbed

habitats. Overall, the fragmentation and the proportion of natural vegetation affect the persistence of parasitic species in the landscape, while the type of habitat influences the dynamics of interactions and coevolutionary processes.

Unfeasible expectations: Structural stability of uncertain networks

Chris Terry[*1]

*[1]University of Oxford, *presenting author*

A core goal of network ecology is to identify the emergent features that influence community assembly and disassembly in changing environments. Recently a family of structural stability approaches that determine the range of intrinsic growth rates compatible with system feasibility have been gaining popularity as a measure of how likely a community is able to persist in fluctuating conditions. These offer a theoretical basis for understanding and predicting the assembly and stability of complex multi-species communities from only interaction network structures. However, in this talk I will show that the high sensitivity feasibility calculations, coupled with empirical uncertainties inherent in estimated interactions, are likely to preclude the approach’s reliable application to empirical settings. Across four reanalyses of previous empirical demonstrations of the structural stability approach, more parsimonious explanations based on species-level connectance provide better explanations for observed patterns of community assembly or dynamic stability. Calculation of structural stability metrics therefore appears to lose, rather than synthesise, information embedded in empirical interaction networks. The relative success of simpler measures is good news for the purposes of scalable prediction using more easily gained information. More broadly, this highlights the value of multiple competing approaches in validation tests to demonstrate the value-added associated with new approaches and highlights ongoing critical questions for network ecology on how the field can close the gap between its ambition and fundamental limits of empirical precision.

Multi-trophic metacommunity responses to habitat fragmentation in the Brazilian Atlantic Forest

*Tiago Souto Martins Teixeira, Omar Khalilur Rahman, Alyssa R. Cirtwill, Kelly A Speer, David Hemprich-Bennett, Alexis Brown, Susan L. Perkins, Nancy B Simmons, Stephen J Rossiter, Ana ClÅLaudia Delciellos, Marcus V. Vieira, Elizabeth L. Clare**

**Department of Biology, York University, presenting author*

The structure of ecological communities is profoundly altered by anthropogenic disturbance to landscapes. However, most reported impacts rely on the quantification of diversity estimates for single trophic levels or impacts on key species of interest. In this analysis we integrate measures of community structure, comparisons of interaction networks and measures of β-diversity across four trophic levels: plants, bats, bat ectoparasites and bacteria within the ectoparasites. Our data show that bat, bat fly, and bacterial communities are significantly nested across forest fragments, with specialist consumers in all groups being found in fewer fragments than generalists. We found substantial β-diversity in both species richness and interaction richness across fragments but no decline in interaction redundancy with decreasing forest area, likely because even intact forest networks had very low redundancy in our dataset. Despite the loss of species and interactions, our data provide support for the conservation value of even the smallest and most disturbed forest patches where essential seed dispersal services are potentially maintained by Artibeus, Carollia and Sturnira and distinct sets of taxa and interactions are supported. These species may be key in the potential recovery of these habitats, but our data highlight the fragility of these communities which have contracted around these disturbance-tolerant species.

Assessing competition between honeybee and wild pollinators in urban allotments and parks

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Cities are important habitats for wild and managed pollinating insects. The increasing popularity of urban beekeeping has led to higher densities of Western Honeybee (Apis mellifera) colonies, prompting concerns about their competitive impacts on wild pollinator communities and the structure of plant–pollinator networks. Recent studies have investigated the potential for competition between honeybees and other wild pollinators in urban settings, but these have largely focused their analysis at group level or been limited to a single pollinator group (e.g. bees), without considering the entire pollinator community. In this study we collected plant-pollinator interaction data and quantified floral resources across urban parks and allotments gardens in Newcastle upon Tyne, UK. Using General Linear Mixed Models and linear regressions we explore the effects of honeybee colony density and honeybee abundance on wild pollinator species richness, abundance, diversity and also the role of honeybee abundance in shaping plant-pollinator networks and species?specific niche overlap (Müller index). Although we found no evidence for direct competitive effects of honeybees on the overall richness and abundance of wild pollinators, floral resource availability appears

to play an important mediating role, offering a wide range of forage opportunities for both honeybees and wild pollinators. At network level increased honeybee abundance was associated with a decrease in network connectance, interaction evenness and pollinator niche overlap. At the species level, honeybee abundance increased specie-specific niche overlap with wild pollinator species. To ensure the future coexistence between wild and managed pollinators we recommend the establishment of a national register of beehives in the UK to monitor and control local hive densities, in addition to greenspace management strategies that enhance floral resources in urban landscapes.

The structure of Amazonian fruit-frugivore interactions across hunting-induced defaunation gradients.

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Hunting-induced defaunation disproportionately impacts large-bodied species, driving downsizing shifts in vertebrate communities that favour smaller species. This imbalance triggers trophic cascades by restructuring plant-animal interactions and disrupting seed dispersal and predation rates. Large frugivore declines limit the dispersal of large-seeded trees, while small-seeded plants continue to be dispersed by non-hunted frugivores. However, a comprehensive assessment of how fruit-frugivore interactions shift along hunting pressure gradients remains lacking. To address this, we used canopy and ground camera traps to investigate the structural properties of plant-frugivore interaction assemblages in six forests across a defaunation gradient in Western Amazonia, Brazil. Between Nov 2022 and Feb 2025, we deployed over 300 camera traps, monitoring for more than 11,000 camera-days >200 individuals of five dominant animal-dispersed tree genera with diverse fruit and seed traits—from small- to large-seeded species (Euterpe spp., Pourouma spp., Virola spp., Iryanthera spp., and Pouteria spp.). Based on a 60% subset of >320,000 videos recorded, we constructed bipartite interaction networks, where nodes represent interaction partners and weighted links reflect fruit-feeding event frequencies. We assembled a metanetwork including all sampled fruiting trees across the gradient, and separate bipartite networks for overhunted, hunted, and non-hunted forests. We evaluated network metrics against null models to assess changes in overall network architecture and frugivore roles along the defaunation gradient. Preliminary results show that network structure and frugivore topological roles change significantly along the gradient. The metanetwork revealed a modular structure: two clusters of interactions between large-bodied frugivores and trees in non-hunted forests, and one cluster of medium- to small-sized frugivores and trees in hunted and overhunted forests. In non-hunted forests, large seed dispersers such as ateline monkeys and toucans were central hubs, whereas in hunted and overhunted forests, medium to small primates like capuchins and seed predators like saki monkeys assumed more central roles. In hyper-diverse tropical ecosystems, the loss of large frugivores results in a cryptic loss of ecological functions, with potentially pervasive long-term impacts on natural forest regeneration. Our study showcases how analyzing plant-frugivore interaction networks can provide early diagnostics of ecosystem functionality loss due to overhunting.

Network-based analysis of niche partitioning across trophic, spatial and temporal axes in neotropical primates

Laura Paltrinieri[1], Iago Ferreiro-Arias[2], Iván Ortiz[1], Brayan A. Cedeño-Panchez[1], Andrea Zampetti[3], Hugo D Díez-Santaolalla[1], Claudia Alfaro-Martínez[1], Carine Emer[4], Ana Benítez López[1]*

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Shedding Light on Solutions: Applying Network Ecology to Test How Streetlight Mitigation Measures Impact Lepidoptera Networks

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Light pollution, caused by artificial light at night (hereafter ALAN) is an emerging global threat, which is acting synergistically with global environmental change, to affect everything around us, including us (Longcore & Rich, 2004; Cupertino et al., 2022). Its rapid advancement is largely a result of technological developments, which allow for cheaper and more accessible lighting technologies (Yam & Hassan, 2005; Pimputkar et al., 2009). Further, an increase in urbanisation and thus demand for lighting (Gaston & Evans, 2010), has resulted in a 10% yearly increase in ALAN (Kyba et al., 2023). Recent switch to light-emitting diodes (LEDs), characteristic of broad-spectrum of wavelengths with a blue peak, have disrupted the temporal and spatial dynamics of ecosystems. Yet, LEDs can be modified, and evidence suggests that these modifications can alleviate the negative impacts of ALAN (Evans, 2023). The most common mitigation measures include changing light colour (CCT), shielding, part-night lighting, adaptive lighting and dimming, but despite the array of mitigations suggested, we lack concrete evidence to support how these mitigations impact ecosystem services and ecological networks.

Whilst a variety of taxa are affected by ALAN, this work focuses on the ubiquitous pollinators and prey food, Lepidoptera (moths). We use a variety of direct sampling methods, and new molecular technologies, to understand how street light mitigation measures impact moth ecological networks. We focus on testing the effects of ALAN mitigations through the lifecycle of the moths, to understand how the network responses change, across flower-visitor and egg-laying networks for adult Lepidoptera to host-parasite networks for the larval stages. This will allow us to assess if there is an "optimal" light pollution mitigation strategy.

On the structure of species-function participation in multilayer ecological networks

Mar Cuevas-Blanco[1], Sandra Hervıas-Parejo[2,3], Lucas Lacasa[1], Anna Traveset[2], Isabel Donoso[2, 4, 5], Ruben Heleno[3], Manuel Nogales[6], Susana Rodrıguez-Echeverrıa[3], Carlos J.*

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It is currently a priority in ecology to unravel how biotic interactions shape ecosystems and influence their functioning, resilience, and biodiversity, especially as climate change heightens environmental challenges. Traditional methods often depict ecosystems as networks of species interacting via a specific biotic interaction (e.g., pollination), thus overlooking both the combined effects of multiple functions and the resulting species–function patterns. Indeed, ecosystems are inherently multidimensional; for example, bees not only pollinate but also facilitate seed dispersal, demonstrating how one species can assume various ecological roles. Hence, to fully capture ecosystem diversity, it is crucial to move from considering a species' singular role (unifunctionality) to its multifaceted roles (multifunctionality). Here, we introduce a framework for standardizing data and its analysis that integrates multiple biotic interaction types into a single model. Alternatively to the traditional ecosystem representations, we focus on how entangled species and functions are by building 'species–function' networks. This new perspective enables quantification of the importance of (i) species and (ii) functions, ultimately identifying key actors with disproportionately important roles for community functioning, among other important ecological questions. As a case study, we apply our framework to the small island community of Na Redona in the Balearic Islands For this, we use recently collected data on species interacting via six different ecological functions, reporting 1,537 interactions. Our analysis reveals a non-random, nested structure in the way plants and functions interact, indicating that both species and functions play heterogeneous and dual roles participating into each other in a non-random way. Woody shrubs and fungal decomposition emerge as key actors whose removal triggers larger-than-random cascading of secondary extinctions. The emergent species–function duality enables a deeper quantification of ecosystem complexity and refines assessment of the impact that multifunctionality plays on ecosystems. Keystone species and functions, a new concept we introduce, emerge as two interconnected sides of the same coin, showing that disruptions in either species or functional interactions can disproportionately undermine ecosystem stability. These insights are instrumental for guiding conservation

efforts and preserving ecosystems in the face of ongoing environmental challenges.

A network-based protocol for monitoring beneficial arthropods in agroecosystems

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Network analysis offers a powerful framework for exploring the organization and functioning of ecological communities, especially in intensively managed systems. Here, we extend co-occurrence approaches into a co-abundance network framework to identify key functional components of agricultural arthropod assemblages.

Our study is based on a large-scale field experiment conducted in the Rolling Pampas of Argentina, one of the most productive agricultural regions globally and a landscape in urgent need of biodiversity-friendly practices. Across three years and twelve crop fields under a soybean–maize–wheat rotation, we collected approximately 1,500 samples and recorded over 750,000 arthropods using Malaise trapping. Each field contained a flower strip and a conventional margin treatment, allowing direct comparison of margin effects. Arthropods were classified into 70 functional groups, including pollinators, predators, parasitoids, and pest species.

We constructed co-abundance correlation networks for each treatment to explore the structure of inter-group associations. Network modularity and the identity of module hubs were used to identify cohesive groupings and organizational keystone groups. Within each module, we proposed candidate indicators based on a combined criterion of centrality and practical ease of field sampling.

This approach illustrates how network science can guide the design of monitoring protocols tailored to complex, multispecies assemblages. By targeting abundant, functionally informative taxa, it offers a scalable tool for tracking biodiversity and ecosystem service providers in agroecosystems.

Physiological and Environmental Factors Predict Protozoan Infection Profiles in Rats

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Heterogeneity in parasite infection is a key feature of host-parasite systems, with implications for transmission dynamics, persistence, and zoonotic spillover. Yet, understanding the physiological and environmental factors shaping individual-level infection patterns remains a major challenge. In this study, we used an integrative network and machine learning framework to detect and predict protozoan infection profiles in a wild population of black rats (Rattus rattus) from northeastern Madagascar, a region where rats are known zoonotic reservoirs. We sampled 841 individual rats across environmental gradients in land use and habitat disturbance, and identified 41 protozoan OTUs from fecal samples. We constructed a bipartite network of hosts and parasites and applied stochastic block modeling (SBM) to detect latent infection profiles—groups of rats and protozoa with similar interaction patterns. This revealed three distinct host infection profiles and eight protozoan profiles, varying in parasite richness and specificity. To investigate the mechanisms underlying profile assignment, we quantified a suite of physiological and environmental variables for each rat. We then trained an XGBoost multi-class classification model to predict host infection profiles from these features, and interpreted model predictions using SHAP (SHapley Additive exPlanations) values. The model exhibited strong predictive performance, consistently outperforming random classifiers across multiple evaluation metrics. SHAP analysis revealed that physiological traits, particularly body mass and gut microbiome composition (notably Prevotellaceae and Lachnospiraceae relative abundances), were stronger predictors of infection profiles than environmental variables. However, environmental features such as non-native species density and vegetation structure also contributed meaningfully to predictions. These results demonstrate that structured infection profiles emerge in host-parasite networks and are shaped by a combination of intrinsic host traits and extrinsic environmental conditions. Our findings highlight the importance of integrating ecological context with host physiology to understand infection heterogeneity in wildlife. Our analytical framework provides a scalable approach for predicting infection risk, identifying functionally distinct host groups, and informing surveillance of zoonotic reservoirs.

Intraguild interactions structure a community of invasive ants: a holistic ecological approach including hypergraphs

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Invasive species can severely impact biodiversity, yet interactions among ecologically similar invaders remain poorly understood. Intraguild interactions—competition and predation among species occupying similar niches—are well known to structure native communities, but their role in invaded ecosystems is underexplored. Here, we investigate intraguild interactions in an assemblage of 18 non-native ant species on a small Indian Ocean islet. Our approach integrates multiple ecological methods, anchored by a novel hypergraph framework that quantifies competitive structures beyond pairwise links.

Using dietary metabarcoding of 755 ant individuals from 12 species, we found that approximately half of all prey detections involved ant-ant predation. This frequency varied substantially between species, from 80% in Monomorium floricola to 30% in Technomyrmex vitiensis. Null model analyses revealed that ants preferentially consumed each other over native arthropods once the superabundant Pheidole megacephala was excluded. Co-occurrence patterns and baiting experiments further indicated that competitive interactions influence spatial resource partitioning. Our hypergraph model highlighted P. megacephala as a structural keystone: despite its abundance, it was consumed less often than expected and was consistently avoided spatially by other species, while simultaneously competing for food resources with much of the community.

We found that 35.4% of food items were contested by two or more species simultaneously, suggesting pervasive exploitation competition. The hypergraph approach allowed us to capture these higher-order, multi-species competitive structures, revealing that both predation and competition operate concurrently across the community.

Our results demonstrate that intraguild interactions—predation and competition alike—are central to structuring invaded ant communities. By combining network ecology with behavioural experiments, metabarcoding, and null modelling, this study highlights the

value of a holistic, systems-level approach to understanding invasion ecology in multi-invader contexts.

Eight-legged Random Walks: Host-tick contact networks, Markov chains, and their application to tick-borne disease

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Tick-borne diseases represent a significant and growing global health challenge, yet the spatial dynamics of tick vectors within host populations remains poorly understood due to sampling and tracking difficulties in natural settings. To address this, we constructed host-tick interaction networks using high-resolution GPS tracking data from free-roaming domestic dog populations across multiple continents. These networks capture host spatial overlap and contact patterns that facilitate tick dispersal. Using stochastic simulations of tick movement and pathogen transmission on these networks, we identify spatial hotspots and key host behaviors driving disease risk. Our results reveal critical nodes and temporal windows that disproportionately contribute to vector spread, providing actionable targets for surveillance and control interventions. This integrative approach offers a novel framework to elucidate vector ecology and inform management of tick-borne diseases in diverse ecological contexts.

Specialized African Ant-following Birds Play Central Roles in Flocks at Dorylus Driver Ant Swarms

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Across the tropics, ant-following birds—those that forage on arthropods flushed by swarm raiding army ants—have been identified as one of the most vulnerable avian guilds to anthropogenic forest disturbance. Despite capturing the attention of naturalists for over a century, research on ant-followers has focused almost entirely on Neotropical species, which track nomadic Eciton army ant colonies through complex cognitive and behavioral adaptations. In Africa, over 150 species have been documented foraging at army ant swarms, but virtually nothing is known of their behavioral ecology or their specialization on Dorylus army ants. Understanding the convergent evolution of behavioral adaptations between these distant, largely unrelated bird species, and the ants they follow, could be the key to unlocking the mechanism behind global patterns of decline in disturbed tropical forests. In Equatorial Guinea, we explored the behavioral adaptations of African ant-following birds, building ecological networks of observed mixed-species flocks at driver ant swarms to identify important species and their role in flocks. Species showed high variation in swarm attendance rates, with eight species identified as putative specialists and occupying central positions in the network. Network centrality in species was strongly correlated with two key behavioral adaptations seen in the most obligate Neotropical ant-following birds, namely bivouac-checking and social information use. Furthermore, the simulated removal of central species from flock networks led to network dissolution, indicating these species were critical for facilitating interactions between flock members. The loss of central species from ant-following bird flocks in disturbed forests could have devastating consequences for birds' abilities to find and form flocks around Dorylus driver ant swarms. These findings highlight a long-overlooked and rapidly declining avian guild, providing critical context necessary for understanding their sensitivity to disturbance.

Learning the Few that Matter: Active Link Prediction for Ecological Network Recovery

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Reconstructing predator-prey networks from limited observations is crucial for understanding ecosystem dynamics and guiding biodiversity monitoring. In this study, we propose an active learning-based link prediction framework to efficiently infer trophic interactions using minimal training data. We evaluate our approach on the Hengill dataset, which includes food webs from 14 stream ecosystems across a natural temperature gradient in Iceland.

By defining core species as those frequently observed across temperature sites, and treating infrequent ones as non-core, we guide active sampling to prioritize species pairs that maximize information gain. Our graph neural network model, trained on only 2,000 strategically selected interactions, successfully recovers over 12,000 predator-prey links with AUC > 0.99 and few false positives. Notably, the selected training set consistently includes all core species and a minimal subset of non-core species.

These results demonstrate that complete food webs can be accurately reconstructed without exhaustive sampling. Our method provides a practical tool for identifying the

smallest effective species subset needed for network recovery, offering new insights into the design of ecological surveys and the structural resilience of food webs under environmental gradients.

Network Position Mediates Species Extinction Risk from Chemical Pollution: A Food Web Modeling Approach

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Chemical pollution is a major driver of biodiversity loss and is projected to triple in the next 3 decades. Traditionally, laboratory measures of pollutant sensitivity for each species in isolation have been employed to estimate how chemical pollution affects biodiversity. However, this approach ignores biotic interactions that couple populations and therefore performs poorly when predicting extinctions in nature. To solve this, we employed simulated food web networks to assess the importance of biotic interactions in modulating chemically-driven extinction. Specifically, we exposed 200 food webs of varying complexity to 140 different concentrations of a hypothetical pollutant. Models including food web traits predicted extinction 25% better than models that only included species' pollutant sensitivity alone. We find that the combination of network parameters, describing trophic level, generality and eigencentrality, with individual pollutant sensitivity can boost the predictions of pollutant effects substantially. Our findings offer a novel framework for understanding and predicting the risk profiles of chemical pollutants in nature.

The Robustness of Temporal Ecological Network

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Species phenology is a key ingredient in determining the structure of ecological networks. Since a species can only interact during its active period (e.g. flowering period), this structure can vary greatly throughout the year. Despite this, many models regard networks as static, aggregating interactions over time. Here we develop a temporal network model of plant-pollinator interactions, and introduce temporal robustness as a metric of pollinator robustness to plant extinctions. Using results from random geometric graph theory, we obtain analytical expressions for the temporal robustness of these model networks, and show how this differs from the robustness of static (time-aggregated) networks. We find that, in contrast to static networks, temporal networks are more robust when the active periods of its pollinators are longer and those of its plants are shorter. This result is obscured when interactions are time-aggregated, suggesting that pollinators which are active over long time periods may be more vulnerable to species loss than predicted by non-temporal network models.

From Ashes to Ecosystems: Recovery of Plant–Animal Networks After Wildfire

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Wildfire is an important driver of ecological diversity and functioning in many ecosystems, however there is growing concern that changing climate and land management strategies are driving more frequent and severe fires. Whilst recovery from fire is well documented in certain ecosystems, responses tend to focus on certain species or habitats, with impacts on species interactions often overlooked. As a result, the effects of changing wildfire disturbance and the resilience of many ecosystems to it are poorly understood. This research aims to address this knowledge gap by investigating the direct and indirect impacts of a recent major (>2000 hectare) wildfire in Ireland’s Killarney National Park on several levels of ecological assemblage. By using a paired burnt-unburnt site design and ecological network theory we investigate the wildfire’s impacts on a mixed temperate heathland across three levels of trophic functioning. 1) Floral diversity and nectar resource availability. 2) Responses of plant-pollinator networks. 3) Composition of bird communities. By utilising a network approach, we connect biodiversity and species interactions, to support informed fire management in Ireland’s oldest National Park and advance understanding of increasing wildfire impacts in temperate heathlands.

Examining above and below ground interactions in managed urban grasslands using a network approach

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In cities, grassland management (particularly mowing frequency) plays a central role in shaping ecological communities and their interactions above and below ground. Intensive mowing remains widespread in urban grasslands, due to recreational use or aesthetic preferences, however this can impact plant diversity, alter soil conditions, and deplete pollinator habitats.

Efforts to improve urban grassland management for biodiversity are increasing, with campaigns such as No Mow May and wildflower planting initiatives. However, these strategies are often implemented in isolation, at limited scale, and without clear evidence that they benefit the entire grassland ecosystem. While reduced mowing can benefit both above and below ground communities, studies typically examine these in isolation. A key knowledge gap remains in understanding how management-induced changes cascade across the entire grassland ecosystem, particularly soil-plant-pollinator ecological networks. As a result, no single management strategy has yet been shown to support biodiversity and ecological function across multiple trophic levels. This project will assess how grassland management influences ecological structure and function across trophic levels using a network approach. We aim to use multi-layer ecological networks to integrate plant-pollinator interactions with soil data. By linking above and below ground components, the research will explore how mowing frequency and alternative management strategies affect the resilience and connectivity of soil-plant-pollinator networks. The goal is to identify management approaches that support biodiversity across multiple ecological levels, providing evidence to inform better practices in urban greenspace management.

In my first field season, I am collecting data across five Newcastle parks under varying management regimes in collaboration with Newcastle City Council, Wild Intrigue and the Ouseburn Trust to examine relationships between soil properties and above ground networks. Sampling transects represent six management types: standard mowing, reduced mowing, uncut areas, scythed plots, sown wildflower patches, and disused bowling greens. Data collected above ground comprise plant-pollinator interactions, floral abundance. Soil measurements include bulk density, temperature, percentage moisture, and other chemical properties.

Future work will explore below ground communities to integrate into multi-layer networks. I will also explore how floral reward provision can mediate links between soil and pollinators and whether alternative strategies can better support ecosystem-level biodiversity.

Cross-feeding networks create tipping points in microbiome diversity

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How the extraordinary diversity of microbiomes emerges from the interactions between individual populations is a important unanswered question in microbial ecology. Key to this process are the cross-feeding networks that structure these systems in which populations release metabolic by-products into the environment for other members of the community to use. Understanding how cross-feeding contributes to coexistence presents a major challenge due to the complex structure of cross-feeding networks and the interdependencies they create between populations. In this work we address this problem by using the tools of network science to develop and analyse a structural model of microbial community cross-feeding. Our model represents the community as a bipartite- or hypergraph in which consumers and resources are linked by the consumption and secretion of metabolites. We consider feasible community states by introducing simple rules that determine the presence of consumers and resources. Using percolation theory and the generating function formalism we derive expressions for the realised diversity of consumers and metabolites in cross-feeding networks with arbitrary degree distributions. We apply our model to random networks where we find tipping points at which community diversity abruptly changes in response to changes in network structure. These points correspond to discontinuous percolation transitions and occur due to the collapse and reassembly of the active cross-feeding network. We also consider how robust these cross-feeding networks are to attack, deriving expressions for the state of the community following the removal of consumers and resources from the system.

EcoMIR: Reconstructing Indirect Dependencies in Ecological Networks

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In the face of accelerating Global Environmental Change, unraveling the full complexity of ecological networks is more important than ever. Traditional approaches—anchored in pairwise interactions—miss many of the indirect and multi-species dependencies that shape ecosystem stability under stress.

To address this gap, we introduce Multi-Node Interaction Reconstruction (MIR), a model-free framework that infers and quantifies indirected and higher-order dependencies directly from time-series data of continuous-state, nonlinear dynamical systems. Rather than relying on predefined coupling functions or invertible embeddings, MIR exploits the way statistical scales with the inclusion of additional variables to determine both the order and strength of interactions.

We benchmark MIR on synthetic networks designed with known three- and four-species couplings, demonstrating near-perfect recovery of the true interaction topology—even when observations are noisy or coupling strengths are weak. By revealing complex, multi-species feedbacks that escape pairwise analyses, MIR offers a more nuanced lens on ecological architecture and a powerful predictive tool for assessing how communities respond to environmental perturbations.

This framework paves the way for deeper insights into ecosystem resilience and provides a flexible platform for mapping intricate interaction webs in any data-rich, nonlinear system.

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