



**E**cological Networks and Molecular Analysis  
of Trophic Interactions

11-15 September 2017, Uppsala, Sweden

# Abstract Book

MONDAY		TUESDAY		WEDNESDAY		THURSDAY		FRIDAY	
Web structure versus functioning: a new understanding		Reconstructing food web structure and dynamics		Dissecting trophic interactions by molecular techniques		New findings achieved through molecular dissection		Applied trophic interactions	
8:45-9:00	Welcome	8:55-9:00	House keeping	8:55-9:00	House keeping	8:55-9:00	House keeping	8:55-9:00	House keeping
9:00-10:00	Dominic Gravel	9:00-10:00	Vojtech Novotny	9:00-10:00	Tom Gilbert	9:00-9:20	Rosemary Moorhouse-Gann	9:00-10:00	Tara Gariepy
10:00-10:30	COFFEE	10:00-10:30	COFFEE	10:00-10:30	COFFEE	9:20-9:40	Emilia Hannula	10:00-10:30	COFFEE
10:30-11:30	Jennifer Dunne	10:30-11:30	Jane Memmott	10:30-10:50	WORKSHOP	9:40-10:00	Vanessa Mata	10:30-10:50	Sarah Wolf
11:30-11:50	Anna Eklöf	11:30-11:50	Talya Hackett	10:50-11:10	WORKSHOP	10:00-10:30	COFFEE	10:50-11:10	Oskar Rubbmark
11:50-12:10	Alyssa Cirtwill	11:50-12:10	Jörg Albrecht	11:10-11:30	WORKSHOP	10:30-10:50	Joris Cromsigt	11:10-11:30	Blas Lavandero
12:10-13:30	LUNCH	12:10-13:30	LUNCH	11:30-11:50	WORKSHOP	10:50-11:10	Sabuj Bhattacharyy	11:30-11:50	Mary Gardiner
13:30-14:30	Ulrich Brose	13:30-14:30	Anna Gärdmark	11:50-12:10	WORKSHOP	11:10-11:30	Deborah Dawson	11:50-12:10	Lolita Ammann
14:30-14:50	Vincent Miele	14:30-14:50	Brendan McKie	12:10-13:30	LUNCH	11:30-11:50	Amair Esnaola Illarreta	12:10-13:30	LUNCH
14:50-15:10	Alireza Tamaddoni-Nezhad	14:50-15:10	Harriet Downey	13:30-14:30	Sara Hallin	11:50-12:10	Julia Tiede	13:30-14:30	Elizabeth Clare
15:10-15:40	COFFEE	15:10-15:40	COFFEE	14:30-14:50	Cancelled	12:10-13:30	LUNCH	14:30-14:50	Marc E. Frischer
15:40-16:00	Christopher Terry James	15:40-16:00	Carol Frost	14:50-15:10	Omar Khalilur Rahman	13:30-14:30	Bruce Deagle	14:50-15:10	Hernani F. M. de Oliveira
16:00-16:20	Miranda Bane	16:00-16:20	Riccardo Bommarco	15:10-15:40	COFFEE	14:30-14:50	Juan Pedro González-Varo	15:10-15:40	COFFEE
16:20-16:40	Daniel Montoya	16:20-16:40	Kate Pereira Maia	15:40-16:00	David Bohan	14:50-15:10	Peter Hambäck	15:40-16:00	Helen Hipperson
16:40-17:00	Ignasi Bartomeus	16:40-17:00	Colin Fontaine	16:00-16:20	David Hemprich-Bennett	15:10-15:40	COFFEE	16:00-16:20	Bastian Egeter
		17:00-20:00	POSTER SESSION starting with flash talks	16:20-16:40	Sara Zamora-Terol	15:40-16:00	Jan Hrcek	16:20-16:40	Marco Benucci
				16:40-17:00	Josep Pinol	16:00-16:20	James Kitson		
				19:00-24:00	CONFERENCE DINNER	16:20-16:40	Rosie Drinkwater		
						16:40-17:00	Tina L. Walters		
						17:00-20:00	POSTER SESSION starting with flash talks		

Dear Reader,

Welcome to the 3rd Symposium on Ecological Networks and 3rd Symposium on Molecular Analysis of Trophic Interactions, arranged back to back in Uppsala from 11 to 15 September, 2017. On the next few pages, you will find the abstracts contributed to our joint meeting. In preparing this booklet, we have done our utmost to make the material easily accessible to you. If you are looking for a specific contribution, you can

1. consult the programme-at-a-glance, found at the start of this booklet.
2. browse the contributions by symposium and theme, arranged as separate sections in this booklet. Within themes, contributions are split by format into plenary talks, oral presentations and posters, consecutively. Within these formats, contributions are sorted alphabetically by first author.
3. use the author index at the end of this booklet to search by author surname. The theme and format are identified in the page header. For each oral presentation, the presentation time can be found on the right of the page.

Posters will be on display for the full time of the respective symposium. Posters contributed to the symposium on Ecological Networks will be presented on Tuesday evening. They will be put up as soon as the presenter arrives and taken down by the end of the poster session on Tuesday. Posters contributed to the symposium on Molecular Analysis of Trophic Interactions will be presented on Thursday evening. They will be put up on Wednesday morning and taken when the symposium closes on Friday. Poster stands will be numbered according to an index found in the poster hall (which is next to the lecture hall).

We wish you an exciting week in Uppsala, and look forward to welcoming you all!

Tomas Roslin, Mattias Jonsson & Michael Traugott

# Contents

Preface . . . . .	1
<b>Ecological Networks</b>	<b>3</b>
<b>Ecological Networks: Empirical work</b>	<b>4</b>
Plenaries . . . . .	5
Oral presentations . . . . .	8
Posters . . . . .	22
<b>Ecological Networks: Network theory</b>	<b>60</b>
Plenaries . . . . .	61
Oral presentations . . . . .	64
Posters . . . . .	70
<b>Molecular Analysis of Trophic Interactions</b>	<b>78</b>
<b>MATI: Applied trophic interactions</b>	<b>80</b>
Plenaries . . . . .	81
Oral presentations . . . . .	83
Posters . . . . .	97
<b>MATI: Empirical dissection of ecol. interact.</b>	<b>114</b>
Plenaries . . . . .	115
Oral presentations . . . . .	117
Posters . . . . .	122
<b>MATI: Methods development</b>	<b>135</b>
Plenaries . . . . .	136
Oral presentations . . . . .	137
Posters . . . . .	143

# Ecological Networks

# Ecological Networks: Empirical work

## Individual variation in trophic interactions shape natural communities

Tuesday  
13:30

*Anna Gårdmark*<sup>1</sup>

<sup>1</sup>*Swedish University of Agricultural Sciences, Department of Aquatic resources, Öregrund, Sweden*

Trophic interactions vary with body size in most animals, and therefore also among individuals within populations. Together with food-dependent body growth, this diversity of interactions and interaction strengths results in feedbacks that govern animal community dynamics. Size-dependent interactions and variation in individual body size (due to energy-dependent body growth) have proven to be fundamental drivers of fish community dynamics. However, their importance in natural food-webs has primarily been demonstrated in closed, often small-scale systems such as lakes, subject to experimental or accidental manipulations.

In this talk I will explain how theory on size-structured community dynamics can guide analyses of observation data to identify (i) size-dependent trophic interactions, (ii) size- and food-dependent individual performance, (iii) size- and food-dependent community dynamics, and (iv) mechanisms that may uphold alternative stable states in food-webs, all in large open systems. The analyzed examples address the interactions between predatory fish in the Baltic Sea, their main fish prey at intermediate trophic levels, and partly shared invertebrate prey lower in the food-web. Combined analyses of dynamic models of these core food-webs, of data on the performance of predator individuals (such as growth and fecundity) and information on prey availability, as well as of time series of population sizes reveal that individual variation in trophic interactions, arising through size- and energy-dependence, are highly important for fish community dynamics also in open, exploited, food-webs, such as the Baltic Sea. Addressing variation in individual performance and in interactions, as well as population dynamics across trophic levels, through dynamic food-web modelling combined with natural observational data can resolve mechanisms underlying food-web dynamics in natural systems, impossible to manipulate experimentally.

**Ecological networks – past, present and future**Tuesday  
10:30*Jane Memmott*<sup>1</sup><sup>1</sup>*School of Biological Sciences, University of Bristol, UK*

This talk will introduce a series of big questions in ecology which can be answered using an ecological network level approach. These will include the impact of alien species and agriculture on communities, predicting and testing the impact of species loss on communities and developing food web measures of conservation success. The projects collect data on a wide range of species including plants, pollinators, herbivores, parasitoids, birds and mammals from field sites around the world. Early work and ongoing work will be presented along with thoughts on what projects lie ahead.



## Empirical study of complex food webs in tropical forests using experiments

Tuesday  
9:00

*Vojtech Novotny*<sup>1</sup>

<sup>1</sup>*Biology Center, Czech Academy of Sciences, Ceske Budejovice, Czech Republic*

Local food webs in tropical forests may comprise as many as 100,000 distinct inter-specific trophic interactions. Unsurprisingly, none of the existing webs has been thoroughly documented. Here we review approaches to food web inventory and argue that manipulative experiments on food webs represent the most promising approach to their study. The manipulation, both insertion and exclusion, of resources and consumers offer opportunities to reveal the dynamics of food web assembly and resilience to changing environmental conditions and disturbance. We provide examples of such manipulations for plants, herbivores, parasitoids and predators in the forests of New Guinea and discuss the lessons learned, in particular in the framework of the bottom-up versus top-down control of individual trophic levels, as well as the future directions of food web research.

## Correlated loss of ecosystem services in coupled mutualistic networks

Tuesday  
11:50

*Jörg Albrecht<sup>1</sup>, Dana G. Berens<sup>1</sup>, Bogdan Jaroszewicz<sup>2</sup>, Nuria Selva<sup>3</sup>, Roland Brandt<sup>4</sup>, Nina Farwig<sup>1</sup>*

<sup>1</sup> *Department of Ecology—Conservation Ecology, Faculty of Biology, Philipps-University Marburg, Marburg, Germany,* <sup>2</sup> *Białowieża Geobotanical Station, Faculty of Biology, University of Warsaw, Białowieża, Poland,* <sup>3</sup> *Institute of Nature Conservation, Polish Academy of Sciences, Krakow, Poland,* <sup>4</sup> *Department of Ecology - Animal Ecology, Faculty of Biology, Philipps-University Marburg, Marburg, Germany.*

Networks of species interactions promote biodiversity and provide important ecosystem services. These networks have traditionally been studied in isolation, but species are commonly involved in multiple, diverse types of interaction. Therefore, whether different types of species interaction networks coupled through shared species show idiosyncratic or correlated responses to habitat degradation is unresolved. Here we study the collective response of coupled mutualistic networks of plants and their pollinators and seed dispersers to the degradation of Europe's last relict of old-growth lowland forest (Białowieża, Poland). We show that logging of old-growth forests has correlated effects on the number of partners and interactions of plants in both mutualisms, and that these effects are mediated by shifts in plant densities on logged sites. These results suggest bottom-up-controlled effects of habitat degradation on plant–animal mutualistic networks, and predict that the conversion of primary old-growth forests to secondary habitats may cause a parallel loss of multiple animal-mediated ecosystem services.

## Enough is enough: How to sample plant-pollinator networks to make relative comparisons

Monday  
16:40

*Ignasi Bartomeus*<sup>1</sup>

<sup>1</sup> *EBD-CSIC, Sevilla, Spain*

Characterizing complex networks on interacting species is challenging. Two major stumbling blocks are a) correctly identifying species identity and b) having a sufficient sampling size for detecting all occurring links. A revision of recently published plant-pollinator networks shows that most published networks group several species into morphospecies or even work at the genus level. In addition, when evaluated, sampling completeness is never reached. This has clear implications for describing the network structure, but it is unknown how it affects relative comparisons among networks. Ecologists are often more interested in the relative comparison among communities with contrasting environments or treatments rather than in the absolute values. When two networks are sampled using the same methods, low taxonomic resolution and limited sampling effort may not change its relative comparison, but this has never been tested empirically. I use an intensive sampling of 16 fully resolved plant-pollinator networks across an environmental gradient to compare if the relative ranking of the main network properties changes when increasing taxonomic resolution (from morphospecies to species) and sampling effort. Then, I tested to which degree recently developed techniques for predicting missing links enhance the relative comparisons of poorly sampled networks. Determining which methods and indexes are robust to relative comparisons is needed in order to empirically test for pressing environmental changes that interacting communities are facing.

## Food web ecology can inform biodiversity-ecosystem functioning relationships

Tuesday  
16:00

*Riccardo Bommarco*<sup>1</sup>

<sup>1</sup> *Swedish University of Agricultural Sciences, Department of Ecology, Uppsala, Sweden*

Trophic interactions are important for ecosystem functions and related services. For instance, herbivorous insects cause damage to agricultural crops, and predatory arthropods consume these herbivores but also other prey including other predators (intra-guild predation). The composition of these communities and their interaction structure most probably thereby impact the delivery and stability of ecosystem functions such as population regulation of the herbivores and primary production. There are several research gaps to be addressed with regards to functioning in such trophic settings. A wealth of indices of community functional composition have been developed, but few have used these to predict actual measured functions resulting from trophic interactions in diverse communities. We show how including traits to describe communities improves predictions of multiple functions in nature. Further, taking information on food web interaction structure and abundance dynamics into account might further improve our ability to predict multi-trophic functioning. Allowing for this, food web theory has made notable recent advances. In particular, it has been suggested that considering body size composition in dynamic food web models, departing from metabolic theory, could allow for drastically decreasing the number of model parameters needed to be estimated to replicate dynamics of real trophic networks. We tested the ability of body size based food web models to predict real abundance dynamics by confronting such a model with empirical data. Food webs were experimentally varied with respect to guild and body size composition of predators feeding on cereal aphids in cage mesocosms and their abundance dynamics over time was tracked. When mapped to experimental data, the model showed great ability to reproduce prey dynamics and, to some extent, intra-guild predation in the cages. Matching food web models with empirical information on interaction structure, trait composition and abundance is a promising approach for informing biodiversity-ecosystem functioning relations in multi-trophic settings, and highlights the applied relevance of recently developed theory.

## Investigating the influence of shared enemies in diverse tropical tree communities

Tuesday  
14:50

*Harriet Downey<sup>1</sup>, Owen Lewis<sup>1</sup>, Michael Bonsall<sup>1</sup>, Sofia Gripenberg<sup>1</sup>*

<sup>1</sup>*Department of Zoology, University of Oxford, Oxford, UK.*

Insect herbivores are thought to play a key role in the maintenance of diversity in tropical plant communities. Compared to other types of enemies, pre-dispersal insect seed predators have received little attention although they have the potential to drastically reduce plant fecundity by killing seeds. Some insect seed predators are associated with multiple host plant species, typically within the same genus or family. Where this is the case, these non-specialised seed predators have the potential to link the regeneration dynamics of their host plants via so-called enemy-mediated indirect interactions. Where present, such interactions have the potential to influence the abundance of one or more of the plant species and provide a mechanism contributing to the structure of plant communities. We constructed a quantitative food web to investigate the potential for seed-predator mediated indirect interactions between tree species within the Lauraceae family on Barro Colorado Island (BCI) in Panama. In this study we use the Lauraceae-seed predator system to assess 1) whether closely related Lauraceae species and/or species with similar traits are more likely to share enemies than more distantly related species and/or species with greater trait dissimilarity, and 2) whether trees experience higher attack rates by pre-dispersal insect seed predators when surrounded by conspecific and/or confamilial trees than elsewhere in the landscape. We also aim to present results from a molecular study testing whether the principal insect seed predator of Lauraceae at our field site forms a panmictic population across all host species or cryptic host races – information that will aid the interpretation of the food web data.

**Artificial light effects on plant-pollinator networks**

Tuesday

16:40

*Colin Fontaine<sup>1</sup>, Eva Knop<sup>2</sup>, Leana Zoller<sup>2</sup>, Remo Ryser<sup>2</sup>, Christopher Gerpe<sup>2</sup>, Maurin Hürler<sup>2</sup>*

<sup>1</sup>*CNRS - Muséum national d'Histoire naturelle, Paris, France* <sup>2</sup>*University of Bern, Institute of Ecology and Evolution, Bern, Switzerland*

Pollinators are declining worldwide and this has raised concerns of a parallel decline of the essential pollination service they provide to both crops and wild plants. The main drivers of this decline are related to human activity, namely habitat loss, use of pesticides, introduction of alien species, spread of pathogens and climate change. Recently, the rapid global increase of artificial light at night has been proposed as a new threat to terrestrial ecosystems with currently largely unknown consequences for ecosystem functioning. Here, we show that artificial light disrupts nocturnal pollination networks with negative consequences for plant reproductive success. On artificially illuminated plant-pollinator communities, nocturnal visits to plants were reduced by 62% compared to dark areas. Most importantly, this resulted in an overall 13% reduction of fruit set of a focal plant even though the plant received also numerous visits of diurnal pollinators. Further, by merging diurnal and nocturnal pollination sub-networks we show that the structure of these combined networks tends to facilitate the spread of negative consequences of disrupted nocturnal pollination to daytime pollinator communities. Our findings demonstrate that artificial light is a threat to pollination and that negative effects of artificial light on nocturnal pollination are predicted to propagate to the diurnal community, thereby aggravating their decline. Our findings provide novel perspectives on both the functioning of plant-pollinator networks, with nocturnal pollinators not being redundant to diurnal ones, and our understanding of the human-induced decline of pollinators and their ecosystem service.

**Apparent competition drives community-wide parasitism rates and changes in host abundance across ecosystem boundaries: predicting future states of complex systems with quantitative food webs**

Tuesday  
15:40

*Carol Frost*<sup>1</sup>, *Guadalupe Peralta*<sup>1</sup>, *Tatyana A. Rand*<sup>2</sup>, *Raphael K. Didham*<sup>3,4</sup>, *Arvind Varsani*<sup>1,5,6,7</sup>, *Jason M. Tylianakis*<sup>1,8</sup>

<sup>1</sup> Centre for Integrative Ecology, School of Biological Sciences, University of Canterbury, Private Bag 4800, Christchurch 8140, New Zealand, <sup>2</sup> USDA-ARS Northern Plains Agricultural Research Laboratory, Sidney, Montana 59270, USA, <sup>3</sup> School of Animal Biology, The University of Western Australia, 35 Stirling Highway, Crawley Western Australia 6009, Australia, <sup>4</sup> CSIRO Land & Water, Centre for Environment and Life Sciences, Underwood Ave, Floreat Western Australia 6014, Australia, <sup>5</sup> Biomolecular Interaction Centre, University of Canterbury, Private Bag 4800, Christchurch 8140, New Zealand, <sup>6</sup> Structural Biology Research Unit, Department of Clinical Laboratory Sciences, University of Cape Town, Observatory, Cape Town 7700, South Africa, <sup>7</sup> Department of Plant Pathology and Emerging Pathogens Institute, University of Florida, Gainesville, Florida 32611, USA, <sup>8</sup> Department of Life Sciences, Imperial College London, Silwood Park Campus, Buckhurst Road, Ascot, Berkshire SL5 7PY, UK.

Species have strong indirect effects on others, and predicting these effects is a central challenge in ecology. Recently, information about shared predators in quantitative food webs has been used to successfully predict indirect interactions among selected pairs of prey species within a given habitat. However, it remains unclear whether these predictions can be scaled up to encompass all the indirect interactions in a food web, and whether the movement of predators between habitats has community-wide indirect effects on herbivores in adjacent habitats. We tested this using parasitoid-host food webs sampled at habitat edges between plantation and natural forests, where spillover of predators may significantly impact ecosystem functioning in the recipient habitat. We constructed an empirical quantitative food web of cross-habitat interactions collected over two years at ‘training’ sites (68 Lepidoptera hosts and 43 parasitoid species, with parasitoids identified morphologically and by DNA barcoding), and used this to predict parasitism rates on hosts at separate ‘validation’ sites following a large-scale experimental reduction of host abundance on the plantation side of the habitat edges. We hypothesized that if apparent competition is an important mechanism structuring community-wide interaction networks, then parasitism rates of hosts should be predictable given information on the proportions of shared parasitoids between hosts, initial attack rates, and changes in host abundance. We found that observed parasitism rates in the validation sites following experimental prey reduction were significantly correlated with the predicted parasitism rates based on apparent competition, whether the predictions were made based on just one or both of the habitats. This provides strong evidence that apparent competition is a community-wide and cross-habitat structuring mechanism. These findings could have broad application in landscape planning, invasion biology, and biological control.

## Food webs at the landscape scale: are we missing the wood for the trees?

Tuesday  
11:30

*Talya Hackett<sup>1</sup>, Alix Sauve<sup>2</sup>, Ian Vaughan<sup>3</sup>, Daniel Montoya<sup>4</sup>, Jane Memmott<sup>1</sup>*

<sup>1</sup> *University of Bristol, UK,* <sup>2</sup> *University of Bordeaux,* <sup>3</sup> *Cardiff University,* <sup>4</sup> *CNRS Moulis*

Research in ecological networks has been improving dramatically in quality over the last 20 years with networks becoming fully quantified and well established in the literature. However, for practical reasons, the vast majority of terrestrial network science is both guild-specific and habitat-specific. In reality, ecosystems host a variety of guilds and transcend different habitats; and multiple guilds in multiple habitats can interact in unexpected ways. Our aim is to determine how working at the landscape scale, defined as a mosaic of habitats, affects our understanding of the structure, robustness and ecosystem service provision of ecological networks. Thus, are landscape webs simply the sum of their habitat webs, or do they have emergent properties that cannot be predicted from component webs? Working at 30 sites consisting of one, two or three habitats (monads, dyads and triads), we sampled plants, flower-visitors, leaf miners, externally feeding herbivores, seed feeders and parasitoids to create a series of networks-of-networks. To determine the effect of habitat diversity on ecosystem services in the form of pollination, we placed strawberry plants at monads and triads and recorded the resulting fruit weight and quality. Here we link the results from this experiment with changes in species richness and diversity, network properties and functional diversity of the monads, dyads and triads. Understanding how communities are interacting at the landscape scale allows for restoration projects to be targeted and applied in a more specific way to achieve the highest likelihood of success.



## Soil networks and food-webs in a chronosequence of abandoned agricultural fields

Thursday  
9:20

*Emilia Hannula*<sup>1</sup> *E. Morrien, B. Snoek, W. de Boer, J. A. van Veen, W. H. van der Putten*

<sup>1</sup> *Netherlands Institute of Ecology (NIOO-KNAW)*

Land abandonment is considered an effective tool for restoring biodiversity and ecosystem functions. Thus far little attention is given to the role of soil species interactions, diversity and network configuration on development of plant community. Here, we present results of a soil biodiversity and ecosystem functioning study from a chronosequence of ex-arable fields in The Netherlands. These fields are typically managed by low-intensive grazing while undergoing a transition from an arable system into species-rich grassland. Abandoning agricultural fields triggers a change in the species composition and possibly in the way species interact. By using a combination of molecular and morphology based approaches, we were able to reconstruct the full soil food web (from microorganisms to earthworms) at 9 fields that were taken out of production at different points in history (10-31 years prior to sampling). In total ~18000 species were found in these soils. By using co-occurrence networks we investigated the links between these organisms and found out that soil species networks become more connected when nature restoration progresses.

In the same fields a mesocosm experiment was conducted using intact soil cores to look at fate of plant derived carbon in the soil food-web by using <sup>13</sup>C-CO<sub>2</sub> pulse labeling. Samples were collected of aboveground and belowground plant tissues, soil bacterial and fungal PLFA biomarkers, nematodes, enchytraeids, mites, collembola, earthworms, and other soil fauna. Furthermore, the fungal community was analysed in detail using DNA-SIP in combination with NGS-sequencing. We could show that early successional fields the bacterial channel was predominant while at the mid- and long-term abandoned fields the carbon went through the fungal channel. We also show that the fungal community changed during succession further influencing the fungal feeding organisms.

Here we synthesize this data and discuss these results in relation to the soil network analyses and <sup>13</sup>C tracer studies in order to predict the change in ecosystem processes during land abandonment and secondary succession.

## Taking the lab to the field: ecological analysis with ‘field-friendly’ PCR and sequencing

Wednesday  
14:50

*Omar Khalilur Rahman*<sup>1</sup>, *Elizabeth Clare*<sup>1</sup>, *Rob Knell*<sup>1</sup>

<sup>1</sup> *Queen Mary University, London, UK*

Short stretches of DNA are now commonly used for non-invasive monitoring of biodiversity and ecosystem interactions. A key limitation is the reliance on non-portable laboratory settings for genetic analysis and the resulting time lag between sample acquisition and analysis. This limits the utility of the approach when rapid diagnostics are key. Samples collected in the field must be preserved and stored correctly, and overcome obstacles in transport and handling before laboratory work can begin. Here we aim to assess the potential for mobile laboratories for the recovery and analysis of DNA *in situ* using the latest technological advances. As a model we target the recovery of mammalian COI (cytochrome C oxidase subunit 1) DNA barcodes from vampire bat faeces. Our aim is to identify both the species of bat and their local prey using only equipment and analysis methods that would be sustainable in the field, limiting both wet-lab and analytical steps. We collect and preserve DNA using Whatman® FTA® cards, which lyse cells, trap nucleic acids, and preserves them at room temperature, eliminating the need for DNA extraction. We conducted PCR amplification using the battery-operated and portable miniPCR™ platform and conventional PCR reagents. We then sequenced the DNA on the MinION flowcell (Oxford Nanopore) generating sequencing reads in real-time. We successfully recovered 1.5 million reads from a sequencing run and demonstrate that these ‘field-friendly’ alternatives to conventional protocols can answer simple ecological questions that are urgent, from materials that are difficult to preserve, or when it is prohibitively difficult to remove samples from the collection site. We observed high sequencing error rates which limits the scope of the questions that can be answered and increases the risk of false-negatives and false-positives. However, enough information was acquired to answer basic ecological questions and pinpoint the main food source for the bat colony. We explore methods of streamlining bioinformatics steps to complete the analyses without the need of high performance computing. While requiring additional preparation prior to fieldwork, our results open up possibilities that will revolutionise ecological research taking the lab to the field.

**Using nested metabarcoding to assess changes in herbivore-parasitoid food webs following insecticide application to control invasive species.**

Thursday  
16:00

*James Kitson*<sup>1</sup>, *Christoph Hahn*<sup>2</sup>, *Helen Kimbel*<sup>3</sup>, *Nigel A Straw*<sup>4</sup>, *David H. Lunt*<sup>5</sup>, *Darren M. Evans*<sup>1</sup>

<sup>1</sup> Newcastle University, Newcastle upon Tyne, UK, <sup>2</sup> Karl-Franzens-Universität, Graz, Austria, <sup>3</sup> Lausanne, Switzerland, <sup>4</sup> Forest Research, Farnham, UK, <sup>5</sup> University of Hull, Kingston upon Hull, UK

The Oak Processionary Moth (*Thaumetopoea processionea*) is native to southern Europe but has increasingly become a serious invasive urban and forest pest in France, Germany and the Netherlands with both agroforestry and public health effects. In 2006 it arrived in the UK and although it is currently restricted to London, it is the subject of a major control program involving both manual nest removal and the application of *Bt* (*Bacillus thuringiensis*) based insecticides. Although studies have been performed on the efficacy of these methods for controlling Oak Processionary Moth, the broader effects on other Oak tree insect herbivores and their parasitoids are less well known, particularly the knock-on effects on network structure. We demonstrate a simple extension to current metabarcoding practices that allows us track sequences and link them back to the metadata for thousands of samples to generate highly-resolved host-parasitoid networks. We sequenced approximately 13,000 insects across 160 trees grouped into 20 sets of sprayed and unsprayed trees for 3 time points. By maintaining individual sample level metadata and using a replicated experimental design we are able to build Oak tree herbivore-parasitoid networks and look for changes in network structure attributable to both temporal change and insecticide treatment. We demonstrate how merging metabarcoding with ecological network analysis provides a novel way of examining the indirect effects of spraying on non-target species and their interactions.

## Effects of land use on cross-habitat resource subsidies in stream-riparian networks

Tuesday  
14:30

*Brendan McKie<sup>1</sup>, Peter E. Carlson<sup>1</sup>, Leonard Sandin<sup>2</sup>, Richard K. Johnson<sup>1</sup>*

<sup>1</sup> *Department of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden,* <sup>2</sup> *Institute of Freshwater Research, Department of Aquatic Resources, Swedish University of Agricultural Sciences, Drottningholm, Sweden*

Adult aquatic insects with a terrestrial life-stage are important vectors transferring resources assimilated in freshwater environments to terrestrial consumers. Key factors regulating the incorporation of aquatic subsidies into terrestrial food webs include subsidy productivity, timing of adult aquatic insect emergence relative to the resource requirements of terrestrial consumers and the dispersal patterns of adult aquatic insects, and rates of consumption of aquatic subsidy by terrestrial consumers. Additionally, both the timing and extent of dispersal by adult aquatic insects are also potentially strongly regulated by their species-specific life history traits. In a field study conducted in nine streams in Sweden's Uppland region, we assessed how land use (agriculture vs. forest) affects in-stream and stream-side riparian habitats, the functional trait composition of aquatic insects, and the dispersal of adult aquatic insects. Abundances of aquatic insects were greater at agricultural than at forested sites. Larval insect assemblages from the agricultural streams were characterized by traits indicative of more limited adult dispersal, including small adult size and weak flying strength, and also by traits indicative of strongly pulsed peaks in emergence, including univoltinism and well-synchronised emergence. Traits associated with reduced dispersal were similarly characteristic of insect assemblages in pools, which also supported the highest proportion of invertebrates completely lacking an adult flying stage, a result likely to have implications at larger scales, given the dominance of soft-bottomed pool habitats and scarcity of riffles in agricultural landscapes. Most (64%) adult insects emerging from the agricultural streams were caught close to the stream edge. In contrast, catches of adult aquatic insects declined relatively little with increasing distance from the forest streams. Overall, our analysis indicates that while overall production of aquatic insects with a winged adult was greater in agricultural streams, availability of this productivity for terrestrial consumers is more likely to be spatially restricted closer to the stream channel and especially adjacent to riffle habitats, and also more strongly temporally pulsed. A key question for future research is whether the deposition of large quantities of aquatic subsidy in agricultural riparian habitats exceeds the resource requirements and processing capacities of terrestrial consumers.

**Exploring the organization of multiplex ecological networks**Monday  
14:30***Vincent Miele<sup>1</sup>, Sonia Kéfi<sup>2</sup>, Evie A. Wieters<sup>3</sup>, Sergio A. Navarrete<sup>3</sup>, Eric L. Berlow<sup>4</sup>***

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*Vibrant Data Inc., San Francisco, California, United States of America*

Species are linked to each other by a myriad of positive and negative interactions. This complex spectrum of interactions constitutes a network of links that mediates ecological communities' response to perturbations, such as exploitation and climate change. In the last decades, there have been great advances in the study of intricate ecological networks. We have, nonetheless, lacked both the data and the tools to more rigorously understand the patterning of multiple interaction types between species (i.e., "multiplex networks"), as well as their consequences for community dynamics. Using network statistical modeling applied to a comprehensive ecological network, which includes trophic and diverse non-trophic links, we provide a first glimpse at what the full "entangled bank" of species looks like. The community exhibits clear multidimensional structure, which is taxonomically coherent and broadly predictable from species traits. Moreover, dynamic simulations suggest that this non-random patterning of how diverse non-trophic interactions map onto the food web could allow for higher species persistence and higher total biomass than expected by chance and tends to promote a higher robustness to extinctions.

## Does plant community relatedness explain context dependency on keystone plant species roles?

Tuesday  
16:20

*Kate Pereira Maia<sup>1</sup>, Alix Sauve, Ian Vaughan, Jane Memmott*

<sup>1</sup> *School of Biological Sciences, University of Bristol, Bristol, United Kingdom*

Restoration is an important tool to promote biodiversity and, in terrestrial systems, it usually starts with the creation of plant communities. Plant community diversity and composition can have strong bottom-up effects enriching higher trophic levels, and turning the replanting stage of restoration into a real opportunity to improve biodiversity. However, not all plant species have equal potential for promoting positive multi-trophic effects, and ecological networks could be a useful tool to identify species that could act as keystone resources for higher trophic levels, defined as plant species that support more individuals at higher trophic levels than expected by their abundance. We asked whether keystone plant species could be identified in 20 plant-herbivore-parasitoid networks from UK farms, and tested the importance of plant relatedness (i.e. the presence of closely related species that act as alternative hosts to their herbivores) to determine plants' network role. We found that, while keystone plants were present in most networks, the identity of the keystone species varied from network to network; keystones from one network did not act as keystones in every network they occurred, rather a plant's role was context dependant. Here, we link the results on context dependency of plant's keystone roles with measures of plant community phylogenetic composition. Keystone plants, as well as being interesting from a network perspective, could also create a focus for restoration projects, providing land managers with a fast track approach to the restoration of biodiversity in both managed and natural habitats.

**Do predator food webs change in response to fertilization type?**

Friday

10:50

***Oskar Rennstam Rubbmark<sup>1</sup>, Daniela Sint<sup>1</sup>, Lena Manzl<sup>1</sup>, Nina Egger<sup>1</sup>, Michael Traugott<sup>1</sup>***

<sup>1</sup> *Mountain Agriculture Research Unit, Institute of Ecology, University of Innsbruck, Technikerstraße 25, 6020 Innsbruck, Austria*

Predator-prey dynamics in agricultural fields are driven by an interaction between biotic factors (e.g. predation or competition for resources) and abiotic factors (influenced by e.g. organic fertilization that could change nutrient availability for both plants and decomposers). Agricultural inputs such as fertilization have been shown to affect both resource availability and habitat conditions through either of these pathways; however, how this occurs could vary with the type of fertilization used. So far we know little of the processes controlling these changes, and consequently a deeper understanding of food-web dynamics under different fertilization management is needed. Such insights can have implications for both fundamental and applied ecology.

Using a molecular approach, we investigated how ~7000 generalist predators changed their consumption of functionally important food items including aphids, springtails and earthworms in response to fertilization type. Manure, compost, conventional fertilizer or no fertilizer was applied in experimental plots during two years in cereal fields located in the Inn-valley of Tirol/Austria. Our findings show that organic fertilizers such as manure or compost not only provide nutrients, but that they contribute to restructure food-webs, as alternative prey becomes more available for predators. We show how this occurs by coupling community data of both prey and predator taxa, with trophic-interaction networks. This allowed us to describe how predator communities, occupied niche space and diet preference changed within predator communities in response to different fertilization types and co-occurring prey and predator species. Often predator-prey networks are complex and difficult to generalize, however our findings show that agricultural inputs such as fertilization have a real potential to regulate food-web dynamics. As we gain a deeper mechanistic understanding of predator-prey food webs, this knowledge will help contributing to and ultimately aid a more sustainable agricultural management.

## Characterization of food web structures and ecosystem services in agroecosystems

*Guillermo Aguilera<sup>1</sup>, Kirsten Miller<sup>1</sup>, Tomas Roslin<sup>1</sup>, Riccardo Bommarco<sup>1</sup>*

<sup>1</sup> *SLU, Sweden*

Pest control and crop pollination are important services provided by natural arthropod communities in agricultural habitats. Landscape ecology have investigated the relation between pests and their natural enemies in agroecosystems of different landscape composition. Yet, most of our knowledge about pest control services are based on natural enemy diversity, abundances or pest damage . Likewise, most of our understanding about how pollination is affected by the landscape is based on how pollinator communities differently perform to the proportion of natural habitats or connectivity between habitat patches. However, little is known about how landscape configuration directly affect the network-level associations between pests and natural enemies, and plants and their pollinators. We have designed a field experiment to quantify how differences in food web structure are driven by landscape and local characteristics. We have selected a total amount of 20 fields selected as pairs of adjacent oilseed rape and ley fields (local) in two types of landscapes dominated by oilseed rape or ley (landscape). We will characterize pest-predator, pest-parasitoid and plant-pollinator networks by sampling the arthropod communities and using molecular tools to identify who predate, parasites or pollinate whom. We aim to find out how local and landscape variables shape the overall food web structure in terms of connectivity, nestedness or specialization among other metrics. Additionally we will directly measure the ecosystem services of pollination, yield and pest control. Thus, we will establish the degree to which food web metrics can be used to reliably predict the degree and quality of the ecosystem services that these webs provide.



## Quantifying floral resources from the flower to the landscape scales and perspectives for plant-pollinator networks

*Mathilde Baude*<sup>1</sup>, *Bill Kunin*<sup>2</sup>, *Nigel Boatman*<sup>3</sup>, *Simon Conyers*<sup>3</sup>, *Nancy Davies*<sup>4</sup>, *Mark Gillespie*<sup>2</sup>, *Dan Morton*<sup>5</sup>, *Simon Smart*<sup>5</sup>, *Jane Memmott*<sup>4</sup>

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The lack of floral resources is suspected to be one of the main factors involved in pollinator decline. However, floral resources are rarely quantified at large scale making difficult 1-to assess the value of species and habitats in feeding pollinators and 2- to study the changes in the availability of floral resources across time. We created a floral resource database of nectar values for 260 common plant species from the flower to the landscape scale through empirical sampling, flower density counting and statistical modeling based on plant traits. We then combined the nectar database with vegetation data from the Countryside Survey, a national-scale representative survey of British plant communities. We found that a few productive species and habitats increasingly dominate national nectar supplies and that the total nectar production of Great Britain showed a marked decline in floral resources from 1930s to 1970s, followed by a period of stable low production and then increased post-2000. These results will be discussed in the context of opportunities for conservation and restoration efforts dedicated to pollinators and we will present how this database could be used to improve our understanding of the role of floral resources in plant-pollinator networks.

Reference: Baude, M; Kunin, WE; Boatman, ND; Conyers, S; Davies, N; Gillespie, MAK; Morton, RD; Smart, SM; Memmott, J; Historical nectar assessment reveals the fall and rise of floral resources in Britain, *Nature*, 530, 7588, 85-88, 2016

## The effects of accelerated snowmelt on subalpine pollination network structure and function

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Mutualistic networks are key for the creation and maintenance of biodiversity, yet their structure and functioning may be threatened by environmental changes. Global climate change is one such potential driver, and may be a critical factor disrupting plant-pollinator interactions given the potential for phenological (timing) mismatches between pollinator activity and plant blooming. Very few studies have taken a manipulative approach to understanding the effects of perturbations on mutualistic network structure. In addition, even fewer empirical studies have measured ecological functioning associated with different network structures, or the effects of perturbations on structure-function relationships. While several excellent studies have examined the effects of experimental alterations in phenology, both for pollinators and plants, these studies have focused on one or a few taxa, and we are unaware of any studies that have focused on the whole-network level. To address these gaps, we are studying the effects of snowmelt acceleration on the structure and functioning (plant seed production) of pollination networks with replicated, manipulative experiments.

In spring 2017, we experimentally accelerated snowmelt timing in field plots in subalpine meadows (~3,000m ASL) in Colorado, USA. We conducted these manipulations via a standard method: placing black greenhouse shade cloth over the snowpack to increase snow surface temperature, accelerating melt date by approximately three weeks. The plots measure 10 x 14m and are replicated at the landscape scale, with each manipulated plot paired with a control plot located ~50m away. We expect that these manipulations will strongly affect plant flowering phenology, but not have a noticeable effect on local pollinator phenology because of the mobility of foraging pollinators. In spring-summer 2017, we are examining the effects of accelerated snowmelt on flower visitation network structure, across most of the duration of the growing season. We are also assessing potential changes in ecological functioning (pollinator-dependent plant reproduction) in several focal plant species, using hand-pollination treatments. We hypothesize that snowmelt acceleration will alter several key elements of network structure and that it will decrease pollination functioning, relative to controls.

## Understanding cross-habitat linkages between stream and riparian networks to optimize biodiversity, ecosystem services and human uses.

*Francis Burdon*<sup>1</sup>, *Nikolai Friberg*<sup>2</sup>, *Geta Risnoveau*<sup>3</sup>, *Peter Goethals*<sup>4</sup>, *Martin Volk*<sup>5</sup>, *Brendan McKie*<sup>1</sup>

<sup>1</sup> *Department of Aquatic Science and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden,* <sup>2</sup> *NIVA - Norwegian Institute for Water Research, Oslo, Norway,* <sup>3</sup> *Department of Systems Ecology and Sustainability, University of Bucharest, Bucharest, Romania,* <sup>4</sup> *Department of Applied Ecology and Environmental Biology, Ghent University, Ghent, Belgium,* <sup>5</sup> *Department of Computational Landscape Ecology, Helmholtz Centre for Environmental Research, Leipzig, Germany*

Connectivity is an ecological concept with multiple dimensions. In coupled stream and riparian networks, connectivity can encompass hydrological, landscape, and food-web connections within and across habitats. These spatial networks are also key components of green and blue infrastructure (GBI) that underpin landscape integrity by transporting nutrients, regulating floods, buffering human impacts and supplying fresh water. However, stream-riparian networks are also subject to multiple human pressures (e.g., from hydropower generation and agriculture) that affect longitudinal and lateral connectivity, driving habitat and diversity losses, threatening ecosystem services, and causing management conflicts. Thus, there is a pressing need to understand the importance of connectivity within these networks, and to apply this understanding in managing stream-riparian GBI for both natural values and societal needs.

Here we present a new project, CROSSLINK, which aims to: 1) evaluate how the extent, spatial arrangement, and connectivity of riparian-stream GBI affects biodiversity, ecosystem functioning, ecosystem services, and resilience indicators in forested, rural, and urban settings, and 2) produce an optimization framework capable of balancing multiple uses with greater resilience in riparian-stream GBI. The project will analyze existing data on stream-riparian GBI and conduct extensive field studies in four case-study networks located in Sweden, Norway, Belgium, and Romania.

One key component of CROSSLINK will be to better understand the food-web linkages between stream and riparian communities. Ecological theory predicts that productivity gradients in both donor and recipient ecosystems determine the strength of cross-habitat connections. However, the interaction strength may also be contingent on the trophic level the resource subsidy enters, and additionally, the quality of that input. Thus, in CROSSLINK, efforts will be made to quantify the extent of aquatic resource subsidies to terrestrial communities using biomarkers including stable isotopes and fatty acids. This, in combination with assessing resource stocks and flows, means CROSSLINK will help explain how differing riparian land-uses and network positions influence cross-habitat linkages and food-web interactions. A greater appreciation for these connections should enhance our ability to manage biodiversity, ecosystem services, and multiple human uses at the land-water interface.

## Macroecology of avian seed-dispersal networks

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Studying the structure and the dynamics of mutualistic interactions is essential for understanding the underlying mechanisms that originates and maintains patterns of biodiversity in time and space. The number of studies revealing the structure of mutualistic networks has grown extraordinarily in the past few decades, and currently their main focus is to understand the extrinsic factors driving their organization. Despite these efforts, the knowledge of macroecological patterns is still lacking. Therefore, our goal was to investigate macroecological patterns of seed-dispersal networks formed by plants and birds, using novel and published data (n=19 networks). We described the general mutualistic network patterns in terms of nestedness, connectance and modularity. We used a genetic algorithm, within an information-theoretic framework, to test the association between network metrics and bioclimatic and geographical predictors. Nestedness was a common feature in almost every network, while only 47.37% of the networks presented a significant modular structure. The lack of modularity could be an effect of network size, since most of the networks were small (<100 species). Nestedness was best predicted by the precipitation and the mean temperature of the warmest quarter, connectance by precipitation of the wettest month and mean temperature of the wettest quarter and modularity by the precipitation of the driest month. Probably the differences in temperature and seasonality between temperate and tropical and subtropical regions influence the interaction specificity. The climatic conditions of the warmest quarter seem to be important to nested networks, maybe influencing resource availability and consequently, species interactions. Seed-dispersal networks between plants and birds showed macroecological patterns, with precipitation and temperature affecting the structure of these networks and without any effect of geographical (e.g., latitude) predictors. Our next step is to increase our dataset and test the prevalence of these results, since macroecological studies with small sample sizes should be considered with caution.

## Understanding ecosystem functioning in natural predator-prey communities by confronting dynamic food web models with population time series data

*Alva Curtsdotter*<sup>1</sup>, *H. T. Banks*<sup>2</sup>, *J. E. Banks*<sup>3</sup>, *Mattias Jonsson*<sup>4</sup>, *Tomas Jonsson*<sup>1,4</sup>, *A. N. Laubmeier*<sup>2</sup>, *Michael Traugott*<sup>5</sup>, *Riccardo Bommarco*<sup>4</sup>

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Most ecosystem functions and related services involve interactions among organisms at different trophic levels, e.g. pollination and biological pest control. Despite this our mechanistic understanding of ecosystem functioning in multi-trophic communities is poor, and research has been limited to experiments on small study systems, or to statistical descriptions in larger communities. To correct this deficit approaches that can overcome the existing trade-off between mechanistic insight and ecological realism are needed.

Dynamic food web modeling of predator-prey communities potentially allows for this, thanks to recent advances in trait-based parameterization of food web models and molecular tools to detect feeding interactions. We here make use of these advances, and provide the first test of an allometric food web model's ability to replicate temporally non-aggregated abundance data from the field and provide mechanistic insight into the function of predation. Specifically, we attempt to reproduce the population dynamics of the aphid herbivore *Rhopalosiphum padi* in ten Swedish barley fields, with a food web model which mechanistically relates predation rates to body size and abundance. The mathematical approach involving inverse problems is used to simultaneously optimize model fit and estimate the allometric constants for model parameterization.

In half of the fields, the dynamic food web model explained more than 70% of the variation in aphid abundance, and reproduced aphid dynamics well when the observed population trajectory was strictly increasing. In other fields, the increasingly in-depth model assessment criteria revealed knowledge gaps, ranging from aspects of the autecology of the focal herbivore to allometric theory. The deeper analysis of model processes highlighted the importance of developing arthropod sampling methods better suited for quantitative modeling.

We demonstrate the multiple usefulness of matching empirical time series data with dynamic food web models. When the model performs well, this approach can help identify functionally important predators and disentangle whether this importance is due to traits or abundance, while when it does not, it can reveal knowledge gaps and research needs. Generally, the approach holds promise to provide mechanistic insight into ecosystem functioning in multi-trophic communities.

## Host-virus-viophage population dynamics governed by mutualisms and parasitism interactions

*Ana Del Arco*<sup>1</sup>, *Matthias Fisher*<sup>2</sup>, *Lutz Becks*<sup>1</sup>

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Microbial systems are at the base of every food web. We only recently discovered host-virus-viophage interactions but the ecological role of these interactions are still unknown. Virophages are unique obligate parasites of giant virus and they disrupting the interaction of the giant virus and its host by suppressing replication of the giant virus as shown in a recent study with *Cafeteria roenbergensis* (host) - CroV (virus) - mavirus (virophage). In order to gain a better understanding of the species interactions, the conditions allowing long-term coexistence and disentangle the roles of parasitism and mutualism in this tripartite system, we use long-term chemostats experiments. In this experiment we follow population dynamics and species interactions over time. We found that the activation of the virophage reduced species interaction strength of the host and virus which lead to dampened population cycles over time. We currently establish multiplex-digital-droplet-PCR methods to be able to follow abundances and changes in species interactions in higher temporal resolution. Our results will contribute to the understanding of the coexistence of this system governed by parasitism and mutualism and the potential evolutionary responses in host and viruses. Our methodological aim is to establish the use of molecular based techniques to follow such changes and being able to link with the observed ecological responses.

## Conservation of plant-pollinator networks in agroecosystems: soybean and its field margins in the Argentinian Pampas

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The Pampean region of South America is an extended flat area, once dominated by grasslands, that has been dramatically modified by intensive agriculture and livestock grazing. Currently, 60% of the sown area is dominated by a single annual crop, soybean (*Glycine max*). Spontaneous vegetation (including many native species) is mostly confined to field margins, which altogether represent a very small fraction of the landscape. However, plant-pollinator communities in these margins are crucial to sustain the pollination service to various crops (sunflower, rapeseed and soybean, among others). Our objectives were twofold: (1) to understand the local and landscape factors that affect the structure of plant-pollinator networks in field margins, and (2) to explore the factors that affect the role played by the single dominant mass-flowering crop (soybean) in the networks. Along two years we studied 59 soybean plots and constructed the plant-pollinator networks comprised by the crop, the plants in its field margins and their flower visitors. We included plots with margin widths ranging from 1.5 to 40m, and within surrounding landscapes of varying complexity. We found that field margin width was far more important than landscape factors (e.g. diversity of land cover types) in structuring plant-pollinator networks. In addition, the complexity of the networks, the evenness of its interactions and its robustness to species loss was positively related to field margin width, but only up to a width of 8-10m. This has direct management implications, as it sets a maximum width beyond which there is no apparent benefit to the conservation of plant-pollinator networks. Regarding the role played by soybean in the networks, our results suggest that it is not an attractive floral resource and, thus, its importance in networks' structure is negatively related to the abundance of floral resources in field margins. In this sense, the behaviour of soybean is somewhat different to that of other mass-flowering crops such as sunflower or rapeseed. All in all, our study is a good example of the usefulness of the network approach to understand and sustainably manage a crucial ecosystem function, such as pollination, in agroecosystems.

## Community phenology of insects on oak – evolutionary adaptations and predictions for climate change

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Global anthropogenic change is causing rapid shifts in climate, thus advancing the onset of many phenological events. As different trophic levels, and species within trophic levels, may be unequally sensitive to climatic variables, changes in climate can result in species becoming asynchronised in time. In terms of food web structure, asynchrony can induce shifts in interaction strengths or result in extinction of specialized species. Yet, we lack insights in how diverse multitrophic communities respond to global warming. Moreover, some geographically isolated populations of the same species may show different responses to temperature. To investigate how geographically isolated communities respond to changes in climate, we implemented a reciprocal transplant experiment. We sampled acorns and a subset of the oak insect community in five locations along a climatic gradient from southern to northern Europe in the autumn of 2016. Each local community were exposed to five different temperature regimes in growth chambers, where each regime corresponded to the local temperature in one of the sampling locations. We observed root and shoot development of acorns, and spring emergence date of herbivores and parasitoids insects on a weekly basis. This approach allow us to expose potential differences in acorn development and insect hatching dates among local populations from different latitudes, thereby probing for local adaptation. Likewise, we will achieve a community wide understanding of how altered temperatures can affect the structure of the food web. The experiment is currently ongoing and during the conference I want to present the preliminary findings.



## A meta-network of bird seed dispersal interactions in a tropical biodiversity hotspot

*Carine Emer*<sup>1</sup>, *Marco A. Pizo*<sup>2</sup>, *Milton C. Ribeiro*<sup>3</sup>, *Suelen Moraes*<sup>4</sup>, *Augusto Piratelli*<sup>4</sup>, *Pedro Jordano*<sup>5</sup>, *Mauro Galetti*<sup>3</sup>

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Fast-paced deforestation has created fragmented forests that besides negative impacts on biodiversity can still hold many species. However, maintaining effective gene flow and connectivity across the fragmented landscape strictly depends on maintaining functional species interactions (e.g., seed dispersal, pollination) favouring species persistence. Here we use a metanetwork approach to understand how remnant bird-plant interactions for seed dispersal (BSD interactions) across fragments may contribute effective connectivity among forest fragments and whether species traits identify key central BSD interactions potentially connecting the landscape. We gathered data from 16 Atlantic Forest fragments, a threatened biodiversity hotspot. BSD interactions showed a high turnover among fragments of the metanetwork, resulting from high beta-diversity in local assemblages, forming a highly diverse, modular and poorly connected metanetwork structure. High-centrality BSD interactions constituted a distinct, small subset of the regional pool, including small-bodied bird species and plant species with intermediate seed-size and reduced wood density, typical of secondary growth forest. BSD interactions functioning as mobile links tend to favour the persistence of secondary-forest, involving super-generalists in most fragments. The pristine forest tracts harbour distinct interactions (e.g., large-bodied frugivores and large-seeded plants) that vanish in the forest fragments, which may lead to long-term changes in forest structure.

## Spatial variation in trophic interactions - The warming Arctic from a topological perspective

*Rasmus Erlandsson<sup>1</sup>, Anders Angerbjörn<sup>1</sup>, Fredrik Dalerum<sup>1</sup>*

<sup>1</sup> *Zoology department / Stockholm University*

Global warming is expected to be especially pronounced in the Arctic with a major impact on species interactions within Arctic ecosystems. Although arthropods dominate the interspecific interactions in the Arctic, accounting for the most complex networks, terrestrial vertebrate prey species such as small rodents, hares and birds have important ecosystem roles through top-down regulation of plant communities. These species interact strongly with terrestrial predators, such as birds of prey and arctic foxes, and vertebrate predator-prey dynamics are thus important for the regulation of Arctic ecosystems. Irregularities in small rodent cycles, which may be linked to warmer winter temperatures and effects such as changes in snow cover, has already affected the population dynamics of arctic foxes and snowy owl in Greenland and Scandinavia. The influx of marine resources is also important in Arctic systems as for example many birds depend on marine food resources. In winters, the sea ice is hunting ground for polar bears that prey on seals that are also scavenged by other predators. However, to date limited attention has been given to the topology of Arctic predator-prey interactions, nor in geographic variations in such topologies. This is unfortunate, since the effect of global warming is likely different in different regions of the Arctic, and the structure of trophic interactions can be a strong determinants to community responses to perturbations. With a combination of our own empirical data supplemented with literature data we will quantify interactions between terrestrial vertebrate herbivores and carnivores in different parts of the Arctic. We will compare the topologies of these interactions and interpret geographic variation in relation to global warming on ecosystems in different parts of the Arctic.

## Trait-associated loss of frugivores in fragmented forest does not affect seed removal rates

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Seed dispersal by frugivorous animals forms the basis for regeneration of numerous plant species. Habitat fragmentation has been found to be one major factor perturbing frugivore communities and dependent plant species. Yet, community-wide consequences of fragmentation for both frugivore and plant communities are still hardly understood. Here, we studied the effects of habitat fragmentation on the seed removal by frugivorous birds and mammals from nine fleshy-fruited plant species in Białowieża Forest (Eastern Poland). This last relict of old-growth lowland forest in Europe poses an exceptional reference site for studying the impact of habitat fragmentation on seed dispersal processes in temperate forest ecosystems. In particular, (1) we tested for associations between forest fragmentation and response traits of frugivores, i.e., forest specialization and body mass; (2) we studied the relationship between frugivore response and effect traits, i.e., centrality (number of consumed plant species) and interaction type (mutualistic vs. antagonistic); and (3) we assessed the feedback of fragmentation-induced changes on plant–frugivore interactions and seed removal rates. We found that fragmentation led to shifts in the frugivore community, associated with the response traits forest specialization and body mass, with fewer forest specialists and large-bodied frugivores in fragmented than in continuous forests. However, forest generalists and small-bodied frugivores were more central in the plant–frugivore associations than forest specialists and large-bodied frugivores. Therefore, the loss of vulnerable species did not result in reduced seed removal rates in fragmented compared with continuous forest. These results indicate, that seed removal may be relatively robust in spite of shifts in the frugivore community in forest fragments. The correlation between response and effect traits of frugivores highlights the importance of forest generalists and small-bodied frugivores for maintaining dispersal processes in fragmented forests in temperate regions. Yet, future studies should aim at quantifying the consequences of seed disperser loss on other aspects of dispersal, such as long-distance dispersal, spatial patterns of seed deposition, seed germination and plant regeneration.

## RETROMAR Thesis – Trophic functioning of coastal marine systems in Marquesas’ Islands, French Polynesia.

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The thesis project RETROMAR aims to characterize and understand the trophic functioning of reef ecosystems that are preserved from significant human activities in Marquesas’ Islands (French Polynesia), a highly isolated archipelago. In the face of ever-increasing human impact and climate change, information on the functioning of these systems, beyond structural description, is needed. The functional approach of the project is based on the study of the organic matter pathways within marine trophic networks, and will depend on the trophic level of organisms on one hand and, on the other hand, of the environmental characteristics of the studied sites. We will develop a multi-marker study that will give an approach combining several efficient techniques (bulk stable isotopes, compound specific analyses and fatty acids analyses; and then mathematic modeling of trophic processes). This combination will allow a very detailed reconstruction of the paths taken by the organic matter from the base of the trophic network to high-level predators. In addition, this combined approach will determine if, in Marquesas’ Islands, seasonal nutrient-rich upwellings are a major factor for interactions between pelagic and coastal ecosystems. Marquesas’ Islands are also characterized by a high endemism rate (~20% on average), and a focus on the place of endemic species within food webs will be useful to understand the global trophic functioning. Finally, similar results already known from other coral reefs submitted to anthropogenic influences in the South Pacific -and in other regions- will highlight the major functional differences between preserved coral reefs and those under impacts from human activities. Marquesas’ Islands are currently under discussion as part of the future UNESCO World Heritage, this work will provide knowledge on marine ecological and biological processes conducive to the implementation of consistent management plans.

## Climate change rocks the balance of power between trophic levels in the High Arctic

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With an overall change in climate, local abiotic conditions change differently in different areas, and individual taxa respond differently to specific climatic cues. These idiosyncratic effects will inevitably change the structure of interaction webs, causing further, cascading effects. How changes in interaction structure translate to changing patterns of apparent competition, and to changes in the top-down versus bottom-up influences, is yet to be established.

Here, the Arctic offers a convenient observatory: the arctic climate is warming twice as fast as the rest of the world, and the limited arctic species pool makes it feasible to accurately trace interaction structure. In this project, we focus on interactions among three trophic levels. First, a dominant flowering plant, second, insect herbivores feeding on this plant, and third, a community of parasitoids (flies and wasps) preying upon the herbivores. We aim to explain the changes seen in the food web structure with species-specific traits, such as the timing of species-specific life history events (phenology).

To dissect interactions, we employ molecular identification of adult parasitoids and their hosts, combined with molecular screening and identification of parasitoids from within lepidopteran larvae. For this purpose, we draw on our pre-existing, comprehensive reference library of DNA-barcodes from the study region. Ultimately, we link food web structure to ecosystem functioning, *sensu* the level of seed damage inflicted on the focal plant. To separate climate driven patterns from demographic dynamics, we use several spatial and temporal scales of: local environmental gradients, interannual variation at our focal study area, and geographic variation at a pan-Arctic scale.

By characterizing natural, small scale variance and annual turnover in a tritrophic food web, by assessing what proportion of this variance is due to climatic variables, and by examining how this translates into changes in ecosystem functioning, we seek to bridge a major knowledge gap: how complex natural systems respond to climate change.

## Experimental test of the effects of plant invasions on the structure of plant-flower visitor networks

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Invasions of nonnative plants into natural habitats are a pervasive threat to ecological communities. However, the consequences of plant invasions for plant-flower visitor networks are complex and difficult to predict. At a small spatial scale, invasive plants can either compete with native plants for pollinators, or enhance visitation of nearby native plants by attracting more flower visiting insects to the area. In either case, not only visitation of native plants, but also the structure of the entire plant-flower visitor network changes as the nonnative plant is incorporated into the local community. We conducted a field experiment to test the effects of the introduction of nonnative plants on plant-flower visitor interactions in several small grassland patches. We manipulated the structure of plant-flower visitor networks by introducing two species of nonnative plants, *Calendula officinalis* and *Dracocephalum moldavica*, in pots. We tested the effects of these two plant species separately and together. This allowed us to evaluate also the interactive effect of introduction of two plant species at the same time. We found that the introduced plants competed with native plants for flower visitors in most cases, thus decreasing visitation of native plants. However, a facilitative effect, i.e. increased native plant visitation was observed at one site after *Dracocephalum moldavica* was introduced and at another site after the introduction of *Calendula officinalis*. Introduction of both plants simultaneously produced non-additive, site-specific effects on visitation of native plants compared to experiments when the two plant species were introduced separately. Moreover, we observed fine-scale changes in the structure of plant-flower visitor networks after the introduced plants were incorporated into the networks. We highlight that the response of local plant-flower visitor networks to plant introductions depends on the composition of the local community, particularly in terms of species traits. Our experiment thus revealed varied effects of plant introductions on plant-flower visitor networks at a small spatial and temporal scale, which may help us understand how invasive plants affect natural communities of plants and flower-visiting insects.

## Interaction patterns among generalized plants species and their pollinators: are these interactions less structured?

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Species abundance and traits play an important role in plant-pollinator interactions. Morphological traits may act as a barrier, limiting the type and number of interactions and thus may affect species specialization degree and plant-pollination interaction structure. In this study we investigated how flower density, nectar tube depth, display size and the frequency distribution of flower-visitor proboscis length affect plant species specialization degree and plant-flower-visitor interaction structure. We studied the interactions among 16 co-occurring Asteraceae species and their flower-visitors, including bumblebees, solitary bees, butterflies and flies and analysed interaction generalization, asymmetry and size matching.

Overall, interactions were more connected, more even and more generalized compared to other networks. Despite these characteristics, the plant species differed largely in generalization degree and degree of size-matching, and interactions were asymmetric and nested. We found that the number of flower-visitor species increased with flower density and display size and decreased with nectar tube depth. Together these characteristics explained 82% of the variation in plant generalization degree. In contrast, the number of visiting individuals did not increase with flower head density and nectar tube depth. This can be explained by underlying correlations between nectar tube depth, flower head density, flower-visitor proboscis length and abundance. Shallow flowers, which were more dense, were visited by shorter-tongued insects which were less abundant. Size-matching occurred among flies, solitary bees and bumblebees, as species with a long proboscis avoided shallow flowers, while species with a short proboscis avoided deep flowers. The exact pattern differed among these insect groups and among butterflies, this pattern did not occur.

Our results indicate that even among generalized species, interactions are structured and predictable and influenced by species density and morphology. They highlight that size distributions of flower-visitors and correlations among plant traits are key determinants of pollination community structures. Overall, our results provide a better understanding on how plant and flower-visitor traits and their frequency distributions affect plant-pollinator interactions.

## Frugivory networks across a fragmented landscape

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Habitat fragmentation causes species with previously continuous spatial distributions to become metapopulations - local populations connected by dispersal. Species loss in fragmented ecosystems also poses a threat to ecological interactions, such as complex mutualistic bird-plant networks and their associated ecosystem functions. These metacommunity networks will likely be influenced by dispersal among patches, fragment size, and potential over-representation of exotic species that can exist in the matrix outside of the fragments. We investigated seed dispersal by birds for native and exotic fleshy-fruited plants within and among forest fragments of various sizes, across an urban ecological corridor in New Zealand. We constructed frugivory networks using faecal samples, focal observations and video recordings of birds feeding. We found that both native and exotic bird species play an important role in the dispersal of native plants but this depends on the season, fruit availability and fragment size. The majority of interactions occurred in larger fragments. It is important to recognise the role of exotic birds in the system and their contribution to native seed dispersal. We found that exotic birds preferred native fruit, but switched to exotic fruit when food availability was scarce. Therefore, food preference by exotic birds could facilitate the dispersal of native seeds without posing a major threat to the system as weed vectors.



## Four- trophic level food webs reveal the cascading impacts of an invasive plant targeted for biocontrol

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Biological invasions are a major threat to biodiversity and as such understanding their impacts is a priority. Ecological networks provide a valuable tool to explore such impacts at the community level, and are particularly insightful for biocontrol programs, including the potential for their seldom evaluated indirect non-target effects. *Acacia longifolia* is among the most widespread invasive species in Portugal, and has been recently targeted for biocontrol by a highly specific gall-wasp. We used a replicated network approach to: (1) identify the mechanisms by which direct and indirect impacts of *A. longifolia* can cascade from plants to galls and their parasitoids and inquilines; (2) disentangle the interaction networks between plants, galls, parasitoids and inquilines before the biocontrol; and (3) explore the potential for indirect interactions among galls, including those established with the biocontrol agent, via apparent competition. During 15-months, we collected a total of 219 plants and 31737 galls from native plants and identified 49 galler-, 65 parasitoid- and 87 inquiline-species. No galls were found on any of the 16 alien plant species. Invasion by *A. longifolia* simplified alarmingly the plant communities, with bottom-up effects, namely decreasing overall gall biomass, and richness, abundance and biomass of galls, their parasitoids, and inquilines. Correspondingly, we detected a significant decline in the interaction richness between plants and galls. The invasion tended to increase overall interaction evenness by promoting the local extinction of native host-plants of gall species. However, highly idiosyncratic responses hindered the detection of further consistent changes in network topology. Predictions of indirect effects of the biocontrol agent on native galls via apparent competition ranged from negligible to highly significant. Such scenarios are incredibly hard to predict, but even if there are risks of indirect effects it is critical to weigh them carefully against the consequences of inaction and invasive species spread.

## Using species interaction networks to understand community response to agricultural intensification

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With agricultural landscapes dominating Earth's terrestrial area and causing biodiversity declines worldwide, understanding and predicting how ecological communities respond to agricultural intensification is a critical conservation issue. Although interaction networks are a powerful tool for quantifying changes in community structure and could potentially be used to predict which species will persist in agricultural areas, we still have much to understand about how species interaction networks are influenced by agricultural intensification. In this study, we ask how agricultural intensification impacts network structure and whether network characteristics can be used to predict species' relative success in agricultural areas. To explore this relationship, we constructed plant-hummingbird interaction networks from 19 sites along an intensification gradient in a coffee-producing region of southern Costa Rica. We found that agricultural intensification led to a decline in specialization at both the whole network and individual species level. This indicates that while reciprocally specialized and rare species may be the most vulnerable to habitat conversion, some species are capable of changing their behavior to interact more opportunistically in agricultural areas. We expected hummingbird species' success (abundance) in agriculture to be predicted by its network characteristics: its abundance in non-agricultural sites, its overall specialization value, or its ability to change its interaction behavior (represented by a change in specialization value). However, we found that none of these factors alone nor combined predicted hummingbird success in agriculture. This suggests that, in this case, network characteristics do not predict the success of species in agricultural areas. While we found evidence that agricultural intensification impacts species interactions at the community and species level, more empirical research is needed to understand the drivers behind changes in community composition before network theory can be incorporated into predictions of community response to agricultural intensification.

## Indirect interactions between herbivores

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Most plants are attacked by a multitude of herbivores. When these herbivores share the same host plant, one herbivore might affect the other herbivore through induced plant responses. These plant-mediated indirect interactions between herbivores have been given little attention compared to direct plant-herbivore interactions. Indirect interactions can have large effects on community composition, population dynamics of herbivores and also on the levels of herbivory. The aim of our research is to study how browsing by large ungulates (mostly moose) affects tree growth and stand composition and the effects of those changes on insect herbivore on Scots pine. Understanding these indirect interactions can aid the understanding of ecosystem function and the relationships to biodiversity. From an applied perspective, understanding these interactions could contribute to development of wild life management and forest management strategies for land owners with the aim to reduce the risk of herbivore damage, which is especially important if it turns out that effects of different types of herbivores are synergistic in their effect on community composition and predation. Therefore we ask the following questions:

- How is the insect community on Scots pine affected by moose browsing?
- How is predation of insect herbivores by natural enemies affected by moose browsing?

We used an observational field study and an experiment to answer these questions. We found that excluding ungulate browsing affects the density of insect herbivores and the predation rates, while the diversity of the community was not affected.

## Opportunistic attachment assembles plant-pollinator networks

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Species and interactions are being lost at alarming rates and it is imperative to understand how communities assemble if we are to prevent their collapse and restore lost interactions. Using an eight-year dataset comprising nearly 20,000 pollinator visitation records, we explore the assembly of plant-pollinator communities at native plant restoration sites in an agricultural landscape. We find that species occupy highly dynamic network positions through time, causing the assembly process to be punctuated by major network reorganizations. The most persistent pollinator species are also the most variable in their network positions, contrary to what preferential attachment --- the most widely studied theory of ecological network assembly --- predicts. We suggest assembly instead occurs via an opportunistic attachment process. Our results contribute to our understanding of how communities assemble and how species interactions change through time while helping to inform efforts to re-assemble robust communities through restoration.

## Determinants of insect and bacterial communities in boreal forest mushrooms

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Fungi represent one of the key organisms interweaving different elements of the boreal forest into an integral whole. Despite explosive advances in detangling belowground networks, understanding aboveground interactions involving fungal fruitbodies lags behind. However, ectomycorrhizal mushrooms form the largest fungal biomass in boreal forests, providing abundant resources for many organisms. Our studies aimed to understand the role of mushroom diversity and identity on the community structure of bacteria and insects residing in fruitbodies. We sampled fruitbodies of ectomycorrhizal and saprotrophic fungi to test the hypotheses that mushroom's a) unpredictable and ephemeral nature preclude specialization of their consumers, b) bacterial communities are determined by characteristics of underlying soil.

Analyses of interactions revealed that mushroom identity significantly affected the community structure of their insect consumers and bacterial associates. Structure of both communities differed most between ectomycorrhizal and saprotrophic fungi, but also among different host taxa. In case of bacteria, these patterns were captured by high throughput sequencing but not the traditional culturing method. The former also revealed the superior effect of soil pH on the structure of bacterial communities, supporting the idea of their origin from surrounding soil. We suggest that the contrasting selection pressure resulting from host unpredictability and taxon-specific chemistry, has resulted in the prevalence of oligophages with mostly host genus-level preference among mushroom-feeding fungus gnats (Mycetophilidae, Diptera). In line with literature, exclusive specificity tends to be rare but the potential host range broad among mushroom fungivores, regardless of the degree of host specialization. However, we showed that the structure of host-consumer networks and the degree of ecological specialization involved, can be revealed only by individual-based analyses capturing differences in partner-to-partner interaction intensities. As a result, we suggest to reconsider the prevailing idea of considering fungivorous insects largely polyphagous due to the unpredictability of their hosts.

## Resource switching in a quantitative dung beetle – mammal interaction network

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Dung beetles rely upon mammal dung as their primary food source. Although associations between individual dung beetle species and dung from particular mammal species have been established through correlative studies, research directly identifying and quantifying the frequency of these pairwise interactions is lacking. Most dung beetle species are thought to be generalist feeders and may therefore show flexibility in their feeding in response to changes in resource availability. Here we present the first quantitative dung beetle - mammal interaction network enabling us to investigate possible responses of dung beetle communities to mammal species extinction through resource switching. Dung beetle data were collected in the Southern Atlantic forest, Brazil, using dung of native mammal species to identify dung beetle species diet breadth. Mammal surveys were carried out to identify sources and volume of mammal dung available to dung beetles. These data were combined to create a quantitative network that represents the association between mammal species, mammal dung volumes and dung beetle species. We present a bipartite network of seven mammal species and 15 dung beetle species, created from data of 435 dung beetles collected from 100 traps, and 56 mammal records. The network showed a structure and associations that were significantly different from random, and showed low levels of specialism in the dung beetle species which interacted with on average 5.8 mammal species. The mammal extinction scenarios simulated included mammal extinction based on mammal rarity, total dung volume and mammal extinction proneness. Mammal extinction based upon the total dung volume resulted the most rapid loss of dung beetles through secondary extinction in terms of dung beetle species richness, abundance and biomass. The generalist feeding preferences of many of the dung beetle species included in the network could explain the low impact of the loss of endangered or rare mammal species on dung beetle populations.

## Subsidy quality determines the direction of trophic cascades in an agroecosystem

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The “subsidy hypothesis” states that ecosystems receiving subsidies will experience stronger trophic cascades. Subsidies can, however, enter different compartments in the food-web and vary in their quality to the receiving compartment, but little is known how these factors will determine the relative importance of top-down versus bottom-up cascades. The effects of anthropogenic subsidies on trophic cascades in agroecosystems have received little attention, despite their implications for pest regulation and crop yield. Using large cage mesocosms in a long-term agricultural fertilisation experiment, we tested the hypothesis that subsidies in form of organic and mineral fertilisers will strengthen the regulation of herbivores via an increase in either top-down or bottom-up regulation forces. We also tested the idea that the magnitude and the direction of these will depend on whether the plant or the decomposer compartment of the food-web receives the subsidy, and on the quality of the subsidy. In support of the subsidy hypothesis, adding subsidy did indeed increase top-down regulation of herbivore abundances. The direction and strength of the trophic cascade depended on where the subsidy entered the food-web and the quality of the subsidy. Top-down forces dominated in food-webs where the detrital compartment was subsidized with organic fertilisation, while bottom-up forces were stronger when the plant received a subsidy of mineral fertilisation. Furthermore, the high quality, easily degradable organic subsidy propagated through the food chain faster than the less degradable organic subsidy, leading to a positive top-down trophic cascade of predators on plant, with potentially important implications for biological pest control in agriculture.

## Dissecting interaction structure - an empiricist's view

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The Spatial Foodweb Ecology Group is a Nordic research team active at two universities: the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden, and the University of Helsinki, Finland. We are particularly interested in how interaction webs are built from first principles: how (meta)populations of multiple species interact, and how species-specific characteristics blend with interspecific interactions in shaping what species occur where and at what abundances. To dissect interaction structure, we draw on a wide variety of techniques, with a particular fondness for molecular methods. In this poster, we will give a flash overview of some recent approaches and insights, with pointers to specific contributions during the two symposia.



## Landscape effects on pollination networks in Mediterranean gypsum islands

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Habitat fragmentation has operated historically on Mediterranean ecosystems. However, more needs to be understood about how fragmentation influences ecological interactions, particularly pollination. Gypsum outcrops are historically fragmented Mediterranean habitats and settings for the evolution of many endangered soil-specialist plants with narrow ranges. In this study, we aimed to determine how fragmentation (area and connectivity) affects: (i) the pollinator community composition, and (ii) the structural properties of pollination networks; and whether there are differences in the effects of fragmentation on: (iii) the number of interactions and visits among pollinator functional groups; and (iv) the number of interactions and specialization degree between soil-specialist and soil-generalist plants. We characterized the degree of fragmentation and the pollination network structures in 12 gypsum habitat fragments embedded in a cropland matrix during two consecutive years. We found significant relationships between fragmentation and network structure. The effects of fragmentation differed among pollinator functional groups, but not between soil-specialist and soil-generalist plants, in terms of number of interactions. However, the relatively higher pollinator specialization of soil-specialist plants suggests greater dependence on pollinators. Interannual variations in the network structures demonstrated the importance of temporal replication. These findings may help to identify the potential drivers of persistence of endangered soil-specialist plants with narrow ranges in a changing scenario.

## Plant-fungal mutualistic networks in arbuscular mycorrhizal symbioses: structure and seasonal dynamics in an alvar grassland community

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Arbuscular mycorrhizal (AM) fungi are obligate plant symbionts that have been interacting with plants since plants first invaded land. The long co-evolutionary history of these fungi with their hosts (about 85% of all land plant species), in conjunction with the relatively low diversity of these fungi has for quite some time raised the question of host specificity, that has yet to be answered. In recent years, applying the concept of ecological networks on mycorrhizal interactions has shown great promise in disentangling the issues of host specificity and the relationship between phylogenetic or functional groups of plants and mycorrhizal fungi. In this study, we use a unique dataset where all plant species in a 0.1 ha homogeneous plot of calcareous alvar grassland were molecularly sampled for root-colonizing AM fungi in two seasons (summer and autumn). We found a highly significant effect of both host plant species and host plant functional affiliations on AM fungal richness and community composition. Sampling season, while not affecting AM richness, did drive a shift in overall community composition. We shall discuss: (1) whether and how the symbiotic network of plants and fungi is structured; and (2) does the structure of the mutualistic network show temporal dynamics within growing season. The study tries to eliminate one of the most prevalent shortcomings of AM fungal community ecological studies – the inclusion of only a fraction of host plants – and enables us to make conclusions based on the entire active part of the mycorrhizal community.

## Specialized and facultative nectar-feeding bats have different effects on pollination networks in mixed fruit orchards in Southern Thailand

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Recent advances in the study of pollination networks have improved our ability to describe species interactions at the community level. In this study, we compared the abundance and network strength of facultative and obligate nectar-feeding bats to determine their roles in pollinating mixed fruit orchards. We were particularly interested in the effect of distance from forests and caves on the foraging activity of these two bat groups. For this study, we examined 10 pairs of orchards; each pair consisted of one orchard near to (< 1 km) and one orchard far from (> 7 km) the forest edge. We estimated the abundance of each bat group (nectarivorous vs. frugineectarivorous) using video observations to determine floral visitation rates. A pollination network was then created for each of the 20 study orchards and network strength was calculated for each bat group at each orchard. We found that nectarivorous bats showed higher abundance and network strength than frugineectarivorous bats. Both bat abundance and network strength were negatively correlated with distance to the nearest cave, however, only network strength was affected by distance to the forest. These results corroborate the importance of nectarivorous bats in pollinating crops within southern Thailand's mixed fruit orchards. Higher network strength of bats near forests and caves emphasizes the role of natural habitats as pollinator sources.

## Trophic Structure in Brown and Green Web Arthropods of a Temperate Hardwood Forest Using Stable Isotope Analysis: Preliminary Results and Future Directions

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Understanding trophic structure of an ecosystem is critically important for untangling interactions and food web dynamics. In forest ecosystems, arthropods function within all ecological roles, as prey to numerous animals, decomposers and nutrient cyclers, predators and parasitoids, and primary pollinators. As indisputable as their contribution to the ecosystem may be, their trophic structure in many places is not well understood. We sampled a wide range of arthropod taxa associated with both brown and green webs within a temperate hardwood forest at the Hubbard Brook Experimental Forest, NH, USA, and analyzed their stable carbon and nitrogen isotopes values for trophic resolution. In many ways, our results were consistent with known natural history and behaviors. For example, great variation in  $\delta^{15}\text{N}$  values were found among Coleoptera, Araneae, and Hemiptera, reflecting their wide dietary breadth and slight variation in specialists, such as Eulophidae. High isotopic values were found for predatory groups, such as Ichneumonidae, Araneae, and Staphylinidae, however, Staphylinidae were significantly higher than other arthropods tested. The high  $\delta^{15}\text{N}$  of the Staphylinid species may indicate that they are preying on second level taxa in both the brown and green webs. Staphylinidae is largely a facultative predatory family, so while they may feed primarily on other arthropods, they can feed on other nutrient sources. For example, some *Philonthus* species are known to associate with dung. Furthermore, this high trophic level was matched by a brown web taxon, Silphidae (carrion beetles). Here we present, in accordance with other studies, the deceptively high trophic signature of many brown food web arthropods, mistaking their trophic position. This preliminary investigation of food web structure has left us with many unanswered questions about the resolution of trophic structure in the brown food web using stable isotope analysis. We intend to expand the scope of the current study to include molecular methods to further understand the structure of the brown food web, linkages between the brown and green webs, and the relative contribution of these webs to forest stability.

## Multilayer networks reveal the spatial structure of seed-dispersal interactions across the Great Rift landscapes

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Species interaction networks have been analyzed as discrete and static entities, but this oversimplification can impair their applicability. We applied a multilayer network approach, explicitly accounting for the connectivity between layers, to investigate the spatial structure of seed-dispersal interactions across the habitats of the landscape of the Gorongosa National Park, Mozambique. We used multilayer modularity to identify seed-dispersal communities across habitats, for a range of inter-layer connectivity strengths. We found that the seed-dispersal network of Gorongosa is highly structured and modular, and influenced by the strength of the inter-layer connectivity. This influence is particular evident for low values of inter-layer strength. Many of the communities of dispersers span across several habitats, thus contributing to the spatial continuity of seed-dispersal. The modular structure of the spatial network was tested against two different null models: a) an intra-layer null model revealed that the structure of each habitat's network largely influences the modular structure of the multilayer network, being always significantly less modular than that of the null model, and b) an inter-layer null model revealed that the multilayer modularity is also significantly affected by the identity of the dispersers connecting the different habitats, and is always greater than that predicted by the inter-layer null model. The high multilayer versatility of primates, elephants, and civets, revealed their critical role maintaining seed-dispersal cohesion across habitats, securing both local (habitat level) and global (landscape level) dispersal of seeds. The relative importance of the dispersers could not be captured by other less complex metrics. We also show how the results from the multilayer approach differs from those of an aggregated network, which may reflect the information gain from considering the explicit connectivity between the different layers of a network.

## Mountain avens and muscid flies as key parts of the pollination network of the High Arctic

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Biodiversity is known to enhance ecosystem functioning and ecosystem services. The mechanisms, however, remain partly unclear – in particular what role individual species play in sustaining overall ecosystem functioning. Under natural conditions, most networks of interactions are simply too diverse to allow the dissection of contributions from individual nodes and links within the networks. High Arctic ecosystems with reasonable-sized species communities offer a rare opportunity for revealing these mechanisms.

To resolve the importance of different flowering plants for the insect community, I monitored flower abundances of plant species across 24 sites within the Zackenberg valley in North-East Greenland. I then related the visitation rates of pollinators to the local abundance of flowers. Out of 35 flowering species found, Mountain Avens *Dryas* sp. was the second most abundant accounting for 31 % of all the flowers observed at the study sites. However, *Dryas* received a full 99 % of all insect visits.

To examine the more specific role of insect visits for *Dryas* seed set, I focused on 15 sites within the Zackenberg valley. To describe the flower-visiting community at each site, I used sticky flower mimics to sample local insect communities and DNA-methods to identify them. This approach resulted in a highly-resolved dataset. In total, I captured 8 504 individuals and 185 species of arthropods with the sticky traps, including 70 % of all insect species known from the area. In terms of ecosystem functioning, the presence of pollinators significantly increased the seed set of *Dryas*. However, overall insect abundance and species richness had little or no effect on seed set. Instead, Muscid flies, especially *Spilogona sanctipauli*, significantly contributed on the successful seed set of *Dryas*.

All in all, most of the pollination function in this Arctic system seems to be carried out by only a few species – despite the diversity of insects visiting even a single plant species.

## Changes in the pollination network structure along an altitudinal gradient in Tenerife (Canary Islands)

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Previous experimental research has shown that diet breadth is a flexible pollinator trait partially affected by behavioural adaptation to resource availability. Yet, variation in diet breadth and its effects at the community scale remains largely unexplored. These community-wide patterns of plant–pollinator interactions can be studied with a species interaction network approach. Based on the Functional Biodiversity hypothesis FBH, which predicts higher pollinator biodiversity in species-rich plant communities, we asked whether the decrease in nutritional resources available for pollinators due to plant community simplification modifies pollinator niche breadth and species richness, and whether these changes affect network structure. For this purpose, we compared quantitative plant–pollinator visitation network assemblages along an elevational plant-diversity gradient in the oceanic high-mountain ecosystem of El Teide (Canary Islands). Variation in the composition of flower-visitor assemblages was wide, and mainly driven by the spatial replacement of species rather than by the loss of species along the diversity gradient. As predicted by FBH, pollinator richness decreased with elevation (i.e., with plant community simplification), but their niche breadth increased (e.g., higher linkage and lower specialization  $d'$ ). Accordingly, network specialization ( $H'2$ ) and modularity (Q) decreased whereas weighted linkage ( $lwp$ ,  $lwa$ ) increased suggesting higher generalisation (greater niche overlap) with reduction in plant diversity. Furthermore, plants at higher elevations showed significantly higher linkage level and strength, given that they were visited by more pollinator species which also visited them more frequently overall. This suggests increased plant-plant competition for shared pollinators in impoverished plant-communities, although facilitative interactions among plants -as found in other studies performed at higher altitudes- cannot be discarded. From an applied perspective, our results highlight the importance of considering the spatial variation of species interactions when aiming to build functionally consistent interaction networks across environmental gradients.

## Structure of pollination networks along an altitudinal gradient of Mt. Cameroon

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Plant-pollinator interactions are one of the most important biodiversity drivers. Studying of these relationships on an entire community level can help us to understand various patterns of current biodiversity, as well as history of its forming. Nevertheless, our knowledge on pollination networks changes along environmental gradients, crucial for our understanding of biodiversity organisation in time and space, is still highly limited. Such lack of data is even more apparent in some species rich tropical regions, especially in the Afrotropics. To fill this gap, we are studying pollination networks on Mt. Cameroon, a West African mountain offering the only complete altitudinal gradient of rainforest from lowlands to natural timberline in the whole continent. In four different elevations (650, 1100, 1400 and 2200 m a.s.l.), we record flower visitors of all plant species occurring along six 200m transects per elevation. To cover all plant-pollinator interactions, we record flowers by video-cameras for 24-h sessions. It allows us to efficiently cover visitors during whole days and nights, to increase amount of collected data, and to observe behaviour of individual visitors and thus consider potential pollinators only. Our methodology also covers all vegetation layers, including forest canopy, as well as both dry and wet season. Besides changes of network specialisation with altitude and season, we also focus on other network characterisations, including their modularity, nestedness or connectance. In the first phase of the project, we have focused presumably on the higher elevations, getting over 450 records of 100 plant species with diverse flower morphology and morphological specialisation. Although we are still processing the records, we have already detected numerous flower visitors from various groups of insects and vertebrates. In the symposium, first results from upper altitudes will be presented.



## More is less: consequences of eutrophication in insect food webs

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Eutrophication is one of the greatest threats of biodiversity of this century. In terrestrial systems, it is a successional process in which some plant species outcompete others becoming more abundant. It not only affects plant diversity by decreasing species richness and evenness, but also plant traits of importance for their consumers. Such modification of plant community is likely to have a bottom-up effect on emergent properties of networks and species interactions turnover threatening the resilience of the system. This study aims to analyse the process of eutrophication using an ecological network approach in order to understand its bottom-up effects on insect food webs in grasslands. The study was performed in a long term experiment in England, in which four fertilizers treatments (mineral, FYM, FYM+mineral and control) have been applied annually for 27 years. Plants, pollinators, leaf miners and parasitoids were sampled in 2016 with data being gathered on species richness and abundance, along with data on the interactions between the species. Preliminary results show that fertilizers increased herbivore and parasitoid abundance but not pollinator abundance, showing different responses between insect guilds but also within plant species since abundance of herbivores increased only in certain plant species. Current work involves analysing the structure of insect food webs in terms of emergent properties, interaction turnover and change in the role of plant species within the network.

## The effects of early-season caterpillar herbivory on the late-season oak-associated insect community

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The relationships between plants and their insect herbivores are among the most common ecological interactions. By consuming plant tissue, insects can trigger substantial changes in the physiology and chemical composition of their host plant. These changes can affect the quality of the plant as a food source for other herbivore species. This can lead to changes in the structure of the associated herbivore community, and the effects can spread further in the interaction web to include several trophic levels. We studied whether abundant insect herbivores affect other herbivore species through herbivory-induced changes in their host plant. As a study system, we used early-season free-feeding moth caterpillars and the leaf miner and galler community associated with oak trees at our study site in Oxfordshire, southern UK. We hypothesised that intense early-season feeding by caterpillars would change the quality of oak leaves as a food source, thus causing changes in the composition of the leaf mining and galling community colonizing the trees later in the season, and in patterns of parasitism on these herbivores. We manipulated early-season caterpillar densities on a set of 72 oak trees, to create trees with either suppressed or increased caterpillar abundance alongside non-manipulated control trees. Later, we surveyed the abundance of leaf miners and gallers. Preliminary analyses suggest that the abundance of miners and gallers was lower on trees with increased herbivory, while there were no changes in the diversity or community composition of late-season herbivores. Since herbivory-induced changes in the oaks may also affect higher trophic levels, we hope to assess this possibility through molecular analyses of leaf miner and galler larvae to detect patterns of parasitoid attack. The resulting data set could be used to test whether herbivory by hypothesised ‘keystone herbivores’ can change the structure of the interaction networks between herbivores and their parasitoids.

## Microhabitat use, mesocosms and models in multitrophic communities; using traits to predict community dynamics

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Ecological communities can be described as networks, with species as nodes and interactions as links. While the structure of these networks and strength of the links is important for ecosystem functioning, elucidating this for empirical communities is difficult, expensive, and time consuming. A promising method to elucidate structure and interaction strength without such a laborious process is to use species traits, such as body size and hunting mode, to predict species interactions. While there is a substantial body of evidence supporting this concept, there is still much to be understood before it can be used to accurately predict interactions. Here, we use a tritrophic community in controlled cage experiments to closely examine the effect of species traits – in this case, body size and habitat use – on trophic and non-trophic interactions and thus the population dynamics of the interacting species. We hypothesize that the body-size ratio of predator and prey, as well as overlap in habitat use, affects the strength of the predator-prey trophic interaction, but also the non-trophic effect of predators on each other. Predators which overlap in their habitat use to a greater extent with their prey should have a greater effect on their population dynamics, while predators which are more likely to be intraguild prey to a second predator may spend more time avoiding the predator and thus have less effect on the prey. We then use the information from the cage experiments to parameterize a model incorporating these traits to predict population dynamics of the interacting species. This is a crucial step, as any attempt to use species traits to predict network structure and ecosystem function effectively must be able to relate those traits to the effect on the interacting populations. Furthermore, there is frequently a disconnect between how and what is studied empirically vs theoretically. This is due to the particular strengths and difficulties of both methods, however it complicates comparisons and applications of findings between the two types of studies. By combining empirical mesocosm studies with a theoretical model, we aim to bridge this disconnect.

**Deciphering competition of alien (*Rhithropanopeus harrisi*, *Anadara kagoshimensis*) and native (*Brachynotus sexdentatus*, *Cerastoderma glaucum*) species in trophic networks using stable isotope analysis.**

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The comparison of two different trophic networks using stable isotope analysis can shed light on the character and position of common introduced species in these communities. The two adjacent marine basins – Black and Azov Seas have similar invaders, but differ by environmental conditions and species diversity. The crab *Rhithropanopeus harrisi* is one of the earliest known alien species in these seas (1930s). It is similar in size and life history traits to the native crab *Brachynotus sexdentatus*, which was common throughout the Sea of Azov prior to the invasion. The native species is no longer found in the area, whereas the alien crab is found throughout the sea. Presently there are no known areas where both of these species would coexist. Thus, a direct comparison is not possible. In the Black Sea (where the alien crab is not found) *B. sexdentatus* occupies similar trophic position to that of *R. harrisi* in the Sea of Azov, although higher crab predators are present in the Black Sea and absent in the Sea of Azov. This could be one of the possible reasons for the inability of *R. harrisi* to disperse in the North-Eastern Black Sea, even though it is likely that it has outcompeted *B. sexdentatus* in the Sea of Azov.

The invasion of *Anadara kagoshimensis* is more recent (1980s). *A. kagoshimensis* is present in both ecosystems. In the Sea of Azov it is mostly found together with *Cerastoderma glaucum*, which is one of the main dominant species there, but is rarely found in the Black Sea. Isotope analysis of *C. glaucum* has shown broad variability of its trophic position, possibly due to low selectivity during feeding; while *A. kagoshimensis* occupies a trophic position similar to that of *Mytilus galloprovincialis* in both seas. Based on the results of isotopic analysis and life history traits of these species it can be seen that *A. kagoshimensis* does not directly compete with *C. glaucum*, i.e. occupies different trophic niche, while it does compete with *M. galloprovincialis*, but generally occupies a different spatial niche. Overall *A. kagoshimensis* has incorporated into the invaded ecosystems without changing its structure or substituting local species.

## Topography affects plant-pollinator networks in a subtropical forest by altering plant sexual diversity

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Understanding the determinants of network dynamics of plant-pollinator communities is important for biodiversity conservation and ecosystem restoration. At a fine scale, topography affects microclimate, spatial distribution of species, and thus species composition. In turn, it may affect the network between plants and pollinators. Here, we studied the effects of topography on plant-pollinator networks to address the question: how do plant-pollinator interactions and network structures change between ridge and valley sites across different seasons? We observed 1776 interactions between 84 pollinator morphospecies and 28 flowering plants (9 dioecious plants) in the understory throughout the February to November flowering season in 2013 and 2014. From these data, we created plant-pollinator networks across four plots and four seasons and calculated three common network indices for each: interaction evenness, weighted nestedness and complementary specialization. We found that plant-pollinator communities had a high turnover between seasons, while the network structure properties remained unchanged. The diversity of plant sexual phenotypes and pollinator functional groups did not show significant difference between rainy and dry seasons. The compositions of plant-pollinator communities displayed a high turnover between ridge and valley sites. Floral abundance and pollinator visiting frequencies were higher in ridge sites than in valley sites. The diversity of plant sexual phenotypes and pollinator function groups were higher in ridge sites than in valley sites. In ridge sites, our networks displayed lower complementary specialization and interaction evenness. In networks with greater plant sexual diversity, our network indices indicated higher pollinator group diversity and lower network specialization, with most of the pollinators being generalists of the dioecious plants. This suggests that dioecious plants can provide quality resources for pollinators and communities with high plant sexual diversity can support and sustain robust plant-pollinator networks.

# Ecological Networks: Network theory

## Body-masses, food-web structure, animal diversity and ecosystem functioning

Monday  
13:30

*Ulrich Brose*<sup>1</sup>

<sup>1</sup> *German Centre for Integrative Biodiversity Research (iDiv)*

The distribution of body masses across species in general and the scaling of resource body mass with consumer body mass in particular have strong implications for food-web structure, community stability and ecosystem functioning. In this talk, I will present a novel global data base on consumer and resource body masses, which was compiled based on the collaboration among a global group of food-web scientists. The data allows unprecedented analyses of consumer-resource body-mass relationships across different interaction types (predators and herbivores), ecosystem types, movement types and species' metabolic categories. Together, these analyses provide deepened insight into the body-mass structure of natural communities and their consequences for the network structure of food webs.

These principles of food-web structures are used to formulate generic network models using consumer and resource body mass distributions as the only input parameter. These network models are used to predict the consequences of varying the diversity of animal consumers for different ecosystem functions (primary productivity, herbivory, predation, carbon respiration). Prior studies suggested that increasing animal diversity can lead to higher primary productivity via trophic cascades or to lower primary productivity if intraguild predation dampens the top-down pressure on plants. In the food-web simulations, we found that despite higher intraguild predation in more diverse animal communities, both the exploitation rates on plants and the animal community biomass increased. Unexpectedly, this did not negatively affect the plant community biomass because of a dynamic adjustment of the community body-size structure, which exhibited a shift towards larger, and thus energetically more efficient, species in more diverse communities. The plasticity of community body-size structure reconciles the debate on the consequences of animal species loss on primary productivity.

## The Roles, Function and Impacts of Humans in Complex Ecological Networks: Data and Theory

Monday  
10:30

*Jennifer Dunne*<sup>1</sup>

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Traditionally, most ecological research has studied ecosystems separate from humans. Network approaches provide a potentially powerful quantitative framework for understanding the roles, function and impacts of humans as a part of ecosystems, in terms of their direct and indirect interactions with other species. This talk will discuss recent approaches to data compilation, analysis, and modeling of food webs and interaction networks that explicitly include humans. Such research can provide a new lens for understanding aspects of the function and sustainability of coupled natural-human systems.



## Predicting the architecture of biodiversity

Monday  
9:00

*Dominique Gravel<sup>1</sup>*

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Ecologists have always been fascinated by the spatial distribution of species richness. But biodiversity is more than the distribution of species, it is also the collection of interactions among them driving ecosystem processes and supporting diversification of life. The representation of communities as networks of interacting species, populations and individuals, is a convenient formalism to describe the spatial distribution of biodiversity. It is however fairly limited by our capacity to document such networks over space and time. Another challenge is to predict the emergence and re-assembly of communities following species responses to global changes, such as range shifts, invasions and extinctions.

Predicting interactions among species that never co-occurred proves challenging, as traditional empirical methods of food web sampling (such as gut content analysis) cannot be performed. Inferring potential interactions among species of an arbitrary defined pool is a major step to predict the structure of emergent communities and their functioning. Development of predictive models of trophic interactions could greatly improve our understanding of large-scale food web structure and our capacity to anticipate major changes in ecosystem functioning. I will first review current approaches used to predict ecological networks of interactions, using information such as functional traits, phylogenies and co-occurrence. I will show that there are essentially two broad categories of methods, phenomenological and mechanistic, each of them with pros and cons.

Then I will present an analysis I performed to reconstruct trophic interaction networks among marine pelagic fishes, at the global scale. This unprecedented effort reveals that, surprisingly, marine food webs are remarkably well connected because of significant range overlap between species. While this connectivity provide considerable robustness to node extinction, it also suggest that disturbances can rapidly spread across the globe and has the potential to generate significant indirect interactions. I expect that, with the upsurge of interaction data availability, such methods will be more common and could potentially change our view of the conundrum of biodiversity's architecture.

## Robustness of weighted bipartite networks and skew due to structurally correlated extinctions

Monday  
16:00

*Miranda Bane*<sup>1</sup>, *Michael Pocock*<sup>2</sup>, *Richard James*<sup>3</sup>

<sup>1</sup> *Centre for Networks and Collective Behaviour, University of Bath, Claverton Down, Bath, BA2 7AY, UK,* <sup>2</sup> *Centre for Ecology and Hydrology, Wallingford OX10 8BB, UK,* <sup>3</sup> *Department of Physics, University of Bath, Bath BA2 7AY, UK*

Declines in insect pollinators suggest that pollinator communities may be sensitive to environmental change. Assessing the robustness of a network to secondary extinctions is a popular approach for predicting the sensitivity of such ecological systems. Long-standing approaches, such as deterministic co-extinctions with sequential primary extinctions, and recent advances, such as stochastic cascading extinctions, are applied to binary interaction data. There is demand for methods to work with weighted networks and a need to better understand the mechanisms leading to variations in robustness. Building on previous work, we have developed a new deterministic approach for modelling robustness with or without secondary cascades. Our model can directly incorporate information on interaction weights and so is suitable for weighted or binary networks. We show how this relates to existing robustness approaches.

Robustness varies due to the sequence of primary extinctions, but under random extinctions robustness varies markedly between networks. We explored mechanisms driving this variation and found that robustness is strongly influenced by the structural heterogeneity of the network. Also, the presence of cascades (when permitted), and hence the overall order of extinctions, is determined by the local structure of the network, resulting in a skewed distribution of robustness. We found this skew was driven by the presence of highly connected plant species. However, alternative models of robustness can also be developed in which effects are transmitted rather than attenuated (e.g. disease transmission) in which case the presence of highly-connected species decreases overall robustness.

Overall, it is valuable for ecologists to have methods to assess robustness to primary extinctions for weighted networks. However our findings indicate that care must be taken when interpreting the results of extinction models, and that robustness simulations should be used with an understanding of the specific mechanisms of the given model.

## Which traits of marine species explain the most variation in their food-web roles?

Monday  
11:50

*Alyssa Cirtwill<sup>1</sup> , Anna Eklöf<sup>1</sup>*

<sup>1</sup> *Linköping University*

Species' traits can affect their trophic interactions with other species, but it is not clear how these effects scale up from single interactions to shape species' roles within food webs. While previous work suggests that a small number of traits may be able to explain patterns of interactions within food webs, efforts to identify which traits are related to specific patterns have met with limited success. Here we use a motif framework (based on the simple building blocks of complex networks) to relate seven basic traits of marine organisms to their roles in six empirical food webs. As different traits are likely to shape the roles of basal resources, top predators, and intermediate consumers, we analyzed each group separately. First, we determined the motif positions associated with the major axes of variation in the roles of each group. Next, we identified the traits most strongly associated with the frequency of each position. This allowed us to interpret variation in species' roles in light of ecologically important traits.

We find that species' positions in three motifs (apparent competition, direct competition, and three-species food chains) are most strongly associated with the major axes of variation in the roles of all three trophic groups. The traits associated with these positions, however, vary between trophic groups. For basal resources, feeding environment and body mass are most strongly associated with species' roles. For intermediate consumers, a wider variety of traits are important. For top predators, trophic level is the trait most strongly associated with species roles. Taken together, our results suggest that relatively simple traits can provide a great deal of insight into species' roles within food webs. In particular, traits such as body mass and trophic level are strongly associated with positions in motifs with clear biological meanings (e.g., apparent competition). As these motifs have previously been studied in isolation, our results suggest that these smaller-scale results may also be relevant to large empirical communities. Our results also highlight trophic level and body weight as particularly important in shaping species roles, lending support to food-web models based on these traits.

## Assessing ecosystem services in ecological networks - the role of species traits

Monday  
11:30

*Anna Eklöf*<sup>1</sup>

<sup>1</sup> *Linköping University*

Ecosystem services are most often evaluated from a single species perspective, despite the fact that we do know species are existing in entangled networks of direct and indirect dependencies with other species. These dependencies are in many cases determined by the specific traits the species possesses. We also know how some single species provide multiple services, for example Mangroves sequester carbon, provide shoreline protection, serve as a nursery for other species and provide fuel for people. Each of these services arises from different species traits. Therefore, a deeper understanding of how ecosystem services relate to ecosystem structure and different traits will allow for a much more complete accounting of the total services provided by single key species or functional groups.

Here we aim to disentangle the actual role certain species traits play in ecosystem service provisioning. By analysing a set of complex ecological networks, where both species-specific traits and ecosystem service contribution has been defined on single species level, we can address the question whether certain traits - including species roles in the network - are particularly important for ecosystem service provisioning.

## Beyond species numbers: the effects of habitat loss on multi-trophic communities

Monday  
16:20

*Daniel Montoya<sup>1</sup>, Chris McWilliams<sup>2</sup>, Alan Champneys<sup>2</sup>, J. M. Montoya<sup>1</sup>, Miguel Lurgi<sup>1</sup>, Alix M. C. Sauve<sup>3</sup>*

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Changes in habitat are a key factor behind the current biodiversity crisis. With habitat loss it is not only species that ecosystems are losing, but also their inter-specific interactions. Further, interaction loss has the potential to significantly alter fundamental structural and stability properties of biological communities. However, little is known about how habitat destruction impacts diversity, structure and stability in communities with multiple interaction types. In this study, we present a synthetic theoretical analysis of community responses to habitat loss, which includes diversity and network properties, as well as several spatial and stability metrics. We use spatially-explicit, individual-based models to simulate the dynamics of multi-trophic communities, with both antagonistic and mutualistic interactions, under two habitat loss scenarios. We address three questions: (i) how do communities with multiple interaction types respond to habitat loss? (ii) does the proportion of mutualism to antagonistic interactions influence these responses?, and (iii) do communities respond differently to different habitat loss patterns? Our results suggest that habitat destruction affects the temporal stability of biological communities by shifting the distribution of interaction strength within the community and altering its trophic structure and spatial variability. These findings are not sensitive to the proportion of interaction types within a community, but they do strongly depend on the spatial pattern of habitat destruction. Given that landscape disturbances, including habitat destruction, are seldom randomly distributed (rather, they operate in a self-organised manner or are subjected to multi-scaled randomness), these results provide important insights into how communities respond to global change.

**Integrative machine learning and verification of trophic networks**Monday  
14:50*Alireza Tamaddoni-Nezhad<sup>1</sup>, David Bohan<sup>2</sup>, Stephen Muggleton<sup>1</sup> Alex Dumbrell<sup>3</sup>, Guy Woodward<sup>4</sup>*

<sup>1</sup> Dept. of Computing, Imperial College, London, UK, <sup>2</sup> Agroécologie, INRA, Dijon, France, <sup>3</sup> School of Biological Sciences, University of Essex, Essex, UK, <sup>4</sup> Dept. of Life Sciences, Imperial College, London, UK

Food -webs are important for explaining ecosystem structure and dynamics. However, establishing trophic interactions between the many hundreds of species in an ecosystem is usually resource intensive, requiring considerable investment in field observation and/or laboratory experimentation (e.g. molecular analysis). Machine Learning approaches can be used to narrow down the space of possible interactions, e.g. by inferring trophic interactions directly from species abundance data. These hypothetical trophic interactions can then be verified by empirical and experimental approaches such as molecular analysis. For example, a logic-based machine learning method was used (Tamaddoni-Nezhad et al., 2013) to automatically generate probabilistic trophic networks from an extensive sampling of invertebrates from 257 arable fields across the UK. The learned trophic networks were examined and it was found that many of the trophic links were corroborated by the literature. In some cases novel, high probability links were suggested, and some of these have been tested and confirmed by subsequent molecular analysis. In this paper we describe an integrative framework for automated discovery of trophic networks. The main elements of this framework are a) machine learning of trophic interactions (hypotheses generation), b) text-mining to identify potential novel hypotheses (trophic interactions under-represented in the literature) and c) molecular verification of novel hypotheses. Verified hypotheses are used as new background knowledge for machine learning of new hypotheses in the next cycle. We compare several machine learning approaches for trophic network inference and discuss their suitability for the proposed framework. We also discuss our current research project where this framework is used to model the impacts of global warming on trophic networks.

## Identifying significant trophic interaction modifications for population dynamics in ecological communities

Monday  
15:40

*J. Christopher D. Terry<sup>1</sup>, Michael B. Bonsall<sup>1</sup> Rebecca J. Morris<sup>2,1</sup>*

<sup>1</sup> *Department of Zoology, University of Oxford, UK,* <sup>2</sup> *Biological Sciences, Faculty of Natural and Environmental Sciences, University of Southampton, UK*

Conventionally, efforts to understand the dynamics of ecological communities have focussed almost exclusively on pairwise trophic interactions. However, it has been repeatedly demonstrated that trophic interactions can be strongly influenced by other species in the community. Improvements to our understanding of the impact of these trophic interaction modifications have been slow, in part due to the overwhelming complexity that these processes can introduce and the highly multi-dimensional demands on data. There is therefore a need for theoretical work to explore how significant processes can be identified to direct experimental work.

As an initial step to move from demonstrations of the potential impact of interaction modifications to an understanding of how they lead to consequences in a food web context, we have developed a set of approaches to conceptualise and quantify the different aspects of the strength of trophic interaction modifications. A feature of these metrics is that they stay closer to the underlying mechanism by maintaining the multi-species nature of the interaction, in contrast to traditional approaches that attempt to coerce the processes into pairwise non-trophic interactions. We apply these models of randomly-generated allometrically parameterised food webs to identifying properties of interaction modifications that distinguish those that are particularly significant in determining the dynamics of food webs. This theoretical work allows us to make suggestions of where experimental emphasis should be placed in practical efforts to understand the effect of interaction modifications in communities.

## Habitat Heterogeneity and Edge Effects in Model Metacommunities

*Michaela Hamm<sup>1</sup>, Barbara Drossel<sup>1</sup>*

<sup>1</sup> *Technische Universität Darmstadt, Institut für Festkörperphysik, Germany*

Spatial heterogeneity is an inherent property of any living environment and expected to favour biodiversity due to a broader niche space. Edges between different types of habitats can provide additional possibilities for species coexistence. In order to identify suitable strategies to protect or retain biodiversity in the face of anthropogenic changes in the spatial habitat structure, a deep understanding of how spatial structure affects diversity is essential. We explore the influence of spatial heterogeneity on species diversity using computer simulations. Heterogeneous landscapes are modelled by using two resource pools that have different sizes. The evaluation comprises the combined effect of dispersal and heterogeneity on local and regional species diversity. Species diversity is obtained by running population dynamics and evaluating the robustness (i.e., the fraction of surviving species). The key results for regional robustness are in agreement with the habitat heterogeneity hypothesis: The largest robustness is found in heterogeneous systems with intermediate dispersal rates. Robustness is larger than in homogeneous systems with the same total amount of resources. The edge effect was studied by arranging the two types of resources in two homogeneous blocks, creating an edge between these blocks. Different edge responses in diversity are observed, depending on dispersal strength. Local robustness is highest for edge habitats that contain the smaller resource in combination with intermediate dispersal. The results show that dispersal is relevant to correctly identify edge responses on community level.



## Biodiversity Atlas Sweden - Integrated biodiversity analyses

*Veronika Johansson<sup>1</sup>, Anders Telenius<sup>1</sup>*

<sup>1</sup> *Swedish Museum of Natural History/GBIF-Sweden*

Driven by scientific opportunity and societal challenges, biodiversity and ecosystems research are rapidly developing into big-data sciences, modeling processes that affect entire biotas and predicting system-wide effects of environmental change. Biodiversity Atlas Sweden (BAS) is designed to be the key driver and facilitator of these changes in Sweden, providing data and analysis services that offer rich opportunities for innovative, interdisciplinary research on biodiversity and ecosystems.

BAS will serve as the national Swedish GBIF node and have a joint data and analysis portal ([www.bioatlas.se](http://www.bioatlas.se)) presently covering occurrence and event-based data. Currently, data from molecular studies are not easily accessible for integrated biodiversity analyses but in the near future we hope to include sequence data in the BAS infrastructure.

A key function of BAS is to provide interoperable data and analysis services that can be flexibly combined by researchers to support innovative workflows, typically through the use of e.g. R packages or Python libraries. BAS will also provide graphical Web user interfaces for integrated analyses, through the Spatial Portal and related ALA modules, for users that prefer this approach. Primary BAS data sources will include biotelemetry, species observations, collections, environmental metagenomics and systematic monitoring programs. We further aim to broaden the evidence base of the portal to include molecular biodiversity data and data on microbial diversity (prokaryotes, unicellular eukaryotes, and microscopic fungi). BAS will allow users to combine these data with a wide range of environmental and climate data, “from soils to satellites”, which will open up exciting new possibilities for integrative analyses of biodiversity and ecosystem services nationally and internationally.

BAS fully subscribes to the principles of Open Science and its tools and services will be designed to facilitate reproducible research. The portal will be entirely based on software developed in international collaboration within the Atlas of Living Australia (ALA) – “The Living Atlases Community” - and the Global Biodiversity Information Facility (GBIF). Only during the last two years seven countries outside Australia has started national ALA-based portals; additionally twelve more countries are about to, or are considering implementing the ALA-system, including Sweden.

## Higher dimensionality of ecological networks under a unifying mechanistic framework

*Danis Kiziridis<sup>1</sup>, Lynne Boddy<sup>2</sup>, Dan E. Eastwood<sup>1</sup>, Mike S. Fowler<sup>1</sup>, Cheng-gui Yuan<sup>1</sup>*

<sup>1</sup> *College of Science, Swansea University, Swansea, United Kingdom,* <sup>2</sup> *School of Biosciences, Cardiff University, Cardiff, United Kingdom*

The mechanistic, trait-based study of direct interactions addresses proximate and evolutionary questions for various systems of trophic, parasitic, mutualistic, commensalistic, competitive, cooperative, and antagonistic interactions. However, interest in particular questions or systems has led to specific theoretical approaches. In response, we propose a framework for multilayer networks that unifies direct interactions in three stages. Specifically, direct interactions in any system: (1) appear directed by goals, with each goal dictating one network layer; (2) follow alternative subgoal pathways to goal success; and (3) occur via the confrontation of subgoal performance traits. We apply our framework to 563 empirical networks to compute their mechanistic dimensionality, i.e. the minimum number of traits that must be involved to mechanistically explain all the observed outcomes of a network. We show that dimensionality is: (1) underestimated when ignoring failures (so-called ‘forbidden links’); (2) higher than in previous analyses with phenomenological dimensions assuming one pathway to success; and (3) even higher under our novel assumption of alternative pathways to success. Alongside, our dimensionality offers a mechanistic explanation of rock–paper–scissors, intransitive networks in even well-mixed environments. In general, the framework provides a standardised and hence comparable form of how direct interactions occur. It could provide the mechanistic basis for proximate and evolutionary questions, inspiring hypotheses and trait-based models in coevolution, community assembly or invasion, and animal social network dynamics.

## A step towards multispecies MSY assessment by comparing singlespecies to pairwise perturbations in food webs

*Ágnes Mór  h<sup>1</sup>, Anett Endr  di<sup>1</sup>, Ferenc Jord  n<sup>1</sup>*

<sup>1</sup> *Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary*

Marine ecosystems are expected to feed more and more people, while we want to minimize the disturbance on them. The solution may be the improvement of maximum sustainable yield (MSY) assessments by putting them into multispecies context.

In spite of frequent critiques, singlespecies approaches are routinely used in determining MSY ignoring any interactions between species. However, it is clear that fish stocks are interdependent and should be considered simultaneously. The behavior of species depends on the context of the community, for example, on their position in a food web. To make strides for improving the multispecies approaches we need to better understand how local or nonlocal are the effects of changing the elements of a large interaction network.

We analyzed a hypothetical food web topologically and determined the key nodes, built a dynamical model and performed sensitivity analysis on it. After determining the community response to all singlespecies and all pairwise combinations of double species perturbations, we quantified the additivity of the effects for particular pairs of species.

Our results suggest that additivity is higher if both species have stronger indirect interactions, are quite central in the network and are involved in larger trophic flows.

In these cases, predictability is quite high and single-species MSY is useful in the context of multispecies fisheries.

## National scale patterns in plant-pollinator interaction networks

*John Redhead<sup>1,2</sup>, Ben Woodcock<sup>2</sup>, Michael Pocock<sup>2</sup>, Richard Pywell<sup>2</sup>, Adam Vanbergen<sup>3</sup>, Tom Oliver<sup>1</sup>*

<sup>1</sup> *School of Biological Sciences, University of Reading, UK,* <sup>2</sup> *Centre for Ecology & Hydrology, Wallingford, UK,* <sup>3</sup> *Centre for Ecology & Hydrology Edinburgh, UK*

Understanding the spatial structure and stability of plant-pollinator networks in relation to anthropogenic drivers is key to mitigating declines and maintaining pollination services. Using biological recording data, we constructed potential plant-pollinator networks at a 10km resolution across Great Britain. We developed a novel method for assessing robustness of multiple networks to global sequences of simulated plant extinctions. We analysed spatial patterns in network structure and their robustness to simulated extinctions in response to the spatial coverage of agricultural land. Metrics describing plant-pollinator network structure showed clear spatial patterns at the national scale. Coverage of agricultural land showed a positive relationships with generality (number of plants per pollinator) and with robustness to simulated extinctions. Our results suggest that landscapes dominated by agriculture have plant-pollinator networks are actually more robust to simulated extinctions. This is potentially driven by positive associations between the traits required to persist in highly agricultural landscapes (e.g. generalist pollinators and plants tolerant of anthropogenic disturbance) and the network properties conferring robustness to particular extinction scenarios.

## *Species Area Relationships and Lifetime Distributions in an Evolutionary Meta Food Web Model*

*Tobias Rogge<sup>1</sup>, David Jones<sup>1</sup>, Korinna T. Allhoff<sup>2</sup>, Barbara Drossel<sup>1</sup>*

<sup>1</sup> Technische Universität Darmstadt, Institut für Festkörperphysik, Darmstadt, Germany,

<sup>2</sup> Université Pierre et Marie Curie, Institute of Ecology and Environmental Sciences, Paris, France

Evolutionary food web models in space provide important insights into the stability and the functioning of ecosystems on long time scales and on large spatial networks, since the network structure is a highly nontrivial outcome of the ongoing processes of species addition, migration and extinction. Here, we investigate a spatial evolutionary food web model that includes no population dynamics but generates nevertheless a large variety of complex, multi-trophic networks. In this model, trophic species are characterized by a few traits that are based on their body mass and that determine the connections to other species in the network. The system of food webs on a grid of habitats evolves due to migration of species over the grid and addition of new species, which are modifications of existing species. Species survival depends on a criterion that takes into account the predators, the prey, and the competitors of the new species. We investigate this model depending on the parameters, which are mutation rate, migration rate and extinction rate. The long-term dynamics of the network can show layered structures and highly dynamical configurations with frequent extinctions. We find that species-area distributions as well as species lifetime distributions obey power laws the exponents of which depend on the parameters. We discuss these findings in an ecological context.

## Interactions between green and brown food webs: consequences on ecosystem functioning and stability

*Elisa Thebault<sup>1</sup>, Pierre Quévreux<sup>1</sup>, Kejun Zou<sup>1</sup>, Gérard Lacroix<sup>1</sup>, Sébastien Barot<sup>1</sup>*

<sup>1</sup> *IEES-Paris - CNRS, Paris, France*

Classical food-web theory on ecosystem functioning and stability has focused either on food webs based on primary production (green food webs) or on food webs based on detritus (brown food webs) and generally ignored nutrient cycling. However, nutrient cycling connects the two food webs, which questions traditional concepts of food web theory. Studying the mechanisms driving the interactions between green and brown food webs is crucial to understand the functioning and the stability of ecosystems.

We integrated these two food webs and nutrient cycling into ecosystem models.

First, our results show that cascading effects between green and brown food webs depend on distinct mechanisms. The direction and strength of cascading effects of the green food web on decomposer production are determined by the carbon/nutrient limitation of decomposers whereas the effects of the brown food web on primary production are mainly driven by the relative proportion of direct/indirect nutrient cycling in the brown web.

Second, our results question the stabilizing effect of asymmetry between energy channels in ecosystems predicted by recent models. We show that asymmetry between green and brown food web channels has either stabilising or destabilising consequences depending on the stoichiometric mismatch between producers and decomposers.

## Impact of stochastic migration on species diversity in meta-foodwebs consisting of several patches

*Tatjana Thiel<sup>1</sup>, Barbara Drossel<sup>1</sup>*

<sup>1</sup> *Technische Universität Darmstadt, Institut für Festkörperphysik, Germany*

The structure of space has an appreciable influence on the diversity of ecosystems. So far, there are only few theoretical studies investigating the population dynamics of food webs consisting of many species that can migrate between several patches, and in most of these models migration is a continuous, deterministic process. However, when migration events are rare (for instance because the patches are far apart), migration is a stochastic process and should be modelled accordingly.

For this purpose, we place a food web model consisting of many species on a spatial network of several patches and evaluate the stable configurations and long-time patterns that arise due to the population dynamics. These dynamics have a deterministic contribution from the processes within a patch, and a stochastic contribution due to migration events, which are implemented using the Gillespie algorithm.

We will discuss how the frequency of migration events impacts species diversity on local and regional scales. Furthermore, we investigate in particular the adiabatic limit in which population dynamics always reaches an equilibrium before the next migration event and we will discuss which long-term scenarios are possible.

# Molecular Analysis of Trophic Interactions



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## **MTI introductory workshop**

Michael Traugott & MTI-Plenary Speakers

This workshop aims at introducing ecologists into the basic technologies and concepts of molecularly analysing trophic interactions and to provide a common starting point for the MTI talks and posters. The workshop will start with an introductory presentation followed by a Question & Answer/Discussion section. Michael Traugott will introduce the basic concepts and technical approaches of molecularly analyzing food web interactions. The presentation will cover the characteristics of different sample types destined to assess predator-prey, herbivore-plant and host parasitoid interactions. The collection of samples in both aquatic and terrestrial systems as well as their storage will be briefly addressed followed by an overview on the most typical laboratory procedures such as DNA extraction, PCR, and the specifics of trophic molecular diagnostic work which often includes processing large sample numbers. Typical genes targeted for the detection of plant and animal food and their characteristics to assess trophic interactions at different taxonomic levels will be presented. This will be followed by introducing the basic concepts of diagnostic and sequence-based food and host identification as well as the quantification of food DNA. Finally, some considerations for the interpretation of molecularly derived trophic data and suggested Do's and Don'ts for MTI work will be given. After this presentation, the MTI plenary speakers plus the presenter are happy to engage in a discussion with the audience and to answer questions.

# MATI: Applied trophic interactions

## Conservation, DNA, and Ecological Networks: Methods and Challenges

Friday  
13:30

*Elizabeth Clare*<sup>1</sup>

<sup>1</sup> *Queen Mary University of London, London UK*

Over the last decade, DNA based methods for inferring diet and network analyses of ecological systems have exploded with new technologies and analytical techniques emerging faster than manuscripts can be published. This has generated excitement among a variety of research communities and particularly among conservation ecology where species' niche requirements are fundamental to understanding systemic perturbations and community response. However these developments also presents significant challenges in field, lab and analytical systems. It is often a race to keep up with developments rather than a solidification and validation of techniques. How then are we to actually apply these methods to real systems and address real questions?

In this seminar I will provide examples of analyses conducted across a diversity of habitats including deserts, tropical jungles, temperate forests and agricultural landscapes which cover antagonistic, mutualistic and parasitic interactions. I will discuss how to approach questions such as species co-existence, the conservation impacts of climate changes like El Niño and species response to forest modification and I will address the problems and challenges we face in these research frontiers.

In particular how should we view the molecular operational taxonomic unit (MOTU)? What is the impact of technological shifts and analytical choices? And what biases must we consider in our analysis? I will make recommendations, but also suggest what avenues are vital for validation and exploration.

In this seminar I will consider the shift from “diet analysis” to “network analysis”. This represents not just a scaling up of techniques, but presents very novel challenges we must consider if we are to truly measure and quantify community conservation of interactions between predators and prey, the dispersal of seeds and pollination and the relationship between parasites and their hosts. I will particularly focus on terrestrial systems involving bats, bees, plants and insects, but I will draw general conclusions relevant to a variety of applications in ecology, biodiversity and conservation.

## Molecular Analysis of Trophic Interactions: Defining and Evaluating Host-Parasitoid Associations in Biocontrol Programmes

Friday  
9:00

*Tara Gariepy<sup>1</sup>*

<sup>1</sup> *Agriculture and Agri-Food Canada, London Research and Development Centre, London, Ontario, Canada*

Biocontrol programmes involve the purposeful release of natural enemies to control or manage a pest. Ideally, these programmes reduce the population of a target pest below the economic threshold, and are expected to have minimal impact on non-target species, including rare, beneficial, and non-pest species. From the identification of the natural enemy community associated with a pest, to the release and establishment of an agent, a thorough understanding of trophic interactions improves the safety and success of biocontrol programmes. However, conventional approaches for the evaluation of trophic interactions do not always provide a complete picture of the species linkages in the system being studied. For example, rearing of target and non-target hosts to obtain their natural enemies is often plagued by high levels of mortality, which precludes the detection and identification of biocontrol agents that are developing inside these hosts. This can be an issue if the agent was responsible for the death of the host, but failed to complete development to a detectable or identifiable stage. Similarly, dissection may provide an indication that a given host is attacked by a natural enemy; however it typically yields an immature stage of the agent, which may lack the morphologically-distinguishing characteristics necessary to get species-level identification. Molecular tools facilitate the detection of trophic links as they permit the detection of small quantities of DNA and can provide species-level identification of both the host and the biocontrol agent(s), regardless of the life stage of the individuals of interest. Furthermore, there is the potential to detect DNA from multiple species and trophic levels simultaneously, thereby providing a more thorough view of interactions and key players which may impact the success and safety of a biocontrol programme. Here, examples of the application of molecular analysis of trophic interactions are presented across the continuum of biocontrol – in particular their use in defining the host range and host specificity of parasitoids used in biological control programmes that target agricultural insect pests.

## Analysis of spatio-temporal food resource exploitation by aphid predators may help to promote pest control services

Friday  
11:50

*Lolita Ammann*<sup>1</sup>, *Amy Ellison*<sup>2</sup>, *Rosemary Moorhouse-Gann*<sup>2</sup>, *Colette Bertrand*<sup>3</sup>, *Laia Mestre*<sup>4</sup>, *William O. C. Symondson*<sup>2</sup>, *Martin H. Entling*<sup>4</sup>, *Matthias Albrecht*<sup>1</sup>, *Felix Herzog*<sup>1</sup>

<sup>1</sup> Agroscope, Institute for Sustainability Sciences ISS, Zürich, Switzerland, <sup>2</sup> School of Biosciences, Cardiff University, Cardiff, United Kingdom, <sup>3</sup> French National Institute for Agricultural Research, Department of Environment and Agronomy, <sup>4</sup> University of Koblenz-Landau, Institute for Environmental Sciences, Landau/Pfalz, Germany, <sup>5</sup> Agroscope, Institute for Sustainability Sciences ISS, Zürich, Switzerland

Ladybeetles (Coleoptera: Coccinellidae) are major predators of aphid pests. However, pest aphids sustain ladybeetles only during brief infestation periods, and ladybeetle survival may be strongly impaired by insecticide applications. Thus, alternative aphid prey as well as floral resources outside crops are needed during the remainder of the year. Consequently, an understanding of ladybeetles' spatio-temporal resource use in agricultural landscapes is needed to predict their distribution and pest control delivery. To identify key aphid and pollen species consumed by ladybeetles, sampled during the season in different habitats of 24 agricultural landscapes in Switzerland and Germany, we applied molecular gut content analysis, targeting parts of the COI primer region in aphids and the ITS2 primer region in plants. The results from the genetic pollen analysis were complemented by visual pollen identification. Insights into the spatio-temporal food resource use of ladybeetles will hopefully inform landscape management aimed at enhancing pest control services by ladybeetles.

## Untangling molecular foodwebs to investigate the impacts of invasive non-native species on invertebrate communities in the UK

Friday  
16:20

*Marco Benucci<sup>1</sup>, Bernd Haefling<sup>1</sup>, Helen Roy<sup>2</sup>, Lori Lawson-Handley<sup>1</sup>*

<sup>1</sup> *University of Hull, Hull, United Kingdom,* <sup>2</sup> *Centre for Ecology and Hydrology, Wallingford, United Kingdom*

Invasive non-native species (INNS) are one of the main drivers of biodiversity loss worldwide and are also linked to changes in community structure and network complexity. These changes are likely to be a consequence of the ability of INNS to outcompete local species for shared prey, resources, and through direct predation of members of the same guild, so called intraguild predation (IGP). Detection of these interactions is essential for understanding the impacts of INNS on invaded communities, but this remains a considerable challenge for arthropod communities. Recent developments in DNA metabarcoding and Next-Generation Sequencing (NGS) provide powerful tools for assessing trophic interactions by extracting and analysing gut content. These interactions can then be modelled using ecological network analysis to describe community foodwebs. Here, we use this approach to investigate the impacts of two British INNS, *Harmonia axyridis* (Coccinellidae) and *Dikerogammarus villosus* (Gammaridae), on, respectively, arboreal and benthic freshwater communities in the UK. We first used controlled feeding experiments to investigate the accuracy and sensitivity of DNA metabarcoding for detection of prey DNA in *D. villosus* guts. Second, we performed gut content analyses of wild-sampled *D. villosus* and *H. axyridis* to determine the prey-predator and IGP interactions happening in the wild. The composition of their respective communities was also surveyed, pairing molecular and standard methods. Benthic communities were surveyed in paired invaded and non-invaded reservoirs; while arboreal communities were surveyed along a spatial transect ranging from the core to the edge of the invasion range. The main objectives of the study were to investigate i) the possibility to detect prey DNA in gut contents of *D. villosus* in experimental trials; ii) the diet breadth of *D. villosus* and *H. axyridis* wild populations in the UK; iii) the importance of IGP against native guild member taxa; and iv) the changes in structure and complexity of prey-predator networks in UK freshwater and arboreal communities influenced by these two INNS.

## Factors affecting diet diversity in a climate sensitive alpine small mammal in Himalaya

Thursday  
10:50

*Sabuj Bhattacharyya<sup>1</sup>, Deborah A. Dawson<sup>2</sup>, Helen Hipperson<sup>2</sup>*

<sup>1</sup> Centre For Ecological Sciences, Indian Institute of Science, Bangalore, India and Department of Animal and Plant Sciences, University of Sheffield, U.K., <sup>2</sup> Department of Animal and Plant Sciences, University of Sheffield, U.K.

Climate change is considered to be one of the greatest threats to world biodiversity. It can affect the distribution and population dynamics of a species directly or by altering its trophic interactions. Recent research has indicated population extinction and range contraction of herbivores due to change in food plant availability and composition during the late Miocene. Alpine small mammals, such as pikas (*Ochotona* spp.), a relative of rabbits and hares, play an important ecological role and are thought to be particularly vulnerable because they as well as many of the plant species upon which they feed are climate sensitive. Pika's live in isolated mountain top talus habitat, have limited dispersal ability and are strict herbivores. In spite of high pika species diversity, detailed information about Himalayan pikas and their interactions with native plants is scarce. Therefore, we selected the Royle's pika (*Ochotona roylei*) a widely distributed pika species in the Himalaya and investigated its diet across various habitats. We conducted habitat surveys and collected pika fecal pellets from five protected areas along an elevation gradient of 2600m to 4300m in the state of Uttarakhand, India, in Western Himalaya. Fecal DNA was extracted from 124 individuals using a commercial kit. Two genes (ITS2 and *rbcl*) were amplified and sequenced on an Illumina MiSeq sequencer to identify the plant species present. We blasted the sequences obtained against the NCBI sequence database to identify taxonomic units. We were able to identify 100 unique plant genera in the fecal samples, in contrast to 26 species that pika have been observed to eat, highlighting the increased sensitivity of molecular methods. We compare the diversity of plants in the pika diet across all of the regions sampled and examine possible drivers determining food selection, such as habitat structure, topography (elevation, aspect) or the availability of rock cover, using statistical models in an Information Theoretic framework. Finally, we will assess the vulnerability of pika to climate change mediated alterations in the plant species available by comparing their dependency on C3 versus C4 species.

## Beyond Moose: resource partitioning patterns in novel ungulate assemblages

Thursday  
10:30

*Joris Cromsigt<sup>1</sup>, Robert Spitzer<sup>1</sup>*

<sup>1</sup> *Dept. Wildlife, Fish & Environmental studies, SLU*

During recent decades, Europe's ungulate communities have changed dramatically, both through strongly increasing population numbers and through changing species compositions. Humans have strongly contributed to these changes through introduction of native and non-native species, range expansion of native species due to climate change and through changing land use. This human impact is rapidly creating assemblages with species compositions and relative abundances beyond any historical reference; i.e., novel species assemblages. The multi-species ungulate communities in Sweden are an excellent example of novel assemblages. New communities have been created by the introduction of non-native species, such as fallow deer and mouflon, and the ranges of native species such as red deer and wild boar have expanded far north. Very little is known about the functioning of these communities and their interaction with the environment. Novel assemblages include new interactions among species such as competitive interactions over food. These novel interactions might cause shifts in the species realized niches and thereby alter the functioning, structure and performance of species populations and communities and ultimately also their impact on the environment. In 2015 we started a 3+3 year program, Beyond Moose, which aims to understand trophic interactions in multispecies ungulate systems in Sweden's human-modified landscapes, and how these interactions affect the performance of these species and their impacts on the landscape. We will introduce the program and present initial results of a study where we use DNA metabarcoding to quantify how dietary niches may shift as a consequence of changing ungulate community compositions and land uses. Understanding how novel species communities work is essential for science-based management and our ability to protect biodiversity and ecosystem functioning.



## El Niño effects on nestedness and modularity of tropical seed dispersal networks revealed by DNA barcoding

Friday  
14:50

*Hernani F. M. de Oliveira<sup>1</sup>, Stephen J. Rossiter<sup>1</sup>, Elizabeth L. Clare<sup>1</sup>*

<sup>1</sup> *Queen Mary University of London*

The frequency of strong El Niño events is expected to increase in the near future with the cycle of 2015-2016 registered as one of the strongest on record. El Niño is one of the main drivers of fluctuations in precipitation, and this influences fruit production in the tropics, with potential cascading effects on frugivores. As environments get wetter, mutualistic interactions between frugivores and the plants they visit are thought to become more modular and less nested. To assess the impact of changes in rainfall associated with the 2015-2016 El Niño on nestedness and modularity of mutualistic networks, we constructed networks for frugivorous bats and plants for dry and wet forests of Costa Rica, which experienced, respectively, drier and wetter rainy seasons than average. We identified network links through DNA barcoding of fruit and fruit pulp in bat faeces, and tested the significance of the values of nestedness and modularity using null models and a Monte Carlo procedure. Despite the predicted contrasting effects of droughts and floods on network structure, we observed similar changes on nestedness and modularity for both dry and wet forests. We found higher values of modularity, but lower of nestedness in comparison to the null models. We found higher nestedness in the dry forest than the rainforest and reduced seasonality. Lower nestedness might decrease the number of species supported by the habitat as well as increase species competition. Although increased modularity might reduce the number of coexisting species in the environment, associated higher compartmentalization is thought to lead to greater stability, increasing resilience to disturbance, and reducing the chances of trophic cascades. Therefore, changes in network structure arising from El Niño are likely to have dual effects, leading to greater stability to external network impacts, but increasing competition among species within the community.

## Investigating the feeding preferences of two blood-feeding terrestrial leeches, using invertebrate-derived DNA analysis

Thursday  
16:20

*Rosie Drinkwater<sup>1</sup>, Joshua Potter<sup>1</sup>, Henry Bernard<sup>2</sup>, Matthew Struebig<sup>3</sup>, Elizabeth Clare<sup>1</sup>, Thomas Gilbert<sup>4</sup>, Stephen Rossiter<sup>1</sup>*

<sup>1</sup> School of Biological and Chemical Sciences, Queen Mary University London, London, UK, <sup>2</sup> Institute of Tropical Biology and Conservation, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia, <sup>3</sup> Durrell Institute of Conservation and Ecology, School of Anthropology and Conservation, University of Kent, Canterbury, UK, <sup>4</sup> Centre for Geo-Genetics, Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark

Blood-feeding terrestrial leeches are widely distributed across the tropics and assumed to be generalist ectoparasites, opportunistically attaching to passing vertebrates. However, this assumption has not been formally tested for common leeches in Borneo and it is expected resource partitioning among species might occur. The aim of this study was to investigate the dietary differences between two congeneric leeches, *Haemadipsa picta* and *Haemadipsa zeylanica*, in Malaysian Borneo, which display different searching behaviour and occupy different niches and strata in the forest.

We applied a recently developed invertebrate-derived DNA (iDNA) approach, which here refers to the isolation of mammal DNA from the guts of the leeches. Individuals from both species were collected from multiple degraded forest fragments, logged forest and primary forest sites at an experimental fragmentation project (SAFE project) in Sabah. To increase efficiency and throughput, for each species, multiple individuals were pooled for whole DNA extraction. Short fragments of mammalian 16S mitochondrial gene were amplified and sequenced using Illumina MiSeq technology, and the results compared to a reference database of candidate mammals from the region.

We report on the host preferences of our two focal leeches, and discuss the potential usefulness of applying iDNA to leeches for assaying and monitoring mammalian diversity in human-modified landscapes, as well as for gaining a better understanding the role of leeches in trophic networks.

## Prey DNA Detectability Half-Lives: Turning PCR Positives into Quantitative Predation Rates

Friday  
16:00

*Bastian Egeter<sup>1</sup>, Luke Easton<sup>2</sup>, Cailin Roe<sup>2</sup>, Bruce C. Robertson<sup>2</sup>, Phillip J. Bishop<sup>2</sup>*

<sup>1</sup> *CIBIO-InBIO, Research Centre in Biodiversity and Genetic Resources, Porto, Portugal,*

<sup>2</sup> *University of Otago, Dunedin, New Zealand*

Predation affects every facet of species ecology, either in the context of being a predator or being prey, including distribution, resource partitioning, population fluxes, circadian rhythms and evolution. Furthermore, predation influences important conservation and resource management issues such as the impact of introduced fauna on native prey or the impact of pest predators on commercially valued prey (e.g. pollinators, game or fish).

Diet analysis remains one of the most important tools in predation studies and PCR has largely surpassed traditional morphological diet analysis as a means of detecting prey items in animal gastrointestinal and faecal samples. Usually, DNA-based diet analysis results in qualitative (or semi-quantitative) Frequency of Occurrence data. Depending on the objective, these data alone can be useful, but where the objective is to measure the impact of one species on another, quantitative predation rates are necessary.

Here we present a case study that combined DNA-based diet analysis, prey detectability half-lives, predator density and prey availability to estimate the impact of introduced ship rats (*Rattus rattus*) on New Zealand's Archey's frog (*Leiopelma archeyi*), which is currently ranked as the world's most endangered amphibian (ZSL Amphibian EDGE list). Predation rates were estimated in a unit of frogs consumed per rat per night, information that was utilised by the Department of Conservation in the decision making process on providing rodent control. The study represents the first to measure prey DNA detectability half-lives in mammal stomachs, the first to compare half-lives of stomach and faecal contents for any vertebrate, and the first to report a quantitative predation rate from PCR diet analysis.

## Distribution, ecology and role of a parasitic ciliate on commercial penaeid shrimp in the US Southeast Atlantic: Insights gained using molecular interactions tools

Friday  
14:30

*Marc E. Frischer<sup>1</sup>, T. L. Walters<sup>1,2</sup>, A. R. Price<sup>1,2</sup>*

<sup>1</sup> *University of Georgia, Skidaway Institute of Oceanography, Savannah, Georgia 31411, USA,* <sup>2</sup> *Savannah State University, Savannah, GA, USA*

Parasites, parasitoids and pathogens are important components of complex ecosystems that, at times, can function as the most important predator in a food web. In the US Southeast Atlantic, penaeid shrimp including *Litopenaeus setiferus* (white shrimp), *Farfantepenaeus aztecus* (brown shrimp), and *Farfantepenaeus duorarum* (pink shrimp) support one of the most valuable commercial fisheries and are a critical prey species supporting a diverse and highly productive estuarine and coastal food web. However, since the late 1990's the shrimp fishery, especially in coastal Georgia and South Carolina, USA has experienced a significant decline. A contributing factor to this decline has been hypothesized to be due to a severe outbreak of shrimp black gill caused by a ciliate. DNA sequence-based analysis of the gill parasite small subunit rRNA gene identifies the proposed causative agent as being closely related to the non-pathogenic apostome ciliate *Hyalophysa chattoni*. However, morphological characteristics of the ciliate observed by electron microscopy are inconsistent with this identification. Although studies are ongoing to identify this ciliate, it was possible to develop a diagnostic PCR-based assay targeting the small subunit rRNA gene and use it to investigate the seasonal and geographic distribution of the parasite in wild shrimp populations and to discover its potential environmental reservoirs. Next Generation Sequencing of the gill microbiome confirmed that when black gill is at its peak, microeukaryotic communities were dominated by apostome-related ciliates, but over the year highly diverse communities of gill associates, including other potential ciliate, fungal, euglenozoid and amoeboid parasites are commonly observed. Improved molecular diagnostics and the ability to explore the diversity of potential parasites in shrimp provide important new insights into the impact and interactions of parasites on an ecosystem keystone species.

## The richness of predators containing striped cucumber beetle (*Acalymma vittatum*) DNA predicts pest suppression.

Friday  
11:30

Mary M. Gardiner<sup>1</sup>, Molly E. Dieterich Mabin<sup>1</sup>, Celeste Welty<sup>1</sup>

<sup>1</sup> The Ohio State University, Department of Entomology, Columbus, OH 43210 USA

The biodiversity-ecosystem function (BEF) hypothesis predicts that increased species richness within a trophic level supports greater resource capture. However, the increased predator richness commonly found within organic versus conventional agroecosystems does not always result in greater pest suppression. This variation may be due in part to inaccurate assessment of the taxa contributing to biological control. The striped cucumber beetle, *Acalymma vittatum* (Coleoptera: Chrysomelidae), causes damage via direct feeding and pathogen transmission to crops in the family Cucurbitaceae. The aims of this study were to: 1) identify the predators that contribute to *A. vittatum* suppression, and 2) determine if the richness of predators testing positive for *A. vittatum* DNA was negatively correlated with prey abundance. To accomplish this, we collected pitfall traps and hand-collected individual predators from four organic and four conventional summer squash farms during two 14-day time periods in 2015. DNA was extracted from all hand-collected samples and PCR was used to amplify *A. vittatum* DNA, if present within the gut contents of a sample. Of 1,215 hand-collected predators tested for the presence of *A. vittatum* DNA, 139 individuals from eight arthropod families were positive. We found that the community composition of predator families testing positive for *A. vittatum* DNA differed between organic and conventional farms ( $F_{3,6}=2.64$ ,  $p=0.02$ ); yet there was no effect of farm management ( $F_{1,23}=2.4$ ,  $p=0.14$ ) on the total abundance of predators testing positive. Additionally, there was no effect of farm management on the family richness ( $F_{1,23}=2.42$ ,  $p=0.13$ ) or the species richness ( $F_{1,23}=2.67$ ,  $p=0.12$ ) of predators testing positive. Across all sites, we found a neutral relationship between pest abundance and total predator abundance ( $F_{1,14}=2.90$ ,  $p=0.11$ ) and richness ( $F_{1,14}=51.69$ ,  $p=0.21$ ) measured in pitfall traps. However, when we compared cucumber beetle density and the richness of hand-collected predators testing positive for *A. vittatum* DNA we found a negative relationship ( $F_{1,14}=5.67$ ,  $p=0.03$ ), supporting the BEF hypothesis. This study illustrates that estimates of predator richness and abundance may not accurately predict the strength of pest suppression. Application of molecular gut content analysis proves a useful tool in advancing both the theory and practice of biological pest control.

## A DNA metabarcoding approach to analyse diet and foraging habitat preference in Bechstein's bat *Myotis bechsteinii*

Friday  
15:40

*Helen Hipperson<sup>1</sup>, Ian Davidson-Watts<sup>2</sup>, Natalie dos Remedios<sup>1</sup>, David C. Lees<sup>3</sup>, Terry A. Burke<sup>1</sup>, Roger K. Butlin<sup>1</sup>*

<sup>1</sup> Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield, S10 2TN, UK, <sup>2</sup> Davidson-Watts Ecology Ltd, Sunnymead, Watery Lane, Minsterworth, Gloucester, GL2 8JQ, UK, <sup>3</sup> Department of Entomology, Natural History Museum, London, SW7 5BD, UK

The technique of DNA metabarcoding of faecal samples is revolutionising studies of animal diet and providing greater insights into species' life histories and habitat use, information which can be a great aid to conservation. Here we use this approach to identify invertebrate prey species from faecal samples collected from Bechstein's bats across their UK range. We amplified two barcoding genes (COI and 16S) for faecal sample DNA from 98 Bechstein's bats to generate an average of 20,000 (following sequence data quality control) Illumina MiSeq sequencing reads per sample. We compared these data to a reference database of sequences from known invertebrate species, and identified Lepidoptera, Dermaptera (earwig) and Diptera (particularly crane flies) as being the most common prey items. Examining habitat preferences for many of these species revealed a strong habitat preference for deciduous oak-beech woodland with some birch and Salicaceae. These data give us new insights into the foraging habits of one of the rarest UK mammals and will help in guiding their conservation.

## Can landscape context affect intraguild predation of cereal aphid natural enemies?

Friday  
11:10

*Blas Lavandero*<sup>1</sup>, *Sebastian Ortiz-Martinez*<sup>1</sup>, *Karin Staudacher*<sup>2</sup>, *Michael Traugott*<sup>2</sup>

<sup>1</sup> *Universidad de Talca, Talca, Chile,* <sup>2</sup> *Innsbruck University, Innsbruck, Austria*

Landscape complexity may provide ecosystem services to agriculture through the provision of natural enemies of agricultural pests. Strong positive effect of adjacent semi-natural habitats on natural enemies in croplands has been evidenced, but the resulting impact on biological control remains unclear. In this study, the population dynamics of aphids, two groups of predators (coccinellid and parasitoids) were examined. Insects were sampled in 20 wheat fields, surrounded by structurally simple and complex landscape contexts in the Chilean central valley. Sampling was carried out throughout the wheat growing season every two weeks. The most abundant aphid species was *Sitobion avenae* (Hemiptera: Aphididae). Using molecular methods, the diet of the four most abundant coccinellid species was studied using species-specific and group-specific primers at each sampling date for all fields. Aphid detection followed temporal differences in coccinellid abundances between both landscape contexts. Most variation between contexts was due to temporal differences in intraguild predation (IGP) (predation of parasitoids and of other coccinellid species). Higher parasitism was observed in simple landscape contexts, than in simple ones, accordingly higher parasitoid consumption was also observed early in the complex set of fields. Contrastingly, the simple set of fields presented increased parasitoid consumption by coccinellids as abundance of coccinellids increased (mid to late season). More IGP among coccinellid species was observed late in the season for the simple set of fields, when compared to the complex set of fields. As discussed previously, there seems to be a temporal partitioning of the aphid resource by different natural enemy guilds, with some temporal overlap in IGP in response to the environmental and management context.

## Understanding ecological replacement through trophic interactions: The impact of introduced giant tortoises on island plant and animal communities

Thursday  
9:00

**Rosemary Moorhouse-Gann<sup>1</sup>, Nik Cole<sup>2</sup>, Martine Goder<sup>3</sup>, Michael Bruford<sup>1</sup>, Richard Young<sup>4</sup>, Nicolas Zuël<sup>3</sup>, William Symondson<sup>1</sup>**

<sup>1</sup> Cardiff University, Cardiff, UK, <sup>2</sup> Durrell Wildlife Conservation Trust and Mauritian Wildlife Foundation, Vacoas, Mauritius, <sup>3</sup> Mauritian Wildlife Foundation, Vacoas, Mauritius, <sup>4</sup> Durrell Wildlife Conservation Trust, Trinity, Jersey, Channel Islands

Species extinctions on islands are commonplace throughout history. Such extinctions can lead to dysfunctional ecosystems, especially when keystone species are lost. When the target species is extinct, a surrogate species can be introduced to restore ecosystem function (known as ecological replacement). In Mauritius, exotic giant tortoises (*Aldabrachelys gigantea*) have been introduced to restore dysfunctional ecosystems after the loss of their endemic counterparts, which were thought to be keystone grazers. Dietary analysis is essential to understand the impact that tortoises have on the plant community, food web, and ecosystem function. Metabarcoding of plant DNA from faecal samples provides us with an invaluable tool to recover detailed dietary information. Such dietary analysis is often inhibited by the absence of comprehensive DNA barcode libraries. Here we discuss what the dietary analysis of introduced tortoises and two endemic species, Telfair's skinks (*Leiolopisma telfairii*) and Pink Pigeons (*Nesoenas mayeri*), alongside field data is revealing about the impact of ecological replacement on food webs and ecosystem functioning on two ecologically important Mauritian islands. This work is assisted by the development of a comprehensive plant DNA barcode library. To the best of our knowledge, this is the first time that entire island plant communities have been barcoded in order to carry out dietary analysis and it lays the foundations for the construction of more comprehensive food webs to further our understanding of ecological restoration.



## Molecular gut profiling of the globally significant pelagic tunicate *Dolioletta gegenbauri* in the US South Atlantic Bight continental shelf: What are they eating?

Thursday  
16:40

*Tina L. Walters*<sup>1</sup>, *M. E. Frischer*<sup>1</sup>, *D. M. Gibson*<sup>2</sup>

<sup>1</sup> *University of Georgia Skidaway Institute of Oceanography and Savannah State University, Savannah, Georgia, USA,* <sup>2</sup> *Hampton University, Hampton, Virginia, USA*

Gelatinous metazooplankton play a crucial role in marine planktonic food webs. However, due to methodological challenges and reliance on laboratory cultivation approaches, the *in situ* diet of zooplankton with complex life histories and diverse prey choices remains poorly investigated. This is particularly true for the gelatinous zooplankton including *Dolioletta gegenbauri*, a pelagic marine tunicate that forms large blooms in productive subtropical continental shelf environments. Recently, molecular methods have become available which now make it feasible to directly identify the diets of predators. To investigate the diet of *D. gegenbauri* we developed a molecular gut profiling approach based on the use of a Peptide Nucleic Acid (PNA) PCR blocker. Using a doliolid-specific PNA blocker, it was possible to enrich the amplification of prey and parasite DNA from whole animal DNA extracts of doliolids. Gut contents from the water column, wild and captive-fed doliolids were profiled after PNA-PCR by denaturing HPLC (dHPLC), clone library (CL) and next generation sequencing (NGS) approaches. Studies were conducted during 5 summer cruises in the mid-shelf of the South Atlantic Bight. Prey sequences related to picoplanktonic dinoflagellates dominated the captive –fed doliolid diet. Comparison of gut profiles to available prey in the water column suggests evidence of prey selection towards larger prey species, including diatoms and metazoans. Metazoan prey were likely captured as larvae and eggs. Wild-caught doliolids contained more metazoan sequences than did the captive-fed doliolids representing 49% and 21% of the total sequence reads, respectively. Ingestion of metazoan prey suggests that metazoans may contribute both to the nutrition of doliolids and the potential role of doliolids as trophic cascade agents in continental shelf pelagic food webs.

## A simple and cost-effective molecular way to track predation on *Drosophila suzukii* in the field

Friday  
10:30

*Sarah Wolf*<sup>1</sup>, *Christiane Zeisler*<sup>2</sup>, *Daniela Sint*<sup>2</sup>, *Jörg Romeis*<sup>1</sup>, *Michael Traugott*<sup>2</sup>, *Jana Collatz*<sup>1</sup>

<sup>1</sup> Agroscope, Biosafety group, Reckenholzstrasse 191, 8046 Zurich, Switzerland, <sup>2</sup> Mountain Agriculture Research Unit, Institute of Ecology, University of Innsbruck, Technikerstrasse 25, 6020 Innsbruck, Austria

The invasive vinegar fly *Drosophila suzukii* (Matsumara) uses ripening fruits and berries for oviposition, in contrast to native *Drosophila* species that can only lay eggs into decaying fruit. The developing larvae of *D. suzukii* initiate a process of rapid fruit decay, resulting in dramatic losses in fruit production. So far, management of *D. suzukii* chiefly relies on chemical and cultural control, but additional measures such as biological control are asked for. Natural enemies, e.g. generalist arthropod predators, can play a role in pest management, but up to now those predators remain to be identified in the invaded areas.

We developed a simple and cost-effective assay with species-specific primers to detect DNA of *D. suzukii* in the guts of predators. Additionally, we also developed *Drosophila* group-specific primers to compare *D. suzukii* predation rates to those of other *Drosophila* species. When field-collected arthropod predators were tested with the assay, frequent consumption of *D. suzukii* by earwigs, spiders and predatory bugs was revealed. Therefore, these predators should be taken into account in management practices. On the one hand they can be susceptible non-target organisms, on the other hand they can be supported by conservational efforts and serve as potential biological control agents.

## Molecular gut content analysis of the invasive pest *Drosophila suzukii*

*Felix Briem*<sup>1</sup>, *Christiane Zeisler*<sup>2</sup>, *Karin Staudacher*<sup>2</sup>, *Michael Traugott*<sup>2</sup>, *Heidrun Vogt*<sup>1</sup>

<sup>1</sup> *Julius Kühn Institute - Federal Research Centre for Cultivated Plants, Institute for Plant Protection in Fruit Crops and Viticulture,* <sup>2</sup> *University of Innsbruck, Institute of Ecology, Technikerstrasse 25, 6020 Innsbruck, Austria*

The invasive pest *Drosophila suzukii* Matsumura (Diptera: Drosophilidae), commonly named Spotted Wing Drosophila, is native to the Sino-Japanese realm and increasingly threatening agriculture in the Americas and Europe with severe ecological and economic impacts. *Drosophila suzukii* is well adapted to feed on fruit-juice using its haustellum. Thus, studying its feeding ecology is challenging as no microscopically identifiable food remains can be found within its gut content. The current knowledge of host plants used is mainly based on studies dealing with egg laying and developmental success in fruits. Here, we present a DNA-based approach to examine plant DNA ingested by *D. suzukii* to provide a tool for accurate determination of host plants. Feeding experiments were performed with adult *D. suzukii* which were fed for 1 h with raspberry (*Rubus idaeus*) and then allowed to digest for up to 72 h. Applying diagnostic PCR, plant DNA was detectable for 24 h post-feeding in male and 48 h post-feeding in female *D. suzukii*. A significantly negative effect of time since feeding on *R. idaeus* DNA detection success was observed. To exclude contamination by DNA sticking on the flies' body surface, a bleaching protocol was tested. Fed female *D. suzukii* were dipped into mashed mistletoe (*Viscum album*) simulating an authentic contamination of the flies' body surface. All individuals were tested by diagnostic PCR for DNA of *R. idaeus* and *V. album* and we found that the bleach treatment was effective in removing non-gut content DNA. The bleaching protocol is currently applied to field-collected flies using a next generation sequencing approach. This will provide an important prove of concept how to assess the feeding ecology of *D. suzukii* under natural conditions.

## **There's something fishy going on: a stable isotope analysis of marine derived nutrients in the diet of Eurasian otters (*Lutra lutra*)**

*Lorna Drake*<sup>1</sup>, *W. O. C. Symondson*<sup>1</sup>, *R. A. McDonald*<sup>2</sup>, *E. A. Chadwick*<sup>1</sup>

<sup>1</sup> *School of Biosciences, Cardiff University, Cardiff, United Kingdom,* <sup>2</sup> *Environment and Sustainability Institute, University of Exeter, Tremough, United Kingdom*

Nutrient transfer between terrestrial and marine ecosystems usually refers to movements from inland regions to the sea, however, transfer of marine derived nutrients (MDN) upstream is also often significant. Nutrients from marine sources can be incorporated into terrestrial ecosystems through anadromous fish spawning, excreting or decomposing in freshwater streams and via consumption of marine species by piscivorous predators. MDN contribution to freshwater ecosystems can be detected through analysing carbon and nitrogen stable isotopes, which tend to be more enriched in marine ecosystems. We used stable isotope analysis to assess the contribution of MDNs to freshwater ecosystems in Wales and bordering areas in England using bone collagen and muscle tissue from Eurasian otters (*Lutra lutra*), an apex predator in Northern Europe. This allowed us to investigate the diet of otters along with the MDN contribution through consumption of marine prey at the coast followed by dispersal inland and through the consumption of anadromous fish in freshwater streams. Here we present our findings showing the significance of MDNs to freshwater ecosystems and the implications of these results for otter diet and behaviour. Further investigations into the diet of otters will be conducted using next generation sequencing to analyse prey identity and choice.

## Elucidating trophic functional groups of carabid beetles in cereal fields

*Britta Frei<sup>1</sup>, Yasemin Guenay<sup>1,2</sup>, Michael Traugott<sup>2</sup>, David Bohan<sup>3</sup>, Sandrine Petit<sup>3</sup>, Corinna Wallinger<sup>1</sup>*

<sup>1</sup> Mountain Agriculture Research Unit, Institute of Ecology, University of Innsbruck, Technikerstraße 25, 6020 Innsbruck, Austria, <sup>2</sup> Institute of Interdisciplinary Mountain Research, IGF, Austrian Academy of Sciences, Technikerstraße 21a, 6020 Innsbruck, Austria, <sup>3</sup> INRA Centre Dijon, 17 Rue Sully, 21000 Dijon, France

The frequent use of pesticides in arable land is strongly questioned for the threats to human health and biodiversity. Over the last few years, the regulation of weed and pest species via biological agents has gained considerable traction as a promising alternative. Carabid beetles have been identified to play a key role in biological control in temperate systems. However, apart from feeding on weed seeds and pest species, they also consume non-pest prey (alternative prey) such as collembolans and earthworms, which can play a contradictory role in the efficacy of pest and weed control. Most carabids are described as generalist predators, although some species appear to be predominantly carnivorous whereas others are rather strict granivorous. The trophic plasticity in omnivorous species i.e. how they switch between prey types according to environmental conditions, however, is poorly understood. Here, we sampled carabid beetles in cereal fields in three regions in Austria and France. Regurgitates of three most common species, *Poecilus cupreus*, *Pterostichus melanarius*, and *Pseudoophonus rufipes*, were screened with diagnostic PCR, targeting abundant cereal pest species, weed seeds and detritivorous non-pest prey groups. The outcomes of these analyses will contribute to a better prediction of pest and weed control ecosystem services provided by carabid beetles and their species specific role in the functioning of agroecosystems.

## Characterising the diet of brown trout: traditional prey identification versus DNA sequencing

*Bruno Gallo<sup>1</sup>, Guy Woodward<sup>1</sup>, Alex Dumbrell<sup>2</sup>, Emma Ransome<sup>1</sup>, Michelle Jackson<sup>1</sup>*

*<sup>1</sup> Department of Life Sciences, Imperial College London, Silwood Park Campus, Ascot, Berkshire SL5 7PY, UK, <sup>2</sup> School of Biological Sciences, University of Essex, Wivenhoe Park, Colchester, Essex, CO4 3SQ, UK*

Food webs are commonly characterised using visual observation of gut contents and feeding habits of predators, but new advances in molecular tools can provide more complex and sophisticated insights into trophic interactions. Molecular approaches are very powerful and can overcome several issues that are encountered with traditional approaches. Soft-bodied species are hard to identify as they get digested very quickly, cryptic species can't be separated by eye, damaged specimens and early instar larvae are almost impossible to distinguish under a microscope. By using molecular approaches and sequencing the DNA of prey species, there is the potential to resolve all links more efficiently and completely. In order to prove the efficacy of molecular gut content analysis, I studied a common and widespread predator with a wide diet and another species with a poorly known diet as a proof of concept in a model system where the food webs have already been characterised using traditional methods. These novel molecular approaches still need refining, but have the potential to overcome and replace what scientists have traditionally been doing, picking and identifying species under the microscope. Nevertheless, more research needs to be developed in this field to improve the depth and breath of molecular reference libraries and thus increase the speed of future molecular analysis.

## Deep sequencing unravels the dynamics of trophic links between carabids and weed seeds in arable land

*Yasemin Guenay<sup>1</sup>, Britta Frei<sup>2</sup>, Michael Traugott<sup>2</sup>, David Bohan<sup>3</sup>, Sandrine Petit<sup>3</sup>, Corinna Wallinger<sup>1</sup>*

<sup>1</sup> Institute of Interdisciplinary Mountain Research, IGF, Austrian Academy of Sciences, Technikerstraße 21a, 6020 Innsbruck, Austria, <sup>2</sup> Mountain Agriculture Research Unit, Institute of Ecology, University of Innsbruck, Technikerstraße 25, 6020 Innsbruck, Austria, <sup>3</sup> INRA Centre Dijon, 17 Rue Sully, 21000 Dijon, France

In agroecosystems, trophic interactions between species provide ecosystem services such as weed seed predation. Carabid beetles are an abundant and diverse group in arable land across Europe and are known to play a key role in regulating weed seeds. However, attempts to link carabid abundance to the level of weed seed predation have delivered ambiguous results. Moreover, the trophic functional groups of the different carabid species are not that clear-cut. Most findings are based on laboratory feeding experiments making it difficult to evaluate the actual role of carabid beetles as seed predators in agroecosystems. Here, we used next generation sequencing (NGS) to analyze the range of seed species in the gut content of different carabid species. Beetles were collected in organic wheat fields in three different regions in France and Austria during two collection periods, in May/June and July/August 2016. Regurgitates of the three most frequent carabid species, *Poecilus cupreus* (Linnaeus, 1758), *Pseudoophonus rufipes* (DeGeer, 1774), *Pterostichus melanarius* (Illiger, 1798), were molecularly analyzed using a general plant primer targeting the *trnL* region of the chloroplast DNA. The information which plant seeds are consumed by which carabids and how variable these trophic linkages are in space and time will provide fundamental information for assessing if this ecosystem service provided by carabid beetles is robust and resilient and whether it might be used in achieving international goals of reducing herbicide applications without compromising crop yields.

## Predation by anthocorid bugs (Heteroptera) on the common pear psyllid *Cacopsylla pyri* (Homoptera, Psyllidae)

*Bjørn Arild Hatteland*<sup>1,2</sup>, *Elena Therese Wulff-Vester*<sup>3</sup>, *Ida Gundersen*<sup>3</sup>, *N. Agusti*<sup>4</sup>, *L. Sigsgaard*<sup>5</sup>, *Nina Trandem*<sup>3,6</sup>

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Anthocorid bugs are among the most abundant predators in fruit orchards, and are considered a significant part of the natural control of pome fruit pests. In this study we focused on *Anthocoris nemorum* and *A. nemoralis*, assessing their importance as predators of the pear psyllid *Cacopsylla pyri*, which is a common pest in pear orchards. Semi-field experiments as well as a field survey using spatial and temporal scales were used to study predation by these two anthocorids on *C. pyri* in a Norwegian pear orchard. Molecular gut-content analyses of the predators were also carried out, using conventional PCR. The semi-field experiments showed that anthocorid bugs may effectively reduce the numbers of psyllids, and that commercially available *A. nemoralis* (imported) were inferior to locally collected *A. nemorum*. The abundance patterns in the field survey together with the gut-content analyses confirmed the importance of anthocorids in conservation biological control in fruit orchards. More specifically we also found differences between the two species of predators. *Anthocoris nemoralis* is used in augmentative biological control in Europe and is considered to have a high preference towards psyllids, while *A. nemorum* is regarded to be more polyphagous. Our results support the former assumption to some degree, but *A. nemorum* still seems more important in Norwegian fruit orchards, being much more abundant and showing high predation rates. A complicating factor was the presence of ants, which reduced the anthocorid predation of psyllids regardless of species.



## Food webs in barley fields: implications for biological control

*Mattias Jonsson<sup>1</sup>, Eve Roubinet<sup>1</sup>, Klaus Birkhofer<sup>2</sup>, Barbara Ekbom<sup>1</sup>, Gerard Malsher<sup>1</sup>, Karin Staudacher<sup>3</sup>, Michael Traugott<sup>3</sup>*

<sup>1</sup> *Swedish University of Agricultural Sciences,* <sup>2</sup> *Brandenburg University of Technology, Cottbus-Senftenberg, Germany,* <sup>3</sup> *University of Innsbruck, Austria*

The feeding patterns of generalist predators have important implications for biological control, but in the past it has been difficult to get a comprehensive picture of predator food webs due to difficulties in quantifying feeding links. We have constructed food webs of generalist carabid beetles and spiders and their prey in Swedish spring-sown barley fields using multiplex molecular gut content analysis, and explored implications for cereal aphid biological control. We investigated the presence of DNA of 13 different intraguild and extraguild prey types in the guts of >3500 generalist predators in 10 barley fields during the aphid colonization and population growth phase. We found that although carabid beetles and spiders frequently fed on a range of different prey types, they maintained high levels of aphid pest predation during both phases of aphid population dynamics. Neither feeding on intraguild prey or alternative extraguild prey diverted the predators from aphid feeding. Overall we found strikingly low levels of specialization in the food webs, suggesting a high level of functional redundancy in the predator communities. However, we still detected certain changes in prey choice over time with small carabids and spiders preferring to feed on aphids early in the season, while larger carabids preferred to feed on aphids later on. In a newly started project we will explore whether the high redundancy observed in these generalist predator communities can provide resilience against climate change and environmental variability.

## High-throughput molecular methods reveal the importance of farming practices as driver of the trophic structure and the biological control potential in carabid beetles

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Quantitative food webs provide a powerful framework for understanding and sustainably managing fundamental ecological functions. However, drawing a comprehensive picture of trophic interactions in real food webs is challenging because of (i) their inherent complexity; (ii) our limited capacity to empirically quantify trophic interactions. DNA-based methods such as barcoding and metabarcoding are already revolutionizing our capacity to deal with biological complexity and offer a robust methodological framework for studying complex species interactions. Here, we aim at understanding how the delivery of key ecosystem service such as biological control could be optimized through the management of multitrophic interactions. Focusing on a methodologically challenging group of generalist insect predators - carabid beetles - we present a unique approach combining DNA metabarcoding diet analysis and diagnostic multiplex PCR. We hypothesized that agronomical factors such as the type and the intensity of farming practices (i.e. conventional vs organic farming) would be the main determinant of carabids' trophic choice in a representative cereal agroecosystem in Central France. More than 700 individuals from two dominant carabid species were collected in the Long-Term Research Area "La Cage" near Versailles. Their gut contents were analyzed using (i) a combination of four universal animal and plant primers and Illumina MiSeq high-throughput sequencing; (ii) a set of three 'ready to use' multiplex PCR assays comprising 45 prey-specific PCR primers that target a wide range of common invertebrate taxa. Plants and arthropods comprised 95% of the carabid diet with the type of farming practices explaining significant part of the variation ( $p < 0.01$ ). No significant differences in trophic choice were observed between the two carabid species ( $p > 0.5$ ). Differences in prey availability most likely explain our findings. For instance, carabid diet was the most diversified in the fields under organic farming where the consumption of pest species (weeds and aphids) was also the highest. Taken together these results highlight the importance of agronomic factors as drivers of the trophic structure and the biological control potential of service-providing carabid communities. We discuss specific actions for informed, data-driven agroecosystem management, and emphasize the value of DNA-based methods for tackling questions of ecological and societal relevance.

## Can protist predation help protect plants against diseases?

*Ida Karlsson*<sup>1</sup>, *Zhilei Gao*<sup>2</sup>, *Giel Scheepers*<sup>2</sup>, *Hanna Friberg*<sup>1</sup>, *Alexandre Jousset*<sup>2</sup>

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Soil protists is a highly diverse but often overlooked group of microbes. Most free-living soil protists are consumers of other microbes and exert a considerable selection pressure on microbial populations in the rhizosphere. Protist predation contribute to nutrient release in the soil and increased plant growth. However, their effect on other functions performed by the soil microbiome, such as disease suppression, is less well known. We hypothesize that protists can help protect plants against diseases in two ways: 1) by directly feeding on plant pathogens and 2) by selecting for beneficial microbes and stimulating their biocontrol activity.

In a series of experiments, ranging from lab to field scale we study the effect of soil protists on disease suppression. First, we study the impact of grazing on bacterial community structure and the prevalence of biocontrol genes in soil microcosms containing semi-natural bacterial communities with four protist species. Second, we are testing the ability of different protist species to induce disease suppression of *Fusarium* foot rot of wheat in a pot experiment. Third, we will assess the potential of protists as predictors of soil disease suppressiveness in field trials in Sweden where we will relate protist and bacterial communities in agricultural soils to disease suppression in the *Fusarium*-wheat pathosystem. Our aim is to develop more sustainable strategies to protect plants from pathogens.

## Quantitative significance of different prey types in the *in situ* diet of *Dolioletta gegenbauri*

Lauren Lamboley<sup>1</sup>, T. L. Walters<sup>1,2</sup>, M. E. Frischer<sup>1</sup>

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Gelatinous zooplankton, including the globally significant pelagic tunicate *Dolioletta gegenbauri*, play a crucial role in marine planktonic food webs on productive subtropical continental shelves. However, because of their fragile nature, *in situ* investigations of these organisms, including feeding studies, are rare. Consequently, little is known about their trophic interactions including feeding behavior, prey selection, and *in situ* feeding rates. Based primarily on laboratory studies with captive animals, microalgae are believed to comprise the primary diet of *D. gegenbauri*. However, recent investigations utilizing PCR-based molecular gut content analysis (MGCA) approaches that avoid bias associated with cultivation have suggested that nanoplankton and metazoan prey comprise a significant portion of the doliolid diet. Additionally, these studies have also suggested that doliolid prey DNA digestion is minimal, indicating that prey ingestion can be reliably estimated using quantitative PCR (qPCR) targeting prey-specific 18S rRNA genes. In this study we developed and empirically validated qPCR assays targeted to 4 prey types representative of the size spectrum of the *in situ* diet of *D. gegenbauri* on the continental shelf of the US South Atlantic Bight (SAB). These assays are being utilized to investigate the diet of wild caught *D. gegenbauri*. Nearly 200 individuals representing various life history stages and oceanic conditions were captured during a series of monthly cruises in the SAB from 2015 and 2016 and subsequently analyzed. These studies are providing novel insights into the diet and trophic interactions of a globally significant gelatinous zooplankter, *D. gegenbauri*.

## Impacts of habitat modification on predator-prey interactions in an upland, insectivorous passerine

*Lisa Malm*<sup>1,3</sup>, *Nick Littlewood*<sup>2</sup>, *Alison Karley*<sup>3</sup>, *James Pearce-Higgins*<sup>4</sup>, *James Kitson*<sup>1</sup>, *Darren Evans*<sup>1</sup>

<sup>1</sup> Newcastle University, Newcastle, UK, <sup>2</sup> The James Hutton Institute, Aberdeen, UK, <sup>3</sup> The James Hutton Institute, Dundee, UK, <sup>4</sup> British Trust for Ornithology, Thetford, UK

Changes in landscape management and habitat modifications are common reasons for declines of many bird species. To understand the cause of these declines in insectivorous species, we need a better understanding of how their foraging resources are affected. Studying prey abundances alone can give an inaccurate picture of prey availability and confirmed predator-prey interactions are preferred over independent observations of the two. New non-invasive methods of analysing diets are necessary for undertaking repeatable and large scale surveys to understand the scale of environmental change impacts on breeding birds. A growing number of studies have shown that it is possible to identify the DNA of prey species found in avian faeces, but few have examined the impacts of habitat modification on bird-insect interactions.

This study was carried out at Glen Finglas, Scotland, where a fully-replicated, landscape-scale experiment examining the effects of different livestock grazing intensities on upland plant and animals has been running since 2003. Previous studies have shown that grazing intensity affects the abundance and foraging behaviour of breeding meadow pipits (*Anthus pratensis*). However, it is unclear what insects nestlings are provisioned by parents and whether this differs between grazing treatments. In this study, we investigated the effects of grazing pressure on the composition of arthropod prey provisioned to meadow pipit nestlings. Faecal sacks were systematically collected across four grazing treatments during different stages of nestling development. DNA was extracted and a region of the mitochondrial cytochrome c oxidase subunit 1 (CO1) was targeted using universal primers suitable for arthropods and all samples were tagged, pooled and sequenced using a high-throughput protocol. Here, I present the results of the study and discuss the consequences for meadow pipit productivity.

This work highlights the applicability of molecular techniques in the process of answering land management questions based around avian food-webs. By merging DNA-metabarcoding with ecological network analysis I discuss how previously intractable questions in avian ecology can be answered as well as how these techniques can be used in conservation and restoration of habitats and for species of conservation concern.

## Jellyfish in albatross diets and implications for ecosystem monitoring

*Julie McInnes<sup>1</sup>, Rachael Alderman<sup>2</sup>, Mary-Anne Lea<sup>1</sup>, Ben Raymond<sup>3</sup>, Bruce Deagle<sup>3</sup>, Richard Phillips<sup>4</sup>, Andrew Stanworth<sup>5</sup>, David Thompson<sup>6</sup>, Paulo Catry<sup>7</sup>, Henri Weimerskirch<sup>8</sup>, Cristián G. Suazo<sup>9</sup>, Simon N. Jarman<sup>10</sup>*

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Gelatinous zooplankton form a large biomass component of marine ecosystems, but are considered to be uncommon in the diet of most marine top predators. However, diet of key groups like seabirds have conventionally been assessed from stomach content analyses, which cannot easily detect soft-bodied prey. We investigated albatross diet using DNA metabarcoding of scats to assess whether gelatinous zooplankton have been underestimated in seabird diets. Black-browed and Campbell albatross scats were collected from eight circumpolar breeding colonies over consecutive breeding seasons to provide a broad scale assessment of prey groups consumed. Fish was the main dietary item at most sites, however Scyphozoa jellyfish comprised 19.8% of DNA sequences (present in 36.8% of samples) and made up 50% of sequences (present in 80% of samples) at some sites. We also found that cephalopod DNA was detected less frequently than by conventional methods. The diet of marine top predators can be used to identify changes in the overall species composition of an ecosystem. However, each method of diet analysis has its own inherent bias in prey detection. Such biases may impact our detection of important ecosystem regime shifts. Warmer oceans and overfishing of fish are predicted to favour jellyfish populations, therefore there is a need to review dietary assessment methods used for ecosystem monitoring. Future seabird monitoring programs should be designed to detect diet changes across the full prey spectrum, including jellyfish, so any potential impact on seabird breeding success and survival can be evaluated.

## **StraDiv Project: System approach for the TRAnSition to bio-DIVersified agroecosystems, from process analysis to multi-scale co-conception with actors**

*Gregory Mollet<sup>1</sup>, Jean-François Martin<sup>1</sup>, Philippe Tixier<sup>2</sup>*

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The intensity of pest control relies to a great extent on the community structure in which pests and their natural enemies are embedded. The structure of the community of plants affects other communities, with direct bottom-up effects (quantity and quality of primary resources supporting food webs) and with indirect effects especially through the modification of habitats. Disentangling how plant diversity alters the functioning of communities and pest control is not easy task due to the difficulty involved in measuring real interactions in natura. We will use DNA metabarcoding to identify trophic link occurring between consumers and resources (including pests) within the complex network of the agroecosystem. This method leads to a full reconstruction of the food web structure and enables a comprehensive analysis of the pest regulation processes (Mollet et al. 2014). The use of the method in a set of contrasted situations is one of the most ambitious initiatives in community ecology applied to agroecosystems. Since the method will be applied strictly using exactly the same protocols across sites, our dataset will provide a generic understanding of the relationship between plant diversity, the structure of food webs and pest control. We will focus on the most important pests in each type of agroecosystem: white grubs in rice, banana weevil and root-feeding nematodes, aphids in fruit orchards, and the coffee borer. In parallel, in each situation investigated, pest abundance will be measured to quantify the control provided by the community. DNA will be extracted from dietary samples, followed by cloning, sequencing, and finally taxonomic assignment of sequences, which will make it possible to establish binary matrices of resource-consumer events. From a practical point of view, DNA metabarcoding will help identify species directly involved in pest control along with other species that may interfere with them (for instance through intra-guild predation).

## Field predation of winter moth defoliator by soil arthropods revealed using PCR

*Lucija Šerić Jelaska<sup>1</sup>, Ivan Šapina<sup>1</sup>, Milivoj Franjević<sup>2</sup>*

<sup>1</sup> Division of Biology, Faculty of Science, University of Zagreb, Rooseveltov trg 6, 10000 Zagreb, Croatia, <sup>2</sup>, Faculty of Forestry, Svetošimunska cesta 25, 10000 Zagreb, Croatia

Winter moth *Operophtera brumata* is a serious defoliator than can cause significant damages to broadleaf trees. Late spring, after feeding on buds and leaves, the caterpillars drop from the host tree to the soil to pupate and remain in the soil until the adults emerge in late autumn. To prevent damages to larger scale, population density has been regularly monitored and treated with insecticides in population outbreaks. For winter moth pupae that live in a soil there are no controls other than natural predation. Using molecular analyses we screened terrestrial predatory arthropods (e.g. carabid beetles and spiders) for presence of winter moth within their gut. Predatory arthropods were sampled at two forest sites: one treated with Btk due to pest outbreak and one untreated. Newly designed primers that amplify *O. brumata* were used in singleplex PCR and results were scored on gels after electrophoresis. Winter-moth presence was confirmed in the guts of carabids and spiders. So far, 183 individual carabid beetles were tested for winter-moth presence in their guts, and 7.1% were positive. Of 14 species tested, almost third individuals positive for winter moth belongs to *A. parallelepipedus*. Since 2017 has very high density of winter moth populations, we expected higher proportions of detected predations by predatory arthropods. These preliminary results will be complemented with additional sampling in late spring 2017.



## Phylogenetic and functional composition of arctic herbivore assemblages

*James D. M. Speed<sup>1</sup>, Eeva M. Soininen<sup>2</sup>, Ina Åsnes Skjelbred<sup>1</sup>, Michael D. Martin<sup>1</sup>, Isabel C. Barrio<sup>3</sup>*

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To understand trophic interactions we need to understand both the diversity and linkages in a vertical dimension (between trophic levels) and also the diversity in a horizontal dimension (within a trophic level). A trophic level may consist of a large range of taxa and encompass multiple ways of interacting with other trophic levels and the wider environment. It is rare for the horizontal dimension of diversity to be analysed in a trophic context, and efforts to date have largely looked only at species diversity within trophic levels. However, incorporating phylogenetic and functional dimensions of diversity can both broaden and deepen our understanding of ecological mechanisms and hence trophic interactions.

In this study we present a phylogenetic and functional assessment of a whole trophic group at a biome scale. We will focus on vertebrate herbivores of the Arctic biome. A previous study mapped the species richness of arctic herbivores, finding it peaked in the western Nearctic and was positively associated with plant productivity and predator diversity. In this study we created a phylogeny of all vertebrate arctic herbivores and used this to form the basis of a spatial analysis of the phylogenetic diversity and structure of this trophic level across the Arctic biome. We also used functional traits of the Arctic herbivores to classify how the species of this trophic level interact with their environment.

Results from our study show that both phylogenetic and functional diversity are correlated with species diversity across the arctic. However, assemblages of herbivores that differ in terms of species composition are more similar in terms of phylogenetic and functional composition. These together suggest that regional species differentiation does not reflect strong evolutionary divergence or functionally different herbivore communities. However, the ratio of phylogenetic diversity to functional diversity suggests that assemblages are functionally-dispersed. This may be due to competition within arctic herbivore assemblages in structurally simple ecosystems. Our study demonstrates the power of combining spatial analysis of phylogenetic and functional diversity, in order to increase our understanding of trophic ecology and interactions.

## Using DNA Barcode to track the effect of habitat fragmentation on food webs

*Tiago Teixeira<sup>1</sup>, Stephen J. Rossiter<sup>1</sup>, Elizabeth Clare<sup>1</sup>*

<sup>1</sup> *Queen Mary University of London*

Habitat fragmentation is of major conservation concern, with potentially negative consequences for biodiversity, ecosystem services, and the structure of ecological communities. Network theory provides a framework for studying how fragmentation processes might influence ecological interactions, however, network approaches often suffer from a lack of taxonomic resolution. Molecular techniques, including DNA barcoding, provide a powerful means of identifying species without a need for morphological characters. These methods can be applied to identify the species origin of trace materials, such as hairs, degraded tissues, and faecal matter. To assess changes in network structure with fragment size and isolation, we reconstructed mutualistic networks among bats and their food plants in the Brazilian Atlantic forest, using DNA barcoding to identify plant material contained in bat guano. Our analysis indicates that habitat fragmentation leads to more simple networks with fewer bats and plant resources. We discuss the potential negative consequences of fragmentation for seed dispersal, as well as the longer-term persistence of sensitive species in the environment.

## Linking agricultural management, host-parasitoid interactions and natural pest control in Mediterranean olive farms: a molecular-based food web approach

*Sasha Vasconcelos<sup>1</sup>, Mattias Jonsson<sup>2</sup>, Ruben Heleno<sup>3</sup> Pedro Beja<sup>4</sup>*

<sup>1</sup> *Research Network in Biodiversity and Evolutionary Biology, Instituto Superior de Agronomia, Lisbon, Portugal,* <sup>2</sup> *Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden,* <sup>3</sup> *Department of Life Sciences, Centre for Functional Ecology, University of Coimbra, Coimbra, Portugal,* <sup>4</sup> *Research Network in Biodiversity and Evolutionary Biology, Instituto Superior de Agronomia, Lisbon, Portugal*

Agricultural intensification in the form of increased use of agrochemicals, mechanisation and landscape simplification, has been found to reduce farmland biodiversity and hinder the provision of natural pest control through changes to interactions between pest species and their natural enemies. However, the effects of management practices on biotic interactions across space and time, and how this influences the stability of pest control services remains largely unknown. A better understanding of this relationship is crucial, as greater spatio-temporal stability of natural pest control can contribute to more reliable crop productivity. This study will address this knowledge gap in 38 Mediterranean olive (*Olea europaea*) farms under varying degrees of management intensity. Olive tree pests and their primary controllers – parasitoids – will be sampled within each olive farm, and a novel molecular approach will be used to describe the network of interactions between both trophic groups. Diversity of parasitoids, as well as the complexity of species interactions, will then be related to the level and spatio-temporal variability of parasitism rates across a gradient of management intensity and landscape complexity. These findings would allow the creation of guidelines to maximize olive farm productivity while ensuring the provision of this key ecosystem service, thus contributing to the sustainable management of this agroecosystem.

# MATI: Empirical dissection of ecological interactions

**The wonderful (?) world of eDNA**Wednesday  
9:00*Tom Gilbert<sup>1</sup>*

<sup>1</sup> *Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark*

Environmental DNA (eDNA) is increasingly being recognised as a unique means with which to assay the biodiversity present within ecosystems. Originally built around PCR coupled to molecular cloning, with the advent of GS FLX, and then later the Illumina and IonTorrent sequencing platforms, the power of such methods leapt by orders of magnitudes, in theory representing the means to economically and rapidly achieve this goal. With successful recovery of eDNA from a remarkable array of sources, its promise seems endless. But is it? With great power comes great responsibility, and greater still headaches. In this regard, I explore what can be done, what gets in the way, and where we need to go to provide a truly helpful tool for modern ecology.

## Co-occurrences among microbes producing and reducing inorganic nitrogen compounds within the nitrogen cycle

Wednesday  
13:30

*Sara Hallin*<sup>1</sup>

<sup>1</sup> *Swedish University of Agricultural Sciences, Uppsala, Sweden*

Microbial communities in the environment are highly diverse and can only be detected using indirect methods. Today, molecular techniques offer standard tools for dissecting the composition of microbial communities and the interactions between their members. They also allow us to examine how microbes with different functions affect each other. Inorganic nitrogen compounds are transformed through reduction-oxidation reactions by microbial communities in the biogeochemical nitrogen cycle. Their activity regulates the retention or loss of nitrogen from ecosystems, and determines in which form nitrogen is lost. Products formed in one process is the substrate in other processes. These product-substrate-links occur across both large and small geographical or temporal scales and involve both direct and indirect interactions among the microorganisms mediating the processes. A tight association between processes minimize accumulation of reactive intermediates, such as nitrite and nitrous oxide, in the environment. Two examples will be presented. The first involves field-scale spatial variation in co-occurrence patterns of organisms performing the overall process of nitrification, which is split across bacteria and archaea oxidizing ammonia to nitrite and bacteria that oxidize nitrite further to nitrate. The co-occurrences between these three functional communities was explored across a 44-hectare farm. The results demonstrate the importance of accounting for biotic interactions in defining the niche space of the nitrifier communities at scales compatible to land management. The second example focuses on microorganisms that can sustain growth by reducing nitrous oxide to harmless dinitrogen gas emitted to atmosphere. In a study using a range of soils across Europe, we demonstrated that a newly described nitrous oxide-reducing microbial group was important for the capacity of a soil to reduce nitrous oxide. Analyses of interactions and niche preference similarities suggest niche differentiation or even competitive interactions between different nitrous oxide reducers. Several recurring communities, comprised of co-occurring nitrous oxide-reducing bacterial genotypes, were significant indicators of the soil nitrous oxide sink capacity across different soils. Overall, these examples illustrate general principles for how microbial interaction networks may serve as templates for understanding functional relationships within natural communities, allowing important cross-fertilization among the macroscopic and microscopic ecology.

## A pilot dietary study using multiple primers to overcome prey detection biases in the generalist insectivore Pyrenean desman

Thursday  
11:30

*Amaiur Esnaola Illarreta*<sup>1</sup>, *Aitor Arrizabalaga-Escudero*<sup>1</sup>, *Jorge Gonzalez-Esteban*<sup>2</sup>, *Arturo Elosegui Irurtia*<sup>3</sup>, *Joxerra Aihartza Azurtza*<sup>1</sup>

<sup>1</sup> Department of Zoology and Animal Cell Biology, University of the Basque Country UPV/EHU, Leioa, Basque Country, <sup>2</sup> DESMA Estudios Ambientales, Sumbila, Basque Country, <sup>3</sup> Department of Plant Biology and Ecology, University of the Basque Country (UPV/EHU), Leioa, Basque Country

The Pyrenean desman (*Galemys pyrenaicus*) is an endangered semi-aquatic insectivore mammal endemic to the northern Iberian Peninsula and the Pyrenees. Due to its small populations, evasive behaviour and nocturnal activity, the basic ecological requirements of the Pyrenean desman are still poorly known. Detailed knowledge of the trophic interactions between predator and prey is required to understand the ecology and conservation of species as well as ecosystem functioning. Molecular tools are facilitating the non-invasive analysis of elusive or endangered species, but the completeness of diet characterization depends on the taxonomic coverage of primers and the spectrum of consumed prey species. In this pilot study we aimed to test the range of primers needed to cover the prey diversity consumed by the Pyrenean desman, a generalist forager. We non-invasively collected 24 fecal samples, extracted DNA from them, and PCR amplified different fragments of the standard barcode region (COI) by using seven different primer sets. PCR outputs were sequenced on the Illumina MiSeq platform, sequences were bioinformatically processed, clustered into OTUs using UPARSE algorithm and BLASTed against the NCBI nt database. Four out of seven primer sets successfully amplified their target fragments but they considerably differed in the amounts of sequence reads, OTU composition and assignments of OTUs to prey species. They were consistent identifying some few and most frequent prey taxa, probably corresponding to the staple food of the Pyrenean desman. However, they considerably differed in the less frequent prey groups. This study highlights the ecological relevance of considering varying primer sets to successfully characterize the prey spectrum of generalist insectivorous predators. It also sets the combination of primers needed to non-invasively characterize the diet of the evasive and critically endangered Pyrenean desman.

## Unravelling seed dispersal by frugivorous animals through DNA barcoding

Thursday  
14:30

*Juan Pedro González-Varo<sup>1</sup>, Pedro Jordano<sup>2</sup>*

*<sup>1</sup> Conservation Science Group, Department of Zoology, University of Cambridge, Cambridge, UK, <sup>2</sup> Integrative Ecology Group, Estacion Biologica de Doñana (EBD-CSIC), Sevilla, Spain*

Many plants crucially depend on frugivorous animals to disperse their seeds. Frugivores promote key ecological functions such as local recruitment, connectivity and initial colonization, playing a pivotal role in plant community dynamics. Besides, by fostering vegetation recovery after disturbance, frugivores provide important ecosystem services, including erosion prevention or habitat provisioning for other taxonomic groups. Information on the way in which frugivores operate is therefore essential to understand and forecast these functions and services. Yet, there is still an important knowledge gap on *how* multiple frugivore species disperse seeds through space and time, especially in a context of global change. In this contribution, we will show how DNA barcoding can be used to unravel seed dispersal networks in an unprecedented way. DNA of animal origin can be efficiently extracted from the surface of defecated or regurgitated seeds sampled in the field, allowing unambiguous identification of the frugivore species that contributed each dispersal event. Given that seeds are sampled at the end of the dispersal process, this technique enables to link the identity of the frugivore species responsible for each dispersal event to plant traits and environmental features, bridging frugivory outcomes and the delayed consequences of seed deposition patterns. We will present novel empirical evidence about how different frugivores select for different fruit sizes, disperse seeds at specific space-time combinations, and foster connectivity and colonization through fragmented landscapes. Thus, we will show how DNA barcoding can help us to uncover relevant and diversified functional components underlying seed dispersal networks.



## Using a combination of molecular gut content and stable isotope analyses to unravel the connections between marine and terrestrial food webs

Thursday  
14:50

*Peter Hambäck<sup>1</sup>, Love Dalén<sup>2</sup>, Rodrigo Esparza Salas<sup>2</sup>, Tomas Roslin<sup>3</sup>, Alma Strandmark<sup>4</sup>, Vasiliki Verschut<sup>4</sup>, Elisabeth Weingartner<sup>4</sup>, Helena Wirta<sup>5</sup>*

<sup>1</sup> Dept Ecology, Environment and Plant Sciences, Stockholm university, <sup>2</sup> Natural History Museum, Stockholm, <sup>3</sup> SLU, <sup>4</sup> DEEP, SU, <sup>5</sup> University of Helsinki

Food webs close to the border between ecosystems typically contain connections to the neighboring system. One example is shore-line communities, where the terrestrial species on the shore may strongly depend on the flow of matter or organisms from the marine or limnic system. The traditional approach for examining these dependencies use the fact that basal resources in the two systems have different carbon isotope ratios. Because these ratios are more or less conserved up the food chain, they provide a quantitative estimate of the food web relations. The problem with using stable isotopes is that these provide only very coarse estimates of diets, and can therefore not be used to delineate highly resolved food webs. However, by combining these analyses with molecular analyses of gut contents, it is possible to provide a more complete food web. We have used this dual approach to study food webs on shore-lines at the Baltic Sea, and specifically to examine the dependence of terrestrial shore-line predators on marine versus terrestrial prey. In one study, we compared spider diets, a major shore-line predator, between open and reedy shores. The dual approach allowed us to show that spiders on open shores mainly feed on prey from the marine environment whereas spiders on reedy shore feed on prey from the reeds. There was also a fairly good fit between the proportion chironomids in the diet and the stable isotope composition, indicating that the molecular analysis can provide quantitative information. In a second study, examining the seasonal variation in spider diets, we confirmed a fairly close relationship ( $R^2 = 0.54$ ) between the molecular and stable isotope analyses. This study also showed that the marine dependence varies over time. In spring and summer, spiders mainly feed on flies that have developed in wrack deposits on the shore, while in fall then the spiders mainly feed on chironomids that have developed in the water. Besides these ecological results, our study also interesting methodological experiences. In particular, we found that spiders have a very diverse diet and contain on average DNA from slightly more than 3 different prey species per individual spider.

## Using molecular methods to establish a new food web study system: wild *Drosophila*, their parasites and symbionts

Thursday  
15:40

*Jan Hrcek*<sup>1</sup>, *Christopher T. Jeffs*<sup>2</sup>, *Joel J. Brown*<sup>1,3</sup>, *Megan Higgie*<sup>4</sup>, *Owen T. Lewis*<sup>2</sup>

<sup>1</sup> *Institute of Entomology, Biology Centre CAS, Ceske Budejovice, Czech Republic,* <sup>2</sup> *Department of Zoology, University of Oxford, Oxford, UK,* <sup>3</sup> *University of South Bohemia, Ceske Budejovice, Czech Republic,* <sup>4</sup> *College of Science & Engineering, James Cook University, Townsville, Australia*

Advances in food web ecology depend on a combination of approaches, and it is thus important to study food web systems which are rich enough to be realistic, yet still amenable to experimentation in addition to food web surveys and ecological modelling. We focus on a promising system of wild *Drosophila* and their parasites as an example of how metabarcoding and other molecular methods can be used to survey a system and quickly enable and inform food web level experiments. We metabarcoded *Drosophila* pupae from banana baits exposed at three locations, each spanning an altitudinal gradient, in tropical Australia and recovered interactions between *Drosophila* hosts and parasitic wasps that attack them. Identifying the interaction partners required construction of a reference library using standard barcoding. We further metabarcoded the microbiome associated with the hosts and used PCR detection and barcoding to survey trypanosomatid parasites of *Drosophila*. The molecular methods thus enabled a survey of food web structure changes along altitudinal gradients and prepared the ground for experiments exploring the mechanisms underlying structural changes in food webs.

## Multitrophic interactions in a plant diversity experiment analyzed by gut content sequencing

Thursday  
11:50

**Julia Tiede<sup>1</sup>, Bernd Wemheuer<sup>2</sup>, Michael Traugott<sup>3</sup>, Rolf Daniel<sup>2</sup>, Teja Tscharn-  
tke<sup>4</sup>, Anne Ebeling<sup>5</sup>, Christoph Scherber<sup>6</sup>**

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Plant diversity has been shown to affect species richness and abundance of associated consumer communities. Species in diverse communities are likely connected by interspecific interactions. Omnivores, in particular, may link multiple trophic levels in interaction webs. However, it has remained unclear if and how changing plant diversity affects interactions of omnivores, because appropriate methods were lacking. A promising approach is the DNA-based analysis of gut contents using next generation sequencing (NGS) technologies in combination with universal primers allowing the detection of interactions from a wide range of taxa.

Here, we use the framework of a grassland biodiversity experiment where plant taxonomic and functional diversity were manipulated to analyse how three species of ground dwelling invertebrates with varying degree of omnivory respond to plant biodiversity. We released and recaptured ground beetles (*Pterostichus melanarius*, and *Harpalus rufipes*) and sampled slugs (*Deroceras reticulatum*) in 138 fenced plots. Beetle regurgitates and slug faeces were collected and DNA from these dietary samples was sequenced (Illumina Miseq). We analyzed trophic- and nontrophic interactions using general primers for plants, animals, fungi, and bacteria.

In a pilot study, we detected a wide range of taxa with the NGS approach in regurgitates of *P. melanarius*, including organisms representing trophic, phoretic, parasitic, and neutral interactions. Our findings suggest that plant diversity positively affects multitrophic interactions involving omnivorous consumers (Tiede et al. 2016, PLoS ONE). With the extended study we will elucidate this trend and advance fundamental biodiversity research by providing novel insights into ecological interactions.

## The effects of climate and prey availability on dietary partitioning in warblers

*Sarah Davies<sup>1</sup>, Robert Thomas<sup>1</sup>, Ian Vaughan<sup>1</sup> Stuart Bearhop<sup>2</sup> William Symondson<sup>1</sup>*

<sup>1</sup> School of Biosciences, Cardiff University, Cardiff, United Kingdom, <sup>2</sup> School of Biosciences, University of Exeter, Penryn, Cornwall, UK

The advent of Next Generation Sequencing (NGS) in the field of molecular ecology has led to significant advances in our understanding of ecological interactions in nature. To date, few molecular studies have considered the future impacts of environmental change on levels of resource overlap and dietary partitioning among sympatric species. Over the course of my PhD I will use molecular methods and field ecology to examine dietary competition among coexisting warbler species in European reed bed habitats and determine the influence of overarching ecological drivers, invertebrate prey availability and local climate, on patterns of prey selectivity. The first year of my research focuses on two latitudes within the UK using a "space for time" approach to mirror a changing climate. Faecal samples collected from adult and juvenile warblers during bird ringing sessions throughout the summer of 2017 will be screened for prey DNA using general invertebrate primers, allowing between-species dietary comparisons to be made at different stages of the breeding season within and among sites. Relative prey abundance and diversity will be quantified in the field through monthly monitoring of invertebrates present in reed beds and their adjacent habitats to give a measure of prey availability for each site. Following NGS of faecal samples and subsequent prey identification from DNA sequences, prey species consumed by each warbler species will be compared with local prey availability to determine the extent of dietary overlap in warbler assemblages of each study site. My results will generate more accurate predictions with respect to the potential influence of future warming on invertebrate resources for predators and provide a greater understanding of dietary selectivity and partitioning ability in birds in response to environmental change, both of which can be used to inform and implement effective conservation strategies.

## Predicting the future of arthropod food webs in a changing Arctic

*Bernhard Eitzinger<sup>1</sup>, Tomas Roslin<sup>1</sup>*

<sup>1</sup> *Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland*

Animal communities in the arctic Tundra are currently confronted with massive transformation processes due to global climate change, affecting biological interactions networks such as food webs. Among the species-rich and abundant arthropod community, wolf spider *Pardosa glacialis* occupies a key position as top generalist predator. Climate change-driven shifts in food availability, habitat structure and animal body sizes are expected to alter prey preferences and affect competition for shared food resources. In this study we use a combination of NGS-based gut content analysis with functional response models to quantify local food web structure along an altitude gradient in the high arctic region of Zackenberg (NE-Greenland), chosen to represent variation in microclimatic conditions as predicted by IPCC climate scenarios. High variation in local prey abundances as well as predator body size are significantly shaping prey choice of *Pardosa*. Flexible feeding behaviour allows optimal exploitation of prey resources suggesting high adaptive capacity under changing conditions.

## **Influence of forest type and microhabitat on trophic interactions of microarthropods and their bacterial-feeding nematode prey**

*Kerstin Heidemann<sup>1</sup>, Mark Maraun<sup>1</sup>, Stefan Scheu<sup>1</sup>*

<sup>1</sup> *Georg August University Göttingen, JF Blumenbach Institute of Zoology and Anthropology, Untere Karspüle 2, 37073 Göttingen, Germany*

Soil microarthropods are widely distributed and live in various forest types including coniferous and deciduous forests, but also in microhabitats such as dead wood at different decay stages, in mosses, fungal mats and grass patches. Microarthropods reach high densities in soil and have been assumed to function mainly as decomposers, but recent studies indicated that they are omnivores also feeding on free-living nematodes. Bacterial-feeding nematodes are among the most important bacterial grazers and form a key prey in soil food webs due to their high abundance at microbial hot spots. Thereby, they channel carbon via the bacterial energy channel to higher trophic levels such as microarthropods contributing to their nutrition as high quality food. However, nematodes are an understudied group in soil food webs. They are lacking in many studies due to methodological problems relating to their small body size and the lack of skeletal structures which can be traced in the gut of consumers. Moreover, many microarthropod species ingest only prey fluids. Therefore, the importance of this predator-prey interaction and its implications for food web structure is little understood. Molecular approaches are needed to uncover these trophic links in different soil food webs. We investigated the role of free-living bacterial feeding nematodes as prey for microarthropods, i.e. collembolans and mites, and if their trophic interactions change with different forest types and microhabitats. Therefore, specific primers as molecular markers for bacterial feeding nematodes were used for molecular gut content analyses of several mite and collembolan taxa. Our findings indicate that nematodes form an important component of the diet of many soil microarthropod species including those being assumed to predominantly function as detritivores. Further the results suggest that trophic niches of microarthropods are plastic and this plasticity likely contributes to the coexistence of the many soil animal species in forest ecosystems.

## Free-living nematodes as prey for higher trophic levels as indicated by molecular gut content analysis

*Kerstin Heidemann*<sup>1</sup>, *Liliane Ruess*<sup>2</sup>, *Stefan Scheu*<sup>1</sup>, *Mark Maraun*<sup>1</sup>

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Molecular methods are a novel tool to study trophic interactions between predator and prey on the level of species. They are particularly suited for analysing ‘invisible interactions’, such as predators ingesting only liquids of their prey, the prey lacks of detectable hard remnants predators feeding on small prey or living in opaque habitats, as in interactions of microarthropods feeding on nematodes in soil. Although among the most numerous invertebrates, until today nematodes are an underestimated prey in soil food web studies.

Molecular gut content analysis overcomes most of limits of other techniques investigating trophic links by analysing predator individuals in a PCR using molecular markers specific for certain prey taxa. General primers at the level of prey groups or families allow analysis of the dietary range of predators, whereas specific primers allow identifying trophic links at the level of genera or species. Development of specific primers, however, poses a challenge as target DNA fragments need to be short, allowing long detection of prey DNA in the gut of predators, but also need to be specific to the respective prey taxon. Further, the primers need to be sensitive allowing detection of even small amounts of prey DNA. Once established, however, specific primers allow screening of many individuals of predator species and thereby detection and comparison of the predator spectrum of the prey taxa the primers have been developed for.

We designed and optimized three specific primer pairs for free-living bacterial-feeding nematodes abundant in forest and other ecosystems: *Acrobeloides buetschlii*, *Plectus* spp. (*P. minimus* and *P. velox*) and *Panagrellus redivivus*. The markers were tested for specificity, sensitivity and detection time of nematode prey in microarthropod predators in the laboratory and the field. They proved to be a promising tool to uncover the contribution of nematode prey to the nutrition of microarthropods, thereby allow answering some of the most challenging questions in soil food web ecology, i.e. the contribution of microfauna to the nutrition of higher trophic levels of soil food webs and the trophic links between micro- and mesofauna.

## Jellyfish on the menu: cryptic predation revealed

*Philip Lamb<sup>1</sup>, Ewan Hunter<sup>2,1</sup>, John Pinnegar<sup>2,1</sup>, Simon Creer<sup>3</sup>, Richard Davies<sup>1</sup>, Martin Taylor<sup>1</sup>*

<sup>1</sup> *School of Biological Sciences, University of East Anglia, Norwich, UK,* <sup>2</sup> *Cefas,* <sup>3</sup> *Bangor University*

Jellyfish populations, and the frequency of localised outbreaks of jellyfish known as blooms, are thought to be increasing globally. These increases have caused negative economic and ecological effects such as, fish death in aquaculture installations, blocking marine infrastructure, bursting fishing nets, and stinging bathers. Understanding the ecology of jellyfish is paramount if these blooms are to be predicted and controlled. Overfishing, releasing jellyfish from predation and competition, has been suggested as a possible cause of population increases. Simultaneously, it has been asserted that jellyfish are trophic dead ends and increases must be abiotic in origin. To help resolve this debate, we developed 16S jellyfish-specific primers to screen stomach samples of potential marine predators. We demonstrate that jellyfish are not trophic dead-ends - numerous species were identified as jellyfish predators at different times of the year. These findings highlight that jellyfish may occupy a far more important position in the marine food web than previously acknowledged.



## The foraging strategy and digestion rate of generalist and specialist spiders

*Lenka Petráková<sup>1</sup>, Gabriel Pompozzi<sup>2</sup>, Luis Fernando García<sup>3</sup>, Stano Pekár<sup>1</sup>*

<sup>1</sup> Department of Botany and Zoology, Masaryk University, Brno, Czech Republic, <sup>2</sup> Instituto de Ciencias Biológicas y Biomédicas del Sur, Universidad Nacional del Sur, Bahía Blanca, Argentina, <sup>3</sup> Centro Universitario Regional del Este, Universidad de la República, Treinta y Tres, Uruguay

The optimal foraging theory assumes that predators should select prey in order to maximize their net rate of energy intake. It was used to explain the conditions under which predators should either specialize on a certain prey or keep a broad diet. Generalists may capture more prey items and extract only specific nutrients, while specialists have to extract all nutrients from a single type of prey. Given trade-offs in adaptations, specialists should exploit the most profitable prey and they should consume a single prey item longer than the generalist. We compared the feeding frequencies of three generalist spider species (*Cybaeodamus taim*, *Harpactea hombergi*, *Hersiliola sternbergi*) and three phylogenetically related specialist species (*Zodarion rubidum*, *Nops* aff. *variabilis*, *Palpimanus orientalis*). Generalists fed more frequently than specialists: they accepted prey on average every 4.7 days, while specialists accepted prey every 11.7 days. Generalists consumed significantly more prey than specialists but gained significantly less mass than specialists. We also compared the digestion efficiencies of generalists and specialists by detecting prey DNA in their guts. The digestion rate was not significantly different between specialists and generalists. However, ant-eating specialist had much longer 50% detection half-life than generalist fed with ants (8 and 21 days, respectively). Specialists exploited a single prey more than generalists, probably because they are adapted to extract all available nutrients from a single prey type. Generalists regulate any imbalances in nutrient intake by capturing more prey items and extracting only specific nutrients, or they feed less to avoid overconsumption of some nutrient types. Specialists have evolved a foraging strategy that is based on maximizing the exploitation of a single prey that provides the full spectrum of required nutrients. In contrast, generalists have evolved a strategy that seems to regulate any imbalances in nutrient intake by capturing more and different prey items and extracting only specific nutrients from each one.

## Using DNA barcoding to link seed removal with seed deposition patterns in the context of forest degradation

*Jan Schlautmann<sup>1</sup>, Jörg Albrecht<sup>2</sup>, Bogdan Jaroszewicz<sup>3</sup>, Dana G. Schabo<sup>1</sup>, Nina Farwig<sup>1</sup>*

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Frugivory and the associated removal of seeds is an important ecosystem function, which - in temperate regions - is carried out mainly by mammals and birds. While much attention has been paid to plant-frugivore interactions, there is a lack of knowledge about the processes which follow the removal of seeds. The ability to link frugivore activity to later seed deposition and plant establishment is the key to understand the seed dispersal process. This project aims to fill this gap by quantitatively linking plant-frugivore interactions to seed deposition in Białowieża Forest in Eastern Poland. To achieve this, we will combine our comprehensive datasets from previous studies on interactions among frugivore and plant communities with newly collected seed deposition data from the same study sites. Transect walks in old-growth and degraded forests were carried out to collect defecated or regurgitated seeds of 16 focal fleshy-fruited woody plants, and DNA barcoding is currently used to identify the disperser of each seed. This will allow us to (i) compile seed deposition patterns (seed quantity and seed species richness) for different disperser species as well as to (ii) establish the link between seed removal and seed deposition. It is of particular interest if the observed loss of interactions and partners in plant-frugivore interactions in degraded compared to old-growth forests is also found in the seed deposition networks. By assessing the importance of different disperser species our study will allow for unique insights into the consequences of the loss of seed disperser species in degraded forest habitats for plant communities.

## Variation in the trophic ecology of a marine generalist: a DNA metabarcoding diet analysis on the brown shrimp, *Crangon crangon*

*Andjin Siegenthaler*<sup>1</sup>, *Owen S. Wangensteen*<sup>1</sup>, *Chiara Benvenuto*<sup>1</sup>, *Stefano Mariani*<sup>1</sup>

<sup>1</sup> *School of Environment & Life Sciences, University of Salford, UK.*

The trophic ecology of opportunistic predators can provide important ecological insights on a wide range of ecological areas ranging from the individual to the ecosystem level. Recent advances in next generation sequencing allow for a detailed description of animal diets which is essential for linking animal feeding habits, prey community structure and environmental variation. Here, we apply a DNA metabarcoding approach, using versatile primers, to assess the diet of the brown shrimp, *Crangon crangon*. This decapod crustacean is an ecologically and commercially important species occurring in coastal waters across Europe. Based on morphological diet analysis, the brown shrimp has been described as an omnivorous, carnivorous opportunistic and scavenger species. To get an extensive overview of its trophic ecology, over 500 specimens were collected from 24 sites distributed over 6 estuaries across Europe. DNA from the stomach of each specimen was extracted to assess diet composition while environmental DNA from sediment was used to determine prey items availability. Furthermore, environmental variables and heavy metal levels were determined for each site. The feeding habits of *C. crangon* will be presented to discuss its trophic interactions in the light of prey availability and natural and anthropogenic variability. The results of this study will show important insights in the application of molecular trophic ecotoxicology in generalist predators.

## Identification of the Atlantic walrus diet using the molecular scatology

*Ulyana Simakova<sup>1</sup>, Maria Mardashova<sup>2</sup>, Vadim Mokievsky<sup>1</sup>*

<sup>1</sup> *P. P. Shirshov Institute of Oceanology of the Russian Academy of Sciences (IO RAS), Moscow, Russia,* <sup>2</sup> *The Marine Research Center of the Lomonosov Moscow State University, Moscow, Russia*

The Atlantic Walrus population of the southeastern part of the Barents Sea (the so-called Pechora Sea) undergoes the rapid growth during the last decades. The number of walrus in this region did not exceed 100 ind. throughout the XX century. More than 300-600 (up to 900 according to the latest estimates) of individuals are recorded near the islands of the Pechora Sea over the last years. Walrus of this region fed on large burying clams mainly. According to benthic surveys, clam resources do not cover the needs of the growing herd. The Mussels (Mytilidae) could serve as additional food object: extensive stocks of mussels are found on the shallows surrounding the islands inhabited by walrus. However, mussels have never been mentioned as a significant food object for walrus, and it is not known whether walrus are able to utilize this type of food. Direct monitoring of the Atlantic Walrus feeding in the Pechora sea is absent; the gut content analysis is impossible due to conservation status of the species. To study the diet we involved the molecular genetic methods for feces analysis. We have developed a method of inexpensive isolation of DNA from walrus feces. Using the specific mytilid primers (for PCR and sequencing) we showed that the DNA of Mytilidae is at least detected in Atlantic Walrus scats. This need further confirmation and quantification using qPCR and RT-PCR methods.

## Molecular analysis reveals that facultative bacterial endosymbionts structure aphid-parasitoid-hyperparasitoid networks

*Michael Traugott<sup>1</sup>, Zhengpei Ye<sup>1</sup>, Ines M. G. Vollhardt<sup>2</sup>, Nadia Parth<sup>1</sup>, Oskar Rubbmark<sup>1</sup>*

<sup>1</sup> Mountain Agriculture Research Unit, Institute of Ecology, University of Innsbruck, Technikerstrasse 25, 6020 Innsbruck, Austria, <sup>2</sup> Agroecology, Department of Crop Sciences, Georg-August-University Göttingen, Grisebachstr. 6 D-37077 Göttingen, Germany

In aphids, defensive facultative bacterial endosymbionts can confer protection against parasitoids, which should have profound consequences for host-parasitoid-hyperparasitoid networks. To date the effects of such endosymbionts have not been investigated in natural communities of aphids and parasitoids. Here, we used a new diagnostic multiplex PCR system to examine how specific species of defensive endosymbionts hosted by the English Grain Aphid *Sitobion avenae* affect the interactions between this species of aphid and its associated community of primary parasitoids and hyperparasitoids. By individually screening ~ 7,000 aphids and mummies collected in 13 winter wheat fields around Göttingen (Germany), we found that on average 80% of the collected *S. avenae* were infected by defensive endosymbionts. We found strong evidence that endosymbiont occurrence reduces parasitoid survival, supposedly by killing immature parasitoids rather than affecting female oviposition behaviour. The endosymbiont infection rates in aphid mummies were lower in aphids collected from fertilized compared to unfertilized plants, indicating that plant fertilization boosts the protective effect of the bacteria. Our data also suggests that the endosymbionts, independent from other environmental factors such as plant fertilization and landscape complexity, strongly impact parasitoid community composition and the specialisation of primary-hyperparasitoid food webs. The current findings provide evidence that facultative bacterial endosymbionts constitute a hidden force in structuring natural communities of aphids, primary parasitoids and hyperparasitoids in cereal systems.

## Distinctive use of mutualistic fungi by the resident ants inside caulinary domatia of the ant-plant *Humboldtia brunonis* (Fabaceae)

*Arkamitra Vishnu*<sup>1</sup>, *Sathish Desireddy*<sup>1</sup>, *Renee M. Borgess*<sup>1</sup>

<sup>1</sup> *Centre for Ecological Sciences, Indian Institute of Science, Bangalore, 560012, India*

*Humboldtia brunonis* (Fabaceae), an endemic ant-plant of the Indian Western Ghats dominates the rainforest understory and produces extrafloral nectaries on young expanding leaves and floral bud bracts for its resident ants. Some plants produce a hollow domatium in their stem internodes that provides shelter to 16 ant species. The domatia are also occupied by several other invertebrates, most prominently by the arboreal earthworm *Perrionyx pullus*. Here we report on the characteristic fungal communities associated with the ants inside domatia. We have found that the ants use fungi in two distinctive ways inside the domatia: i) building a disc-shaped carton to form a partition between the ant and the zone occupied by other inhabitants especially when ants share the domatium with earthworms, and ii) maintaining a group of fungi in the inner wall of domatia, probably as a food source. We attempted pure cultural isolation of these two groups of fungi and preliminary molecular data revealed that the fungal communities represent two fungal clades, i.e. the carton clade (used for the structural component of the partition) and the domatia clade (maintained by the ants in the inner wall of the domatia) in this system. A diverse group of tropical Ascomycota found predominant in these clades and it is possible that some fungi is not yet isolated successfully in culture. We hypothesized that, when there is another domatium occupant present in the same domatium, the ants are probably maintaining a specific group of fungi in the domatia wall by constructing a carton separation using a different group of fungi. The ants also possibly groom the domatia wall fungi so that the domatium entrance is not blocked and control other weedy fungi from affecting their culture. A DNA metabarcoding approach using Illumina MiSeq and targeting fungal ITS region is being taken in order to characterize the complete community profile of these two fungal clades. Our study shows a possible tripartite symbiosis in this ant-plant system involving ants, the plant and fungi first time from the Indian subcontinent.

## Exposing the structure of an Arctic food web with the help of a communal DNA barcode library

*Helena Wirta*<sup>1</sup>, *Eero Vesterinen*<sup>2</sup>, *Peter Hambäck*<sup>3</sup>, *Elisabeth Weingartner*<sup>3</sup>, *Claus Rasmussen*<sup>4</sup>, *Jeroen Reneerkens*<sup>5</sup>, *Niels Martin*<sup>6</sup>, *Olivier Gilg*<sup>7</sup>, *Tomas Roslin*<sup>1</sup>

<sup>1</sup> Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland, <sup>2</sup> Department of Biology, University of Turku, Finland, <sup>3</sup> Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden, <sup>4</sup> Department of Bioscience, Aarhus University, Aarhus, Denmark, <sup>5</sup> Conservation Ecology Group, Groningen Institute for Evolutionary Life Sciences, University of Groningen, Groningen, The Netherlands, <sup>6</sup> Arctic Research Centre, Department of Bioscience, Aarhus University, Denmark, <sup>7</sup> Groupe de Recherche en Ecologie Arctique, Francheville, France

How food webs are structured has major implications for their stability and dynamics. While poorly studied to date, arctic food webs are commonly assumed to be simple in structure, with few links per species. If this is the case, then different parts of the web may be weakly connected to each other, with populations and species united by only a low number of links.

To describe trophic links of a community, we first construct an extensive DNA barcoding library for an Arctic site, covering the vast majority of animal and vascular plant species of the region. With this tool, we provide the first highly resolved description of trophic link structure for a large part of a high-arctic food web. We apply the DNA barcodes to describe the links between three predator guilds (insectivorous birds, spiders, and lepidopteran parasitoids) and their two dominant prey orders (Diptera and Lepidoptera).

The resultant web shows a dense link structure and no compartmentalization or modularity across the three predator guilds. Thus, both individual predators and predator guilds tap heavily into the prey community of each other, offering versatile scope for indirect interactions across different parts of the web. The current description of a first but single arctic web may serve as a benchmark toward which to gauge future webs resolved by similar techniques.

Our findings call for similar explorations of link structure across multiple guilds in both arctic and other webs. The findings suggest that to comprehend the community-level consequences of rapid arctic warming, we should turn from analyses of populations, population pairs, and isolated predator–prey interactions to considering the full set of interacting species.

## Sex specific prey choice of breeding cormorants in the Alpine foreland

*Christiane Zeisler<sup>1</sup>, Bettina Thalinger<sup>1</sup>, Johannes Oehm<sup>1</sup>, Julia Vorhauser<sup>1</sup>, Michael Traugott<sup>1</sup>*

<sup>1</sup> *Institute of Ecology, University of Innsbruck, Technikerstraße 25, 6020 Innsbruck, Austria*

Cormorants (Phalacrocoracidae) are abundant piscivores in marine and freshwater ecosystems. With males being larger than females, they display a size dimorphism that affects the birds' potential foraging abilities: diving performance, foraging area, and response to environmental conditions such as strong winds might differ between the sexes. To develop conservation and management strategies for the Great Cormorant (*Phalacrocorax carbo sinensis*) in Europe, sex-specific differences in prey choice are of particular interest since they can strongly influence predation pressure exerted on prey populations. So far, research has been based on stomach content analysis of shot cormorants and most studies were carried out in coastal lowlands during autumn and winter. Male cormorants in general were found to consume bigger fish than females. However, information on the prey choice during the breeding season and at Central European freshwaters is missing.

Here, we assess sex-specific prey choice of Great Cormorants during two subsequent breeding seasons in the Alpine foreland at lake Chiemsee (Bavaria, Germany). To obtain this information we utilized a unique, non-invasive approach and applied it to regurgitated pellets: molecular sexing combined with molecular prey fish identification and fish-length regression analysis based on prey hard parts contained in the pellets. Altogether, 212 pellet samples delivered information on both, bird sex and consumed prey and were used for the analysis. The main food source in both sexes were perch (*Perca fluviatilis*) and roach (*Rutilus rutilus*), but additionally, male diet was characterized by a broader prey spectrum. Furthermore, males were found to consume significantly larger fish than females.

The current findings show that the sexes differ in their prey choice and therefore probably have a different effect on fish populations in Alpine foreland freshwaters. Further on, the non-invasive approach employed here provides a new means for future studies on sex-specific aspects of cormorant trophic ecology.



# MATI: Methods development

## Making DNA count: defining and pushing the technical limits of dietary DNA metabarcoding

Thursday  
13:30

*Bruce Deagle*<sup>1</sup>

<sup>1</sup> *Australian Antarctic Division, Tasmania, Australia*

Over the past ten years genetic technological advances have revolutionised the field of molecular analysis of trophic interactions. The unattainable ‘holy grail’ of dietary DNA metabarcoding is to retrieve perfect quantitative description of trophic interactions in a study system. In this talk, I will focus on the factors that impact the accuracy of dietary DNA metabarcoding and best practice approaches to limit their effects. I will present data from the literature and our own work to illustrate some of the problems that may be encountered in high-throughput amplicon sequencing workflows. A particular focus will be on our attempts to validate the use of proportional data based on sequence read counts rather than working only with frequency of occurrence datasets.

## Next-generation Global Biomonitoring – large-scale, automated reconstruction of ecological networks

Wednesday  
15:40

*David Bohan<sup>1</sup>, Corinne Vacher<sup>2</sup>, Alireza Tamaddoni-Nezhad<sup>3</sup>, Alan Raybould<sup>4</sup>, Alex J. Dumbrell<sup>5</sup>, Guy Woodward<sup>6</sup>*

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We foresee a new global-scale, ecological approach to biomonitoring emerging within the next decade that can detect ecosystem change accurately, cheaply and generically. Next-generation sequencing of DNA sampled from the Earths' environments, would provide data for the relative abundance of operational taxonomic units or ecological functions. Machine-learning methods would then be used to reconstruct the ecological networks of interactions implicit in the raw NGS data. Ultimately, we envision the development of autonomous samplers that would sample nucleic acids and upload NGS sequence data to the cloud for network reconstruction. Large numbers of these samplers, in a global array, would allow sensitive automated biomonitoring of the Earths' major ecosystems at high spatial and temporal resolution, revolutionising our understanding of ecosystem change.

## Detection and distribution of otters and their prey on the river Don in South Yorkshire

Thursday  
11:10

*Deborah Dawson<sup>1</sup>, Amy Withers<sup>1,2</sup>, Sabuj Bhattacharyya<sup>1,3</sup>, Natalie dos Remedios<sup>1</sup>, Gracie Adams<sup>1</sup>, Helen Hipperson<sup>1</sup>, Hannah Dugdale<sup>2</sup>*

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The Eurasian otter (*Lutra lutra*) underwent a severe decline in the UK due to pollution caused by pesticides, becoming locally extinct in much of England by the 1960s. Bans on pesticides and improvements in water quality, alongside legal protection and targeted conservation efforts have led to the return of otters to parts of their original range. In 2016 camera traps revealed that otters have returned to the River Don in Sheffield. We performed DNA analyses of otter spraints (faecal samples) to confirm species, and identify otter numbers, sex, distribution and diet. Spraints were collected from 24 km of the River Don surrounding Sheffield (2016-17). Genomic DNA was extracted and amplified with mitochondrial markers (12S and cytochrome b; to indicate species present and diet), and seven microsatellite markers and a sex marker (to estimate otter numbers). Individually-tagged amplicons of the mitochondrial markers were pooled and sequenced on an Illumina MiSeq sequencer. Mitochondrial sequences were compared against the NCBI sequence database revealing otter (and mink) at various sites. Microsatellite genotyping and sex-typing was performed on an ABI DNA Analyzer and DNA profiles were compared. Seven individual otters were identified, including at least two males. A female otter was also detected to the north of Sheffield in a more rural location. Several species of fish (including bullhead, common minnow and trout) and birds (including grey heron and moorhen) were detected in the otter spraint DNA. Additional markers (such as COI and 16S) will be used to detect other potential prey species, such as crayfish and water vole. The markers developed are currently being used to identify otter individuals in the Peak District surrounding Sheffield, to investigate if the same individuals are crossing between river systems, between urban and rural areas, whether this is seasonal, and if any barriers/drivers affecting distribution can be detected.

## Adaptive network rewiring, MOTU clustering pipelines, and applications for molecular network ecology

Wednesday  
16:00

*David Hemprich-Bennett<sup>1</sup>, Joshua Potter<sup>1</sup>, Stephen Rossiter<sup>1</sup>, Elizabeth Clare<sup>1</sup>*

<sup>1</sup> *Queen Mary University of London*

In the current age of anthropogenic extinctions it is crucial to understand the behaviour of ecological networks following the loss of species. To date, most efforts to model network responses have focussed on deterministic secondary extinctions of species at the stage when they no longer have any resources, yet this takes no account of the ability of species to switch diets. Allowing for changes in ecological interactions, whereby species can ‘re-wire’ their connections upon the loss of their partners, likely gives a more realistic view of the behaviour of an ecosystem during an extinction cascade. Understanding these switches might be further complicated in empirical networks that rely on molecular operational taxonomic units (MOTUs) as proxies for species, particularly in cases where multiple taxonomic groups are present in the data. Indeed, despite studies showing inter-order variation in marker gene divergence, it is standard practice to apply a uniform MOTU clustering level to all sequences obtained. To address these challenges, we have modelled resource-switching behaviour using a combination of empirical and simulated datasets. Here we present our results on adaptive network rewiring during extinction cascades, and consider the switching characteristics that maximise ecosystem robustness. We also discuss findings with respect to whether MOTU approaches should be standardised or fitted to the taxonomic composition of each dataset.

## How much is enough? Estimating individual bat diet using metabarcoding

Thursday  
9:40

**A. Mata<sup>1</sup>, Francisco Amorim<sup>1</sup>, Hugo Rebelo<sup>1,2</sup>, Simon Jarman<sup>1</sup>, Pedro Beja<sup>1,3</sup>**

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Dietary studies based on DNA metabarcoding have boomed during the last decades. This technique offers a powerful tool to tackle old ecological questions by providing ecologists with unprecedented data resolution. At the moment, diet analysis of species, or populations, based on DNA metabarcoding techniques are commonly limited to the use of frequencies of occurrence (FO), i.e., the frequency a prey is present in a number of samples. This means that in order to have good FO estimates, an adequate number of samples is required. However few studies have assessed the impact of sampling design on molecular diet analysis and the advantages and disadvantages of the different approaches. Here we aim to assess how different experimental designs affect the accurate estimation of FO in metabarcoding studies of bat diets. We investigated the effects on FO estimates of: sequencing depth, number of PCR replicates per fecal sample, number of fecal samples per individual, and pooling of samples before extraction. One of the main goals is to understand the sources of variability in FO estimates, thereby devising sampling and analytic strategies that maximize FO estimate accuracy. For this we assessed the diet of the European free-tailed bat *Tadarida teniotis* in an orthogonal set-up, and sequenced a small fragment of the COI gene of 20 bat individuals, using 15 pellets per individual as well as a pool of 15 pellets (all from the same foraging night), 3 PCR replicates, and 2 levels of sequencing depth. Overall, results suggest that maximizing the number of individuals analyzed is the most important factor for accurately estimating FO, with the number of pellets per individual also affecting significantly FO estimates for each given sample size of individuals. PCR replicates were fairly consistent given similar sequencing depths, with rarer species disappearing at lower sequencing depths. These results will give us fundamental baseline information to propose guidelines for the sampling design of future studies.

## Computer simulation shows that DNA metabarcoding can provide quantitative estimates of the relative abundance of species in heterogeneous mixtures

Wednesday  
16:40

*Josep Pinol<sup>1</sup>, Miquel Angel<sup>2</sup>*

<sup>1</sup> CREAF, UAB, Bellaterra, Spain, <sup>2</sup> Senar, Department of Computer Architecture & Operating Systems, UAB, Bellaterra, Spain

DNA metabarcoding is a promising technique to survey biodiversity in many ecological settings, including the analysis of animal diets. However, there are reasonable doubts that this technique can provide quantitative results, i.e. the actual proportion of each species in the mixture as opposed to the species list. Here we provide a rationale to understand why the technique might or might not be quantitative, and explore the above ideas by simulating artificial mixtures of insects.

*Rationale.* Let's consider a mixture of DNA of  $S$  species with original abundances of  $O_i$  that is PCR-amplified with a certain primer pair to provide a final concentration  $F_i$ . Each species increased its concentration following a certain efficiency  $e_i$ , so that  $F_i = e_i \cdot O_i$ . The final concentration of DNA  $F_i$  will reflect the original one  $O_i$  when  $e_i$  is the same for all species; on the contrary, when  $e_i$  is very different among species,  $F_i$  would poorly reflect  $O_i$ .

*Simulation.* We simulated artificial mixtures of DNA of  $S$  species by repeatedly and randomly sampling a database of mitogenomes of ca. 1000 insect species. Then we randomly assigned the initial concentration of DNA  $O_i$  to each species using theoretical models of species distribution in natural communities. We estimated the amplification efficiency  $e_i$  of each species from the number of primer-template mismatches using published relationships. Finally, known  $O_i$  and  $e_i$  we calculated  $F_i$  as their product and studied the resulting relationship  $F_i$ - $O_i$ .

*Results.* Depending on the primer pair (4 analysed so far), between 68% and 96% of the 10000 simulated communities showed a positive and statistically significant ( $P < 0.05$ ) correlation  $F_i$ - $O_i$ . The original DNA concentration  $O_i$  explained more than 50% of the variance on  $F_i$  on between 18% and 71% of the cases. The correlation  $F_i$ - $O_i$  was higher in richer communities and when the distribution of the original abundance of the species was more heterogeneous. In conclusion, depending on the primer pair used in the PCR amplification and on the structure of the mixture analysed, DNA metabarcoding provides a quantitative estimate of the relative abundance of species in most cases.

## Untangling trophic interactions in marine plankton communities through DNA barcoding approaches

Wednesday  
16:20

*Sara Zamora-Terol<sup>1</sup>, Andreas Novotny<sup>1</sup>, Monika Winder*

<sup>1</sup> *Department of Ecology, Environment and Plant Sciences, Stockholm University, Sweden*

A continuous challenge in aquatic ecology has been to accurately identify prey of microbial consumers in the natural environment, which in turn influences the productivity of primary producers and of their predators. Genetic and molecular tools have transformed research areas such as biology and biomedicine and their potential to elucidate unknown aspects of the biology and ecology of microbial communities has only begun to be exploited over the last years. Novel molecular advances now allow the identification of dietary uptake of small-sized organisms, such as microbial plankton species under complex natural conditions. For instance, DNA barcodes are useful tools to accelerate species-level analysis of marine biodiversity, and they have been recently used for identification of prey in gut contents. Here we present the application of a new tool to investigate trophic interactions in the pelagic ecosystem including different zooplankton grazers under temporal and spatial variation of food resources. We obtained quantitative data on the relative amounts of diverse suspected prey species consumed by zooplankton using DNA barcoding. For that purpose, a laboratory experiment with copepod *Eurytemora* sp. as a model species and fed with different combination of algal prey was set up to estimate variance due to difference in gene copy number barcodes. Combining the DNA-based approach with grazing estimates using traditional methods of microscopy helped to optimize the molecular methods, and provide a baseline for the accurate interpretation of samples from subsequent field surveys. Our study suggests that molecular analysis has the potential to elucidate unknown aspects of the biology and ecology of plankton food web interactions.



## eDNA metabarcoding as a tool for detecting the herbivores that feed on a common plant resource

*Mehdi Cherif<sup>1</sup>, Carin Olofsson<sup>1</sup>, Kerstin Richau<sup>2</sup>, Nicolas Delhomme<sup>3</sup>*

<sup>1</sup> Ecology and Environmental Science Department, Umeå University, <sup>2</sup> Umeå Plant Science Centre, Umeå University, <sup>3</sup> Umeå Plant Science Centre, SLU Umeå

Metabarcoding has emerged as a powerful tool for the detection of trophic interactions that are hardly revealed otherwise. Examples abound of its use in drawing a more complete picture of realised predator-prey interactions in nature. In comparison, its application to herbivore-plant interactions is less common, mostly due to methodological issues in finding a unique sequence to barcode the diverse set of plants usually encountered. Another limitation, common to all types of trophic interactions, is that only the diet of consumers can be metabarcoded, thus resulting in a consumer bias to our view of food webs. Here, I try to develop a method to metabarcode the eDNA left by insect herbivores on the plant parts they consume, in order to bring the focus on the spectrum of consumers that eat a given plant resource. The method can thus be used to test the effects of resource quality and quantity on food web structure. Many theories in food web ecology are bottom-up, so the method should prove useful for both empirical and theoretical developments.

## Browsing the web: design and evaluation of primers for the analysis of spider diets and predation on aphids

*Jordan P. Cuff*<sup>1</sup>, *Pablo Orozco-terWengel*<sup>1</sup>, *Carsten T. Müller*<sup>1</sup>, *Ian Vaughan*<sup>1</sup>, *James R. Bell*<sup>2</sup>, *William O. C. Symondson*<sup>1</sup>

<sup>1</sup> *School of Biosciences, Cardiff University, Cardiff, United Kingdom,* <sup>2</sup> *Rothamsted Research, Harpenden, United Kingdom*

The burden aphids and other crop pests impose on agriculture is increasingly pertinent given the projected food security issues of the 21st century. Biological control of crop pests by naturally-occurring predators offers an ecologically and environmentally sustainable alternative to inorganic pesticides. Spiders are abundant predators in cereal crops that consume aphids and many other pest and non-pest prey. Analysis of spider diet in the field would allow us to determine the role of aphids vs. non-aphid prey in their diets and to analyse the mechanisms behind prey choice. Molecular methods, such as Next Generation Sequencing (NGS), allow accurate identification of consumed prey species. This, however, requires amplification of degraded prey DNA without amplifying non-degraded predator DNA that would otherwise dominate PCR reactions. No PCR primers have yet been developed which broadly amplify spider prey DNA without amplifying spider DNA.

Currently, we are designing and testing new and existing PCR primers suitable for metabarcoding of spider gut contents. Existing primers were identified from the literature and previous work within our lab, and new primers designed *in silico*. Primer specificity and taxonomic coverage were evaluated *in silico* and then *in vitro*. Once fully developed, these primers, and an accompanying barcode library, will be used to study spider diet in cereal crops, specifically focussing on the predation of aphids. This will ultimately contribute to the development of management strategies that maximise the ability of spiders to control aphids without compromising agricultural productivity and improving sustainability.

## A comparative study on the use of traditional DNA barcoding and next-generation sequencing for determining the trophic interactions of herbivorous insects

*Jane Hardwick<sup>1</sup>, Alison Shapcott<sup>2</sup>, Sarah Maunsell<sup>3</sup>, Nigel Stork<sup>1</sup> Roger Kitching<sup>1</sup>*

<sup>1</sup> *Environmental Futures Research Institute, Griffith University, Brisbane, Australia,* <sup>2</sup> *Faculty of Science, University of the Sunshine Coast, The Sunshine Coast, Australia,* <sup>3</sup> *Museum of Comparative Zoology, Harvard University, Cambridge, United States of America*

Measuring insect-herbivore trophic interactions is challenging, but the emerging field of ecological genomics is helping to overcome previous limitations with its increasing technological advances. This study compares the efficiency of traditional single-species barcoding using Sanger sequencing with novel next-generation sequencing (NGS) using an Illumina Miseq. These two sequencing methods are trialled on the same selection of Orthopterans to analyse their diets when host-plant species and diet breadth are predominantly unknown. We tested four standard plant DNA barcode markers (rbcL, MatK, psbA-trnH and ITS) and developed a hybrid method for NGS to allow for multiple marker PCR products to be sequenced simultaneously. By sequencing more than one marker in the Illumina Miseq cell, DNA fragment diversity is increased which helps to reduce issues caused by low diversity that can cause lower quality reads and yield output. Overall, we found that the NGS method gave much more exhaustive results than the Sanger method in terms of number of sequences obtained. However, the Sanger sequences were longer in length and therefore could be matched more confidently to a plant species or genus level. One major drawback with Sanger sequencing for the use of diet analysis is that it often fails to deliver a readable sequence from a sample when there is DNA from multiple species within the gut-contents; a limitation which is overcome by the NGS method. We suggest that only for known specialist species, the Sanger method is a more appropriate approach for measuring trophic interactions. Although both methods have valuable uses across many fields, NGS has a more extensive potential for developing a wider understanding of trophic interactions in ecological systems.

## Exposing the long-term dynamics of arthropod communities at high Arctic using recent advances in metagenomics

*Tea Huotari<sup>1</sup>, Yinqiu Ji<sup>2</sup>, Douglas Yu<sup>3,2</sup>, Otso Ovaskainen<sup>1</sup>, Tomas Roslin<sup>4,1</sup>, Niels Martin Schmidt<sup>5</sup>, Nerea Abrego<sup>1</sup>*

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The Arctic, as other parts of the globe, is dominated by arthropods, which sustain many ecological functions. The Arctic is also one of the fastest warming regions on the planet, but we still know little about how current change affects both arthropod communities, whole ecosystems, and their functioning. Despite the advantages of the Arctic for analyzing change at the community and ecosystem -level, longer records of species level information from high latitudes are still very few. In this project we are analyzing the single most comprehensive time series of arthropod samples from high altitudes derived from the Zackenberg research station in Northeast Greenland, where arthropod samples have been collected over 18 years. Our objective is to use the collection, utilize recent advances in genomics and statistical modelling to come up with species-level correlates to climatic response, temporal patterns in community structure, and evidence of structural and functional tipping points during two decades of rapid climatic change. We use a PCR-free mitochondrial metagenomic approach to resolve the collection to the species level data and show that this method is valid for analyzing environmental monitoring data and revealing changes at community level. Changes happening at the high Arctic can be seen as an indicator of changes about to happen in other parts of the world, and therefore our results provide crucial information when aiming to predict future change.

## Primer design of ecto-mycorrhizal fungi from temperate forests to unravel the effect of forest type on the fungivory of soil mesofauna species

*Melissa Jüds<sup>1</sup>, Kerstin Heidemann<sup>1</sup>, Mark Maraun<sup>1</sup>, Stefan Scheu<sup>1</sup>*

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Forest soils with their dense root system are inhabited by a variety of microbes and animals. Microbes as fungi and bacteria often live in symbiosis with plants and are of crucial importance for ecosystem processes such as leaf litter decomposition, carbon sequestration and nutrient cycling. However, they also function as food resource of soil dwelling invertebrates including microbivores and detritivores. Fungi are considered to be the major food source of soil animal food webs channeling carbon to higher trophic levels. Fungi in soil comprise saprotrophic and mycorrhizal species with very different roles in ecosystems. Feeding on fungi by soil invertebrates therefore may have very different consequences for ecosystem processes. In temperate forest ecosystems the ecto-mycorrhizal (EM) fungi are predominating comprising a large number of species with different resource exploitation strategies. However, which fungal species are preferred by fungal feeders and if they alter their feeding preferences in presence of other fungal species is little known. Isopoda, Collembola and Oribatida form main fungal consumers in forest soils. Unfortunately, the diet of these taxa and their interrelationships with fungal species in soil is difficult to study under field conditions. We aim at investigating these interrelationships using molecular gut content analysis, i.e. by tracing fungi in the diet of consumers. To achieve this goal we designed primers for abundant and widespread species of saprotrophic and EM fungal specific of forest ecosystems. We use these primers to identify the fungal diet of detritivore soil invertebrates using molecular gut content analyses in laboratory and field experiments. As precondition of that work we established a washing protocol to eliminate false positive results by fungal spores and hyphae attached to the animal cuticle. In the field the interrelationship between fungi and fungivores will be analyzed as affected by forest type and region within the Biodiversity Exploratories project.

## Waiter, there's a fly in my mushroom soup! Actually, hundreds of them. . .

*Janne Koskinen<sup>1</sup>, Tomas Roslin<sup>2,3</sup>, Tommi Nyman<sup>1</sup> Eero J. Vesterinen<sup>3,4</sup>*

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Mushrooms (Fungi: Basidiomycota) are a substantial economical and nutritional resource in boreal forests. Yet, surprisingly little effort has been put into revealing the communities of other organisms within and around mushrooms. These studies have traditionally been limited by methodological difficulties, particularly in identifying the highly specious fungivorous insects and their cryptic larvae. However, recent advances in molecular methods have offered novel tools to dissect networks consisting of multiple trophic levels and a vast number of species. Despite these advances, some fundamental methodological challenges have persisted in the processing of large fruiting bodies of mushrooms, especially concerning the critical DNA extraction step. We introduce a validated DNA purification method for any mushroom material. The method has been developed to be efficient, simple and adjustable for nearly any starting material. First, we use a traditional and widely applied salt isopropanol precipitation method in high volume to extract the DNA. We then further purify the DNA samples using high throughput SPRI purification method. We demonstrate the power of this method by purifying DNA from a set of various fungi sampled in situ and then metabarcoding the fungi, the fungivorous arthropods and microbe communities from these the samples. This method will make large-scale fungivory interaction research easier, faster and more affordable than before.

## Metabarcoding in passerine diet analyses: efforts, biases and results

*Vanessa A. Mata<sup>1</sup>, Luis P. da Silva<sup>2</sup>, Pedro Lopes<sup>3</sup>, Simon Jarman<sup>1</sup>, Ricardo J. Lopes<sup>1</sup>, Pedro Beja<sup>1,4</sup>*

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The use of metabarcoding has grown exponentially in the study of animals' diets. The accuracy and detail of this technique is invaluable for a better understanding of biotic interactions characterizing natural and human-dominated ecosystems, and thus to their conservation and sustainable use. However it has seldom been applied to passerine birds, though this order accounts for about half the bird species and encompasses a wide range of trophic niches. One of the problems is that many species have a wide trophic niche, feeding on both plants and on variety of arthropod orders, which is challenging for metabarcoding studies. For instance, a wide feeding spectrum may lead to methodological problems, due to primer selection and bias. Here we compare the effectiveness of metabarcoding against traditional microscopic analysis in evaluating the diet of the black wheatear *Oenanthe leucura*. This is a generalist passerine of conservation concern in Europe, occurring in semi-arid areas of Iberia and North Africa. It is known to feed on several berries, a large variety of arthropods and even small lizards. Here we apply a multi-marker approach, with different levels of taxonomical resolution (18S, 16S, trnL, and COI), as well as standard microscopic analysis of prey fragments, in order to assess the diet of this species. In general, genetic analysis was able to recover a higher number of taxa than microscopic analysis, with group specific primers showing also a higher taxonomic resolution. The COI primer used however, completely failed to amplify some invertebrate groups, showing the importance of using multiple markers when evaluating the diet of a species.

## Optimised scat collection protocols for dietary DNA metabarcoding and its application to investigate albatross diets

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DNA metabarcoding of food in animal scats provides a non-invasive dietary analysis method for vertebrates. Universal approaches which can recover DNA from all diet items are ideal; however, these also recover non-food DNA. Blocking primers can be used to inhibit amplification of non-target DNA, but their use is not always feasible, especially when multiple distinct non-target groups are present. As part of a broad study on albatross diet, we developed scat collection protocols to optimise detection of food DNA in scat samples. In this experiment, we used a universal metabarcoding approach, but the generalised findings have implications for all vertebrate diet metabarcoding studies. We investigated how DNA amplification success and the proportion of food DNA detected are influenced by both environmental and physiological parameters. The data show that both the amount and type of non-target DNA varies with sample freshness, collection substrate, fasting period and developmental stage of the consumer. Based on our observations, we recommend the following procedures for field scat collections to ensure high quality samples for dietary DNA metabarcoding studies. Ideally, i) collect fresh scats; ii) from surfaces with minimal contamination; iii) collect scats from animals with minimum time since feeding and avoid fasting animals; iv) avoid young animals that aren't feeding directly or target larger/older individuals. These optimised field sampling protocols will improve the quality of dietary data from vertebrates by focusing on samples most likely to contain food DNA. The ability to collect quality dietary data using DNA metabarcoding is valuable for evaluating and monitoring marine based threats to threatened seabird groups such as albatross. We have applied universal markers to shed light on the importance of gelatinous prey in albatross diet, these prey cannot easily be recovered using conventional diet methods. We have also used group specific markers with higher taxonomic resolution to assess overlaps with commercial fisheries. The continued development of DNA dietary analysis techniques enable researchers and conservation efforts around the world to non-invasively obtain information on ecosystem linkages and monitor and evaluate marine threats to seabird populations.



## The plasticity of multi-trophic networks in agriculture

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Naturally occurring predators and parasites of crop pests provide protection and increase crop yields via biological control. As such, the richness and composition of biological communities within agri-ecosystems is strongly linked with ecosystem functioning. However, the underlying mechanisms linking biodiversity and ecosystem functioning remain unclear. Although the majority of studies in this field have focused solely on species richness, there is evidence to suggest that the interactions between species are at least partly responsible for this trend. Complementarity between coexisting species is one possible explanation for how increased biodiversity can enhance functioning and network ecology can help us to understand whether this is the case.

There is mounting evidence that ecological interactions vary across space and time. The occurrence and strength of a relationship between two species is dependent upon influences from the local environment. In agricultural systems, disturbance via management is likely to play an important role in determining network characteristics and as such, the degree of agricultural intensification present within a landscape is expected to influence ecological network properties.

This project aims to characterise a variety of ecological networks in oilseed rape (OSR) and ley habitats in both high and low intensity agricultural landscapes in the south of Sweden. We aim to describe the variation in network properties across treatments to examine the impact of landscape complexity and agricultural intensification on interspecific interactions.

Molecular techniques such as DNA metabarcoding are increasingly used to determine feeding associations within ecological communities. They provide a number of advantages over traditional methods such as improved node resolution, the identification of cryptic species, faster and cheaper processing leading to increased sample sizes, and the ability to determine links at multiple trophic levels simultaneously. Here we use these techniques to characterise predator-prey, parasitoid-host and host-symbiont interaction networks in multiple agricultural landscapes.

We expect that networks will differ significantly in structure both between OSR and ley habitats and between high and low intensity habitats. Landscape complexity is predicted to be positively correlated with network complexity, and different types of network are expected to show divergent trends according to the properties of the species present.

## Can next generation sequencing provide higher resolution of food-web interaction dynamics in marine microbial communities?

*Andreas Novotny<sup>1</sup>, Sara Zamora<sup>1</sup>, Rodrigo Esparza Salas<sup>2</sup>, Monika Winder<sup>1</sup>*

<sup>1</sup> *Stockholm University, Department of Ecology, Environment and Plant Sciences, Stockholm, Sweden,* <sup>2</sup> *National Museum of Natural History, Department of Bioinformatics and Genetics, Stockholm, Sweden*

The traditional model of marine pelagic food webs based on phytoplankton, zooplankton and predatory fish, is changing fast. From being a three-step food chain, it is becoming a complex and dynamic network of species interactions. Most studies today are conscious that an individual's trophic level can depend on more than taxonomic identity. Life stages, food availability, predation and external environmental factors are influencing foraging behavior and makes trophic levels dynamic entities, rather than fixed discrete units.

Microorganisms play a vital part in the cycling of energy and nutrients in the oceans. Even though the implementation of Next Generation Sequencing (NGS) techniques has brought invaluable insights on the microbial composition, species interactions within the microbial community are still mainly based on size structure and do not account differences between species. Lack of mechanistic understanding of the microbial community has been identified as one of the major knowledge gaps for predicting both vulnerability of local marine ecosystems as well as global climatic feedback alterations.

Using NGS metabarcoding and metagenomics, we are developing a method for studying food-web interactions among the microbial community and relate this with interactions of upper trophic levels. The aim is to increase the mechanistic understanding of feeding-, parasitic- and symbiotic interactions in the microbial community. We also want to identify what species are the key players in the transport of organic compounds to the upper food web. In order to enhance the quantitative properties of the NGS methods we have established simple feeding interactions consisting of different organisms of bacteria, picophytoplankton, flagellates, ciliates and rotifers. The controlled laboratory systems are used as standard models for calibrating the NGS analysis of *in situ* environmental samples of the microbial community under different environmental conditions.

The methods used in this study will shed new light on the complexity and dynamics of microbial food-webs and facilitate the study of the key players. These insights are prerequisite for further investigation of the mechanistic impacts of warming, ocean acidification and other anthropogenic factors on the marine microbial community.

## Molecular diet analysis in arthropod predators – when to use NGS or diagnostic PCR

*Daniela Sint*<sup>1</sup>, *Oskar Rennstam Rubbmark*<sup>1</sup>, *Sandra Cupic*<sup>1</sup>, *Michael Traugott*<sup>1</sup>

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For molecular diet analysis two methods are commonly applied. Either diagnostic PCR is used to screen for targeted types of food-DNA, or thousands to millions of DNA sequences are read using next generation sequencing (NGS) and matched to reference databases. To compare the information attained by the two methods, we analysed twenty regurgitates from carabid beetles (*Poecilus cupreus*) and staphilinid beetles (*Philonthus* sp.) repeatedly with each method. For diagnostic PCR, a multiplex system targeting different aphid species, collembolans and earthworms was used. For the NGS approach, an approx. 300 bp long fragment of COI was amplified with a set of general primers with a wide taxonomic coverage and little taxonomic bias and sequenced on an Illumina MiSeq.

Although we selected regurgitates for the analysis, which contain significantly less consumer DNA than full-body DNA extracts, consumer DNA accounted for over 90 % of the returned reads from NGS. The detected prey diversity per individual sample was higher with NGS, however, also the species turnover between the five replicates of the same sample was significantly higher. Moreover, prey that was constantly detected in a sample with multiplex PCR was often missed with NGS.

This shows that results obtained by diagnostic PCR are much more robust and stable, while NGS-results are strongly influenced by random and unknown factors that complicate comparisons between replicates or samples. Consequently, in situations like here, where it is anticipated that NGS-results will be biased by one or few dominating DNA-types, this method is better suited for obtaining general knowledge on an *a priori* unknown diet. As NGS has difficulties in reliable detecting rare species and thus cannot describe absences well, it is, with a sufficiently high sequencing depth, rather suited for descriptive studies. To study functional changes however, it is advisable to investigate the consumption of selected, ecologically important food items with diagnostic PCR as this method delivers more robust information on both, presence and absence of the targeted species. Also, due to lower costs per sample, larger sample numbers can be analysed individually with diagnostic PCR, increasing the reliability of results and drawn conclusions even further.

## Pellets of proof: First glimpse to the dietary composition of adult odonates as revealed by metabarcoding of faeces

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Recent advances in molecular techniques allow us to resolve the diet of new taxa. Odonates are potentially important top-down regulators of many insects. Yet, to date, our knowledge of odonate prey use is based mainly on limited observations of odonates catching or eating their prey. In this study, we examine the potential use of metabarcoding in establish the diet of three odonate species (*Lestes sponsa*, *Enallagma cyathigerum* and *Sympetrum danae*) at a site in southwestern Finland. To this purpose, we compared three different methods for extracting DNA from faecal samples: Macherey-Nagel Nucleospin XS kit, a traditional salt extraction, and Zymo Research Fecal Microprep kit. From these extracts, we amplified group-specific mitochondrial markers (COI and 16S rRNA) from altogether 72 odonate individuals, and compared them to comprehensive reference libraries. The three odonate species show major overlap in diet, with no detectable differences between individuals of different size and/or gender, reflecting opportunistic foraging of the odonates. Of a total of 41 different prey species detected, the most frequently-consumed ones were Diptera, with additional records of six other orders. Based on our data, the best DNA extraction method would be the traditional salt extraction, since it provides best results while being the most economical at the same time. To our knowledge, this is the first study to resolve the species-level diet of odonates. Armed with these molecular tools, we are ready to examine the ecological role of odonates in both terrestrial and aquatic food webs, and in transferring subsidies between these two realms.

## A rapid identification system for earthworm prey

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Earthworms are amongst the most important invertebrates in soils worldwide, playing a key role in soil ecology. Constituting up to 90% of the soil invertebrate biomass they occupy a central position in food-webs both above and below ground. Moreover, earthworms are sustaining populations of generalist predators, which can be important biocontrol agents. The species identification of earthworms, however, poses substantial challenges. Molecular approaches have become vital for prey detection offering a high potential also for reliable earthworm identification. The aim of this study was to develop a diagnostic multiplex PCR targeting for fast and cost-effective earthworm-prey identification via gut content analysis or in faeces. Primers are targeting the the most common Central European earthworm species occurring in arable land: *Dendrobaena octaedara*, *Dendrodrilus rubidus*, *Octolasion tyrtaeum*, *Lumbricus rubellus*, *A. rosea*, *A. longa*, *A. tuberculata* s.l. and the genus *Lumbricus* spp.. Additionally, a general primer pair amplifying a ~600bp for the family Lumbricidae was developed to be used as an internal PCR control. The assay was tested against an extensive number of arthropods, gastropods and vertebrates inhabiting arable ecosystems to exclude false amplification of non-target organisms. The approach presented here provides an efficient, highly sensitive, and cost-effective (~consumable costs of 1.3 € per sample) tool for assessing the dietary choice of the numerous earthworm consuming predators species specifically.

# Index

- Abrego, Nerea, 146  
Adams, Gracie, 138  
Aguilera Nuñez, Guillermo, 151  
Aguilera, Guillermo, 22  
Agusti, N., 102  
Aihartza Azurtza, Joxerra, 117  
Akter, Asma, 36  
Albrecht, Jörg, **8**, 33, 128  
Albrecht, Matthias, 83  
Alderman, Rachael, 108, 150  
Allhoff, Korinna T., 75  
Ammann, Lolita, 83  
Amorim, Francisco, 140  
Angel, Miquel, 141  
Angerbjörn, Anders, 32  
Arrizabalaga-Escudero, Aitor, 117  
Ayes, Matthew, 50
- Bahram, Mohammad, 43  
Bane, Miranda, 64  
Banks, H. T., 27, 57  
Banks, J. E., 27  
Barot, Sébastien, 76  
Barrio, Isabel C., 111  
Bartomeus, Ignasi, 9  
Bartos, Michael, 54  
Bastazini, Vinicius A.G., 26  
Baude, Mathilde, 23  
Bearhop, Stuart, 122  
Becks, Lutz, 28  
Beja, Pedro, 113, 140, 149  
Bell, James R., 144  
Benucci, Marco, 84  
Benvenuto, Chiara, 129  
Berens, Dana G., 8  
Berlow, Eric L., 19  
Bernard, Henry, 88  
Bertrand, Colette, 83  
Bhattacharyya, Sabuj, **85**, 138  
Biella, Paolo, 36  
Birkhofer, Klaus, 103
- Bishop, Philip J., 89  
Björkman, Christer, 41  
Boatman, Nigel, 23  
Boddy, Lynne, 72  
Bohan, David, 68, 99, 101, **137**  
Bommarco, Riccardo, **10**, 22, 27, 45, 57, 151  
Bonsall, Michael B., 11, 69  
Borgess, Renee M., 132  
Brandl, Roland, 8  
Briem, Felix, 97  
Brose, Ulrich, 61  
Brosi, Berry, 24  
Brown, Joel J., 120  
Bruford, Michael, 94  
Burdon, Francis, 25  
Burke, Terry A., 92  
Butlin, Roger K., 92
- Carlson, Peter E., 18  
Casas, Grasiela, 26  
Catry, Paulo, 108  
Chadwick, E. A., 98  
Champneys, Alan, 67  
Cherif, Mehdi, 143  
Cirtwill, Alyssa, 65  
Clare, Elizabeth L., 16, **81**, 87, 88, 112, 139  
Cole, Nik, 94  
Collatz, Jana, 96  
Conyers, Simon, 23  
Correia, Marta, 51  
Creer, Simon, 126  
Cromsigt, Joris, 86  
Cuff, Jordan P., 144  
Cupic, Sandra, 153  
Curtsdotter, Alva, **27**, 57
- da Silva, Luis P., 149  
Daily, Gretchen, 40  
Dalén, Love, 119  
Dalerum, Fredrik, 32  
Daniel, Rolf, 121  
Davidson-Watts, Ian, 92

- Davies, Nancy, 23  
 Davies, Richard, 126  
 Davies, Sarah, 122  
 Dawson, Deborah A., 85, **138**  
 de Boer, W., 15  
 de Oliveira, Hernani F. M., 87  
 Deagle, Bruce, 108, **136**, 150  
 Del Arco, Ana, 28  
 Delhomme, Nicolas, 143  
 Desireddy, Sathish, 132  
 Devoto, Mariano, 29  
 Didham, Raphael K., 13  
 Dieterich Mabin, Molly E., 91  
 Dirzo, Rodolfo, 40  
 Dobbs, Emily, 24  
 dos Remedios, Natalie, 92, 138  
 Downey, Harriet, 11  
 Drake, Lorna, 98  
 Drinkwater, Rosie, 88  
 Drossel, Barbara, 70, 75, 77  
 Dugdale, Hannah, 138  
 Dumbrell, Alex J., 68, 100, 137  
 Dunne, Jennifer, 62  
  
 Easton, Luke, 89  
 Eastwood, Dan E., 72  
 Ebeling, Anne, 121  
 Edenius, Lars, 41  
 Egeter, Bastian, 89  
 Egger, Nina, 21  
 Eitzinger, Bernhard, 123  
 Ekbom, Barbara, 103  
 Ekholm, Adam, 30  
 Eklöf, Anna, 65, **66**  
 Ellison, Amy, 83  
 Elozegi Irurtia, Arturo, 117  
 Emer, Carine, 31  
 Endrédi, Anett, 73  
 Entling, Martin H., 83  
 Erlandsson, Rasmus, 32  
 Escudero, Adrián, 47  
 Esnaola Illarreta, Amaiur, 117  
 Esparza Salas, Rodrigo, 119, 152  
 Evans, Darren M., 17, 107  
  
 Farwig, Nina, 8, **33**, 128  
 Fernando García, Luis, 127  
 Ferreira, Pedro M.A., 26  
 Fey, Pauline, 34  
  
 Fisher, Matthias, 28  
 Fontaine, Colin, 12  
 Fowler, Mike S., 72  
 Franjević, Milivoj, 110  
 Frei, Britta, **99**, 101  
 Freitas, Helena, 51  
 Friberg, Hanna, 105  
 Friberg, Nikolai, 25  
 Friedemann, Pâmela V., 26  
 Frischer, Marc E., **90**  
 Frischer, Marc. E., 95, 106  
 Frost, Carol, 13  
  
 Gaiarsa, Marilia P., 42  
 Galetti, Mauro, 31  
 Gallo, Bruno, 100  
 Galzin, René, 34  
 Gao, Zhilei, 105  
 Gardiner, Mary M., 91  
 Gariepy, Tara, **82**  
 Gerpe, Christopher, 12  
 Gibson, D. M., 95  
 Gilbert, Thomas, 88  
 Gilbert, Tom, 115  
 Gilg, Olivier, 133  
 Gillespie, Mark, 23  
 Goder, Martine, 94  
 Goethals, Peter, 25  
 González-Varo, Juan Pedro, 118  
 Gonzalez-Esteban, Jorge, 117  
 Gravel, Dominique, 63  
 Gripenberg, Sofia, 11, 56  
 Guenay, Yasemin, 99, **101**  
 Gundersen, Ida, 102  
 Gårdmark, Anna, 5  
  
 Hackett, Talya, 14  
 Haenfling, Bernd, 84  
 Hahn, Christoph, 17  
 Hallin, Sara, 116  
 Hambäck, Peter, **119**, 133  
 Hamm, Michaela, 70  
 Hannula, Emilia, 15  
 Hardwick, Jane, 145  
 Hatteland, Bjørn Arild, 102  
 He, Fangliang, 59  
 Hebert, Paul, 52  
 Heidemann, Kerstin, **124**, **125**, 147  
 Heleno, Ruben H., 39, 51, 113

- Hemprich-Bennett, David, 139  
 Herzog, Felix, 83  
 Higgin, Megan, 120  
 Hipperson, Helen, 85, **92**, 138  
 Hrcek, Jan, 120  
 Hunter, Ewan, 126  
 Huotari, Tea, 146  
 Hürler, Maurin, 12  
  
 Jackson, Michelle, 100  
 James, Richard, 64  
 Janecek, Stepan, 54  
 Jarman, Simon N., 108, 140, 149, 150  
 Jaroszewicz, Bogdan, 8, 128  
 Jeffs, Christopher T., 120  
 Ji, Yinqiu, 146  
 Johansson, Veronika, 71  
 Johnson, Richard K., 18  
 Jones, David, 75  
 Jonsson, Mattias, 27, **103**, 113  
 Jonsson, Tomas, 27, 57  
 Jordán, Ferenc, 73  
 Jordano, Pedro, 31, 118  
 Jousset, Alexandre, 105  
 Jüds, Melissa, 147  
 Jürgenstein, Siiri, 43  
  
 Kaasik, Ants, 43  
 Kamenova, Stefaniya, 104  
 Kankaanpää, Tuomas, 35  
 Karley, Alison, 107  
 Karlsson, Ida, 105  
 Kaunisto, Kari M., 154  
 Kéfi, Sonia, 19  
 Khalilur Rahman, Omar, 16  
 Kimbell, Helen, 17  
 Kitching, Roger, 145  
 Kitson, James, **17**, 107  
 Kittelberger, Kyle, 50  
 Kiziridis, Danis, 72  
 Klapwijk, Maartje, 41  
 Klečka, Jan, 36  
 Klinkhamer, Peter, 37  
 Klomberg, Yannick, 54  
 Klumpers, Saskia, 37  
 Knell, Rob, 16  
 Knop, Eva, 12  
 Koeb, Marco, 155  
 Kolyuchkina, Galina A., 58  
  
 Koskinen, Janne, 148  
 Kremen, Claire, 42  
 Kunin, Bill, 23  
 Kurina, Olavi, 43  
  
 Lacroix, Gérard, 76  
 Lamb, Philip, 126  
 Lamboley, Lauren, 106  
 Lara Mendoza, Carolina, 38  
 Laubmeier, A. N., 27, 57  
 Lavandero, Blas, 93  
 Lawson-Handley, Lori, 84  
 Lea, Mary-Anne, 108, 150  
 Lees, David C., 92  
 Letourneur, Yves, 34  
 Lewis, Owen T., 11, 44, 120  
 Littlewood, Nick, 107  
 Lopes, Pedro, 149  
 Lopes, Ricardo J., 149  
 López Núñez, Francisco Alejandro, 39  
 López-Angulo, Jesús, 47  
 López-Carretero, Antonio, 29  
 Loy, Xingwen, 24  
 Lunt, David H., 17  
 Lurgi, Miguel, 67  
  
 Malm, Lisa, 107  
 Malsher, Gerard, 103  
 Manzl, Lena, 21  
 Maraun, Mark, 124, 125, 147  
 Marchante, Elizabete, 39  
 Marchante, Hélie, 39  
 Mardashova, Maria, 130  
 Mariani, Stefano, 129  
 Martin Schmidt, Niels, 133  
 Martin, Jean-François, 109  
 Martin, Michael D., 111  
 Martinez Bauer, Angelica E., 56  
 Mata, Vanessa A., **140**, **149**  
 Maunsell, Sarah, 145  
 McDonald, R. A., 98  
 McInnes, Julie, **108**, **150**  
 McKie, Brendan, **18**, 25  
 McWilliams, Chris, 67  
 Memmott, Jane, **6**, 14, 20, 23, 55  
 Mendenhall, Chase, 40  
 Mertens, Jan, 54  
 Mestre, Laia, 83  
 Miele, Vincent, 19



- Mikich, Sandra B., 44  
 Miller, Kirsten, 22, **151**  
 Mokievsky, Vadim, 130  
 Mola, Iñaki, 47  
 Mollot, Gregory, 109  
 Monasterolo, Marcos, 29  
 Montoya, Daniel, 14, **67**  
 Montoya, J. M., 67  
 Moora, Mari, 48  
 Moorhouse-Gann, Rosemary, 83, **94**  
 Moraes, Suelen, 31  
 Móréh, Ágnes, 73  
 Morozumi, Connor, 24  
 Morrien, E., 15  
 Morris, Rebecca J., 69  
 Morrison, Beth, 40  
 Morton, Dan, 23  
 Muggleton, Stephen, 68  
 Müller, Carsten T., 144  
  
 Navarrete, Sergio A., 19  
 Nogales, Manuel, 53  
 Nordkvist, Michelle, 41  
 Novotny, Andreas, 142, **152**  
 Novotny, Vojtech, 7  
 Nyman, Tommi, 148  
  
 Oehm, Johannes, 134  
 Oliver, Tom, 74  
 Olofsson, Carin, 143  
 Ornosá, Concepción, 47  
 Orozco-terWengel, Pablo, 144  
 Ortiz-Martinez, Sebastian, 93  
 Ovaskainen, Otso, 146  
  
 Parravicini, Valériano, 34  
 Parth, Nadia, 131  
 Pearce-Higgins, James, 107  
 Pekár, Stano, 127  
 Pent, Mari, 43  
 Peralta, Guadalupe, 13  
 Pereira Maia, Kate, 20  
 Perez-Delgado, Antonio, 53  
 Petit, Sandrine, 99, 101  
 Petráková, Lenka, 127  
 Phillips, Richard, 108  
 Pillar, Valério D.P., 26  
 Pinnegar, John, 126  
 Pinol, Josep, 141  
  
 Piratelli, Augusto, 31  
 Pizo, Marco A., 31  
 Plantegenest, Manuel, 104  
 Pocock, Michael, 64, 74  
 Pompozzi, Gabriel, 127  
 Ponisio, Lauren, 42  
 Potter, Joshua, 88, 139  
 Price, A. R., 90  
 Pywell, Richard, 74  
 Pöldmaa, Kadri, 43  
  
 Quévieux, Pierre, 76  
  
 Raine, Elizabeth H., 44  
 Rand, Tatyana A., 13  
 Ransome, Emma, 100  
 Rasmussen, Claus, 133  
 Raybould, Alan, 137  
 Raymond, Ben, 108, 150  
 Rebelo, Hugo, 140  
 Redhead, John, 74  
 Reneerkens, Jeroen, 133  
 Rennstam Rubbmark, Oskar, **21**, 131, 153  
 Ribeiro, Milton C., 31  
 Ribeiro, Sérgio, 39  
 Richau, Kerstin, 143  
 Riggi, Laura, 45  
 Riordan, Philip, 44  
 Risnoveau, Geta, 25  
 Riutta, Terhi, 56  
 Robertson, Bruce C., 89  
 Rodríguez-Echeverría, Susana, 51  
 Roe, Cailin, 89  
 Rogge, Tobias, 75  
 Romeis, Jörg, 96  
 Romero, Carlos-Lara, 53  
 Roslin, Tomas, 22, 30, 35, **46**, 52, 57, 119,  
     123, 133, 146, 148, 151, 154  
 Rossiter, Stephen J., 87, 88, 112, 139  
 Roubinet, Eve, 103  
 Roy, Helen, 84  
 Ruess, Liliane, 125  
 Ryser, Remo, 12  
  
 Sánchez, Ana M., 47  
 Sandin, Leonard, 18  
 Šapina, Ivan, 110  
 Santamaría, Silvia, 47  
 Sauve, Alix M. C., 14, 20, 67

- Schabo, Dana G., 33, 128  
 Scheepers, Giel, 105  
 Scherber, Christoph, 121  
 Scheu, Stefan, 124, 125, 147  
 Schlautmann, Jan, 128  
 Schmidt, Niels Martin, 52, 146  
 Seguí, Jaume, 53  
 Selva, Nuria, 8  
 Sepp, Siim-Kaarel, 48  
 Šerić Jelaska, Lucija, 110  
 Shapcott, Alison, 145  
 Siegenthaler, Andjin, 129  
 Sigsgaard, L., 102  
 Simakova, Ulyana, 130  
 Sint, Daniela, 21, 96, **153**, 155  
 Skjelbred, Ina Åsnes, 111  
 Slade, Eleanor M., 44  
 Smart, Simon, 23, 55  
 Snoek, B., 15  
 Soininen, Eeva M., 111  
 Spatial Food web Ecology Group, 46  
 Speed, James D. M., 111  
 Spiridonov, Vassily A., 58  
 Spitzer, Robert, 86  
 Sritongchuay, Tuanjit, 49  
 Stang, Martina, 37  
 Stanley, Margaret, 38  
 Stanworth, Andrew, 108  
 Staudacher, Karin, 93, 97, 103, 104  
 Steltzer, Heidi, 24  
 Stork, Nigel, 145  
 Strandmark, Alma, 119  
 Straw, Nigel A, 17  
 Struebig, Matthew, 88  
 Studer, Liz, 50  
 Suazo, Cristían G., 108  
 Symondson, William O. C., 83, 94, 98, 122, 144  
 Sääksjärvi, Ilari E., 154
- Tack, Ayco, 30  
 Tamaddoni-Nezhad, Alireza, **68**, 137  
 Tammaru, Toomas, 43  
 Taylor, Martin, 126  
 Teder, Tiit, 43  
 Teixeira, Tiago, 112  
 Telenius, Anders, 71  
 Terry, J. Christopher D., 69  
 Thalinger, Bettina, 134
- Thebault, Elisa, 76  
 Thiel, Tatjana, 77  
 Thomas, Robert, 122  
 Thompson, David, 108  
 Tiede, Julia, 121  
 Timóteo, Sérgio, 51  
 Tiusanen, Mikko, 52  
 Tixier, Philippe, 109  
 Trandem, Nina, 102  
 Traugott, Michael, 21, 27, 93, 96, 97, 99, 101, 103, 104, 121, **131**, 134, 153, 155  
 Traveset, Anna, 53  
 Tropek, Robert, 54  
 Tschardt, Teja, 121  
 Tylianakis, Jason M., 13, 38
- Vacher, Corinne, 137  
 van der Putten, W. H., 15  
 van Veen, J. A., 15  
 Vanbergen, Adam, 74  
 Varsani, Arvind, 13  
 Vasconcelos, Sasha, 113  
 Vaughan, Ian, 14, 20, 122, 144  
 Vaz-de-Mello, Fernando Z., 44  
 Verschut, Vasiliki, 119  
 Vesterinen, Eero J., 35, 133, 148, **154**  
 Villa-Galaviz, Edith, 55  
 Visakorpi, Kristiina, 56  
 Vishnu, Arkamitra, 132  
 Vogt, Heidrun, 97  
 Volk, Martin, 25  
 Vollhardt, Ines M. G., 131  
 Vorhauser, Julia, 134
- Wallerger, Corinna, 99, 101, **155**  
 Walters, Tina L., 90, **95**, 106  
 Wangenstein, Owen S., 129  
 Weimerskirch, Henri, 108  
 Weingartner, Elisabeth, 119, 133  
 Welty, Celeste, 91  
 Wemheuer, Bernd, 121  
 Wieters, Evie A., 19  
 Wilmer, Chelsea, 24  
 Winder, Monika, 142, 152  
 Wirta, Helena, 119, **133**  
 Withers, Amy, 138  
 Wolf, Sarah, 96  
 Woodcock, Ben, 74

Woodward, Guy, 68, 100, 137  
Wootton, Kate, 57  
Wulff-Vester, Elena Therese, 102  
  
Ye, Zhengpei, 131  
Young, Richard, 94  
Yu, Douglas, 146  
Yuan, Chenggui, 72  
  
Zalota, Anna, 58  
Zamora, Sara, 152  
Zamora-Terol, Sara, 142  
Zeisler, Christiane, 96, 97, **134**  
Zhang, Minhua, 59  
Zobel, Martin, 48  
Zoller, Leana, 12  
Zou, Kejun, 76  
Zuël, Nicolas, 94  
Öpik, Maarja, 48