



Oikos-Finland 2025 Conference

“Ecology And Evolution: Patterns, Processes, and Applications”

Abstract book

March 11-14 Jyväskylä, Finland

Novogene

BioName
DNA analyses as turnkey solutions

 Suomen ympäristökeskus
Finlands miljöcentral
Finnish Environment Institute


Federation of Finnish
Learned Societies



NSO
NORDIC SOCIETY OIKOS



WILD ANIMAL PHENOTYPING INFRASTRUCTURE
WildAP
UNIVERSITY OF HELSINKI

Table of Contents

Keynote 1: J. Kotiaho	4
Keynote 2: A. Narwani.....	5
Keynote 3: M. Leibold	6
Keynote 4: C. De Pasqual.....	7
Keynote 5: B. Mohring	8
Keynote 6: M. Saastamoinen.....	9
Session A1: Urbanization	10
Session A2: Genetic diversity	16
Session A3: Eco-evo-devo experimental research	21
Session A4: Predation.....	27
Session B1a: Themed session 4: Biodiversity monitoring for the future	33
Session B1b: Themed session 4: Biodiversity monitoring for the future	39
Session B2a: Methodological advances in ecology and evolution	45
Session B2b: Methodological advances in ecology and evolution	51
Session B3a: Conservation biology and sustainability	56
Session B3b: Conservation biology and sustainability	62
Session B4a: Metacommunity processes and dynamics	68
Session B4b: Metacommunity processes and dynamics	74
Session C1: Experimentally testing the effects of environmental change.....	80
Session C2: Population dynamics	88
Session C3: Themed session 8: Biodiversity footprint of human activities	96
Session C4: Host-parasite and disease dynamics.....	104
Session C5: Themed session 3: Citizen science approaches in ecological research	113
Session D1a: Themed session 7: Environmental sequencing for biodiversity research ...	120
Session D1b: Themed session 7: Environmental sequencing for biodiversity research ...	125
Session D2a: Ecophysiology	131
Session D2b: Ecophysiology	137
Session D3a: Themed session 5: Experimental community ecology.....	142
Session D3b: Life-history traits	148
Session D4a: Themed session 1a: Forest management	154
Session D4b: Themed session 1b: Human-wildlife interactions	160

Session D5: Microbiome research.....	166
Session E1a: Restoration.....	173
Session E1b: Temporal community dynamics.....	180
Session E2a: Macroecology and global change.....	184
Session E2b: Macroecology and global change.....	190
Session E3a: Ecosystem processes	196
Session E3b: Palaeoecology	203
Session E4a: Foodwebs and interaction networks.....	206
Session E4b: Science communication.....	212
Session F1: Spatial modelling in conservation and management	215
Session F2: Animal behavior	223
Session F3: Evolutionary processes	232
Session F4: Themed session 2: Statistical approaches in multispecies modelling	240
Session F5: Themed session 6: Microbial ecology	248
Poster session	255

Keynote 1: J. Kotiaho

Wednesday, 09.30-10.30, Room L304

Ecological applications and evidence-based policy making

Janne S. Kotiaho

School of Resource Wisdom, University of Jyväskylä

Planetary well-being is a state in which the integrity of Earth system and ecosystem processes remains unimpaired to a degree that lineages can persist to the future as parts of ecosystems, and organisms (human and nonhuman) can realise their typical characteristics and capacities. Planetary well-being may not be reached without a profound change in our world views and the structures and functions of our society. We need to promote the construction of sustainable lifestyles, curb consumption, protect and restore nature, and combat climate change. The planning, decision-making and implementation of the sustainability transformation policy must be based on scientific evidence.

In this talk my intention is first to discuss the state of nature from global and Finnish perspective. While doing this I will also discuss the role of academics in providing advice to various decision makers. Once I have established the nature of the existential risk, I will turn into solutions. I will start by making a claim that we can't manage what we can't measure. I will explore the biodiversity equivalent impact assessment methodology and biodiversity offsetting as well as scrutinize the buzzwords biodiversity handprint and nature positive actions. I may end with a few recommendations.

Keynote 2: A. Narwani

Wednesday, 13.00-14.00, Room L304

Phyt to compete in a warming world? Ecological and evolutionary responses to resource limitation across scales

Anita Narwani

Swiss Federal Institute of Aquatic Science and Technology (Eawag)

Resource limitation is a major driver of ecological and evolutionary dynamics of all organisms, including phytoplankton. Short-term responses to resource limitation include plastic re-wiring of the molecular and metabolic phenotypes of cells. Less is known about the evolution of resource requirements and the molecular phenotype after longer-term selection by resource limitation. Can competitive abilities adapt to limiting resources? Do requirements for different resources evolve independently or are trade-offs intrinsic? What is the metabolic basis of this evolutionary adaptation? To answer these questions we have employed a variety of approaches, from highly controlled evolution experiments of a single model green alga in chemostats, to outdoor mesocosm experiments exposed to natural climatic and biotic community complexity. We have investigated ecological and evolutionary change in individual-level traits, protein expression and population-level resource requirements. Across these experiments and levels of biological organization, we find that selection by limiting resources results in adaptive evolutionary change, including reductions in resource requirements. At the molecular level, we find a surprising degree of convergent evolution of core metabolic functions across multiple different low-resource selection environments. We also do not observe the evolution of trade-offs between competitive abilities in different low-resource environments. As many resources are becoming increasingly limiting in pelagic environments as the climate is warming, I will also present our most recent work investigating the combined impacts of warming and resource limitation on phytoplankton metabolism, growth and competitive ability. I discuss the potential consequences of our findings for competitive community assembly.

Keynote 3: M. Leibold

Thursday, 09.00-10.00, Room L304

Inferring process from patterns in metacommunities: How well can we hope to do? And why we need to do better

Mathew Leibold

University of Florida

Variation among communities in metacommunities is the result of the interplay among species that involve a handful of basic processes. However, these processes become ‘entangled’ with each other in highly complex ways when they involve more than a very small number of species in very simple landscapes. Predictive models of species distributions have improved dramatically, even in highly diverse biotas in complex landscapes so that it is not uncommon to predict in excess of 75% of the variation. However, the task of inferring or explaining (rather than predicting) this variation remains a substantial challenge. In this talk, I’ll try to define this challenge and highlight how process-based models can be improved to facilitate this link. I’ll examine methods based on ‘partially-structured’ modifications of disordered systems models and transition-based community assembly models to meet this challenge. I’ll also discuss how data-based pattern analysis models might be modified to link with these improvements in theory. Overall, I argue that these rapidly improving tools promise a much more coherent understanding of metacommunities.

Keynote 4: C. De Pasqual

Thursday, 13.00-13.45, Room L304

On the maintenance of intrapopulation genetic variation: The interplay between sexual selection, chemical communication, and fitness in the wood tiger moth (*Arctia plantaginis*)

Chiara De Pasqual

Swedish University of Agricultural Sciences

Within population phenotypic variation is often maintained by intricate interactions among multiple selective pressures. Genetic associations between color traits and life-history traits can create context-dependent advantages and affect intrapopulation dynamics. In my PhD thesis, I investigated the role of sexual selection, chemical communication, and fitness of the different genetic color morphs (i.e., WW, Wy, yy) in maintaining the two male color morphs in the polymorphic wood tiger moth (*Arctia plantaginis*). Overall, I found that the presence of one or two copies of the yellow (y) allele affected several life-history traits, leading to context-dependent (dis)advantages across the reproductive sequence. For example, yy females were generally more attractive to males in a high-density scenario, while WW females were more attractive when females were simultaneously calling. yy males were faster to reach females than white (WW, Wy) males in a low-density scenario, while white males and males with denser antennae (i.e., higher lamellae count) located females faster in a high-density scenario. At the reproductive level, Wy females benefit from higher likelihood of reproductive output leading to strong heterozygote advantage, while yy males had the lowest reproductive output. These results show that the color locus has pleiotropic effects on several life-history traits, offering a mechanism of balancing selection that enables the persistence of genetic and phenotypic variation in natural populations.

Keynote 5: B. Mohring

Thursday, 16.15-17.00, Room L304

Evolution under fluctuating predation pressure: A case study of common eiders and white-tailed eagles in Finland

Bertille Mohring

University of Liverpool

Predation is a key selective force shaping prey trait evolution. Predators can directly select prey phenotypes through killing, whereas the risk of predation can induce plastic adjustments of prey phenotypes. Importantly, the extent to which predator-consumptive and predation risk effects drive the evolution of prey phenotypes is still poorly understood. Predator-prey interactions between white-tailed eagles *Haliaeetus albicilla* and common eiders *Somateria mollissima* in Finland provide an ideal backdrop to assess the relative contributions of selection and plasticity in enabling individuals and populations to cope with fluctuating predation threat. Using a long-term monitoring of common eiders facing the rapid recovery of their native predator (the white-tailed eagle), I investigated behavioural and physiological responses of breeding common eiders to fluctuating predation pressure. I showed that the temporal increase in white-tailed eagle abundance was accompanied by several behavioural and physiological changes, including a reduction of risk-taking, breeding propensity and investment in reproduction. Observed responses were driven by both within-individual adjustments (i.e., plasticity) and among-individual variation (i.e., selection). However, plastic responses were predominant, supporting the idea that predation risk effect may be more important in explaining prey trait evolution than predator-consumptive effects. Altogether, these results provide valuable insight into the short- and long-term responses of prey individuals and populations to a changing predation regime. Understanding how both plastic and selective mechanisms drive predator-prey interactions is key to assessing the resilience of species and populations to changes in their environment.

Keynote 6: M. Saastamoinen

Friday, 09.00-10.00, Room L304

Unveiling responses to anthropogenic change through long-term monitoring of natural populations

Marjo Saastamoinen

University of Helsinki

Natural populations and communities are greatly affected by environmental changes, with habitat loss and climate change being key drivers. However, species and communities exhibit diverse responses to these pressures. Long-term, systematic monitoring is crucial for identifying the factors and potential adaptive mechanisms that enable species to mitigate the impacts of anthropogenic change. In this presentation, I will first highlight how the long-term monitoring data of the Glanville fritillary butterfly in the Åland Islands, in combination with experimental and genomic approaches, reveals critical insights into factors that enhance its resilience to anthropogenic disturbances. Next, I will draw on moth and butterfly monitoring data from across Finland to provide examples of the determinants of whether species thrive or decline under climate change. Finally, I will present findings from two multi-taxon studies that assess biodiversity-stability relationships and compare occupancy patterns between protected and unprotected boreal sites over decades. Together, my talk aims to demonstrate how long-term monitoring data, as a uniquely valuable and essential resource, can uncover patterns and mechanisms that may help protect populations and communities facing anthropogenic pressures. Natural populations and communities are greatly affected by environmental changes, with habitat loss and climate change being key drivers. However, species and communities exhibit diverse responses to these pressures. Long-term, systematic monitoring is crucial for identifying the factors and potential adaptive mechanisms that enable species to mitigate the impacts of anthropogenic change. In this presentation, I will first highlight how the long-term monitoring data of the Glanville fritillary butterfly in the Åland Islands, in combination with experimental and genomic approaches, reveals critical insights into factors that enhance its resilience to anthropogenic disturbances. Next, I will draw on moth and butterfly monitoring data from across Finland to provide examples of the determinants of whether species thrive or decline under climate change. Finally, I will present findings from two multi-taxon studies that assess biodiversity-stability relationships and compare occupancy patterns between protected and unprotected boreal sites over decades. Together, my talk aims to demonstrate how long-term monitoring data, as a uniquely valuable and essential resource, can uncover patterns and mechanisms that may help protect populations and communities facing anthropogenic pressures.

Session A1

Urbanization

Wednesday, 11.00-12.00, Room L304

Session chair: TBA

Moth reproduction and the city

Tuomas Kankaanpää¹, Riina-Kaisa Autti¹, Mahtab Yazdanian¹, Thomas Merckx², Sami Kivelä¹

¹*University of Oulu*

²*Vrije Universiteit Brussel*

Urban areas are characterised by hostile built-up land cover, higher temperatures, light pollution and high but alien plant diversity. These features have been shown to favour generalist moth species. Urban environments also include many hazards for adult moths, which should favour producing more eggs from the resources collected as a larva. Such reproductive strategy is called capital breeding. We wanted to test the hypothesis that increased adult mortality would: 1. lead to ecological filtering favouring a higher degree of capital breeding in urban moth communities and 2. affect the evolution of resource allocation within a species accordingly. We did this by using relative abdomen size as a proxy for the degree of capital breeding and modelling how the amount of urban land cover is associated with relative abdomen size in a subset of European geometrid moth observations sourced from the Global Biodiversity Information Facility (GBIF). We also reared *Chiasmia clathrata* moths belonging to urban and rural populations in common garden conditions and then measured their relative abdomen weights post eclosion. We found that urban environments favour species with higher degree of capital breeding in species living on herbaceous host plants but the opposite for tree feeding species. The latter effect can be explained by both urban tree species and thermal conditions mirroring those of a lower latitude. In the experimental part, we found no difference in the allometric scaling of body parts, but urban moths had relatively slightly larger abdomens by the virtue of growing a little larger overall.

Keywords: urban evolution, urban ecology, lepidoptera, resource allocation

Codes of conduct: Towards coexistence with urban animals

Karolina Lukasik

University of Helsinki

Urban animals usually fall outside the frameworks of protection established for their wild and domesticated counterparts. However, as we share urban spaces with them and interact on a daily basis, a mode of coexistence with them is much needed. Urban allotment gardens, as areas designed for interaction with nonhuman nature, offer practical insights into how such coexistence could look like. The local knowledge of urban gardener communities can be applied to other urban spaces as well. My study combines interviews with urban gardeners and camera observation of urban animals in 24 allotments across three gardens in the Helsinki capital region. Following Donaldson's and Kymlicka's concept of urban animal denizenship, I review the garden practices in the light of the three clusters of issues for denizens: security of residency, reciprocity of denizenship, and anti-stigma safeguards. I analyze how the gardeners develop and use strategies of controlling urban animal population and movement (barriers, disincentives, reduced food supply, habitat corridors, safe zones). I also discuss the ways in which those strategies may fail, drawing conclusions for broader coexistence framework for urbanites, both human and nonhuman.

Keywords: socio-ecological linkages, urban ecology, human-wildlife interactions

Movement activity of brown rats (*Rattus norvegicus*) in four populations in Helsinki

Suvi Sallinen, Viktor Zöldi, Tuomas Aivelo

University of Helsinki

The brown rat (*Rattus norvegicus*) is a common urban species that lives in close proximity to humans. Rats are commonly controlled for by pest management companies due to concerns for human health and structural integrity of buildings. Despite the control efforts, rats remain abundant in cities. Effective mitigation of rats requires knowledge on the basic ecology and spatial movement behaviour of rats. Furthermore, the effects of pest management on the ecology of rat populations remain unknown. In this multi-year project, we combine data of rat movement across the sites, population genetic data, pathogen data, and parasite data, to investigate the variation and effects of pest management on rat ecology. Here, I present initial results from the first data collection year on rat movement. We tagged rat individuals in four populations (Helsinki, Finland) with RFID-chips and followed their movement using 10-15 RFID-chip reading antennas placed across the sites. In addition, we collected population level movement activity data using track plates and trail cameras. Combined, these data provide a first glance into differences and similarities in rat activity across populations and individuals in this project.

Keywords: *Rattus norvegicus*, spatial ecology, movement

Temporal alpha and beta diversity of diving beetles (Coleoptera: Dytiscidae) reveals biotic heterogenisation in urban ponds

Wenfei Liao, Janne Soininen

University of Helsinki

Temporal biodiversity is a sensitive indicator of community change and the relative importance of different underlying drivers; thus it can be utilised to forecast urban biodiversity change in the future. Cities have suffered from biodiversity loss due to decreasing quantity and quality of both aquatic and terrestrial habitats. Here, we surveyed diving beetles in 20 ponds in Helsinki Metropolitan Area, Finland, for six years and investigated how alpha and beta diversity of beetles changed through time, and if pond structural connectivity (i.e., clustering of the ponds) and the presence or absence of fish affected the temporal change. We found that (a) dytiscid alpha diversity decreased through time, while dytiscid temporal beta diversity increased. (b) Clustered ponds had higher alpha diversity, lower species losses and higher species gains than isolated ponds, but temporal beta diversity did not differ between the categories. (c) Ponds with fish had little change in alpha diversity and experienced lower species losses and higher species gains than ponds without fish throughout time, but ponds without fish experienced declining alpha diversity through time. Our results indicate that dytiscid assemblages experienced biotic heterogenisation during the six years, but the heterogenisation processes are different in the presence and absence of fish. Dytiscids in clustered ponds are more likely to maintain more stable populations due to immigration via the rescue effects than in isolated ponds. The temporal dynamics of aquatic invertebrates suggest that improving landscape connectivity and local habitat conditions can mitigate species losses and support biotic communities in urban ponds.

Rapid change in community composition of carabid beetles in urban remnant forests of Helsinki

Basile Finand, Heikki Setälä, D. Johan Kotze

University of Helsinki

Habitat fragmentation is a major threat to biodiversity. Several studies have investigated the impact of current habitat fragmentation on contemporary carabid beetle communities. However, some studies suggest that the past configuration of the landscape can also explain contemporary communities through the extinction debt. While many of these studies have been performed on plants, few have done so for insects. Our study aims to fill this gap by studying the impact of past habitat fragmentation on contemporary carabid beetle communities and populations in remnant forests in Helsinki, Finland. We sampled ten recently fragmented urban forests (less than 35 years ago), ten historically fragmented urban forests (more than 35 years ago), and five less fragmented control forests in the summer of 2023. We compared the communities in terms of species richness, species composition and functional diversity. Moreover, we investigated changes in individual traits (size, dispersal) of the most commonly collected species at the population level. Our results showed no effect of fragmentation age on species richness and community composition. However, there is a clear difference in community composition between the fragmented and control forests. This suggests that community change is faster than expected after forest fragmentation. At the population level, no differences in size or dispersal were observed in the selected species. Our study highlights the rapid consequences of urban habitat fragmentation on biodiversity and the importance of considering time in the study of habitat fragmentation.

Keywords: habitat fragmentation, community ecology, Carabid beetles, urbanization

Session A2

Genetic diversity

Wednesday, 11.00-12.00, Room L303

Session chair: TBA

From wild to weeds: The evolutionary journey of a major agroecosystem threat

Célia Neto, Paul Neve

University of Copenhagen

Arable weeds provide great examples of rapid evolution in response to strong anthropogenic selective pressures, by invading, colonizing and adapting to agroecosystems. The evolution of weediness therefore provides unique and fundamental insights into the genetic basis of adaptation to novel human-influenced environments. In northern and western Europe, blackgrass (*Alopecurus myosuroides*) has emerged as a major arable weed, threatening crop yields. Here, we aimed at reconstructing its spread across European agricultural landscapes, to gain insight into its evolution from wild to weed, using contemporary agricultural populations and wild germplasm collected prior to modern agricultural intensification. We traced blackgrass history in space and time, conclusively pinpointing its origin to the Black Sea region and following its spread across Europe. Non-native contemporary weedy populations are more recent and genetically uniform, with reduced diversity, while wild past populations were large and highly diverse. Expansion patterns indicate a northward spread from the native region, beginning with dispersal to the Iberian Peninsula. Furthermore, our findings indicate that weediness in blackgrass has a polygenic genetic architecture, with loci under positive selection linked to tropism and growth, organ development and reproduction, and response to environmental stimuli. These traits likely allowed blackgrass to thrive in disturbed environments, via a “weediness syndrome” with parallels with crop domestication. This study reveals the genetic basis of adaptation to new environments and the evolutionary mechanisms behind responses to anthropogenic pressures. It highlights polygenic adaptation’s role in weed evolution, offering insights into eco-evolutionary processes that drive plant invasions and persistence in agroecosystems.

Keywords: adaptation, novel environments, weediness evolution

Resolving the genetic paradox of invasions

Antti Miettinen¹, Carol Stepien², Aja Noersgaard Buur Tengstedt¹, Michael Møller Hansen¹

¹*Aarhus University*

²*Smithsonian Institution*

Invasive species threaten global biodiversity and human well-being. Understanding the drivers involved in their spread is critical for preventing and mitigating future invasions. Using genomic approaches, we address the “paradox” of biological invasions: how do species sometimes spread to new habitats so efficiently, when their invading populations should suffer from inbreeding and loss of genetic variation due to low numbers of founder individuals? To explain this, we propose a new hypothesis that genetic “purging” (removal of deleterious recessive alleles exposed to selection because of inbreeding) is a decisive factor in invasiveness. We assume that without purging of strongly deleterious variation, inbreeding depression frequently leads to failure of invasions. We test this by analysing levels of inbreeding and deleterious alleles in populations of the invasive zebra mussel (*Dreissena polymorpha*) that poses a threat to freshwater ecosystems worldwide. Our results suggest strong and recent inbreeding in invasive zebra mussel populations and are in line with our hypothesis. The improved understanding of genomic processes underlying biological invasions will be broadly relevant across taxa and could fundamentally change our view of the dynamics of invasions. This may ultimately help guide conservation actions to prevent and reduce the impact of invasive species.

Keywords: invasive species, population genomics, inbreeding, whole-genome sequencing

Insights from analysing structural variants in *Neurospora crassa*

April Snøfrid Kleppe, Ilkka Kronholm

University of Jyväskylä

Identifying structural variants (SV) is to identify genetic biological diversity. As with all tasks concerning mapping biological diversity, the selected method of sampling will impact data. Identifying SV is a challenging task as different software approaches yield different results. We have applied nanopore sequencing to 53 wild strains of *Neurospora crassa*. We identified structural variants by applying three different methods for identifying SVs: sniffles2, mum&co, and cactus. We created de novo assemblies for the 53 strains that were applied for cactus and mum&co. We compare the results yielded by the three methods and cross-check which SVs are common, and which ones are unique for each mapping method. We further analyse physical properties of the SVs in relation to their allele frequencies and estimated distribution of fitness effects. Furthermore, we investigated whether heterochromatic regions harbour more diversity in SVs than euchromatic regions.

Keywords: structural variants, mutations, *Neurospora crassa*, molecular evolution

What can museum specimens reveal on temporal changes of genetic diversity in Finnish butterflies with varying population trends?

Audrey Bras¹, Lauri Kaila², Anssi Teräs³, Nathalie Puggaard Elkær A Ibsen⁴, Marie Djernæs⁴, Jeppe Bayer Pedersen⁴, Mads R. Jensen⁴, Trine Bilde⁴, Philip F. Francis Thomsen⁴, Jesper Bechsgaard⁴, Marjo Saastamoinen¹

¹*University of Helsinki*

²*Finnish Museum of Natural History*

³*Zoological Museum*

⁴*Aarhus University*

Insects have been reported declining worldwide in both numbers of species and population densities. Several factors such as climate change, pollution or land-use changes have been pointed out as main drivers of these declines. Whereas species losses are quantifiable through long term biodiversity monitoring, genetic losses remain difficult to quantify over time. Yet, genetic diversity is underlying the adaptive potential of species, and is consequently critical for species ability to respond to environmental changes. The long-term monitoring surveys of butterflies in Finland indicate that species responses, reflected by changes in temporal population trends, vary across species. This baseline offers a unique opportunity to assess how factors responsible for insect decline has shaped genetic diversity over time. Using a museomics approach, we are investigating temporal changes in genetic diversity during the last century for five butterfly species showing stable or declining population trends overtime. We have sequenced whole genomes of museum specimens collected at three historical time points in two areas in southern Finland and their corresponding contemporary populations. After accounting for postmortem damage in museum samples, we are comparing historical populations to the contemporary ones for each species to assess for signs of genetic erosion and increased inbreeding across the species studied. Here we will be presenting our latest results

Keywords: population genomics, conservation, Lepidoptera

Session A3

Eco-evo-devo experimental research

Wednesday, 11.00-12.00, Room L302

Session chair: TBA

Developmental effects and endocrine disrupting potential of In Ovo exposure to per- and polyfluoroalkyl substances in mallard ducklings

Silje Peterson¹, Anne-Fleur Brand¹, Kang Nian Yap¹, Junjie Zhang¹, Tomasz Maciej Ciesielski¹, Céline Arzel², Veerle Jaspers¹

¹*Norwegian University of Science and Technology*

²*University of Turku*

Waterbird populations are declining globally. Additionally, concerning observations of male-skewed sex ratios and increased hatching failures are being reported in the Baltic. Environmental contaminants and endocrine disrupting chemicals, such as per- and polyfluoroalkyl substances (PFASs), are potential contributors to these declines. PFASs have been linked to multiple adverse health effects in wildlife species, yet the specific modes of toxicity in avian models remain uncertain and establishing clear links between exposure and toxicity is complicated by factors such as co-contaminants, environmental conditions and biological variables. Thus, controlled exposure studies are valuable when addressing these challenges. This study experimentally investigated the developmental toxicity and endocrine disrupting potential of two unregulated PFASs, Perfluoro-4-ethylcyclohexanesulfonic acid (PFECBS) and Perfluorododecanesulfonic acid (PFDoDS), alongside the regulated Perfluorooctanesulfonic acid (PFOS), using the mallard duck (*Anas platyrhynchos*) as a model organism. Farmed mallard eggs were exposed to PFASs via in ovo injections at environmentally relevant doses. A lower hatching success was observed in eggs exposed to PFECBS and PFDoDS compared to controls and PFOS exposed eggs. Additionally, a potential shift in sex ratio was observed in the exposed groups. Changes in plasma levels of corticosterone, 11-deoxycorticosterone and progesterone levels were found, with significant differences in corticosterone levels between the PFAS-exposed groups. These findings highlight PFASs' potential for developmental and endocrine disruption, particularly among unregulated PFASs, emphasizing the need for further research on their effects on avian health and population dynamics.

Keywords: ecotoxicology, PFAS, experimental exposure, mallard duck

Effects of early-life gut microbiome disruption on development and survival in wild birds

Suvi Ruuskanen¹, Charli S Davies¹, Clemence Furic², Julie Fleitz², Jenna Palttala¹, Sophie Reichert²

¹*University of Jyväskylä*

²*University of Turku*

Microorganisms are everywhere, all organisms carry them, and the gut microbiome varies vastly across individuals and species. Microbiome adds a whole new layer of complexity in understanding phenotypic variation. A current key challenge is to understand if and how the microbiome may help the host respond and adapt to environmental variation. Yet, most literature is focused on laboratory model species, which do not reflect the complexity of natural conditions, life-history variation and different selection pressures. Furthermore, developing individuals are known to be particularly sensitive to gut microbiome disruption in human and rodent models, with long-lasting effects of early disruption, but it is poorly understood if similar patterns are found in other taxa. To this end, we experimentally studied the effects of early-life gut microbiome disruption using wild great tits (*Parus major*) as the study system. Developing individuals were exposed to antibiotics and respective controls during nestling period in wild populations, and their development and survival was monitored. Our study contributes to our understanding of the causal effects of gut microbiome on phenotypic variation and fitness, and opens a new avenue for studying host-microbe interactions.

Keywords: microbiome, bird, development, survival

Dilute or cooperate? Density-dependent selection for cooperation and freeloading in collective chemical defence

Carita Lindstedt¹, Sophie Van Meyel¹, Raphael Ritter¹, Heikki Helanterä²

¹*University of Helsinki*

²*University of Oulu*

Selection for cooperation is expected to be density-dependent as the relative fitness of cheats should increase with increasing population density. We tested this hypothesis in the context of collective chemical defence by using the gregarious haplodiploid pine sawfly *Neodiprion sertifer* as a study system. In this species, larvae live mostly in kin-groups where they perform a collective chemical defence by raising their head and secreting an individually costly defence fluid in concert. There is also individual variation in larvae's willingness to secrete the defence fluid. By manipulating both the group size and the individual's ability to deploy the defensive fluid, we show that larval survival against predation is higher in cooperative and larger groups. However, benefits of collective defence were more pronounced in small cooperative groups in terms of survival against predation. Our factorial rearing experiment revealed no life-history costs or benefits dependent on the larval group size, but individuals participated less to the collective defence in larger than in smaller groups. Overall, females contribute more to the group defence than males. Together our results suggest that higher densities do not promote cooperativeness in collective goods but instead increase the fitness of freeloaders. Therefore, cooperation can be more likely to evolve in low population densities.

Keywords: public goods, Hymenoptera, social insects, cooperation

Social environment changes forest pest insect's responses to pathogen infections and thermal variation

Katja Koskenpato, Magnus Jonsson, Connor Hendrich, Ville-Petri Friman, Carita Lindstedt

University of Helsinki

Currently, many insect species are endangered or extinct due to climate change, habitat fragmentation and biodiversity loss. At the same time, there are also insect species benefitting from these environmental changes, many known as forest pests. It is predicted that forest pest insect outbreaks will become more regular and intensive in the future. However, while the population dynamics of forest pest insects are influenced by various abiotic and biotic factors, the interactive effects of these factors are often overlooked. Specifically, we lack information about the role of social behaviour in shaping insects' adaptive capacity. In this study, we examined how ecological and social factors affect the survival of *Neodiprion sertifer* pine sawfly larvae, a forest pest insect with social behaviour. We conducted a full-factorial rearing experiment to analyse the effects of temperature, pathogen (*Serratia marcescens*) infection, and group size on larval survival and life-history traits. Our findings indicate that responses to temperature and bacterial infection are significantly influenced by larval group size. Non-infected larvae had higher survival rates in large groups, while infected larvae had higher mortality in large groups. Furthermore, infected larvae in large groups survived better in high temperature (24 °C) than in cold temperature (15 °C), whereas infected larvae in small groups survived better in cold temperature than in high temperature. These results emphasise the importance of examining the interactive effects of multiple factors, particularly social behaviour, in understanding the outbreak dynamics of forest pest insects.

Keywords: adaptation or evolution, population ecology, life history

Transgenerational effects of temperature and diet on performance in Mývatn threespine stickleback (*Gasterosteus aculeatus*)

Alessandra Schnider¹, Katja Räsänen², Zophonías O. Jónsson³, Bjarni K. Kristjánsson¹

¹*Hólar University*

²*University of Jyväskylä*

³*University of Iceland*

How phenotypic variation can arise and be maintained is still not fully understood. Threespine stickleback (*Gasterosteus aculeatus*) have served as a model organism to study environmentally induced phenotypic variation and rapid changes in phenotypes within and across generations. The aim of this project was to study how environmental drivers shape the phenotype within and across generations. To this end we reared multiple generations of threespine stickleback from the spatio-temporally varying system Lake Mývatn, Iceland under differing experimental conditions, which reflect contrasts observed in the wild (temperature: 12°C vs. 21 °C; diet: Cladocera vs. bloodworms). We collected phenotypic information at juvenile (weight) and sexually mature life stage (weight, length, clutch size and egg size). We found clear environmental effects on traits directly associated with fitness, such as maternal investment and body condition. Females (F1) reared at 12°C produced fewer but larger eggs, that were more likely to be fertilized and to hatch, resulting in a significantly higher reproductive success. Further, F2 juveniles showed a higher body weight in the cold and on a Cladocera diet. Thus, maternal environment substantially affected offspring performance. In conclusion, this study deepens our understanding of the importance of transgenerational effects, and they can shape phenotypic variation. It further stresses the importance of multigenerational experiments to understand the long-lasting effects of contrasting environmental conditions on phenotypic variation.

Keywords: phenotypic variation, maternal investment, Threespine stickleback

Session A4

Predation

Wednesday, 11.00-12.00, Room L209

Session chair: TBA

Something smells ducky! Using odour as chemical camouflage to protect waterfowl against over-predation by mesopredators

Purabi Deshpande¹, Vesa Selonen¹, Andreas Linden², Toni Laaksonen¹

¹*University of Turku*

²*Natural Resources Institute Finland (Luke)*

Animals, and in particular mammals, who have a keen sense of smell, use odour cues in the environment to track prey. In Finland, waterfowl numbers are declining in response to habitat loss and climate change but also possibly due to high predation pressure. The increasing number of invasive mesopredators such as raccoon dogs (*Nyctereutes procyonoides*) and increasing population of local predators like foxes (*Vulpes vulpes*) can have adverse effects on waterfowl populations which act as prey. These predator species are also known to be active nest predators for waterfowl. However, currently hunting is the only strategy used to manage predator populations in Finland. Questions are being raised around the ethics and sustainability of such a management strategy. Here, we use a means of chemical camouflage, flooding the areas around wetlands with an odour that mimics waterfowl nests, hence making it harder for the mesopredators to follow this odour cue. The resulting increased costs of searching and low reward could encourage predators to direct their attention to other prey items, hence, providing a non-invasive conservation method to protect waterfowl nests. We have extracted the “duck odour” ourselves in the lab. This was then spread on 8 treatment wetlands around south and south-west Finland and compared to 8 control wetlands in the same region. After first year of the experiment, we have encouraging results that treatment wetlands show an increase in chick numbers as compared to control wetlands, while comparing the trends in the wetlands for data collected over four years.

Keywords: conservation biology, waterfowl, mesopredators, raccoon dog, wetland ecology

De novo synthesized pyrazines in tiger moths: Ecology, evolution and prevalence

Zowi Oudendijk¹, Johanna Mappes¹, Niklas Wahlberg², Simeão Souza de Moraes³, Junia Yasmin Oliveira Carreira³, Kimmo Silvonen⁴, Nicolas J. Dowdy⁵

¹*University of Helsinki*

²*Lund University*

³*University of Campinas*

⁴*No affiliation*

⁵*Wake Forest University*

Predation is one of the most potent and pervasive forces driving the evolutionary trajectory of prey species, shaping their characteristics, behaviours, and adaptations. Among the diverse array of antipredatory defence strategies, the utilization of defensive toxins has become a pervasive tactic adopted by animals, plants, and microorganisms to deter their natural enemies. While traditionally believed to be acquired from the diet, recent discoveries have revealed some species' ability to synthesize complex compounds de novo, internally. This ability raises intriguing questions about the prevalence and mechanisms of de novo synthesis, removing the need for resource-intensive searches for external sources. Pyrazines, volatile nitrogen-containing compounds, serve as odour signals to repel predators and are widely found in plants, insects, fungi, and bacteria. Herbivorous insects have been believed to acquire methoxypyrazines (MPs) primarily through sequestration from their host plants, while the exploration of de novo synthesis of MPs remained largely unexplored. We examined 56 Arctiinae species, that are known to have complex chemical defences across their phylogeny from diverse geographic regions to investigate reflex bleeding as a defensive strategy, the presence of pyrazines in their defensive fluids, and the occurrence of methoxypyrazine de novo synthesis. Our findings suggest that reflex bleeding is widespread in this group, but pyrazine production is limited to the *Arctia* and *Spilosoma* genera and exclusively to the Holarctic species. We discuss the ecological drivers that may have shaped the evolution of these defensive strategies in this group.

Testing flash coloration in wild avian predators: delayed detection of conspicuous prey in motion

Theo Brown, Johanna Mappes, Sandra Winters

University of Helsinki

Colouration serves diverse functions in the natural world, from extravagant displays for sexual selection to crypsis for evading predators. While the protective role of colouration against predation has been extensively studied across taxa, empirical testing of colour's function when prey is in motion presents inherent challenges. In this study, we employ a novel Touchscreen Operant Chamber (TOC) to investigate how wild avian predators respond to prey exhibiting flash colouration. Flash colouration theory posits that prey utilize conspicuous, bright colours that are only visible when in motion to bewilder pursuing predators. Focusing on wild avian predators, specifically blue tits (*Cyanistes caeruleus*), we assess their reactions to prey employing flash colouration compared to continuously cryptic prey. We found that conspicuous hindwing colour does not increase survival rate of digital moths. Contrary to previous research, our results do not support flash colouration theory and highlight that its function is likely context specific. While previous research has predominantly centered on anatomy-based ecological predictions and empirical testing involving humans, our study provides a pioneering exploration of flash colouration's empirical testing in the context of wild predators.

Keywords: visual ecology, predator-prey interactions, protective colouration

What lies behind a successful pest and vulnerable forest ecosystem? Effect of diversity, forest structure and prey defence strategy on predation risk

Magnus Jonsson, Emy Guibault, Venla Korhonen, Katja Koskenpato, Carita Lindstedt

University of Helsinki

Climate change and environmental homogenization are expected to facilitate the expansion of new potential pest insects as well as increase the vulnerability of forest ecosystems to outbreaks. However, at present, we lack empirical data on how the ecology of pest insects interacts with the local environmental conditions and shape outbreak risk. Here we study this from predator-prey interaction perspective. We ask 1) how do antipredator defences of pest insects affect their success in boreal forests, and 2) how is predation risk shaped by the diversity and structure of forests and predator communities? We tested these questions by conducting a field predation experiment where we manipulated the gregariousness, unpalatability and defensive colouration of dummy prey and tested their effects on predation risk. We also measured environmental variables along the prey transects to analyse how they shape overall predation risk across defence treatments. Our results show that the predation risk was always lowest for gregarious prey irrespective of other defence strategies. Furthermore, our results indicate that intensive forest management, homogeneous tree structure and a low dead wood continuum increase the susceptibility to pest insect invasions as the predation risk was lower in those locations in comparison to more natural state forests. Altogether, our results indicate that maintaining diversity in forests can make them more resistant to pest outbreaks. Furthermore, gregariousness can facilitate pest insects to form outbreaks by increasing their survival against generalist predators.

Keywords: invasiveness, predator-prey interaction, forest management, pest outbreaks

Presence of an apex predator controls alien mesopredator occurrence and reduces ground-nest predation

Elina Tuomikoski¹, Vesa Selonen¹, Heidi Krüger², Veli-Matti Väänänen², Toni Laaksonen¹, Sari Holopainen¹

¹*University of Turku*

²*University of Helsinki*

Apex predators induce trophic cascades, and their absence leads to increased mesopredator populations, followed by decreased survival of prey species. After worldwide extirpations, some apex predators, such as the grey wolf (*Canis lupus*), are now recolonizing their natural habitats. The return of apex predators is shaping trophic cascades anew, but their effects on alien mesopredators and ground-nesting birds are understudied, especially in human-affected landscapes. We examined whether the recovering native apex predator, the grey wolf, reduces the nest predation risk of artificial forest grouse nests by suppressing mesopredator occurrences. This was done by comparing nest predation risk and mesopredator occurrences in 16 wolf territories to areas outside these territories. We focused especially on the effect of wolves on the invasive alien mesopredator, the raccoon dog (*Nyctereutes procyonoides*). We found artificial grouse nest survival to be lower outside wolf territories than inside, and that raccoon dog was the main mesopredator driving this pattern. Although this invasive species appears to be the most common mammalian nest predator in the boreal forested landscape, our results indicate that the grey wolf can have a prominent effect on its occurrence and impact. We also found that the area of agricultural land around artificial grouse nests had a negative effect on nest survival and a positive effect on mesopredator occurrences, indicating that human land use is affecting predator-prey dynamics. We conclude that apex predators induce trophic cascades and can provide a nature-based solution to suppress invasive alien mesopredator populations and help protect native prey species.

Keywords: alien species, ecosystem restoration, large carnivore, mesopredator release

Session B1a

Themed session 4: Biodiversity monitoring for the future

Wednesday, 14.00-15.00, Room L304

Session chairs: Jarno Vanhatalo, Päivi Sirkiä, Elina Numminen

Multidimensional evaluation of nature monitoring in Finland

Jarno Vanhatalo, Elina Numminen, Jukka Siren, Nourhan Shafik, Tuuli Rissanen, Anna-Liisa Laine, Tomas Roslin, Marjo Saastamoinen

University of Helsinki

Long-term nature monitoring programs have typically been initiated for different reasons, are implemented by multiple actors, remain focused on a few selected taxonomic groups (e.g., birds, butterflies and game species), and utilize a specific design. More, the resulting taxon-specific assessments are rarely combined into holistic analyses of the general state of biodiversity. Motivated by this, we analysed the state of the Finnish nature monitoring programs and their usefulness for biodiversity monitoring. For this, we conducted a comprehensive analysis on how representatively the single-taxa study designs capture the diversity of climatic- and environmental landscapes in the country. In parallel, we developed and applied a novel statistical framework to evaluate between different candidate sampling designs for collecting the monitoring data in future, and to select indicator species to efficiently monitor species communities. Our results show, that the spatio-temporal configurations of the current monitoring vary a lot between the datasets and most of the current monitoring programs do not provide statistically representative data on Finnish biodiversity – calling for advanced statistical methods to analyse the data. We also suggest ways to improve the current monitoring programs.

Keywords: biodiversity, monitoring

LIFEPLAN: A massive global biodiversity survey

Tomas Roslin¹, Otso Ovaskainen², Bess Hardwick¹, Deirdre Kerdraon³, Brendan Furneaux², Panu Somervuo¹, David Dunson⁴, Patrik Lauha¹, Tommi Mononen¹

¹*University of Helsinki*

²*University of Jyväskylä*

³*Swedish University of Agricultural Sciences*

⁴*Duke University*

While humanity is planning on conquering other planets, we still know little about how life is structured across our own. Of species globally, an estimated four out of five are still undescribed by science. To understand the structure of global biodiversity, we need standardized data collected through known sampling processes – and methods for dealing with the massive amount of dark diversity. In LIFEPLAN, we are collecting an unprecedented biodiversity dataset on fungi, arthropods, mammals, and birds at over 150 locations all over the world. We collect physical and digital samples and identify species with molecular and machine learning methods. Through standardized and semi-automated data collection methods, standardized species identification and novel statistical methods, we aim to establish the current state of terrestrial biodiversity across the globe. We will report on the state of the project and cool recent findings.

Monitoring sounds globally

Panu Somervuo¹, Tomas Roslin¹, Bess Hardwick¹, Deirdre Kerdraon², Patrik Lauha¹, Otso Ovaskainen³

¹*University of Helsinki*

²*University of Uppsala*

³*University of Jyväskylä*

In project LIFEPLAN, we have recorded soundscapes over one hundred sites across six continents. We have characterised these soundscapes by 15 metrics and quantified the seasonal and diurnal patterns in the soundscapes. Across the globe, we have found consistent and predictable temporal patterns. Latitude, time of day, and day of year predicted a substantial proportion of the variation in many of the metrics. Our data contained soundscapes from pairs of sites where one member was urban green space and the other member was a neighboring natural site. This allowed to make comparisons between urban and natural sites. The soundscape of urban green spaces proved generally noisier and more diverse than the soundscape of nearby natural sites. Interestingly though, the amount of animal sounds was larger in urban green spaces compared to natural sites. In this talk we present the results and methods used to analyze the data. We conclude that existing methods allow to find interesting patterns in global soundscapes but we also want to emphasize that there is plenty of room to improve and develop sound event and animal species classification methods further.

Keywords: soundscape, passive acoustic monitoring, animal sound identification

Piloting state-of-the-art methodologies in expanding the Finnish National Forest Inventory into comprehensive biodiversity monitoring

Mira Kajanus¹, Arto Ahola², Mikko Heikkinen³, Aino Juslèn⁴, Kari T. Korhonen², Raisa Mäkipää², Veera Norros⁴, Otso Ovaskainen¹, Tomas Roslin⁵, Jouni Sorvari², Petteri Vihervaara⁴, Nerea Abrego¹

¹*University of Jyväskylä*

²*Natural Resources Institute Finland*

³*Finnish Museum of Natural History*

⁴*Finnish Environment Institute*

⁵*Swedish University of Agricultural Sciences*

Ongoing species declines emphasize the urgent need to generate insights into shifts in multitaxonomic communities. Recent advances in high-throughput data collection and processing methods have greatly expanded the potential for semi-automated biodiversity monitoring. While these technologies allow the rapid accumulation of extensive biodiversity data, standardized large-scale implementation is still lacking in Finland. In summer 2023, we conducted a pilot study to extend the Finnish National Forest Inventory (NFI) to a comprehensive biodiversity monitoring program. Our approach included audio recording (birds), camera traps (mammals), and three DNA-based methods (soil and air sampling for fungi, and Malaise trapping for arthropods) across 44 NFI sites with broad spatial distribution. We assessed the feasibility of this approach and analyzed diversity patterns across various taxonomic groups within three managed forest types: clear-cut, thinned, and control forests. These innovative methods were successfully implemented by the NFI teams, although the planning and execution of the work still needs improvements to increase cost-efficiency. Sampling proved to be highly informative about poorly known and species rich groups such as arthropods and fungi. We consider that the NFI would most benefit from the Malaise trapping since it informs directly about the organisms living in the site whereas the airborne sampling informs about the diversity at larger spatial extents. All methods detected spatial patterns across habitat types in the diversity of the different taxa, but some methods detected stronger changes than others. Still, expanding an established, standardized monitoring scheme offers a promising approach to generate comprehensive long-term biodiversity data in Finland.

Keywords: biodiversity, community ecology, ecological monitoring

Technology readiness level of biodiversity monitoring with molecular methods – where are we on the road to routine implementation?

Tiina Laamanen¹, Veera Norros¹, Petteri Vihervaara¹, Jacqueline Jerney², Pirkko Kortelainen¹, Katharina Kujala³, Stefan Lambert³, Janne Mäyrä¹, Lilja Nikula⁴, Ida Palmroos⁵, Mikko Tolkkinen⁶, Kristiina Vuorio¹, Kristian Meissner¹

¹*Finnish Environment Institute*

²*Umweltbüro GmbH*

³*University of Oulu*

⁴*University of Helsinki*

⁵*Ministry of the Environment Finland*

⁶*Metsähallitus*

Molecular monitoring methods, such as environmental DNA (eDNA) and DNA metabarcoding, offer significant benefits for biodiversity monitoring and environmental assessment: high sensitivity and accuracy, non-invasive sampling, broad taxonomic range and cost and time efficiency. However, the diverse methodological approaches lead to poor comparability between studies and surveys, highlighting the need for standardized assessments. We used the Technology Readiness Level (TRL) framework to evaluate the maturity of Molecular monitoring methods, providing a structured assessment of their readiness for routine use. In a systematic literature review 420 articles fulfilling the study criteria were assessed and both individual studies and method categories ranked according to the TRL scale. The findings revealed a growing number of studies, particularly in aquatic environments, with most studies validating molecular technologies on a small scale but lacking large-scale system demonstrations. Aquatic eDNA-based methods targeting fish showed overall higher technology readiness compared to other sample types and taxa, and applications of molecular monitoring methods ranked into the highest TRL were predominantly freshwater studies. Key barriers to the broader implementation of molecular monitoring methods to monitoring include the need for international standards, better quantitative estimates, and comprehensive reference libraries. National and international cooperation is crucial for establishing common standards, ensuring reliable and comparable results, and expediting the routine use of molecular monitoring methods in biodiversity monitoring. Recent efforts towards international standardization are encouraging, but further coordinated actions are necessary for the global implementation and acceptance of these methods.

Session B1b

Themed session 4: Biodiversity monitoring for the future

Wednesday, 15.00-16.00, Room L304

Session chairs: Jarno Vanhatalo, Päivi Sirkiä, Elina Numminen

Detecting indicator species to monitor understorey communities in boreal forests

Tuuli Rissanen¹, Jukka Siren¹, Raisa Mäkipää², Jarno Vanhatalo¹, Anna-Liisa Laine¹

¹*University of Helsinki*

²*Natural Resources Institute Finland*

It is said that Finland lives from the forest and our forest resources indeed are well known and continuously monitored. However, this does not hold in terms of forest understorey even though it hosts majority of forest biodiversity and plays a crucial role in ecosystem processes such as different biogeochemical cycles. Vascular plants contribute fundamentally to both abiotic and biotic processes interacting with other taxa for example via herbivory, pollination and decomposition. Therefore, to detect changes in forest biodiversity and ecosystem functioning, for example in relation to forest management practices or other environmental changes, continuous monitoring of the understorey would be important. More frequent monitoring could be enhanced by using indicator species since they can provide information on the whole community with less effort. In this study we provide a model-based approach to select potential indicator species to represent boreal understorey communities. We focus on vascular plants as they are identifiable on the field and their occurrence links to the presence of other taxa representing forest diversity more broadly. With joint species distribution models, we investigate species-species and species-environment relationships across Finland utilising long-term monitoring data from 1985 to 2023 covering nearly 3000 study sites. Our results suggest that potential indicator species can either have a high covariance with other species and/or a strong response to climate and habitat conditions. Therefore, both aspects should be considered when choosing species to future forest monitoring.

Keywords: ecological monitoring, indicator species, vascular plants, biodiversity

Combating biodiversity loss requires high-quality information and effective collaboration: The National Coordination Group for Nature Information (Lukki)

Päivi Sirkiä¹, Katja Holmala², Saku Härkönen³, Mikko Impiö¹, Meri Kallasvuo², Hanna Koivula⁴, Veera Norros¹, Ida Palmroos³, Minna Pekkonen¹, Riikka Venesjärvi², Nadja Weisshaupt⁵, Petteri Vihervaara¹

¹*Finnish Environment Institute*

²*Natural Resources Institute Finland*

³*Ministry of the Environment*

⁴*CSC - IT Center for Science Ltd.*

⁵*Finnish Meteorological Institute*

There is a significant demand for high-quality nature-related data in society, as addressing biodiversity loss requires solutions grounded in a comprehensive knowledge base. For the first time in Finland, 17 organizations from diverse sectors have united to enhance the quality and accessibility of nature-related data. The National Coordination Group for Nature Information (Lukki), led by the Finnish Environment Institute, has published a joint proposal for a National Nature Information Development Program for 2024–2035. The primary objective of this program is to establish a national coordination hub for biodiversity and ecosystem monitoring. We focus on four key themes: data utilization, monitoring, innovative methods, and data interoperability. Our main goals are: 1. Both the public and private sectors have easy access to the best possible information for assessing environmental impacts, preventing environmental harm, and improving the state of nature. 2. The status and changes in biodiversity are monitored and coordinated as comprehensively as possible. 3. New methods that produce and utilize nature-related data are being developed and used on a large scale. 4. Nature-related datasets and their metadata are easily accessible, as open as possible, and as closed as necessary. The data sets are interoperable for various purposes. For each theme, we have formed thematic working groups that will plan and execute more detailed aspects of the program. More information of biodiversity monitoring and Lukki is available at a Finnish Nature Information Hub www.luontotieto.fi. In this presentation, we will outline our plan and highlight the initial actions we have undertaken.

Keywords: biodiversity, monitoring, interoperability, coordination

Towards genetic diversity monitoring in Finnish nature - GenMonFin

Aapo Kahilainen

Finnish Environment Institute (Syke)

Intraspecific genetic diversity (GD) is a key component of biodiversity (BD), influencing e.g. long-term population persistence and functioning of ecosystems. Despite its importance, GD has been neglected in policy and biodiversity monitoring, an oversight historically justified by a lack of cost-effective methods. However, with recent advancements, this is changing. Technical development has made detailed genetic studies possible for most species, and the growing body of academic population genetic research on natural populations can offer feasible foundations for GD monitoring. Furthermore, the increasing recognition of GD in international policy, as seen in the Kunming-Montreal Global Biodiversity Framework (KMGBF), has already led some countries to develop plans for GD monitoring. Incorporating GD into BD monitoring schemes can significantly improve BD assessments by identifying declining population abundances across populations of species, including those currently common, and tracking long-term historical trends with the aid of museum samples, an opportunity rarely possible for other aspects of BD. Nevertheless, questions remain about optimal GD monitoring strategies, such as which species to prioritize, how to ensure that sampling represents diverse environments, and whether proxies based on abundance estimates adequately substitute direct GD data, as may suffice under the KMGBF. With constantly developing technical and policy frameworks, strategic planning is essential to develop effective, scalable GD monitoring. The GenMonFin project aims to enhance GD's integration into Finland's national BD monitoring and policy. By assessing Finland's technical capacity for GD monitoring and comparing it to relevant reference countries, GenMonFin provides a roadmap for embedding GD into national biodiversity frameworks.

Keywords: biodiversity, wildlife genomics, conservation science and policy

Modelling and assessment of freshwater biodiversity loss with monitoring data

Anna Suuronen, Heikki Mykrä, Annika Vilmi, Minna Kuoppala, Krister Karttunen, Kristiina Vuorio, Jarno Turunen, Jukka Aroviita

Finnish Environment Institute

Freshwater community data has been extensively collected over 20 years in several monitoring programs covering all major land use gradients in Finland. We compiled all available macroinvertebrate, diatom, macrophyte, phytoplankton and moss data sets from streams and lakes to assess the biodiversity status of freshwaters. We used RIVPACS-type multi-taxon distribution modelling to estimate the near-natural communities of each taxonomic group and then compared species prevalences in current and expected near-natural conditions to estimate the degree of regional biodiversity change. We found significant declines in regional biodiversity with often marked declines in common taxa in regional biodiversity with often marked decline in common taxa. The results indicate that stream macroinvertebrates and bryophytes show similar changes in their species compositions whereas diatoms model did not show as strong changes compared to macroinvertebrates and bryophytes are. Biodiversity loss of macroinvertebrates and bryophytes were considerable in smaller streams in all regions due to forestry. The prevalence of common taxa of macroinvertebrates had decreased in all stream size groups in multiple regions. In all taxonomic groups agricultural land use increased the species that gain from nutrient increase and to species that decreased because of it. Our results suggest that the ecological status class “good” by the national classification for the EU Water Framework Directive may not be fully sufficient to safeguard the freshwater biodiversity. Our results provide key information to implement policies more effectively (e.g. in European Union Water Framework Directive, Habitats Directive, Biodiversity Strategy, and Nature Restoration Law) aiming to halt freshwater biodiversity loss.

Keywords: freshwater biodiversity, RIVPACS modelling, biodiversity assessment, monitoring data

Systematic surveying and monitoring of habitat types is gaining attention, but how to sample the unknown?

Aapo Ahola

Finnish Environment Institute (Syke)

Habitat type is an important practical unit for studying β -level biodiversity. Monitoring habitat types reveals trends in key functional, structural, and community characteristics, providing essential understanding of changes in ecosystems. Such monitoring may also produce valuable background data for species- and genetics-focused research, establishing a better linkage between species and habitat change. The importance of habitat types has become increasingly recognized in national and multinational biodiversity policies, which has led to a rising demand for systematically collected and statistically robust field monitoring data. However, because habitat type locations are typically largely unknown, designing a probabilistic sampling scheme for nationwide habitat monitoring poses notable challenges. We present a sampling and field survey system that utilizes randomized line transects and balancing of features from background datasets. Results from our field tests in Finland suggest that this approach can offer a cost-effective framework for probabilistic sampling of poorly known habitat type localities on a large spatial scale. In addition, we discuss some general best practices for designing a field monitoring system, particularly with the goal of integrating ground data with remote sensing.

Keywords: habitat types, β -level biodiversity, sampling

Session B2a

Methodological advances in ecology and evolution

Wednesday, 14.00-15.00, Room L209

Session chair: TBA

Wild animal derived cells as a tool for cross-species comparative studies

Kateryna Gaertner¹, Mügen Terzioglu¹, Sina Saari¹, Eric Dufour¹, Riikka Tapanainen², Craig Mitchell², Zsófia Fekete², Steffi Goffart², Jaakko Pohjoismäki²

¹*Tampere University*

²*University of Eastern Finland*

The research community relies on a small number of model organisms to study large themes in evolution and medicine. However, incorporating non-traditional models offers new inspirations for scientific breakthroughs. The aim of my doctoral work is to demonstrate the utility of wild animal derived cells for ecophysiological and biomedical studies. Using skin fibroblasts harvested from mountain hares and brown hares, we applied various methods, including transcriptomics, metabolomics, imaging and respirometry, to uncover species-specific molecular features. Furthermore, we generated hybrid cell lines (cybrids) to study effects of mito-nuclear compatibility that may reinforce species separation and cause mitochondrial-associated disorders. The results show that brown hare fibroblasts are faster in wound closure and proliferation, while mountain hare cells exhibit increased glycerol 3-phosphate (G3P) shuttle activity, consisting of cytosolic (GPD1) mitochondrial (GPD2) enzymes. Alterations in G3P shuttle is implicated in multiple human diseases including cancer. GPD2 knockdown led to the increase in proliferation and migration of mountain hare fibroblasts, while caused no such changes in brown hare cells. Additionally, we uncovered that mitochondria of cold-adapted animals potentially function at lower temperatures than in temperate-adapted, for the first time demonstrating differences in basal mitochondrial temperature between animals. This could impact, for instance, mtDNA replication activity. Cybrid model revealed that mito-nuclear incompatibilities emerge under specific genetic backgrounds and manifest in various pathophysiological changes. In conclusion, this work demonstrates that cells retain species-specific molecular features, allowing to draw parallels between cells and whole animal physiology and so reducing the need for animal experimentation.

Keywords: cell models, hares, metabolism, mito-nuclear compatibility

Exploring the diverse chemistry of Scots pine deadwood via hyperspectral imaging

Mariina Günther, Markku Keinänen, Pemelyn Santos, Ville Nissinen, Timo Kekäläinen, Janne Jänis, Tuomas Aakala

University of Eastern Finland

Currently Finnish forests are mainly managed in a way that is not convergent with the natural dynamics of boreal forests. Thus, in unmanaged forests wood properties can differ from managed forests as trees grow older and are exposed to various disturbance agents, biotic interactions and growing conditions. Wood quality, e.g. density and chemical characteristics, is important for species dependent on deadwood: for example, lichens require more longer lasting deadwood due to their slow colonization. Some *Pinus sylvestris* trees stay standing for even centuries after death whereas others decompose much faster. Chemical composition of wood can largely influence this variability in wood quality and decay resistance. We are developing novel methods to study the variability in chemical composition of *P. sylvestris* deadwood, by imaging increment core samples in high spatial and spectral resolution with hyperspectral cameras. The images are calibrated with high resolution mass spectrometry data from the same samples, and we aim to create chemical abundance maps for the samples. We use these maps to study the within- and among-tree differences in the chemistry of *P. sylvestris* deadwood with different growth histories, and we compare *P. sylvestris* trees from Finnish old-growth forests and trees that have been injured in a restoration experiment. Final aim is to use our results to plan restoration measures that form natural-like deadwood structures.

Keywords: hyperspectral imaging, mass spectrometry, old-growth forest, deadwood restoration

Using unlabelled data to train automatic bird sound identification models

Patrik Lauha¹, Panu Somervuo¹, Otso Ovaskainen²

¹*University of Helsinki*

²*University of Jyväskylä*

Inexpensive passive acoustic recorders and deep learning -based species detection models are revolutionizing bioacoustic monitoring. Training of accurate species classifiers requires representative training data from the target domain. While unlabelled audio data are easy to collect on a large scale, a practical bottleneck in training species classification models is the amount of properly annotated training data. Recent advances in machine learning research have shown that semi-supervised learning holds great potential for exploiting unlabelled data. In practice bio-monitoring data are typically noisy and species counts are highly imbalanced. We test semi-supervised learning (SSL) methods under a controlled setup in three different scenarios: a) balanced data set of high-quality bird recordings, b) highly imbalanced data set of high-quality bird recordings and c) a truly unlabelled, possibly very noisy and imbalanced passive acoustic monitoring data set. In addition, we train bird sound identification models for birds of Madagascar to demonstrate the model performance in a real-world bio-monitoring application. We compare the performance of two different SSL frameworks MeanTeacher and SimCLR to supervised baseline models with different amounts of labelled training data. Our results show that both SSL methods improve the classification accuracy when the amount of labelled training data is very limited. When the unlabelled data set is noisy or unbalanced, labelled data are required to guide the training. Our results encourage the use of SSL for training identification models when only little training data are available. This is a typical case with many species found outside of North-America and Europe.

Keywords: bio-monitoring, bird species classification, neural networks

Framework for evaluating sampling efforts in Schnabel censuses for reliable population size estimates

Su Na Chin

University of Southampton

Accurate population size estimation is essential in various ecological and wildlife management disciplines. The Schnabel census, a widely applied capture-recapture method, is commonly used to estimate populations, but the sampling effort required for reliable results in Schnabel census studies is not well understood. This study addresses the necessary sampling effort for Schnabel census studies, with a focus on varying capture success rates and population heterogeneity. To explore this, we adjusted the number of capture occasions T , to achieve specific probabilities of missed observations p_0 , aiming to maintain a reasonable confidence interval. Findings indicate that keeping p_0 below 0.5 can limit uncertainty to within 20% of the true population size, N , for populations where $N \geq 100$. Zero-truncated counting distribution was used, fitted with three models: binomial, beta-binomial, and binomial mixture. Results demonstrate an exponential relationship between the desired capture success rate and the necessary number of capture occasions. Additionally, our findings show that lower detectability requires more capture occasions to reach the same level of capture success as higher detectability. This methodological framework provides efficient and reliable strategies for estimating population size, thereby enhancing the feasibility and sustainability of long-term population monitoring efforts. The insights provided offer practical guidance for optimizing sampling strategies in ecological research and wildlife conservation, especially when resources are limited.

Keywords: statistical ecology, population estimation, Schnabel census, capture-recapture, sampling effort, zero-truncated distribution

AI-based species identification method for global camera trap data

Tommi Mononen

University of Helsinki

Camera trap datasets can be huge, containing millions of images. Globally, the number of species captured in camera trap images can be counted in thousands – mainly mammals and birds. An AI system for species identification, where you could feed in all your camera trap images and get back annotated species data, is in great demand. Wildlife Insights (by Google) approaches this aim, but uploaded data can be further sub-licensed and partly end up for example on social media. Training a classifier for species identification requires good training data. High-quality sets are not commonly available. However, iNaturalist has a broad uncleaned image data of a large number of species. For some species, many of the annotated images do not represent the animal itself, but all kinds of indirect evidence of animal presence, like tracks. On the other hand, nocturnal or shy species can be largely represented by images of carcasses. I will explain how to semi-automatically exclude unwanted and lower-quality images, and then build a high-quality species library for model training purposes. Many endemic species outside the Western world have a very limited collection of images on iNaturalist. Therefore, their automatic detection must be based on scarce data coming solely from trail cameras. Small species-wise training data usually leads to poor accuracy over new camera scenes, because the model does not have enough data to separate the target from its background. I will present a novel data parsimonious deep learning method aimed to solve this problem.

Keywords: animal identification, camera trap, deep learning

Session B2b

Methodological advances in ecology and evolution

Wednesday, 15.10-16.00, Room L209

Session chair: TBA

Permafrost in peril: high-resolution insights into palsa mire evolution

Bendik Sivertsen¹, Geir Arnesen¹, Floris Groesz², Martjin Vermeer²

¹*Sállir Natur AS*

²*Field Geospatial*

This study develops an advanced remote sensing monitoring program for palsa mires in Norway, detecting shifts linked to permafrost thawing under changing climatic conditions. In collaboration between ecologists and geospatial analysts, high-resolution orthophotos and LiDAR data were used to design and train a deep learning model that identifies and classifies the micro-topographic features of palsa systems. The model integrates semi-supervised learning techniques and data augmentation to enhance classification accuracy, even in geographically limited datasets. Our methodology includes a coarse-scale mapping to estimate the national extent of palsa mires, complemented by fine-scale classification to enable analysis of volume changes within these systems. Additionally, historical data are employed to estimate trends for the potential extent and degradation of palsa systems. Findings from this approach contribute to understanding the cyclical nature of palsa mires and provide a framework for assessing the impacts of warming climates on permafrost-bound ecosystems. By integrating this data into the Norwegian national nature indexation program, the project directly supports adaptive conservation strategies to address the ecological impacts of Norway's warming climate.

Keywords: palsa, permafrost, monitoring, deep learning, remote sensing

Sonic pointillism and biodiversity

Jari Rinne

Freelancer postdoc/Uniarts

This presentation investigates how sonic pointillism, utilizing organic acoustic lenses and amplifiers, can be applied to understand nature's communication mechanisms as processes characterizing the idea of democracy as a mode of communication for planetary biomass. Democracy is defined as the ability to use lenses and amplifiers in living worlds to sound larger than oneself while simultaneously building sonic relationships with other actors within the reach of sound. Communication reaches those for whom it is meaningful. The speculative exploration employs THE BOXES art installation as both a research method and a medium for public engagement. Art installations enable the exploration of various worldviews and alternative realities. By integrating artistic processes with inquiry, the installation creates an immersive experience that fosters a deeper understanding of ecological soundscapes and the interconnectedness of all living systems. The artistic research offers preliminary insights into nature's communication as a dynamic interplay of universal vibrations and particular resonations. The findings suggest that sonic pointillism, combined with acoustic lenses and amplifiers available in the habitats of various life forms, reveals how different species and ecological systems interact and convey information. This study advances acoustic ecology and environmental communication by providing a framework for analyzing nature's complex sonics. It highlights sonic pointillism as a valuable tool for ecological research and conservation, emphasizing the interconnectedness of all living systems through sound. Consequently, biodiversity is presented as the most effective form of democracy, where all means of sustaining life are permitted within the resources of one's local environment.

Keywords: nature communication, biodiversity, artistic research, sonic pointillism

Machine learning outcompetes human assessment in identifying parasitic eggs in barn swallows (*Hirundo rustica*)

Michal Šulc¹, Anna E Hughes², Lisandrina Mari³, Jolyon Troscianko⁴, Václav Jelínek¹, Tomáš Albrecht¹

¹Czech Academy of Sciences

²University of Essex

³University of Jyväskylä

⁴University of Exeter

Avian brood parasitism provides an exceptional system for studying coevolution. Most species that use this reproductive strategy are conspecific brood parasites, making it more challenging for researchers to identify parasitic eggs because they closely resemble those of the host. While molecular genotyping provides a definitive method for identification, its high cost has led researchers to explore egg appearance as an alternative identification signal. Barn swallows (*Hirundo rustica*) are suspected conspecific brood parasites, but identifying parasitic eggs has traditionally relied solely on human visual assessment. In this study, we used UV-visible photographs of non-parasitized barn swallow clutches and simulated brood parasitism to compare the accuracy of human assessment with that of advanced automated methods. We designed two games: one where both human participants and the automated models identified the parasitic egg from six options, and another where they chose between two eggs. Our findings show that while human assessment was fairly accurate at identifying parasitic eggs (72% and 85% accuracy), supervised automated methods proved more reliable, achieving 93% and 96% accuracy. The superior performance of automated methods may be partly attributed to their ability to incorporate UV information, which is not visible to human observers. In fact, egg colouration (including the UV component) and egg dimensions were the most informative characteristics for automated identification. This study demonstrates that, in barn swallows, a combination of low within-clutch variation and high between-clutch variation enables the accurate identification of conspecific parasitic eggs, highlighting the effectiveness of supervised automated methods for this task.

Keywords: ornithology, brood parasitism, egg phenotype, machine learning, human assessment

Prototype digital twins of biodiversity: What is it and examples from species distribution models to population dynamics

Gabriela Zuquim¹, BioDT Consortium

¹CSC - IT Center for Science

Digital twins (DTs) represent a highly promising solution to address the needs of modern biodiversity research. A digital twin can be defined as a virtual, interactive replica of a real-world entity or process, comprised of data, a model (the digital representation of a real-world process), and ways to connect the data and model. By bringing together experts in high-performance computing and ecology to develop advanced prototype digital twins (pDTs), the BioDT project is developing 10 biodiversity prototype digital twins (pDTs) tackling a wide range of biodiversity topics, from grassland and forest management and biodiversity dynamics to species interactions with each other and with humans. Two pDTs have been successfully deployed: one to model beehive dynamics and honey productivity in different regions and as a response to environmental conditions, land use and pollen availability; and a second one that quantifies the recreational potential of a national park by combining the ecosystem services provided by physical landscapes and species distribution models of tens of species. While traditionally the processing of biodiversity data has not required substantial computing resources, research in the field is becoming increasingly data-intensive. Moreover, there is a need for improved modelling approaches that can handle big data and produce reliable predictions of biodiversity shifts in response to pressures including changes in climate and land use. In this talk, I will describe the outputs of BioDT project and how it is contributing to advance in our understanding of specific biological phenomena and to deliver timely results to a wide range of public, from the research communities to non-experts.

Keywords: high-performance computing, cultural ecosystem services, grasslands, forests

Session B3a

Conservation biology and sustainability

Wednesday, 14.00-15.00, Room L303

Session chair: TBA

The contribution of short rotation plantations and Natura 2000 forest habitats to landscape connectivity in Europe

Sara Pineda¹, Alejandra Moran-Ordóñez², Blas Mola-Yudego¹, Remi Duflot³

¹*University of Eastern Finland*

²*University of Lausanne*

³*University of Jyväskylä*

The European Union's biomass demand is expected to rise in the coming decades to promote carbon neutrality and enhance energy independence. Short Rotation Plantations (SRP) are viewed as a promising solution due to their high biomass yield over short rotation cycles (2–20 years). However, large-scale biomass cultivation through tree plantations poses risks to biodiversity, as it may lead to landscape homogenization, which reduces species diversity. Nevertheless, SRP, often established on marginal agricultural lands or in riparian zones, could potentially support functional connectivity between otherwise fragmented natural forest patches. In this study, we assessed how SRP contribute to forest bird connectivity across three sub-watersheds in Spain, France, and Sweden. We examined changes in connectivity metrics across three scenarios with varying SRP and forest coverage within and outside Natura 2000 areas. This included analyzing the current land use scenario (including all forests and plantations) and then systematically removing SRP and forest patches until only Community Interest Forest habitats (Directive 92/43/EEC) within Natura 2000 areas remained. We used the Probability of Connectivity Index to quantify each patch's connectivity contribution and measured connectivity changes across scenarios. Preliminary results indicate that SRP significantly support landscape-wide connectivity for short-dispersal forest birds, especially in sub-watersheds with higher agricultural land coverage. However, the overall net connectivity contribution of plantations across scenarios was not significant. We propose that strategically deploying SRP within European landscapes could enhance species connectivity while supporting ecosystem services. Nonetheless, large-scale biomass expansion requires careful landscape planning.

Keywords: landscape connectivity, short rotation plantation, Natura 2000

The strengths and weaknesses of the new biodiversity offsetting law in Finland

Heini Kujala¹, Minna Pappila², Paula Leskinen², Johanna Tuomisaari³, Joel Jalkanen¹, Veera Salokannel⁴, Eini Nieminen³, Atte Moilanen⁵, Panu Halme³, Marianne Aulake², Essi Pykäläinen³, Linda Mustajärvi³, Iikka Oinonen², Juha Kotilainen⁶, Janne Kotiaho³

¹*Natural History Museum of Finland*

²*Finnish Environment Institute*

³*University of Jyväskylä*

⁴*University of Lapland*

⁵*Finnish Natural History Museum*

⁶*Akordi Ltd.*

In biodiversity offsetting, biodiversity losses are compensated by producing commensurate gains elsewhere. Offsetting is the last step of mitigation hierarchy, where biodiversity losses are first to be avoided, then minimized and finally offset. The goal is to achieve no net loss of biodiversity which calls for an explicit loss-gain calculation. Offsetting is guided by internationally set criteria, yet offset planning, execution and monitoring face well-known challenges that can prevent them from achieving the goal of no net loss of biodiversity. Here, we assess the strengths and weaknesses of the new Finnish biodiversity offsetting policy, introduced in 2023, against these challenges. The new policy is in many ways advanced, outlining an exact way to calculate biodiversity losses and gains and setting clear rules for what actions can be called biodiversity offsetting. The policy includes several central criteria, such as the additionality and in-perpetuity of offsets and accounting for time-lags and uncertainty in future gains. All implemented offsets will also be listed in an open biodiversity offset register. The policies' weaknesses include the illogical definition of avoided loss offsetting, which diverts from the international definition and likely prevents its use. Adherence to mitigation hierarchy or confirming that offsets deliver biodiversity gains are not required, reducing the scheme's incentive towards avoidance. Offsetting is also entirely voluntary, hampering its uptake. These weaknesses illustrate the challenges of creating credible biodiversity offset policies that can set biodiversity on a net positive trajectory.

Keywords: conservation science and policy, biodiversity offsetting, no net loss of biodiversity

Developing and piloting biodiversity offsetting with Finnish cities

Panu Halme¹, Jani Hohti¹, Suvi Huttunen², Joel Jalkanen³, Heini Kujala³, Elisa Lähde⁴, Venla Leppilampi¹, Emma Luoma⁵, Olivia Mahlio⁴, Atte Moilanen³, Eini Nieminen¹, Inka Ojanen⁶, Essi Pykäläinen¹, Johanna Tuomisaari¹, Liisa Varumo²

¹*University of Jyväskylä*

²*Finnish Environment Institute*

³*University of Helsinki*

⁴*Aalto University*

⁵*Akordi*

⁶*Ramboll*

Biodiversity offsetting is a conservation tool or policy where unavoidable negative impacts on biodiversity are offset with biodiversity-positive actions elsewhere. Several growing Finnish cities have openly stated to aim for no net loss, or net positive state on biodiversity within their land use practices. Since 2021 we have been developing biodiversity offsetting as a tool to mitigate negative biodiversity effects in the context of the land use decisions of Finnish cities. We started with a series of workshops to outline the necessary tasks, followed by the development of a general protocol for biodiversity offsetting in the given context. We then proceeded with different pilot studies to develop practical calculations, required knowledge and data requirements for successful biodiversity offsetting. Currently we are developing biodiversity offsetting as an integrated tool with the green area factor tool to aim for no net loss state of both biodiversity and ecosystem services. This presentation provides an overview of our work to give the audience an example of a transdisciplinary and co-creational research process that has been carried out with land use specialists of participant cities, and in close collaboration with decision makers, public authorities and other key stakeholders.

Keywords: biodiversity offsetting, conservation, land use

POOL_an art-science project to raise awareness of a deficiently known habitat: the temporary wetlands

Céline Arzel¹, Aurélie Davranche², Petri Nummi³, Janne Sundell⁴, Kimmo K. Kahilainen⁴, Hanna Rosti⁴, Clarisse Blanchet³, Kari Minkkinen³, Harri Vasander³, Henrik Lindberg⁵, Heikki Seppä³, Mohamed Maanan⁶, Uma Sigdel³, Jonas Suomalainen-Sallinen⁷

¹*University of Turku*

²*University of Angers*

³*University of Helsinki*

⁴*Lammi Biological Station*

⁵*Hämeen Ammattikorkeakoulu*

⁶*Nantes University*

⁷*University of Jyväskylä*

POOL_an art-science project to raise awareness of a deficiently known habitat: the temporary wetlands Temporary wetlands have been lost or degraded by lack of understanding of their uniqueness and role for Finnish forest diversity. The POOL project funded by the Kone Foundation aims at raising awareness on their crucial features for watershed functioning and biodiversity at the landscape level via a Science art approach. Hence, their specific seasonality and fishless characteristics promote biodiversity. The POOL project focuses on temporary wetlands within and in the vicinity of the Evo Natura 2000 area. We will present how interdisciplinary projects such as POOL can contribute to 1) improving knowledge on deficiently known habitats functioning and their biodiversity and 2) raising awareness on their importance to the public and decision-makers.

Keywords: biodiversity, wetlands

Improving insect species digital conservation requires more effort from all stakeholders

Gideon Deme Gywa¹, Yoila David Malann²

¹*University of Jos*

²*University of Abuja*

Species occurrence records on databases have arguably become important tools in assessing biodiversity. However, the exciting research opportunities presented by GBIF have resulted in biased occurrence records, which can impact our ecological research, biodiversity assessment, and global conservation efforts. Because the deterministic and idiosyncratic response of species to anthropogenic global climate change affects changes in their distribution patterns of organisms, given that the rates at which species are colonizing, being extirpated, recolonizing, and extirpating may vary across different ecoregions, biodiversity assessments research opportunities quantifying the level of biases in species occurrence records on global databases are needed to facilitate evidence-based application of these research outputs to maximize species conservation. To address this, we downloaded insect occurrence data to compute for the Bray-Curtis measures of insect species community metric. We used these indexes as response variables in generalised linear mixed models, with continents as explanatory variables to understand the differential global insect occurrences as represented in GBIF. We found that although insect species community assemblages did not significantly differ among continents, insect species abundance and richness were higher in Oceania, South and North American continents, and not the African continent. Our results indicate that the African continent recorded fewer insect species populations on GBIF, compared to other continents. The implication of our study shows that for global evidence-based conservation to succeed, there is a need for the African stakeholders to support a long-term, extensive, and systematic insect monitoring program that will aggressively contribute to insect species occurrence records.

Keywords: biodiversity assessment, digital data, Insect occurrence, biased data, conservation science

Session B3b

Conservation biology and sustainability

Wednesday, 15.10-16.00, Room L303

Session chair: TBA

How does METSO compare to other payment for ecosystem services schemes?

Khorloo Batpurev¹, Heini Kujala¹, Mar Cabeza¹, Maria Trivino², Terhi Koskela³, Kimmo Syrjänen⁴, Steve Sinclair⁵

¹*University of Helsinki*

²*University of Jyväskylä*

³*Natural Resources Institute Finland (Luke)*

⁴*Finnish Environment Institute (Syke)*

⁵*Arthur Rylah Institute*

The effectiveness of Payment for Ecosystem Services schemes is difficult to assess because of the sheer diversity of programs. Cross-program learning, and knowledge sharing is crucial to design and therefore the success of future schemes. More importantly, there has been little syntheses on the shared challenges of the programs and how these may be expressed in terms of on ground actions in the context of ambitious biodiversity targets such as the European Biodiversity target 2030. We conduct a bi-directional (through interpolation and extrapolation) policy analysis of Finland's METSO scheme, a biodiversity focused voluntary conservation scheme, to illustrate shared challenges and lessons learnt from its 15-year experience. We communicate the strengths and weaknesses of the scheme using fundamental PES design concepts to characterize the pros and cons of METSO scheme design and effectiveness. Secondly, we estimate how much privately owned forests Finland must protect to meet European Biodiversity 2030 boreal bioregion protection target. This study illustrates what lays ahead for countries with high private land ownership to reach biodiversity targets such as the EUBS 2030, and how we may be able to use the Finnish example to pave the way forward.

Keywords: PES, METSO, private land conservation

A climate-conscious gap analysis for biodiversity protection

Thiago Cavalcante, Heini Kujala

University of Helsinki

Climate change is rapidly altering species distributions and ecosystems globally, challenging the effectiveness of current protected area (PA) networks. As species ranges shift, conventional gap analyses based on static distributions risk overlooking future conservation needs. This research employs the spatial prioritization tool Zonation across Europe to evaluate the adequacy of current protected areas in preserving biodiversity under present conditions and two projected climate change scenarios (low and high emissions, corresponding to SSP1 and SSP3), as modeled by species distribution models. We quantified the coverage of most European terrestrial vertebrate species' current and future ranges within existing PAs, identified species most at risk of underrepresentation due to climate-driven shifts, and pinpointed priority regions for PA expansion to accommodate these changes. By comparing PA coverage to an ideal, unconstrained analysis (not limited by the current PA network), we evaluated the effectiveness of existing protection and identified gaps in the conservation network amid biodiversity redistribution. This strategy provides an adaptable framework for enhancing resilience in biodiversity conservation in the face of ongoing climate change.

Keywords: conservation science and policy, climate change, biodiversity redistribution

The socioecological benefits and consequences of oil palm cultivation in Africa

Michael Pashkevich¹, Cicely Marshall², Benedictus Freeman³, Valentine Reiss-Woolever², Jean-Pierre Caliman⁴, Julia Drewer⁵, Becky Heath⁴, Brogan Pett⁶, Ari Saputra⁷, Jake Stone², Jonathan Timperley², William Draper³, Abednego Gbarway⁸, Bility Geninyan⁸, Tiecanna Jones⁷, Marshall Guahn³, Andrew Gweh³, Peter Hadfield⁹, Morris Jah⁸, Edgar Turner²

¹*Luonnonvarakeskus*

²*University of Cambridge*

³*University of Liberia*

⁴*Sinar Mas Agro Resources and Technology Research Institute*

⁵*UK Centre for Ecology and Hydrology*

⁶*University of Exeter*

⁷*Golden Veroleum Liberia*

⁸*Forestry Development Authority, Government of Liberia*

⁹*Ecology Solutions Ltd.*

Oil palm (*Elaeis guineensis*) is the most productive vegetable oil crop worldwide and economically important to > 45 tropical countries. The impacts of oil palm cultivation have been studied extensively in Southeast Asia, but relatively little is known about its impacts in Africa: oil palm's native range, and where cultivation is expanding rapidly in many regions. We conducted extensive systematic mapping to semi-quantitatively describe the existing evidence base on oil palm-related research in Africa. We found 757 relevant publications across 36 African countries. Mapping indicated that oil palm-related research in Africa has tended to focus on the impacts of palm oil consumption on human health and wellbeing. Relatively few studies have evaluated oil palm's impacts on multi-taxa biodiversity and multifunctionality. In light of this, we introduce the Sustainable Oil Palm in West Africa (SOPWA) Project: a recent collaboration between international researchers, the Government of Liberia, a palm oil industry partner, and local Liberian communities that is assessing the socioecological impacts of oil palm cultivation in southeast Liberia (West Africa). Over the last three years, we have surveyed environmental conditions and the biodiversity of trees, understory vegetation, birds, bats, spiders, and ground-dwelling insects across 54 ecological monitoring plots in rainforest, areas where oil palm is cultivated by local communities, and industrial oil palm plantations. Our findings indicate that traditional and industrial approaches to oil palm cultivation present trade-offs between biodiversity conservation and palm oil yields. Enhanced research activity is needed to guide the sustainable development of the African palm oil industry.

Keywords: land use change, tropical agriculture, community ecology, Africa, systematic map

Can marine protected areas in Finland protect phytoplankton?

Michail Pipinis Troupakis¹, Laura Antão¹, Marjo Saastamoinen¹, Sirpa Lehtinen²

¹*University of Helsinki*

²*Finnish Environment Institute (Syke)*

Climate change and overexploitation are an increasing threat in marine ecosystems as human activities have risen over the past decades. One of the main tools for protecting biodiversity and ecosystem functions is the designation and implementation of Marine Protected Areas (MPAs). Despite their potential for conservation, recent assessments question the effectiveness of MPAs to conserve ecologically resilient ecosystems. Here, we aim to assess the effectiveness of MPAs in Finland using long-term phytoplankton data, which have been collected for almost 60 years (1960-2020) in the Finnish territorial waters from over 700 sites and contain 991 different phytoplankton taxa. Phytoplankton is the basis of marine food webs and thus shifts in phytoplankton communities can affect higher trophic levels. We compared the total biomass, species richness and species diversity of the phytoplankton communities between protected and unprotected sites. To control for the confounding effects of environmental variables that affect phytoplankton biomass and distribution, and to isolate the effect of protection, we employed nonparametric distance matching; essentially, this process selects comparable pairs of samples from protected and unprotected sites. We found that even though there was a general increase in species diversity with time, protection had no effect on phytoplankton biomass, species richness or species diversity. The size and age of the MPAs did not affect the protection outcomes. However, strictly protected MPAs harbored lower biomass compared to unprotected sites, which could indicate that MPAs can help reduce the effects of eutrophication. These results suggest that MPAs in Finland still have room to be improved and there is a need to accurately assess their effectiveness in order to successfully safeguard biodiversity. Considering the phytoplankton component during the designation and planning of the MPA network in Finland could be valuable for marine conservation.

Keywords: phytoplankton, marine protected areas, diversity metrics, protection effectiveness

Biodiversity as the foundation of ecological and evolutionary processes with focus on ecosystem approach in conservation

Skúli Skúlason^{1,2}, Camille Leblanc^{2,3}, Ole Martin Sandberg^{2,3}, Bjarni Kristófer Kristjánsson²

¹*Hólar University*

²*Icelandic Museum of Natural History*

³*University of Iceland*

In this presentation we will discuss the integrated nature of biodiversity and ecosystem structure and function, focusing on the nature of the organism-environment relationship and ecosystem approach in conservation and management. The dynamics of this association will be explored considering the ecological, evolutionary and developmental (eco evo devo) processes that shape the generation and maintenance of biodiversity. We will use conceptual and empirical examples, primarily from aquatic ecosystems. The conclusions will be applied in the context of the global biodiversity crisis, future environmental change and how biologists are creating and contributing knowledge in this area.

Keywords: ecosystem approach, evolution

Session B4a

Metacommunity processes and dynamics

Wednesday, 14.00-15.00, Room L302

Session chair: TBA

How are local communities defined? A mismatch between metacommunity theory and empirical studies

Lluís Serra, Otso Ovaskainen, Nerea Abrego

University of Jyväskylä

Metacommunity theory seeks to understand the drivers of local diversity through the interdependence of processes operating at different spatial scales. A set of potentially interacting individuals constitutes a local community, and local communities are in turn interconnected through dispersal. This dichotomy between local and regional processes has limited theory to communities bounded within habitat patches. However, local interactions are not only restricted to patchy landscapes and local communities may occur in any landscape configuration. The aim of this study is threefold. First, we investigate how local communities are defined in the ecological literature by reviewing empirical studies framed within the metacommunity framework. Our findings indicate that local communities are often loosely defined, relying on criteria that do not align with the underlying theory, such as landscape structure or sampling design. Considering these results, we propose conceptual and methodological definitions for local communities. We distinguish between space-based definitions, where a local community is defined as a subset of space without explicit consideration of biotic or abiotic interactions, and network-based definitions, where a local community is defined non-spatially as a collection of interacting individuals. Finally, we implement these definitions using a spatially explicit simulation approach and compare their performance across various landscape configurations and dispersal scenarios.

Keywords: metacommunity, community ecology

Food web robustness depends on network type and threshold for extinction

Patrik Ståhl¹, Riikka Puntila-Dodd¹, Marie Nordström³, Susanne Kortsch³, Lai Zhang⁴

¹*Finnish Environment Institute (Syke)*

²*Åbo Akademi*

³*University of Helsinki*

⁴*Yang Zhou University*

Species loss in ecological communities can trigger cascading extinctions, the extent of which likely depends on network type and extinction thresholds. Traditionally, network responses to node removal are analysed using unweighted food webs, ignoring interaction strengths and extinction thresholds. Here, we examine how food web robustness varies with network type (unweighted vs. weighted), extinction thresholds, and species removal sequences, and explore how network properties - connectance and relative ascendancy both unweighted and weighted - predict robustness. First, our results show that network robustness, measured by the R50 index, can be up to 40% lower in weighted networks compared to unweighted ones. Furthermore, by incorporating extinction thresholds we find consistent reduction in robustness when species deletions proceed from the highest to the lowest species degree or sum of link weights. This indicates that measures of robustness without inclusion of extinction thresholds overestimate of ecological network robustness. Second, relative ascendancy was identified as the strongest predictor of food web robustness, providing the clearest temporal and ecological signals related to changes in energy fluxes. This metric reflects both link distribution (skewness) and pathway architecture (energy flux constraints), underscoring the importance of these network properties in assessing food web stability. Therefore, these properties should be considered in ecosystem management recommendations.

Keywords: trophic interactions, energy fluxes, weighted networks, secondary extinctions, ecosystem functioning

Metacommunity dynamics shape multi-scale biodiversity patterns in fragmented landscapes

Zachary Hajian-Forooshani, Beatriz Prado Bastos Monteiro, Jonathan Chase

The German Centre for Integrative Biodiversity Research (iDiv)

Habitat loss and fragmentation are interacting phenomena that can shape patterns of biodiversity. While some studies attempt to understand patterns at the landscape scale, others use the scale of individual fragments within a landscape. The scale-dependent nature of biodiversity coupled with the variable structure of ecological communities have made it difficult to make general statements regarding biodiversity dynamics in fragmented landscapes. Here we take an approach that focuses on the ecological processes of communities to understand how biodiversity patterns are shaped at landscape and fragment scales across a gradient of habitat loss. We use a theoretical metacommunity model to explore how the breadth of habitat preference, the structure of competition and dispersal dynamics jointly structure biodiversity patterns in fragmented landscapes. We highlight the importance of these processes and show the conditions under which contrasting and counterintuitive responses of biodiversity to habitat loss across spatial scales are expected

Keywords: biodiversity, metacommunity, habitat loss, fragmentation

Herbivory modifies the role of spatial processes in a grassland metacommunity

Lena Huovinen, Anu Eskelinen

Oulu University

Plant biodiversity depends on the interplay between spatial factors, such as dispersal, connectivity, and habitat size, and local biotic and abiotic factors, such as trophic interactions, competition and environmental conditions. In plant communities, mammalian herbivory is a key factor altering community composition, biomass, and diversity. Herbivores can facilitate plant coexistence on small scales by both reducing extinctions and promoting colonisations. However, if herbivores consistently select for grazing-tolerant species, this could lead to a reduction in the size of the regional species pool and homogenization on larger scales. We examined the relative roles of mammalian herbivory and spatial context for plant community composition and diversity in 90 spatially distributed grasslands in a real-world metacommunity system in the Åland archipelago, Finland. We found that herbivory significantly increased plant species richness and diversity in local communities. We also found that herbivory modified the effect of habitat area on diversity: in grazed habitats, plant diversity increased with habitat area, while there was an opposite effect in ungrazed habitats. This result was linked to increased dominance of tall plants especially in larger ungrazed grasslands, suggesting that herbivory interacts with plant competition to alter plant-area relationships. Our results highlight the importance of incorporating trophic interactions into plant metacommunity theory.

Keywords: metacommunity theory, herbivory, biodiversity

Marked variability in distance-decay patterns suggests contrasting dispersal ability in abyssal taxa

Erik Simon-Lledó¹, Andrés Baselga², Carola Gómez-Rodríguez², Anna Metaxas³, Diva Amon⁴, Guadalupe Bribiesca-Contreras⁵, Jennifer Durden⁵, Bethany Fleming⁶, Alejandra Mejía-Saenz⁵, Sergi Taboada⁷, Loïc Van Audenhaege⁵, Daniel Jones⁵

¹*Institut de Ciències del Mar (ICM) - CSIC*

²*CRETUS, Universidade de Santiago de Compostela*

³*Dalhousie University*

⁴*University of California*

⁵*National Oceanography Centre (NOC)*

⁶*University of Southampton*

⁷*Museo Nacional de Ciencias Naturales, Spain*

Species spatial turnover induces a decrease in community similarity with geographic distance known as the distance-decay relationship. Distance-decay patterns can reflect environmental and biotic controls on species distributions, but remain poorly assessed in the abyssal seafloor (3000-6000m water depth), where knowledge on ecological patterns and processes is urgently lacking. Here, we analysed beta-diversity patterns across space, depth and biotic components of benthic megafauna communities (animals > 10 mm), based on seabed imagery data (>36,000 specimens across 402 species) collected across the Clarion Clipperton Zone (NE Pacific), an abyssal seascape spanning over 4,000 km. We unveil consistently steeper species turnover rates in benthic communities below 4,500 m and variations among functional groups. Our results support Young's deep ocean dispersal hypothesis; turnover was higher for sessile taxa growing only on scattered hard bottom patches than sediment-dwelling or swimming organisms, depicting a more restricted dispersal in polymetallic nodule-dependant fauna. Overall, our study suggest that carbonate saturation boundaries associated with depth are a very relevant factor driving community turnover via niche-sorting with respect to a threshold, whereas dispersal limitation seems to be a more relevant mechanism within the regions above and below that threshold. We provide some of the first empirical evidences of regionally shifting turnover rates and contrasting dispersal abilities across functional groups in wide abyssal seascapes, key to assess the resilience of deep ocean biodiversity and functions to rapidly growing human disturbances in one of Earth's last wildernesses.

Keywords: deep-sea ecology, benthic fauna, image analysis, distance-decay, macroecology, dispersal limitation, niche-sorting

Session B4b

Metacommunity processes and dynamics

Wednesday, 15.10-16.00, Room L302

Session chair: TBA

Does size matter? Assessing the role of surface area on diatom diversity in subarctic lentic systems

Janne Heikkinen¹, Sonja Granqvist¹, Paula Laksela¹, Janne Soininen¹, Virpi Pajunen²

¹*University of Helsinki*

²*Aalto University*

Lentic systems are often small experiencing the harsh consequences of climate change through shifts in chemical properties and community assembly processes. Such vulnerable systems support a majority of regional freshwater biodiversity in Fennoscandian subarctic. Despite an increase in subarctic freshwater diatom research, and especially how their biodiversity relates to various chemical factors, knowledge on the effects of habitat size gradients for benthic diatoms remains limited. This study compared diatom diversities and water chemistry between and within subarctic lakes and ponds. The results showed significant differences in diatom species richness, water pH, Ca, Cl, and Na between lakes and ponds but the variation within systems was insignificant. The data demonstrated size-dependent differences in community composition, assembly processes, and local contributions towards beta diversity. The results indicated that surface area is important in shaping benthic diatoms and water conditions in subarctic lentic systems. Microhabitat size and the level of harsh environmental conditions are likely to cause such area-effects, but further investigation is required on catchment extent, isolation, dispersal limitations, and water depth. Overall, subarctic lentic systems are important in maintaining regional biodiversity highlighting their conservational value. Studying them and their benthic communities will give further insight into the effects of climate change.

Keywords: biodiversity, climate change, diatoms, subarctic

Snow as one of the drivers of subarctic lichen epiphyte assemblage

Lilith Weber¹, Annina Kantelinen², Pekka Niittynen³, Leena Myllys², Julia Kemppinen¹, Nick Pepin⁴

¹*University of Helsinki*

²*Finnish Museum of Natural History Luomus*

³*University of Jyväskylä*

⁴*University of Portsmouth*

Arctic ecosystems are changing rapidly, with widespread reports of increasing air temperature and decreasing snow cover area and duration. Previous studies investigating the composition and spatial patterns of cryptogam communities in the Arctic and Subarctic have mainly considered large warming thermal gradients and were limited in their representation of small-scale and near-ground spatial variability of snow and vegetation. The general importance of snow conditions for lichens has been widely acknowledged, but snow information and microclimatic data are rarely available or utilized. In our study, we inventoried the complete lichen community present at 74 sites in two areas of Finnish Lapland. We are utilizing microclimatic data from a network of loggers, which directly provide information on temperature and humidity from the sampling plots. This was supplemented by manual snow depth measurements on-site, as well as fine-scale satellite imagery. Focusing on the epiphytic lichen community in the typical mountain birch (*Betula pubescens* ssp. *chzerepanovii*) forests, we found a previously unknown diversity of species as well as a significant impact of snow on the species composition and distribution of taxa along the birch stems. This is not only noticeable for such well-known examples as *Parmeliopsis ambigua* and *Melanohalea olivacea* but also for several crustose species. Identifying specialists that are adapted to specific snow conditions is crucial for assessing the effect of climate change on subarctic lichen communities.

Keywords: community ecology, microclimate, Cryptogam

Spatial factors drive beta-diversity in invertebrate communities of water-filled tree holes

Francesca Cerroti¹, Thibaut Rota², Francisco Valente Neto³, Fahis K.T.K.T.⁴, Red Calore⁵, Gustavo Q. Romero³, Anoop K.S. Das⁴, Andreas Bruder⁵, Martin M. Gossner⁶

¹*WSL/SUPSI/ETH Zürich*

²*SUPSI/WSL*

³*Universidade Estadual de Campinas*

⁴*Centre for Conservation Ecology*

⁵*SUPSI*

⁶*WSL/ETH Zürich*

A fundamental question in ecology aims to understand which factors shape biodiversity at different spatial scales. Knowing how communities are formed and maintained is vital for managing natural resources and protecting biodiversity. We addressed this question using water-filled tree holes (WHs) as a model system. WHs, ubiquitous in forests, are dynamic freshwater microcosms that are crucial for forest biodiversity by serving as interconnected hubs within and beyond forest boundaries. We investigated beta-diversity components and the relative importance of environmental and spatial factors on these components in invertebrate assemblages from WHs in near-pristine tropical and Mediterranean forests in Brazil, India, and France. We conducted standardized field surveys of 35 WHs in each forest during the rainy season. We assessed the physical and chemical parameters of each WH as environmental factors and used Moran's eigenvector maps as spatial variables. To elucidate the importance of spatial and environmental factors for beta-diversity and its components, we conducted distance-based redundancy analysis (db-RDA) and variation partitioning. Our results show that beta-diversity patterns in WH were consistent across forests. Spatial factors influenced community assemblages stronger than environmental factors, and differences in species richness among WH dominated beta-diversity. This suggests that in unstable environments like WHs, colonization and extinction dynamics are pronounced due to frequent disturbances. This was particularly important in the Mediterranean forest with its pronounced seasonality. Maintaining the integrity of WH and their interconnected ecosystems is essential for protecting biodiversity in forests and necessitates coordinated conservation strategies at local and regional scales.

Keywords: beta-diversity, metacommunities, water-filled tree holes, spatial factors, environmental factors

Effect of lake morphology on the diversity of metaphyton and phytoplankton

Áron Lukács¹, Enikő T-Krasznai², Zsolt Nagy-László², Balázs Lukács², Gábor Várbíró², Verona Lerf², Csaba Békési², Caio Roza¹, Gábor Borics²

¹*University of Helsinki*

²*HUN-REN Centre for Ecological Research*

Research on lake algae typically considers two main assemblages: the open water phytoplankton and the surface-attached periphyton or phytobenthos. In contrast to phytoplankton and phytobenthos, algal assemblages in the vegetated littoral (metaphyton) are under-represented in the literature. However, recruitment of phytoplankton from the metaphyton via metacommunity processes (source-sink dynamics, mass effects) can be significant, especially in lakes with extensive littoral zones. This suggests that the extent of the littoral could strongly influence phytoplankton diversity by shaping metaphyton communities. In this study, we monitored 33 lakes and oxbows over two years, collecting metaphyton and phytoplankton samples to examine biodiversity in relation to lake morphology metrics, such as shoreline development (ratio of perimeter to surface area), percentage of vegetation cover, estimated water volume and also other abiotic factors. We studied both species and functional diversity. For the calculation of functional diversity metrics, we used life-forms and several morphological traits of algae. We hypothesized that lakes with higher values of shoreline development and vegetation cover would have a more pronounced effect of the littoral vegetation and therefore would support more diverse algal assemblages (both at the species and functional level) and host more rare taxa than those with lower values. Our findings indicate that lake morphology and the extent of macrovegetation significantly shape metaphyton and phytoplankton diversity, although other environmental factors also contribute to the structuring of these communities. These results show the importance of macrophyte beds in biodiversity conservation and might serve as the basis for lake management practices in the future.

Keywords: metaphyton, phytoplankton, diversity, lake morphology

Linking taxonomic and functional diversity: Insights from the community dynamics of Finnish forests understorey

Andréa Davrinche¹, Elina Kaarlejärvi¹, Raisa Mäkipää², Tiina Tonteri², Anna-Liisa Laine¹

¹*University of Helsinki*

²*Natural Resources Institute Finland (Luke)*

To understand the dynamics of forest understorey communities, taxonomic and functional diversity are often used interchangeably. However, whether taxonomic changes translate into shifts in the functional community composition remains unclear. By integrating two decades of understorey vegetation data across Finland and functional traits, we compare taxonomic and functional species turnover. Using a modified Price equation, we partition changes in functional diversity into the functional contribution to the community of species loss, gain, and persistence. We found that, while functional diversity follows the trend of taxonomic diversity, increasing in the south and decreasing in the north, species turnover had surprisingly little effect, with compensatory species loss and gain. Instead, changes in functional diversity were mostly driven by abundance shifts in the community. With this framework, we make a first step towards better assessing biodiversity change across time and space, and improving our understanding of its link to changes in the functioning of the ecosystem.

Keywords: species richness, plant traits, community turnover, boreal forests

Session C1

Experimentally testing the effects of environmental change

Thursday, 10.30-12.00, Room L209

Session chair: TBA

Chasing the light: Geographic origin determines adaptive success of antarctic hair grass across high latitudes

Emilia Mäkinen, Kari Saikkonen

University of Turku

Climate warming is expanding ice-free habitats in the Antarctic, challenging poleward-dispersing species to adapt to the more extreme climate conditions of higher latitudes. In this experimental study, I assess the adaptability of the Antarctic hair grass (*Deschampsia antarctica*)—one of only two vascular plant species native to Antarctica—in response to divergent latitudinal regions. To determine how geographic history affects adaptive responses, plants collected from several Chilean Patagonian and maritime Antarctic populations were arranged in a transplantation experiment at two locations in Finland: Turku (60°26'N) and Utsjoki (69°45'N). At these latitudes, the sites represent the species' current mid-range and southernmost distribution in the Southern Hemisphere. After two consecutive growing seasons, the results revealed an origin-dependent response in the plants' adaptability to the contrasting light and temperature conditions. Consistent with their latitude of origin, Patagonian plants had higher survival rates and were the only ones to flower in Turku, whereas Antarctic plants exhibited greater survival and flowered predominantly in Utsjoki. Overall, plants performed better in Utsjoki, with higher survival and flowering rates and a greater vegetative volume. The superior performance of plants in Utsjoki is likely linked to more stable temperature conditions and a more protective snow cover during winter. These findings highlight the role of geographic history in shaping the species' adaptability to varying light and temperature regimes. Though Antarctic ice sheets continue to retreat, these results suggest that *D. antarctica* can adjust its phenology to the increasingly extreme light conditions of higher latitudes.

Keywords: Antarctica, climate change, light environment, plant adaptations, phenology

Warming strengthens food web effects of predator phenotypic variation

Tiina Salo¹, Casey Yanos², Martine Maan², Maïté Jacquot¹, Andrea De Cervo³, Johan Eklöf³, Britas Klemens Eriksson²

¹*Åbo Akademi University*

²*University of Groningen*

³*Stockholm University*

Intraspecific variation modifies ecological processes and ecosystem functioning. Still, we know relatively little of how the nature and strength of ecosystem effects caused by intraspecific variation may interact with climate change. We conducted a mesocosm experiment to test if, and to what extent, ocean warming modifies the ecological impacts of intraspecific variation in a predatory fish. The mesocosms consisted of a simplified coastal food web with threespine stickleback (*Gasterosteus aculeatus*) as the top predator, from a population where two stickleback phenotypes with either complete or incomplete lateral armor plating coexist and display differentiated predation behavior. Presence of stickleback per se caused a trophic cascade that was strengthened by warming (+4 °C): stickleback reduced biomass of arthropod shredders (crustaceans, insect larvae), indirectly releasing benthic primary producers (diatoms) from top-down control. This strengthened trophic cascade was attributed to one of the plate phenotypes: the completely plated stickleback increased their predation on shredders under warming, while incompletely plated stickleback instead decreased their predation. Diatom biomass responded accordingly: warming increased diatom biomass in the presence of completely plated stickleback but not when incompletely plated stickleback were present. Our results suggest that different plate phenotypes of threespine stickleback differentially affect lower trophic levels, and that warming may exacerbate these cascading effects. This highlights that climate change may drastically modify eco-evolutionary dynamics and the effects of intraspecific variation on ecosystem functioning.

Keywords: climate change, intraspecific variation, eco-evolutionary dynamics, dietary divergence, trophic interactions

Glow-worm reproduction under light pollution: The impact of light color

Linnea Kivelä, Christina Elgert, Topi Lehtonen, Ulrika Candolin

University of Helsinki

Light pollution (artificial light at night) is a severe threat to dark-adapted species, especially insects. As many species are particularly sensitive to short wavelength light, one potential mitigation measure is to adjust light spectra towards longer wavelengths. Here, we investigated the impact of artificial light color spectrum on reproductive behavior in the European common glow-worm, a nocturnal beetle with sedentary bioluminescent females that glow to attract flying males. Through a series of both field and laboratory experiments, we found that long wavelength (yellow and red) light is less disruptive than short wavelength (blue and white) light to both mate finding and female glowing behavior, but has the downside of attracting male glow-worms. These results show that while spectral adjustment of outdoor lighting can alleviate ecological effects of light pollution situationally, the effectiveness of this measure varies both among and within species as well as over different behaviors. As there is no universally safe color of light, the focus of mitigation should instead be on limiting the intensity and distribution of artificial light.

Keywords: environmental change, light pollution, behavior, mitigation

Which aspects of environmental heterogeneity are associated with higher thermal plasticity in European *Hypericum* populations?

Susanna Koivusaari¹, Maria Hällfors², Marko Hyvärinen³, Martti Levo¹, Miska Luoto¹, Charlotte Møller³, Øystein Opedal⁴, Laura Pietikäinen³, Andrés Romero-Bravo⁵, Anniina Mattila³

¹*University of Helsinki*

²*Finnish Environment Institute*

³*Finnish Museum of Natural History*

⁴*University of Lund*

⁵*University of Sussex*

Phenotypic plasticity is likely to play a crucial role in ensuring the persistence of plant species in a rapidly warming world. While many studies have shown that plastic responses evolve in reaction to environmental heterogeneity, the relative influence of different landscape features, each subjected to varying degrees of human pressures, remains poorly understood. In this study, we use high-resolution (10-meter) remote sensing data combined with data from greenhouse experiments testing thermal responses of European populations of three *Hypericum* species to assess how compositional and configurational land cover heterogeneity, along with topographic roughness, influence the degree of thermal plasticity. We germinated and cultivated seeds collected from natural habitats and obtained from European managed seeds banks in four temperature treatments within greenhouse compartments and growth chambers. We estimated population-level thermal plasticity in five key life-history traits using Random Regression Mixed Models (RRMMs) and analyzed the effects of landscape features across five spatial scales. Our preliminary results show variation in the importance of different landscape features for different traits and species. Overall, this study highlights the various mechanisms through which human activities can influence the ability of species to respond to climate change and how remote sensed data can be combined with traditional experiments to gauge such patterns.

Keywords: phenotypic plasticity, landscape ecology, climate change

Cuckoo hosts respond to a geographic mosaic of selection

Rose Thorogood, William Smith, Katja Rönkä

University of Helsinki

Behavioural defences against enemies are ubiquitous across taxa, from bacterial communication to avoid antibiotics to brood parasite hosts attacking cuckoos and rejecting their eggs. Yet behavioural traits such as these are conspicuous in their absence of almost all tests of the Geographic Mosaic Theory of Coevolution (GMTC) - the predominant explanation for how ecology shapes the evolution of enemies and victims (as well as mutualisms). In part, this is because (i) the predictions of GMTC are challenging to test in the field without reciprocal transplants or common-garden experiments, (ii) plasticity is assumed to homogenise responses to variable selection, and (iii) behavioural ecologists rarely measure variation in behavioural traits and genomic data at the geographic scales required. Here we will present results that show geographic variation in selection between the common cuckoo and their reed warbler hosts across their European breeding range. We find that by experimentally inducing plasticity, geographic variation in parasitism correlates with variation in behavioural defences and at genomic SNPs typically associated with learning and immunity.

Keywords: behavioural ecology, range shifts, climate change, field experiment

To the edge and beyond – do clines in expansion-facilitating traits persist across Europe following a rapid range expansion of a philopatric passerine, the reed warbler?

Nora Bergman¹, Edward Kluen¹, Juho Jolkkonen¹, Katja Rönkä¹, Malin Klumpp², Daniela Campobello³, Renzo Ientile⁴, Lucyna Hałupka⁵, Dariusz Jakubas⁶, Petr Procházka⁷, Michal Šulc⁷, Katarzyna Wojczulanis-Jakubas⁶, Rose Thorogood¹

¹*University of Helsinki*

²*Lund University*

³*University of Palermo*

⁴*University of Catania*

⁵*University of Wrocław*

⁶*University of Gdańsk*

⁷*Czech Academy of Sciences*

Numerous species are experiencing range shifts in response to environmental change, but why some successfully track their niche while others do not remains unclear. One key process is spatial sorting of expansion-facilitating traits, which increase in frequency at the expanding range front. Sorting of behavioural traits may be especially important for philopatric species that have low dispersal rates in equilibrium populations – more dispersive individuals are expected to be the ones reaching new areas and high aggression can bring a competitive advantage against resident species. However, while the advantage of these traits is expected to decline rapidly after colonisation, whether spatial sorting remains detectable across the range has rarely been investigated. Here we tested whether clines in expansion-facilitating behaviours and morphological traits, plus associated allele frequencies, can still be detected across the European breeding range of the reed warbler (*Acrocephalus scirpaceus*), a philopatric long-distance migrant that has undergone a rapid northward range expansion during the past 150 years. Previous work has shown that the rate of the expansion cannot be explained by range core dispersal rates alone, suggesting a role for behavioural changes. We tested 286 individuals across a latitudinal gradient spanning the European breeding range and including the leading northern range edge in Finland. Exploratory behaviour was measured using a standardised open field test, combined with repeatable measures of aggression and breath rate. We found persistent clines in typical expansion-facilitation behaviours, providing new insights into the mechanisms underpinning successful range expansions.

Keywords: behavioral ecology, range shifts, population genomics

Vernal pools, temporary wetland which enhance duckling success

Marteau Basile¹, Nummi Petri¹, Sundell Janne¹, Arzel Céline²

¹*University of Helsinki*

²*University of Turku*

In Fennoscandia, the decline of invertivorous waterbirds in recent decades is worrying and may be linked to deteriorating foraging conditions. Fewer wetlands are suitable for dabbling ducks as many shallow lakes and wetlands have been drained for agriculture or forestry. Moreover, not all boreal lakes are suitable for rearing ducklings due to limited food resources; aquatic invertebrates are crucial for young ducklings. Therefore, temporary wetlands can be good habitats as they are generally abundant in aquatic invertebrates. However, the relationship between duckling, food availability, and habitat remains poorly understood and rarely studied in detail. Vernal pools are small temporary wetlands, usually filled with precipitation in autumn and winter. They dry seasonally, making them fishless ponds devoid of large aquatic predators. In this research, we used imprinted mallard ducklings (*Anas platyrhynchos*) to study the effect of aquatic invertebrate availability on duckling growth. Ducklings were divided into two groups and assigned to forage in either lakes or vernal pools. Ducklings foraged at the study sites for four hours daily and were weighed before and after. Aquatic invertebrates were sampled with traps emergence and activity traps. Results showed ducklings' daily weight gain was linked to macroinvertebrate availability. Temporary ponds were richer in aquatic macroinvertebrates than lakes, and more ducklings survived in temporary ponds due to the absence of fish predation. However, no significant relationship was found between ducklings' weight and habitat type. We highlight the crucial role of aquatic invertebrates in ducklings' mass gain and the importance of temporary wetlands for duckling success.

Keywords: vernal pool, temporary wetland, ducklings success, waterbird population

Session C2

Population dynamics

Thursday, 10.30-12.00, Room L139C

Session chair: TBA

The influence of climatic variables on the seasonality of deaths in Asian elephants

Hansraj Gautam¹, John Jackson², Martin Seltmann¹, Mirkka Lahdenperä¹, Virpi Lummaa¹

¹*University of Turku*

²*Estación Biológica de Doñana (Spain)*

With climate change becoming more prominent in recent decades, several studies have explored how climatic variables affect mortality in animals. However, studies based on large and long-term demographic records of very long-lived species are limited. Here, we examined if climate, along with vegetation, explains the seasonality patterns of mortality in the Asian elephant (*Elephas maximus*), a mammal with extremely long life-span. Specifically, we analysed a large, long term demographic dataset on a large population of Myanmar's semi-captive timber elephants to understand if their mortality pattern corresponds with the seasonal patterns of temperature, rainfall and primary productivity of vegetation. We first assessed the intra-annual patterns of Myanmar's bioclimate for the period 1981-2018. We found that temperature, rainfall and primary productivity showed clear peaks (and troughs) but in different months; notably, peak primary productivity lagged the rainfall peak by three months. We then analysed the demographic database and quantified monthly mortality rates, to examine if there is a distinct intra-annual pattern in elephant mortality in four different age classes in males and females. Despite pronounced seasonality in climate and vegetation, high elephant mortality did not clearly correspond with lowest rainfall or vegetation productivity months. Instead, there appears to be a weak trend for mortality to be higher in the months with highest temperature but moderately low rainfall and primary productivity. These trends offer a baseline understanding for future studies on what shapes “environmental adversity” for such long-lived mammals in Asia's tropical and subtropical habitats.

Keywords: climate, elephants, demography, mortality, ecology

Density-dependent sexual selection in a polymorphic moth

Eetu Selenius¹, Johanna Mappes¹, Chiara De Pasqual², Sandra Winters¹

¹*University of Helsinki*

²*Swedish University of Agricultural Sciences*

Density-dependent sexual selection plays a pivotal role in the maintenance of color polymorphism, yet its intricate dynamics remain inadequately understood. Here, we investigate how varying population densities influence sexual selection in the polymorphic wood tiger moth (*Arctia plantaginis*). In this species, male hind wing coloration, either yellow (yy) or white (WW or Wy), is determined by a two-allele single locus system, intricately intertwined with behavioral and morphological traits. Our study reveals that larval population density has significant survival and life-history effects on adults, albeit with minimal impact on sexual behavior in both males and females. Interestingly, differences in adult population density have morph-specific effects on female attractiveness, where heavier yy females are more attractive than Wy females at higher male densities, and male mate-finding ability, where white male morphs benefit from higher population density. Remarkably, despite these nuances, mating success remains unaffected by population density, with WW males consistently outperforming yy counterparts across density gradients. These findings underscore the complex role of density-dependent sexual selection in the maintenance of color polymorphism, wherein traits crucial for sexual selection—including female attractiveness, male size, and mate location—respond dynamically to population density across different life stages.

Keywords: Sexual selection, behavioral ecology

Extreme arid adaptation in South African mole-rat populations along an environmental gradient

Hana Merchant¹, Daniel Hart², Nigel Bennett², Chris Faulkes³, Steve Portugal⁴

¹*Uppsala Universitet*

²*University of Pretoria*

³*Queen Mary University of London*

⁴*Royal Holloway University of London*

Understanding the adaptation of distinct populations can be key in predicting how organisms will respond to future environmental changes, such as shifts in temperature. Mole-rats occupy a wide range of habitats, and despite being subterranean, populations are impacted by both local and broad-scale environmental conditions that occur above ground. Using respirometry, morphometrics and genome-wide single nucleotide polymorphisms (SNPs) we assessed the population level differences of wild non-breeding individuals across five different populations. Our results demonstrate that metabolic rate and evaporative heat loss did not differ significantly between the populations. However, individuals from different populations employed distinct behavioural cooling techniques at higher temperatures. This indicates they have developed alternative strategies to deal with extreme high temperatures, and that metabolic rate may not be a determining factor in temperature adaptation. Morphology differed between the populations, as individuals in arid regions had unique skull shapes to accommodate increase muscle mass for digging through the rocky soil found in the Karoo. Genome-wide SNPs demonstrated significant evidence for population structure, between arid and mesic populations, and genetic diversity was greater in arid regions. This indicates that these populations have unique adaptations in response to aridity and greater connectivity and gene flow within arid populations than previously thought. Such findings have important implications for the conservation of non-migratory subterranean mammals.

Keywords: extreme adaptation, molecular ecology, environmental adaptation, arid evolution

Habitat preferences of the Crested Tit in Southwest Finland: Conservation insights from passive acoustic data

Pegah Hamedani Raja¹, Daniele Baroni², Toni Laaksonen¹, Jon Egbert Brommer¹

¹*University of Turku*

²*Istituto Superiore per la Protezione e la Ricerca Ambientale*

The Crested Tit (*Lophophanes cristatus*), although relatively common in Finland, is experiencing a population decline likely due to increasing human pressures and habitat degradation. This study investigates habitat preferences of the Crested Tit in Southwest Finland. We conducted a passive acoustic survey during spring 2020, recording presence and absence data over one week across 285 sites spaced approximately 1 km apart. Results indicate that Crested Tits favor areas with greater pine foliage within a 100-meter radius, likely due to insect availability for foraging. Unexpectedly, Crested Tit occurrences showed no specific preference for mature forests. Additionally, Crested Tits were found to avoid artificial surfaces and human-made structures, possibly to reduce competition with other bird species around developed areas. Despite their declining numbers in Finland, Crested Tits were present in 68% of surveyed sites, highlighting the effectiveness of passive acoustic surveys for assessing avian habitat preferences and monitoring populations. These findings offer important insights into the ecology of the Crested Tit in the context of habitat loss and support targeted conservation efforts in the region.

Keywords: birds, mature forest, passive acoustic survey, human-created structures

Temperature optima of a natural diatom population increases as global warming proceeds

Conny Sjöqvist¹, Giannina Hattich¹, Sami Jokinen², Sirje Sildever³, Maximilian Gareis¹, Janni Heikkinen¹, Nadja Junghardt¹, Mara Segovia⁴, Miguel Machado⁵

¹*Åbo Akademi University*

²*Geological Survey of Finland*

³*Tallinn University of Technology*

⁴*Valencia University*

⁵*Malaga University*

Studies in laboratory-based experimental evolution have demonstrated that phytoplankton species can rapidly adapt to higher temperatures. However, adaptation processes and their pace remain largely unknown under natural conditions. Here, by comparing resurrected *Skeletonema marinoi* strains from the Baltic Sea during the last 60 years we show that modern *S. marinoi* have increased their temperature optima by 1°C. With the increasing ability to grow in higher temperatures, growth rates in cold water decreased. Modern *S. marinoi* modified their valve:girdle ratio under warmer temperatures, which likely increases nutrient uptake ability. This was supported by the upregulation of several genes related to nitrate metabolism in modern strains grown under high temperatures. Our approach using resurrected strains demonstrates the adaptation potential of naturally occurring marine diatoms to increasing temperatures as global warming proceeds and exemplifies a realistic pace of evolution, which is an order of magnitude slower than estimated by experimental evolution.

Keywords: evolution, global warming, experimental ecology, gene expression

Long-term biodiversity monitoring of multiple ground-water fed ponds and its future

Camille Leblanc¹, Skúli Skúlason^{1,2}, Grant Haines¹, Bjarni Kristófer Kristjánsson¹

¹*Hólar University*

²*Icelandic Museum of Natural History*

Small populations can be the result of habitat fragmentation, population bottleneck(s) and/or colonisation event(s). Knowing what shapes the genetic and phenotypic diversity of small populations is important in predicting their adaptability and persistence in the light of rapid ecological changes. We present the results of a 13-year monitoring program focusing on the Arctic charr (*Salvelinus alpinus*), found in lava ponds in Iceland. First, we overview the respective study system, methods and standardisation of data collection, and what we have learned in terms of ecology, evolution and population dynamics. We show that these fish form a collection of small unique populations, with low genetic diversity, little connectivity across ponds, and subtle phenotypic divergence among ponds. Local ecological factors, such as temperature and macroinvertebrate composition, vary among caves and may affect phenotypic traits in these populations. Our findings strongly suggest that evolutionary and ecological factors interplay in shaping genetic and phenotypic structures of wild populations at contemporary time scale. This system offers a replication of wild unique populations, rarely seen in nature, allowing in the near future a direct estimation of fitness and adaptation in a highly polymorphic species. We discuss the urgent need and feasibility of maintaining long-term monitoring of a focal species in multiple populations, along with simple but standardised measures of local environmental factors, using available technologies such as remote sensing, automation of phenotypic traits collection, eDNA, and the use of machine learning.

Keywords: Intraspecific diversity, freshwater, long-term monitoring, small populations

An epigenetic clock to monitor penguins and other birds

Robin Cristofari¹, Mikaela Hukkanen², Flavia Fernandes², Celine Le Bohec³, Simon Jarman⁴, Miina Ollikainen², Leyla Davis⁵, Klemens Pütz⁶, Emiliano Trucchi⁷, Maite Arriagada⁸, Aurora Fernandez Duran⁸, The Avian epigenetic clock Consortium²

¹*Institute of Biotechnology*

²*University of Helsinki*

³*CNRS*

⁴*Curtin University*

⁵*Zoo Zurich*

⁶*Antarctic Research Trust*

⁷*University of Ancona*

⁸*Reserva Natural Pinguino Rey*

Age is one of the basic data needed to assess vital rates in matrix-based demography: for long-lived species in the wild, this means that assessing intrinsic population growth required, up to now, decades of preliminary work. This burden has recently started to shift with the discovery of epigenetic clocks, now a well-established tool to assess the age or age acceleration in mammals based on DNA methylation level at selected CpG sites: thanks to these predictors, a known-age population can be built in a cross-sectional way. The deep divergences between mammalian and avian physiology, however, prevent the direct transfer of this tool to birds. We are addressing this problem by building an avian epigenetic clock, primarily centered on the King penguin, but designed to function in other bird species too. We demonstrate that (1) this clock shows deep homology with its mammalian equivalent, thus supporting the idea of shared / convergent aging mechanisms in warm-blooded vertebrates, and that (2) this tool can effectively allow the construction of a known-age study population in long-lived penguins in little more than one year.

Keywords: epigenetics, penguins, aging, long-term monitoring

Session C3

Themed session 8: Biodiversity footprint of human activities

Thursday, 10.30-12.00, Room L304

Session chairs: Maiju Peura, Sami El Geneidy, Janne Kotiaho

From Net Zero to Nature Positive: assessing the contribution of greenhouse gas emissions towards organisational biodiversity footprints.

Charlotte Maddinson¹, Janne Kotiaho¹, Sami El Geneidy¹, Joseph Bull²

¹*University of Jyväskylä*

²*University of Oxford*

Climate change and biodiversity loss are closely linked crises, but typically addressed separately within sustainability strategies. Net Zero targets and greenhouse gas (GHG) accounting frameworks have been widely adopted by organisations to address their climate impacts. Analogously, Nature Positive targets and associated biodiversity footprinting approaches have emerged as concepts for tackling biodiversity loss. Identifying synergies between Net Zero and Nature Positive implementation is vital if we are to achieve either. Many questions remain unanswered, however, regarding the connections between the two targets and their underlying methodological frameworks. Firstly, for organisations that have previously measured and set targets for GHG emissions only (i.e., Net Zero), how much additional work is required to further quantify and address biodiversity impacts (i.e., Nature Positive)? What factors influence the ease -or difficulty- for organisations to extend their sustainability strategies to include both Net Zero and Nature Positive? Finally, what are the implications for organisations transitioning from Net Zero to Nature Positive from a strategy perspective? We aim to answer these questions through a qualitative review of carbon and biodiversity footprinting literature, characterising how GHG emissions contribute towards biodiversity footprints. The literature review will be supplemented by a qualitative analysis, evaluating how footprinting methods such as LC-IMPACT weight GHG emissions against alternative drivers of biodiversity loss. Preliminary results indicate that GHG emissions contribute a large proportion of organisational biodiversity impacts, but this varies according to sector and location. Our work implies pathways towards achieving both Net Zero and Nature Positive targets in tandem.

Keywords: biodiversity footprinting, climate change

Carbon and biodiversity footprint of the Finnish transportation system

Venla Leppilampi^{1,2}, Stefan Baumeister^{1,3}, Sami El Geneidy^{1,3}, Janne Kotiaho^{1,2}

¹*University of Jyväskylä*

²*School of Resource Wisdom*

³*School of Business and Economics*

Transportation systems have diverse, generally negative, impacts on biodiversity and climate. Traditionally we have focused on the direct environmental impacts of the transport systems, such as land use of the infrastructures and emissions from the vehicles and have largely ignored the indirect impacts arising from consumption that exports the local impacts around the globe along supply chains. The goal of this research is to assess the carbon and biodiversity footprints of the Finnish transportation system. We will apply hybrid life cycle impact assessment methods that combine environmentally extended input-output analysis methods with life cycle assessment methods and other databases and frameworks, such as LC-IMPACT or ReCiPe. The biodiversity footprint will be estimated with biodiversity equivalent, a common currency for measuring biodiversity impact across the planet, with desirable characteristics similar to the carbon dioxide equivalent. Assessing the carbon and biodiversity footprint requires four items of information: 1) the amount and type of consumption, 2) the amount and type of the driver of biodiversity loss and 3) the geographical locations of the drivers and 4) the damage to biodiversity caused by the driver in each specific location. In this conference I will be presenting the methodological background of the research and preliminary results of the carbon and biodiversity footprint assessment. This study will amplify knowledge of how many species will potentially disappear globally due to the use and maintenance of the Finnish transportation system and pave the way for more comprehensive assessments of carbon and biodiversity footprints of civil society.

Keywords: planetary wellbeing, sustainability, transportation system

Biodiversity footprint of construction

Krista Pokkinen

University of Jyväskylä

The construction industry is one of the fastest-growing sectors. Currently, construction industry is responsible for approximately half of global raw material consumption and 37% of global carbon emissions. The goal of this research is to examine how to calculate the biodiversity footprint and handprint of construction. Biodiversity footprint caused by construction is evaluated through real-life construction projects and by assessing the biodiversity footprint of a construction company. While carbon footprint assessments are widely used by organizations to measure climate impacts, few similar tools exist for evaluating biodiversity footprints or biodiversity impacts. Four things are needed to calculate the biodiversity footprint: type and amount of consumption, type and volume of the cause of the biodiversity loss resulting from the consumption (driver of biodiversity loss), location of the driver of biodiversity loss, and biodiversity loss caused by the driver. Calculations are conducted by using a method that integrates two databases, EXIOBASE and LC-IMPACT, along with life cycle assessment calculation methods. Methods used in the research assess the global extinction risk caused to different species under one unit of measurement, similar to a carbon footprint. Calculations performed for a street renovation project in Tampere revealed that materials caused the biggest biodiversity footprint. The footprint for this renovation was evaluated for two different scenarios: the first scenario represented 'traditional' street construction, while the second modeled resource-efficient construction based on circular economy principles. The results showed that, in the resource-efficient scenario, the biodiversity footprint was 40% smaller than in the traditional scenario.

Keywords: construction

Biodiversity impacts of Finnish organic and conventional crops: assessment with three life cycle impact assessment methods

Anna-Elina Karimaa^{1,2}, Venla Kyttä¹, Iryna Herzon², Hanna L. Tuomisto², Merja Saarinen¹

¹*Natural Resources Institute Finland (Luke)*

²*University of Helsinki*

Agriculture has significant impacts on biodiversity. Life cycle assessment (LCA) is frequently used to assess these impacts, but assessment methods are still under development. The available methods differentiate agricultural production systems to varying extent, which may affect their ability to distinguish between organic and conventional products, for example. More differentiating methods are typically highly site-dependent and developed for a certain country or ecoregion. In this case study, we will examine the suitability of existing methods for evaluating the biodiversity impacts of Finnish organic and conventional crops. Three LCA methods will be used: (1) SALCA-Biodiversity, which calculates a biodiversity score expressing impacts on 11 indicator species groups, (2) Biodiversity Value Increment (BVI), which assesses impacts based on the naturalness of the assessed land area, and (3) a recent land-use-based method behind a new GLAM endpoint method expressing impacts as potentially disappeared fraction (PDF) of species. Additionally, the SALCA-Biodiversity scores will be converted into PDF with a method currently under development. Data on management and crop yields on organic and conventional fields will be taken from ProAgria Field Plot Database. Our upcoming publication will discuss the differences of the assessment methods and their suitability for assessing organic and conventional production systems. Based on the results, we will make recommendations for future development of biodiversity impact assessment methods within LCA.

Keywords: biodiversity, life cycle assessment, agriculture, land use

Bridging the gap: enhancing biodiversity reporting and assessment in the private sector for sustainable practices

Heidi Herlevi, Johan Malmberg, Magnus Hellström, Anna Törnroos-Remes

Åbo Akademi University

In light of the escalating biodiversity crisis and the adoption of initiatives such as the Kunming-Montreal Global Biodiversity Framework (GBF), there is a pressing need for all sectors of society, including the private sector to enhance its focus on biodiversity. The European Union's regulations mandate that companies report their biodiversity impacts and mitigation strategies by 2025, yet significant knowledge gaps remain regarding the methodologies required for such reporting. This paper presents an interdisciplinary approach that merges concepts from industrial management and accounting with ecology and marine biology to address these challenges. We emphasize the necessity for clear definitions of biodiversity and biodiversity impacts, alongside the development of standardized methods for biodiversity assessments, reporting, and outcome evaluation. Our case study of an industry-science collaboration illustrates the complexities of benchmarking biodiversity assessments and highlights the urgency for a comprehensive framework that integrates diverse methodologies and data requirements from environmental impact assessments and biodiversity reporting. By establishing clearer guidelines and standardized practices, this research aims to effectively incorporate biodiversity considerations into company strategies and policies, ultimately contributing to the global effort to mitigate biodiversity loss. This collaborative effort seeks to bridge the gap between scientific understanding and industry application, fostering a more sustainable approach to biodiversity management within the private sector.

Keywords: biodiversity, socio-ecological linkages, conservation science and policy, sustainability

From biodiversity footprint calculation to action: What makes a nature positive university?

Ulla Helimo

University of Jyväskylä

Higher education institutions can have a potentially large biodiversity footprint that we have only recently begun to measure and understand. There are still many uncertainties related to the calculations of organization's biodiversity footprint, handprint and offsetting. Despite of the uncertainties, several universities have already given pledges to become Nature Positive. As organizations universities have taken the lead in the society extending their carbon neutrality goals to no net loss of biodiversity. Because currently no external independent and accredited verifier exists to prove the claim to be Nature Positive, a risk of greenwashing exists. My research examines the Nature Positive claim in general and more specifically in a university context. Using literature review and results of expert workshops, criterion on how universities should prove their nature positive claim is proposed.

Keywords: Biodiversity, footprint, human activities

Defining ecosystem condition metrics and area multipliers of offset actions for Finnish habitat types in biodiversity offsetting

Joel Jalkanen¹, Eini Nieminen², Aapo Ahola³, Minna Pekkonen³, Panu Halme², Heini Kujala¹

¹*Finnish Natural History Museum*

²*University of Jyväskylä*

³*Finnish Environment Institute (Syke)*

Biodiversity offsetting (ecological compensation) is a new tool in Finland for mitigating human-caused biodiversity losses. Offsetting aims at compensating development projects' biodiversity losses by restoring or/and protecting nature elsewhere so that No Net Loss (NNL) for biodiversity would be reached. Such a policy scheme can only work if biodiversity losses and offset gains can be assessed and matched in a transparent and ecologically appropriate manner. Furthermore, the areas required to reach NNL would, and should, depend on the effectiveness and time-lags of the selected offset actions. I will present the joint project of the 'BOOST' research consortium and Finnish environment institute Syke for defining (i) metrics to assess habitat types' ecological condition on-the-field and (ii) estimates of the effectiveness and time-lags of different offset actions. Condition assessment matrices were derived for all habitat types in the Finnish Red book of habitats, and total of 216 response estimates for ecosystem type/restoration action pairs were defined in a large-scale expert collaboration. These estimates allow calculating the action-specific offset multipliers needed to reach NNL in offsetting, i.e., the area needed to fully compensate losses. Naturally, our results inform nature assessments and restoration planning also outside the offsetting context.

Keywords: biodiversity offsetting, Finnish habitat types, restoration

Session C4

Host-parasite and disease dynamics

Thursday, 10.30-12.00, Room L303

Session chair: TBA

Describing the diversity of gregarine-microsporidian symbiosis in marine polychaetes

Anna-Lotta Hiillos, Micah Dunthorn, Torsten H. Struck

Natural History Museum, University of Oslo

Symbiotic interactions have played a significant role in ecological and evolutionary processes through the history of life and have ultimately shaped the biodiversity we witness today. Still many fundamental questions, particularly concerning interactions between micro-organisms (e.g., protists) and their hosts, remain unresolved. Marine polychaete worms (Annelida), key organisms in benthic ecosystems, are hosts to protist symbionts (gregarines), which themselves are infected by microsporidian parasites, forming a tripartite symbiosis. However, it is unclear how common this tripartite interaction is in nature and its diversity and function in benthic ecosystems is still unknown. Using a metabarcoding approach targeting both symbiont taxa within two polychaete species, as well as environmental samples around the Kattegat-Skagerrak region of the Baltic Sea, we aim to unravel the diversity and occurrence of this tripartite symbiosis. Gregarine and microsporidia species composition and diversity is described and compared between host species. Generally, because most of the gregarine and microsporidian diversity in marine hosts is still unknown, we expect new species in both groups to be discovered. This study is a first step towards disentangling what consequences the tripartite symbiosis has on the functioning of benthic ecosystems. Given the ecological importance of polychaetes, gregarines could potentially reduce polychaete populations size and therefore impact the functioning of benthic communities and other marine fauna that is dependent on these animals. Consequently, microsporidians could play an important role in controlling the possible antagonistic interaction between polychaetes and gregarines.

Keywords: parasites, pathogens or wildlife disease, symbiosis, marine animals

Fungal parasites associated with seasonal phytoplankton blooms along a Baltic Sea salinity gradient

Jonna Kangas¹, Simon Bilik², Lumi Haraguchi³, Kaisa Kraft³, Maliheh Mehrshad⁴, Silke Van den Wyngaert¹

¹University of Turku

²University of Lappeenranta

³Finish Environmental Institute

⁴Swedish University of Agricultural Sciences

Parasites of phytoplankton are an integral part of marine ecosystems, yet they are often overlooked in studies of phytoplankton blooms. While chytrid fungi are well-known parasites of freshwater phytoplankton, their interactions with phytoplankton in brackish environments remain largely unexplored. To address this knowledge gap, we aimed to (i) characterize the diversity and abundance of chytrid parasites infecting phytoplankton and (ii) identify potential drivers of their occurrence and diversity during a phytoplankton spring bloom along a horizontal salinity gradient in the Baltic Sea. Samples were collected during five cruises along a north-south salinity gradient spanning from the Gulf of Finland to the Southern Baltic Proper. We applied high throughput quantification and sequencing methods as well as cultivation and single cell sequencing of individual host-parasite associations to characterize the spatial and temporal distribution patterns of chytrid parasites and their phytoplankton hosts. We identified five novel chytrid species infecting cold water diatoms, including *Thalassiosira* spp., *Pauliella taeniata* and *Guinardia delicatula*. The occurrence and relative abundance of parasitic chytrids varied temporally and spatially along the gradient and were linked to host distribution and phytoplankton bloom development. Alpha and beta diversity of parasitic chytrids differed between northern and southern locations. Salinity and host community composition significantly explained parasite community composition along the salinity gradient. Our results indicate that the distribution of chytrid parasites is primarily driven by the distributions of their hosts, which are structured by the salinity gradient. This underscores salinity as an important driver of host-parasite associations in the Baltic Sea.

Keywords: microbial ecology, parasites, pathogens or wildlife disease

Seasonal differences in peaks of abundance allow co-infection of apicomplexan parasites in a shared polychaete host.

K. Emily Knott¹, Anna-Lotta Hiillos², Mathias Colin¹, Jaana Jeskanen¹, Nerea Abrego¹

¹*University of Jyväskylä*

²*University of Oslo*

Parasites co-infecting the same hosts must compete for the shared resource that the host provides. We investigated patterns of infection of apicomplexan parasites in a polychaete host collected from multiple sites at different times of the year using a digital PCR assay. We applied joint species distribution modelling with the framework Hierarchical Modelling of Species Communities (HMSC) to assess how different environmental factors jointly determine the occurrences and abundances of the parasites. Host population was the most important variable explaining occurrence patterns while the variation in abundance was mostly captured at the level of hosts, so that some hosts had high parasite abundances and others not. There were no statistically supported associations between the parasites studied at the level of hosts, but there were at the level of host populations. Namely, when one of the parasites were found in a population, it was likely that the other parasite species was also present. However, the abundance of the parasite species co-occurred negatively in time, one showing peaks of abundance in spring and the other in autumn. Abundance of the two parasites were also differently associated with environmental factors, one being associated with sediment factors, such as C/N ratio and water content, while the other was associated with host density. Ecological differences among the parasites allow them to take advantage of the same host resource.

Keywords: parasites, microbial ecology, species interactions

The lack of *Borrelia afzelii* in bank voles outside urban forests is not explained by the host toll-like receptor 2 (TLR2) genotype

Nosheen Kiran, Phillip Watts, Eva R. Kallio, Tapio Mappes, Ilze Brila

University of Jyväskylä

Earlier studies have shown that Toll-like receptor 2 (TLR2) genotypes affect *B. afzelii* infection probability in the bank vole in Sweden. I investigated the association between TLR2 genotypes and *B. afzelii* infection in Finnish bank voles. A total of 383 individuals were collected from 20 locations in Central Finland, and TLR2 genotyping was conducted through Sanger sequencing. I identified 70 TLR2 haplotypes grouped into three clusters: TLR2C1, TLR2C2, and TLR2C3, showing that genetic variation is present in Finnish bank voles. However, when examining the associations between the *B. afzelii* infection and TLR2 genotypes, no significant association was detected. These results suggest that the patchy distribution of *B. afzelii* in rodents is not driven by the TLR2 polymorphism in bank voles in Finland. The findings suggest that *B. afzelii* infection risk may be shaped more by regional factors like environmental conditions than by TLR2 variation, deepening our understanding of Lyme disease spread across ecosystems.

Keywords: rodents, *Borrelia afzelii*

Amplification or dilution? Quantifying the role of hosts in tick-*Borrelia* interplay with natural islands mesocosms

Eva Kallio

University of Jyväskylä

Identifying the drivers of zoonotic hazards of tick-borne pathogens is challenging as an increase in host abundance may cause amplification or dilution of the pathogen and/or the vector, depending on the role of the host in the disease system. For instance, it remains unclear whether the hazard of Lyme Borreliosis (LB), measured as the density of *Borrelia burgdorferi*-infected ticks, is driven by the hosts that support tick reproduction, such as cervids (e.g., deer and Moose), which are typically not competent hosts for the pathogen, or the availability of pathogen-competent hosts, typically rodents. We quantified the roles of cervids and rodents on LB hazard across 41 islands with varying tick, cervid and rodent abundances in southern Finland in 2017-2021. Structural equation models showed that cervids amplified ticks by increasing the density of nymphs (DON) but caused pathogen dilution by decreasing the nymphal infection prevalence (NIP). Rodents, in turn, increased NIP, i.e. pathogen amplification, without having a detectable effect on DON. The density of infected nymphs (DIN) was positively associated with NIP and DON, the latter having a stronger effect. Our study shows that LB hazard is driven by cervids supporting ticks, and rodents supporting the pathogen, while the dilution is unlikely to decrease the overall LB hazard.

Keywords: disease ecology, wildlife hosts, zoonotic hazards, Lyme disease, *Borrelia*

The impact of anthropogenic disturbance on disease in boreal forest understory: Insights from *Vaccinium myrtillus*

Sara Leino

University of Helsinki

Anthropogenic disturbances, such as clear-cutting, are reshaping boreal forest ecosystems, with significant implications for both biodiversity, and disease dynamics. Plant diseases are influenced by host biodiversity, spatial structure, and abiotic conditions—all of which are being altered by human activities. Understanding how these changes impact disease prevalence is crucial for predicting their broader ecological consequences. This study investigates the effects of forest management practices on disease dynamics in *Vaccinium myrtillus*, a widespread boreal forest understory species that is sensitive to clear-cutting. *V. myrtillus* offers an interesting lens through which to study how disturbance and following biodiversity shifts may affect disease risk. We conducted field surveys at over 120 forest sites across Finland, collecting data on plant species richness, abundance, and environmental variables alongside measurements of disease occurrence and severity in *V. myrtillus*. This extensive dataset enables us to assess the relationships between host community diversity, structure, and disease risk in both disturbed and undisturbed environments. By linking biodiversity patterns to plant-pathogen interactions, this research provides valuable insights into how human-induced habitat changes disrupt ecological processes and affect disease dynamics in boreal forest ecosystems.

Keywords: anthropogenic disturbance, biodiversity–disease relationship, host-pathogen interactions, boreal forest understory

Freshwater mussels – endangered parasites and service providers

Jouni Taskinen

University of Jyväskylä

Freshwater mussels Unionida belong to the most endangered animals globally. Characteristic to freshwater mussels is the parasitic stage (glochidium) in fish, sessile way of life, filter feeding, bivalved shell and in some species extremely long life. Important role of freshwater mussels in aquatic ecosystems, e.g. in nutrient cycling and in supporting biodiversity has been recently understood. I present results of studies that explored host-parasite relationship between an endangered freshwater mussel and its host fishes, including host preference, local adaptation and density dependence. In addition, I present results of studies examining the effect of glochidia infection on susceptibility of fish to co-infections by other parasites and pathogens, as well as on the efficacy of mussels in filtering fish pathogens and larvae of fish parasites. Results show adaptation to local host fish species population and (unexpected) positive density-dependence of glochidia growth, indicating an Allee effect, in the freshwater pearl mussel (*Margaritifera margaritifera*)-salmonid host relationship—bearing important conservation implications for this endangered species. Furthermore, infection of brown trout by *M. margaritifera* glochidia increased susceptibility of fish to subsequent trematode parasite infection, but, unexpectedly, lowered fish mortality rate when exposed to a pathogenic bacterium. Finally, filtration by the duck mussel *Anodonta anatina* removed fish pathogen *Flavobacterium*, and filtration by *M. margaritifera* removed larvae of trematode parasite of fish from water. Thus, with extirpation of endangered freshwater mussels we may lose potential ecosystem services and important interactions between species in aquatic ecosystems.

Keywords: biodiversity, ecosystem functions and services

Enemy release hypothesis: Parasitism in invasive and native freshwater bivalves

Binglin Deng, Jouni Taskinen

University of Jyväskylä

The invasion of exotic bivalves can threaten native freshwater mussels (Unionida) and freshwater ecosystems. The Enemy Release Hypothesis (ERH) proposes that reduction of natural enemies will bring competitive advantage to invaders and contrite to the success of invasion. In this study, ERH was tested on the invasive freshwater bivalves *Sinanodonta woodiana*, *Corbicula fluminea* and *Dreissena polymorpha* with perspective of parasitism. First, parasite pressure, measured by parasite taxon richness and sum of prevalences was compared between native and invasive freshwater bivalves living in sympatry in two separate field studies covering a total of 11 European. In the native bivalves the mean site-specific parasite taxon richness was 2.3–3.4 times and the mean sum of prevalences of infection of different parasites was 2.4–2.6 times that of those in the invasive bivalves. Second, the parasite pressure in the invasive bivalves *S. woodiana* and *C. fluminea* was compared between populations in the original range (China, 5 waterbodies) and the invaded range (Europe, 11 waterbodies). For *S. woodiana*, the average site-specific parasite taxon richness in China was 2.1 times and the sum of prevalences of infection was 3.0 times of those in Europe. For *C. fluminea*, the average site-specific parasite taxon richness was 1.3 and the sum of prevalences of infection was 13.8 in China, while all the studied European *C. fluminea* populations were free of parasites. These results indicate a reduction in the parasite pressure among invasive species, and thus support ERH.

Keywords: invasive species, parasites, pathogens or wildlife disease

Session C5

Themed session 3: Citizen science approaches in ecological research

Thursday, 10.30-12.00, Room L302

Session chairs: Ossi Nokelainen, Aleksi Lehikoinen, Otso Ovaskainen

Citizen science based bird monitoring schemes in Finland

Aleksi Lehikoinen

Finnish Museum of Natural History

Monitoring of biodiversity is widely based citizen science in the globe, and this is also the case in Finland. Finnish common bird monitoring has been running for decades with a help of thousands of voluntary birdwatchers. In this presentation, I will explain the main national bird monitoring schemes coordinated mainly by the Finnish Museum Natural History. These schemes include various types of surveys and bird ringing where the data is gathered to the Finnish Biodiversity Information Facility (Laji.fi). The longest time series are from winter bird surveys, which started in 1956 and ringing activity started in 1913. The annually updated monitoring data are widely used by researchers but also environmental authorities including red listing, EU bird directive reporting and restoration law. In addition, I will present the main results of a recent online questionnaire to clarify what motivates people to participate biodiversity monitoring.

Keywords: biodiversity monitoring, citizen science, bird surveys, ringing, Finnish Biodiversity Information Facility

A mobile application–inspired citizen science initiative to compile bird observations

Ossi Nokelainen¹, Patrik Lauha², Ari Lehtiö¹, Otso Ovaskainen¹

¹*University of Jyväskylä*

²*University of Helsinki*

Citizen science encompasses various initiatives, yet differences in terminology, project goals, and cultural contexts often limit its effectiveness. Our study demonstrates how citizen science can support large-scale avian wildlife monitoring using a mobile app-based campaign (Muuttolintujen kevät), an automated bird sound classifier for Finnish birds. Over 250 000 users have downloaded the application and obtained 9 million recordings with 20 million bird observations in less than two years. We analyzed the spatial and temporal distribution of the data, user behavior, and the reliability of AI-based species identifications. To ensure data quality, raw audio is stored for ongoing validation. Citizen science may not only enhance public engagement and education, but also aid conservation efforts. Future expansions will incorporate advanced analytics to further support conservation strategies.

The involvement of Ukrainian refugees in citizen science activities on biodiversity: first practical experience from Finland

Mykyta Peregrym

University of Oulu

Due to the large-scale Russian invasion, Finland now hosts around 65,000 Ukrainian refugees, many of whom face mental health challenges and difficulties adapting to a new culture, language, and climate. Despite these obstacles, many are interested in exploring Finland's natural environment. Their motivations vary: some find comfort in nature's healing effects, while others see it as a source of income through berry and mushroom picking or as recreation. Nature also offers educational opportunities, especially for children. Our initiative aims to help Ukrainian refugees adapt to Finland's natural environment and values through citizen science activities. These activities not only educate participants and offer potential income opportunities but also improve mental and physical well-being. The skills gained could also be useful when refugees return home. Additionally, this initiative contributes to the collection of biodiversity data, which is important for Finnish researchers and conservation efforts. In 2023-2024, we organized workshops in Oulu, Vaasa, and Tampere, introducing participants to iNaturalist and other citizen science platforms. They then took part in bioblitzes to apply their skills. Local NGOs representing Ukrainian refugees were instrumental in organizing these workshops. Our experience can be expanded within Finland and applied in other countries as well. Further details on the outcomes of the initiative will be presented during the conference.

Keywords: data collection, iNaturalist, nature exploration, NGOs

New methods for collecting and processing audio data in professional and citizen science research

Otso Ovaskainen¹, Ari Lehtiö¹, Patrik Lauha², Ossi Nokelainen¹, Panu Somervuo², Tomas Roslin³, Aleksi Lehikoinen²

¹*University of Jyväskylä*

²*University of Helsinki*

³*Swedish University of Agricultural Sciences*

I describe three recent initiatives for collecting and processing large-scale audio data for bird research, and discuss their pros and cons in terms of their potential for European-wide monitoring schemes. (1) In the ERC-synergy project LIFEPLAN, we implemented a globally distributed sampling scheme with AudioMoth recorders, resulting in 120 years of data from >200 locations. (2) In the context of the Finnish Digital Citizen Science Centre, we created a smartphone app that was used in 2023-2024 by 250,000 citizen scientists, resulting in 20 million bird observations. (3) We have recently developed a prototype of a semi-autonomous monitoring station that sends audio wirelessly to a computational cluster, enabling real-time inference. All three approaches store also the raw audio in addition to the AI-based classifications, enabling rigorous validation and reclassification with continuously improving AI-based models. We consider all three approaches to hold potential for European-wide audio monitoring, and are keen to discuss possible collaborations in this context.

Keywords: citizen science, muuttolintujen kevät, bird classification

The potential of nocturnal flight calls in bird migration research evaluated by citizen science and weather radar observations

Nadja Weisshaupt¹, Jarmo Koistinen¹, Juha Saari

¹*Finnish Meteorological Institute*

The study of nocturnal bird migration brings observational challenges because of reduced visibility and observability of birds at night. Radars have long been the preferred choice of scientists to study nocturnal migrations. A known challenge in radars is the lack of species-level information required in activities targeting biodiversity questions. With recent technological advances and with improved accessibility and affordability of acoustic tools, bird sound recordings have steeply increased in popularity. However, the potential of bioacoustics for nocturnal migration monitoring is unknown. The present work contrasts acoustic recordings with citizen science observations and weather radar data to assess the qualitative and quantitative yield of acoustic recordings for migration-related research. Acoustic migration phenologies are compared to citizen science migration schedules. We identify seasonal and annual patterns observed in combined acoustic and radar analyses and discuss underlying behavioural and phenological species-level dynamics. Our study shows that about 70% of the nocturnal long-distance migrant populations and about 50% of the nocturnally migrating passerines in total is migrating silently. Hence, this affected the capacity of acoustic data to represent migrant populations aloft when long-distance migrants dominate the airspace surveilled by weather radar. On the other hand, some highly vocal and numerous species, such as thrushes, may correlate well with weather radar observations if they outweigh the silent migrants during the respective migration season. Overall, the ability of acoustic records to act as a proxy of overall migration dynamics is highly dependent on the migration period and species involved.

Keywords: bioacoustics, radar, citizen science, bird migration, monitoring

Mobilizing large datasets to infer spatial and temporal biodiversity changes: example on macrolepidoptera in Finland

Rémi Duflot¹, Jérémy Cours¹, Risto Heikkinen², Aleksi Lehikoinen³, Miska Luoto³, Otso Ovaskainen¹, Anssi Vähätalo¹

¹*University of Jyväskylä*

²*Finnish Environment Institute (Syke)*

³*University of Helsinki*

To halt and reverse biodiversity loss, reliable knowledge of its distribution and dynamics is essential. Acquiring biodiversity data at large spatial and temporal scales is challenging. Thus, the development and structuring of ‘citizen’ science is often viewed as a great opportunity to develop extensive complementary datasets. However, such data are usually biased because of unknown and unequal sampling intensity, and, therefore, typically analysed at the species level, focusing on a limited number of species. Using the example of macrolepidoptera in Finland, we aimed to demonstrate how accumulation curve analyses and careful data filtering can be used to infer biodiversity trends of species communities. We explored how the species richness and spatial beta-diversity of macrolepidoptera have changed over time in Finland at three spatial scales: nationwide, in the 21 bioregions, and in 10x10km grid squares. The results show a general increase in macrolepidoptera species richness at all spatial scales. However, the changes were more pronounced in the northern bioregions and 10x10km grid squares. In addition, local trends were more diverse as species richness significantly decreased in some of the 10x10km squares, especially in the most recent periods. Finally, beta-diversity at the national scale across the bioregions and across the 10x10km squares decreased over time, suggesting biotic homogenization. Additional analyses will be conducted to link species gains and losses with functional traits. We conclude that conservation planning and understanding the drivers of biodiversity changes could benefit from the use of consolidated multi-sourced biodiversity data.

Keywords: biodiversity, citizen science, climate change, community ecology

Session D1a

Themed session 7: Environmental sequencing for biodiversity research

Thursday, 13.45-14.45, Room L304

Session chairs: Sten Anslan and Brendan Furneaux

Long-reads or short-reads? That is the question

Sten Anslan

University of Jyväskylä

The DNA library preparation methods and high-throughput sequencing (HTS) technologies are rapidly developing; thus, the market offers a variety of sequencing machines and methods to choose amongst. Although the 2nd generation sequencing-by-synthesis technologies (such as by Illumina) have conquered the field of DNA metabarcoding, the 3rd generation real-time single molecule sequencing methods are becoming more established. While the former (2nd gen.) methods benefit from very high sequencing depths, and thus generally cheaper costs per sequence, the latter (3rd gen.) offers possibilities to generate order of magnitude longer sequences for more accurate classification. In this presentation, I will tackle the question of ‘long or short-reads’ in the example of mitochondrial COI amplicons (300 - 1200 bp) to identify microarthropod communities from soil eDNA samples.

Keywords: metabarcoding, PacBio, Illumina, eDNA

POAnoise: a hybrid denoising framework for high-throughput DNA sequencing accuracy

Muhammad Ardiyansyah, Otso Ovaskainen, Brendan Furneaux

University of Jyväskylä

In high-throughput DNA metabarcoding, denoising methods attempt to accurately distinguish true biological sequences from errors introduced during sequencing. This project aims to combine two powerful approaches – model-based error correction such as implemented in DADA2, and Partial Order Alignment (POA) – to improve accuracy and sequence recovery. DADA2 leverages a quality-aware error model to differentiate true sequence variants from noise, providing high-resolution amplicon data suitable for ecological and clinical studies. However, it struggles to recover rare species, especially for longer amplicons. We propose a more sophisticated error model which represents each putative biological sequences (ASV) using a multiple sequence alignment rather than a representative sequence. To ameliorate the cost of computing large multiple sequence alignments, we use Partial Order Alignment (POA), which represents a multiple sequence alignment as a directed acyclic graph, and allows efficient operations especially when the sequences are similar. We anticipate that this integrated approach will improve the sensitivity and specificity of sequence variant detection while keeping computational costs tractable. This research has the potential to set new standards for processing large-scale amplicon data, enabling more efficient analyses in environmental metabarcoding and beyond.

Keywords: DNA sequence denoising, error correction model, graph-based alignment

OptimOTU: Taxonomically informed dynamic OTU clustering

Brendan Furneaux

University of Jyväskylä

Metabarcoding studies generate amplicon sequences from a chosen marker gene, derived from a mixed sample of genomic DNA from multiple organisms. Amplicon sequences originally deriving from a single species are typically not all 100% identical, with variants produced by both true biological processes and technical noise. Consequently, sequences are typically clustered to form approximately species-level operational taxonomic units (OTUs). In many workflows, a single clustering threshold is chosen a priori, often 97% sequence similarity, despite well-known variability in the level of intra-species sequence variation in marker genes within different taxonomic groups. Alternatively, in recent years denoising or “ASV” workflows, which attempt to retain all biological sequence variants while suppressing technical noise, have gained in popularity. Although this approach is likely warranted for prokaryotes where strain-level differences may be ecologically relevant, for sexually-reproducing eukaryotes, it may instead lead to the inflation of “species” numbers and the complexity of downstream statistical analyses without adding ecologically relevant information. Here I present OptimOTU, a workflow for bioinformatic analysis of large amplicon datasets which uses preliminary denoising, followed by probabilistic taxonomic identification and clustering based on optimized thresholds for different taxonomic groups, in order to generate OTUs which more accurately approximate the true underlying species pool, even in the presence of many unknown species.

Keywords: metabarcoding, eDNA, bioinformatics, biodiversity

DNA Metabarcoding for landscape restoration: towards comprehensive biodiversity assessments

Cristian N Waghershauser¹, Jack Bamber², Kenny Kortland³, Pip Gullet⁴, Nancy Ockendon⁵

¹*University of the Highlands and Islands*

²*University of Aberdeen*

³*Forestry and Land Scotland*

⁴*Cairngorms Connect*

⁵*Endangered Landscapes and Seascapes Programme*

The natural world is threatened by species loss, yet the evidence to document it is spatially coarse, taxonomically incomplete, observationally biased, and debated, reflecting the complexities of biodiversity monitoring and the limitations of current approaches to quantifying the changing state of nature. Thus, bending the curve of species loss and habitat degradation needs not only ambitious restoration efforts but monitoring tools that align with the scale of the challenge. In this project, we showcase the potential of DNA metabarcoding to address gaps in current monitoring frameworks by implementing it in a landscape under restoration, with an emphasis on soil health. Specifically, we test the effects of a common restoration practice, ungulate control, by comparing below-ground communities of fungi, invertebrates, and bacteria at sites that had ungulate carrion 1 year and 2 years before sampling against a control >10 m away. We find a diverse below-ground community with >5,000 taxa. However, up to two thirds of identified taxa remain undescribed, especially in prokaryote groups. We also find significant differences in species richness between treatments, with increased diversity of bacteria at carrion sites but only in some groups of invertebrates (e.g., bacterivorous nematodes) and fungi (e.g., Agaromycetes). These results highlight the value of DNA-based methods to revolutionise monitoring schemes and understand below-ground processes supporting biodiversity, while it outlines the limitations derived from incomplete reference databases.

Keywords: eDNA, metabarcoding, soil, biodiversity

Session D1b

Themed session 7: Environmental sequencing for biodiversity research

Thursday, 14.55-15.45, Room L304

Session chairs: Sten Anslan and Brendan Furneaux

Wind is a primary driver of fungal dispersal across a mainland-island system

Domenica Naranjo Orrico, Jenna Purhonen, Brendan Furneaux, Otso Ovaskainen, Nerea Abrego

University of Jyväskylä

Dispersal is one of the main processes shaping ecological communities, but how it influences the distribution of fungi remains poorly understood. While spore size and trophic guild have been suggested as key traits affecting fungal dispersal abilities, empirical evidence on how these traits influence community-level distributions is lacking. In this study, we model air-borne fungal communities in a Finnish mainland-island system to evaluate how fungal communities change across a connectivity gradient depend on spore size, fungal guild, and the rarity of the species. The study includes 71 sites on an 18 x 18 km semi-regular grid, including sites on mainland, islands, and on top of the water, where cyclone samplers collected air-borne fungal spores. We found that the probability of occurrence of most species (and consequently species richness) decreased in low-connectivity sites (water and island) compared to high-connectivity sites. Yet, when windspeed increased, the probability of occurrence of fungi in the air increased especially in water and island sites. While the rarity of the species did not affect the spatial distributions of the species along the connectivity gradient, the community-weighted sexual spore sizes were smaller in low connectivity sites, and some fungal guilds (e.g., ectomycorrhizal fungi and wood saprotrophs) were more impacted by isolation than others. Overall, this study demonstrates that fungi can be dispersal limited already at small spatial scales, but fungal dispersal distance depends on windspeed. Likewise, our study supports that small spores reach longer dispersal distances and that different trophic groups vary in their dispersal abilities.

Keywords: fungal dispersal, windspeed, community ecology, fungal diaspores

Drivers of marine eukaryotic biodiversity along the Danish coasts

Eva Egelyng Sigsgaard¹, Karoline Bruun Degn¹, Marcelo de Paula Avila¹, Sune Agersnap¹, Marc Zoega Sandal Jørgensen¹, Mads Reinholdt Jensen¹, Adrià Antich², Owen Wangensteen³, Derek Corcoran¹, Pil Birkefeldt Møller Pedersen¹, Anders Jespersen¹, Emil Sloth Thomassen¹, Mary S. Wisz⁴, Jacob Carstensen¹, Henrik Glenner⁵, Søren Rysgaard¹, Peter Rask Møller⁶, Philip Francis Thomsen¹

¹*Aarhus University*

²*Centre for Advanced Studies of Blanes*

³*University of Tromsø*

⁴*World Maritime University*

⁵*University of Bergen*

⁶*University of Copenhagen*

Marine biodiversity is threatened by human activities and coastal areas in particular harbour vulnerable ecosystems. However, these ecosystems are often less studied than open waters, due to difficulties in sampling. Additionally, only a limited number of marine organisms are normally included in monitoring programs. Denmark has >8,000 km of coastline, which spans a strong east-west salinity gradient. This makes Denmark optimal for investigating drivers of coastal biodiversity patterns. **Methods:** We conducted an extensive national-scale sampling of >1,000 water and sediment samples along the Danish coast together with measurements of relevant environmental variables. We then analysed samples using tree-of-life eDNA metabarcoding for investigating general patterns of coastal biodiversity. **Results:** We find salinity to be the main factor explaining the variation in eukaryotic richness and community composition between sampling sites. This was true across water and sediment samples and across metabarcodes, with salinity often leading to increases and rarely to decreases in richness for the individual eukaryote taxa. However, the relative importance of environmental variables for richness varied greatly between taxa, and the majority of the variation in richness remained unexplained. **Conclusions:** Our project shows the importance of salinity in structuring entire coastal eukaryotic communities, and demonstrates the usefulness of eDNA metabarcoding for marine ecology. Perspectives and challenges in our project constitute important lessons for future large scale eDNA research.

Keywords: biodiversity, macroecology & biogeography, microbial ecology, molecular ecology

Bacterial networks in soils along environmental gradients

Jesse Jorna¹, Sonia Kéfi², Byron Adams³

¹*University of Jyväskylä*

²*ISEM*

³*Brigham Young University*

Facilitative interactions are widespread in natural systems, and the Stress Gradient Hypothesis predicts that these interactions increase in proportion to environmental stress. In bacterial soil systems remains investigations of the SGH remain rare. The structure of co-occurrence networks can elucidate the importance of facilitative interactions and give insight into the changes to interaction strength and type because of environmental stress. Here, we compare bacterial co-occurrence networks in three drylands: Arctic tundra on Victoria Island, CA, the McMurdo Dry Valleys of Antarctica and the Jornada Experimental Range in the Chihuahuan Desert, NM, USA. Whole soil communities are characterized by 16S metabarcoding inventories and resulting co-occurrence networks are combined with environmental null models and spatial data to describe the relative proportion of positive interactions across a holistic gradient of environmental stress in the form of water limitation, elevation and vegetation cover. Broadly, community alpha diversity remained similar, but beta diversity was distinct between the investigated stress levels. Though positive associations were much more dominant than negative ones (75-95% of all inferred interaction), we found no correlation between environmental stress and community interaction types. In some sites, the effects of habitat filtering or dispersal were stronger than biotic interaction, but this was not general to any of the investigated ecosystems or stress levels. These results do not provide general evidence for the SGH in natural bacterial communities and highlight the difficulties in describing interactions and inferring environmental stress at the scale relevant for microbial life.

Keywords: soil bacteria, facilitation, stress-gradient hypothesis, co-occurrence networks, ecological theory

Fungal transport via bird vectors revealed using environmental DNA metabarcoding and microscopy

Niko Johansson^{1,2}, Ulla Kaasalainen¹, Jouko Rikkinen^{1,2}

¹*Finnish Museum of Natural History*

²*University of Helsinki*

Birds appear as intuitive dispersal vectors for various plants, fungi, algae and other organisms, but concrete evidence of bird-mediated transfer of biological material is scarce for most taxa. This is especially true for biota producing microscopic propagules, such as fungi. To investigate which taxa can be associated with bird vectors, we used a dual approach of light microscopy and environmental DNA metabarcoding to identify biological material present in bird feathers and feet. Firstly, fresh preserved bird specimens from the Finnish Museum of Natural History were screened with light microscopy. Secondly, swabs of live birds sampled during bird ringing were analyzed using environmental DNA metabarcoding targeting fungal taxa. Based on both surveys, a diverse set of transported organisms were identified. Using microscopy, most common recovered propagules were fungal spores, lichen symbiotic dispersal units and bryophyte fragments. The eDNA survey identified diverse taxa with multiple ecologies and lifestyles, including wood-decaying fungi, saprotrophic and mycorrhizal fungi, plant and animal pathogenic fungi and lichenized fungi. The structure of the detected fungal assemblage reflects the habitat preferences of the bird transporting them. Our results identify a large and diverse pool of species for which birds may function as a dispersal vector. For many taxa, this is the first evidence of their potential interaction with birds. Birds could be especially important in the dispersal of specialist taxa, providing directed transport to suitable microsites for establishment, or as strong fliers contribute to long-distance dispersal events.

Keywords: dispersal, environmental DNA, species interactions, fungi, birds

From larva to adult – following microbiota patterns across mosquito populations in Greenland

Diana Laura Rojas Guerrero¹, Viktor Gårdman², Tomas Roslin², Piotr Łukasik¹

¹Jagiellonian University

²Swedish University of Agricultural Sciences

Microbial symbionts play a crucial role in the biology of many insects, offering insights into host ecology and evolution. In the case of mosquitoes, symbionts such as *Wolbachia* may be able to control and manipulate host populations. On the other hand, other mosquito species, such as adult *Ochlerotatus* spp. from Greenland, may have low-abundance and highly variable microbiota, suggesting that they do not rely on specific symbionts for survival. Thus, we hypothesized that they may have more consistent microbial associations during their aquatic pre-adult stage. In this study, we investigate how the microbiota composition changes across the life stages of *Ochlerotatus* mosquitoes. We do this using high-throughput sequencing of insect, bacterial and fungal marker gene amplicons, in parallel with a microbial amplicon quantitative approach, across a large collection of wild-caught larvae, pupae, and adult mosquitoes sampled systematically from four regions of Greenland. Further, using a reference collection of aquatic invertebrates – larval and adult stages – inhabiting the same environments as *Ochlerotatus* and comparing microbial composition among species and life stages, we aim to further understand the significance of the microbiota for the development and survival of *Ochlerotatus* mosquitoes in Greenland. Our results will provide valuable insights into the diversity, distribution, and dynamics of the microbiome within species across Greenland. This will allow us to understand how these mosquitoes cope with rapidly changing environmental conditions and contribute to a broader understanding of the ecological and evolutionary significance of microbial associations.

Keywords: environmental, sequencing, biodiversity, symbiosis

Session D2a

Ecophysiology

Thursday, 13.45-14.45, Room L139C

Session chair: TBA

Fungicides and heatwaves: impacts on a key freshwater detritivore

Akshay Mohan¹, Blake Matthews², Katja Räsänen¹

¹*University of Jyväskylä*

²*Swiss Federal Institute of Aquatic Science and Technology*

As freshwater ecosystems face increasing threats from chemical pollutants and climate change, understanding the combined impact of fungicides and rising temperatures on aquatic species is crucial. In this study, we examine how *Asellus aquaticus*, a keystone detritivore, responds to both fungicide exposure and thermal stress. In a three-phase experiment, we first exposed individual isopods to fungicides at 17°C for three weeks, followed by a one-week heatwave period at 22°C, and concluded with a three-week recovery phase at 17°C. We measured growth, feeding, pigmentation, survival, and fecal pellet production—key indicators of the species' role in nutrient cycling. Preliminary results show that fungicide exposure, particularly in combination with heat stress, significantly slows growth and reduces feeding efficiency, impairing the organism's ability to process detritus. The three-phase design helps in distinguishing immediate stress responses from long-term effects and evaluating the potential for recovery after the removal of stressors. The results could provide valuable insights on managing multiple stressors in freshwater habitats, particularly for species crucial to nutrient cycling.

Keywords: fungicides, heat stress, freshwater ecosystems, detritivores, nutrient cycling

Poison frog behaviour and physiology vary across a deforestation gradient in a biodiversity hotspot

Bibiana Rojas¹, Mileidy Betancourth Cundar², Virginie Canoine³

¹*University of Veterinary Medicine Vienna*

²*University of Los Andes*

³*University of Vienna*

In a planet undergoing constant and accelerated transformation of its natural ecosystems, it is crucial to understand not only how organisms are affected by the changing environment, but also how they can adapt, or not, to the new conditions. As reliable indicators of ecosystem health, amphibians are an excellent model to study human-induced environmental impact. Among them, poison frogs (Dendrobatidae) stand out by their aposematic phenotype, diurnal habits and complex social behaviours, which involve high degrees of territoriality and elaborate parental care. We investigated the impact of habitat alteration on the morphology, physiology and behaviour of the Devil's poison frog, *Oophaga sylvatica*, a nearly threatened species whose habitat is currently subject to alarming rates of deforestation. We collected data on body condition, glucocorticoid (GC) concentration, perch use, vocal activity and male aggressive response in three populations across a gradient from low to high degrees of deforestation, and predicted that, in comparison to frogs from pristine sites, individuals from disturbed environments would (1) use lower perches and have (2) lower body condition; (3) higher amounts of GC (cortisol and corticosterone); (4) lower vocal activity and (5) a more pronounced aggressive response. In line with our predictions, we found individuals from disturbed environments to have a lower body condition and to use lower perches than individuals from pristine environments, but the levels of GC did not differ significantly among populations. We discuss the implications of these results in relation to communication processes, adaptation to modified environments and the conservation of the species.

Keywords: glucocorticoids, tropical rainforest, agonistic behaviour

Egg turning behaviour in common eider and common goldeneye: the association to thyroid hormone, ambient and egg temperature

Farshad S. Vakili¹, Scott Shaffer², Pentti Runko³, Bertille Mohring⁴, Amalie Ask¹, Markus Öst⁵, Kimm Jaatinen⁶, Bin-Yan Hsu¹, Titiksha Peetumber¹, Nora M. Wilson³, Céline Arzel¹

¹University of Turku

²San Jose State University

³No affiliation

⁴University of Liverpool

⁵Åbo Academy

⁶The Finnish Environment Institute

Reproduction is the most vulnerable stage in vertebrates, posing immediate risks to parents and developing embryos. Environmental stressors can disrupt the reproductive success by interacting with hormonal-behavioural pathways. In many avian species, turning the eggs during incubation is essential for embryo development. Little is known about the egg turning behaviour in waterbirds during incubation and its link to environmental factors and the physiological state of individuals. In 2022 and 2023, we utilized logger technology embedded in artificial eggs, to evaluate the egg turning behaviour of common eider (*Somateria mollissima*) and common goldeneye (*Bucephala clangula*) during incubation in relation to hormonal levels related to energetic consumption, as well as ambient and egg temperature. Our model revealed that, among thyroid hormones, T4 was associated with higher rate of average hourly turning rate in common goldeneye. In contrast, a significant negative relationship was observed between average egg temperature and turning rate in goldeneye females, while eiders showed a positive association between the average hourly egg turn and egg temperature. Additionally, ambient temperature positively influenced turning frequency in common goldeneye. In both species, clutch size negatively affected the average turning rate frequency by female. Our study provides unprecedented insight into the egg turning behaviour of waterbirds and is the first to highlight an association between thyroid hormones and egg turning behaviour. Different turning responses of incubating females to egg temperature may reflect species-specific nesting habitat and incubation biology. Complementary results will be presented at the OIKIS conference, 2024.

Keywords: incubation, egg turning, behaviour, waterbirds

Neophobia in a changing world: does metal pollution affect the birds physiological and behavioral response to novelty?

Lisandrina Mari¹, Lea Hipolite¹, Michal Šulc², Suvi Ruuskanen¹

¹*University of Jyväskylä*

²*Czech Academy of Sciences*

Neophobia, the fear of novelty, has important implications for decision-making in response to novel habitats, foraging opportunities, or predator cues. Both the environment and an individual's physiological response to stress (e.g., glucocorticoids release) can influence their reaction to novelty. However, we have little knowledge on how environmental stressors can influence the interplay between neophobic responses and physiology. Here, we exposed captive male Japanese quails (*Coturnix japonica*) to an ecologically relevant dose of lead. We evaluated neophobia towards a novel object and novel food items, tonic immobility (a measure of fearfulness), and measured plasma and fecal corticosterone concentrations prior to, during, and up to 40 days after exposure. We expected corticosterone levels to be higher in lead-exposed birds, especially early during exposure, compared to non-exposed birds. Considering that lead possesses neurotoxic properties, we expected the ability of lead-exposed birds to categorize fearful stimuli to be impaired, hence they should exhibit lower neophobia levels. Lastly, we expected neophobia to be more repeatable in non-exposed birds. Our results (currently being analyzed) will bring important insights into how metal pollution affects the physiological and behavioral mechanisms behind the birds' response to novelty, an essential trait to their adaptability to a changing world.

Keywords: bird, pollution, behavior, fear, hormones

Life in an asphyxiating world: the different responses of two stickleback populations exposed to hypoxia over multiple generations

Ludovic Toisoul, Alycia Valvandrin, Luisa Bermejo Albacete, Katja Anttila, Amélie Crespel

University of Turku

The frequency of climate change-induced hypoxic events (i.e. decrease in dissolved oxygen levels in water) is increasing at an unprecedented rate. Enclosed ecosystems are particularly vulnerable as hypoxia cannot be avoided and organisms need to cope with chronic hypoxia effect to avoid extinction. When exposed to short-term hypoxia, fish can quickly adjust their phenotype, through direct plasticity, and when the environment is similar across generations, intergenerational plasticity can also occur. If the stressor becomes persistent, adaptation can happen. Therefore, more studies are needed to better understand the responses of fish to multigenerational hypoxia. To investigate this, two populations of *Gasterosteus aculeatus* were collected from two streams, one exposed to hypoxia for a decade and one not. Two generations were created within each population and each generation of offspring were exposed to normoxia (100% dissolved oxygen, DO), or fluctuating hypoxia (night 30% DO and day 100% DO), resulting in eight groups reflecting direct plasticity, intergenerational plasticity (when matching parental environment), and adaptation between the populations. We measured different fitness-related traits such as the fish social and risk-taking behavior, their metabolic rate (standard metabolic rate), and hypoxia tolerance. When directly exposed, fish will reduce their social and risk-taking behavior with no change in metabolic rate. However, fish exposed to multiple generations maintain active social and risk-taking behavior while decreasing their SMR. This study showed that fish might cope to multigenerational hypoxia through direct plasticity of their behavior at first and then through modulation of their metabolism over multiple generations.

Keywords: hypoxia, ecophysiology, phenotypic plasticity, intergenerational plasticity, adaptation

Session D2b

Ecophysiology

Thursday, 14.55-15.45, Room L139C

Session chair: TBA

Understanding the current and future consequences of seasonal changes on damselflies thermal tolerance

Md Tangigul Haque¹, Shatabdi Paul¹, Md Kawsar Khan², Marie E Herberstein¹

¹Macquarie University

²Freie Universität Berlin

An animal's response to climate warming is predominantly governed by its thermal tolerance. Seasonal variation in climate may influence insect thermal tolerance across spatio-temporal scales, which is crucial for predicting the capacity to adapt to the rapidly changing climate. Here, we aim to assess the changes in thermal breadth (the difference between the critical thermal maximum (CTmax) and critical thermal minimum (CTmin)) and estimates thermal safety margin using *Ischnura heterosticta* and *Xanthagrion erythroneurum* damselflies across different seasons. We used dynamic ramping methods, and measured CTmax and CTmin individually to calculate population specific thermal breadth. For both species, we found a narrow thermal breadth during summer which gradually wide as temperature decreases in autumn and spring. CTmax and CTmin increased with monthly temperature for both species, however, rainfall had no impact on damselflies thermal tolerance. Our results highlight the seasonal plasticity of both species in response to climatic variations, suggesting that phenotypic plasticity of thermal tolerance might provide a degree of resilience to rapidly changing climate.

Keywords: climate change, thermal tolerance, insects, seasonal change, phenotypic plasticity

Early-life adversity modulates growth trajectories and mitochondrial metabolism in king penguin chicks

Nina Cossin-Sevrin¹, Katja Anttila¹, Mathilde Lejeune², Céline Bocquet², Maëlle Fusillier², Thomas Faulmann², Camille Lemmonnier², Natacha Garcin³, Pierre Bize⁴, Jean-Patrice Robin², Suvi Ruuskanen⁵, Vincent A Viblanc²

¹*University of Turku*

²*Université de Strasbourg*

³*Université Claude Bernard Lyon1*

⁴*Swiss Ornithological Institute*

⁵*University of Jyväskylä*

In many avian species, variation in breeding phenology has been shown to impact reproductive success. In king penguins, the onset of egg-laying is biphasic with early breeders laying around December and late breeders around February. Because of their reduced growth period, late-born chicks are smaller, with survival chances drastically reduced compared to early-born chicks, but the physiological determinants explaining such variation remain unclear. Variation in metabolic rate is one important pathway driving differences in growth patterns, as it is directly involved both in energy allocation processes and fitness. The conversion of resources into energy occurs in mitochondria, and the efficiency of this conversion is likely to play a fundamental role in explaining individual heterogeneity in growth and survival. The purposes of this study were to investigate the differences in red blood cell mitochondrial metabolism between early- and late-born king penguin chicks and to assess whether morphometric phenotypes could be explained by differences in mitochondrial metabolism. At similar ages and during winter, late-chicks expressed higher mitochondrial metabolism compared to early-chicks, probably linked to the stress related to winter environmental conditions and a decrease in parental feeding rates. We did not find a clear association between chick mitochondrial metabolism and growth patterns, suggesting that mostly environmental conditions contributed in explaining different metabolic phenotypes. As king penguin populations in Crozet may face lower breeding success in relation to global changes, studying the physiological traits and adaptations underlying the chick growth and survival may help understanding the response of king penguins facing challenging conditions.

Keywords: ecophysiology, molecular ecology, cellular metabolism, breeding success, phenology

Endocrine disrupting contaminants in Finnish breeding waterbirds

Céline Arzel¹, Veerle L.B. Jaspers², Amalie Ask¹, Anne-Fleur Brand², Silje Peterson², Sajjad (Farshad) Vakili Shahrabaki¹, Prescillia Lemesle³, Sunniva Frøyland²

¹*University of Turku*

²*Norwegian University of Science and Technology*

³*Centre of Biological Studies of Chizé*

Human and wildlife populations worldwide are exposed to contaminants released by human activities. Among these, endocrine-disrupting chemicals (EDCs) are of growing concern in aquatic environments. EDCs are found in various pollutant classes, including pesticides, dioxins and furans, polychlorinated biphenyls, per- and polyfluoroalkyl substances (PFAS), phthalates and bisphenols, brominated flame retardants, and trace metals/metalloids. These chemicals impact ecosystems extensively, ultimately affecting humans and raising increasing concern. The DISRUPT project, funded by the Research Council of Finland, aims to investigate EDCs of emerging concern. We identified a cocktail of contaminants in breeding female waterbirds in Finland and in their eggs confirming maternal transfer. We discuss the implications of these findings at both individual and population levels.

Keywords: ecotoxicology, common eider, common goldeneye, baltic sea, wetlands

Effect of environmental alterations on the selective feeding and fatty acid retention of freshwater pearl mussel

Mahsa Hajisafarali, Marco L. Calderini, Mikko Kiljunen, Niklas Moser, Sabrina Nykänen, Jaakko Litmanen, Sami Taipale, Jouni Taskinen

University of Jyväskylä

Land use activities within a catchment can increase nutrient loads in rivers, consequently, affecting the quantity and quality of food sources for filter feeders. Freshwater pearl mussel (*Margaritifera margaritifera*, FPM) is a critically endangered keystone species, found in oligotrophic headwater rivers. Essential fatty acids are important biomolecules that consumers usually need to obtain from their diet, as the body cannot synthesize them. Therefore, dietary intake is essential for maintaining overall health. As a result, we analyzed the fatty acid compositions in the stomach of FPM and their diet (seston) to investigate how anthropogenic pressures in catchments affect their availability and retention. Environmental factors (26 in total), that reflect anthropogenic activities, such as chlorophyll-a, nutrients concentrations, intensity of forestry activities, the extent of ditched areas, the size of conservation areas, and latitude were assessed. The fatty acid compositions and content in seston were compared to the ingested fatty acids in stomach content of FPM. Anthropogenic activities increased the availability and contribution of phytoplankton fatty acids to FPM diets, but terrestrial contribution declined. Moreover, by comparing fatty acid from seston and stomach content, we found that FPM selectively fed on phytoplankton. Additionally, rivers with less anthropogenic activities showed reduction in contribution of phytoplankton fatty acids but greater reliance on bacterial sources. FPM actively retained physiologically essential fatty acids, indicating a high dietary reliance on these fatty acids. Our findings revealed that filter-feeder mussels may rely on essential dietary fatty acids and anthropogenic activities can modify how these nutrients are retained.

Keywords: accumulation index, catchment characteristics, climate change, fatty acids, land use

Session D3a

Themed session 5: Experimental community ecology

Thursday, 13.45-14.45, Room L302

Session chairs: Paulina Arancibia and Nerea Abrego

Experiments in community ecology across time: a look into the last three decades of experimental research

Paulina Arancibia, Nerea Abrego, Otso Ovaskainen

University of Jyväskylä

The complexity of assembly processes makes it challenging to disentangle their roles from observational data. As repeatedly claimed in the community ecology literature, experimental manipulations offer a powerful tool to disentangle the mechanisms underlying community dynamics, and consequently link empirical to theoretical research in community ecology. However, the cost and often elaborate logistics of community-level experiments can restrict their scope and/or scale of inquiry. Thus, despite the clear advantages experiments offer for addressing topical questions in community ecology, experiments may often not be the first choice for empirical ecologists. In this review, we took a deep look into the “evolution” of experiments in community ecology over the last three decades. We found that although studies in community ecology increased over time, those explicitly mentioning experiments have decreased in the last 30 years. The close linkage between experiments and ecological theory remains strong, as well as the interest in testing questions regarding changes in community structure. The experimental approaches used continue to be very context-dependent, but field experiments are still the most frequent. Although terrestrial ecosystems remain the most represented, there has been a shift away from experiments in marine ecosystems and an increased interest in below-ground communities, which can be attributable to the massification of molecular methods. The main challenges moving forward seem to be related to increasing the scale of experiments—both temporally and spatially—which can be achieved by incorporating new technologies both in the data collection and data processing, as well as encouraging collaboration among research groups.

Keywords: community ecology, experiments, review

Components of soil biodiversity respond differently to taxonomic and functional plant diversity in agricultural soils

Paula Thitz¹, Luiz Domeignoz-Horta², Rashmi Shrestha¹, Seraina Cappelli³, Emy Guibault¹, Stephanie Gerin⁴, Mikko Tiusanen⁵, Sampsa Malmberg⁶, Juha Mikola⁷, Elina Numminen¹, Jussi Heinonsalo¹, Marleena Hagner⁷, Anna-Liisa Laine¹

¹*University of Helsinki*

²*INRAE AgroParisTect Palaiseau*

³*University of Minnesota*

⁴*Finnish Meteorological Institute*

⁵*ETH Zürich*

⁶*Metsähallitus*

⁷*Natural Resources Institute*

Agriculture drives biodiversity loss. Monoculture farming in particular strongly filters local species pools, thereby limiting potential biotic interactions. Increasing vegetation diversity in agroecosystems promotes more diverse interactions between plants and heterotrophs, and earlier studies show major impacts on ecosystem functioning with even small increases in vegetation diversity. To investigate how vegetation diversity affects the heterotroph communities in grain monocultures, we sampled fauna and microbes from a field experiment where 1–8 undersown cover crops were grown with barley at different diversity levels (1, 2, 4, and 8 co-occurring species). We use joint species distribution models accounting for phylogeny to test for the effects of richness or identity of crops, their functional traits (N₂-fixation or root architecture) or environmental covariates (plant aboveground biomass, soil N, microclimate or particle size) on heterotroph communities. We determine which community (above- or belowground invertebrates, root and soil fungi or bacteria) responds most strongly to undersown diversity, which aspect of diversity (species or functional richness vs. specific species or functions) has the strongest effect on communities, and identify which species respond positively or negatively to vegetation diversity. Our preliminary results suggest that cover crop composition shapes heterotroph communities, and that N₂-fixing and deep-rooted undersown affect especially soil faunal and bacterial communities, respectively. Overall, taxonomic groups respond differently to different aspects of plant diversity.

Keywords: biodiversity, community ecology, microbial ecology, sustainability

The effects of brownification on benthic diatom communities in boreal streams

Aino Juutinen¹, Jussi Jyväsjärvi², Virpi Pajunen³, Maria Rajakallio⁴, Timo Muotka⁴, Jukka Aroviita¹, Ari Huusko, Kaisa-Riikka Mustonen⁴, Kaisa-Leena Huttunen¹

¹*Finnish Environment Institute*

²*ELY-centre*

³*Aalto University*

⁴*University of Oulu*

⁵*Natural Resources Institute Finland*

Brownification is currently one of the main environmental concerns of northern freshwaters. In brownification increased humic substances, dissolved organic carbon and iron are decreasing water transparency and changing the water color. The mechanisms behind browning are complex, but it seems to be accelerated by land-use actions, especially forest drainage. The changes in light environment by decreased water transparency is expected to influence benthic primary producers, in rivers mainly epilithic algae, which are dependent on light. Here we combined data from field surveys in northern Finland and an mesocosm experiment to study the effects of brownification on diatom communities. The field survey showed that diatom community composition was mainly affected by water pH, but water color and nutrient availability were important as well. As changes in these key variables may be intertwined in forestry actions, we conducted an mesocosm experiment concentrating on the role of light environment by manipulating water color while keeping the water chemistry otherwise similar. The diatom communities differed significantly between the three brownification treatments brownification increasing the occurrence of low profile and planktic species. In addition, it decreased alfa diversity (Shannon). The results from the experiment combined with the field survey data underline the individual importance of water color as a factor that is part of the ecological changes occurring in freshwaters under brownification trend. As epilithic diatoms are the key primary producers in lotic ecosystems further effects in the food webs can be expected.

Keywords: biodiversity, algae, forestry, freshwaters, DOC

Greater vulnerability of lowland communities to extreme heat events across seasons

Gerard Martínez De León¹, Ludovico Formenti¹, Jörg-Alfred Salamon², Madhav P. Thakur¹

¹*University of Bern*

²*University of Veterinary Medicine Hannover*

Ecological responses to climate extremes vary drastically in different spatiotemporal contexts. The seasonal timing could be a major factor influencing community responses, but its importance is likely to vary across geographic gradients, such as at different elevations. Here, we tested how soil communities at high- and low-elevation sites respond to extreme heat events at different seasons (spring, summer and autumn). We simulated one-week heat events based on site-specific climatic history in a laboratory experiment using field-collected soil cores, and measured the resistance and recovery of two major groups of soil biota: Collembola and fungi. We found that collembolan communities from low elevations were most sensitive to extreme heat in spring and summer, with complete recovery only occurring in spring. Although fungal communities generally remained stable, pathogens increased and saprotrophs declined following extreme heat. Association networks of Collembola and fungi increased their connectance in high elevation communities exposed to autumn extreme heat events, suggesting a greater dependence of Collembola species on their fungal resources. Our findings highlight that extreme heat events can restructure ecological communities mainly in lowlands, followed by seasonal-dependent recovery.

Interactive effects of heat waves and drought on grassland plants across seasons

Nicolò Tartini, Itzel Lopez, Yu Sun, Ludovico Formenti, Gerard Martínez-De León, Nicholas Ofiti, Hang Zhao, Madhav P. Thakur

University of Bern

Climate extremes are becoming more frequent and severe, dramatically affecting plant communities. The effects of such extremes are likely to be more severe on native plant communities than on invasive species. Moreover, within native plant communities, different life strategies of plants (e.g., slow versus fast growth rates) may show variable responses to climate extremes. Yet, we lack studies under realistic settings aiming to understand the interactive effects of climate extremes like drought and heat waves on plant communities. Using an outdoor mesocosm experiment, we address this research gap by investigating the performance of grassland communities consisting of four slow and four fast-growing native plants and an invasive plant species. We expect that the interactive effects of drought and warming will be most severe on plants when drought is applied. We hypothesize that the invasive species will suffer the least, whereas fast-growing plants will suffer the most due to the interactive effects of warming and drought. Our results indeed confirm that the invasive plant *Solidago canadensis* suffers least from the interactive effects of warming and drought. Moreover, we observe a general trend where slow-growing species appear more resistant to drought and warming than fast-growing ones. We aim to use trait-based approaches to examine the underlying mechanisms for variable plant responses to warming and drought.

Session D3b

Life-history traits

Thursday, 14.55-15.45, Room L302

Session chair: TBA

Juvenile and total reproductive values for sexual reproduction under any genetic system

Petri Rautiala, Jussi Lehtonen

University of Jyväskylä

Reproductive value (RV) is the expected contribution of genes by an individual or class of individuals to the gene pool in the distant future, and it plays a crucial role in understanding adaptation in long-term evolution. Class RVs are linked to the genetic system and to life history: for diploid genetics, Grafen derived expressions for relative RVs of female and male juveniles, and for the absolute RVs of all females and of all males. Subsequently, Gardner presented a derivation for relative RVs of juvenile females and males under haplodiploidy. We have generalised these results to any genetic system for biparental sexual reproduction, such that RV is explicitly linked to parameters of the genetic system and life history. The earlier results by Grafen and Gardner arise as special cases. We have also derived expressions for absolute juvenile and total reproductive values of both sexes under any genetic system.

Keywords: reproductive value, kin selection, theory, evolutionary ecology

Thermal plasticity of seed germination traits in European flora

Laura Pietikäinen¹, Anniina Mattila¹, Maria Hällfors², Susanna Koivusaari¹, Mari Miranto¹, Øystein Opedal³, Annisa Satyanti⁴, Marko Hyvärinen¹

¹*Finnish Museum of Natural History*

²*Finnish Environment Institute*

³*University of Lund*

⁴*Australian National University*

Biodiversity is under threat because of climate change and other human-induced pressures. Our ability to predict how species will adapt to endure the rapid environmental change is limited, because the extent of phenotypic plasticity of most species and traits is poorly known. Thermal plasticity has been found to covary with the climatic variation experienced by species and populations. A deeper insight into how this varies within and between species can enhance our predictions regarding the impact of climate change on population viability across species' ranges. We hypothesized that widespread species and populations at range edges have greater thermal plasticity compared to narrowly distributed species and core populations. To test this, we examined germination responses of 300 edge and core populations from 30 widely and narrowly distributed European plant species under different thermal conditions. Our findings revealed that seed mass, together with distribution area and extent, strongly influenced the thermal response. In narrowly distributed species and core populations heavier seeds were associated with a higher germination percentage, an effect that was more pronounced under warmer temperatures. Given that seed mass, largely determined by maternal genetic and environmental effects, may play a key role in plant adaptation to climate change, and that different types of populations and species show varied germination responses in interaction with seed mass, these findings highlight the importance of geographic representation in seed collection and broader plant conservation efforts in a changing climate.

Keywords: phenotypic plasticity, adaptation

Overcoming the constraints of low sample sizes to study the growth and longevity of the endangered freshwater pearl mussel

Sabrina Nykänen, Jouni Taskinen, Mahsa Hajisafarali, Anna Kuparinen

University of Jyväskylä

Information on key life-history traits, such as growth and age, is crucial to effectively conserve imperilled freshwater mussel species. However, traditionally growth and age studies require large sample sizes covering all age classes, which can pose risks to populations of conservation concern. To avoid destructive sampling and to overcome the constraints of low sample sizes ($n = 1\text{--}6$ per population), we applied retrospective shell growth at age reconstructions to 98 critically endangered freshwater pearl mussel (FPM) individuals from 34 populations across Finland and Sweden. We also compared the performance of six different growth models using the reconstructed size-at-age data across FPM juvenile and adult life stages. The growth reconstruction model showed reasonable skill in reconstructing FPM growth patterns. The von Bertalanffy model served as a good general descriptor of growth for FPM, but it systematically underestimated the asymptotic size. The power law model was the most accurate in estimating juvenile growth. FPM exhibited great variability in longevity (54–254 years) and growth constant ($0.018\text{--}0.057 \text{ year}^{-1}$) within our study area. Our results demonstrate that reasonable growth estimates can be obtained even with extremely limited sample sizes. The results can be further applied to gain knowledge on the population's age structure, size at maturation, and recovery potential. The methodology used in our study is applicable also to other freshwater mussel species of conservation concern. Our approach provides a valuable alternative to destructive sampling, allowing researchers to gain insights into mussel life-history traits while minimizing risks to vulnerable populations.

Keywords: life history, back calculation, *Bivalvia*, endangered species, growth models

Phytoplankton thermal performance determines the distinction of their life strategies

Patch Thongthaisong, Sabine Wollrab

Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB)

Life strategies of phytoplankton can be defined using three quantities: maximum growth rate (μ), carrying capacity (K) and minimum required resource (R), relative to others in the community. These quantities are modulated by temperature, where phytoplankton groups (e.g. diatom, chrysophyte, cyanobacteria, and chlorophyte) exert different thermal performance curves, affecting the three quantities. Here, we mathematically derived predictions on shifts in life strategies along a temperature gradient from 4 to 35°C, based on empirically derived thermal performance curves. We differentiated three size classes per phytoplankton group and contrasted oligo- from eutrophic environments. Our results suggest that below 10 to above 30°C, diatoms shift from the combination of high μ and R (typical for a copiotroph strategy known from bacteria) to only high R, while cyanobacteria shift from high K (K-strategy) to high $\mu_{\max}$ (r-strategy). Between 10 and 30°C, we found that cyanobacteria, chrysophytes and chlorophytes can have positive μ -K correlation (r-K trade-up), instead of the typically assumed r-K trade-off. Above 30°C, the four groups express distinctive strategies: high values of μ (cyanobacteria), K (chrysophytes), R (diatoms), and intermediate μ and R^* but low K (chlorophytes). Our results further indicate that in general strategies (via its impact on the respective quantities) of larger sized cells are more sensitive to changes in environmental N:P and strategies of cyanobacteria express high N:P sensitiveness below 20°C. Our theoretical results provide an explanation for the fact that cyanobacteria can thrive both under cold and very warm conditions and provide a helpful framework for predictions on shifts in life strategies and correspondingly species performance with global warming.

Keywords: phytoplankton, life strategies, r/K selection, biodiversity, competition

Impact of light pollution on reproduction in the threespine stickleback

Sini Bäckroos, Ulrika Candolin

University of Helsinki

The use of artificial light at night is rapidly growing around the world. Research has so far focused on effects on terrestrial ecosystems, but aquatic ecosystems - and especially coastal ecosystems – are also increasingly affected. The purpose of this project is to assess the effects that artificial light at night, ALAN, has on the reproductive success of a key species of the Baltic Sea, the threespine stickleback (*Gasterosteus aculeatus*). The species regulates the abundance of a range of other species, through its consumption of herbivores (which in turn influences the algal biomass) and by serving as prey for piscivorous fishes and birds. Thus, changes in the population dynamics and distribution of the stickleback could have far reaching consequences for the ecosystem. By altering light conditions during the night, using white and yellow LEDs, we are investigating the impact that ALAN has on reproductive maturation and behaviour in the stickleback. We are further assessing how changes in these behaviours and physiological states influence reproductive success, as well as the consequences ALAN has for the hatching success and viability of the offspring. The initial results from the experiments will be presented.

Keywords: behavioral ecology, sexual selection or reproduction

Session D4a

Themed session 1a: Forest management

Thursday, 13.45-14.45, Room L303

Session chair: Rémi Duflot, María Triviño and Jérémy Cours

Enhancing resilience of boreal forests through management under global change: A review

María Triviño¹, Mária Potterf², Julián Tijerín³, Paloma Ruiz-Benito³, Daniel Burgas¹, Kyle Eyvindson⁴, Clemens Blattert⁵, Mikko Mönkkönen¹, Rémi Duflot¹

¹*University of Jyväskylä*

²*Technical University of Munich*

³*University of Alcalá*

⁴*Norwegian University of Life Sciences*

⁵*Swiss Federal Institute WSL*

Boreal forests provide a wide range of ecosystem services that are important to society. The boreal biome is experiencing the highest rates of warming on the planet and increasing demand for forest products. Climate change and its associated extreme events (e.g., windstorms) put at risk the capacity of these forests to continue providing ecosystem services. Thus, enhancing forest resilience recently gained a lot of interest from theoretical perspective. Yet, it remains unclear how to translate the theoretical knowledge into practice and how to operationalize boreal forest management to maintain forest ecosystem services and functions under changing global conditions. In this study, we review the concept of resilience in forest sciences, how extreme events may put boreal forests at risk, and how management can alleviate such risks or make them more severe. We identify and summarize the main management approaches (natural disturbance emulation, landscape functional zoning, functional complex network, and climate-smart forestry) that can promote forest resilience. We further analyze the role of forest management to increase forest resilience to the combined effects of climate change and extreme events. We found that the combined effects of increased temperatures and extreme events are having negative impacts on forests. Then, we discuss how the main management approaches could enhance forest resilience and multifunctionality (simultaneous provision of high levels of multiple ecosystem services and species habitats). Finally, we identify the complementary strengths of individual approaches and report challenges and opportunities on how to implement them in practice.

Keywords: adaptive management, biodiversity, disturbances, silviculture

Future of forest management in Finland: implications for biodiversity

Ekaterina Shorokhova¹, Matti Koivula¹, Leena Hamberg¹, Tomi Heilala², Aku Korhonen¹, Aija Kukkala², Ville Pietilä¹, Pekka Punttila², Hannu Salminen¹, Juha Siitonen¹, Kimmo Syrjänen², Ilkka Vanha-Majamaa¹

¹*Natural Resources Institute Finland (Luke)*

²*Finnish Environment Institute (Syke)*

The assessments of threatened forest species and habitats indicate continuous decline of biodiversity in Finnish forests. The threatened forest-dwelling species are associated with such critical forest characteristics as the proportional area of old-growth and mixed forest stands, number of old trees, large trees, and deciduous trees, as well as the amount of deadwood. We use empirical data and theoretical estimates based on the species-area relationships and ecological thresholds to identify the minimum requirements for critical forest characteristics by vegetation sub-zones and site types in Fennoscandian boreal forests. Our specific objectives are to analyse: (1) current state of forest biodiversity, using reference data on structures and processes in old-growth forests along with evidence on species-resources relationships, (2) theoretically estimated and observed threshold values for the forest characteristics ('resources') particularly for red-listed species, and possible need to increase the amount of a resource in managed forests, (3) spatial targeting of closer-to-nature forest management using various methodological approaches and (4) review tools for safeguarding biodiversity in boreal managed forests. Finally, based on this assessment, we discuss the management implications and knowledge gaps to identify research needs.

Keywords: resilience, ecosystem functioning, nature-based solutions

Continued exploitation of high biodiversity value forest outside of protected areas in Finland

Pihla Kortessalmi¹, Ninni Mikkonen², Mária Potterf³, Jani Hohti¹, Rémi Duflot¹

¹*University of Jyväskylä*

²*Finnish Environment Institute*

³*Technical University of Munich*

In Finland, intensive forestry is the biggest threat for forest biodiversity. The degraded ecological state of Finnish forests is the result of even-aged management based on clear-cutting harvest. Our aim was to evaluate if the most valuable forests in terms of biodiversity conservation are still being lost due to recent harvesting activities. We compared the biodiversity values of harvesting sites to those of all forests, in the Finnish administrative regions. Additionally, we assessed the extent of harvesting and protection within the top 10% of forests with the highest biodiversity value. We used two complementary sources of harvesting data: the Global Forest Change data, showing annual loss of forest cover based on Landsat satellite images, and forest use notifications, compulsory administrative declarations for forestry operations. The biodiversity value of forests was based on the national map of high biodiversity value forests. Our findings indicate that the biodiversity values of harvesting sites increase from north to south and were slightly higher than the average biodiversity values of all forests, in all regions. A significant proportion of the 10% most valuable forests is already under protection, demonstrating that conservation efforts are targeting the right areas and is efficient. Our results show that harvesting target all forests outside of protected areas irrespective of their biodiversity value. Assessing the extent of harvest in valuable forests is crucial for evaluating the success of current conservation practices and planning future measures. This information is vital for ensuring the continued protection and preservation of high biodiversity forests.

Keywords: forest conservation, forest management, clear-cutting, Global Forest Change

Impact of EU biodiversity strategy on forest habitat quality in Europe

Anna Repo¹, Pekka Lauri², Mykola Gusti², Melissa Chapman³, Nicklas Forsell², Piero Visconti², Martin Jung², Fulvio Di Fulvio²

¹*Natural Resources Institute Finland (Luke)*

²*International Institute of Applied Systems Analysis IIASA*

³*National Centre for Ecological Analysis and Synthesis NCEAS*

The EU Biodiversity Strategy (EUBDS) aims to protect and restore ecosystems to halt biodiversity loss. While the expansion of protected areas is essential to achieve these goals, it may lead to increased forest use outside protected areas to meet the demand for timber production potentially undermining biodiversity conservation efforts. Previous studies have identified priority areas for protected area expansion and shown the effects of increased forest protection on future harvests and the bioeconomy. However, the effects of EUBDS on forests outside protected areas have received less attention. We use the integrated species distribution modelling (iSDM) approach, GLOBIOM-forest, a global forest sector model and the Global Forest Model (G4M) to assess how different forest protection area allocations under the EUBDS affect key biodiversity-supporting structures, such as forest age and deadwood, across Europe. We investigate i) how the expansion of protected areas under the EU Biodiversity Strategy (EUBDS) affects the structural features important for biodiversity inside and outside protected forests in Europe, and ii) whether this development is consistent with the objectives of the EUBDS. We find that the success of the EUBDS in improving forest habitat quality largely depends on the allocation of protected areas and the management practices applied. We highlight that increased protection may intensify forest use outside protected areas leading to a decline in structural attributes critical for biodiversity. This study provides important insights into the trade-offs involved in forest management under the EUBDS and assesses its effectiveness in moving forests from poor to good ecological condition.

Keywords: forest policy, modelling, habitat quality, conservation

Trade-offs between timber production and forest grouse occupancy at multiple spatial scales in the boreal production forests

Adriano Mazziotta¹, Reijo Mykkänen¹, Annika Kangas¹, Jukka Forsman¹, Andreas Lindén¹, Kyle Eyvindson²

¹*Natural Resources Institute Finland (Luke)*

²*Norwegian University of Life Sciences (NMBU)*

Forest management affects viability of biodiversity causing alterations to habitat quality. Sustainable forest management aims to find win-win solutions for economy and biodiversity, ensuring that timber flow is maintained while minimizing degradation of forest characteristics affecting habitat quality. As forest-dwelling species are related to different forest characteristics at different spatial scales, the impact of forest management on their habitat can also vary. In this context, the aim of our study was evaluating whether the trade-offs between timber production and habitat availability varies across species with different habitat requirements and spatial scales. We simulated and optimized three boreal production landscapes in Finland interested by a gradient of management intensities with MELA2.0 forest simulation package. We compiled production possibility frontiers to reveal the trade-off between the forest economic (Net Present Value of timber) and ecological value (grouse occupancy). Occupancy for four forest grouse species (hazel grouse, black grouse, capercaillie and willow grouse) was modeled using nationwide wildlife triangle census data with variables related to forest structure and composition at local (stand), home-range (1-km) and regional (5-km) scales. We show that the trade-offs between timber production and forest grouse occupancy are species- and scale-specific. A decrease in the economic value of the landscape mildly increased the landscape occupancy of all the grouse species. Our research demonstrates that the evaluation of the trade-offs between timber harvesting and species occupancy at multiple spatial scales can better inform forest managers about the species' potential use of the landscape and help target management at the relevant scale.

Keywords: spatial scale, species distribution models, optimization, ecosystem services

Session D4b

Themed session 1b: Human-wildlife interactions

Thursday, 14.55-15.45, Room L303

Session chair: Rémi Duflot, María Triviño and Jérémy Cours

Relieving human-wildlife conflicts may result in unwanted negative consequences for other species

Jukka Forsman¹, Tuomas Seimola¹, Maria Honkaniemi², Mikko Jokinen¹, Markus Piha¹

¹Natural Resource Institute Finland

²University of Oulu

Protection of the barnacle geese (*Branta leucopsis*) is one of the success stories of nature conservation. Its population size has increased from about 40 000 up to 1.5 M individuals since 1980's. Now, the Arctic breeding barnacle goose population stage or over-winter in western Europe, including SE Finland, and cause substantial damage in the fields that has inflicted severe human-wildlife conflict. Accommodation fields – safe havens for geese to rest and forage, and no-go fields – where geese are repelled – are used to relieve the conflict. However, it is not known how they affect breeding birds. Accommodation fields attract large number of geese that may tramp nests, while repelling may disturb breeding birds. We examined this by monitoring and tagging 186 lapwing (*Vanellus vanellus*) and 26 curlew (*Numenius arquata*) nests in SE Finland with thermometers that provided estimates about nesting success and source of the failure. We found that predation caused highest (59%) nest mortality, particularly due to nocturnal mammalian predators, while farming activities had smaller impact (22%). The density of the barnacle geese had a negative impact on the offspring production, while repelling activities did not have an effect. In contrast, the significant interaction between geese density and repelling intensity suggests that repelling decreases the negative effects of geese on the offspring production of waders. Our results suggest that the breeding bird diversity should be considered in the placement of both accommodation and repelling fields and that human disturbance may provide protection for breeding waders against crowding effect of super-abundant geese.

Keywords: human-wildlife conflict, nature conservation, species interactions, offspring production

Exploring genetic and environmental factors affecting trehalose digestion in Finnish mushroom consumers

Cristina Ottocento¹, Tapio Nevalainen², Mikko Hurme², Johanna Mappes¹

¹*University of Helsinki*

²*University of Tampere*

Mushrooms are highly valued in diverse diets worldwide, with increasing awareness of their health benefits driving global consumption. However, some individuals experience gastrointestinal symptoms after eating edible mushrooms, possibly due to the low activity of trehalase, the enzyme needed to digest trehalose. Finland's natural landscape contains hundreds of edible mushroom species, and wild mushroom foraging, supported by the cultural tradition of everyman's right, is widely practiced. This study aimed to (1) assess genetic variation in the trehalase gene within the Finnish population to evaluate potential links to gastrointestinal symptoms, and (2) analyze trehalose concentrations in Finnish mushrooms from the genera *Albatrellus*, *Boletus*, and *Leccinum*. Genotyping results revealed that genotypes associated with low trehalase activity are rare in the Finnish population, and no significant association was found between trehalase gene variants and mushroom consumption, suggesting that genetic variation in trehalase alone may not explain reported symptoms. Additionally, although trehalose concentration did not vary significantly by latitude or longitude, it differed notably between genera, with *Albatrellus* mushrooms displaying distinct levels of trehalose compared to *Boletus* and *Leccinum*. While not statistically significant, humidity and maggot presence appeared to influence trehalose levels. These findings suggest that factors beyond genetics and trehalose concentration may contribute to gastrointestinal symptoms related to mushroom consumption.

Keywords: mushrooms, trehalose

Climate associated changes in overwintering populations of widely hunted waterbirds in the EU: Implications for sustainable harvest strategies

Jon Brommer¹, Elie Galet²

¹*University of Turku*

²*Tour du Valat*

Harvest of waterbirds is of cultural and economic importance to local communities. Here we focus on 12 species of waterbirds that are huntable in all 27 European Union (EU) member states, and use winter counts from 1993-2020 (174,392 surveys collected at 18,872 sites) to model their wintering population growth rate in 50kmx50km grid cells covering the EU. Waterbirds typically show a northward temporal shift of their wintering distribution. If climate change is an important driver of this shift, we expect population growth at grid cells that historically represent a relatively cold thermal environment for the species, but declining populations at grid cells that are relatively warm. We used temperature measures over 1970-2000 to compute the Thermal Niche Position (TNP) of each grid cell by relating average temperature of the grid cell to the distribution of average temperatures over the species' wintering range. We find a strong negative correlation between winter population growth rate and TNP for 7 of the 12 species, suggesting climate change is an important driver for their local winter population dynamics. We use EU member-state level data on hunting bags to qualitatively consider the association between hunting pressure and expected winter population growth rate to illustrate how harvest pressure for some species may be substantial in regions where the climatic conditions are not favorable in terms of winter population growth rate. Our work illustrates how developing sustainable long-term harvest strategies may benefit from considering consequences of climate change for local population dynamics.

Keywords: macro-ecology, range shift, climate change, hunting, EU policy

Defining what matters in Finnish state-owned forest management: A stakeholder-driven approach to shaping future optimization models

Bekir Afsar¹, Johanna Silvennoinen¹, Kyle Eyvindson², Kaisa Miettinen¹, Otso Ovaskainen¹

¹*University of Jyväskylä*

²*Norwegian University of Life Sciences*

Finland's state-owned forests are essential for timber production, biodiversity conservation, and recreation, leading to decisions where different objectives often conflict. Multiobjective optimization can help navigate these trade-offs, but its effectiveness depends on accurate problem formulation, which requires a clear understanding of what stakeholders value most. Existing literature on multiobjective forest management often assumes that problems are well-defined from the outset, leaving the crucial structuring phase underexplored. This study focuses on the preparatory steps for creating a multiobjective optimization model by engaging with stakeholders involved in Finnish state-owned forest management. Through interviews and qualitative thematic analysis, we identify the key components — objectives, decision variables, and constraints — needed for future multiobjective optimization models. By emphasizing stakeholder engagement in problem structuring, this research lays a strong foundation for building a multiobjective optimization model that accurately reflects real-world perspectives relevant to public Finnish forests. Our findings contribute to the forest management domain by demonstrating a replicable approach for identifying key model components through stakeholder inputs. This work underscores the importance of problem structuring in complex decision-making contexts, offering a framework for aligning optimization models with stakeholder values in public forest management. Actively engaging stakeholders in problem structuring has revealed a broader range of perspectives for forest management than typically utilized, which can improve biodiversity outcomes.

Keywords: problem structuring, forest planning, identifying objectives, stakeholder interviews

Sustainable management of social-ecological systems: Insights into the importance of resource users

Laura Tuominen

University of Turku

In my interdisciplinary doctoral research, I investigated the ecologically and socially sustainable management of natural resources. I focused particularly on the lowest level of the management system, i.e. the users of natural resources in two different socio-ecological systems: urban gardening in the city of Turku and moose (*Alces alces*) hunting nationwide in Finland. My results suggest that an in-depth knowledge of social dynamics at the local level can significantly impact the sustainable management of natural resources. The sustainable and functional management of the natural resources in my case studies can benefit people and nature in many ways, as they both produce extensive ecosystem services and increase well-being in many ways. My research brings new information about the connection between social and ecological sustainability and confirms that it is complex and context-dependent. My results emphasize that sustainability must be understood and measured with several different metrics and that social sustainability must include more than just economic aspects. My research brings several practical applications to both urban gardening and hunting, about how the activities can be improved, their benefits increased and sustainability promoted. In summary, I can state that the social significance of resource management was emphasized in all my case studies. In achieving high social and ecological results, high social capital, i.e. trust, communication, and face-to-face meetings are particularly important. The Social-Ecological Systems framework and systems thinking applied in my research can improve our possibilities for the necessary sustainability transformations and the interdisciplinary efforts needed for them.

Session D5

Microbiome research

Thursday, 13.45-14.45, Room L209

Session chair: TBA

Microbial symbiosis in Auchenorrhyncha: Effects of geographical isolation and host biology on microbiome diversity

Veronika Andriienko, Kamil Tylek, Adam Stroiński, Małgorzata Sekuła, Jakko Chmura, Piotr Łukasik, Anna Michalik

Jagiellonian University

Geographic isolation and host biology are thought to influence microbiome diversity in insect populations. However, their effects remain understudied in Auchenorrhyncha - a diverse clade, that includes planthoppers, leafhoppers, spittlebugs, and cicadas, that relies heavily on microbial symbiosis to overcome the nutritional limitations of a plant sap diet. These mutualistic relationships represent a critical evolutionary adaptation that has driven their ecological diversification over millions of years. In our study, we assessed the impact of geographical isolation and host sex on microbiome composition across more than 50 populations of Auchenorrhyncha species from Baltic islands (Gotland, Öland, Bornholm) and mainland Northern Europe. Using next-generation amplicon sequencing, we observed significant interspecies microbiome variability. Sex-based differences were also evident, with higher microbiota abundance in females observed in specific species. Additionally, we identified patterns suggesting independent acquisition of new symbionts in isolated populations, highlighting potential adaptive responses to geographic constraints. These findings advance our understanding of how microbial symbioses evolve in isolated populations, providing new insights into the ecological and evolutionary forces shaping microbiome diversity and stability in insects. The research was supported by Polish National Science Center grant no. 2021/41/B/NZ8/04526

Keywords: microbial ecology, evolutionary ecology, adaptation or evolution, macroecology and biogeography, species interactions

Unveiling the impacts of pollution on the bird microbiota across Europe

Lydia Leino¹, Rute Costa², Geert Eens³, Marcel Eens³, Caroline Isaksson⁴, Pere Puigbò¹, Miia Rainio¹, Pablo Sanchez Virosta⁵, Peter Scheys³, Eero Vesterinen¹, Michal Vinkler⁶, Antonio Zamora⁷, Jose Manuel Zamora Marin⁷, Ann-Kathrin Ziegler⁴, Tapio Eeva¹

¹*University of Turku*

²*University of Aveiro*

³*University of Antwerp*

⁴*Lund University*

⁵*Norwegian University of Science and Technology*

⁶*Charles University*

⁷*University of Murcia*

Environmental pollution significantly shapes the community structures of environmental microbiomes. Host-associated microbiota, largely derived from the environment, plays a crucial role e.g., in digestion and immune system development, and acts as the first barrier against toxins in the gut. Thus, pollution-related disruptions in the normal microbiota can adversely affect the host. Despite globally declining bird populations, these mechanisms remain understudied in wild birds. This study examines the impact of pollution and urbanization on the gut bacteria of a common model species, the great tit (*Parus major*), across six European locations: Finland, Sweden, Belgium, Czechia, Portugal, and Spain. Fecal samples from nestlings in both industrial/urban and rural reference areas were analyzed for metal pollutants (e.g., Cu, Ni, As, Pb, Cd, Zn, Al) and bacterial 16S rRNA. Preliminary findings suggest that while the bird gut microbiota was relatively stable across countries regarding the dominant phyla, urban/industrial areas tended to show higher proportions of Firmicutes and lower proportions of Proteobacteria. Notably, the microbial communities in Finland, Sweden, and Spain differed from each other and other locations, while the rest of the locations were more similar. Bacterial groups such as Rhizobiales, Sphingomonadales, and Burkholderiales were positively correlated with fledging, some of them also exhibiting negative correlations with metals such as nickel, aluminum, and zinc – highlighting the complex interactions between pollution and bird health. This research provides insights into the levels of wildlife's exposure to metal pollution in urban and industrial areas across Europe and emphasizes the potential consequences of microbiota alterations for wild birds.

Keywords: microbial ecology, urban ecology, metal pollution, bird microbiota

Climate warming and dietary shifts impacts lizard's gut microbiome

Emma Fromm, Julien Cote, Lucie Zinger

Center for Research on Biodiversity and the Environment (CNRS)

The gut microbiome is now a well-established major driver of its host metabolic, physiological, and behavioral functions. Understanding its response to climate change is hence a pressing challenge, especially in ectotherms. Several studies have shown that climate warming decreases the gut microbial diversity and elevates ectotherm hosts' metabolic and food consumption rates. However, we still do not know whether such responses result from warming-induced changes in the quantity, quality and composition of available resources or changes of the host's consumption rates or prey selection behavior. Here, we experimentally test the long-term effects of climate warming and warming-induced dietary changes on the common lizard' (*Zootoca vivipara*) gut microbiota. To this end, we relied on a semi-natural experimental setup that allows manipulating climatic conditions and monitoring over six experimental years the prey populations, the lizard's the gut microbiota, as well as lizards diet through isotopic signature of both lizard's and prey's populations to estimate the contribution of invertebrate predators, detritivores and herbivores in lizards' diet. We found that climate and diet have interactive effects on lizard's gut microbial diversity in adults. In warmer climates, lizards consume more invertebrate predators than in colder climates, which is associated with greater gut microbial diversity. Moreover, dietary specialization and climate conditions are intertwined factors inducing compositional dissimilarity in gut communities. Our results illustrate the importance of direct and indirect effects of climate change on host-microbe interactions with potential consequences for host physiology and behaviour.

Keywords: microbial ecology, community ecology, climate change, species interactions

Gut microbiota of insular rodents: Testing the island biogeography theory

Ilze Brila¹, Yingying X. G. Wang², Anni Hämäläinen¹, Tapio Mappes¹, Phillip Watts¹, Eva Kallio¹

¹University of Jyväskylä

²One Health Institute

The gut microbiota provides its host with many important services and is an essential part of the host's physiology and health, making understanding the determinants of gut microbiota composition crucial. The effects of the host's local environment, for example, the host's diet, exposure to pollution or contact with conspecifics are well-known. Yet, whether the gut microbiota of hosts exhibits large-scale biogeographical patterns is uncertain. In this study, we examine whether the theory of island biogeography can explain the diversity of gut microbiota of insular rodents. We captured 336 wild bank voles (*Clethrionomys glareolus*) from 22 islands in the Porvoo archipelago in southern Finland across two years (2019–2020) and analyzed their gut bacterial communities using 16S rRNA gene amplicon sequencing. Using the core principles of the theory of island biogeography, we hypothesize that (1) larger island area will be associated with higher α -diversity and β -diversity of the gut microbiota, while (2) higher island isolation will be associated with lower α -diversity and β -diversity. Though the area of an island was not associated with variation in the gut microbiota of bank voles, the increased distance to the mainland was associated with lower mean α -diversity, but higher variation of α -diversity and mean β -diversity. Our findings suggest that certain principles of island biogeography could indeed be extended to host-associated microbial communities of wild rodents.

Keywords: gut microbiota, theory of island biogeography, microbial macroecology, host-associated microorganisms

The effects of climate change and host population dynamic on the microbial community associated with a butterfly across a 30-year period

Linyang Sun, Natalie van Dis, Marjo Saastamoinen, Johan Ekroos, Anne Duplouy

University of Helsinki

Gut microbial communities play a key role in the fitness of their hosts. They can however be susceptible to changes in the host environment, with drastic consequences for their host. The lasting effect of disturbances, such as temperature changes, and their indirect effects through changes in the host population dynamics, on the host associated microbial communities however often remains unclear. In this study, we investigate three decades of changes in the bacterial community associated with diapausing caterpillars of the Glanville fritillary butterfly, *Melitaea cinxia*, from the Åland Islands in the Baltic Sea. We hypothesize that a) climate warming in Åland leads to changes in the structure of microbial communities, by affecting thermos-sensitive bacterial species; and b) drastic host population crash will select for particular microbial profile due to bottlenecks. To explore this, we will use amplicon sequencing of the 16S rRNA gene to get the profiling of bacteria and assess the relationship between microbial community and butterfly population dynamic and local temperature. This study aims to reveal how climate warming and host population dynamics jointly influence changes in the composition, functional diversity, and adaptive responses of host-associated microbial communities. This will provide crucial insights into the dynamics of host microbial communities under environmental pressures.

Keywords: climate change, gut microbiota, *Melitaea cinxia*, extreme events

The effect of prey toxins on the predator gut microbiome and foraging behaviour

Liisa Hämäläinen¹, Gabrielle Davidson², Charlotte Davies¹, Phillip Watts¹, Suvi Ruuskanen¹

¹University of Jyväskylä

²University of East Anglia

Aposematism is a widespread antipredator defence where prey advertise their chemical defence with warning signals. Previous work has demonstrated high within-species variation in how quickly predators learn to avoid aposematic prey, and this heterogeneity among predators is suggested to play an important role in the evolution of prey defences. Here, we aimed to investigate what maintains the observed variation in predator behaviour by focusing on an unexplored mechanism: a predator's gut microbiome. Evidence from humans and laboratory animals shows that gut microbiome can influence learning, memory and foraging choices (the microbiome-gut-brain axis), and theoretical models predict feedback loops between gut microbiome, diet and host behaviour. We investigated this in the predator-prey context using wild great tits (*Parus major*) as predators. We first manipulated birds' diet with i) prey chemical defences (pyrrolizidine alkaloids), ii) antibiotics (known to alter the gut microbe community), or iii) water (control), and quantified gut microbial compositions from faecal samples using 16S rRNA sequencing. To investigate whether changes in the gut microbiome were associated with foraging behaviour, we conducted behavioural experiments that tested birds' avoidance learning and dietary wariness which are important cognitive processes influencing predation pressure on aposematic prey. In my talk, I will present preliminary results from the experiment, which suggest that the diet manipulation influenced birds' behaviour. Overall, our study will address the current knowledge gaps in the predator-prey field by providing insights into the mechanisms that underly variation in predator behaviour.

Keywords: predator-prey interactions, species interactions, behavioural ecology, microbial ecology

Session E1a

Restoration

Thursday, 17.00-18.10, Room L303

Session chair: TBA

Can restoration counteract biotic homogenization? A long-term study of boreal peatland butterflies

Merja Elo¹, Jenni Niku², Norbertas Noreika³, Otso Ovaskainen², Pekka Punttila¹, Anssi Vähätalo², Leo Vähätalo², Janne S. Kotiaho²

¹*Finnish Environment Institute (Syke)*

²*University of Jyväskylä*

³*Estonian University of Life Sciences*

Biotic homogenization is expected to accelerate due to land-use change and climate change. To counteract this, restoration should benefit especially specialist species. However, restored sites may lack specialists, and hence it has been suggested to even contribute to biotic homogenization. Here, we report results from a long-term before-after control-impact experiment on restoration of forestry-drained boreal peatlands in Finland. We use Bayesian joint species distribution modeling (Hierarchical Modeling of Species Communities; HMSC) to study (i) whether generalist and mire specialist butterfly species respond to restoration differently 9-19 years after restoration, (ii) does the species' response depend on its association to temperature, and (iii) what is the consequent effect of restoration on butterfly community composition. We show that five out of nine specialist species responded positively to restoration. By contrast, generalists responded both positively and negatively. During the study period, many *Boloria* species (including both specialists and generalists) declined, while especially warm-dwelling generalists increased. Overall, butterfly community composition in restored sites changed towards those in pristine control sites. Yet, the effect was variable, and in some cases the community composition in pristine sites merely tended to change towards those in restored and drained sites. Hence, restoration benefits specialists, but it may not enough to fully counteract the effect of on-going land-use change and climate change to biotic homogenization.

Keywords: biotic homogenization, butterflies, joint species distribution modeling, peatland, restoration

Mapping uncharted territories: Investigating cryptic interactions of cryptic species to understand recovery of reforested tropical ecosystems

Coen Westerduin^{1,6}, Sille Holm², Geoffrey Malinga³, Saskia Wutke¹, Ryosuke Nakadai⁴, Jaakko Pohjoismäki¹, Ilari Sääksjärvi⁵, Anu Valtonen¹

¹*University of Eastern Finland*

²*University of Tartu*

³*Gulu University*

⁴*Yokohama National University*

⁵*University of Turku*

⁶*University of Oulu*

Global forest cover has greatly diminished over the last century, with the last decades having seen especially and increasingly severe declines in tropical Africa. Even if active deforestation were to be halted, the lingering effects on impacted ecosystems may persist for prolonged periods of time. Bucking regional trends, reforestation efforts have been undertaken in Kibale National Park, Uganda, for almost 30 years. In this study, we investigated arthropod communities—specifically: lepidopteran larvae and parasitoids preying upon them—from sites across a restoration chronosequence from this area, in order to understand whether and how quickly the species and their food-web interactions would naturally recover, and resemble those of local primary forests. We combined DNA-based methods with morphospecies assignments and phylogenetic trait assessments to overcome the substantial obstacles posed by this study system: one which features poorly described species from taxonomically highly diverse tropical arthropod groups involved in usually obscure parasitoid-host interactions. Our findings highlight this diversity and complexity, while showcasing the possibilities and limitations regarding the use of molecular methods in studying scarcely described systems.

Keywords: food webs, molecular ecology, conservation and restoration

Modeling the impact of restoration and climate change on the potential habitats of red-listed peatland plant species

Priscillia Christiani¹, Aleksi Isoaho¹, Merja Elo^{2,3}, Lassi Pääkkilä⁴, Hannu Marttila⁴, Aleksi Räsänen¹

¹*Natural Resources Institute Finland (Luke)*

²*University of Jyväskylä*

³*Finnish Environment Institute (Syke)*

⁴*University of Oulu*

Peatlands are crucial ecosystems for biodiversity conservation and carbon storage, but largely degraded due to drainage and climate change. Ecological restoration is required to reverse the degradation trend, yet limited research has addressed whether restoration can safeguard the presence of red-listed species under future climate conditions. Therefore, we investigate the potential impacts of restoration efforts and future climate change on habitat suitability for 28 red-listed peatland plant species in Finland. We utilized Maxent modeling approach with predictors representing drainage conditions, climate, and other environmental factors. We modeled four restoration scenarios (0%, 30%, 50%, and 100% of drained peatlands restored) under three climate change projections (RCP2.6, RCP4.5, RCP8.5) for the periods 2040-2069 and 2070-2099. Our models showed high predictive performance for the species habitat suitability (mean AUC = 0.892), with drainage and climate variables being the most important predictors. Restoration generally increased suitable habitat area across climate scenarios, but its effectiveness varied among species and climate projections. Species responses to climate change were diverse, with potential range expansions for some species and habitat loss for others. Under severe warming scenarios, many red list species were predicted to experience declining suitable habitats. The effectiveness of restoration declined under the most extreme climate projection (RCP8.5), especially for 2070-2099, indicating potential limits to restoration as a climate change adaptation strategy for many red list species. Therefore, protecting remaining suitable habitats for these species should be the highest priority, followed by restoration of degraded sites, while simultaneously working towards reducing greenhouse gas emissions to minimize future climate impacts.

Keywords: biodiversity, climate change, restoration

Highways as barriers: Restoring connectivity for natural gene flow

Ira Topličanec¹, Rok Černe², Urša Fležar³, Teodora Sin⁴, Jakub Kubala⁵, Tomislav Gomerčič¹, Magda Sindičić¹, Miha Krofel³

¹*University of Zagreb*

²*Slovenia Forest Service*

³*University of Ljubljana*

⁴*Association for the Conservation of Biological Diversity*

⁵*Technical University in Zvolen*

To save the Dinaric lynx population from extinction, 18 lynx were translocated from the Carpathians to the southeastern Alps and Dinaric Mountains over a five-year period within the LIFE Lynx project (2019-2023). This strategy aimed to reinforce the existing Dinaric population, mitigate inbreeding, and establish a stepping stone population in the southeastern Alps to reconnect the Alpine and Dinaric lynx populations. However, monitoring of five lynx with telemetry collars in the Slovenian Dinarics, both before and during the reinforcement process, confirmed that the A1 Ljubljana – Koper highway is a major barrier to lynx movement from the Dinarics toward the Alps. The remnant female Lojzka had a home range clearly bounded by the highway which she never managed to cross, while Puhi, a subadult male in dispersal, turned back upon encountering it. During the reinforcement process, the translocated adult male lynx Maks reached the highway 18 days post-release but was stopped south of the highway after multiple failed crossing attempts, which likely affected his settlement behavior. He eventually crossed the highway four months later and moved towards the southeastern Alps. Conversely, two other translocated adult males, Doru and Catalin, reached the highway but did not cross it. This poor connectivity additionally threatens the lynx population already struggling with inbreeding. To counteract this, it is crucial to create and maintain functional linkages between remnant populations. Conservation efforts should focus on enhancing habitat networks, such as constructing wildlife passes, to facilitate natural gene flow and support a viable lynx population in the Dinarics.

Keywords: movement, *Lynx lynx*, telemetry collars, dispersal

The role of sediment characteristics for *Chara tomentosa* in shallow, sheltered bays in Åland

Irma Puttonen, Henna Raitanen, Sonja Salovius-Laurén

Åbo Akademi University

Charophytes, belonging to freshwater green algae, give rise to important habitats in shallow, sheltered areas of the Baltic Sea. They bind carbon and nutrients, and as they attach to their substrate, they trap and bind sediment, preventing the resuspension and turbidity of the water. Charophytes may constrain phytoplankton growth and clarify the water by taking up nutrients. They form valuable habitats, providing food, shelter and reproduction ground for diverse benthic communities and fish. Charophyte abundances have declined in the Baltic Sea due to eutrophication. Charophytes are sensitive to water turbidity and are used as eutrophication indicators. Sheltered charophyte meadows are included in the Nature Conservation Act in Finland as a priority habitat type. Knowledge of the species' environmental requirements is fundamental for making the right management decisions to aid the species' survival and to achieve successful restoration and conservation. Charophytes anchor to their substrate by root-like rhizoids. Although they take up nutrients directly from the water, they may also use their rhizoids for nutrient uptake. Charophytes are closely related and reminiscent of vascular plants. Hence, we assume that they interact with their substrate. We hypothesised that the sediment properties define the *C. tomentosa* distribution. We studied sediments and pore water related to *Chara tomentosa*, a charophyte species occurring in soft seafloor substrates in shallow sheltered bays in Åland. The results show a narrower range in sediment chemistry for *C. tomentosa* sediments than in the sites without charophytes. Sediment properties need to be considered when planning charophyte restoration into new areas.

Keywords: Baltic Sea, Charophyta, restoration, priority habitat, sediment

The effect of river channel modification on benthic microbial diversity and aquatic ecosystem resilience

Virpi Pajunen

Aalto University

Fluvial ecosystems and the biodiversity within are threatened by the multiple stressors stemming from human actions. Rivers may be dammed or affected by the nutrient and sediment loads from non-point sources. The goal of river restorations or wetland constructions is to restore ecological integrity to rivers and manage the anthropogenic loads by using Nature-based Solutions. Fostering aquatic biodiversity is vital as the global change is more likely to be buffered by ecologically diverse and functionally intact fluvial systems. This project seeks a novel understanding of the effects of river channel modification on aquatic microbial diversity and ecosystem resilience by monitoring two dam removal and three wetland construction sites in Finland. The study aims 1) to investigate the effects of river modification on the composition, diversity, function and resilience of benthic microbial communities, 2) to identify the key drivers of microbial communities, diversity and ecosystem functions from physical and chemical factors, 3) to disentangle the effect of habitat suitability for benthic microbial communities prior and after the modification using hydro- and morphodynamic and physical habitat modelling, and 4) to evaluate the restoration success by estimating the ecological status of the rivers by using the diatom-based index and test the suitability of existing bioindicator indices for river restoration evaluation. This study adds to the aquatic research, which seeks science-based justifications for Nature-based Solutions for environmental protection and restoration purposes, as it disentangles the effects of river channel modifications on ecosystem resilience from microbial perspective.

Keywords: biodiversity, ecosystem processes or function, microbial ecology, restoration ecology

Session E1b

Temporal community dynamics

Thursday, 18.20-19.00, Room L303

Session chair: TBA

Cross-taxa analysis of long-term data reveals a positive biodiversity-stability relationship with taxon-specific mechanistic underpinning

Arthur Rodrigues¹, Tuuli Rissanen¹, Mirkka Jones², Ida-Maria Huikkonen³, Otso Huitu⁴, Erkki Korpimäki⁵, Mikko Kuussaari³, Aleksi Lehikoinen⁶, Andreas Lindén⁴, Hannu Pietiäinen¹, Juha Pöyry³, Pasi Sihvonen⁶, Anna Suuronen³, Kristiina Vuorio³, Marjo Saastamoinen¹, Jarno Vanhatalo¹, Anna-Liisa Laine¹

¹*University of Helsinki*

²*Aalto University*

³*Finnish Environment Institute (Syke)*

⁴*Natural Resources Institute Finland (Luke)*

⁵*University of Turku*

⁶*Finnish Museum of Natural History*

Anthropogenic environmental change is altering biodiversity at unprecedented rates, threatening the stability of ecosystem services on which humans depend. However, most of what is known about biodiversity-stability relationships comes from experimental studies making extrapolation to real ecosystems difficult. Here, we ask whether the shape and underlying mechanisms of the biodiversity-stability relationship vary among taxa in real-world communities. Our study harnesses the power of six terrestrial and aquatic long-term monitoring datasets, encompassing entire assemblages at hundreds of georeferenced sites providing 20 years long community measurements, covering a 1200 km latitudinal gradient across Finland. In general, we detect a positive relationship between species richness and stability. Structural equation modeling reveals that this relationship is modified by functional trait community composition, with specific mechanisms varying among the taxa. Our study is among the first to highlight the importance of functional traits in elucidating both general and taxon-specific impacts of biodiversity on community stability.

Keywords: community ecology, functional traits, ecosystem processes or function, biodiversity

The succession of lichens on standing deadwood based on a multi-century chronosequence

Aleksi Nirhamo, Pemelyn Santos, Mariina Günther, Jari Kouki, Tuomas Aakala

University of Eastern Finland

Deadwood has an important role in forest ecosystems by providing habitat for a myriad of species. Lichens growing on the surface of deadwood are a distinctive part of the biotic communities of deadwood, especially on standing dead trees (i.e., snags). We studied lichen communities on Scots pine (*Pinus sylvestris*) snags in Fennoscandian old-growth forests, and assessed how lichen communities on snags are driven by substrate age. Here, substrate age refers to the time the snag has remained standing after its death, which was determined with dendrochronological methods. Our data comprises a chronosequence of several centuries. Lichen species richness increased during the first 60–70 years of the chronosequence, after which it stabilized. Species composition continued to change throughout the chronosequence, although the rate of species turnover decelerated toward late succession. Several species, including ones that are known to occur only on deadwood, were found exclusively on high-longevity snags. Our results show the special significance of high-longevity snags for lichen diversity, underlining the importance of not only deadwood quantity, but also its quality. This type of deadwood has become exceedingly rare due to widespread commercial forestry, and current evidence implies that it is not generated in managed forests at all. Thus, the conservation of lichens on deadwood entails significant challenges in managed forest landscapes.

Keywords: community ecology, biodiversity, management of natural resources, old-growth forests, deadwood

Spatio-temporal patterns of benthic biodiversity in a stream network – headwaters as upholders of variation

Wille-Pekka Lepo¹, Timo Muotka¹, Venla Virtanen¹, Joel Nyberg¹, Kaisa-Leena Huttunen^{1,2}

¹*University of Oulu*

²*Finnish Environment Institute (Syke)*

The “small but mighty” headwaters often contribute disproportionately to network-scale benthic biodiversity as differences in community composition between separate headwater branches can be high; headwaters harbour high variation between local communities, even though their local (alpha) diversity may be quite low. In spatially isolated headwaters, environment is the main driver of community composition, whereas in mainstream dispersal rates are high and so called “mass effect” swamps any effects of local environmental factors on metacommunity structure. This stream network position (SNP) hypothesis has become a major framework in metacommunity dynamics of stream ecosystems. Temporal community variation, on the other hand, has not been studied extensively from the SNP perspective. In our study, we studied both spatial and temporal variation of benthic macroinvertebrate communities in boreal stream networks, at same time in the same area: we sampled five similar-size catchments in NE Finland, and one of them was also sampled annually from 2016 to 2020. We found that headwater and mainstem communities differed significantly from each other, both having strong indicator taxa. Headwater communities had higher environmental and biological variation between sampling sites (spatial beta diversity) and higher temporal community turnover between annual sampling occasions (temporal beta diversity) compared to their mainstem counterparts. However, we found strong “variation in variation” in headwater communities, some being exceptionally stable and some highly variable through time. Moreover, we found that the differences in environmental characteristics are the main driver of differences in communities in catchment scale.

Keywords: community ecology, freshwaters, beta diversity, macroinvertebrates

Session E2a

Macroecology and global change

Thursday, 17.00-18.00, Room L304

Session chair: TBA

Human pressure homogenises species and traits globally

Caio Graco-Roza¹, Mark Wong², Florian Altermatt³, Martin Gossner⁴

¹*University of Helsinki*

²*The University of Western Australia*

³*Swiss Federal Institute of Aquatic Science and Technology (EAWAG)*

⁴*Swiss Federal Institute for Forest*

Human pressures, particularly urbanisation and agricultural expansion, profoundly affect biodiversity by reshaping species and functional trait distributions, with critical consequences for ecosystem resilience and multifunctionality. Yet, the extent and strength of these impacts across diverse taxa and ecosystems remain poorly understood. Here, we analyse 160 spatial datasets, encompassing over 13,000 local communities and nine major taxa in freshwater and terrestrial ecosystems worldwide. Our results reveal that human pressure is the dominant driver of species and trait replacement, consistently outweighing the effects of climate and spatial distance. Despite observing a prevalence of biotic differentiation across landscapes, we reveal that the occurrence of biotic homogenisation is consistently linked to the dominant effects of human pressure. These homogenising effects are particularly pronounced in the trait composition of terrestrial communities and the species composition of freshwater communities, suggesting distinct mechanisms across realms. We find that rates of species and trait replacement increase rapidly along the human pressure gradient, especially between low and medium pressure, before they stabilise. Importantly, an exception occurs in urban landscapes, where species replacement increases exponentially. Although ecological communities generally exhibit species turnover along the human pressure gradient, we find that they are disproportionately homogenised in traits. While this provides resilience to environmental changes, it can delay the recognition of species collapse until key functional traits are lost, risking sudden ecosystem breakdown. Our findings underscore the urgent need for conservation strategies that prioritise the preservation of minimally impacted habitats to sustain ecosystem resilience and multifunctionality.

Keywords: community turnover, functional diversity, beta diversity, human footprint, global change

Impacts of climate change and forest management on thermal preference of boreal forest understory

Daniel Fernández García¹, Elina Kaarlejärvi¹, Jarno Vanhatalo¹, Anna-Liisa Laine¹, Andréa Davrinche¹, Raisa Mäkipää², Tiina Tonteri², Erik Welk³, Gunnar Seidler³, Jesse Kalwij⁴

¹*University of Helsinki*

²*Natural Resources Institute Finland (Luke)*

³*Martin-Luther-University Halle-Wittenberg*

⁴*University of Johannesburg*

Understanding how climate change and forest management jointly influence forest understory plant communities is crucial, as understory plays a key role in boreal biodiversity and ecosystem functioning. The Community Temperature Index (CTI) provides insights into the temperature preferences of species within these communities, serving as a valuable tool for assessing climate-induced community shifts. Here, using long-term plant monitoring data from 1985, 1995 and 2023, we assess changes in the community-weighted mean of CTI in understory communities. By analysing the influence of management history, and local climate trends, we disentangle the drivers of CTI changes in forest understory communities. Given the temporal stability of old forests, we anticipate that young forests will exhibit an increase in CTI values amplified by local warming. These results will shed light on the potential of forest management to accelerate or decelerate biodiversity change under changing climatic conditions.

Keywords: community ecology, climate change, forest management, thermal preference, boreal forests

A global comparison of stream diatom beta diversity on islands vs. continents across scales

Ramiro Martín-Devasa¹, Aurélien Jamoneau², Sophia Passy³, Juliette Tison-Rosebery², Saúl Blanco⁴, Alex Borrini⁵, Sébastien Boutry², William R. Budnick⁶, Marco Cantonati⁷, Adelaide Clode Valente⁸, Cristina Delgado⁹, Gerald Dörflinger¹⁰, Vítor Gonçalves¹¹, Jenny Jyrkänkallio-Mikkola¹, Bryan Kennedy¹², Julien Marquié², Helena Marques¹³, Virpi Pajunen¹, Anette Teittinen¹, Janne Soininen¹

¹*University of Helsinki*

²*INRAE*

³*University of Texas at Arlington*

⁴*University of León*

⁵*ERSE soc. coop. s.t.p. (Ecological Research and Services for the Environment)*

⁶*Michigan State University*

⁷*University of Bologna*

⁸*Secretaria Regional de Ambiente*

⁹*University of Vigo*

¹⁰*Water Development Department, Cyprus*

¹¹*University of the Azores*

¹²*Environmental Protection Agency, Ireland*

¹³*Centro de Investigação em Biodiversidade e Recursos Genéticos*

In this work, we aim to evaluate the patterns of stream diatom beta diversity in islands vs. continents across scales. We used beta diversity partitioning to compare diatom beta diversity between islands and continents at large (between islands / continental) and small (within islands / equivalent continental areas) scales, partial Mantel test and distance-decay curves to assess how diatom beta diversity on islands and in continents is affected by spatial and environmental distances, and linear mixed models to evaluate the relationship between island beta diversity their latitude, area, age, and isolation. Diatom beta diversity on islands vs. continents is scale- and region-dependent. Beta diversity was mainly caused by species turnover, with spatial and environmental distances shaping diatom beta diversity at large, but not at small scales. Moreover, diatom beta diversity on islands was affected by island latitude, age, and isolation, but not by island area.

Keywords: beta diversity, distance–decay, incomplete colonisation, island biogeography

Microclimate, an important part of ecology and biogeography

Julia Kemppinen¹, Jonas Lembrechts², Koenraad Van Meerbeek³, Pieter De Frenne⁴

¹*University of Helsinki*

²*Utrecht University*

³*KU Leuven*

⁴*Ghent University*

Microclimate science has developed into a global discipline. Microclimate science is increasingly used to understand and mitigate climate and biodiversity shifts. Here, we provide an overview of the current status of microclimate ecology and biogeography in terrestrial ecosystems, and where this field is heading next. We highlight the latest research on interactions between microclimates and organisms, including how microclimates influence individuals, and through them populations, communities, and entire ecosystems and their processes. We also briefly discuss recent research on how organisms shape microclimates from the tropics to the poles. Microclimates are also important in ecosystem management under climate change. We showcase new research in microclimate management with examples from biodiversity conservation, forestry, and urban ecology. We discuss the importance of microrefugia in conservation and how to promote microclimate heterogeneity. We showcase the recent advances in data acquisition, such as novel field sensors and remote sensing methods. We discuss microclimate modelling, mapping, and data processing, including accessibility of modelling tools, advantages of mechanistic and statistical modelling, and solutions for computational challenges that have pushed the state-of-the-art of the field. We identify major knowledge gaps that need to be filled for further advancing microclimate investigations, applications, and methods. These gaps include spatiotemporal scaling of microclimate data, mismatches between macroclimate and microclimate in predicting responses of organisms to climate change, and the need for more evidence on the outcomes of microclimate management.

Keywords: Microclimate, ecology, biogeography

Vulnerability of seed dispersal networks globally

Emma-Liina Marjakangas

Aarhus University

Mutualistic seed dispersal interactions are crucial to maintain plant dispersal and forest regeneration under global change, but our knowledge of their global vulnerability remains scarce. Vulnerability of seed dispersal networks consists of components of exposure (degree of human modification locally), sensitivity (proportion of seed dispersers threatened with extinction), and adaptability (capacity to reorganize pairwise interactions in changing conditions) that can together indicate which networks are most vulnerable and require intensive conservation interventions, such as rewilding. In this study, we quantify the vulnerability components of seed dispersal networks consisting of interactions between 1,561 frugivore species and 3,154 plant species globally. Then, we assess how these components (co)vary spatially and identify the most vulnerable networks globally. Our preliminary results show that the potential to reorganize (i.e. rewire) the pairwise interactions, adaptability, tends to be high everywhere. We expect that the areas with high adaptability coincide with areas that are under intense human land use pressure and contain large proportions of threatened species because these human-modified areas often occur in biodiverse regions where functional redundancy among frugivores could be expected to be particularly high. Our results will pinpoint spatial interlinkages among the vulnerability components and localities that would benefit most from intensive conservation interventions, including rewilding, to maintain the seed dispersal functioning in the future. Our results will also allow identifying candidate frugivore species with highest functional capacity to rewire their seed dispersal interactions for conserving the plant dispersal function.

Keywords: functional trait, human footprint, interaction niche, metanetwork, resilience

Session E2b

Macroecology and global change

Thursday, 18.10-19.00, Room L304

Session chair: TBA

Unraveling the influences of biological attributes on benthic marine species' responses to sea temperature

Mauricio Oróstica¹, Paulina Arancibia², Otso Ovaskainen², Navarrete Sergio³, Bernardo Broitman⁴

¹*Centro de Investigación de Estudios Avanzados del Maule (CIEAM)*

²*University of Jyväskylä*

³*Pontificia Universidad Católica de Chile*

⁴*Universidad Adolfo Ibáñez*

One of the primary challenges for ecologists is forecasting the implications of environmental change and biological influences on community assemblage. To this end, we examined the temporal changes in community composition of macroalgae and invertebrates across a broad environmental gradient along the coast of central Chile, South America. Firstly, we determined the responses of the species to different environmental conditions and their co-occurrence patterns at different spatial scales. Second, we evaluated whether the variation in species responses to environmental conditions was phylogenetically structured. Third, we examined the role of species traits in explaining their occurrences in relation to their environment responses. To achieve this, we used Hierarchical Modelling of Species Communities model to integrate data on species abundances (presence-absence), traits, phylogenetic classification, and environmental predictors (sea-surface-temperature, SST). We show that in both the macroalgae and the invertebrates, most species have shown an increasing trend over the 23-year study period. Although invertebrate species only showed responses within intertidal levels, macroalgae were more sensitive to environmental variations. Larger macroalgae were negatively affected by changes in the mean of SST. The co-occurrence of species varied depending on the spatial scale used. Macroalgal species showed higher co-occurrences at the site-scale, while on a finer scale (bench), the co-occurrence increased positively among species of invertebrates. Our finding showed that species responses were less robust than expected when linking phylogenetic classification and species traits to seawater temperatures. Probably, coastal upwelling regions may buffer species' response to changing temperatures.

Keywords: Intertidal-zone, long-term surveys, phylogenetic effects

Gamma bird diversity responses to landscape composition, configuration, and heterogeneity across landscapes in Finland

Jérémy Cours¹, Aleksi Lehikoinen², Rémi Duflot¹

¹*University of Jyväskylä*

²*Finnish Museum of Natural History*

Birds are highly mobile animals and are thus significantly influenced by landscape habitat conditions. However, their responses to forest landscape structure, composition, and heterogeneity remain incompletely understood, largely due to the limited availability of fine-scale habitat mapping on a global scale. In Finland, the multi-source national forest inventory (MS-NFI) provides continuous, high-resolution data on forest structure and composition across the country. Utilizing 336 bird transects in southern and central Finland, along with MS-NFI, Corine Land Cover, and disturbance maps, we investigated bird community responses to landscape habitat conditions. We characterized landscapes based on land cover and forest habitat information (e.g., mean patch size, area of old and broadleaf forests, tree age diversity). Additionally, we applied habitat functional indices based on MS-NFI data. Bird assemblages were analyzed in terms of species composition, functional traits, and specialization indices. Our findings demonstrate that landscape habitat heterogeneity positively impacts bird gamma-diversity, enhancing both abundance and species richness across various ecological groups (e.g., generalist, forest, old-growth, and open-habitat species), particularly in relation to functional habitat heterogeneity, as measured by the Rao's Q index. Moreover, the presence and spatial configuration of old forests were found to be important for bird communities, especially for specialized species. Furthermore, we found several scales of effect for each bird community. Our results highlight that biodiversity is strongly affected by landscape habitat conditions, at different spatial scales regarding their ecological requirements, underscoring the need to prioritize landscape considerations in biodiversity conservation planning.

Keywords: biodiversity, community ecology, functional traits, landscape ecology

Storm of a century - does it matter when disturbances occur in changing climate?

Juha Honkaniemi, Katharina Albrich

Natural Resources Institute Finland (Luke)

Climate change, combined with changes in land-use, is altering the structure and composition of forests worldwide. In the boreal forests of Fennoscandia, forest management has been the main disturbance agent influencing forest dynamics whereas natural disturbances, such as fire, wind, pests, and pathogens, have played a smaller role. However, large-scale disturbances, even though occurring rarely, can significantly affect the landscape dynamics. In 2005, storm Gudrun felled almost the annual harvest of timber in Sweden during 12hrs. An event likely to happen only once in a century. In rapidly changing climate, does it matter when such major disturbance events happen? To study this, we simulated the dynamics of a forest landscape in southern Finland with the forest landscape and disturbance model iLand. Gudrun-intensity storm was simulated at two different time steps ($t_0=2020$ and $t_{30}=2050$) and the development of landscape structure and composition was analyzed under different climate change scenarios with and without forest management. We found that the storm events disturbed approximately 20-30% of the growing stock leading to changes in landscape structure and composition. Storm in 2020 caused larger variation in the landscape dynamics compared to the no-storm scenario whereas the storm in 2050 led to significant increase in subsequent bark beetle disturbances and set the landscape to a new development trajectory. Thus, size and intensity of the future disturbances coupled with changing climate will have a significant role in shaping forest landscapes. Disturbance event today has different legacy, than a disturbance in 30 years.

Keywords: climate change, ecosystem processes, landscape ecology, management of natural resources

Intraspecific trait variation as a functional trait

Pekka Niittynen¹, Julia Kemppinen²

¹*University of Jyväskylä*

²*University of Helsinki*

Functional traits are widely used in ecology to characterize the roles of organisms in ecosystems and their responses to environmental changes. However, these traits are not constant within a species and often vary substantially among individuals of the same species. This intraspecific trait variation (ITV) can be crucial for species' adaptation to heterogeneous environments or changing conditions and can thus be considered a functional trait itself. Here, we present a unique, harmonized dataset of over 32,000 trait measurements for 130 boreal, alpine, and arctic vascular plant species across northern Fennoscandia to quantify species-specific ITV. We examined whether ITV across species demonstrates a phylogenetic signal and whether it correlates with species' habitat preferences or growth forms. We focused on four commonly measured functional traits: specific leaf area (SLA), leaf dry matter content (LDMC), leaf area, and plant height. Initial analyses revealed that high ITV in one trait did not reliably predict ITV in other traits. Among the traits, LDMC exhibited the greatest ITV, followed by leaf area, SLA, and height. Phylogenetic signals for ITV were generally weak. Forbs demonstrated the highest ITV in general, while evergreen shrubs showed the most variation in leaf area. In contrast, graminoids and sedges exhibited consistently low ITV. In summary, ITV varies widely among northern plant species, with distinct, trait-specific patterns, complicating the use of ITV as a default proxy for species resilience to environmental change.

Keywords: vascular plants, functional traits, intraspecific trait variation, Arctic, boreal

Scots pine (*Pinus sylvestris*) and mountain birch (*Betula pubescens* subsp. *czerepanovii*) seedlings on the treeline ecotone of subarctic Finnish Lapland

Johanna Toivonen¹, Henri Wallen², Sari Stark², Jouko Kumpula³, Tuomas Aakala¹

¹University of Turku

²University of Lapland

³Natural Resources Institute Finland

The range expansion and growth of tree seedlings on treeline ecotones are influenced by a combination of biotic and abiotic factors, including impacts of different land uses. Subarctic treeline ecotones are excellent manifestations of a stress gradient, where facilitation can be expected to increase and competition to decrease from favorable climatic conditions of closed forests to harsh climatic conditions of open tundra. We studied the growth and abundance of Scots pine (*Pinus sylvestris*) and mountain birch (*Betula pubescens* subsp. *czerepanovii*) seedlings on the treeline ecotone in the Finnish subarctic. We sampled 135 plots from an extensive reindeer pasture monitoring plot network, distributed in the main biomes of the ecotone: boreal coniferous forests, mountain birch forests and open tundra. In each plot, we measured seedling height, growth during the last three years (for Scots pine), described their microtopographic position, took soil samples and extracted climate data from the Finnish Meteorological Institute's data. Our preliminary results show that Scots pine seedlings have grown faster in the open tundra and mountain birch forests than in boreal forests, and that their density is as high in mountain birch forests as in boreal forests. Mountain birch seedling density is similar in the tundra and mountain birch forest. We will further continue with the analysis of microtopography, climate and soils, aiming to shed light on the potential and requirements of these two species to maintain their dominance and to expand their ranges to open tundra, as the climate warms and environmental stress decreases in subarctic treelines.

Keywords: treeline ecotone, subarctic, seedling, growth, range expansion

Session E3a: Ecosystem processes

Thursday, 17.00-18.00, Room L302

Session chair: TBA

Dinner is served: Decomposition and release of nutrients from decaying pink salmon carcasses

Aino Erkinaro¹, Hannu Marttila¹, Sami Kivelä¹, Kaisa-Leena Huttunen²

¹*University of Oulu*

²*Finnish Environment Institute*

Pink salmon (*Oncorhynchus gorbuscha*), an alien species in northern Europe, has over the past few years experienced dramatic growth in numbers and distribution. The 2-year lifecycle of pink salmon ends in mass death of all spawning individuals. Nutrients and other resources provided by decaying pink salmon carcasses are expected to have various direct and indirect ecological effects in its non-native distribution area. So far little is known about the rate of carcass decomposition and consequent release, concentrations, and storage of nutrients, all partly affected by decomposer community compositions. In 2023 we monitored pink salmon carcass decomposition and nutrient release for 9 weeks in six Barents Sea catchment rivers in an experimental set-up mimicking hotspots of carcass accumulation sites. While pink salmon carcasses on shore disappeared in a few days, carcasses in stream were decomposed notably slowly, still present and releasing nutrients even after 9 weeks. Decomposing carcasses had no significant effects on water chemistry in free-flowing stream water compared to control areas. However, in hyporheic zone water, nutrients accumulated into the sediment in considerable amounts, and on average we observed 18 times higher nitrogen and 25 times higher phosphorous values in carcass compared to control areas, although there seemed to be high among- and within-sites variation. More information on compositions of decomposer communities as well as on local effects of pink salmon carcasses on ecological processes and biotic communities will be available after further laboratory work and statistical analyses.

Keywords: community ecology, ecosystem processes, invasive species, microbial ecology, subsidy resources

Fish resource use and trophic position is dependent on sampling season – year-round stable isotope study from boreal lake fish community

Emmi Eerola¹, Brian Hayden², Alexander Piro¹, Kimmo Kahilainen¹

¹*University of Helsinki*

²*University of New Brunswick*

Boreal lakes experience variable conditions throughout the year, but we know comparatively little about seasonal variation in fish ecology in these systems. We examined this seasonal variation with stable isotopes of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) in a boreal seasonally ice-covered lake and estimated changes in the habitat and resource use, and trophic level of the fish between seasons. Monthly sampling of the fish community was conducted throughout 2020 and repeated in both March and August between 2021-2023. Our study was designed to address three principal questions: 1. Do fish stable isotope ratios differ seasonally in these habitats? 2. How do the trophic position and pelagic resource use change? 3. What kind of effects different variables (e.g. gonadosomatic index, condition, diet, water temperature) have on the seasonal changes in the isotope values, trophic position, and resource use? Nitrogen isotope ratios of most fishes increased in winter and spring and decreased in summer. For most species, trophic position was highest in spring. These changes could potentially be related to winter starvation or the approaching spawning time. Pelagic resource use was generally higher in summer when plankton production is high. These results indicate that stable isotope ratios are subject to seasonal change even in boreal lakes. Changes in trophic position and pelagic reliance could affect the food web metrics, for example food web width, food chain length and pollutant biomagnification patterns. Variability on the isotope ratios suggests a need to standardize sampling timeframe when comparing among years and different lakes.

Keywords: d13C, d15N, spring, summer, winter

Study on food composition of six nemacheiline loaches and related morphological adaptations

Hanxi Chen¹, Zhaobin Song²

¹*University of Helsinki*

²*Sichuan University*

The fish species in Nemacheilidae are abundant and widely distributed, with various morphological and structural characteristics that allow them to adapt to different habitats and ecological habits. Feeding habit is an important aspect of the study of fish ecological adaptation, while the research on feeding habits for species in Nemacheilidae is currently limited. In this study, a total of 345 fish samples and 1012 gastrointestinal tract samples of six species of Nemacheilidae, including *Claea dabryi*, *Homatala variegata*, *Triplophysa bleekeri*, *Triplophysa stoliczkai*, *Triplophysa scleroptera*, and *Triplophysa obscura*, were collected from five rivers in upper reaches of the Yangtze River and the Yellow River in China for fish feeding habits detection under the microscope, structural characteristics of feeding and digestive related organs, as well as their correlation with feeding habits, were analyzed, aiming to explore the morphological and ecological adaptations of their feeding habits. There was a significantly larger feeding intensity of nemacheiline loaches in non-breeding seasons than in breeding seasons. *T. stoliczkai* represented some differences in food habits between different river individuals with morphological and structural adaptation changes in feeding and digesting organs. The results of the study have enriched the data on the feeding habits of nemacheiline loaches and would have important reference significance for the study of the feeding ecology of fishes.

Keywords: adaptation, morphological structure, feeding habit, nemacheiline loaches

Does mercury biomagnification in a boreal lake food web vary year-round? – A comparison using bulk $\delta^{15}\text{N}$ and compound-specific $\delta^{15}\text{N}$ of amino acids

Alex Piro¹, Sami Taipale², Emmi Eerola¹, Eszter Megyeri¹, Kimmo Kahilainen¹

¹*University of Helsinki*

²*University of Jyväskylä*

Seasonality characterizes northern latitude lakes, however, limited knowledge exists regarding seasonal fluctuations in mercury (Hg) biomagnification. This study tested for these fluctuations year-round in the food web of a boreal humic lake (Lake Pääjärvi, in southern Finland) and to what extent two methods differed regarding trophic level (TL) determination. A representative sample of the food web was collected in three open-water seasons and one ice-covered season. TL was calculated from $\delta^{15}\text{N}$ measured from bulk stable isotopes of $\delta^{15}\text{N}$ and compound-specific stable isotope analysis of $\delta^{15}\text{N}$ in amino acids. Although biomagnification of total Hg (THg) was detected in all seasons using both methods, no significant differences in seasonal trophic magnification slope (TMS) in- and between methods were found. However, [THg] baseline estimates were significantly different in the same seasons between methods. TMS was highest during summer and lowest in winter in both isotope methods, while the reverse was found for [THg] baselines, i.e. regression intercepts. TMS and [THg] baselines values were generally higher in all seasons in bulk than compound-specific stable isotope methods. Calibrating methods using algae as the base to enable comparison generated a food chain length that was one TL longer in compound-specific than bulk stable isotopes. Results highlight relatively stable biomagnification among the seasons, however, a clear need remains for development of system- or region-specific trophic discrimination factors (TDF) for broader comparisons across varying spatial and temporal settings.

Keywords: basal THg, CSIA-AA, season, trophic magnification slope, winter

The use of amino acid isotopes and fatty acids to track the utilization of blue, green and brown carbon by predators in riparian habitats

Bastiaan Drost¹, Grégoire Saboret², Carmen Kowarik², Carsten Schubert², Martin Gossner¹, Maja Ilić³

¹*Swiss Federal Institute WSL*

²*Swiss Federal Institute of Aquatic Science and Technology (Eawag)*

³*Research Department for Limnology*

Global change represents a challenge for biodiversity and has a impact on the interactions that are crucial for ecosystem functioning. Since it can be difficult to study interactions in natural systems directly, analytical approaches are generally used. We investigated trophic interactions in riparian meta-ecosystems, focusing on the connections between aquatic (blue), terrestrial (green), and decomposing (brown) ecosystems. We focused on riparian predators, namely ground-dwelling and web-building spiders, which differ in their hunting strategy. Using carbon isotopes of amino acids (AAs) and polyunsaturated fatty acid (PUFA) profiles, we aimed to decipher dietary preferences and carbon fluxes across interconnected ecosystems. Our results show distinct patterns in PUFA abundance and AA isotope values between blue, green, and brown sources, which was also reflected in the PUFA abundance and AA profiles of the spiders. Mixing models based on either PUFA abundance, AA carbon isotope values or their combination consistently showed that ground-dwelling spiders rely predominantly on brown sources, whereas web-building spiders have a mixed diet with higher reliance on green sources. Our results show that riparian spiders depend on three different energy channels, namely blue, green and brown sources. This highlights the importance of spatial heterogeneity and shows that these types of interactions in meta-ecosystems need to be studied as they may be sensitive to global change. Moreover, it demonstrates the importance of the overlooked brown sources in food webs. Overall, our study suggests that AA isotopes and PUFA profiles can be used to study trophic interactions for a range of organisms and ecosystems.

Keywords: ecosystem processes or function, food webs or networks, species interactions

From forest to heath: moth outbreaks reshape ecosystem functioning and vegetation dynamics in northern Finland

Mirella Karppinen¹, Tamara Hiltunen¹, Jeffrey Welker^{1,2}

¹*University of Oulu*

²*University of Alaska Anchorage*

Climate change has intensified insect pest outbreaks, profoundly altering ecosystem processes, including nutrient cycling and vegetation ecophysiology. In the subarctic, defoliation by the geometrid moths has transformed mountain birch forests, driving transitions in understory vegetation from dwarf shrub-dominated to grass-dominated systems, and over time, converting forests into open secondary heaths with distinct carbon and nutrient cycling dynamics. We conducted a study in northern Finland's wilderness areas, investigating vegetation changes and plant ecophysiological responses in post-outbreak landscapes and their long-term effects on ecosystem functioning. Using foliar stable isotope analysis ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) as surrogates for C fixation and plant mineral nutrition processes, we compared secondary heaths with intact forests and primary heaths. Our findings indicate that secondary heath systems resemble primary heaths in appearance and terms of plant ecophysiological performance as well as ecosystem services. We discovered that plants in primary forests had the most depleted $\delta^{13}\text{C}$ values, indicating favorable water conditions and high rates of leaf gas exchange, while primary heath plants showed enriched $\delta^{13}\text{C}$ values, reflecting drier conditions, likely with reduced stomatal conductance. Interestingly, the $\delta^{13}\text{C}$ values of plants in secondary heaths were intermediate between those of the two primary habitats. Nitrogen dynamics also differed, with primary forest plants showing the lowest $\delta^{15}\text{N}$ values and secondary heath plants the highest, reflecting possible changes in plant nitrogen sources and mycorrhizal associations. Overall, these changes signify an ecological shift with broader implications for carbon sequestration and nutrient cycling, shedding light on how climate-driven disturbance reshapes ecosystem function in subarctic landscapes.

Keywords: ecosystem function, secondary heaths, geometrid moths, $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, carbon cycling, nutrient dynamics

Session E3b: Palaeoecology

Thursday, 18.20-19.00, Room L302

Session chair: TBA

Alongside dinosaurs: environmental and ecological reconstructions of a freshwater ecosystem in the Late Cretaceous of France

Olivier Jansen, Olga Otero, Xavier Valentin, Géraldine Garcia

Université de Poitiers

Freshwater environments are among the richest continental ecosystems but are threatened by climate change, pollution, and land-use. Yet, deep-time evolutionary dynamics in these ecosystems and their resilience to environmental stressors are still largely unknown. The Late Cretaceous (100 – 66 Ma) was marked by numerous environmental disturbances and a biological crisis at the Cretaceous-Paleogene boundary that wiped out 75% of life on Earth, including non-avian dinosaurs. However, the impacts of these disturbances on freshwater ecosystems have received little attention. Amphibians and squamates (lizards and snakes) are sentinel species, particularly susceptible to changes in their environment. In the European Late Cretaceous only a few studies have sought to determine whether their diversity changed over time and whether this was related to environmental changes in freshwater ecosystems. The Villeveyrac locality (Hérault, France) has yielded fluvio-lacustrine deposits from the early Campanian (~80 Ma). An exceptional diversity of vertebrates and fossil plants was recovered from those levels, including unprecedented remains of amphibians and squamates. Based on morphological analysis six new amphibian and six new squamate taxa were identified. Palaeoecological and palaeoenvironmental implications are discussed. Amphibians and squamates are represented by aquatic, semi-aquatic, and terrestrial forms, consistent with other animal and plant remains discovered on the site. We interpret the paleoenvironment as a subtropical floodplain characterized by braided rivers and surrounding riparian habitats. Together, this new material contributes to the characterization of a lower Campanian freshwater ecosystem in southern Europe and represents a milestone in our understanding of the evolution of these specific environments.

Keywords: palaeoecology, palaeoenvironment, freshwater, Lissamphibia, Squamata

Ecometric reconstruction of past environments from mammalian community traits

Abigail Parker, Mikka Tallavaara, Jeremias Glöggler, Liping Liu, Alexander Bakhia, Oscar Wilson, Juha Saarinen, Indrė Žliobaitė

University of Helsinki

Paleontological and archeological research often centers on questions of what environments animals of the past inhabited. Ecometrics is the study of how the distributions of traits (e.g. body size, diet, locomotion) within co-occurring communities relate to the environment. Ecometric models can be used to estimate paleo-environmental conditions (in terms of climate or vegetation) based on measurements of co-occurring fossil species. These models are typically trained using data from modern communities with known environments; therefore, ecometric modelling also serves to describe how modern community trait composition varies across environmental clines and biogeographic regions. This study focuses on ecometrics of large herbivorous mammals, which are the most completely sampled in the fossil record. We present a set of ecometric models based on body size and dental trait distributions within communities of large herbivorous mammals. First, we describe how dental traits, which describe the morphology of molars used to process ingested plant material, relate to temperature and precipitation variables in modern communities. Then, we apply an ensemble of ecometric models, employing varied statistical techniques, to estimate paleoclimatic conditions at a set of 483 fossil sites in Eurasia dating to the Pleistocene/Holocene (2.58-0 million years, drawn from the NOW database). We compare these model outputs against coupled ocean-atmosphere paleoclimate models' estimates for the same sites to evaluate model accuracy and investigate whether each site likely represents a fauna from a glacial stage, interglacial stage, or time-averaged fauna. These ecometric models capture how climate and vegetation change over time and space affect mammalian trait structure.

Keywords: macroecology and biogeography, paleoecology, mammal, community ecology, paleoenvironments

Session E4a: Foodwebs and interaction networks

Thursday, 17.00-18.00, Room L209

Session chair: TBA

Advances in understanding tropical moths in pollination: Exploring systems, communities, and knowledge gaps in nocturnal pollination research

Michal Bartak^{1,2}, Robert Tropek^{2,3}

¹*Charles University*

²*University of Helsinki*

³*Czech Academy of Sciences*

Despite the tropics harbouring tremendous species diversity and moth-plant interactions, tropical moths have received limited attention as pollinators. We synthesised available knowledge on the role of moths in plant pollination systems, the importance of moths in tropical pollinator communities, and their adaptations and specialised relationships. We identified significant research gaps and methodological challenges, discussed geographical biases, and provided cues for future research. We found that moths are crucial pollinators for numerous tropical plants across more than 25 plant families. In communities, plants with moth-attracting flowers account for 4% to 13% of species, while moth-pollinated plants represent up to 20% of species in communities across tropical habitats. This highlights moths' potential to shape the structure and composition of plant communities, mediating long-distance pollen transfer for maintaining populations of rare plants and their high efficiency as pollinators. Current knowledge of tropical moth pollination is geographically biased and constrained mainly by the methodological challenges of nocturnal research in the generally understudied tropical ecosystems. These research complications stem from the complexity of nocturnal moth adaptations and their nectaring behaviour, observational difficulties, and equipment limitations. Future research should broaden sampling efforts to include nocturnal pollinators, utilise advanced technologies like video recordings and AI-driven identification, and integrate generalised pollination systems and community-level studies. We stress the need for new comprehensive datasets on nocturnal pollinators in the tropics. Filling these gaps is critical to understanding the full scope of moths' ecological and evolutionary roles, particularly in the context of changing climate.

Keywords: Lepidoptera, pollination, community ecology

The cascading consequences of herbicide residues in soil on trophic interactions in agroecosystems.

Lena Falk Nielsen¹, Benjamin Fuchs², Valter Weijola¹

¹*University of Turku*

²*Aarhus University*

Glyphosate's extensive use as an herbicide has raised concerns about its impact on biodiversity and ecosystem function. For sustainable agriculture, understanding trophic interactions and creating favorable conditions for beneficial species interactions is essential. Examples of such ecosystem services include the natural regulation of pests, plant pollination, and plant-fungi symbiosis. With biodiversity declining at a critical rate, it is increasingly important to identify potential harms and disturbances to these species interactions. Our research focuses on the cascading impact of glyphosate residues in soil on plant-plant, plant-fungi (specifically arbuscular mycorrhizal fungi, AMF), and plant-insect interactions. Previous work from our group has shown that glyphosate alters the composition of plant phytohormones, potentially affecting the biosynthesis of plant defense metabolites. Our recent findings further demonstrate how these changes impact insect communities, including both flying and ground-dwelling species, with a focus on herbivores and insect predators in three different crops; wheat, oats and beans. Moreover, as expected, inoculation with AMF reduces the abundance of several herbivores and decreases herbivore damage on plants. However, for certain populations, the interaction between AMF and glyphosate residues leads to an increase in the abundance compared to glyphosate treatments without inoculation. We conclude that glyphosate residues in soil have a significant impact on trophic interactions, interacting with AMF and affecting the abundance of herbivores and predators, with effects varying depending on species.

Keywords: +herbicides, trophic interactions

Drivers of food webs in Fennoscandian cold-water freshwaters

Antti P. Eloranta¹, Matthew R.D. Cobain¹, Henna Kangosjärvi¹, Michael Power², Per-Arne Amundsen³

¹*University of Jyväskylä*

²*University of Waterloo*

³*UiT The Arctic University of Norway*

Lakes and rivers in high-latitude and alpine regions are experiencing rapid environmental changes due to both local and global anthropogenic stressors. In Fennoscandia, factors such as non-native species, hydropower operations, land-use activities, and climate change are significantly altering the assemblages and dynamics of ecological communities. This presentation will give an overview of our recent projects utilizing stable isotope data from numerous Fennoscandian lakes and rivers to explore the natural and anthropogenic drivers of freshwater food webs. Our results demonstrate that fish community composition and lake area are crucial to determining the littoral versus pelagic resource use and trophic position of generalist salmonids. However, hydropower-induced water level regulation and non-native species can rewire food webs by modifying nutrient flows and the resource use of native top predator salmonid fishes. Land-use activities like forestry and agriculture can further complicate impacts through their influence on the reliance of aquatic consumers on terrestrial (allochthonous) energy sources. By integrating aspects of biodiversity and ecosystem function, food web ecology offers a robust framework for ecosystem-based monitoring and management actions. This is particularly vital for remote, cold-water high-latitude and alpine freshwater ecosystems, which, despite being relatively species-poor, are highly sensitive to environmental change. Our research enhances the understanding of ecological processes in cold environments and highlights the necessity for data compilations and sustainable management practices to monitor and mitigate negative human impacts.

Keywords: Arctic, community dynamics, habitat coupling, top predators, trophic interactions

Evidence for bottom-up effects of moth abundance on forest birds in the north-boreal zone alone

Mahtab Yazdanian¹, Tuomas Kankaanpää², Thomas Merckx³, Ida-Maria Huikkonen⁴, Juhani Itämies⁵, Jukka Jokimäki⁶, Aleksi Lehikoinen⁷, Reima Leinonen⁸, Juha Pöyry⁴, Pasi Sihvonen⁷, Anna Suuronen⁴, Panu Välimäki⁹, Sami M. Kivelä²

¹*University of Oulu*

²*Ecology and Genetics*

³*Vrije Universiteit Brussel*

⁴*Finnish Environment Institute (SYKE)*

⁵*Kaitoväylä 25 A 6*

⁶*University of Lapland*

⁷*Finnish Museum of Natural History*

⁸*Kainuu Centre for Economic Development*

⁹*Albus Luontopalvelut Oy*

Insect declines are raising alarms regarding cascading effects on ecosystems, especially as many insectivorous bird populations are also declining. Here, we leveraged long-term monitoring datasets across Finland to investigate trophic dynamics between functional groups of moths and birds in forested habitats. We reveal a positive association between the biomass of adult- or egg-overwintering moths and the biomasses of resident and long-distance migrant birds reliant on caterpillars as breeding-season food in the north-boreal zone. Contrary to expectations, similar signs of moth bottom-up effects on insectivorous birds were not observed in other Finnish regions or for moths overwintering in other life stages. In fact, some negative associations between moths and birds were even detected, possibly attributable to opposite abundance trends. While supporting the existence of bottom-up effects in the north-boreal zone, our study emphasizes the need for further investigation to elucidate moth-mediated trophic dynamics in areas characterised by insect decline.

Keywords: insectivores, Lepidoptera, trait-based analysis, trophic interaction, joint dynamic species distribution model

Competition between sinking and buoyancy regulating algae along vertical gradients of light and nutrients

Sabine Wollrab¹, Arthur Rossignol²

¹Leibniz Institute of Freshwater Ecology and Inland Fisheries

²Université Paris-Saclay

Global warming leads to extended periods of summer stratification. While algae growth typically occurs during stratified periods where the warmer and shallower epilimnion layer provides enough light for growth, lake stratification also increases the risk of sinking out of the upper water column. Planktonic primary producers have developed diverse strategies to counteract sinking such as specific morphologies, flagella, or the ability to regulate cell buoyancy. A cyanobacteria with buoyancy regulation is *Planktothrix rubescence*, for which a strong increase has been observed in several deep stratifying lakes across Europe. One suggested reason is that they strongly profit from lengthened periods of summer stratification, with their ability to move below the thermocline giving them a unique advantage over passive sinking algae to overcome nutrient limitation in the epilimnion. So far models on phytoplankton competition and seasonal plankton succession (such as the PEG model) largely ignore vertical gradients in resource availability and specifically do not consider vertical movement strategies. This limits our ability to assess how changes in stratification regimes will impact algal growth and community composition. In this study, we theoretically investigated resource competition between two phytoplankton species along a 1D water column, contrasting passively sinking algae with taxa that can regulate buoyancy to ascend or descend along the water column according to optimal resource availability. We investigated how competition between sinking and buoyancy regulating taxa is influenced by physiological traits related to resource use efficiency of light and nutrients as well as by environmental conditions such as background turbidity and eddy diffusion. Our results show that coexistence between buoyancy-regulating and sinking algae is critically influenced by differences related to light and nutrient use efficiencies. This also applies to the occurrence of a deep chlorophyll maximum (DCM), its location along the water column as well as which species is forming the DCM.

Keywords: plankton phenology, stratification, global warming, buoyancy regulation

Session E4b: Science communication

Thursday, 18.10-19.00, Room L209

Session chair: TBA

Ice Fish Research: A new science communication platform for Icelandic fish research

Alessandra Schnider¹, Lieke Ponsioen², Theresa Henke², Michelle Valliant²

¹*Hólar University*

²*University of Iceland*

Science communication is still an undervalued and underfunded area of scientific work, which makes it challenging to do this work in addition to all the other duties a researcher has. Even more so for early career researchers, who already juggle so many new tasks on top of keeping up with their studies. Furthermore, as scientists we all have a duty to inform the public of our ongoing research efforts. That is why we founded Ice Fish Research in May 2024. We communicate ongoing fish research in Iceland, as well as giving researchers a platform to start sharing their science with minimal efforts associated. By sharing researchers' everyday work in an accessible way on social media and more extended blog posts on our website, the public gets a first-hand experience of what life as a researcher really looks like, whilst also learning about the nature that surrounds them. Moreover, by introducing the people behind the research, we aim to highlight the diversity among researchers and hope to inspire children and young adults through representation. We also engage directly with the public through in-person events and through our "Ask a scientist" column. Finally, we also aim to increase collaborations among researchers by increasing visibility of ongoing research within Iceland. We at Ice Fish Research hope to inspire researchers to share their work more broadly and to celebrate all the outstanding work that is being done.

Keywords: science communication, fish research, Iceland

Are Open Science instructions targeted to ecologists and evolutionary biologists sufficient?

Elina Koivisto, Elina Mäntylä

University of Turku

Open Science (OS) skills are an essential part of scientific work as e.g., many journals require data sharing. Following an OS workflow can seem challenging at first, and thus instructions and guidelines are important. But how comprehensive are they in the field of ecology and evolutionary biology (Ecol Evol)? We reviewed 20 published OS guideline articles aimed for Ecol Evol researchers, together with the data policies of 17 Ecol Evol journals to chart the current landscape of OS guidelines in the field, find potential gaps, identify field-specific barriers and discuss solutions. We found that many of the guidelines covered similar topics, despite being written for specific target audiences. They also mentioned similar obstacles that could hinder data sharing. Thus, there could be a need for a more widely known, general OS guideline for Ecol Evol. Following the same guideline could also enhance the uniformity of the OS practices carried out in the field. However, long-term experiments and physical samples were mentioned surprisingly seldom, although they are typical issues in Ecol Evol. These topics could require specific instructions for example for data sharing. Of the journals, 15 out of 17 expected or at least encouraged data sharing and 10 of those required data sharing at the submission phase. The coverage of journal data policies varied greatly between journals. As journals can contribute greatly by leading the way and making open data useful, we recommend that the publishers and journals should invest in clear and comprehensive data policies and instructions for authors.

Keywords: Open Science, science communication

Session F1: Spatial modelling in conservation and management

Friday, 10.30-12.00, Room L303

Session chair: TBA

Why we need distribution models for ecosystem management - a case study from Norway

Adam Eindride Naas¹, Anders Bryn¹, Rune Halvorsen¹, Peter Horvath¹, Lasse Torben Keetz², Trond Simensen³, Olav Skarpaas¹, Ingrid Vesterdal Tjessem¹, Joachim Paul Töpper³, Vigdis Vandvik⁴, Liv Guri Velle⁵, Catharina Caspara Vloon⁶

¹*Natural History Museum, University of Oslo*

²*Department of Geosciences, University of Oslo*

³*Norwegian Institute for Nature Research*

⁴*University of Bergen*

⁵*Norwegian Institute of Bioeconomy Research*

⁶*Western Norway University of Applied Sciences*

Ecosystem-based management relies heavily on field survey data. Even though field-based ecosystem mapping normally is too time-consuming to acquire information over large extents, distribution models that can inter- and extrapolate to areas that are not mapped in the field are rarely used. To illustrate the need for distribution models in ecosystem-based management, we trained a distribution model to differentiate 54 ecosystem types based on remote sensing, climate, and geology data. We estimated (1) the proportion of Norway that is not mapped by field surveys, (2) the proportion that is not mapped and is regulated to future land use, (3) the model's performance and uncertainty, and (4) the area in which different ecosystem types would be replaced by land use (unnoticed) if the regulations are realized. We found that (1) 96% of Norway is not mapped by field surveys. Land use is planned in 0.6 % (21 000 km²) of the country but (2) 81% of this area is not mapped. We will present results on (3) model performance and uncertainty, and (4) the potential loss of different ecosystem types estimated by distribution modelling. We emphasize that distribution models would benefit spatial planning as a supplement to field surveys. Wall-to-wall maps allow nature managers to identify focus areas (e.g., potential conservation areas), and land-use planners to propose projects where 'land use-biodiversity conflicts' are less likely. Still, distribution models have challenges related to training and test data quality, which calls for a focus on transparent accuracy assessments and uncertainty quantification.

Keywords: distribution modeling, land use, remote sensing, spatial planning, vegetation mapping

Protected area network from the perspective of modelled habitat suitability for birds: a case study from Latvia

Andris Avotins¹, Ivo Vinogradovs², Jekaterina Butkevica¹, Ainars Aunins³

¹*University of Latvia Faculty of Medicine and Life Sciences*

²*University of Latvia Faculty of Science and Technology*

³*Latvian Ornithological Society*

Species distribution modelling (SDM) is a valuable tool for understanding species distributions and ecological requirements, and for conservation planning. In this study, we used SDM to map the nationwide distribution of over 70 bird species from forests, farmland and wetlands at 1 hectare pixel resolution. The species selected include recognised biodiversity indicators, key umbrella species for conservation, and species that are red-listed or protected. We then used the results for multi-species site prioritisation for conservation. Species were categorised based on their typical home range sizes, informed by a literature review. Environmental data were analysed at the site, home range and landscape levels. We collected all available species observation data since 2016, filtering to retain only credible breeding-related records at sites where no significant land-use and land-cover changes had occurred since the observation. Using maximum entropy analysis as our SDM tool, we created habitat suitability maps and used them to prioritise sites for conservation using a weighted multi-species approach. Each species was assigned a specific weight based on factors such as national population size, percentage of the European population breeding in Latvia, annual rate of population change, lifetime reproductive success, area and extent of distribution, association with protected areas, and breadth of ecological niche. Finally, we analysed the results of the prioritisation, both for individual species and based on a multi-species approach, to assess the level of conservation and the condition of the existing conservation network, thus identifying gaps in it.

Keywords: species distribution modelling, nature conservation planning, multi-species site prioritisation for conservation, protected area network evaluation, landscape ecology

Partitioning beta diversity to explore community compositional change along a habitat degradation gradient in boreal forests

Faith Jones¹, Alwin A. Hardenbol¹, Albin Larsson Ekström¹, Anne-Maarit Hekkala¹, Mari Jönsson¹, Matti Koivula², Joachim Strengbom¹, Jörgen Sjögren¹

¹*Swedish University of Agricultural Sciences (SLU)*

²*Natural Resources Institute Finland (Luke)*

Understanding the effects of habitat degradation on biodiversity is essential for undertaking conservation initiatives, but commonly used metrics of biodiversity can miss important signals of habitat degradation. Partitioning beta diversity into nestedness, relating to species losses, and turnover, relating to species replacements, offers more detailed insights into the mechanisms behind biodiversity change with increasing habitat degradation. Using an extensive assessment of lichen, polypore and bryophyte species composition in 240 boreal forest locations across Sweden and Finland, we examined how beta diversity, nestedness and turnover vary when comparing assemblage pairs from the same or different habitat degradation levels. Additionally, we pooled all local assemblages into regional habitat degradation comparisons to evaluate the influence of scale on the importance of turnover and nestedness. Turnover rather than nestedness was the main driver of beta diversity. We also detected a small increase in nestedness in lichen assemblage pairs comparing between habitat degradation levels but negligible increases in nestedness when comparing polypore or bryophyte assemblages between habitat degradation levels. Turnover declined in regional comparisons compared with local pairwise comparisons, whereas nestedness remained comparable or increased. Our results highlight the importance of local scale species replacements with habitat degradation, as differences in assemblage composition between habitat degradation levels were driven predominantly by turnover rather than nestedness. At the regional scale, there was some evidence for biotic homogenisation, as we found higher nestedness values when comparing the most extreme differences in habitat degradation levels for some taxa.

Keywords: biodiversity, beta diversity, lichens, wood fungi, bryophytes

Cascading effects of forest decline on habitat conditions and biodiversity in temperate forests

Jérémy Cours¹, Aurélien Sallé², Laurent Larrieu³, Christophe Bouget⁴

¹*University of Jyväskylä*

²*Université d'Orléans*

³*INRAE DYNAFOR*

⁴*INRAE EFNO*

Climate change is leading to more severe, frequent, and widespread natural disturbances in forests, resulting in increased tree mortality across European forests. This process of tree cohort mortality, known as forest decline, can alter habitats in ways that may benefit deadwood-dependent biodiversity (i.e., saproxylic organisms). We hypothesized that habitat changes associated with forest decline would promote saproxylic biodiversity. To investigate this, we examined the cascading effects of forest decline on habitat structure and biodiversity in three distinct European settings: (i) fir-dominated forests in the French Pyrenees highlands, affected by drought; (ii) spruce-dominated forests in the German Alps highlands, affected by windstorms and bark beetle outbreaks; and (iii) oak-dominated forests in the lowlands of central France, affected by drought. Within each study plot, we inventoried living trees, deadwood, tree-related microhabitats (TreMs), and saproxylic beetles. Forest decline was associated with significant changes in deadwood quantity and TreMs across all contexts. The overall amount of deadwood increased, with highly decayed deadwood occurring primarily in coniferous forests. In drought-affected forests, TreMs diversity rose, and in all contexts, the abundance of lignicolous fungal fruiting bodies and tree injuries increased due to forest decline. These habitat changes promoted saproxylic beetle species richness and led to shifts in community composition. Our findings suggest that, in managed forests with typically low levels of deadwood, areas of forest decline could be utilized opportunistically to support deadwood-dependent species.

Keywords: biodiversity, community ecology, functional traits

Conserving apollo butterflies: habitat characteristics and conservation implications in Southwest Finland

Jonna Kukkonen¹, Mikael von Numers², Jon Brommer¹

¹*University of Turku*

²*Åbo Akademi*

The conservation of insects, particularly endangered species such as the Apollo butterfly, is a pressing global concern. Understanding the habitat requirements and factors influencing species occupancy is crucial for designing effective conservation strategies. We focused on investigating the habitat characteristics expected to affect the occupancy of the nationally endangered Apollo butterfly in Southwest Finland. We conducted field surveys and GIS analysis to assess the impact of larval host plant and adult nectar resources, habitat encroachment, elevation, connectivity, and spatial variation on Apollo larval occupancy in rocky outcrop habitats. We found that rocky outcrops with abundant host plants and those less isolated from nectar patches play a significant role in supporting Apollo reproduction, whereas encroachment, specifically increased tree volume, negatively affected occupancy. We additionally observed spatial variation in occupancy across different blocks within the study area. Our findings emphasise the importance of resource availability for Apollo butterflies and highlight the dynamic nature of their habitat requirements. Maintaining a network of intact rocky outcrops with suitable resources is essential for the long-term persistence of the Apollo butterfly population in the region. Our research underscores the critical need to protect and restore habitats for the Apollo butterfly, particularly by addressing threats such as habitat encroachment and construction projects that pose risks to their breeding sites.

Keywords: conservation, monitoring, resources, host plant, butterfly

Habitat composition outweighs climate in driving terrestrial biodiversity variability.

Emy Guilbault¹, Laura Antao¹, Mirkka Jones¹, Andrea Santangeli², Anna-Liisa Laine¹, Tomas Roslin¹, Marjo Saastamoinen¹, Jarno Vanhatalo¹, Pasi Sihvonen¹, Juha Poyry³, Andreas Linden⁴, Aleksi Lehikoinen¹, Mikko Kuussaari³, Otso Huitu⁴, Heikki Henttonen⁴, Erkki Korpimäki⁵, Janne Heliölä³

¹*University of Helsinki*

²*Mediterranean Institute for Advanced Studies (IMEDEA CSIC-UIB)*

³*Finnish Environment Institute (SYKE)*

⁴*Natural Resources Institute Finland (Luke)*

⁵*University of Turku*

While changes in land use and climate are major threats to biodiversity, evaluating their joint impacts remains challenging, especially over larger extents and timescales. We used joint species distribution modelling associated with a conditional variance partitioning approach to characterize the relative importance of climate and habitat drivers, and their context dependency on both occurrence and abundance patterns for 503 species of terrestrial taxa monitored across Finland in the last 20 years. Overall, habitat composition was the main driver of biodiversity patterns, but its dominance and uncertainty in explaining species occurrences were highly context-dependent. Specifically, habitat was the dominant driver for butterflies, birds, and rodents, while habitat and climate were similarly important for large mammals and moths. Additionally, climate mainly explained species patterns between biogeographical regions, while habitat was the main driver within regions. Covariation importance and direction along climate and habitat gradient was taxa and region-specific. Finally, life history pace, habitat and diet specialization, and body size only moderately modulated the relative importance of both drivers. Our findings emphasize the need to fully consider species and local contexts to build effective management and conservation strategies for biodiversity and climate adaptation from the species to the community level.

Keywords: biodiversity, spatio temporal change, hierarchical modelling of species communities, variance partitioning

The importance for conservation of understanding processes that shape intraspecific diversity

Bjarni Kristófer Kristjánsson¹, Camille Leblanc¹, Katja Räsänen², Skúli Skúlason^{1,3}

¹*Hólar University*

²*University of Jyväskylä*

³*Icelandic Museum of Natural History*

The world's biodiversity is facing accelerating, and unprecedented, decline. This can be clearly seen in aquatic ecosystems which have been greatly influenced by humans; destroyed, altered, fragmented, and simplified. However, even though biodiversity has been defined as diversity, within species, among species and among communities and ecosystems, the concept of biodiversity is usually understood as a quite static construct. The focus is commonly on species diversity rather than on intraspecific (within-species) diversity. Furthermore, the focus has emphasized describing patterns of diversity rather than the processes which generate and maintain biodiversity over time. This focus can be seen among scientists studying biodiversity, and among policymakers and is also reflected in the public's general lack of understanding / misunderstanding of biodiversity concepts. Focusing on species as the unit of diversity in a static way carries great conservation risk as it does not account for individual- and population level processes and their interactions. It furthermore ignores distinctiveness of populations, that may be both evolutionary and ecologically different. Today, populations are being lost at higher rate than species, and this loss of populations is what determines the survival or disappearance of a species. It is therefore crucial that we put the focus on intraspecific diversity in research, conservation, planning, and management. Here, we will discuss the importance of intraspecific diversity, how we can move from a more static, pattern-oriented view towards a more process-oriented view to enable us to better conserve biodiversity in nature.

Keywords: conservation, ecology, evolution, intraspecific diversity

Session F2: Animal behavior

Friday, 10.30-12.00, Room L209

Session chair: TBA

The role of neighbour phenotype and nest dispersion on host choice decision in the Common cuckoo

Abaurrea Teresa¹, Robert Thomson², Rose Thorogood¹, Michael O'Brien³

¹*Helsinki Institute of Life Sciences*

²*Fitzpatrick Institute of African Ornithology*

³*Experimental Station for Arid Zones*

The behaviour of other individuals can provide a rich source of social information about the local environment. There is a growing body of work showing that social information can influence acquisition and use of resources and breeding decisions and has potential to influence how selection operates within and between species. However, the availability and utility of social information is highly determined by the distance in time, space and ecology between the source of information and user. Despite extensive research accounting for neighbour proximity and interactions in other fields of ecology (e.g. plant ecology), this approach is yet to be adopted in studies of behaviour. Here I will present how we can use neighbourhood models with maximum likelihood approach to explore how the laying decisions of brood-parasitic cuckoos are influenced by information of foster parent quality acquired from local host neighbourhoods. We used a 9-year long monitoring dataset to study parasitism probability depending on a host (focal) phenotype, while incorporating characteristics (number, phenotype, and distance) of surrounding host neighbours. We found that neighbour characteristics are more important than focal host phenotype, and that distance between neighbour and focal host had a stronger impact on neighbour characteristics than neighbour phenotype. Our results suggest that neighbourhood is more important on cuckoo host choice than host phenotype, and highlights the importance of accounting for neighbours in brood parasitism studies or in any knowledge area interested on how individuals respond depending on who is around.

Keywords: social information, density dependence, neighbourhood, common cuckoo

Biotic and abiotic factors affect winter cavity use in a nocturnal raptor

Gian Luigi Bucciolini¹, Chiara Morosinotto², Jon Brommer¹, Daniele Baroni³, Al Vrezec⁴, Patrik Karell⁵

¹*University of Turku*

²*University of Padova*

³*ISPRA*

⁴*University of Ljubljana*

⁵*Lund University*

Natural cavities are crucial role for the survival and reproduction of many forest-dwelling species, providing roosting and nesting sites and serving as refuges against cold temperature. This may help to survive to cold winters, or against predators and mobbers to reduce stress and risk of being predated upon. Despite the importance of cavity availability and use for animal survival, a deep understanding of cavity use throughout the year, and in particular how biotic and abiotic factors involved in their use is still lacking. To fill this gap in the knowledge, we investigated winter cavity use by tawny owls (*Strix aluco*), in four European populations (Finland, Sweden, Slovenia and Italy), each with different environmental and climatic conditions, in order to understand conspicuousness and behavioural strategies adopted in diverse habitats. Our findings reveal that cavities are primarily used in occupied territories and not by floaters passing through and that nest boxes are sparsely used outside the breeding season in all populations except Italy, where they are frequently occupied. Cavity use, in winter, is more common in deciduous forests than in coniferous forests, and northern populations (Finland and Sweden) seldom utilized cavities during winter, even in cold conditions, whereas cavities were more commonly used in Italy's milder climate. This study offers valuable insights into behavioural strategies of tawny owls during the non-breeding season and highlights factors influencing cavity use across different European habitats. These findings will help us understand the year-around survival strategies of this owl species and the potential threats they face.

Keywords: biodiversity monitoring for the future, from biodiversity to ecosystem functions and services

How do parents coordinate care? Moving beyond provisioning might explain reproductive success in pied flycatcher.

Gloria Murari¹, Rose Thorogood¹, Robert Thomson²

¹*University of Helsinki*

²*University of Cape Town*

The emergence of parental care represents a major evolutionary transition in animals and is thought to give rise to more complex forms of social structures. Therefore, families provide an ideal social environment to understand how individuals work together. In species where parents both provide care, conflicts of interest arise and understanding how they are resolved has long been a major focus of behavioural ecology. However, despite decades of research testing the key theory proposed to explain why parents cooperate, how parents assess each other and decide their relative investment in care (i.e. sexual conflict) remains unresolved. Partly, this is because of a major gap in our knowledge: most tests have focused on only one aspect of care (provisioning), ignoring that parental care comprises many activities that can be used by parents to gain information. In the first paper of my PhD, I have tackled this problem by testing coordination in different aspect of parental care – provisioning and nest defence against two types of predators (woodpecker and sparrowhawk) in 25 nests of pied flycatchers (*Ficedula hypoleuca*). I then assessed whether they covary with improved survival of the brood, monitored as number of hatched eggs and fledged chicks. I expected coordination to improve when facing threats that are more dangerous for the nestlings (e.g. woodpecker) and to result in improved survival of the brood.

Keywords: parental care, coordination, sexual conflict, pied flycatcher

Tracing the geographic origins of behavioural variation using genomics

Malin V. Klumpp¹, William J. Smith¹, Bengt Hansson², Rose Thorogood¹

¹*University of Helsinki*

²*Lund University*

Consistent behavioural differences between individuals (i.e., animal personality) can explain much of the behavioural variation within species. Understanding how such differences arise and are maintained within populations represents a frontier in personality research. One hypothesis is that personality differences evolve in response to geographically varying selection and persist within populations through migration, but testing this requires knowing individuals' geographic origins, which is challenging in wild populations. Here we leverage genomic (RADseq) data to examine whether behavioural variation in Finnish Eurasian reed warblers (*Acrocephalus scirpaceus*) relates to differences in genetic ancestry. Over the past century, reed warblers have expanded their range into Finland, escaping brood parasitism by the common cuckoo (*Cuculus canorus*). This range expansion seems linked to population-level differences in personality traits: Finnish reed warblers are more aggressive and exploratory than those in their European breeding range core and show reduced defence behaviours against brood parasitism. Yet, some individuals have retained defences, and it is unknown if the more exploratory and aggressive birds are recent immigrants or represent persistent traits at the range front. By using genomic data from Finnish reed warblers and those from the range core, we will assess evidence for recent admixture and assign Finnish individuals to their geographic origin. This novel approach will reveal whether behaviours present in the Finnish population are maintained across generations or influenced by recent immigration. Overall, this study will provide insights into how intraspecific behavioural diversity is shaped by individuals' geographic background, increasingly relevant as anthropogenic influences cause animal redistributions worldwide.

Elephant astrology? Birth season is linked to later life personality in Asian elephants

Martin Seltmann¹, Victor Gomez², V  rane Berger¹, U Kyaw Nyein³, Htoo Htoo Aung³, Virpi Lummaa¹

¹*University of Turku*

²*University Sorbonne Paris Nord*

³*Myanma Timber Enterprise*

Personality differences between individuals can play an essential role in population ecology. Early life experiences can have long-term fitness consequences and also influence the development of personality and its expression later in life. However, except for humans and other primates, only few studies have addressed the link between early life conditions and later personality in long-lived and highly social species. Here, we investigated the association between personality differences in later life of semi-captive Asian elephants (*Elephas maximus*) from Myanmar and four early life experiences: birth origin (wild-caught or captive-born), birth season (hot-monsoon-cold), birth order (1st born vs later born), and the presence or absence of their mother during the first five years of life. We used a previously evaluated model for elephant personality in our study population, which is represented by three factors: Attentiveness, Sociability, and Aggressiveness. Measurement invariance was given only for birth season, therefore other early life experiences could not be further investigated. However, we found that Asian elephants born during the monsoon season (June to September) had higher mean scores in Attentiveness and Sociability compared to elephants born during the cold season (October to January). We discuss how these differences could be due to strong environmental differences between the seasons, as elephants experience more stress during the colder months. Furthermore, we discuss how several physiological mechanisms could potentially influence the development of elephants' personality. This study is the first to demonstrate that certain early life experiences can drive personality differences later in life in Asian elephants.

Keywords: *Elephas maximus*, behavioural consistency, early life conditions, factor analysis, measurement invariance

Biologically inspired warning patterns deter birds from wind turbines

Sandra Winters¹, George Hancock¹, Heta Lehtonen¹, Theo Brown¹, Amine Ejite¹, Ossi Nokelainen², Johanna Mappes¹

¹*University of Helsinki*

²*University of Jyväskylä*

Wind power plants have been at the forefront of investment and innovation in renewable energy. However, bird fatalities from collisions with wind turbines present an ecological and social challenge to the growing deployment of wind power. Increasingly, research has focused on utilizing the sensory ecology of animals to provide passive or active cues that minimize collision risk by increasing the detectability and/or aversiveness of the turbines. In nature, numerous aposematic species use contrasting colors and striped patterns to warn birds of their unpalatability. These common signal elements are effective due to their salience across natural scenes, memorability, generalizability across taxa due to mimicry, and exploitation of the innate color preferences of birds. This begs the question: might biologically inspired turbine blades that mimic aposematic patterns help to protect birds by increasing their avoidance of the blades? Here, we use a screen-based ‘bird game’ experimental setup to test the behavioral responses of wild-caught great tits (*Parus major*) to three blade patterns currently used for wind turbines (white, red striped, and single black blade) as well as a novel biologically inspired aposematic pattern. Birds took significantly longer and were less likely to approach patterned compared to uniform white blades irrespective of whether they had prior experience with them. This effect was strongest for the aposematic pattern compared to all other patterns tested, highlighting the utility of our bio-inspired approach. Our work suggests that adding red, black and yellow warning patterns to wind turbine blades will likely reduce the risk of bird collisions.

Keywords: biomimicry, bird conservation, collision mitigation, vision, warning signals

Impact of artificial light at night on movement and behaviour of glow-worm females

Aurélien Boulez, Linnea Kivelä, Sitara Palecanda, Ulrika Candolin

University of Helsinki

Artificial light at night (ALAN) is a rapidly increasing environmental problem that is transforming natural cycles of light and dark that have been constant over species' evolutionary history. In particular, ALAN poses a threat to nocturnal organism that are dependent on the darkness for survival and reproduction. One such species is the common glow-worm, *Lampyrus noctiluca*, a beetle with bioluminescent females that glow in the night to attract flying males. Previous research show that females stop glowing or glow for shorter times when exposed to ALAN, but whether they move away from the light when exposed to it for several nights is unknown. We investigated female movements in relation to artificial light in outdoor experimental arenas that were illuminated from one end with white artificial light to form a light gradient. Females were placed at the lit end of the arena, and their glowing and movements were monitored over ten nights. Preliminary results indicate that females fail to move away from the light and fail to increase the intensity of their glow under ALAN, indicating that glow-worms lack adaptive responses to artificial light. Moreover, they seem to glow for a shorter number of nights than the control and switch from an open to a sheltered microenvironment. These results highlight the vulnerability of glow-worms to ALAN, and, more broadly, the challenge species face when exposed to light pollution while lacking adaptive responses.

Keywords: behavioral ecology, dispersal or movement

Effect of beaver presence on reproduction of nesting birds

Eszter Megyeri¹, Juha Tiainen¹, Sami Taipale², Kimmo Kahilainen¹

¹*Lammi Biological Station, University of Helsinki*

²*University of Jyväskylä*

The importance of the connection between different habitats has been increasingly recognised, especially the pulsed resources provided by aquatic invertebrates to land-based communities. However, the relative significance of aquatic invertebrate fluxes to terrestrial consumer fitness has remained understudied. The main objective of this research is to understand how beaver can influence cross-habitat ecological linkages, i.e., aquatic-terrestrial coupling via the emerging aquatic insects on a passerine bird, the European pied flycatcher nesting performance at riparian areas of boreal lakes. The study is carried out in Evo area, southern Finland where beaver has been present for decades and long-term data are available regarding its habitat occupancy. In this study, the prey availability in terms of quantity and quality as well as prey selection of pied flycatchers is studied at beaver influenced lakes, and lakes without beaver, and forested control areas near the study lakes. Insect abundance was higher at beaver-influenced site compared to non-beaver area in 2022 and 2023. During the first sampling year, pied flycatchers' mean clutch size, number of hatchlings and fledglings at beaver-influenced lake site were higher than at non-beaver lake, while in the second sampling year, measures of breeding performance were similar. Hence, cross-habitat linkages can be an important part of understanding local interactions, especially the significance of beaver promoting riparian passerines and potentially wider communities.

Keywords: beaver, invertebrates, birds, aquatic-terrestrial linkages

Session F3: Evolutionary processes

Friday, 10.30-12.00, Room L302

Session chair: TBA

Too “Hulk” for love? Sex-specific effects of radiation exposure in tardigrades

Sara Calhim, Jussi Lehtonen

University of Jyväskylä

Tardigrades are famous for surviving radiation exposure thousands of times the human lethal dose. The molecular mechanisms for the latter are relatively well studied. However, the physiological impacts, namely in terms of reproductive success of sexually reproducing taxa, remain unknown. We exposed males and females of a moss-living tardigrade (*Macrobiotus ripperi*) to ionizing radiation between 0 and 550 Gy. We show that despite high survival overall, there was a considerable cost in offspring production at higher dosages. Moreover, this effect is mainly due to a negative impact on the female, but not male, gonad. This study highlights the importance of research into sex-specific responses to stress.

Keywords: evolution, reproduction, invertebrates

How chromatin structure influences genetic and epigenetic variation

Ilkka Kronholm, Mariana Villalba de la Peña

University of Jyväskylä

The genomes of eukaryotes are not uniform in their structure. Parts of the genome, called heterochromatic regions, are packed more tightly in the nucleus. Heterochromatic regions can be distinguished by epigenetic modifications, particularly histone 3 lysine 9 methylation (H3K9me) that marks constitutive heterochromatin, and histone 3 lysine 27 methylation (H3K27me) that marks facultative heterochromatin. We are studying how chromatin structure influences patterns of variation in the genome, using the filamentous fungus *Neurospora crassa* as a model system. We performed a mutation accumulation experiment to measure variation in mutation rate across the genome. We observed that genetic mutation rate was around tenfold higher in regions marked by H3K9me and in the centromeric regions, a slight increase relative to euchromatic regions was also observed in regions marked by H3K27me. Variation in mutation rate was also correlated with the amount of genetic variation segregating in natural populations. We also investigated de novo epimutations, spontaneous changes in DNA methylation or H3K9me, happen in *N. crassa*. We observed that patterns of DNA methylation change over time in centromeric regions, but not elsewhere in the genome. Furthermore, while overall patterns of H3K9me were constant, we did observe some events of new H3K9me peaks that appeared in euchromatin, were transmitted across transfers but were frequently lost again, so spontaneous changes in H3K9me seem ephemeral. We are currently investigating patterns of recombination in the genome to examine how variation in mutation, recombination, and chromatin structure shape patterns of natural genetic variation.

Keywords: epigenetics, population genetics, mutation, mutation accumulation, fungi

Evolution of proboscidean dental functional traits in relation to Neogene vegetation and climate changes

Juha Saarinen¹, Adrian Lister²

¹*University of Helsinki*

²*Natural History Museum, London*

Proboscideans have been the largest herbivorous terrestrial mammals on most continents since their dispersal out of Africa during the early Neogene, and they have had a profound ecological role as keystone megaherbivores since then interacting with their environment and other species. On the other hand, they were ecologically versatile and non-selective feeders, and their diets and adaptations have tracked changes in climate and vegetation through time. We explored the evolution of proboscidean dental traits in East Africa during the last 26 million years in relation to climatic aridification and changes in diet and local vegetation patterns. We show that some proboscideans started to adapt to locally grass-rich environments in East Africa first by behavioral shift, which preceded evolutionary change in dental traits. This happened in some lineages of proboscideans earlier than has been thought, starting in Early Miocene, in parts of East Africa where the environments were locally more grass-dominated than in surrounding areas. Also, around 7 million years ago in the lake Turkana region, increasingly grass-rich diets of the earliest true elephants were associated with dryer and more grass-rich savanna environments than elsewhere in East Africa. Our results suggest that aridification of climate in East Africa during the last 10 million years was the major driving factor that led to the evolution of multi-ridged, high-crowned teeth in true elephants to increase functional durability and shearing efficiency of the teeth. Moreover, we show that the major evolutionary changes in these traits happened in steps following the strongest peaks of aridification.

Keywords: palaeoecology, evolutionary ecology, eco-evolutionary dynamics, adaptation, climate change

Shifts in phenological reaction norms – can we see signs of evolution in bird egg laying timing?

Maria Hällfors¹, Aleksi Lehikoinen², Albert Phillimore³

¹*Finnish Environment Institute*

²*Finnish Museum of Natural History*

³*University of Edinburgh*

Biodiversity is threatened by increasing climate change. In many cases phenotypic plasticity might not be enough for adjusting. Evolutionary processes are often slow but have in experimental studies been shown to act even over short time spans. While experiments are logistically challenging and can provide information on only individuals species, using large observational datasets would provide a possibility to gauge patterns across a wider spatial and taxonomical range. Using nest card data for 40 bird species across Finland from which egg-laying dates can be discerned, we define climatic windows under spring to estimate response norms over 5-year and 60-year periods and compare them by extending the within-subject centering approach to evaluate changes in the slopes and intercepts of the phenological response over a temporal gradient. We postulate that evolutionary adaptation in egg-laying time should be discernible through a steeper long-term than short-term response or through a gradual but directional change in the short-term response norm. We observe gradual but directional change in the response norm over time with a strong effect of generation time. We conclude that more long-lived and bigger birds show signs of evolutionary adaptation while smaller birds are potentially mainly adjusting their phenology through plasticity.

Keywords: adaptation, global change, long-term data, nest cards, within-subject centering

Microevolution in dynamic natural systems: The case of lake Mývatn threespine stickleback

Katja Räsänen¹, Kasha Strickland², Blake Matthews³, Zophonías Jónsson⁴, Árni Einarsson⁵, Bjarni K Kristjánsson⁶

¹*University of Jyväskylä*

²*The University of Edinburgh*

³*Swiss Federal Institute of Aquatic Science and Technology*

⁴*University of Iceland*

⁵*Mývatn Research station/University of Iceland*

⁶*Hólar University*

The organismal phenotype, which is determined by environmental and genetic sources of variance, is a key mediator between dynamic ecological and evolutionary processes, and the direct target of natural selection. While both spatial and temporal heterogeneity is common in natural ecosystems, with major implications for the evolution of biological diversity, spatio-temporal variation is rarely investigated jointly in the wild. Here we combine spatially replicated time-series data with genomic and quantitative genetic approaches to assess spatio-temporal variation in trophic and defense traits of threespine stickleback (*Gasterosteus aculeatus*) in the highly heterogeneous lake Mývatn in Iceland. We demonstrate that over space, the stickleback population is panmictic on the genome wide scale, reflecting extensive dispersal across the lake, while some regions of the genome have diverged in face-of-gene flow. Over time, the stickleback population shows evidence of microevolution of trophic traits, with different modes of selection on different traits. Jointly with evidence for within and cross-generational plasticity from laboratory experiments, our time-series data demonstrates the contribution of different sources of phenotypic variance and selective agents on microevolutionary change in a dynamic natural system. We highlight the power of integrative approaches in spatio-temporal studies of natural populations to understand the dynamic evolution of biological diversity in the wild.

Keywords: adaptive divergence, natural selection, microevolution, dynamic ecosystems

How transgenerational sublethal pyrethroid exposure shapes Colorado potato beetle resistance and transcriptome

Aigi Margus, Maaria Kankare, Santtu Tikka, Juha Karvanen, Leena Lindström

University of Jyväskylä

The evolution of insecticide resistance in the pest species has historically been attributed to strong directional selection caused by lethal insecticide concentrations. However, there is growing evidence that sublethal doses may also drive resistance through the hormetic effects. Our previous research demonstrated that transgenerational exposure to sublethal doses in the Colorado potato beetle induces hormetic effects such as decreased larva-to-adult survival, adult body mass, and egg hatching in the invasive pest, the Colorado potato beetle. However, the mechanisms by which the sublethal doses affect the subsequent populations remain unclear. Here we investigated the transgenerational effects of sublethal insecticide doses across multiple generations by examining differentially expressed genes and KEGG pathways at the transcriptome level in two generations. Our preliminary results indicate that low-dose exposure to low doses leads to 17 differentially expressed genes and two KEGG pathways, and high-dose to six differentially expressed genes and four KEGG pathways. A similar trend was observed in a comparison between the second and third generations, where low-dose exposure led to 34, compared to five genes in the high-dose group. Our results provide insights into underlying genetic mechanisms and the potential for hormetic responses to shape resistance over multiple generations.

Keywords: hormetic effects, transcriptome, transgenerational effects, sublethal doses

Transcriptomics reveal molecular signatures of a resolved sexual conflict and respective association with colour polymorphism in tawny owls

Miguel Baltazar-Soares

University of Turku

Genome sharing in gonochorous species is expected to result in intraspecific conflicts due to intersexual competition. The emergence of sexual dimorphism is thus connected to the evolution of mechanisms that, starting from a similar genomic background, produce sufficiently disparate phenotypes to attenuate sexually antagonistic selection. From a molecular perspective it can be briefly summarised by sex-specific differences in gene expression, splicing, non-coding regulation or epigenetic marks. The tawny owl (*Strix aluco*) is a reverse sexually dimorphic species where females and males evolved distinct body sizes (smaller males), which results in sex-specific roles and therefore are a robust example of resolved sexual conflict. Here we explore, transcriptional variation among 27 juvenile tawny owls with the objective of investigating molecular signatures of resolved sexual conflict. Tawny owls also exhibit melanin-based colour polymorphism, which, given the body size differences between sexes, suggest a sex-specific onset of pigmentation. Our results show substantial sex-specific variation in terms of differentially expressed genes, single nucleotide polymorphisms and alternative exon usage in genes involved in life history traits (ZGRF1, VLDLR), behaviour (GSK3B, SLC12A) and aspects of growth (GHR, EGF, EPS8L2). Exploring sex-specific DEG revealed enrichment for biological functions associated with melanogenesis and pigment granulation in males, which together with the identification of a single up-regulated gene involved in melanogenesis (RAB38) in brown males strongly suggests different timings for the onset of pigmentation between sexes. Overall, our results reveal some of the sex-specific molecular signatures expected to be observed in the context of a resolved sexual conflict.

Keywords: evolution of sexual conflicts, sexual dimorphism, colour polymorphism, transcriptomics

Session F4

Themed session 2: Statistical approaches in multispecies modelling

Friday, 10.30-12.00, Room L304

Session chair: Nerea Abrego

Common to rare transfer learning (CORAL) enables inference and prediction for a quarter million rare Malagasy arthropods

Otso Ovaskainen¹, Steven Winter², Gleb Tikhonov³, Nerea Abrego¹, Sten Anslan¹, Jeremy and Stephanie L. deWaard⁴, Brendan Furneaux¹, Bess Hardwick³, Deirdre Kerdraon⁵, Mikko Pentinsaari⁶, Dimby Raharinjanahary⁷, Eric Rajoelison⁷, Sujeewan Ratnasingham⁴, Panu Somervuo³, Jayme Sones⁴, Evgeny Zakharov⁴, Paul Hebert⁴, Tomas Roslin⁵, David Dunson²

¹*University of Jyväskylä*

²*Duke University*

³*University of Helsinki*

⁴*University of Guelph*

⁵*Swedish University of Agricultural Sciences*

⁶*Agriculture and Agri-Food Canada*

⁷*Madagascar Biodiversity Center*

Modern DNA-based biodiversity surveys result in massive-scale data, including up to millions of species – of which most are rare. Making the most of such data for inference and prediction requires modelling approaches that can relate species occurrences to environmental and spatial predictors, while incorporating information about taxonomic or phylogenetic placement of the species. Even if the scalability of joint species distribution models to large communities has greatly advanced, incorporating hundreds of thousands of species has been infeasible to date, leading to compromised analyses. Here we present a novel “common to rare transfer learning” approach (CORAL), based on borrowing information from the common species and thereby enabling statistically and computationally efficient modelling of both the common and the rare species. We illustrate that CORAL leads to much improved prediction and inference in the context of DNA metabarcoding data from Madagascar, comprising 255,188 arthropod species detected in 2874 samples.

Keywords: joint species distribution modelling, transfer learning

Disentangling the role of intraspecific trait variation in community assembly with joint species-trait distribution modelling

Nerea Abrego¹, Pekka Niittynen¹, Julia Kemppinen², Otso Ovaskainen¹

¹*University of Jyväskylä*

²*University of Helsinki*

The links between intraspecific trait variation and community assembly remain little studied, partially due to the lack of statistical methods to efficiently model variation in individual-level traits and species abundances at the community level. Here we extend the joint species distribution modelling (JSDM) framework into the joint species-trait distribution modelling (JSTDM) framework to explicitly link species abundances to phenotypic variation in traits for multiple species simultaneously. Using a case study of 65 tundra plant species abundances and three key functional traits measured across 325 plots, we show how the JSTDM approach (i) estimates the statistical associations among species abundances, species-level traits and individual-level traits, relative to environmental variation; (ii) improves predictions on trait variation by using information on species abundances; and (iii) generates hypotheses about trait-driven community assembly mechanisms. The JSTDM methodology provides the much needed modelling tools to quantify the role of phenotypic trait variation in eco-evolutionary community assembly.

Keywords: Alpine community, community assembly, community modelling, phenotypic variation, trait hierarchy

Linear-time phylogenetic mixed effects component for joint species distribution modelling

Gleb Tikhonov¹, Otso Ovaskainen²

¹*University of Helsinki*

²*University of Jyväskylä*

Joint Species Distribution Modelling (JSDM) is a powerful and increasingly widely used statistical methodology in biodiversity modelling, enabling researchers to assess and predict the joint distribution of species across space and time. However, JSDM can be computationally intensive and even prohibitive, especially for large datasets and intricate model structures. One of such limitations of existing JSDM software has been related to the incorporation of information on phylogenetic similarities between species to the model. In practice, this computational limitation restricted the phylogeny-accounting JSDM applications to moderate amount of species only, greatly detracting these models' utility for increasingly available massive community datasets acquired via sequencing techniques. In this work we focus on one of the most popular JSDM software – the Hmsc R package, and scrutinously revise its component responsible for accommodating phylogenetic information. We build on the advances in the domain of macrotrait evolution comparative methods and derive an enhanced formulation of phylogenetic component in Hmsc. This revised formulation simultaneously enables assessment of covariate-specific phylogenetic strengths and linear-time scaling of computational load with respect to the number of modelled species. We implement our novel algorithm to the Hmsc package, as well as to its addon Hmsc-HPC for GPU deployment of model fitting. We supplement our presentation of the developed method with a simulation study, illustrating the computational efficiency boost. Additionally, we aim to present the practical gains of enhanced ecological inference available with our advance through a motivating real-data example case study.

Keywords: joint species modelling, phylogeny, species community

Likelihood-based methods for fitting agent-based models to data

Niklas Moser¹, Dmitri Finkelshtein², Georgy Chargaziya², Sara Hamis³, Dagim Tadele⁴, Stephen Cornell⁵, Otso Ovaskainen¹

¹*University of Jyväskylä*

²*University of Swansea*

³*Uppsala University*

⁴*Oslo University*

⁵*University of Liverpool*

Statistical ecology is facing a mismatch between commonly applied models and data, resulting in two key modelling challenges: (1) reliable predictions under global environmental change and (2) the inference of mechanisms that drive the observed ecological patterns to broaden system understanding. As most ecological processes are based on discrete interacting agents, agent-based models (ABMs) seem especially well poised to appropriately represent ecological phenomena and thus to overcome these challenges of prediction and inference. However, due to their complexity leading to intractable likelihood equations, fitting ABMs to data has been relying on heuristic approaches such as pattern-oriented modelling which lack mathematical rigour. In this study we consider a broad range of ABMs that can be defined as spatio-temporal point processes, specifically the reactant-catalyst-product models (RCP-models) that operate in continuous space and time. We derive for any model closed-form expressions for moments and cumulants of any order by applying a systematic perturbation expansion allowing us to include information beyond mean field. This results in a general, rigorously derived and asymptotically exact expression for the conditional density of any agent type given information about the distribution of other agents. We derive likelihood expressions based on the conditional density which we use in a Bayesian parameter estimation framework. We exemplify our framework with simulated and empirical snapshot and time-series data for multispecies communities in transient and stationary regimes in homogeneous and heterogeneous space.

Integrated joint distribution modeling to estimate the biomass of commercial fish in the Baltic Sea from acoustic and trawl data

Mikhail Shubin¹, Jarno Vanhatalo¹, Nicolas Goñi², Valeria Mobilia³

¹*University of Helsinki*

²*Natural Resources Institute Finland (Luke)*

³*Deltares*

Integrated species distribution models (ISDMs) have seen rapid development in the recent years. By integrating multiple data sets under single hierarchical Bayesian model has been demonstrated to improve parameter identifiability and prediction in multiple works. However, applications of ISDMs to multispecies modeling are few. In this work, we developed a Integrated Joint species distribution model (IJSDM) for three commercially important fish in the Baltic Sea. We combine annual acoustic and trawl survey data on herring (*Clupea harengus*), sprat (*Sprattus Sprattus*) and stickleback (*Gasterosteus aculeatus*) within our JSDM to provide estimates on the spatiotemporal distribution and trends in their biomasses. Herring, sprat and stickleback constitute a major part of the Baltic sea fish biomass so their biomass estimates are of great importance to fisheries management and assessment of the ecological status of the Baltic Sea. We compare our results to the results obtained with the current acoustic stock assessment method StoX, which approximates the fish stock by synthesizing data collected by Baltic International Acoustic Survey (BIAS). Unlike StoX, our IJSDM explicitly models fish abundance and its dependence on environmental covariates and provides uncertainty quantification for the estimates.

Keywords: Joint species distribution model, Bayesian statistics, Baltic Sea

Improving connectivity maps with multispecies models

Julia Hämäläinen¹, Alex Lechner², Johan Ekroos¹, Susanna Lehvävirta¹

¹*University of Helsinki*

²*Monash University*

Connectivity is crucial for population viability and biodiversity conservation by facilitating species' movement and gene flow. Connectivity conservation and enhancement is particularly important in fragmented urban landscapes. Nevertheless, connectivity is still mainly considered as either structural connectivity or from single species' perspective. Multispecies connectivity modelling is needed to study connectivity comprehensively in a feasible way; however, results should also be applicable to city planning to have an actual effect on biodiversity conservation. In this study we modelled multispecies connectivity by using expert- and literature-based parameters and resistance values for selected target species. Firstly, we modeled urban habitat connectivity of three distinctly different species: Siberian flying squirrel (*Pteromys volans*), common lizard (*Zootoca vivipara*) and European crested tit (*Lophophanes cristatus*). Then we compared connectivity outcomes with the existing connections identified by city planners, and finally, we tested the planned connections by adding those to our land cover data and rerunning the models. Graphab and Circuitscape software were used for modelling the connectivity. Delta integral index of connectivity (dIIC) was used as connectivity metrics in Graphab. Differences in the degree of isolation and delta integral index of connectivity (dIIC) values were due to dispersal capacities, modes, and habitat size and quality requirements. Circuitscape outputs revealed several areas where connectivity should be enhanced within interconnected areas. The comparison with city connectivity maps indicate that these maps are overly optimistic for connectivity from perspective of our target species. Nevertheless, the planned connections seem to enhance connectivity especially if implemented with quality requirements of each species.

Keywords: urban forests, connectivity, multispecies modelling, habitat network design

Hierarchical modelling of changing planktonic communities in the Helsinki Archipelago

James de Haast, Aleksandra Lewandowska, Janne Soininen

University of Helsinki

Understanding how communities respond to environmental changes is critical for mitigating the impact of changing oceans. Phytoplankton form the base of the food web, thus changes in their composition can have cascading effects on higher trophic levels. Hierarchical modelling of species communities (HMSC) is a Bayesian joint species distribution model that allows the inclusion of both environmental and random factors, including spatial-temporal effects, when modelling the key drivers of community change. HMSC was used to model summer phytoplankton communities recorded over the years 1966-2018 across 29 sites in the Helsinki Archipelago, Finland. The results showed that, despite long-term temperature changes and a strong nitrogen gradient related to changes in sewage processing over time, the major driver of species responses were random temporal effects. Environmental change over the past 52 years did not drive the phytoplankton community change in the Helsinki Archipelago.

Keywords: biodiversity monitoring, HMSC, plankton, marine ecology

Session F5

Themed session 6: Microbial ecology

Friday, 10.30-12.00, Room L139C

Session chair: Carlos Aguilar-Trigueros

Testing the extreme plastic mycelium hypothesis: Does grazing induce developmental plasticity in saprotrophic fungi?

Carlos Aguilar-Trigueros

University of Jyväskylä

Phenotypic plasticity—the ability of a genotype to alter its phenotype in response to environmental changes—is widespread across the tree of life and has been a focal point of research in ecology and evolution. However, the phenotypic plasticity of filamentous fungi, a dominant group of organisms in terrestrial ecosystems is little understood. Yet, the fungal body has structural flexibility that is assumed to enable them to dramatically alter their morphology in response to environmental changes. This flexibility has contributed to the hypotheses of fungi having an extreme plastic phenotype. Based on the assumption of extreme morphological plasticity in fungi, we tested whether grazing pressure induces convergence towards a common mycelial phenotype or, alternatively, if genotypes exhibit distinct trajectories of grazer-induced plasticity based on species identity. We found that each species followed a distinct developmental trajectory when exposed to grazing pressure. This species-specific response suggests that, rather than converging on a single optimal phenotype, fungi exhibit different levels of plasticity to grazing within species specific limits. Our results show that morphological traits of cord-forming mycelia have limited plasticity, the extent of which varies depending on the species, and suggest weak evolutionary pressure for the emergence and maintenance of grazer-induced plasticity.

Keywords: fungi, intraspecific trait variation, traits, microorganisms

Species sorting vs. dispersal limitation in fungal communities revealed by airborne eDNA, Earth surface data and atmospheric modelling

Jussi Mäkinen¹, Veera Norros¹, Mikhail Sofiev², Yalda Fatahi², Nerea Abrego³, Otso Ovaskainen³

¹*Finnish Environment Institute*

²*Finnish Meteorological Institute*

³*University of Jyväskylä*

Much of global microbial biodiversity has remained unexplored as its monitoring has been expensive or technically out of reach for researchers. Especially the realized dispersal ability of wind-dispersed microscopic organisms, such as fungal spores, in natural conditions has been poorly understood despite the interest among theoretical ecology, environmental management and pathogen control on this topic. In our project, SPORELIFE, we ask how habitat associations and dispersal abilities vary among fungal species with different morphological and life history traits. The question is tackled by integrating globally extensive and taxonomically comprehensive empirical fungal spore occurrence data with state-of-the-art Earth observation products. Airborne spore occurrences and Earth surface characteristics are linked using atmospheric dispersion projections (footprints) which highlight potential particle source areas under realized meteorological conditions. We integrate species, trait, atmospheric and Earth observation data in a joint species distribution model to estimate habitat requirements and the importance of different traits for sorting species. Our results show that species occurrence patterns cluster in relation to the habitat and Earth surface characteristics and that species' dispersal potential is associated with their morphology and trophic guild. Adding information on atmospheric dispersion through footprints adds to the explanatory power of the species distributions models. Our results showed that we can infer properties of fungal dispersal with the integration of spore, air circulation and Earth surface data. We present the framework as a proof of concept -type of work to highlight the progress and future potential in studying dispersal of microbial organisms.

Keywords: fungal ecology, dispersal, atmospheric modeling, joint distribution modeling

Microbial pathways of bioplastic degradation in the Baltic Sea revealed by genome-resolved metagenomics

Igor Pessi, Eeva Eronen-Rasimus, Hermann Kaartokallio

Finnish Environment Institute (Syke)

Plastic pollution is a serious threat for the oceans, particularly in coastal ecosystems. Petrochemical plastics take centuries to decompose in the marine environment, and even bioplastics – i.e. plastics that are biodegradable and/or bio-based – may decompose very slowly. Microorganisms play a central role in the cycling of organic matter in marine ecosystems, but we lack a systematic knowledge of the microbial pathways involved in the breakdown of different bioplastics. Here we studied the decomposition of biodegradable (CA, CAP, PHB and PBS) and non-biodegradable (PA and PE) bio-based plastics during a 22-month mesocosm experiment in the Baltic Sea (Southern Finland, 59°N). The biodegradable plastics decomposed at different rates, and metagenomics analyses showed that their microbiomes differ from the surrounding environment and from the non-biodegradable plastics. Different genera of Alphaproteobacteria (e.g. *Devosia*, *Hwanghaeella*, *Hyphomonas*, *Kordiimonas*, *Roseovarius*), Bacteroidota (e.g. *Fulvivirga*, *Roseivirga*), Gammaproteobacteria (e.g. *Acidovorax*, *Hydrogenophaga*, *Rubrivivax*) and Myxococcota (e.g. “JADJRH01”, *Polyangium*) were consistently detected across many biodegradable plastics and with significantly higher abundances compared to the surrounding environment and the non-biodegradable plastics. Genome-resolved analyses are being carried out, which will yield information on the microbial traits and pathways involved in bioplastic degradation. This, in turn, will provide crucial information on the effect of bioplastics in the marine food web and their impact at higher trophic levels.

Keywords: metagenomics, bioplastics, Baltic Sea

Dispersal of environmental bacteria in the context of human well-being

Mira Grönroos

University of Helsinki

Growing evidence suggests that contacts with environmental microbial communities are necessary for human health and immune system development. Thus, it is of great importance to find out how environmental microbes are transferred to human beings. However, studies on microbial dispersal in this context are rare. In a recently published correlative study, we used the relative number of bacteria shared between environmental and human samples as a measure of dispersal and studied how this measure was associated with living environment and lifestyles. Now we use an intervention set-up to study how nature activities change human microbiota and if the bacteria in different kind of green areas is transferred on human skin and in saliva. Four ninth grade classes from four schools in southern Finland participated in either hiking, geocaching, playing location-based mobile games, or a drama camp indoors. The drama camp served as control for outdoor activities. Skin swab and saliva samples were taken before and after the activity periods. Also, swab samples of collector tapes attached to participants shoes were taken once during each activity. Of these samples, quantitative PCR was used to study total bacterial abundance and 16S rRNA gene sequencing to study bacterial diversity and community composition. Bacterial total abundance in collector tapes was significantly highest for hikers, next highest for geocaching and mobile game player and the lowest for drama campers. The bacterial abundance, however, in skin and saliva samples did not change due to the intervention. Results of bacterial diversity and community composition were more variable.

Keywords: biodiversity hypothesis, dispersal, human health, immune system, microbiome

Field-based enhancement of soil microbial function in barren brownfields through soil mixing and artificial root exudate addition

Nina Goodey, Eshariah Dyson

Montclair State University

Barren, metal-contaminated soils that lack microbial activity require revitalization of microbial function prior to successful revegetation or phytoremediation. New strategies to revitalize extracellular enzyme function in inactive soils are needed. In this field study, we investigated the effect of soil mixing and artificial root exudate treatment on soil microbial function, plant germination, and plant productivity in a barren, contaminated, microbially inactive brownfield. We hypothesized that some of the previously demonstrated benefits of soil mixing and amending barren brownfield soils with artificial root exudates in the laboratory setting can be replicated in the field setting. Rye grass germination rates were significantly higher in mixed soil ($53 \pm 8\%$) compared to structured soil ($30 \pm 7\%$), demonstrating the benefits of mixing the surface (top 10 cm) of barren soils in-the-field prior to planting. An addition of artificial root exudates to the soil significantly increased phosphatase activity ($1.8 \pm 0.1 \mu\text{mol}/(\text{hrgdrysoil})$) compared to Control ($0.2 \pm 0.03 \mu\text{mol}/(\text{hrgdrysoil})$), highlighting their potential in enhancing soil microbial function in the field setting. The simultaneous application of artificial root exudates and seeds did not result in significant changes in germination rates or plant biomass, emphasizing the importance of applying artificial root exudates before seed introduction in a stepwise manner to revitalize the soil for effective greening. The findings underscore the in-field benefits of soil mixing and artificial root exudate application in promoting germination and soil microbial function, respectively, in a barren, highly contaminated, microbially inactive brownfield.

Keywords: barren brownfield, artificial root exudates, soil ecosystem services, phytoremediation, microbial diversity

Single-cell transcriptomics reveals functional insights into non-model phytoflagellate and metabolically-linked bacterial community

Aditya Jeevannavar¹, Javier Florenza², Stefan Bertilsson³, Manu Tamminen¹

¹University of Turku

²Uppsala University

³Swedish University of Agricultural Sciences

The application of single-cell transcriptomics to non-model microeukaryotes is often limited by the absence of reference genomes and comprehensive annotation databases. This gap presents a significant challenge in environmental transcriptomics, complicating the interpretation of data from non-model organisms. This study aims to demonstrate how cutting-edge bioinformatics tools can be employed to extract biologically meaningful information from a non-model unicellular eukaryote: *Ochromonas triangulata*. We sought to demonstrate the relationship between growth states and associated transcriptomic profiles and to identify potential unexpected transcriptional states. To this end, *O. triangulata* cells from two distinct growth phases were isolated using FACS and single-cell transcriptomic libraries were constructed using the Smart-seq2 protocol. In the absence of a reference genome, transcriptomes were assembled de novo using Trinity, followed by annotation via 2D sequence similarity against Swiss-Prot and 3D structural alignments against AlphaFoldDB. Differential expression was analyzed using DESeq2, and metabolic pathways were mapped using Pathview onto KEGG-Orthology pathways. Clustering read counts by tSNE and DBSCAN revealed two distinct transcriptional states correlating with the growth phases and a third previously unidentified cluster. Differential expression analysis and metabolic mapping revealed the biological basis of the transcriptional states, showing variable oxidative stress responses, ribosome activity, CO₂ fixation, and carbohydrate metabolism. Residual rRNA reads successfully confirmed the taxonomic identity of the cells and the bacterial rRNA reads permitted characterizing the bacterial community associated with the single cells. This study demonstrates the maturity of current bioinformatics to conduct transcriptional studies in environments where the surveyed organisms are not known a priori.

Keywords: Smart-seq2, microeukaryote, single-cell transcriptomics

Poster session

Wednesday, 16.00-19-30, Floor 2 & 3 lobby

Poster 1: Insights into the Pace of Life Syndrome hypothesis from a behavioral selection experiment on *Drosophila*

Anni Hämäläinen

University of Turku

The Pace of Life Syndrome (POLS) hypothesis suggests that life history traits are intricately linked with physiological and behavioral traits that support distinct life history strategies. For instance, a fast pace of life - characterized by a shorter lifespan and higher reproductive rate - is hypothesized to depend on rapid resource turnover, facilitated by an accelerated metabolism and increased activity levels to secure necessary resources. Conversely, a slow life history strategy may be optimized by reduced metabolic rates and lower activity levels. The core of the POLS hypothesis is that certain behavioral traits closely covary with life history traits, providing adaptive advantages in particular ecological contexts. Due to the high plasticity of many behavioral traits, behavioral traits may also be critical in adapting to novel environmental conditions. The “behavior evolves first” hypothesis suggests that behavioral adjustments in response to environmental shifts can provide immediate fitness benefits, potentially allowing time for subsequent adaptations in other aspects. This study addresses the intersection of these hypotheses through an artificial selection experiment on *Drosophila simulans*, in which flies were selected for high and low spontaneous activity levels, with unselected lines maintained as controls. By the fifth generation, significant divergence in intrinsic activity levels was observed, with high-activity lines expressing on average three times higher frequency of spontaneous activity than low-activity lines. I will present preliminary findings on coadapted traits within these activity-selected lines, using these data to evaluate empirical support for the POLS hypothesis under artificial behavioral selection.

Keywords: behavioral ecology, experimental evolution, life history

Poster 2: Epistasis among fungicide resistance mutations

Luka Biočanin, Ilkka Kronholm

University of Jyväskylä

Fungicide resistance poses a significant threat to agricultural productivity, as fungal pathogens increasingly adapt to withstand fungicides. Understanding the genetic interactions, or epistasis, among fungicide-resistant mutations is crucial for predicting the evolutionary trajectories of resistant strains and informing sustainable control strategies. In this study, we investigated the epistatic interactions among resistance mutations by evolving 20 lines of the filamentous fungus *Neurospora crassa*, with 10 lines for each mating type, under incrementally increasing concentrations of the fungicide tebuconazole, culminating at 2 µg/mL. Following the evolution experiment, we will sequence the genomes of the evolved lines to identify mutations conferring resistance. Crosses will be then made between lines harboring distinct resistance mutations to evaluate the extent to which epistasis influences the fitness of resistant strains. By quantifying growth rate variations among offspring with different combinations of resistance mutations, this research aims to clarify whether epistasis hinders, enhances, or has a neutral effect on fungal growth rate in the context of fungicide resistance. These findings will contribute to our understanding of resistance dynamics and provide insights into the potential limitations and strengths of resistant fungal populations under ongoing selective pressures.

Keywords: fungicide resistance, epistasis, *N. crassa*, tebuconazole, evolutionary dynamics

Poster 3: Genetic adaptation to environmental change in evolving populations

Salvatore Bannò, Ilkka Kronholm

University of Jyväskylä

Theoretical models suggest that when the environment fluctuates slowly, over hundreds of generations, populations adapt to the environmental optimum primarily through genetic changes rather than relying on phenotypic plasticity. Furthermore, long-term experimental evolution studies have shown that populations consistently introduce novel mutations over extended periods. We will test the hypothesis that during initial adaptation populations will fix new mutations that allow them to adapt to the new environment. Then as the environment starts to change back, instead of reverting their changes, compensatory mutations that eliminate any possible trade-offs with the original environment will be fixed. When compared to populations where the environment stays constant, we can determine whether environmental fluctuations promote genetic divergence. We will test this using experimental lines of fission yeast that will undergo evolutionary adaptation under slowly fluctuating environments. Allele frequencies will be tracked using time-series pool sequencing data from all populations. To test whether accumulated mutations play an active role in adaptation, the growth rates of evolved and ancestral populations will be measured and compared across different environments.

Keywords: experimental evolution, genetic adaptation

Poster 4: The effect of size-selective harvesting on the epigenetic variation in zebrafish

Stephan Van Dijk, Daniel Sadler, Phillip Watts, Phillip Uusi-Heikillä

University of Jyväskylä

While high genetic diversity in the population can increase its chance to endure environmental changes in the long term, in the short term a population can also adapt if individuals have high levels of phenotypic plasticity. One underlying mechanism defining phenotypic plasticity comes from the epigenetic variation found in the population, such as DNA methylation. However, there is the possibility that, just as with genetic variation, the current fishing practices (i.e., high mortality rates and distinct selectivity) also deplete epigenetic variation. So we wondered, can size-selective harvesting reduce epigenetic diversity and alter methylation patterns and which regions does it alter? We looked into this by sequencing the entire epigenome of individuals originating from experimentally size-selected populations of zebrafish, using whole genome bisulfite sequencing. By doing so, we can determine which genes are most likely to be methylated in the population. By combining this approach with whole genome sequencing, it is possible to get a comprehensive picture of how size-selective harvesting affects the exploited fish stock on a molecular level. This will increase our understanding of the mechanisms underlying fisheries-induced evolution and potentially help in sustainable management planning.

Keywords: fisheries, size-selective harvesting, DNA methylation

Poster 5: Population genomics of the wood tiger moth across time and space.

Melanie Brien¹, Juan Galarza², Johanna Mappes¹

¹*University of Helsinki*

²*University of Oulu*

The wood tiger moth, *Arctia plantaginis*, displays bright hindwing colours associated with unpalatability, and males have discrete colour morphs which vary in frequency between localities. We used long term sampling of the moth in multiple populations across Finland to analyse how phenotypes, including colour, melanisation and size, change across time and how these link to climatic changes. Using long-read haplotagging sequencing, we looked at genomic changes over an 11-year period, focussing on allele frequencies, gene flow and signatures of selection. We also looked at wider-scale differences between populations, comparing monomorphic and polymorphic populations from Georgia, Scotland and Estonia.

Keywords: population genomics, genetics

Poster 6: From species to genetic diversity: patterns of taxonomic and genetic diversity of rock-pool tardigrades

Matteo Vecchi¹, Jakub Godziek¹, Claudio Ferrari², Diego Fontaneto³, Ingemar Jönsson⁴, Daniel Stec¹

¹*Institute of Systematics and Evolution of Animals Polish Academy of Sciences*

²*SCVSA Department*

³*IRSA - CNR Italy*

⁴*Kristianstad University*

Concerns for preserving biodiversity are widespread among the general public and the scientific community. To be conserved, biodiversity needs to be thoroughly understood and quantified. Quantification and catalogation of biodiversity is often laborious and complicated, but molecular techniques such as metabarcoding are proving to be extremely helpful in this task. Tardigrades are a group of microinvertebrates known for their ability to survive complete desiccation. Traditionally tardigrades have been studied from mosses, lichens, leaf litter, ponds, and stream and marine sediments; however, many other habitats have been to date neglected, including rock pools. We surveyed tardigrade diversity in freshwater rock pools in Italy, Poland and Sweden, with the aim to describe their species and genetic diversity patterns through DNA metabarcoding of the markers 18S and COI. Tardigrade alpha diversity was found to be negatively influenced by the rock pool volume, allowing to hypothesize that lower competition and predation from less specialized taxa may allow tardigrades to colonize and persist in smaller pools. Multiple *Ramazzottius* species forming a monophyletic clade were found to be present and abundant in rock pools, often with multiple co-occurring species in the same rock pool. Interestingly, only some of those taxa show genetic patterns congruent with isolation by distance. Our findings highlight the complexity of tardigrade biodiversity and dispersal in freshwater rock pools, underscoring the need for further research into microinvertebrate distribution patterns and the factors that influence genetic diversity across habitats.

Keywords: biodiversity, molecular ecology, Tardigrada, metabarcoding

Poster 7: Metal-induced effects on nest and gut microbiota in two related passerine birds

Miia Rainio, Lyydia Leino, Eero Vesterinen, Tapio Eeva

University of Turku

Metals are well-known antimicrobial agents, and metal pollution may significantly affect the microbial communities of wild birds, leading to various health issues, immune dysregulation, and detrimental effects on gut microbiota function. We examined the effects of metal pollution on the early-life microbial environment of wild passerines by assessing bacterial diversity and community composition in nestling feces and nest materials using 16S rRNA sequencing. Our study focused on two common model species, the great tit (*Parus major*) and the blue tit (*Cyanistes caeruleus*), which frequently nest in metal-polluted areas in Finland. Fieldwork was conducted near a copper-nickel smelter, the most metal-polluted site in Finland. We assessed microbiota responses to pollution, habitat, and microclimate, linking these to individual performance metrics such as brood size, growth, and fledging success. The most common bacterial phyla in nestling feces were Firmicutes, Proteobacteria, and Chlamydiae, while Proteobacteria, Actinobacteria, and Firmicutes were predominant in nest materials. While fecal and nest microbiota displayed some similarities both within and between species, distinct differences were observed across multiple bacterial orders. Our findings revealed that fecal microbial alpha diversity was reduced in polluted areas compared to control areas, whereas nest microbiota showed no significant differences between areas. However, both fecal and nest microbial communities differed between species and study areas. Additionally, several bacterial orders were differentially abundant across study areas. Overall, our results suggest species-specific effects of metal pollution on bacterial diversity and community composition in nestlings, either directly or indirectly through diet or other environmental factors.

Keywords: bacterial diversity, birds, metals, microbiota

Poster 8: The role of the gut microbiome in thermal adaptation in wild birds – PhD research plan

Maria Correia, Suvi Ruuskanen, Charlotte Davies

University of Jyväskylä

Understanding animals' response to temperature provides insights into how animals cope with climate change and temperature shifts across the globe. Therefore, studying mechanisms that can alter host fitness can help predict how wild populations respond to environmental perturbations. Gut microbiome (GM) is a key regulator of host physiology, influencing host phenotypes and impacting fitness. As microbes can adapt to environmental changes quicker than the host, the GM may be crucial in host adaption to environmental perturbations. Currently, there is limited knowledge on how GM influences host thermoregulatory capacity. Short-term exposure to fluctuating temperatures may alter GM composition in wild birds, which can influence the hosts metabolism and thermoregulatory capacity. Diet also plays an important role in the hosts ability to cope with environmental conditions, influencing diversity and composition of GM which may further affect the hosts energy metabolism. Long-lasting effects from early developmental conditions can be passed on through generations, with GM transferred from parents suggested as an important mediator of environmental effects, influencing offspring phenotype and fitness. Overall, this project aims to understand how GM variation caused by environmental temperature can influence the hosts thermoregulatory capacity. This will be achieved by a series of experiments using wild Great tits (*Parus major*) in Finland to investigate (1) the short-term flexibility of the GM to environmental temperatures, (2) and the effect food quality has on this response; (3) the role of the GM in transgenerational thermal plasticity, and (4) its adaptive function in host thermoregulation, cold tolerance, and winter survival.

Keywords: gut microbiome, thermoregulation, birds

Poster 9: Gut microbiome underlying winter adaptations in wild populations of Great tits (*Parus major*)

Charli Davies¹, Andreas Nord², Antoine Stier³, Suvi Ruuskanen¹

¹University of Jyväskylä

²Lund University

³Université Claude Bernard Lyon 1

Winter poses a key environmental challenge to survival in endotherms. Combination of reduced temperatures, resources, and day lengths present energetic and thermoregulatory challenges in wild populations living at high latitudes. By increasing metabolic rate through thermogenesis and mitochondrial bioenergetics, endothermic animals can adapt to decreasing temperatures by maintaining a stable body temperature, but this is energetically costly. One promising mechanism for regulating energy acquisition and heat production and thus enabling the host to adapt to rapid environmental perturbations, is the gut microbiome (GM). To see if the GM can act as a mechanism for winter adaptation, we first study longitudinal associations between winter conditions and the GM in two wild populations of great tits (*Parus major*), which experience varied environmental conditions and wild-caught individuals in captive conditions kept under either summer or winter temperatures. Secondly, to assess whether temperature-induced changes in the GM are linked to thermoregulation we associated GM composition with biomarkers of thermal physiology for both wild and captive populations. Combination of correlative and experimental methods using wild-caught individuals allows assessment of the role of GM-mediated adaptation to environmental changes, demonstrating a new route of thermal adaptation in birds.

Keywords: winter adaptation, gut microbiome, thermoregulation, Great tit

Poster 10: Abundance of brown trout parr in stream habitats with and without large wood

Alisa Koski¹, Reetta Väättäinen², Kimmo Sivonen³, Jukka Syrjänen⁴, Central Finland's Water & Environment Association

¹*University of Jyväskylä*

²*University of Eastern Finland*

³*Co-operative Kala- ja vesistötutkimus Vesi-Visio*

⁴*Co-operative Vesi-Visio*

Large wood has been found to be crucial component in riverine ecosystems. However, because of the heavy channelization of the channel form and intensive forestry practices in the last few decades, the number of large wood has decreased worldwide. River restoration aims to improve the effects of channelization and restore the channel to its original, pre-channelized form, and this can be achieved, among other things, by adding large wood to the channel. In this study, we investigated how large wood affects the density of brown trout parr in a few natural rivers in Southern Finland and Sweden. Also, other microenvironmental factors, including water depth, current velocity at 60 % depth, aquatic moss and macrophyte coverage combined, dominant and subdominant substrate particle size, and shading of riparian bushes and trees were examined as responsible for differences in parr density in different areas. We found 0-year-old brown trout parr density to increase when large wood density increased. We did not find similar results in 1-year-old and 2-year-old or older brown trout parr.

Keywords: salmonid, density, LWD, large woody debris

Poster 11: Intraspecific diversity of salmonids in cold-water lakes

Sini Halonen

University of Jyväskylä

Ecological variation between individuals of a species, i.e. intraspecific variation, can be driven by differences in genetics or expressed traits (phenotype) within and between populations. Intraspecific diversity contributes to speciation and the ability of populations to adapt to changing environmental conditions. Although there is increasing evidence that intraspecific diversity is common, it remains understudied how this variation is driven by large-scale natural and anthropogenic factors. My PhD project focuses on two salmonid species, Arctic charr (*Salvelinus alpinus*) and brown trout (*Salmo trutta*), which show high intraspecific diversity and thus are ideal targets for studies of environmental drivers of individual variation. I use stable isotope and genomic data from numerous cold-water lakes to examine e.g. linkages between phenotypic (trophic) and genomic (microsatellites) diversity under different environmental conditions. To elucidate the temporal stability of intraspecific trophic diversity, I compare the isotopic variation in fish muscle and liver tissues with stomach contents data providing insights to individual's diet at different temporal resolutions. I will present preliminary results based on stable isotope analysis and stomach content data that suggest intraspecific trophic diversity varies with the environment. Cold-water lakes provide essential ecosystem services, but their valuable salmonid populations are declining globally. As highly mobile generalist consumers, the abundance, size structure and trophic ecologies of salmonids have fundamental consequences for overall ecosystem structure and function. Therefore, improved understanding of the drivers of intraspecific variation in salmonids would facilitate conservation and management of cold-water Arctic and alpine lakes.

Keywords: biodiversity, adaptation

Poster 12: Vegetation functional traits, water quality and phenology shape Baltic fish larval productivity

Sum Yi Lai¹, Emy Guilbault¹, Lari Veneranta², Jarno Vanhatalo¹

¹*University of Helsinki*

²*Natural Resources Institute Finland*

Eutrophication and anthropogenic disturbances in coastal areas largely contribute to the decline in aquatic biodiversity. Such stressors alter the water quality and the sea bottom habitat which can limit the abundance and productivity of fish populations in their early life stage. In the Gulf of Bothnia, coastal fish populations are socio-economically and culturally important to the Baltic countries, whilst playing a significant role in the food web of the Baltic ecosystem. The alterations to the coastal environment directly affect the carrying capacity and the diversity of fish larvae yielding critical consequences on the sustainability of fish populations. Despite these growing threats, the ecosystem functions of juvenile fish communities in relation to their habitat diversity and suitability are rarely explored in this region. Therefore, we evaluated the importance of the key vegetation functional traits and physical characteristics that determine the abundance of Baltic herring, pike perch, European perch, and European smelt larvae in the Gulf of Bothnia. Using joint Bayesian species distribution models, we investigated the functional traits and spatial context of benthic vegetation and macroalgae distribution in driving fish larvae abundance. We show that the importance of vegetation diversity, water quality, and within-year variation varies between the four fish species. Thus, our work aspires to bridge the link between biodiversity and ecosystem-functions and stresses the importance of the conservation of habitat diversity to facilitate the growth and productivity of different juvenile Baltic fish species.

Keywords: fish larvae, habitat quality, population ecology, functional diversity

Poster 13: Effects of historical exposure to artificial light at night on the behavior and life history of *Gammarus pulex*: Examining the possibility of adaptation

Johannes Männistö, Dhanushika Wijekoon, Ulrika Candolin

University of Helsinki

1. Artificial light at night (ALAN) is one of the major threats to biodiversity. 2. We investigated if a key species of many freshwaters, *Gammarus pulex*, can adapt to ALAN. We exposed individuals from historically exposed and unexposed populations to ALAN in the laboratory for eight weeks to assess a) whether historical exposure to ALAN influences behavioral responses to present ALAN, which would indicate genetic adaptation, b) whether the impact of past and present ALAN changes across the lifetime of individuals. 3. We found historical exposure to ALAN to influence behavior during both days and nights in a sex-specific manner. Females from historically exposed populations reduced their swimming activity during days and increased it during nights when exposed to ALAN. This differed from females from unexposed populations who increased their swimming activity during days but not during nights. Moreover, females from historically exposed populations reduced their same-sex contacts during nights, while females from unexposed populations increased the contacts. However, the difference between populations in same-sex contacts declined over the eight weeks. Males did not change their daytime behavior when exposed to ALAN, independent of historical exposure, but they altered their night time behavior: males from historically exposed populations reduced the frequency of male-male and male-female contact less than males from unexposed population. 4. The results indicate that *G. pulex* exhibits behavioral responses to long-term exposure of ALAN, potentially driven by mechanisms of phenotypic plasticity or genetic adaptation.

Keywords: light pollution, stream ecology, environmental change, invertebrates, stream ecology

Poster 14: Historical exposure to artificial light shapes *Daphnia* responses across an urban-rural gradient

Yuhan He¹, Huan Zhang², Jiale Guan², Panpan Wang³, Yue Wu², Kangshun Zhao², Ulrika Candolin¹

¹*University of Helsinki*

²*Donghu Experimental Station of Lake Ecosystems*

³*Huazhong Agricultural University*

Artificial light at night (ALAN) is an increasingly pervasive environmental stressor, particularly in urban areas, yet its long-term ecological impacts on organisms remain understudied. We investigated the impact of historical exposure to ALAN (urban contra rural populations) and present experimental exposure in the laboratory on morphological and life-history traits of *Daphnia pulicaria* using a 2×2 experimental design. We assess the responses of clonal populations across three generations to examine both immediate and multigenerational plasticity in reaction to historical and laboratory exposure to ALAN. Our results show that populations historically exposed to ALAN exhibit faster maturation, longer lifespans and have a higher reproductive success than unexposed populations in both the presence and absence of ALAN. In contrast, naïve populations have lower reproductive success when exposed to ALAN, with the artificial light accelerating maturation, reducing clutch intervals and shortening lifespan, with the effect increasing across generations. These findings suggest that local adaptation to historical exposure to ALAN has taken place through selection for phenotypic plasticity. This highlights the potential for ALAN to act as an evolutionary force in urban ecosystems and underscores the need for further research into its long-term ecological and evolutionary consequences.

Keywords: Cladocera, local adaptation, multi-generational effect, phenotypic plasticity, urbanisation

Poster 15: Urban evolution of dispersal ability in the butterfly *Pieris napi*

Juho Kökkö¹, Matthew Nielsen², Marjo Saastamoinen¹

¹*University of Helsinki*

²*University of Bremen*

Dispersal is a key trait in a species' life history, affecting persistence, range, and gene flow. In the fragmented urban landscape, the costs of dispersal are likely high due to individuals having to cross resistant environments to move from habitat patch to patch. How, then, have dispersal characteristics evolved in urban environments? While cities are a relatively novel environment, dispersal is an important trait that can experience rapid evolution. In theory, increased fragmentation could either increase dispersal to overcome the barriers of a fragmented landscape, or conversely decrease dispersal, if moving between habitats is not cost-efficient. Urban dispersal has been researched before by looking at occurring gene flow and community level dispersal traits. Few studies, however, have attempted to gauge the dispersal capability of urban individuals. I aimed to estimate the dispersal ability of the green-veined white butterfly (*Pieris napi*). I collected *P. napi* individuals from rural and urban environments around the city of Helsinki in 2024 and measured the flight metabolic rates and wing parameters of their offspring. Both butterfly flight metabolics and wing metrics have been used to indirectly estimate dispersal ability in prior studies. My results do not show a difference in the flight metabolics between butterflies of urban and rural origin, and do not therefore implicate evolution in the dispersal ability. A lack of evolution could mean that urban fragmentation is not always drastic enough to shift species dispersal traits. While still under analysis, the wing shape data will provide further context for these results.

Keywords: evolution, dispersal, urban ecology

Poster 16: Breeding dispersal in the common eider

Ida Hermansson¹, Markus Öst¹, Mikael von Numers¹, Kim Jaatinen²

¹*Åbo Akademi University*

²*Finnish Environment Institute*

Breeding dispersal, or movement between successive breeding sites, is poorly understood. This process may aid in predator avoidance if individuals adopt a ‘win-stay, lose-switch’ (WSLS) strategy, but dispersal decisions are also influenced by individual traits. We studied the drivers of breeding dispersal within and between breeding islands in female common eiders (*Somateria mollissima*), a ground-nesting site-fidelic sea duck, over a 21-year period (2003–2023) in SW Finland, Baltic Sea. The sharp increase in predation on this population led us to expect a rise in dispersal over time. Using long-term data on individual traits and environmental factors, we investigated which factors influence dispersal, based on GPS-tracked nest locations of known individuals. Breeding dispersal distance was individually repeatable between years ($r = 0.45$). Consistent with the WSLS strategy, both dispersal distances within islands and the likelihood of switching islands increased following predator-induced breeding failure and years with high island-specific nest predation risk. Older females switched islands less frequently, likely due to accumulated experience and age-dependent anti-predator strategies. Island switching was also more likely in years with abundant white-tailed eagles (*Haliaeetus albicilla*), the main predator of adult eiders, suggesting that females are capable of perceiving predation risk beyond the immediate nest surroundings when dispersing outside the previous ‘home’ colony. Together, these findings highlight the complex interactions between predation, environmental cues, and individual traits, underscoring the eiders’ ability to make informed dispersal decisions when facing elevated predation pressure.

Keywords: behavioral ecology, dispersal or movement

Poster 17: Mammals gone urban: Exploring behavioural differences of three medium-sized mammals in Finnish gardens along an urban-rural gradient.

Mélissa Gagnière, Martin Seltmann, Timo Vuorisalo

University of Turku

In Finland, red foxes (*Vulpes vulpes*), European badgers (*Meles meles*), and raccoon dogs (*Nyctereutes procyonoides*) have been observed exploiting anthropogenic food sources and shelters, becoming veritable city dwellers. However, no studies have assessed variation in behaviours towards novelty in these urban species in Finland so far. Therefore, it is essential to conduct such studies to mitigate potential future human-wildlife conflicts, understand how animals adapt to urbanisation, and develop effective wildlife management strategies to help prevent biodiversity loss. We aim to evaluate adaptation in these urban mammals by examining whether their behaviours towards novelty change along an urban-rural gradient. We are conducting behavioural experiments on free-living animals in private gardens and forested areas, using novel objects and camera traps over two-week periods. The study period for 2024 ran from June to September, with 70 gardens studied, resulting in approximately 500 useful video recordings. We plan to continue our experiments annually until 2027. The experiments involve food-baited novel objects (e.g. plastic or aluminium-covered boxes) or surfaces (e.g. bubble wrap, aluminium foil), requiring animals to interact with them to access the food reward. We will measure bold behaviours, defined as any physical interaction with the object/surface (e.g. pushing, biting, sniffing). A similar study by Morton et al. (2023) on red foxes in UK cities found that animals showed bolder behaviours, with greater willingness to interact with objects compared to rural areas. We anticipate similar results, with possible additional effects related to the unique 'midnight sun' phenomenon, offering valuable insights into urban wildlife behaviour.

Keywords: urban ecology, animal behaviour, novel object

Poster 18: The gut microbiome as a driver of foraging behaviour in predator-prey interactions.

Christopher John Irving, Liisa Hämäläinen, Suvi Ruuskanen

University of Jyväskylä

Aposematism is a defensive strategy that combines a deterrent with visual signals. High intra-species variation in learning time to avoid the signal is seen, and this variation in behaviour influences prey defense evolution. Here, we aim to investigate if the micro-gut biome is a driver in maintaining this heterogeneity. Research with mammals establishes a relationship between gut microbiome, diet and behavior. We ask if this relationship impacts ecosystems and test if there is a feedback loop between the predator gut microbiome, cognition, foraging decisions and concentration of prey toxins consumed, and how this influences the selection pressures on chemical defenses. This provides multiple objectives: First, testing the association between the predator gut microbiome and foraging behaviour, quantifying the effect of consuming aposematic prey on the predator gut microbiome, identifying the defensive toxins that impact the predator gut microbiome, measuring the causal effect of the gut microbiome on behavior and then testing the effect of the early-life gut microbiome on foraging behaviour in adulthood. The model predators employed will be wild-caught great tits (*Parus major*), that will undergo altered gut microbiomes, through prey toxins and faecal microbiota transplantations. The microbial gut composition will be measured, and behavioral experiments will assess avoidance learning and dietary awareness. This investigation will deepen our understanding of the role of the predator gut microbiome in aposematism and uncover insights into the variation in predator behavior. Additionally, this investigation can propose if the gut microbiome is a factor in shaping ecology and evolution.

Keywords: microbiome, predator-prey, behaviour

Poster 19: A new method to measure predation activity within the canopy and compare it to ground and shrub level activity

Csaba Béla Eötvös, Melinda Nagy-Khell, Máté Farkas, Bálint Horváth

University of Sopron

The canopy provides a variety of microhabitats, each with its specific microclimate. Climate change is causing accelerating changes in the canopy, with strong negative impacts on specialist organisms in particular, as well as changes to the communities living there. These communities represent 50% of the total terrestrial biodiversity. To help maintain the ecological balance, canopy research is important. In the past, they focused on the canopy of tropical forests, as it was thought that the distribution of species within the canopy was more homogeneous in the temperate zone. However, in the last 15 years, several studies have shown that a similar diversity within the canopy insects can be observed in temperate forests. Predation is one of the most important ecological processes because of its community-structuring effects. I aim to present a method to measure the predation activity in different parts of the canopy and to compare it with the ground and shrub level activity. This method uses sampling columns made of PVC pipes. With the help of the columns, 50 cm long branches placed in water bottles are moved to the appropriate heights by ropes. So we can even reach the canopy surface. Artificial caterpillars made of green plasticine are placed on the branches, imitating a common prey. The activity obtained does not reflect the real predation activity, but the habitats studied are comparable based on the results.

Keywords: canopy predation, dummy caterpillar, artificial prey, forest

Poster 20: Prevalence and ecological impact of zoosporic parasites on harmful cyanobacterial blooms in the northern Baltic Sea

Siru Gestrin, Katja Mäkinen, Jonna Kangas, Saija Saarni, Silke Van den Wyngaert

University of Turku

Zoosporic parasites of phytoplankton are ubiquitous in aquatic environments, yet little is known about their identity, life cycle, or ecological impact. One of the most visible results of eutrophication in the Baltic Sea are the massive summer blooms of filamentous cyanobacteria. These nitrogen-fixing cyanobacteria add nutrients to an already eutrophic ecosystem, and produce toxins harmful to animals and humans. Previous studies suggest that zoosporic parasites may play an important role in modulating cyanobacterial blooms, however, this dynamic remains unstudied in the Baltic Sea. Our study aims to narrow this knowledge gap by characterizing the fungal and fungus-like zoosporic parasites capable of infecting cyanobacteria and quantifying the prevalence of parasite infections on dominant cyanobacterial species in the northern Baltic Sea. Water and sediment trap samples were collected weekly throughout the summer of 2024, in the Archipelago Sea, near the Archipelago Research Institute of Seili. Preserved samples are being analysed microscopically to quantify the total biomass of filamentous cyanobacteria and the prevalence of parasite infections. Initial microscopy analysis has revealed parasite infections on all three dominant filamentous cyanobacterial genera: *Dolichospermum*, *Aphanizomenon* and *Nodularia*. An Oomycete-like parasite was observed infecting *Nodularia*, marking the first discovery of this type of infection in brackish cyanobacteria. Individual infected cyanobacterial filaments were picked manually and their DNA will be amplified using multiple displacement amplification. The 18S rDNA genes of these isolates will be sequenced using Sanger technology, to link molecular data with morphological characteristics.

Keywords: parasites, pathogens or wildlife disease, microbial ecology, species interactions, aquatic ecology

Poster 21: Environmental triggers of resting spore germination in the chytrid parasite *Staurastromyces oculus*

Silke Van den Wyngaert¹, Laura Garzoli², Alena Gsell³

¹University of Turku

²Water Research Institute (CNR-IRSA)

³Leiden University

Many parasites produce resting spores to survive host absence or adverse conditions. Insights into the environmental triggers for switching between active and resting phases is crucial for understanding host-parasite dynamics in nature. Zoosporic fungi from the *Chytridiomycota* phylum, known as chytrids, are widespread parasites of phytoplankton, impacting bloom dynamics and influencing key processes in aquatic ecosystems. Though chytrids produce resting spores, the triggers for their germination remain poorly understood. A previous study found that germination could be induced in cold, dark-stored spores by exposing them to increased temperature and light. To disentangle the effects of temperature, light, and host presence, we conducted a microcosm experiment with the phytoplankton-chytrid model system *Staurastrum* sp. – *Staurastromyces oculus*. Resting spores were stored for 3 months at 4°C or 16°C in darkness or light. They were then exposed to combinations of temperature (4°C or 16°C), light (light or dark), and host presence (with or without host). Using automated fluorescence microscopy, we imaged and quantified resting spores, germination, and new infections daily for the first 5 days, and at days 7, 10, and 14. Our preliminary results indicate that an increase in temperature following 4°C storage is a primary trigger for germination, while light does not appear to significantly influence the process, as infections were observed even in dark conditions. Interestingly, the highest infection rate occurred in spores stored and incubated at 16°C with light. These findings suggest that multiple pathways can induce germination in chytrid resting spores, primarily through temperature shifts or host presence.

Keywords: parasites, species interactions, life history, ecophysiology

Poster 22: Loisen isäntämanipulaatio lisää isännän alttiutta erityyppisille saalistajille

Venla Pekkarinen, Esa Koskela, Anssi Karvonen

Jyväskylän yliopisto

Loiset, joilla on monivaiheinen elinkierto, voivat manipuloida väli-isännän alttiutta saalistajille parantaakseen transmissiota pääisäntään. Tämä voi kuitenkin altistaa isännän myös loiselle soveltumattomien petojen saalistukselle, mikä johtaa loisen elinkierron epäonnistumiseen. *Diplostomum pseudospathaceum* –imumatoloinen loisii väli-isäntäkalan silmän linssissä ja heikentää kalan näkökykyä. Tutkin pro gradu - työssäni sitä, miten *D. pseudospathaceum* infektio merilohessa (*Salmo salar*) ja kirjolohessa (*Oncorhynchus mykiss*) vaikuttaa niiden saalisalttiuteen erityyppisille pedoille. Vertailin saalisalttiutta loisen varsinaisiin pääisäntiin (lokit ja tiirat) ja pääisännäksi huonommin soveltuviin sukeltaviin lintuihin (koskelo) simuloimalla lintujen saalistusta erilaisilla haavintatavoilla, sekä haukeen (*Esox lucius*), joka ei kelpaa loisen pääisännäksi. Havaitsin, että infektio lisäsi kalojen alttiutta lintujen saalistukselle, mutta myös merkittävästi pääisännäksi soveltumattoman hauen saalistukselle. Lisäksi havaitsin eroja kalalajien välillä. Koska manipulaatio altistaa väli-isäntäkalat myös pääisännäksi kelpaamattomien petokalojen saalistukselle, tällä voi olla vaikutusta loisen nettotransmissioon, saaliskalalajista riippuen.

Keywords: parasites, species interactions, behavioral ecology

Poster 23: Influence of water color on aquatic invertebrate communities in boreal wetlands

Clarisse Blanchet¹, Morgane Ducoin², Bastien Parisy¹, Aurélie Davranche³, Kimmo Kahilainen¹, Petri Nummi¹, Céline Arzel⁴

¹*University of Helsinki*

²*Lammi Biological Station*

³*University of Angers*

⁴*University of Turku*

Freshwater browning is affecting the trophic webs of boreal aquatic ecosystems. Aquatic invertebrates' abundance has declined over the last twenty years due to browning, but little is known about its impact on aquatic invertebrates' richness and community composition. We examined aquatic invertebrate community composition and diversity in Finnish lakes and temporary and beaver wetlands across a water color (mg Pt/L) gradient. Using Hierarchical Modelling of Species Communities (HMSC), we analyzed the relationship between water color, habitat type, time, and invertebrate community metrics. Results indicated a decrease in invertebrate taxa richness as water color increased, with stable richness throughout the trapping period, although occurring species may differ. Chironomids were more likely to occur in brown water color, while environmental indicator taxa (Ephemeroptera, Haliplidae and Hydrophilidae) showed negative responses to increasing color. Beaver wetlands exhibited higher taxa richness than other habitats, with community composition varying among habitats. Culicidae were more likely to occur in temporary wetlands, and water beetles had lower occurrence probability in lakes compared to other habitats. This study highlights the general negative effects of brown water color on aquatic invertebrate diversity. The findings suggest that continued browning may lead to reduced taxa richness and altered community structure in impacted wetlands. Our results also support the importance of beaver wetlands at the landscape scale for biodiversity, due to their abundance in resources, despite their usual high water color. This research provides insights for conservation strategies aimed at supporting sensitive species through browning mitigation.

Keywords: community ecology, biodiversity, food webs, species interaction, water quality

Poster 24: Impacts of minnow invasion on the diet of salmonids in Fennoscandian lakes

Henna Kangosjärvi¹, Pär Byström², Kaisa Anttila¹, Antti P. Eloranta¹

¹University of Jyväskylä

²Umeå University

Invasive species are an increasing problem globally, including in Fennoscandian lakes. One example of this is the invasion of the non-native European minnow (*Phoxinus phoxinus*) into previously allopatric Arctic and alpine salmonid lakes. Over recent decades, the minnow has increasingly spread naturally or been introduced into previously allopatric brown trout (*Salmo trutta*) lakes throughout Fennoscandia. Minnows can engage in complex competitive-predatory interactions with trout, potentially leading to reduced trout growth and dietary shifts, which may alter the structure and energy flow of the entire food web. Previously, stomach content analyses have been used to study these competitive-predatory interactions between trout and minnows, with results suggesting that the resource competition between the two species may outweigh any benefits trout gain from preying on minnows. We build on this knowledge and use stable isotopes of carbon and nitrogen to further clarify the balance between competition and predation by examining how the long-term diet of trout varies in lakes with and without invasive minnows in the Abisko area of Northern Sweden. Our results compare the diet and condition of trout in three allopatric trout lakes and in three lakes that now also host an established minnow population. By disentangling the effects of minnow invasion on trout diet, we aim to elucidate how invasive species can alter food web dynamics in cold-water lakes.

Keywords: food web, stable isotopes, salmonids, Arctic, invasive species

Poster 25: Food web structure and ecosystem services across the seascape

Marie Nordström¹, Iara Rodriguez¹, Tiina Salo²

¹*University of Helsinki*

²*Åbo Akademi University*

Food webs form the backbone of functioning and provide communities with the foundation for ecosystem service provisioning. Coastal ecosystems host diverse and highly productive ecological communities delivering valuable services to human society. However, coastal ecosystems are also under severe anthropogenic pressure, including the triple threat of climate change, biodiversity loss and pollution, putting service provisioning in jeopardy. Ultimately, to be able to safeguard ecosystems and their biodiversity in a changing marine environment, we need a better understanding of the links between ecological structure, functioning and service provisioning. Using monitoring data for zoobenthic invertebrates, coastal fishes, and a mammal species (grey seal), together with information on the trophic links among the species, we established 556 food webs across the Archipelago Sea seascape. To each topological network, we added nodes and links for ecosystem services provided by the marine natural capital stocks, here, a subset of benthic invertebrates and mobile fish species. We focused on services leading to societal benefits, namely regulating and maintenance, provisioning, and cultural services. The aim of this work is to use the environmental gradients in the Archipelago Sea and map ecosystem service providers with supporting species in the networks to explore the service robustness of these communities.

Keywords: biodiversity, ecosystem services, food webs or networks

Poster 26: Do food webs studies in apple orchards reveal buffering ability of key natural enemies against plant pests?

Anne Nissinen¹, KS Shameer², Ian CW Hardy², Oliver Bitz¹, Satu Latvala¹, Sari Himanen¹

¹*Natural Resources Institute Finland (Luke)*

²*University of Helsinki*

Maintenance of ecosystem services can depend on understanding the structure of community webs and the consequent promotion and conservation of pest suppression interactions. Research on beneficial insect species that are naturally present in cultivated apple in Finland and their roles in community food webs will contribute to pest management, e.g. through crop and agri-environment diversification, which can provide beneficial insects with alternative food sources when pests are seasonally scarce. The common flowerbug, *Anthocoris nemorum*, is a predatory insect found in apple trees. Coccinellids are known to be influenced by crop management practices. Insects were collected in a 10-year-old orchard at Jokioinen in 2017-18. Predator, prey and plant species were identified by multiprimer metabarcoding sequencing. Two pairs of primer for COI – cytochrome C (arthropods) and primer pairs for ITS2 - internal transcribed spacer 2 and chloroplast trnL intron (plants) were used to amplify DNA. In the preliminary analyses to study the prey range of *Anthocoris*, DNA fragments from taxonomic families among arthropod orders Diptera, Hemiptera, Lepidoptera, Coleoptera, Arachnida, Collembola and Psocoptera were identified. Analyses of Coccinellid prey identities are ongoing. Indirect estimates of community structure based on literature records will be used to compliment these direct empirical assessments of feeding relationships within the community. Trophic interactions identified from empirical and literature study will be visualized and analyzed using metrics that describe and analyze the structure (topology) of trophic webs, including ‘Connectance’ (a proportional measure of community complexity), ‘herbivore overlap’ and the ‘potential for apparent competition’ (a form of indirect ecological interaction).

Keywords: *Anthocoris nemorum*, Coccinellids, feeding relationships, community ecology, NGS

Poster 27: Land use drives terrestrial support of boreal lake food webs

Ossi Keva¹, Matthew Cobain², Antti Eloranta², Heikki Hämäläinen², Mikko Kiljunen², Jos Schilder³, Roger Jones²

¹*University of Helsinki*

²*University of Jyväskylä*

³*Rijkswaterstaat*

There is a growing awareness of the importance of cross-boundary transfers between adjacent ecosystems. Lake ecosystems can receive high inputs of terrestrial organic matter (t-OM) that microbes make available to higher trophic level consumers. However, how environmental drivers influence t-OM support of benthic and pelagic consumers at multiple trophic levels remains underexplored. Using hydrogen stable isotopes as a tracer of t-OM, we found large variation in the contribution of t-OM to biomass of aquatic consumers (i.e., consumer allochthony) among 35 boreal lakes, with benthic consumers being particularly supported by t-OM. Consumer allochthony decreased along the environmental gradient from forested to agricultural catchments, likely due to alteration in the origin of lake organic matter. Our results demonstrate how cross-system transfer of organic matter can influence community dynamics in recipient ecosystems, with anthropogenic management of donor terrestrial ecosystems affecting the structure and function of food webs in recipient aquatic ecosystems.

Keywords: cross-system subsidies, stable isotopes, Bayesian mixing models, food web ecology

Poster 28: Applying metacommunity theory to understand the dynamics of extinction debt

Beatriz Prado Bastos Monteiro, Zachary Hajian-Forooshani, Jonathan M. Chase

German Centre for Integrative Biodiversity Research (iDiv)

Habitat destruction is an important consequence of land use change and is considered to be one of the main drivers of biodiversity loss globally. One of the complications in predicting biodiversity response to habitat loss is the fact that species responses are not instantaneous, creating a time lag to extinctions, what has been termed “extinction-debt”. It has been noted empirically that significant extinction debts can occur during the transient period after habitat loss. A robust understanding of the factors that influence the magnitude (i.e. number of species that go extinct) and the relaxation time (i.e. time-lagged period it takes for the community to reach a new equilibrium) of extinction debts remains elusive for ecologists but has important implications of conservation. Our aim is to understand how metacommunity processes influence the dynamics of extinction debts across a gradient of habitat loss. We used a discrete time spatially explicit metacommunity model to gain a robust understanding of the mechanisms that shape biodiversity dynamics of extinction debts. Our results show that there is an interaction between the amount of the habitat that is lost and the internal processes within a metacommunity (competition and dispersal) which shapes the dynamics of extinction debt in our simulation study. First, we show that the number of species lost following habitat destruction increases with increasing strength of competition in the metacommunity, and that this relationship is strongest when there are large amounts of habitat destroyed. Second, we show that metacommunities with higher dispersal lose fewer species post habitat destruction but that this effect is contingent on the strength of competition in the metacommunity. Finally, we demonstrate that relaxation times post habitat destruction is larger as the strength of competition and dispersal increase. Our results suggest that explicitly taking into account metacommunity processes could help to associate the dynamics of extinction debt with different types of metacommunities.

Keywords: extinction, community ecology, ecological theory, landscape ecology

Poster 29: An experimental approach to disentangle how dispersal through air versus soil structures wood-inhabiting fungal communities

Jenna Purhonen, Domenica Naranjo Orrico, Brendan Furneaux, Nerea Abrego

University of Jyväskylä

One of the most critical obstacles in predicting species responses to natural and anthropogenic environmental gradients is the lack of comprehensive understanding on how assembly processes jointly structure species communities. The present interpretation is skewed towards the role of environmental filtering, which is relatively easy to study with observational study designs, whereas other processes such as dispersal remain poorly understood. We present a study which disentangles the interactions of dispersal and environmental filtering using community-level field experiments on species-rich wood-inhabiting fungi in an island-mainland study system. In particular we study how dispersal through air versus soil structures fungal communities along a connectivity gradient characterized by habitat size and isolation. The experimental design consists of four wood discs of pine and spruce placed at 15 islands and 15 mainland sites. Half of the discs were wrapped with wire mesh to avoid soil contact, and half were placed directly on the forest floor. We utilize metabarcoding of environmental DNA samples from air, soil, and deadwood, which is an efficient tool for characterizing species-rich fungal communities, in their vegetative stages and importantly also in their dispersal stages. For pursuing understanding on the functional modulation of assembly processes we will additionally incorporate data on species traits and phylogeny. The produced knowledge promotes better assessment of dispersal in community ecological theory and supports conservation and forest management planning, as wood-inhabiting fungi are crucial for forest functioning and include threatened species as well as forest pests.

Keywords: community ecology, field experiment, dispersal, wood-inhabiting fungi

Poster 30: Trait-based approaches in macrozoobenthic communities: Unravelling nature's contributions to people in the Finnish Archipelago Sea

Michele Ivone-Formica Rodríguez¹, Tiina Salo², Marie Nordström¹

¹*University of Helsinki*

²*Åbo Akademi*

Macrozoobenthic communities play a key role in coastal ecosystem functioning and services, which are threatened by strong anthropogenic pressures in coastal areas. In this study, we infer how macrozoobenthic assemblages influence the provision of Nature's Contribution to People (NCP), which are the benefits and detriments gained by people from their associations with the rest of the living world. We use the Finnish Archipelago Sea as a case study and macrozoobenthic abundance data from 2013-2021 to assess structural and functional diversity patterns in our study system and area. We also identified and deduce the presence or absence of links between species and functional traits, ecosystem health, resilience and service provision. The results indicate that higher species richness does not ensure a balanced ecosystem, as indicated by weak correlations with evenness. Similarly, weak correlations between species diversity and functional diversity suggest that more species does not guarantee broader functional diversity. Rao's quadratic entropy (Rao's Q), with strong correlations to other functional metrics, emerged as a key measure of ecosystem function and adaptability. The service provision shows geographical patterns with higher value services located in more pristine areas. Future work should focus on assessing the variation in these correlations along coastal pressure in more detail gradients.

Keywords: macrozoobenthos, nature's contribution to people, functional diversity, trait-based approaches, coastal ecology

Poster 31: Strong and weak trait-environment associations in subarctic stream diatoms

Laura Castañeda Gómez¹, Jianjun Wang², Javier Pérez-Burillo¹, Virpi Pajunen³, Mika Sillanpää⁴, Janne Soininen¹

¹*University of Helsinki*

²*Nanjing Institute of Geography and Limnology*

³*Aalto University*

⁴*University for Science and Technology*

Ecological traits are functional characteristics measurable at the species level and provide valuable insights into how organisms respond to environmental constraints. Here, we investigated how diatom trait-groups and individual species respond to environmental variables. Diatoms were sampled at 129 sites in the subarctic streams of Norwegian islands and mainland, and were categorised into three trait groups: high-profile, low-profile and motile diatoms. Data were analysed using a recently developed method known as Hierarchical Modelling of Species Communities, which is a flexible framework for joint species distribution modelling. We found that diatom trait-groups responded relatively weakly to measured environmental variables but showed positive or negative relationships with major ion levels of the water (e.g., conductivity, calcium [Ca²⁺]). Variance partitioning showed a similar, important contribution of the chemical variables for all the trait groups, while the contributions of physical variables and especially random (spatial) factors were notably lower for all trait groups. Our findings also highlighted considerable among-species variation in their relation to environmental variables within the trait groups. Notably, we identified a high number of indicator species within each trait group that were explained by specific environmental factors, mostly chemical variables. Our study suggests that certain diatom species can be considered as useful environmental indicators but the variability in species preferences within the trait group may in some circumstances hamper the use of ecological traits in environmental assessments. Thus, we suggest using species-level ecology combined with trait information to better track environmental change when using diatoms as indicators.

Keywords: community ecology, diatoms, joint species distribution modelling, subarctic streams, traits

Poster 32: Modeling species distributions: do priority effects and dispersal limitation affect the inference of niche determinants?

Tanguy Bernard¹, Virginie Ravigné², Matthieu Barbier², Frédéric Mahé², Benoit Facon³, Patrice David⁴

¹*UiT The Arctic University of Norway*

²*Plant Health Institute Montpellier*

³*Centre for Biology and Management of Populations*

⁴*Centre d'Ecologie Fonctionnelle et Evolutive*

The ability of joint species distribution models (JSDM) to accurately infer the parameters of the fundamental niche for several species and their interspecific interactions is currently under debate. To test this ability, we employed a two-stage approach. First, we simulated metacommunities with patch disturbance regimes and priority effects to slow down species extinctions and delay metacommunity-wide convergence to a stable state, two phenomena detrimental to JSDM performance. These theoretical metacommunities consist of several generalist and specialist species competing with each other. Secondly, we analyzed data sampled from sites of predefined “ages” (time since first colonization) using JSDM. When the data came from younger sites, JSDM were able to correctly identify the degree of specialization of the different species but were unable to detect any negative interactions. In contrast, when the sites were older, JSDM could no longer accurately identify the degree of specialization of generalists, yet they inferred negative interactions consistent with the specifications of the metacommunity model. These results suggest that inferring fundamental niche parameters and species interactions using JSDM remains complex, even in a simple system. However, the application of JSDM to study data collected from sites at various stages of community assembly appears promising.

Keywords: community ecology, statistical ecology, species interactions, multispecies modeling

Poster 33: Standardized diversity estimation uncovers global EPTO distribution patterns and drivers

Guohao Liu¹, Janne Soininen¹, Naicheng Wu²

¹*University of Helsinki*

²*Ningbo University*

Freshwater insect biodiversity is under global threat from anthropogenic impacts, yet how it is affected by natural factors and anthropogenic stressors remain poorly understood. Here, we examine 783 river basins to map the global diversity and explore natural and anthropogenic influences on four major taxa: Ephemeroptera, Plecoptera, Trichoptera and Odonata (EPTO). Our results showed that 62% of these basins had low data availability, especially in the Global South. Standardized diversity metrics (especially Shannon- and Simpson-based) can significantly correct biases in the description of global insect diversity. Standardized taxonomic and functional diversity of 512 well-sampled basins had a consistent global pattern, with a minor peak at the equator and a higher peak at ~40°N/S. Landscape factors had the highest relative impact on taxonomic diversity, while climatic factors played the key role in functional diversity. Positive correlations were found between diversity and both the human development index and the human modification gradient. Overall, in the context of global change and increasing anthropogenic pressures, understanding the drivers of global freshwater insect diversity is crucial for conserve and manage it effectively.

Keywords: statistical approaches in multispecies modeling

Poster 34: Spatial distribution of large mammals during the Late Pleistocene in the upper valley of the Lozoya River (Madrid, Spain)

Beatriz Trejo¹, Theodoros Karampaglidis², Juan Luis Arsuaga¹, Guillermo Rodríguez-Gómez¹

¹*Universidad Complutense de Madrid and Centro UCM-ISCIII*

²*Universidad de Castilla-La Mancha and Hebrew University of Jerusalem*

In the upper valley of the Lozoya River (Madrid, Spain), close to the municipality of Pinilla del Valle, are the Calvero de la Higuera sites, which show evidence of Neanderthal settlements. This study aims to understand the environment inhabited by these humans during the Late Pleistocene and the animal resources available to them by evaluating the potential distribution of nine large herbivorous mammals (i.e., *Bos primigenius*, *Rupicapra pyrenaica*, *Capreolus capreolus*, *Cervus elaphus*, *Dama dama*, *Sus scrofa*, *Equus ferus*, *Stephanorhinus hemitoechus*, and *Castor fiber*) that were present in the Upper Lozoya Valley and are recorded in the Cueva del Camino site (≈90 ka). To estimate their distributions, we used Maxent software, which is widely employed for modelling species distribution, particularly when only presence data are available. For the models, presence data were derived from an estimation of the past distribution of species based on site locations in the Iberian Peninsula with records of these species, as well as values for home range and population density. As a result, potential distribution maps were obtained for each species, representing areas of greater or lesser habitat suitability or species presence probability, with values ranging from 0 to 1, where 1 indicates locations with the highest habitat suitability or presence probability. These maps allow us to estimate the population density of herbivores and the prey biomass that the valley could support, which allows us to evaluate the resources available to Neanderthals and whether these would be sufficient to sustain them.

Keywords: Iberian Peninsula, modelling species distributions, large herbivores, Maxent, Pleistocene fauna

Poster 35: Detecting and modelling the occurrences of fungi of human interest from global airborne fungal data

Laura Ravattinen, Nerea Abrego

University of Jyväskylä

Fungi profoundly impact human life in many positive and negative ways. Thus, knowing what environmental factors determine the occurrences of fungi affecting human life is important for society. In this project, we use published data from the Global Spore Sampling Project (GSSP) to determine the suitability of air fungal sampling to monitor fungi of human interest and to determine what environmental factors influence their dynamics. The data were collected by collecting airborne fungal samples from air with a cyclone sampler and identifying the fungal species through DNA barcoding. The data comprises 47 sampling locations distributed across six continents, each location collecting two 24-hour samples per week for one to two years. From these data, we retrieved data from the fungi of human interest. A fungus of human interest was defined as those being of conservation concern (e.g., endangered), edible (to be of culinary importance), or pose a hazard to human health or food production as plant pathogens. The preliminary results show that airborne fungal data can be used to detect fungi of human interest, especially to monitor plant pathogenic fungi.

Keywords: biomonitoring, eDNA, fungal pathogen, mushroom, spore

Poster 36: Robust Bayesian count regression with applications on species distribution models.

Ilaria Pia, Jarno Vanhatalo

University of Helsinki

In species distribution models it is common to encounter anomalous observations, which strongly deviate from the bulk of the other data-points. Such outliers arise because of two main reasons. First, species abundance observations themselves can manifest as an extremely high or unexpectedly small value, for example, through observation error or an underlying process not accounted for by the regression model. Second, corrupted environmental variables can lead to serious mismatch between the conditional expectation and observed count, for example, through inaccurate covariate map or mismatch between the spatial resolution of observed target values and environmental covariate. Regardless of the underlying reason, outliers can lead to biases in the results. However, detecting and excluding them from analysis is a rather complex task, motivating development of robust models that are capable to automatically reject potential outliers' information without discarding any observation. In this work we focus on Bayesian count regression models with Poisson-mixture target distributions and Gaussian latent variables. We motivate and formulate the models for species distribution modeling. We then test their theoretical robustness against extreme outliers, namely data-points with infinite or zero valued counts, by checking, for the Poisson-mixing distribution, the thickness of its right tail and its ability to handle zero-inflation. We further evaluate models' robustness to moderate outliers, derived by finite but anomalous combinations of count and covariate observations, via simulations and real-world case studies, to shed light on the differences between their theoretical asymptotic robustness and their performance in practice.

Keywords: robustness, outlier, zero-inflation, species distribution modeling

Poster 37: Clustering analysis for community abundance fluctuations

Nourhan Shafik, Arthur Rodrigues, Jarno Vanhatalo

University of Helsinki

Community stability is usually measured as the temporal variation of abundance (or biomass) in a community. However, the dynamics in abundance fluctuations could present different frequency signatures which could be comparable among taxonomic groups or different communities. To understand more about the characterization of community, we developed a novel approach to cluster communities based on the frequency characteristics of their abundance time series data. By clustering these time series, we can reveal different stability regimes and understand how various factors, such as environmental covariates or species interactions, influence community dynamics. This approach enables ecologists to group communities and species with similar fluctuation dynamics. By identifying communities with similar dynamics, we can target conservation efforts to preserve those that are particularly vulnerable to disturbances. Furthermore, recognizing the functional characteristics of communities in maintaining stability helps prioritize conservation efforts to key organisms that may act as stabilizers within their ecosystems as well as can be informative for designing biodiversity monitoring schemes. Ultimately, these insights contribute to better understanding of how biodiversity supports ecosystem stability. With this comprehensive understanding of community dynamics and the factors that drive stability not only enhances our theoretical knowledge but also provides practical guidance for sustaining biodiversity and ecosystem health in the face of environmental change.

Keywords: biodiversity, ecosystem functioning, time series clustering, community stability

Poster 38: The dynamics of rare and common species in shaping ecosystem diversity

Liam Singer, Jarno Vanhatalo, Marjo Saastamoinen, Anna-Liisa Laine, Tomas Roslin

University of Helsinki

Global biodiversity is declining at unprecedented rates, threatening ecosystem stability and human wellbeing. While there is broad consensus on the urgent need to mitigate biodiversity loss, determining where and how to prioritize conservation actions remains challenging. This is especially true when considering rare species, which consist the majority of species in any ecosystem. Rare species, typically defined by low abundance or restricted distribution, face heightened extinction risks yet may contribute unique ecological functions and evolutionary histories. In this study, we address the challenges of incorporating rare species into biodiversity assessments by examining 30-year ecological time-series data from Finland, covering multiple taxa and extensive spatial and temporal variation. Specifically, we investigate how commonly used biodiversity indices, including species richness, taxonomic diversity and functional diversity, correlate between common and rare species groups and assess the effects of varying definitions of rarity on these metrics. Additionally, we determine to what extent rare species and common species respectively contribute to overall biodiversity in a community. Our preliminary results show that rare species likely play an important role in ecosystem functioning, particularly when considering functional diversity. Our multidimensional approach contributes to a more comprehensive understanding of how rare and common species collectively shape ecosystem structure and resilience. Moreover, our results will offer practical insights for conservation management, showing that focusing solely on common species may be insufficient to fully capture ecosystem resilience.

Keywords: ecosystem functions, rarity, biodiversity

Poster 39: Identification and conservation of forest biodiversity using habitat modelling of indicator species

Pinja Saarinen

University of Jyväskylä

Forest ecosystems in Finland are increasingly threatened by land-use changes, making targeted conservation strategies essential for safeguarding biodiversity. Raptors are effective indicator species due to their sensitivity to habitat quality and prey availability. In this study we aim to use species distribution models (SDMs) for five Finnish raptors; Golden eagle (*Aquila chrysaetos*), Northern goshawk (*Accipiter gentilis*), Common buzzard (*Buteo buteo*), Eagle owl (*Bubo bubo*), and Honey buzzard (*Pernis apivorus*). As old-growth forests decline due to logging and other land uses, these species can indicate valuable forest habitats essential for both raptors and overall forest biodiversity. Our research integrates environmental variables, such as forest cover, elevation, and human disturbance, with species occurrence data to build SDMs using various techniques, such as Maxent modelling. Our aim is to identify areas with high conservation value that are important for both raptors and other forest-dependent species. We expect to find areas that serve as biodiversity hotspots. Protecting these habitats not only aids raptor conservation but also supports broader forest biodiversity across Finland. Our research contributes to the development of conservation strategies by providing a freely available tool for prioritizing areas important for biodiversity, with implications for forestry practices, land-use planning, and biodiversity conservation to avoid the decline of forest biodiversity in Finland.

Keywords: biodiversity, ecological monitoring, landscape ecology, species interactions

Poster 40: Temporal variability of active stream microbial communities and their responses to changing water sources through seasons and years

Jonna Tauriainen¹, Kaisa Lehosmaa¹, Kaisa-Leena Huttunen², Aino Erkinaro¹, Saija Ahonen¹, Danny Croghan¹, Jeffrey Welker¹, Kaisa-Riikka Mustonen¹

¹*University of Oulu*

²*Finnish Environment Institute*

Freshwaters of Arctic and Boreal regions are changing rapidly in response to more pronounced warming of the north compared to lower latitude areas. These changes are driven by climate-induced shifts in the Arctic water cycle, which will alter the seasonally predictable hydrological regimes of northern catchments. Catchment hydrology plays a vital role in transporting organic and inorganic carbon, the crucial energy source for freshwater ecosystems. The quantity and quality of carbon further influences the microbial community composition and hence the microbial induced ecosystem processes. While the role of microbes in carbon cycling and in the consequent greenhouse gas emissions is recognized, the role of the communities of small northern freshwater systems meandering through large peatland areas of the north remains poorly understood. This is largely due to a lack of data from these regions. To fill this knowledge gap, we established a three-year timeseries of microbial community data collected weekly from two locations (upstream and downstream) from a typical sub-arctic headwater stream located in Pallas-Yllästunturi National Park, Finland. Combining year-round (incl. winter) microbial community data together with high frequency hydro-chemical measurements from the same stream system enables us to connect the changing water and carbon sources to changes in microbial community attributes, and also identify the microbial groups that are active during the previously unmeasured season; winter. This sort of long-term time series data is crucial to understand the annual variability of these processes and to be able to predict the upcoming climate-induced changes of northern water-carbon interactions.

Keywords: microbial ecology, ecosystem processes or function

Poster 41: Effects of phytoplankton community structure on carbon fluxes along a coastal gradient

Joris Wiethase¹, Catharina Uth¹, Tjardo Stoffers¹, Nicolas-Xavier Geilfus¹, Eero Asmala², Aleksandra Lewandowska¹

¹*University of Helsinki*

²*Geological Survey of Finland*

Globally, coastal ecosystems are under high anthropogenic influences while simultaneously providing important ecosystem functions. The Baltic Sea comprises some 8000 km of coastline and serves as an important net sink for atmospheric CO₂. Phytoplankton is expected to influence carbon cycling in these coastal zones, e.g. transporting carbon to the sediment by sinking. Phytoplankton communities are highly dynamic, driven by factors like salinity, nutrient availability and wind/wave exposure. In this study, we collected phytoplankton and physico-chemical samples along a coastal estuary, utilising the unique environmental gradient provided by this ecosystem to identify drivers on phytoplankton community structure. Using a machine learning model trained on wind speed data from the Finnish Meteorological Institute, we quantify wind exposure at the sampling sites. We analyse species communities from both a taxonomic and functional perspective using joint species distribution models in HMSC, accounting for species traits, taxonomic relatedness and spatial autocorrelation. We find that while no clear effects on community evenness emerged, functional richness decreased with higher wind exposure, while taxonomic richness increased in lower salinity conditions. This increase also resulted in higher total carbon biomass of the community. To assess the interconnected pathways through which environmental drivers influence carbon cycling, we employ structural equation models in R to quantify both direct effects on particulate organic carbon and indirect effects mediated by phytoplankton community structure. This approach will provide valuable insights into the role of phytoplankton dynamics in supporting carbon sequestration in the Baltic Sea's coastal zones.

Keywords: HMSC, phytoplankton, coast systems, carbon cycling

Poster 42: The effects of climate change on mushroom yields and species composition

Perttu Anttonen¹, Esteri Ohenoja², Jarno Vanhatalo¹

¹*University of Helsinki*

²*University of Oulu*

Climate change is affecting species range distributions, but also the ecosystem functions and services the species provide. Fungi interact with other species in numerous ways, offering ecosystem services for example through decomposition and by affecting plant growth through mycorrhiza. Fungal fruiting bodies, i.e. mushrooms, represent fungal investment on sexual reproduction. They are also important source of food for many animals, especially consisting of high amounts of protein. They are also eaten or otherwise used by humans and thus have economical value. Warming climate is known to increase the fungal fruiting season but also drive changes in fungal species composition. Further, as mushroom yields vary highly depending on weather, the effect of climate change on mushroom yields is yet not well known. In this study, we investigate how climate change affects mushroom yields and species composition across a wide variety of species belonging to different functional groups, i.e. ectomycorrhizal and saprophytic fungi. Data were collected in Oulu area, Finland, by collecting and weighing all mushrooms from 2m*50m transect lines for the autumn season. The collection was conducted over two time-intervals, first in 1976-1988 and then in 2014-2018. Using these long-term survey data, we estimate how differences in yearly weather conditions affect mushroom yields and species composition, and how this relates to long term changes in climatic conditions.

Keywords: climate change, biomass, mushroom, species composition, weather

Poster 43: Understanding the effect of habitat conversion on the current state of bird populations in the NW Mediterranean basin

Elisenda Peris-Morente¹, Marc Anton¹, Sergi Herrando^{1,2,3}, Lluís Brotons^{1,3}, Sara Fraixedas³

¹*Catalan Ornithological Institute (ICO)*

²*European Bird Census Council (EBCC)*²

³*Ecological and Forestry Applications Research Centre (CREAF)*

Biodiversity indicators aggregate complex species trends to reflect the overall state of nature and its changes; however, assessing the specific roles of individual species within these indicators is essential for a comprehensive understanding of what they represent. It is therefore necessary to disentangle the environmental factors influencing the abundance of each species and to identify the traits that mediate these environmental responses. In this study, we aimed to analyse bird abundances across a gradient of anthropic intensity in the NW Mediterranean basin to understand how land use changes within major habitat types drive the abundance of 120 bird species. Given the current decline of the farmland bird index at the European level, we also evaluated whether farmland bird species exhibit similar responses to land use changes as compared to other bird species. Additionally, we assessed whether particular traits could help explain similar trends among farmland bird species. For this purpose, we fitted joint species distribution models to data from the Catalan long-term monitoring scheme, which includes over 300 sampling sites and spans more than 20 years. Our results provide a mechanistic understanding of the farmland bird index in the region, its sensitivity to the species it comprises, and the extent to which specific habitats drive the species trends.

Poster 44: Role of community composition on acoustic niche differentiation in avian community

Peng Han¹, Xingfeng Si², Otso Ovaskainen¹

¹*University of Jyväskylä*

²*East China Normal University*

Global variation in abiotic pressures has altered the sensory systems of species, but it has been difficult to distinguish whether these sensory changes are influenced by species interactions within different community compositions or by abiotic factors. Here, using a novel method to conduct acoustic modulation analysis, we test the acoustic niche hypothesis that habitat fragmentation and community diversity can jointly significantly influence the sensory systems of birds. Furthermore, these species interactions in acoustic space can lead to the species modulating their senses in different directions. The overlap of acoustic competition will decrease as the average body size within the community decreases and more distantly related species appear. Ultimately, considering community composition and island area, island isolation together accounts for over 50% of the explanatory power for understanding acoustic niche differentiation through actual spatial structure, community composition, and interspecific competition. These results suggest that variations in species composition are highly likely to reshape species sensory responses, underscoring the importance of considering biotic interactions.

Keywords: acoustic niche competition, community composition, habitat fragmentation

Poster 45: Non-random patterns of co-vocalization bird communication: do birds sing on top of each other or avoid doing so?

Anran Dong¹, Otso Ovaskainen¹, Patrik Lauha², Panu Somervuo¹, Ossi Nokelainen¹, Aleksi Lehikoinen¹, Tomas Roslin^{2,3}

¹*University of Jyväskylä*

²*University of Helsinki*

³*Swedish University of Agricultural Sciences*

The ability to produce and perceive sounds is fundamental to the survival of many species of animals. Animals vocalize for a variety of purposes, such as the protection of their resources from competitors, the assertion of territorial rights, the attraction of mates and the rearing of offspring. The timing of the vocalizations by different individuals (of the same or different species) may not be independent, as individuals may observe each other and accordingly modify exactly when they vocalize. We examined non-random patterns of co-vocalisation among different bird species, thus asking under what kind of circumstances birds co-vocalize more (synchronized vocalization) or less (avoidance in co-vocalization) often than expected by random. We hypothesize that variation in such behaviors is influenced by competition for acoustic space and social signaling needs. We employed autonomous audio-based biomonitoring to gather long-term acoustic data across the globe and used AI-based methods to classify the vocalizations of different species. We then compared the level of vocalization overlap to compute an index of non-randomness in song overlap for each 60-second recording and for each pair of species. We then used linear mixed models to examine the influence of time of day, day of the season, and site on co-vocalization patterns. Our findings elucidate the intricate interrelationship between vocal strategies and environmental factors, emphasizing the significance of co-vocalisation in social communication, territorial defense and mate selection. Our results demonstrate the utility of high-throughput automated methods in deciphering the vast and complex datasets that can be generated by autonomous biomonitoring.

Keywords: avian acoustics, vocal overlap, temporal avoidance, ecological strategies, bioacoustic monitoring

Poster 46: Landscape effects on genetic diversity of range shifting butterflies in Finland

Lola Fernández Multigner, Marjo Saastamoinen, Audrey Bras

University of Helsinki

In response to climate change, numerous species are shifting their range towards higher latitudes, tracking suitable temperature conditions. Although these range shifts are often considered a positive response, the genetic composition of the expanding populations can be altered, and the genetic diversity reduced. The genetic loss can be bigger if the area of expansion presents little available habitat or is poorly connected, as that would make the new populations smaller and more isolated. Although the negative effects of habitat loss and fragmentation on species richness are known, their role during range expansions is still understudied, especially at the genetic level. In this study, we aim to understand the effect of habitat configuration on the distribution of genetic diversity in five butterfly species in Finland, two of which are expanding northwards. We are first studying the role of the landscape on the species distribution through habitat suitability models based on occurrence, climatic, habitat and host plant distribution data. We will present the preliminary models of the five species. In the next step, we aim to integrate species genetic diversity data with the distribution models to perform individual-based simulations, which will allow us to understand the role of landscape on the spatial distribution of genetic diversity. We expect genetic diversity to be reduced in the populations from the expanding area, as well as in areas with little habitat or poor connectivity. This study will help understand the interplay of climate change and habitat loss as drivers of genetic diversity loss.

Keywords: landscape ecology, species distribution models, genetic diversity, climate change

Poster 47: Crowberry expansion drives the long-term homogenization of vegetation in Fennoscandian heathlands and tundra

Petteri Kiilunen¹, Tuija Maliniemi¹, Kari Anne Bråthen², Jutta Kapfer³, Torunn Bockelie Rosendal², John-Arvid Grytnes⁴, Patrick Saccone⁵, Risto Virtanen¹

¹*University of Oulu*

²*Arctic University of Norway*

³*Norwegian Institute of Bioeconomy Research*

⁴*University of Bergen*

⁵*Austrian Academy of Sciences*

Biodiversity loss affects the structure and functions of the tundra biome through altered species composition and community structure. A critical but often overlooked phenomenon is biotic homogenization, where increased compositional similarity—essentially a decrease in beta diversity—occurs across communities. Less is also known about how temporal changes in alpha and beta diversity are interlinked. However, long-term evidence of these changes in high-latitude regions is limited due to a lack of temporal data. We studied multi-decadal changes across oligotrophic mountain heath and tundra plant communities in northern Fennoscandia and within different habitat types, biogeographical zones and continentality classes. Data, that was resurveyed in 2013-2023, includes 275 sample plots that were originally surveyed in 1964-1975. All plots (2 x 2 m) include percentage covers of vascular plants, bryophytes, and lichens. We found that Fennoscandian tundra communities have become more compositionally similar over the decades, with this trend consistent across different biogeographical zones and continentality classes. However, at the same time, species evenness increased among all plant groups except bryophytes, while species richness remained largely unaffected. The observed homogenization trend is strongly linked to pronounced increase in the abundance of crowberry (*Empetrum nigrum*). Our study indicates that regional biotic homogenization may occur strongly even while alpha diversity has remained stable or increased over time. Such trends likely decrease ecosystem functioning and condition.

Keywords: biodiversity, ecosystem processes or function, macroecology and biogeography

Poster 48: Illuminating the Impact: Light pollution threatens biodiversity in aquatic ecosystems through changes in organismal behaviour

Anirban Ganguly¹, Caio Roza², John Loehr²

¹*Organismal and Evolutionary Biology*

²*Lammi Biological Station*

Artificial Light at Night (ALAN) is a rapidly growing environmental disturbance, yet its effects on freshwater ecosystems, particularly streams, remain poorly understood. We investigate ALAN effects on the composition and abundance of stream benthic invertebrates. We conducted a field experiment across 25 sites in five freshwater streams in Finland, following a Before-After-Control-Impact (BACI) design to sample natural and illuminated stretches over 15 weeks. We found that ALAN exposure alters community composition by selectively favouring certain invertebrate taxa, while others exhibit significant declines in abundance. This research demonstrates an interplay between the spatial extent and ecological ramifications of light pollution in freshwater streams. By highlighting changes in invertebrate community structure and biodiversity along ALAN gradients, our study underscores the need for targeted conservation strategies to mitigate light pollution in vulnerable aquatic systems. These results contribute to our broader understanding of how anthropogenic disturbances propagate through interconnected ecological networks, posing implications for freshwater biodiversity management.

Keywords: biodiversity, light pollution, human activities, behavioural ecology, ecosystem disturbance

Poster 49: Diet and reproductive success in birds exposed to metal pollution: A DNA metabarcoding study

H.A.S.S. Alwis, Lydia I. Leino, Miia J. Rainio, Eero J Vesterinen, Tapio Eeva

University of Turku

Avian dietary studies provide insight into nutritional shifts caused by natural and anthropogenic disturbances, such as environmental pollution. In highly polluted areas, insectivorous passerines are directly exposed to pollutants and indirectly affected through their invertebrate diet. Point sources of heavy metals have the capacity to induce shifts in abundance and species composition of invertebrate populations. This shift may in turn lead to variation in the diet of insectivorous birds during their breeding period, potentially influencing their reproductive success. The goal of this study is to link anthropogenic changes in invertebrate prey with changes in the reproductive success of three hole-nesting bird species – great tit (*Parus major*), blue tit (*Cyanistes caeruleus*), and pied flycatcher (*Ficedula hypoleuca*) around a Finnish copper-nickel smelter in Harjavalta. The first chapter of my doctoral thesis will examine the diet of the focal bird species using DNA metabarcoding and assess the variation in the diet of these birds in metal-polluted and reference areas. The dietary information will be combined with nestling growth and other parameters (e.g. clutch size, and fledging success). This work will contribute important perception to ongoing work investigating the health status of these common model bird species in Finland.

Keywords: molecular ecology, passerine birds, heavy metals, prey selection

Poster 50: Oxidative stress response of mallard embryos to in ovo per- and polyfluoroalkyl substances injection

Salla Lahdentausta

Åbo Akademi University

Per- and polyfluoroalkyl substances (PFAS) are a broad group of substances that are utilised widely in consumer and industrial settings. However, some of them are known to have, among other things, a negative developmental, immunological, cardiovascular and hepatic effect on health. The aim of the study is to determine whether different PFAS, identified in Finnish breeding waterbirds, may cause oxidative stress responses to the avian embryo at environmentally relevant doses. The possible oxidative stress responses are changes in the enzyme activity and energy content of the embryo. Farmed mallard eggs were injected with one regulated (PFOS) and two emerging PFAS (PFDoDs, PFECHS). The activities of catalase and glutathione-S-transferase enzymes were measured as well as the lipid peroxidation with FOXII method as well as the content of lipids, glycogen, glucose and protein of the embryo livers. We expected to see some negative impact on the enzyme activity and/or energy content of mallard embryo livers. Nevertheless, we did not find any statistically significant differences between the five groups: control group, PFDoDs low dose (LD), PFECHS LD, PFOS LD and PFOS high dose (HD). A larger sample population would be required to attest the results. Further research is needed to study further potential effects of these chemicals and to evaluate what are the risks when these chemicals occur together in the environment.

Keywords: environmental toxicology, per- and polyfluoroalkyl substances, oxidative stress

Poster 51: Sulphate sensitivity of aquatic organisms in northern Baltic Sea modeled with species sensitivity distribution

Xiaoxuan Hu¹, Kari Lehtonen², Matti Leppänen², Anna Karjalainen³, Johanna Järvistö², Ossi Tonteri², Hansika Sarathchandra¹, Rashmika Samarawickrama¹, Natalija Kolesova⁴, Evita Strode⁵, Hoi Shing Lo⁶, Juha Karjalainen¹

¹*University of Jyväskylä*

²*Finnish Environment Institute (Syke)*

³*Envineer Ltd*

⁴*Tallinn University of Technology*

⁵*Latvian Institute of Aquatic Ecology*

⁶*Stockholm University*

Sulphate is a naturally occurring major ion ubiquitously found in natural environments. Major anthropogenic sources of sulphate include runoff from agricultural lands on acid sulphate soils, effluents from industrial activities, as well as mining and municipal wastewaters. Chronic sublethal effects of sulphate on freshwater aquatic organisms have been explored and observed in many toxicity tests, and the development of sulphate environmental quality standard in freshwater has gained more attention recently. However, the effects of sulphate on the brackish water biota are poorly known and experimental data from biotests are largely missing. We conducted chronic sulphate toxicity tests on various species from northern coastal Baltic Sea areas and used Species Sensitivity Distribution (SSD) modeling to derive the 5th percentile hazardous concentration (HC5) that would protect 95% of the species in the brackish water ecosystem where sulphate concentrations range between 180 to 620 mg/L. Chronic sulphate toxicity varied notably between the species tested. The most sensitive species tested were whitefish *Coregonus lavaretus* and common water moss *Fontinalis antipyretica*. This study provides important knowledge on sulphate sensitivity of various Baltic species of both freshwater origins and marine origins.

Keywords: ecotoxicology, EQS

Poster 52: Glyphosate and phosphate treatments in soil differentially affect crop microbiomes depending on species, tissue and growth stage

Niina Smolander¹, Benjamin Fuchs¹, Marjo Helander¹, Pere Puigbò¹, Technology Center of Catalonia², University Rovira i Virgili², Manu Tamminen¹, Kari Saikkonen¹, Suni Anie Mathew¹

¹*University of Turku*

²*Aarhus University*

Glyphosate-based herbicides (GBHs) are among the most widely used pesticides, controlling weeds by inhibiting the shikimate pathway. However, the effects of GBH on non-target organisms, such as shikimate pathway-containing microbes, are understudied, and their impact on crop microbiomes, crucial for agricultural productivity, remains largely unknown. Furthermore, the complex interactions between GBH and fertilizers are difficult to predict. Hence, for long-term GBH use, we investigated the effects of GBH and phosphate fertilizer on the composition of endophytic bacterial communities of potato, faba bean and oat during early and late summer, and on plant growth in late summer. GBH treatments significantly affected bacterial communities of potato roots and faba bean leaves in early summer, while phosphate treatments significantly affected bacterial communities of potato leaves, tubers and faba bean leaves in late summer. GBH treatments reduced bacterial diversity and abundance of beneficial bacteria but significantly increased the aboveground biomass of all crops. Thus, agrochemicals affected differently in diverse crops, tissues and growth stages. While improved crop yield is often prioritized in chemical-intensive farming, shifts in microbiomes, which may compromise crop health, are overlooked.

Keywords: endophytes, bacterial communities, pesticides, fertilizers, non-target organisms

Poster 53: Environmental contamination by radionuclides alters diet and gut microbiota of wild passerines

Sameli Piirto, Phillip Watts, Tapio Mappes, Suvi Ruuskanen

University of Jyväskylä

Organisms that occupy environments contaminated by radionuclides such as Chornobyl, Ukraine, face putative detrimental effects. How radioactive pollution affects organisms, especially in early life, is not well studied in the wild. Our study focuses on two interconnected factors that might be altered due to radionuclide contamination of the environment and influence fitness: early-life diet and gut microbiota, an important physiological constituent tied closely to diet and host physiology. We quantified fitness components, diet, and gut microbiota from nestlings of two passerine birds, Great tit (*Parus major*) and Pied flycatcher (*Ficedula hypoleuca*), by sampling animals in nest-boxes located in contaminated and uncontaminated areas within the Chornobyl Exclusion Zone, Ukraine. We used amplicon sequencing to identify dietary insects and to quantify the bacterial diversity and composition of the birds' gut microbiota. Environmental radiation had no effect on fitness components (body condition and brood size) of either species. Dietary insect diversity of *P. major* did not show association to radiation, but diversity of *F. hypoleuca* diet was associated with radiation. Composition of the diet was associated to radiation in both species. Neither species showed association between environmental radiation and bacterial species diversity of gut microbiome, however radiation was associated with composition of gut microbiome. Other ecological factors: forest type, brood size and age were associated with *P. major* gut microbiome composition but not in *F. hypoleuca*. Our data show comparable responses in diet and gut microbiome of two wild species when exposed to environmental radionuclide contamination.

Keywords: ecophysiology, molecular ecology, microbial ecology

Poster 54: Linking electromagnetic field exposure to plant response: experimental approaches

Jasmin Nevala¹, Minna Maarit Kytöviita¹, Jonne Naarala²

¹*University of Jyväskylä*

²*University of Eastern Finland*

Background: Low-frequency magnetic fields (LF-MFs) are an emerging environmental factor with potential implications for plant growth and physiology. While studies have shown that electromagnetic exposure can influence biological processes, its effects on plants remain poorly understood. **Aims/Purpose:** This research aims to explore the potential effects of LF-MFs on plants by exposing them to controlled magnetic fields and examining physiological and morphological responses. LF-MFs may affect plant reproduction and growth and thus impact on ecological and agricultural systems **Methods:** Plants are exposed to LF-MFs using a custom-designed exposure system capable of delivering consistent magnetic fields at varied frequencies and intensities. The exposure protocol involves 24-hour exposure of both annual and perennial species, with fields generated by an electromagnetic coil system. End-points include germination rates, biomass measurements, and stress response measurements, allowing for a comprehensive assessment of both morphological and physiological responses. **Significance:** Understanding how LF-MFs affect plant physiology can reveal broader ecological implications of electromagnetic exposure, especially as these fields become more prevalent in natural and agricultural settings. By identifying specific physiological signals of response, this research may inform future studies on electromagnetic stress in plants and support the development of guidelines for managing electromagnetic exposure in sensitive environments.

Keywords: plant ecophysiology, electromagnetic radiation

Poster 55: Real-time spatial mapping of metal contamination in environmental waters for sustainable ecological monitoring using a portable XRF device

Mikhail Sandzhiev

University of Eastern Finland

The monitoring of metal pollution in environmental waters is crucial for the protection of ecosystems, human health and agricultural activities. Traditional laboratory-based metal analysis methods are time-consuming and expensive, which often leads to delays in the availability of information. This study presents a new approach to real-time water quality monitoring using portable X-ray fluorescence (p-XRF) technology coupled with geographic information systems (GIS). Using a custom Python script, p-XRF data is processed and formatted into a GIS-compatible format, facilitating spatial visualization of metal concentrations in QGIS. Field-usable filters, especially bisphosphonate-functionalized thermally carbonized porous silicon (BP-TCPSi), preformed metals such as Mn, Ni, Cu, Zn, and Pb allow direct detection in the field by using p-XRF. Key objectives include robust data collection, spatial visualization and validation processes to ensure accuracy and efficiency. This provides quick and efficient insights into metal contamination trends and allows proactive decision-making.

Keywords: ecological monitoring

Poster 56: Fungicides elicit immunological and variable stress responses in super pest species at the whole transcriptome level

Maaria Kankare, Aigi Margus, Shahed Saifullah, Leena Lindström

University of Jyväskylä

Global insect declines are strongly linked to the common pesticide usage in agriculture and while insecticides appear to be the main driver, fungicides may also play a significant role, although the mechanisms are mostly unclear. Multi-site fungicides are preferred as they work against a broad range of plant pathogens by interfering with the host's multiple metabolic pathways. Single-site fungicides target a narrower range of pathogens by affecting a specific site in a specific pathway and are hence expected to be less toxic to non-target organisms. Here, we studied the effects of two commonly used fungicides, mancozeb and fluazinam treatments on the Colorado potato beetle (CPB) larvae at the whole transcriptome level. Mancozeb is a multitarget fungicide inhibiting several key enzymes, disrupting cell membrane function and generating reactive oxygen species leading to oxidative stress, while fluazinam is a single-site fungicide targeted on the fungal respiratory chains. We treated second instar larvae from two CPB populations with more than a hundred times difference in their insecticide resistance. Beetle larvae were exposed to either of the fungicides or control treatments (solvent and pure water) topically three times during 72 hours. Interestingly, we found that fungicide exposures over all samples caused expression level differences predominantly in genes connected to immunological defense with several attacin genes coding for insect antimicrobial peptides (AMPs) together with major-antigen-like protein gene. Moreover, heat shock proteins related to many types of stress responses were only found as response to mancozeb treatment. We discuss possible implications of these results.

Keywords: fungicides, transcriptome, non-target pest species, immune defense, antimicrobial peptide

Poster 57: Impact of clearcutting on resident bird communities in boreal forests

Pavan Chikkanarayanaswamy¹, Toni Laaksonen¹, Daniele Baroni², Patrik Lauha³, Jon E Brommer¹

¹*University of Turku*

²*Italian Institute for Environmental Protection and Research (ISPRA)*

³*University of Helsinki*

Boreal forests, vital for biodiversity conservation and carbon storage, face significant threats from human activities, especially forestry-driven habitat loss or alteration through clearcutting. This practice significantly alters forest landscapes, reducing old-growth forests, deadwood availability, and habitat diversity. These are crucial elements for specialist species, such as forest birds that thrive in complex ecosystems. In Finland, studies on the effects of clearcutting largely focus on charismatic or indicator species, leaving gaps in data on common forest birds. Notably, few studies have examined the presence of common birds before and after clearcuts. In this study, we investigate the impact of clearcutting on resident boreal forest birds in Southwest Finland over four years. Using a Before-After Control-Impact (BACI) design, we monitored bird activity from mid-March to early May, comparing periods before (2020) and after (2024) clearcut formations. Data were collected from 292 sites in 2020 using Autonomous Recording Units (ARUs) over a week, while in 2024, sampling was conducted at 66 sites—33 control and 33 clearcut impact sites—over three and a half days. The analysis of this data is based on automated species identification. The findings will offer valuable insights into the effects of logging on bird communities at a local scale, assessing changes in species richness and community structure. This research aims to inform sustainable forestry practices that balance resource extraction with biodiversity conservation.

Keywords: Boreal forests, clearcutting, biodiversity conservation, bird activity, Before-After Control-Impact (BACI)

Poster 58: Long-lasting effects of clearcuts on bird communities in Southern Finnish forest landscapes

Jenna Rönttinen, Rémi Duflot, Jérémy Cours

University of Jyväskylä

Forest management practices have remarkably intensified over the past century in Finland. The predominant management practice is clearcutting followed by tree planting, which results in homogeneous and younger forest habitats. These local modifications affect biodiversity as crucial resources are being removed. However, the landscape-level and long-term impacts of clearcutting are still unclear because large-scale time series are scarce. We investigate how the accumulation of clearcutting over time and their size affect forest specialist bird species, whether open-habitat species benefit from clearcutting and for how long, and if there is a threshold defining a maximum viable clearcut area in a landscape. Using data from the Finnish bird monitoring transects and the European disturbance map describing clearcuts, we infer the effects of clearcut accumulation over different spatial and temporal scales on species richness and abundance of different bird functional groups within forested landscapes of Southern Finland. Non-forest habitat heterogeneity positively affects overall bird species richness, especially through smaller clearcuts (edge habitats). Forest birds show short-term benefits from small-sized clearcuts as well, while old-growth forest species experience negative effects from the 20-year accumulation of clearcuts, with threshold level at 20% area of a landscape. Open habitat birds respond positively to clearcuts at longer, 20-year time scales. Additionally, species group responses vary across spatial scales. Some birds benefit from short-term and localized effects, but large and long-term effects and excessive forest cover can negatively impact others. Observed threshold level and the average proportion of clearcuts imply unsustainability of current forest practices.

Keywords: biodiversity, community ecology, landscape ecology

Poster 59: Bees in clear-cuts: changes in diversity over a 30-year succession after final felling

Betija Rubene¹, Andris Avotins², Rūta Starka², Jānis Gailis¹

¹*LBTU Institute of Plant Protection Research “Agrihorts”*

²*University of Latvia*

The loss and degradation of natural and semi-natural grasslands have forced many grassland specialist insects to adapt to human-altered environments such as roadsides, quarries, and other anthropogenic landscapes. Clear-cuts have been identified as potential habitats for various insect species commonly associated with grasslands and open habitats, including vital pollinators like bees. However, the long-term changes in bee communities during the early stages of forest succession following final felling remain unclear. In this study, we investigated bee diversity in clear-cuts over 30 years of post-felling succession and identified the key landscape and vegetation factors influencing these patterns. Using coloured pan traps and generalised additive mixed effects models, we found that bee diversity peaks in younger forest stands, declines until approx. 10 years of age, and remains consistently low thereafter. Larger forest stands and greater diversity of flowering plant genera were positively associated with higher bee diversity, while flower cover and abundance of specific plant genera had no significant effect. Our findings highlight that clear-cuts provide important habitats for bees, but only in the short term. It is therefore important to evaluate the trade-off between supporting temporary bee populations and potentially harming forest specialist species is crucial nevertheless.

Keywords: pollinators, clear-cuts, coloured pan traps, generalised additive mixed effects modelling, landscape ecology

Poster 60: Fine-scale geodiversity and its relation to species richness in northern boreal forests - Case Saariselkä

Henriikka Salminen, Helena Tukiainen, Johanna Kotilainen, Joonatan Lohi, Johanna Ollila, Janne Alahuhta, Tuija Maliniemi

University of Oulu

There is an urgent need to find complementary measures to tackle the current biodiversity loss. Geodiversity could be one such approach as its positive relationship with biodiversity is well established. There is, however, a lack of research that use empirical geodiversity data in explaining biodiversity patterns at finer scales. In this study, we investigated the connection between the fine-scale geodiversity and climatic and topographical variables and species richness of vascular plants, bryophytes and lichens in boreal treeline ecotone in Saariselkä, Finland. Using a recently developed field method to map fine-scale geodiversity, we assessed georichness, i.e. the occurrence of different geofeatures (geological, geomorphological, and hydrological features), within a radius of ten meters from the centre of the study plots (N=82). Our preliminary results show that the georichness is positively associated with species richness of all species groups. Georichness was selected to all multivariate models. Our results suggest that the inclusion of fine-scale geodiversity estimates may improve understanding and predictions of species richness patterns in the northern boreal forests. This further encourages to examine the geodiversity-biodiversity relationship at finer scales and could help to gain better understanding of the resilience of vulnerable northern environments.

Keywords: geodiversity, biodiversity, georichness, species richness, landscape ecology

Poster 61: Tales from the past: re-mapping of rising tree- and forest lines

Ingrid Vesterdal Tjessem¹, Anders Bryn¹, Peter Horvath¹, Adam Eindride Naas¹, Ida Marielle Mienna¹, Inger Kristine Volden¹, Michal Torma¹, Rune Halvorsen¹, Terje Koren Berntsen², Ketil Isaksen³, Kerstin Potthoff⁴

¹*Natural History Museum*

²*University of Oslo*

³*Norwegian Meteorological Institute*

⁴*Norwegian University of Life Sciences*

The global average temperature is rising, and alpine regions at high latitudes currently warm faster than global averages. A warmer climate is expected to move the temperature-limited tree- and forest lines (TFLs) to higher elevations, stretching the forest ecosystem into treeless tundra, and decreasing the extent of the alpine ecosystem. Temperature is the strongest factor limiting the boreal ecosystem and although TFLs are overall advancing, we need to determine where and how fast local tree lines will respond to a warmer climate. Furthermore, long-term studies are needed to account for distributional time lags due to potential setbacks from stochastic effects (e.g., insect infestations, extreme drought) and continuous drivers (e.g., domestic grazing, climate). This may subsequently enable the recognition of TFL feedbacks and interactions, both locally and globally. In this study, we investigated a one-century (1887-2023) TFL response by re-mapping historical TFLs (281 sites) in situ in Norway. We modeled local and regional changes in TFLs through time as a function of climate- and land-use change (and other effects accounted for). We propose potential processes that lead to time lags for elevational change in TFLs (e.g., extreme climate events) and identify continuous drivers that explain TFL dynamics through the investigated period. Lastly, we evaluate the quality of the methods and data used in our investigations and emphasize the profit and importance of reusing and remapping the work of our past century's scientists to better understand the future dynamics of TFLs.

Keywords: Alpine, treeline, forest line, climate change, land-use change

Poster 62: The impact of forestry activities and restoration on spring species composition, the cultural heritage of springs, and the significance of various conservation measures in the protection of springs.

Iina Eskelinen

University of Jyväskylä

Spring Ecosystems Springs are small-scale oases of biodiversity and vital water sources, hydrologically connected to surrounding wetlands and forests. Unfortunately, forestry activities and peatland drainage have disrupted and destroyed many springs. **Cultural Significance of Springs** Springs have historically been integral to everyday life, holding diverse meanings for people. Today, modern society no longer depends on springs as it once did, jeopardizing these cultural-historical values due to forestry impacts and their gradual disappearance from collective memory. **Conservation Status and Restoration** In southern Finland, only 2-5 % of springs are permanently protected, with up to 99 % having lost their pristine state. Approximately 50 springs are protected under the Antiquities Act for their cultural importance, but overall protection remains inadequate for both natural and cultural aspects. Although hundreds of springs have been restored, research on the ecological effects of these efforts is limited. **Research Focus** In my PhD research, I will explore the species composition of springs using traditional identification methods and environmental DNA (eDNA). I will monitor the impacts of restoration on species composition, community structure, water chemistry, and physical characteristics of springs. Additionally, I will document the cultural values, oral histories, and historical uses of springs, including the inventory of structures related to their past use. **Integration of Natural and Cultural Values** In this research, natural and cultural values are not opposing forces, but equally valuable, fascinating, and deserving of greater attention and research, as they can manifest simultaneously at springs.

Keywords: biodiversity, conservation science and policy, ecosystem services, ecological monitoring

Poster 63: Development of vegetation in restored forestry-drained peatlands is partially driven by water table level

Aapo Jantunen¹, Merja Elo², Otso Ovaskainen¹

¹*University of Jyväskylä*

²*Finnish Environment Institute*

Ecosystem restoration is globally increasing due to agreements such as Kunming-Montreal Global Biodiversity Framework and EU Restoration Law. However, restoration effect varies between and within ecosystems. To increase efficiency of future restorations, we need to understand the factors behind this variability. As this also applies to restored forestry-drained boreal peatlands, we studied if restoration increased water table level and whether water table level explained differences in abundances of five vascular plant and moss species and species groups. We used joint-species distribution modelling (HMSC) with data from a 10-year before-after-control-impact restoration study. The study included 151 sites representing six peatland types. Restoration consistently increased water table level in all but the two peatland types with the lowest productivity. In addition, knowing water table level increased predictive power of the vegetation models in 40 % of the species-peatland type pairs, and in several cases, we observed over 100 % increase in predictive power. Even though we confirmed that water table level is an important factor in development of vegetation in restored peatlands, plenty of variation was left unexplained. This could be due to many other factors, such as level of degradation of the site before restoration, and should be studied further. As peatland type affects probability of successful restoration of water table level, higher productivity peatlands could be prioritized for higher restoration efficiency.

Keywords: restoration ecology, ecological monitoring, statistical ecology

Poster 64: The effects of drainage and restoration on peatland tardigrade communities

Hennariikka Mäenpää¹, Merja Elo², Sara Calhim¹

¹*University of Jyväskylä*

²*Finnish environment institute*

Tardigrades are ubiquitous micrometazoans that are most often found in moist terrestrial habitats, such as peatlands. However, nothing is known about the effects of peatland management on tardigrade communities. We collected moss samples from pristine, drained and restored pine mire forests. Management type explains more of the variance in abundance than distribution within site (i.e., distance to ditch). In addition, tardigrade occurrence was more associated with moss species that are common in drier and forested peatland types. We did not find significant differences in the community composition of tardigrades, despite some individual genera being more abundant in certain management types. We conclude that drainage and the following decrease in water table level and habitat heterogeneity of peatlands alter the distribution of tardigrades. The changes in the overall habitat quality for tardigrades probably arise from the combinations of large- (e.g., water table level and tree cover) and small-scale (e.g., substrate type) environmental factors.

Keywords: community ecology, restoration ecology

Poster 65: Which natural wetland characteristics could be used in creating temporary wetlands?

Markéta Nummi¹, Petri Nummi², Sari Holopainen², Aurélie Davranche², Uma Sigdel¹, Céline Arzel¹

¹*University of Turku*

²*University of Helsinki*

Wetland loss resulting from anthropogenic land use and global climate change has drastically accelerated during the past century, leading to a freshwater biodiversity crisis. Temporary wetlands, e.g. vernal pools, have been especially endangered as they have been poorly implemented in freshwater habitat regulations. They are, however, important habitats for many organisms. Some species or species groups, such as amphibians, even require temporary wetlands to complete their life cycle. One possibility to mitigate wetland loss and deterioration is to emulate natural temporary wetlands in wetland construction. For this purpose, we describe seven types of natural temporary wetlands with hydroperiods ranging from less than one month to multi-years floods, and their related biodiversity. The temporary wetland types are: ephemeral ponds, temporary ponds, seasonal ponds, semi-permanent ponds, turloughs, multi-year floods of early succession (e.g. new beaver flood), multi-year flood of late succession (e.g. old beaver flood). Temporary wetlands constructed to enhance biodiversity should be designed to fulfil needs of targeted species. Important aspects to consider when creating temporary wetlands to enhance biodiversity are timing and length of flooding, absence of fish, vegetation structure, shoreline morphology, presence of flats and islands, water depth, landscape connectivity, monitoring and management.

Keywords: vernal pool, wetland creation, biodiversity, flooding

Poster 66: Spring habitats in commercial forests - developing basic understanding and legislation to preserve remaining diversity

Veera Saari

University of Jyväskylä

Spring habitats are essential for maintaining biodiversity in boreal forests due to their unique habitat characteristics. These ecosystems support a wide range of species and have relatively stable abiotic conditions. Despite their ecological importance, many spring habitats in Finland have been degraded or lost, primarily due to forestry activities. Our studies on spring habitats emphasize the urgent need for their better understanding and more efficient protection. The Finnish Forest Act has played a crucial role in conserving these habitats, but recent changes have led to the loss of protection for many areas. Our research highlights the alarming number of undocumented springs and the impact of logging and ditching on these ecosystems. The aim is to create suitable methods for finding spring habitats and help improve their current protection.

Keywords: springs, forestry, conservation, groundwater, legislation

Poster 67: Safeguarding biodiversity and carbon-rich forest networks in Europe

Mikko Peltoniemi¹, Mira Kajanus², Otso Ovaskainen², Eszter Kelemen³, Bill Kunin⁴, Fulvio Di Fulvio⁵, Santiago Saura⁶, Cornelius Senf⁷, Petru Stancioiu⁸, Kyle Eyvindson⁹, Sebastian Seibold¹⁰, Kathrina Albricht¹, Jan-Peter George¹, Matti Koivula¹, Juha Honkaniemi¹, Adriano Mazziotta¹, Anna Repo¹, Sebastiaan Luyssaert¹¹, Sebastian Seibold¹⁰, Jukka Forsman¹

¹*Natural Resources Institute Finland (Luke)*

²*University of Jyväskylä*

³*ESSGR Nonprofit KFT*

⁴*University of Leeds*

⁵*IIASA*

⁶*Technical University of Madrid*

⁷*University of Munich*

⁸*Transilvania University of Brasov*

⁹*Norwegian University of Life Sciences*

¹⁰*University of Dresden*

¹¹*Vrije University Amsterdam*

The EU has developed ambitious policies and regulations to halt biodiversity loss resulting from intensive land use and climate change. Reverting the biodiversity decline requires safeguarding existing biodiversity and fostering the adaptive capacity and resilience of the ecosystems. SafeNet relies on a portfolio of complementary tools to develop anticipatory and sustainable strategies and solutions to safeguard the biodiversity, while considering the needs to use forests also for climate change mitigation, wood and ecosystem service provisioning. SafeNet integrates cutting-edge methods in biodiversity monitoring and mathematical modelling with massive remote sensing and species data repositories to better understand the climate change induced shifts in the distribution of species, communities and ecosystems under different climate and land use scenarios. This enables implementing efficient and anticipatory conservation and management measures, including creating corridors among the primary and old-growth forests and other ecologically valuable forests to enhance connectivity. SafeNet implements a multi-actor approach and engages relevant stakeholders, including policymakers, forest practitioners, regional and national authorities, certification bodies, and forest-value chain stakeholders, in regional Living Labs, and in a European level Policy Lab. Stakeholders will co-create and interact with researchers and modelling to develop conservation-management plans for real landscapes at local scales, and innovate EU-level strategies and policies for reconciling conservation-restoration-management goals at the EU level. Active stakeholder involvement and dissemination-outreach will ensure SafeNet's impact on conservation and management of forest ecosystems and national and European level policy developments. SafeNet (2025-2029) receives funding from Horizon Europe funding programme.

Keywords: primary and old-growth forests, biodiversity, forest management, conservation, policy impacts

Poster 68: Environmental management and societal perception of green spaces in cities: case study of urban islands in Kuopio

Anniina Korhonen¹, Oksana Skaldina¹, Syamili Manoj Santhi¹, Salla Eilola²

¹*University of Eastern Finland*

²*University of Turku*

With growing urbanization, there is an emergency for biomonitoring and further biological conservation of urban biodiversity to enable global sustainable development. In urban green spaces (UGS), floral biodiversity provides essential ecosystem services and citizens can experience nature directly. Evaluating local societal perceptions provides valuable information for the development of UGSs. Such actions support local biodiversity, citizens' well-being, and sustainable urban development. The aim of this research is to evaluate environmental management practices and societal perceptions of biodiversity in different types of UGSs. An assessment of floral biodiversity was conducted in the first half of June, July, and August 2024 in Kuopio (Eastern Finland). The assessments were done in 25 traffic islands and 25 vegetation islands in recreational areas using standard quadrat (1x1) placement method for biodiversity research. Citizen's survey, which was open on Webropol in July-August, was used to evaluate societal perceptions. The survey included two interventions about wildflowers and their role in providing ecosystem services, which were included to examine if environmental education can change societal perceptions. Preliminary results show that total vegetation cover and total number of species were significantly higher in recreational islands compared to traffic islands. Flowering species cover was significantly higher in recreational islands in June and July and number of flowering species was significantly higher in recreational island in July. Islands that were not mowed during the study period had significantly higher plant richness and richness of flowering species than islands that were mowed. Environmental education increased positive perception of floral biodiversity in UGSs.

Keywords: biodiversity, citizen science, urban ecology

Poster 69: Designing for diversity: The role of flower strips in wild bees and butterflies conservation

Wendy Moya, Oksana Skaldina

University of Eastern Finland

Pollinators play a crucial role in the health and productivity of both agricultural and urban ecosystems. Agricultural landscapes support a high biodiversity of pollinators, which provides significant ecological and economic benefits to humans. However, as urbanization continues to rise, it becomes essential to assess and conserve pollinator populations in urban environments. Flower strips —integral Nature-based Solutions— enhance pollinator and plant biodiversity, attract natural enemies for natural pest control, improve soil quality, and contribute to phytoremediation. They offer a sustainable solution for farmers to improve crop yield while positively impacting the economy and the environment. Simultaneously, flower strips are being utilized in urban areas to counteract declines in floral and pollinator diversity. Despite their high importance, pollinators are experiencing significant global declines. In Europe, there is an alarming decrease in butterflies and wild bee's pollinator groups, and conservation efforts are hindered by gaps in local and regional research on pollinators' ecological networks. To develop effective biodiversity conservation strategies for vulnerable pollinators, it is necessary to understand their distribution and the plant species they depend on. This target can be achieved through the selection of specific native floral resources, such as plants with varying sugar compositions, that are less attractive to pests yet beneficial to key pollinators. This research aims to fill the knowledge gap by examining the structure and function of plant-pollinator networks in Finnish agricultural and urban environments. It focuses on designing and optimizing native plant mixtures for flower strips to enhance wild bee and butterfly diversity in both settings.

Keywords: pollinators, biodiversity, monitoring, flower strips, conservation

Poster 70: Synergies between biodiversity and residents' reported valuations in urban forests

Aku Korhonen, Jenni Simkin, Ann Ojala, Marjo Neuvonen, Leena Hamberg

Natural Resources Institute Finland (Luke)

In Finnish urban forestry, recreational and biodiversity values are highly prioritized as management goals. However, it has remained contested how well these goals can be reconciled in practice. For example, some forest structural features that are known to be important for biodiversity, such as dead and decaying trees, have been considered undesirable from the viewpoint of recreational use. We studied people's perceptions of mature spruce-dominated forests in relation to several forest biodiversity indicators, including (1) living tree diversity, (2) deadwood abundance, (3) understory vegetation diversity, and (4) soil ectomycorrhizal fungal (eDNA) richness, to identify potential synergies and conflicts between forest biodiversity and recreational values. Our surveys covered 15 forest sites spread across five Finnish urban centers where we recruited local residents as respondents. Each participant (n=153) visited one forest site and answered a questionnaire about the perceived qualities of the forest after 15 min observation period within the forest stand. We also measured the psychological restoration of participants. Our preliminary results suggest that forests that ranked higher in terms of biodiversity indicators also tended to be more positively perceived by the study participants, indicating stronger synergy than conflict between biodiversity and recreational value in urban forests.

Keywords: dead wood, forest vegetation, ectomycorrhizal fungi, psychological survey

Poster 71: Does the biodiversity hypothesis apply to wildlife health? Introducing the MUUMAA project

Esa Koskela¹, Jussi Heinonsalo², Eva Kallio¹, Saana Kataja-aho¹, Carita Lindstedt-Kareksela², Aigi Margus¹, Phillip C. Watts¹, Elli Liimatainen¹, Saija Vuorenmaa¹, Michaela Casková³, Tiina Arjukka Hirvonen³

¹*University of Jyväskylä*

²*University of Helsinki*

³*Evolution in Action*

According to the biodiversity hypothesis, forests provide children and adults with a wide range of microbial contacts that strengthen immune defenses and prevent disease. Currently, however, human impacts such as silvicultural practices and urbanization are reshaping forest habitats at a rate to which organisms cannot or do not have time to adapt. These changes may be reflected in the structure and diversity of forest microbial communities. Unfortunately, we do not know how these changes will affect the health of non-human forest species. For example, an increase in disease burden in wildlife may be detrimental to humans by increasing the risk of zoonoses. We study how different levels of human impact shape the diversity of forest soil microbial communities, the health of non-human forest species, and the resulting disease threat to humans. Our societal goal is to use environmental and arts education to increase current and future generations' understanding of the complex interactions of forest ecosystems, and to strengthen children's and young people's diverse relationships with nature. In this way, we can contribute to knowledge and skills for planetary life: the ability to understand the many meanings of forests for humans and all other life in the context of planetary well-being. Close collaboration between scientists and environmental and art educators allows the latest research findings to be rapidly translated into openly available educational materials and made available to educators.

Keywords: biodiversity monitoring, forest soil, environmental education, ecosystem services, zoonoses

Poster 72: Understanding public perception of invasive species: the role of social conditions

Akanksha Ingale, Satu Ramula, Aino Kalske

University of Turku

After habitat loss, invasive alien species (IAS) are one of the major causes of biodiversity loss. When introduced to new habitats, invasive species often outcompete native species, disrupt ecosystems, and exert negative ecological and economic impacts. Recent studies show that the direct negative impacts of IAS and their management are associated with 423 billion US\$ global annual cost. Public perception plays an important role in successful management strategies for IAS. Differences in the perception and values of the stakeholders can lead to varied expectations and actions in invasive species management. The social conditions of the stakeholders affect their perception of invasive species, and the better understanding of these conditions is thus vital for crafting effective management strategies for IAS. In our study, we aim to identify various social conditions that affect public perception of IAS. We conducted a literature survey of peer-reviewed publications in the Scopus to examine the socio-economic factors typically used and their impacts on the perceptions of IAS across different taxa globally. Our findings indicate that gender, age, and education background are the most frequently studied variables. We observed a lack of studies on public perceptions of invasive species before 2015, and a geographical bias with the majority of research conducted in Europe during the past years, followed by America. Future investigations will build on these insights to explore specific public attitudes and their implications for effective communication and outreach in invasive species management.

Keywords: invasive species, socio-ecological linkages

Poster 73: A quantitative examination of biodiversity indicators in the context of biodiversity footprint assessment

Essi Pykäläinen¹, Sami El Geneidy², Mari Heikkinen³, Anne Holma³, Aapo Kahilainen³, Veera Norros³, Jani Salminen³, Hannu Savolainen³, Päivi Sirkiä³, Janne Kotiaho², Maria Hällfors³

¹*University of Jyväskylä / Finnish Environment Institute*

²*University of Jyväskylä*

³*Finnish Environment Institute*

Production and consumption of goods and services cause significant biodiversity loss worldwide through global supply chains. Biodiversity footprint assessment enables the quantification of biodiversity impacts from the consumption perspective by modelling the impact of human-induced pressures on biodiversity, i.e., land and sea use, exploitation of natural resources, pollution, climate change, and invasive alien species. Although several approaches and indicators for measuring and monitoring biodiversity impacts already exist while new ones are being developed, the lack of unified and comparable indicators applicable across different sectors hinders the operationalization of common goals to halt biodiversity loss. In this study, we review scientific and grey literature to identify and quantify indicators and methods that are used in biodiversity footprint assessments. Additionally, we identify linkages between 1) indicators and the level of biodiversity measured (genetic, species, ecosystem), 2) indicators and methods (e.g., EEIO, LCA), 3) indicators and assessments of different scope (e.g., product, sector, national consumption), and 4) indicators and the sectoral coverage. We present preliminary findings on how well different levels of biodiversity are captured through the most commonly used methodologies for different scopes and within different sectors. The findings of this study have the potential to direct future development of biodiversity footprint research towards sectors that have been poorly addressed and indicators that have potential in measuring a wider variety of biodiversity impacts.

Keywords: biodiversity footprint, indicator, review

Poster 74: Citizen science in Eurasian lynx reinforcement project - tool for population monitoring and public support

Magda Sindicic¹, Tomislav Gomerčić¹, Ira Topličanec¹, Silvia Blašković¹, Vedran Slijepčević², Ivan Budinski³, Ivana Selance³, Rok Černe⁴

¹*Faculty of Veterinary Medicine University of Zagreb*

²*Karlovac University of Applied Sciences*

³*NGO BIOM*

⁴*Slovenian Forest Service*

Conservation translocations face many challenges, and in the case of large carnivores, public support is one of the top concerns. However, informed and engaged stakeholders can be transformed from obstacles into key partners. In the period 2017 – 2024, the LIFE Lynx project (LIFE16 NAT/SI/000634) was implemented to prevent the extinction of the Eurasian lynx (*Lynx lynx*) in the Dinaric Mountains and the South-Eastern Alps. Eighteen lynx were relocated from the Carpathians to Croatia and Slovenia to stop inbreeding and enable gene flow between the Dinaric Mountains and the Alps. Systematic camera trapping, telemetry and genetics were used to monitor the reinforcement success, and intensive information campaigns were used to gain public support and boost citizen science as a source of opportunistic presence data and genetic samples. In Croatia, special attention was paid to the hunters as they were initially reluctant to support the reinforcement, while in Slovenia hunters were among the project's initiators. Thus, Croatian hunters were approached individually to build trust and friendship with project personnel. Also, they were engaged in camera trapping and all monitoring data was stored in an online database accessible to the public. This personal bottom-up approach and involvement in monitoring eventually led to the Croatian national hunting organization publicly supporting the LIFE Lynx project. Also, the amount of citizen science data collected during the project implementation increased 3 times compared to the previous period, with camera trap photos being the most frequent and substantially improving monitoring of the distribution and population size.

Keywords: *Lynx lynx*, Dinaric mountains, Croatia, camera traps, genetic samples

Poster 75: ‘Fluffy innovations’ – does flexible nest-building behaviour increase fitness at the cold range margin of the reed warbler?

Vilma Palomäki¹, Jules Mourgues², Deryk Tolman¹, Rose Thorogood¹, Nora Bergman¹

¹University of Helsinki

²École normale supérieure de Lyon

The nest as an extended phenotype can determine the reproductive success of its builder. Although once thought a classic example of rigid behaviour, nest-building is now considered to be more adaptable. For example, recent work shows that birds can exhibit significant flexibility in how they decide the shape and material of their nest. This raises the possibility that flexible nest-building behaviour could help to buffer against environmental challenges, but this is only just beginning to be investigated. Here we examine whether a novel nest-building behaviour is an adaptive response to a more marginal climate. The common reed warbler (*Acrocephalus scirpaceus*) has undergone a rapid northward range expansion and is temperature-limited at its northern range edge. In all previous literature, the species is reported to build nests from a variety of plant materials. However, based on our observations, reed warblers often incorporate animal fur in their nests in Finland. Since fur has a high insulation value, we predicted that fur as a nest material would be more prevalent in the cooler early season in the Finnish study population, and that nest size and material use affect nest temperature, incubation behaviour, and ultimately relative fitness. To disentangle active material choice from seasonal variation in material availability, we also experimentally provided fur at nesting sites throughout the breeding season and measured incorporation into the nests. Studying nest building in a recently colonised area presents an excellent opportunity to investigate how behavioural innovations can facilitate range shifts and improve resilience to environmental change.

Keywords: behavioural ecology, range shifts, climate change, field experiment