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Abstract booklet

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Keynote lecture #1

Cutting Edge: The role of forestry in riparian and stream ecology

Lenka Kuglerová, Senior Lecturer
Department of Forest Ecology & Management
Swedish University of Agricultural Sciences (SLU)

In my keynote presentation, I will talk about the interaction between forestry and water, and specifically I will discuss riparian forests and riparian buffer zones. Riparian forests are situated at the edges of all water bodies, but I will focus on riparian forests along streams. Riparian forests provide many ecological functions that keep our streams healthy and our waters clean. For example, they shade water surface, they filter nutrients leaching from the uplands and they supply food to aquatic organisms. Further, riparian zones are some of the most species rich ecosystems in boreal forest. Because the tight link between riparian forests and streams has been well recognized, it is desired that riparian forests are kept uncut in harvested stands. Those uncut forests are called riparian buffers and their purpose is to protect waters from potential negative effects caused by forestry operations and to preserve biodiversity. However, my research has shown that riparian buffers along streams in Sweden are not managed in a way that will secure water protection and riparian and aquatic biodiversity conservation. Many riparian buffers are too narrow, dominated by spruce and they tend to blow down, and as such, they can fail to provide the desired ecological functions. I will explain why is riparian buffer management in Sweden unsatisfactory, and I will give some ideas for how we can design better and more functional riparian buffers today and in the future.

Sensors and AI for seabird research and monitoring

Jonas Hentati Sundberg, Senior Lecturer
Department of Aquatic Resources
Swedish University of Agricultural Sciences (SLU)

New sensor technologies and Artificial intelligence can speed up learning about species and populations and increase the utility of ecological field studies to inform environmental management. My group has developed a range of automated methods for studying seabirds, which are often monitored for their high conservation value and for being sentinels for marine ecosystem changes. Using video surveillance, automated scales and a range of other sensors, we perform continuous monitoring in a semi-natural environment – the Karlsö Auk Lab, an artificial cliff on the island of Stora Karlsö, Sweden. Computer vision-based deep learning methods have been developed to generate high resolution, continuous data on monitoring parameters including bird presence, phenology and chick growth, and we have used such data to quantify effects of extreme weather and white-tailed eagle disturbances. Our ongoing work includes training deep learning models to identify more complex patterns in data such as poses, behaviors and recognition of individuals. I discuss several levels where big data and Artificial intelligence can be useful within ecological field studies, including (1) high resolution feature extraction, (2) linking diverse data to find new patterns in food webs and ecosystems, and (3) obtaining data in real time for performing iterative ecosystem forecasting and informing environmental management.

Plants and pollinators: what we know from space, time, and experiments about how the Arctic is changing

Anne Bjorkman, Senior Lecturer
Department of Biological & Environmental Sciences
Gothenburg University

The Arctic is undergoing rapid environmental change, thus altering the diversity, traits, and phenology of plants and impacting the animals that closely depend on them. A comprehensive understanding of these changes and their consequences must encompass a wide variety of data and approaches. In this talk I will synthesize recent results from spatial, temporal, and experimental approaches that aim to further our understanding of how climate change impacts Arctic plant species and plant-pollinator interactions. In particular, I will discuss how plant species composition, diversity, phenology, and functional traits correspond to variation in both macro- and microclimate, respond to experimental warming, and change over 30 years of monitoring. I will then show how shifts in these properties can influence plant-pollinator interactions, plant reproduction, and ecosystem functions such as litter decomposition. By integrating information across multiple methodological approaches, I hope to shed light on the complex dynamics shaping Arctic plants and plant-pollinator interactions in a rapidly warming Arctic.

Ecological Niche dynamics during adaptive radiation on Oceanic Islands

José Cerca, DDLS Fellow
Swedish Museum of Natural History

Adaptive radiations occur when a single lineage diversifies to exploit a broad range of ecological niches. However, the sequence of ecological occupation remains poorly understood. Two potential scenarios are herein proposed: random occupation, where species fill niches without a discernible pattern, and progressive occupation, where species track specific environmental gradients in a systematic manner. In this study, I examined four well-known adaptive radiations: Galápagos finches (Galápagos), Descurainia (Macaronesia), Aeonium (Macaronesia), and Anoles (West Indies). By analyzing phylogenetic and ecological distances between species, I found evidence supporting the hypothesis of progressive ecological occupation. This suggests that species diversify along a structured niche axis, implying that adaptive radiations may follow a more predictable, directional pattern. These findings are framed within the context of the 'least action principle' described by Gavrilets and Vose (2005).

Climate, calendars and crystal balls: Long-term studies of phenology, climate and abundance in the US and Sweden

Nora Underwood, Professor
Department of Biological Science,
Florida State University

Phenology has long been thought of as a calendar, with the timing of biological events proceeding predictably through each year and differing predictably among species. More recently, scientists have increasingly used phenological responses to climate as a crystal ball to predict how ecological communities might change with changing climate. Using long-term datasets from the US and Sweden, we asked 1. What aspects of climate influence phenology across high-altitude taxa (plants, insects, fish, mammals, birds) and do responses differ among taxa, 2. How climate influences abundances across high-altitude taxa (plants, insects, fish, mammals, birds, protists), and 3. How well predictions based on climate-phenology relationships from 150 years ago hold up when compared to contemporary data. We find that aspects of both current and prior year's climate can influence phenology, but that taxa differ substantially in how they respond to climate. Similarly, we found that the effects of climate on species abundances were highly variable and generally uncorrelated, even for organisms all living in the same valley. These results support previous suggestions that climate change may result in changes to relative abundances and temporal overlap of species within communities. Preliminary analyses suggest caution in using phenology as a crystal ball: current phenological events are rarely well-predicted by historical data.

The timing of winter fur change in the mountain hare in relation to elevation and latitude

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Lars Hillstrom, University of Gävle, Sweden
Petter Hillborg, University of Gävle, Sweden
Marcus Larsson, Swedish Forest Agency, Sweden
Antonio J Carpio, University of Córdoba, Spain

This study examines the timing of winter fur change in the mountain hare (Lepus timidus) concerning elevation and latitude. The transition from brown to white fur is a critical adaptive strategy that allows hares to remain camouflaged in snowy environments. Using data collected with camera traps from various elevations and latitudes, we analysed the influence of environmental factors, including snow presence, altitude, and latitude, on fur colour change. Our findings reveal that snow presence is the most significant determinant, with a strong correlation between snow cover and the transition to white fur. Latitude also significantly influences fur colour, likely reflecting the environmental gradients that vary with geographic location. In contrast, altitude did not have a significant effect on fur colour, nor did it interact with latitude in any meaningful way. However, seasonal altitudinal movements, driven by the availability of food and shelter, appear to influence the hare's habitat choice, with hares moving to lower elevations during winter to access food and higher elevations in summer. This seasonal behaviour may account for the lack of a direct correlation between altitude and fur colour. These results underscore the importance of snow cover and latitude as primary drivers of fur colour change, while altitude plays a secondary role. The findings highlight the need for conservation strategies that consider the potential impacts of climate change on snow cover dynamics.

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

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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. 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. 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 alternative strategies to deal with extreme high temperatures, and that metabolic rate may not be a determining factor in temperature adaptation. Morphology differed between populations, as individuals in arid regions had unique skull shapes to accommodate increase muscle mass for digging through the rocky soil. 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 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.

Genomic vulnerability of north Atlantic ptarmigan in response to climate change

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Patrick Rödin-Mörch, Uppsala University
Jacob Höglund, Uppsala University
Kristinn Pétur Magnússon, University of Akureyri & The Icelandic Institute of Natural History

Using whole genome re-sequencing data we study population level associations with regional climate data and predict the response to future climate change in populations of cold-adapted rock ptarmigan (Lagopus muta) and willow ptarmigan (L. lagopus). We infer the relationships between populations, examine individual adaptations to environmental factors, and calculate genetic offset in the face of expected environmental change. Genomic vulnerability to future climate change scenarios is predicted for each of the populations in the context of predicted range contractions under various global development scenarios using both CHELSA and WorldClim models. SNP data shows that regional populations have different influences of climate on predicted population-level persistence. We find evidence of adaptation towards local annual temperature ranges and precipitation regimes. Ancestry proportions derived from principal components analysis identified genetic similarities between east and west Greenlandic populations of rock Ptarmigan, all Scandinavian willow Ptarmigan, and Willow Ptarmigan in England and Ireland. Based on our evidence of local adaptation, genetic association with these climatic variables, and expected environmental changes across the north Atlantic and Arctic, we suggest that general warming and increased rainfall will be driving pressures on these species with more stochastic weather patterns adding to threats against more geographically isolated groups.

Time in urban ecology: Effect of urban trajectories on bird and plant population trends

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Pierre-Alexis Herrault, LIVE, Strasbourg university, France
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Landscape anthropization profoundly influences ecosystems both spatially and temporally. While the spatial impacts of urbanization are well-documented, its temporal dimensions remain less explored. Cities are hypothesized to act as ecological filters, favoring generalist species or enabling species with specific traits to thrive. Yet, these hypotheses are rarely examined from a temporal perspective: How do urbanization trajectories shape these dynamics, and how do they change over time?

Here, we investigate whether the species abundance and community trait values of plants and birds exhibit delayed responses to urbanization. Focusing on the Paris region, France, we describe urbanization through the current state of the built environment and past urbanization trends (1982–2021). Bird and plant community data come from two long-term citizen science programs. We computed the spatiotemporal responses of 90 bird and 222 plant species to our urbanization metrics, and 14 bird and 15 plant functional traits.

We find that over 10% of the studied species display delayed population trends in response to urbanization trajectories, with some trends deviating from expectations based on their spatial preferences along urban gradients. At the functional level, many of community traits values show delayed responses, often aligning with their spatial patterns. Our results highlight the ongoing dynamics of biotic communities in cities, showing the importance of temporal dimensions in ecology.

Why we disagree about the climate impact of forestry - A quantitative analysis

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Today, there is a heated scientific debate about the climate impact of forestry, which may hamper the implementation of forest-based mitigation strategies. Settling the dispute is therefore warranted. I will use quantitative analyses to demonstrate the conceptual and methodological basis for the disagreement and discuss the roles of paradigms and confirmation bias.

Warmer waters - Riparian buffers protect boreal streams from heating up on clearcuts

Caroline Greiser, Stockholm University
Maria Myrstener, Swedish University of Agricultural Sciences
Lenka Kuglerova, Swedish University of Agricultural Sciences

Warming waters can have severe consequences on aquatic ecosystem communities and functioning. Clearcutting increases temperatures of forest streams, and in temperate zones, the effects can extend far downstream. Here, we studied whether similar patterns are found in colder, boreal zones and if riparian buffers can prevent stream water from heating up. We recorded temperature at 45 locations across nine streams with varying buffer widths and compared upstream (control) reaches with reaches in clearcuts and up to 150m downstream. In summer, we found significant maximum water temperature increases on clearcuts of up to 5 °C in the warmest week, and warming was sustained down to 150m into the downstream forest in three out of six streams with buffers narrower than 15m. Surprisingly, these temperature patterns were also found in autumn, yet with lower effect sizes. Clearcuts in boreal forests can indeed warm streams and because these temperature effects are propagated downstream, we risk cumulative warming effects when streams pass through several clearcuts. Here, buffers wider than 15m protected against water temperature increases, calling for a general increase of riparian buffer width in Sweden.

Large scale, low coverage conservation genomics of the vulnerable Swedish sand lizard

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The Swedish sand lizard (Lacerta agilis) occurs in fragmented populations across the country, with varying population sizes and degrees of isolation. Sand lizards inhabit a large area across Eurasia and these Swedish populations, as many other Swedish species, represent the northern range extreme. These populations face significant threats from habitat degradation and land use change, which further fragmentation and increase risks of inbreeding. Currently red-listed and managed under a national species protection plan, the Swedish sand lizard stands to benefit substantially from an application of population genomics for their conservation. Here, we use low-coverage, whole-genome sequencing of 140 individuals to investigate genetic diversity and population structure among sand lizard populations from across their Swedish distribution. We observe declining diversity with increased latitude, reflecting the historical northward expansion process. We also observe strong population structure, with high differentiation even between closely located populations. Our study adds to the growing field of conservation genomics, demonstrating the utility of genomic approaches in conservation efforts for other threatened populations. Our research contributes crucial insights for the conservation management of this vulnerable species in Sweden and highlights the utility of genomic data for informing conservation decision-making.

Local deadwood abundance and surrounding landscape composition shape saproxylic beetle assemblages in burnt forests

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Understanding how factors at different spatial scales affect species is necessary to determine where conservation restoration efforts will be most effective. We examined how local and landscape variables influence saproxylic beetle populations after prescribed burning. Beetles (Coleoptera) and flat bugs (Hemiptera) were collected at 23 burn sites across three regions in Sweden. We analyzed the relationships between species richness, abundance and composition, and environmental variables at both local and landscape scales. Variables at the local scale were deadwood volume and burn size. Landscape scale variables included forests that were: protected, old (>120 years), clear-cut and burned. We recorded a total of 3088 saproxylic individuals (190 species). At the local scale, saproxylic species richness was positively associated with deadwood volume stressing the importance of conducting prescribed burns in ways that generate large deadwood amounts. At the landscape scale, saproxylic richness was positively associated with protected forest area, whereas abundance showed a negative relationship. In contrast, saproxylic richness was negatively associated with clear-cut forest area, while abundances were positively associated. The landscape context is therefore important to consider when planning prescribed burns. Species richness was similar across regions, whereas species composition varied; suggesting that prescribed burning is an important conservation measure in all regions.

Identifying priority areas for the expansion of the Swedish MPA network to conserve connectivity and vulnerable habitats

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Charlotte Berkström, Swedish University of Agricultural Sciences

Nations across the world have now committed to protecting 30% of land and seas by the year 2030 as part of the Kunming-Montreal Global Biodiversity Framework. As nations seek to expand protected area networks, there is an urgent need for systematic conservation planning and spatial prioritization that considers the broad range of ecological and socio-economic factors that influence the persistence of biodiversity. Here, we present an approach to spatial prioritization that incorporates spatial models of habitat connectivity and habitat vulnerability to isolation caused by anthropogenic disturbance in coastal areas of the Swedish Baltic Sea. We do so by developing connectivity models for 16 actively dispersing fish species using information on dispersal ranges and dispersal kernels. Using these models, we spatially estimate the importance of habitats to connectivity and maintenance of the population. We then incorporate spatial data on anthropogenic disturbance to identify habitats that are vulnerable to disconnect and isolation from the rest of the population. Using these spatial data, we then assess how well the Swedish network of marine protected areas conserves these important habitats. Finally, we perform a spatial prioritization with these data to identify priority areas for expansion of the Swedish marine protected area network to ensure ecological coherence and survival of fish habitats and populations in the future.

Restocking, the rescue or demise of the European eel?

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Philip Jacobson, Swedish University of Agricultural Sciences, Department of Aquatic Resources (SLU Aqua)
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The practice of restocking, i.e. releasing wild-captured or hatchery-bred fish into the wild, is a common conservation and fisheries management tool, often performed with stakeholder and political support. Studies however show that restocking rarely leads to an increase in population size. The European eel has been restocked since the early 1900's, and restocking is a recommended measure according to the EU eel regulation, included in many national eel management plans. The European eel is critically endangered, with a population decline of >99%. Eel cannot be artificially reproduced meaning that restocking relies exclusively on reallocation of wild recruits. The net-benefit of restocking at the population level is unclear, and ICES advice against fishing of glass eel for restocking. This implies an urgent need for studies evaluating restocking. Here we analysed over 20 years of data from restocking and monitoring in Swedish lakes and coastal areas. Our results show that production of eel at restocked areas can be relatively high, and there were no major differences between restocked and naturally recruited eels in condition or growth rate. Amongst recruiting eels in rivers, 4% were restocked, and in the coastal system 26% of the eels were restocked. Hence, despite extensive restocking, most eels are naturally recruited. We conclude that restocking can lead to increased production locally but comparisons with production at donor sites are needed to estimate the net benefit.

The impact of agriculture and agroforestry on down-stream water quality and biodiversity in tropical mosaic landscape

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Freshwater biodiversity is often sensitive to the land use in the focal catchment. To study how water quality and aquatic biodiversity changes along a land use gradient we measured water quality parameters and sampled stream macroinvertebrates from 46 small streams in southwestern Ethiopia. The composition of the land-use of the stream catchments varies in terms of the proportion of natural forest, coffee agroforestry and open agriculture. High resolution satellite images were used to create a land use map. Land use affected the abundance and taxa richness of macroinvertebrates by changing water quality. For example, the amount of dissolved oxygen (DO) was higher in streams coming from forests and lower when running through agricultural landscapes. Contrary to our hypothesis, water temperature, turbidity, conductivity, total phosphorus, total nitrogen and total organic carbon were higher in mosaic landscapes with coffee agroforestry. One possible explanation could be that this is due to higher human pressure and organic waste load from agro-processing (e.g. wet coffee processing wastes) in these landscapes, despite having a high tree-cover. Our findings highlight the urgent need for measures in agriculture and agroforestry-dominated landscapes to reduce the negative impacts of wastes from settlement areas and coffee washing stations on water resources, while simultaneously safeguarding the positive aspects of coffee agroforestry for both people and terrestrial biodiversity.

The usefulness of indicator species in conservation

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Preserving biodiversity requires extensive knowledge on species distribution and effectiveness of conservation actions. This task can be simplified by using indicator species that act as representatives for other species groups. However, it is unclear exactly how useful indicators are in conservation. In view of this, we used systematic review methods to synthesise evidence on whether indicator species can be used to estimate the diversity of other species groups. In addition, we evaluated if different forest species groups respond similarly over time to restoration practices such as prescribed burning and deadwood addition. Our results revealed weak correlations between diversity of indicators and other species, and that different species groups does not necessarily respond the same to forest restoration practices. However, there are some situations when indicators can be more useful, e.g. when used at larger scales and when there are similarities between an indicator and other species. Together, this suggests that indicators often does not represent the status of biodiversity or other species, and that the response of indicators to conservation actions is not necessarily indicative of how other species will respond. As there are few feasible alternatives to using indicators in conservation, we stress the importance of carefully selecting indicators and confirming that there is a strong association between and indicator and the species it is meant to represent.

15 years of monitoring – can we detect changes in tundra plant communities?

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Environmental monitoring programs can provide data to analyze ecosystem processes at large spatial and temporal scales. Here, we use 15 years of vegetation monitoring of the Scandic Mountain chain in Sweden to test whether there has been a shift to a more thermophilic vegetation community, adapted to warmer temperatures, and a changed tolerance to grazing by large herbivores, as well as whether there has been an increase in plant productivity as a consequence of climate change.

We used ecological indicators, i.e. ordinal values that attribute optimal environmental conditions to plant species, to investigate whether the vegetation community changed in its temperature optimum and tolerance to grazing over time. Trends in plant productivity were calculated by remote sensing of the Normalized Difference Vegetation Index (NDVI).

We did not find changes of the community mean values of the temperature optimum, i.e. a trend to a more thermophilic community, nor a change in the grazing tolerance throughout the study period. Plant productivity remained stable on most sites, but increased in a third of the sites largely in the southern part of the study area, most likely due to an increase in shrub cover. The lack of strong trends in vegetation transitions highlights the complex interplay of biotic and abiotic factors, especially mammalian herbivory, which contribute to the resilience of arctic-alpine vegetation amidst climatic and environmental changes.

Competitive interactions modify the direct effects of climate

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As the climate is changing, species respond by changing distributions and abundances. The effects of climate are not only direct, but also occur via changes in biotic interactions, such as competition. Yet, the role of competition in mediating the effects of climate is still largely unclear. To examine how climate influences species performance, directly and via competition with other species, we transplanted two moss species differing in climate niches, alone and together at 59 sites along a climate gradient. Growth was monitored over three growing seasons. In the absence of competition, both species performed better under warmer conditions. When transplanted together, a warmer climate had instead negative effects on the northern moss, while the effects remained positive for the southern species. The negative effect of a cold climate for the southern species was larger when both species were transplanted together. Over three growing seasons, the southern species almost outcompeted the northern in warmer climates. Our results illustrate how competitive interactions can modify, and even reverse, the direct effects of climate on organism performance. A broader implication of our results is that species interactions can have important effects on how environmental and climate change influence performance and abundance.

Invasive lupines in Sweden: limited by climate, or by dispersal?

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The distribution of an invasive species is shaped on one hand by which environments suit the species' niche, and on the other hand by patterns of dispersal since introduction to the new region. Understanding the ecological niche of a given invasive can help management efforts, but dispersal patterns, if not accounted for, can confound attempts to model niches. We conducted a survey of the globally invasive large-leaved lupine (Lupinus polyphyllus) along 2100 km of Swedish roadside, to investigate how its occurrence is shaped by macro- and microclimate, soil characteristics, and dispersal patterns. Our results suggest that the Swedish lupine distribution is broadly shaped by climate at a regional scale, but more strongly shaped by patterns of anthropogenic dispersal at the local scale. We additionally show that local lupine abundance appears to be driven by similar environmental factors as those affecting lupine occurrence, but these same drivers explain little variation in morphology or ground cover. Our study shows how a nested sampling design can be used to model effects of the environment at different spatial scales, and test hypotheses about the drivers and trajectories of invasive species distributions.

Plant abundance drives beta-diversity changes in a warmer Arctic

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Warming of the Arctic is now occurring four times faster than the global average, , altering vegetation patterns and threatening biodiversity. Most studies have focused on α-diversity, but understanding plant β-diversity is crucial. Using various aspects of Arctic plant diversity and a Pan-arctic warming experiment, we found contrasting responses in α-diversity and β-diversity. For α-diversity, we found a warming sensitivity in the cold dry and moist communities, which for moist communities was driven by loss of functional important species. The cold dry communities were instead more sensitive to decreased evenness of species abundance, whereas wet communities did not show any α-diversity responses to warming. For β-diversity, changes in plant abundance were an important driver of increased β-diversity, where warming led to increased dissimilarity for warm wet communities and mid-warm moist communities. Interestingly, we also found that the temperature response window increased with increased abundance weight. Our findings reveal different diversity responses operating in the low Arctic compared to the high Arctic. Additionally, it highlights the sensitivity of β-dissimilarity metrics to climate warming and promotes their use when analyzing the impact of vascular plant diversity on ecosystem functions in the tundra biome.

Responses to extinction drivers vary among specialist plants in Baltic coastal meadows

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Coastal meadows are semi-natural grassland with unique ecological communities due to their disturbance regimes and position between land and sea. However, abandonment and environmental change threaten their characteristic flora and fauna.

We recorded abundance of 9 specialist plant species in 72 coastal meadows along 250 km of coastline in central Sweden, reiterating a 60-year-old inventory. Through aerial image interpretation we also produced maps of Baltic coastal meadows in the 1960s and 2023, enabling us to quantify local and regional changes in habitat amount and management continuity. We analyzed changes in population sizes and distribution in relation to past and present habitat availability, management and habitat quality.

We found that all species have decreased in habitat occupancy, with some now having become regionally extinct. Half of the species that persist still have stable populations in continuously managed meadows, while the other half have declined significantly, even in these areas. Only habitat loss cannot explain these patterns, but rather its interactions with other extinction drivers such as climate change and eutrophication. These results give a rare insight into the varying responses of specialist plant species to the environmental developments in modern times and the ensuing payment of extinction debts. Conservation measures are imperative and must take habitat quality and connectivity into account.

Trait-based higher-order interactions and species coexistence

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A higher-order interaction between three species means that the presence of a third species modifies the interaction between the first two. A trait-based higher-order interaction is the same except between phenotypes instead of species. Higher-order interactions are ubiquitous in both ecological communities and gene regulatory networks, but their relevance in explaining large-scale evolutionary patterns is still contested. In this talk I discuss the ecological and evolutionary effects of trait-based higher-order interactions on species coexistence in model communities. I use one-dimensional traits, such as root depth in the case of soil nutrient competition or height in the case of competition for light. On the surface, a confusing array of possibilities emerge which may be summed up as "adding higher-order interactions can have a positive, negative, or no effect on coexistence". However, I argue that by analyzing the relative widths of the pairwise and higher-order interaction kernels, we will know which outcome to expect in any given scenario and gain a general understanding of how higher-order interactions affect species diversity.

Distinct bacterial and protist plankton diversity dynamics uncovered through DNA-based monitoring in the Baltic Sea area

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Planktonic microorganisms in coastal waters form the base of food webs and biogeochemical cycles. These environments are exposed to pronounced environmental gradients, and often strong salinity gradients. Yet, commonplace ecological assessment overlooks most of their diversity. We analyzed protist and bacterial diversity from new and publicly available DNA metabarcoding data collected in the Baltic Sea and the Kattegat-Skagerrak. We show that salinity, unlike other environmental factors, had a stronger effect on bacterial than protist community composition. Meanwhile, bacterial alpha diversity primarily followed seasonal patterns that we linked to deep water taxa reaching the surface through convective vertical mixing. On the other hand, protists were more diverse in high salinities. Still, Bayesian modeling showed that similarly abundant bacterial lineages were less likely than protists to occur in both lower and higher brackish salinities. We propose that protists are ecologically less sensitive to salinity due to the disconnection of basic metabolic processes from the cell membrane through compartmentalization. Additionally, further and more frequent dispersal of bacteria might have impeded local adaptation following historic salinization events. Ultimately, incorporating DNA metabarcoding into an environmental monitoring program allowed us to connect ecological and biogeographic processes with understudied taxa and biodiversity dynamics.

Phytoplankton adaptation to a browning light spectrum in the Baltic Sea area - community competition

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Phytoplankton are vital in the marine ecosystem and they depend on light for energy. Species able to efficiently utilise light in their environment have an advantage and therefore light is a key driver of adaptation and distribution. The importance of light intensity is well described, but less is known about phytoplankton responses to the light spectrum. The light environment in the northern Baltic Sea is browner than in the south and the Kattegat which mixes with clearer waters. This browning is caused by chromophoric dissolved organic matter (CDOM) which primarily absorbs light in the blue part of the spectrum. Climate change has increased rainfall and, with changing land use, CDOM levels are projected to increase. We determined that phytoplankton communities from northern, southern Baltic and Kattegat area waters differ depending on spectrum using incubations and DNA barcoding. We found greater proportions of heterotrophic plankton and mixotrophs after incubation under browning light than under a bluer spectrum based on oligotrophic ocean waters. In samples from the northern Baltic, we found green algae were better able to cope with the challenge of browning light incubations. These differences are likely to represent adaptations to the browning light in the northern Baltic. Our findings have implications for the health of the Baltic Sea, and improve understanding of CDOM induced changes in phytoplankton communities by determining the spectral aspect of browning.

Carbon cycling below three common plants encroaching the Low Canadian Arctic

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Deciduous shrubs and trees are encroaching on the Arctic tundra due to increasing air temperatures, wildfires and thawing permafrost. The induced shifts in composition and biomass could induce large losses of soil organic carbon due to increased rhizosphere priming. I present a novel dataset on the belowground carbon cycling of three common encroaching plants following a 13CO2 pulse-chase labelling experiment in Inuvik, Canada. 13C flux estimations and partial 13C source isolation, both from field and lab measurements, show that there are major differences in the turnover rate of photosynthates belowground between Alnus viridis, Betula glandulosa and Picea Mariana. Turnover rates of the roots and soil depth were both key influences on the fate of recently assimilated carbon belowground. Our work highlights the importance of plant-soil interactions under changing Arctic climate and pinpoints towards a feedback from northern ecosystems to on-going climate change.

Impacts of large herbivores on mycorrhizal fungal communities across the Arctic

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Plants form symbiotic relationships with mycorrhizal fungi, which are vital for soil carbon cycling. In the Arctic, one of the most soil carbon rich regions of the world, herbivores can strongly influence vegetation, but their impacts on mycorrhizal fungal communities are uncertain. We collected soils from 15 herbivore exclusion experiments across the Arctic. We sequenced across both ITS regions and partial SSU region with two sets of amplicons to determine the composition of soil mycorrhizal fungal communities and assess how these are impacted by herbivore effects, plant communities, and climate and edaphic properties. Ectomycorrhizal fungi (EcM) had the highest number of species, followed by arbuscular mycorrhizal fungi (AM), then Ericoid mycorrhizal fungi. Mycorrhizal fungal communities differed regionally along climatic gradients. Herbivore exclusion had a modest effect on the total mycorrhizal fungal community composition and the AM fungal community composition. AM fungal community composition was most strongly impacted by plant community, whereas EcM fungi composition was correlated with both plant communities and total nitrogen and δ13C in the soil. The large number of AM fungi identified highlights the need for more thorough evaluations of these communities and their potential role in Arctic carbon dynamics as these fungi are currently understudied in the Arctic.

How do decomposers face nutrient limitation?

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Plant residues can contain very limited amounts of nutrients, and yet soil microorganisms decompose them, providing nutrients for plant uptake and precursors of stable organic matter. How can microorganisms grow on these nutrient-poor substrates, despite having high biomass nutrient contents? Here we focus on nitrogen (N) as a key limiting element in most terrestrial ecosystems, and explore different strategies microorganisms adopt to utilize substrates ranging from relatively N-rich leaves to extremely N-poor wood. When feeding on N-poor substrates, microorganisms can lower their N demand by growing less efficiently—i.e., by respiring more or using more carbon (C) for resource acquisition rather than growth. This strategy results in decreasing microbial C-use efficiency (CUE= microbial growth/C uptake) with decreasing residue N content. The soil microbial biomass can also continue to grow despite low N availability by retaining N in their tissue when they senesce. This mechanism has been documented in fungi, which translocate N from old mycelium to the growing hyphal tips, where N is needed to grow new biomass. Using a mathematical model and a database of ~600 residue decomposition time series, we show that both strategies allow explaining the observed C and N changes during decomposition. However, compared to lowering CUE, efficient resorption of N is a more ecologically meaningful strategy as it allows to sustain growth under low N availability without wasting C.

The evolution of thermal performance curves in response to rising temperature across the model genus yeast

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The maintenance of biodiversity crucially depends on the evolutionary potential of populations to adapt to environmental change. Accelerating climate change and extreme temperature events urge us to better forecast evolutionary responses. We harnessed the power of experimental evolution with the microbial model system yeast (Saccharomyces spp.) to measure the evolutionary potential of populations to adapt to future global warming, in real-time and across deep phylogenetic rifts. We tracked the evolution of thermal performance curves (TPCs) in populations of eight genetically and ecologically diverse species under gradually increasing temperature conditions, from 25ºC to 40 ºC, for up to 600 generations. We found that evolving towards higher critical thermal limits generally comes at a cost, causing a decrease in both thermal tolerance and maximum growth performance. The evolution of TPCs varied significantly between species with strong genotype-by-environment interactions, revealing two main trajectories consistent with the "hotter is wider" and the generalist "jack of all temperatures is a master of none" hypotheses. Our results suggest that adaptive strategies to increasing temperatures are complex and highlight the need to consider both within and between species diversity when predicting and managing the impacts of climate change on populations.

Adapting fast and slow: The repeatability and molecular basis of plastic and genetic responses to temperature extremes

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Theory predicts that phenotypic plasticity can play a pivotal role in evolution by impeding or facilitating genetic adaptation. Thus, to predict how populations will respond to climate change, we need to understand how plastic and genetic responses interact during thermal adaptation - and the effects of genetic variation in source populations.

We used experimental evolution in seed beetles to unravel plastic and genetic responses to temperature stress. Replicate lines were generated from three geographic origins, and then adapted to cold, ancestral, or hot temperature for ~100 generations. Gene expression was then measured at the three temperatures.

In line with previous findings, genetic changes in expression often counteracted immediate plastic responses, suggesting that genetic compensation is a major mode of thermal adaptation across the transcriptome. However, this pattern was much stronger and more repeatable across genetic backgrounds for cold-adaptation compared to heat-adaptation. We harness DNA pool-sequencing and phenotypic data from the same lines to explore the underlying mechanisms behind these qualitative differences.

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

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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.

Local adaptation of life cycle regulation in a range expanding butterfly

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In seasonal environments insects cannot perform throughout the year, but only during favourable seasons. The unfavourable seasons are therefore overcome by entering a state of dormancy known as diapause. Diapause is a predictive state, entered before the start of winter through the perception of cues, the perhaps most important being daylength. Due to climate change, higher latitudes and altitudes are becoming warmer, which cause species distributions to shift. As a result of these species range shifts, organisms moving to higher latitudes will encounter novel daily and annual light cycles and will need to adapt to the daylength they encounter. To investigate local adaptation to daylength, we studied diapause induction in the butterfly Lasiommata megera. Using a common garden field experiment we compared populations from the southern Swedish core range with populations from the northern-Swedish margin. Our results show differences between populations in diapause response. In line with adaptive predictions caterpillars from the northern populations entered diapause earlier in the season compared to caterpillars from the southern populations. This shows local adaptation of the northern populations to the novel day length conditions. However, there were no differences between populations just two weeks later in the season. This highlights the importance of local adaptations in northern-Swedish populations, during the early stages of the last annual generation.

Sex-specific growth and lifespan effects of germline removal in the dioecious nematode *Caenorhabditis remanei*

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Germline regulates the expression of life-history traits and mediates the trade-off between reproduction and somatic maintenance. However, germline maintenance in itself can be costly, and the costs can vary between the sexes depending on the number of gametes produced across the lifetime. We tested this directly by germline ablation using glp-1 RNA interference (RNAi) in a dioecious nematode Caenorhabditis remanei. Germline removal strongly increased heat-shock resistance in both sexes, thus confirming the role of the germline in regulating somatic maintenance. However, germline removal resulted in increased lifespan only in males. High costs of mating strongly reduced lifespan in both sexes and obliterated the survival benefit of germline-less males even though neither sex produced any offspring. Furthermore, germline removal reduced male growth before maturation but not in adulthood, while female growth rate was reduced both before and especially after maturation. Thus, germline removal improves male lifespan without major growth costs, while germline-less females grow slower and do not live longer than reproductively functional counterparts in the absence of environmental stress. Overall, these results suggest that germline maintenance is costlier for males than for females in *C. remanei*.

Landscape of genetic diversity in Scots pine across Eurasia

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Scots pine (*Pinus sylvestris* L.) is the foundation species of boreal forests across Eurasia, and displays remarkable ecological breadth, with a distribution ranging from southern Europe to tundra Arctic. Such expansive distributions can be favored by various demographic and adaptive processes, as well as the interaction between them. To understand the impact of neutral and selective forces on genetic structure in Scots pine, we conducted range-wide population genetic analyses on about 3000 trees from 200 populations using genotyping-by-sequencing, reconstructed the recent demography of the species, and examined signals of genetic adaptation. We found a high and uniform genetic diversity across the entire range, with no indication of increased genetic load in expending populations, and minor impact of the last glacial maximum on genetic diversity. Genetic-environmental associations identified only a handful of SNPs significantly linked to environmental gradients. The results suggest that extensive gene flow is predominantly responsible for the observed genetic patterns in Scots pine. The apparent missing signal of genetic adaptation is likely attributed to the intricate genetic architecture controlling adaptation to multi-dimensional environments. The panmixia metapopulation of Scots pine offers a good study system for further exploration into how genetic adaptation and plasticity evolve under gene flow and changing environment.

Distributional thinking and the HerbVar project

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Species interactions are rarely distributed uniformly or randomly in space and time, but instead have high variance. Nonetheless, ecologists typically quantify interaction metrics with only a mean value. The variance, skew, and asymmetry of distributions can be useful as both responses and predictors in ecological studies. We encourage researchers to consider the potential for variance in distributions to be biologically important, as has been suggested by some previous theory and by empirical work.

The 'HerbVar' project is a global collaboration among ecologists using standardized protocols to collect data on the distribution of herbivore damage to plants. We find that biogeographic and phylogenetic patterns in the inequality of herbivore damage (its Gini coefficient) are stronger than patterns in mean herbivore damage. Damage patterns at different hierarchical levels (among leaves within a plant, among plants, among populations or species) are different from expectations from null models, and differences in variances can be caused by plant genotype and plant neighborhoods. We invite people to join phase 2 of HerbVar data collection, which will target data collection within focal plant families and of damage to reproductive structures (flowers, fruits, seeds).

Resource competition between small pelagic fish in the central Baltic Sea

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Small pelagic fish, or forage fish, comprise only few species but are the most abundant pelagic fish stocks. This makes them prone to high fluctuations with consequences for lower and higher trophic levels. Resource competition among forage fish is often reported as the driving factor for population dynamics, but prey preference and interspecific competition is not well quantified. We used DNA metabarcoding, stable isotopes and microscopy to identify resource use and overlap of the two clupeid species, herring (Clupea harengus) and sprat (Sprattus sprattus), and the three-spined stickleback (Gasterosteus aculeatus). The fish and their zooplankton prey were sampled in the central Baltic Sea in May 2022 and 2023 and October 2022. Clupeids shared a similar diet in spring, composed mainly of the copepods Pseudocalanus and Acartia, while stickleback favoured different copepods species and the rotifer Synchaeta, and had a distinct isotopic signature. In fall, all fish preyed on different species, mainly composed by various copepods. Our results show that resource competition was overall limited, except for sprat and herring in spring when prey diversity is low. This suggests that shifts in plankton prey composition have the potential to affect forage fish stocks dynamics, rather than resource competition. Our study illustrates that an improved understanding of species interactions is key to advice ecosystem management for sustainable fisheries and marine biodiversity protection.

Community filtering in wetlands: the role of hydrological processes and dry refuges at different spatial scales

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Flood disturbances act as strong filters on arthropod communities by excluding species that are not adapted to the high water-tables. Sensitive species survive in these areas by either migrating to terrestrial habitats of by using dry refuges within the wetland. To understand the processes driving wetland arthropod communities, it is therefore necessary to combine ecological studies with measurements of hydrological processes at a scale relevant to arthropod species. We used fine-scale (2x2 m2) digital elevation models combined with water table measurements to detect variability in flooding regimes within a wetland. We then selected wetter and drier sites at a range of spatial scales, and found that the scale of wet-dry heterogeneity at 10x10 m2 best explained arthropod communities. We also found differences among taxa in their response to flooding, showing how habitat generalist species can be filtered from wetland communities depending both on species traits and on habitat properties such as the presence of hummocks in the neighborhood. These hummocks can be used as dry refuges at high waters and thereby allow sensitive species to survive, as long as they also can climb the vegetation. There were also differences in the response between predatory and herbivore species, suggesting differences in the driving variables. Our study thus identifies unique community filters that could only be identified through collaborations between ecologists and hydrologists.

Ants protect against fig crop devastation by a community of specialist fig-eating moths

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Insect herbivores can inflict substantial costs on plant reproductive success. Seed herbivory impacts directly by reducing the number of seeds and therefore the dispersal and reproductive potential of the plant. Fig trees, Ficus, provide keystone resources for tropical forests. The pollinating fig wasps develop inside figs, so consumption of unripe figs results in trees not only losing seeds but also their pollen dispersers. Selection to defend figs should therefore be strong. Here we use canopy sampling to identify fig-consuming larvae in central Panama and quantify both their consequences for the fig trees' reproductive success and the defensive value that ants provide against these larvae. Field surveys of 46 crops from nine fig species revealed that larvae could destroy up to 80% of figs on a tree. We barcoded 51 individual fig consuming larvae (mainly Lepidoptera) that grouped into seven molecular operational taxonomic units. Lepidopteran larvae formed two feeding strategies, either stationary within a fig or tunneling between figs. Within the context of our study, stationary larvae were specialists whereas tunneling larvae were either specialists or generalists found on different Ficus species. Trees with ants had significantly fewer figs consumed by larvae than did trees without ants. Our results corroborate earlier findings that hosting ants can be an effective defensive mechanism for trees against seed herbivores or other antagonistic insects.

Where do reindeer graze? A study of the interplay between abiotic factors and human presence in the mountain tundra

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The long history of reindeer herding in the Fennoscandian mountains has shaped vegetation and can mitigate climate change effects on plants. Yet, outdoor tourism is discussed as a major pressure resulting in a changed grazing behavior, potentially leading to shifts in the tundra plant communities. To study this, we tagged reindeer with GPS and accelerometers to follow their time-activity budget in space. Specifically, we investigated reindeer grazing patterns in relationship to tourism infrastructures but also abiotic factors. The effect of grazing duration in relation to plant composition was also studied locally. Regarding abiotic factors, soil wetness was highly influential, with reindeer grazing for longer time in drier than wetter sites. Regarding tourism infrastructures, reindeer on average did not come nearer than a 2-km distance from buildings and tended to graze less when in their proximity. No avoidance of hiking trails was found, and grazing patterns did not differ near trails. On a local scale, soil wetness prevailed as the dominant driver of local vegetation patterns, while grazing duration had weak effects on the vegetation. We therefore encourage to further investigate the interaction between grazing and soil wetness to foresee changes in the tundra vegetation. Our study also highlights the importance to monitor vegetation changes in mountain areas near buildings, as they appear discarded by reindeer, and hence are more prone to climate-driven shrub expansion.

Reindeer grazing counterbalances the treeline expansion in the Scandinavian subarctic

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Herbivory may offset climate change driven treeline expansion into the tundra. This study quantifies the effects of reindeer grazing on mountain birch recruitment and growth in the treeline ecotone in the Scandinavian sub-arctic in an area with contrasting grazing regimes for the past 20 years. We measured seedling density and the allometry of trees below, at, and above the treeline as well as vegetation composition along 20 transects crossing the treeline. Additionally, we investigated nutrient loading of soils and its effects on adult tree growth rate. Our results show that the treeline in the area grazed in winter may be responding to climate forcing by expanding diffusely into the tundra, while no treeline expansion was observed under the year-round grazing regime. High grazing pressure also reduced the numbers of tree basal shoots and the number of leaves below reindeer browsing height (less than 2 m). Additionally, we found a shift in ground layer vegetation composition in the area grazed year-round. Our results suggest that reindeer grazing at high density and when occurring during the growing season has the potential to stabilize the treeline locally, as well as significantly modify field layer vegetation composition in the treeline ecotone.

Pan Svecicus – Linnaeus's innovative large-scale feeding experiment

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In 1749, Linnaeus published Pan Svecicus, a thesis that describes food preference trials with cows, goats, sheep, horses and pigs. It is one of the first ecological experiments, but more important is the stunning scale of the operation: 2325 tests with 643 plant species. The study has several remarkable aspects: (1) The large experiment was made by an almost modern research group structure; (2) methods were described; (3) species names could be tracked to modern systematics thanks an early use of binomial names and reference to Flora Svecica; (4) raw data were published. However, the text merely summarizes conventional wisdom at the time, and is not based on the collected data. After 275 years we have made the first analysis of the results. Goats accepted the highest number of plant species (85% of the 204 plant species that were tested on all animals), followed by sheep (82%), cows (66%), horses (59%) and pigs (32%). The ruminants (especially goats and sheep) had high overlap in food choice, and the pigs were most deviating (despite the fact that pigs are more closely related to the ruminants than horses are). Among plant families, Fabaceae and Poaceae were generally preferred, while Lamiaceae and Ranunculaceae were avoided, especially by cows and horses. Cows and horses were also more keen to avoid toxic plant species.

Pre-weaning body condition maintained during a period of declining birth rates in harbour seals

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Body condition is intrinsically linked to both the survival and welfare of marine mammals. In Koster National Park on the Swedish West Coast, we have seen evidence of nutrient limitation in harbour seals including shifts in diet and a halving of the number of pups born between 2012 and 2023. This likely reflects widescale changes in the ecosystem as evidenced by declining seal abundance during national monitoring. Over four years, we have monitored pup body condition in Koster National Park using a remote sensing system. Despite significant declines in pup numbers, average preweaning body condition has remained constant. We have also found a significant correlation between pup and mother body condition. This may be an indication of year skipping, with a dwindling number of females in good condition giving birth to pups in similarly good condition. At least in the pre-weaning stage, it may indicate that pup welfare is not negatively influenced by declines in birthrates. Our findings have implications for understanding the mechanisms by which population growth rate is modulated by resource availability.

Moderate browsing may promote understory plant diversity under certain conditions

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Our study investigated the effects of browsing by large ungulates on understory plant diversity in the boreal forests of central Sweden. By analysing long-term data on browser density and plant species richness, we observed a non-linear, unimodal relationship between browsing intensity and biodiversity: plant species richness increased with browsing up to a threshold before declining as browsing intensified further. This pattern aligns with the "intermediate disturbance hypothesis," which suggests that moderate disturbance supports the greatest biodiversity, while both low and high levels of browsing lead to reduced diversity due to competition or high plant mortality, respectively.

The findings suggest that intermediate browsing levels support more diverse plant communities even in species-poor boreal production forests, a result that may be obscured in other studies where browsing intensity is lower. This study underscores the importance of balanced management of browsing species to foster biodiversity in northern forest ecosystems.

Insights into the Genetic diversity and Insecticide Resistance of Fall Armyworm (*Spodoptera frugiperda*) in Ethiopia

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The fall armyworm (FAW), Spodoptera frugiperda, a migratory and polyphagous noctuid moth native to the Americas, has become a significant invasive pest, severely affecting maize and other crucial crops worldwide. We analyzed 250 FAW larvae from Ethiopia using Cytochrome oxidase subunit I (COI) and Triosephosphate isomerase (Tpi) genetic markers. Additionally, 30 samples underwent whole-genome resequencing (WGS), and insecticide sensitivity bioassays were conducted against five synthetic insecticides.

The COI marker identified 60.6% and 39.4% of the Ethiopian FAW population as the rice (R) and corn (C) strains, respectively. However, the Tpi marker identified all samples as the C strain. The WGS revealed low genetic diversity and neutral evolution, suggesting a recent introduction and rapid migration. Amino acid substitutions associated with organophosphate resistance i.e. 10% A201S and 71.7% F290V were observed in the acetylcholinesterase-1 gene. Insecticide sensitivity bioassays indicated low sensitivity to Lambda-cyhalothrin, while Indoxacarb emerged as the most effective among the tested chemicals.

These findings support a common origin for the FAW invading Ethiopia and other Eastern regions, highlighting the potential risk of introducing resistance alleles for other insecticide classes. Regular molecular monitoring and integrated pest management strategies are recommended for effective control and mitigation of this pest's damage.

Form, Function, and Fashionably Late Falls: Tundra Ecosystem Productivity Changes Under Warming

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The Arctic, a region with brief summers and huge quantities of carbon stored in permafrost soil, is warming faster than any other biome on the planet. Warming temperatures in the tundra ecosystems of the Arctic can change vegetation traits and assemblies and drive feedbacks between soil, vegetation, and atmosphere with global consequences. One hypothesis posits that with warming and thus longer suitable periods for growth, some plants will extend their period of carbon assimilation via early green-up or late senescence and consequently store more carbon in biomass. However, recent studies have found that there may be a pre-determined limit to a plant's period of assimilation and growth regardless of temperature, and fixed photoperiod at any given latitude makes it unclear how plants will adapt to warmer days of the same length. This novel study will examine the phenological responses of tundra and boreal plants to warming at various latitudes in a fully controlled experiment. In order to compare among populations and predict changes in ecosystem productivity under potential new assemblages, we will grow dominant species from populations along a latitude gradient from the high Arctic to boreal Sweden at four seasonal temperature treatments and two daylength treatments (low Arctic, mid-boreal), and measure biomass growth and differences among phenological and functional traits. This study will begin in a phytotron facility in January 2025, with preliminary results to follow.

Genomic landscape of divergence in a pine species complex

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Species with large geographical distributions often display strong signals of local adaptation in growth and phenotypic traits. However, recovering signals of genetic adaptation in wild populations to complex environments has been challenging by using single-nucleotide polymorphisms (SNPs) analysis alone, due to minor effects of individual SNPs. Structural variants (SVs), which represent larger genomic differences, could have stronger phenotypic impacts and play an important role in mediating ecological transitions. Here we combined whole-genome short-read and long-read sequencing to investigate the genomic landscape of divergence in a pine species complex, Pinus densata, P. tabuliformis and P. yunnanensis, characterized by their distinct differentiation in ecological niche preferences. We discover over 4.9M SVs in a collection 21 samples from the three species, of which 54.6% are insertions, 42.6% deletions, 2.8% other types of SVs (inversions, duplications, and translocations). About 85.2% of genes have SVs overlapping intragenic regions or putative regulatory elements. Population differentiation in SVs is stronger than in SNPs. We further analyzed the fitness effects of different categories of SVs through annotation. Our findings highlight the significant contributions of SVs to species divergence, providing new insights into potential genetic mechanisms underlying environmental adaptation in conifer trees with large genomes.

Plant identity and traits shape above- and below-ground service and disservice provider abundances in flower plantings

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Flower plantings in agricultural landscapes can enhance pollination and biological control, contributing to sustainable crop production. However, selecting plant species that support multiple ecosystem services is challenging, and potential trade-offs must be considered. This complexity increases when accounting for below-ground effects. We evaluated 27 plant species for their ability to support functionally important above- and below-ground organisms—pollinators, natural enemies, herbivores, and decomposers—and assessed the effect of the plant traits floral area, timing of peak bloom, life cycle, and plant cover. We found that certain plant species support several groups of beneficial organisms, suggesting they can enhance multiple ecosystem services. Annual plants supported higher abundances of both above- and below-ground beneficial organisms than perennials. Greater plant cover was positively associated with hoverfly abundance. Several organism groups were correlated across plant species, but not due to shared responses to plant traits. Our findings underscore the importance of plant species identity and traits in designing flower plantings to enhance biodiversity and ecosystem services and highlight the need to include below-ground organisms, like nematodes, in future studies. Our results can be used to design flower mixtures that support beneficial ecosystem service providers while minding potential trade-offs and thus optimize the efficiency of flower plantings.

Wood-inhabiting fungi along macro- and microclimatic gradients

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Fungi are among the most diverse organism groups, and play a crucial role in decomposition. Besides the direct effect of climate on fungal diversity, fungi can be indirectly affected due to deadwood dependent beetles serving as vectors. Considering ongoing global climate and land-use changes, both affecting climate on a small scale, it is important to determine how fungal species communities are affected by macro- and microclimate, and beetle vectors. In this study, we investigated the fungal diversity in dead wood along a macro- and microclimatic gradient, and related it to beetle abundance. The macroclimatic gradient spanned along a 1200 km latitudinal range from southern to northern Sweden, while the microclimatic gradient was due to the varying level of shade from the forest edge to forest interior. Fungal species richness increased from northern to southern Sweden, whereas shade level had only minor effects. Also fungal species composition changed significantly along a latitudinal gradient, but only slightly along the shade gradients. Furthermore, we found that in the south, fungal species richness was best explained by microclimate, whereas in the north, it was best explained by the abundance of a vectoring beetle species (Ips typographus). Thus, macroclimate is the overall key determinant explaining fungal diversity on a regional scale, whereas both microclimate and the abundance of vectoring beetles are important on a local scale.

Three tests for the effectiveness of protected areas

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Protected areas are the cornerstones of biodiversity conservation. However, the evidence for their effectiveness is somewhat mixed. We will use new datasets quantifying land-use change across both Great Britain and Sweden together with climate data to assess the impact of protected areas and other conservation actions on occurrences of plants, butterflies and bird species in an era of rapid global change. Comparing the situation both before and after area protection, as well as trends in locations both receiving and not receiving protection, we will answer the following questions: [1] Do protected areas prevent the loss of valuable habitat?; [2] Do protected areas prevent local extinctions?; [3] Do protected areas facilitate colonisations of range-shifting species? In doing so, we aim to provide the reliable answers that are urgently needed for effective conservation policy and management.

Adaptation to historical climate conditions lowers soil respiration sensitivity to soil moisture and temperature

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Historical climate conditions can influence the current response of soil respiration to variations in soil moisture and soil temperature. This is because the main contributors to soil respiration - soil microbes and plant roots - can adapt to their environmental conditions, and thus retain some memory of past climates. The sensitivity of soil respiration to soil moisture and temperature has been hypothesized to be lower when historical conditions are more variable, and some supporting evidence has been provided by incubation studies. However, this hypothesis has not been confirmed in field studies. Here, we compiled high-frequency soil respiration, soil moisture, and soil temperature data from 25 sites from the COSORE database and defined mathematically the sensitivity of soil respiration to soil moisture and temperature. Using the monthly temperature and drought index (SPEI) from 1990 to 2010, we characterized the variability of historical climate conditions. We then predicted the sensitivity of soil respiration to soil moisture and temperature using historical conditions, vegetation cover and status (NDVI), and soil properties (soil organic carbon, pH, and clay content). Temperature sensitivity depends on NDVI and moisture sensitivity depends on soil properties, indicating indirect effects of climate history on contemporary soil respiration response to soil moisture and soil temperature.

New climate data at organism-relevant scales

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We present SoilTemp, a geospatial database compiling soil and near-surface air temperature data from all terrestrial habitat types over the world. Temperature-organism relationships lie at the heart of understanding, predicting and mitigating climate change impacts on local, regional and global biodiversity. Mechanistic understanding of temperature-driven processes and patterns like growth, performance and distribution of species requires climate data at organism-relevant scales. High-resolution local microclimate data (e.g., air and soil temperature, humidity, light intensity) from small consumer-grade sensors are becoming increasingly available and are now being compiled in the global SoilTemp database (https://www.soiltempproject.com). Currently housing 70,000 temperature logger time series, often complemented with local vegetation data, from 80 countries across all major biomes, the database continues to expand. We present examples of database products, including global soil temperature maps and European forest microclimate maps, as well as highlight key studies on how microclimate is improving our mechanistic understanding of organism and ecosystem responses to climate variation and change. SoilTemp is a large collaborative venture by the scientific community for the scientific community serving as a shining example of how efforts can be pooled to address the climate and ecological crisis.

Investigating the Relationship Between Soil Microbial Diversity and Soil Respiration Under Different Forest Management

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Forest management and disturbance can change soil microbial community composition and activity, which in turn may affect C turnover by altering microbial ecosystem functions such as decomposition. Despite these links, microbial abundance and diversity are often excluded from C turnover models. However, laboratory data suggest that microbial biomass improves model predictions for C turnover, and theoretical studies suggest that microbial functional diversity affects decomposition rates. In this study, we use empirical data collected from multiple forest management experiments across Europe by the HoliSoils consortium (Holistic management practices, modelling and monitoring for European forest soils; https://holisoils.eu/), and test the hypothesis that diversity indices for various fungal and bacterial functional groups contribute to explain variation in soil respiration rates. Preliminary results indicate significant effects of diversity on respiration, but that the relationship between microbial diversity and respiration differs between fungi and bacteria. The results will contribute to model development, to identifying and testing soil management practices for climate change mitigation, and to optimize ecosystem service provision.

Soil carbon simulation, projections and feedback in Earth system models

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Understanding the sensitivity of soil carbon cycling to climate change is key to quantifying future carbon cycle feedbacks. Under increased atmospheric CO2, both carbon input to the soil from vegetation and output from the soil due to heterotrophic respiration will increase, and the balance between these will determine the future ability of the land surface to be a sink or source of carbon. The ability of Earth system models (ESMs) to simulate soil carbon and related processes is therefore vital for reliably estimating global carbon budgets. Soil carbon simulation, projects and feedbacks are evaluated in the latest generation of CMIP6 ESMs. Global soil carbon is compared against observational datasets, highlighting the lack of consistency in northern latitude stocks. Future changes in global soil carbon stores and fluxes are investigated and the feedbacks quantified. The results suggest much of the uncertainty associated with modelled soil carbon stocks can be attributed to the simulation and representation of below ground soil processes in large scale models. These improvements would help reduce the uncertainty in projected carbon release from global soils under increasing levels of global warming.

Can we disentangle climate and microbial diversity effects on soil respiration in managed forests?

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Soils store large amounts of carbon (C), and small changes in C stocks can have large impacts on climate. Microbes affect C stocks by processing soil organic matter (SOM) and releasing greenhouse gases such as CO2 into the atmosphere, but also form and stabilize SOM. Despite their key role, microbes are generally not included in decomposition models to predict respiration rates and soil C turnover times. Microbial respiration rates are affected by various environmental drivers, such as temperature, soil moisture, plant litter inputs and existing SOM content. In addition—and possibly interacting with the environmental drivers—it is theorized that increased microbial diversity would contribute to accelerating decomposition rates, but this relationship needs to be explored with empirical data. For this purpose, we use data from the HoliSoils project (Holistic management practices, modelling and monitoring for European forest soils; https://holisoils.eu/) measured at different managed forest sites across Europe. First, we investigate the relationships between heterotrophic respiration and climatic drivers, and fit a non-linear model for temperature and soil moisture effects on respiration at these sites. Differences across sites and managements in the fitted model parameters such as activation energy, base respiration and moisture sensitivity are then further investigated in light of the different management practices and microbial diversity for each site.

Chapter V: Is the Åland Baltic cod divergent from the Bornholm cod?

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In the last decades, the eastern Baltic cod population has decreased in size and body condition, being small and skinny, however, this picture changes in the Åland Sea. Here cod can range 30cm-141cm, and look much healthier than the cod found in the Bornholm Sea. This opens the possibility that the Åland cod is a healthy population there, nevertheless, as far as we know the cod is not able to reproduce in the Åland sea, due to the low salinity found there. This salinity is too low for egg development, and further, eggs are negatively buoyant, therefore they would sink and die. In this study, we test whether Åland cod is adapted to low salinity at early life stages compared to Bornholm cod by testing: i) larval survival and neutral buoyancy after incubation in low salinity conditions, and ii) whether their eggs can develop and hatch on the bottom.

Trade-offs and synergies in forest management under fire risk

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Forests are managed in order to achieve multiple and often conflicting objectives, including maintaining a stable ecosystem and ensuring reliable production of resources. These goals become particularly challenging in the face of climate change and associated disturbances such as fires. Achieving effective forest management involves understanding the trade-offs between various objectives, such as maintaining stability in the face of disturbances and ensuring reliable production outcomes. However, the dynamics are not always a zero-sum game. In some cases, management strategies can create synergies, simultaneously enhancing both ecosystem stability and productive outputs. This presentation will explore such trade-offs and synergies using simple dynamical models, focusing on forest dynamics under management and fires, to illustrate the complexities and opportunities in managing forests under climate change pressures.

Microbial use of carbon and nitrogen from organic sources

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Soil microorganisms use organic material as carbon (C) and energy source, but they must also meet their demand for nutrients such as nitrogen (N). Prevalent organic material like plant litter is generally depleted in N (high C/N) compared to microbial biomass (low C/N). The C/N of the organic material is thus influencing its decomposability by microorganisms and further fate of C and N in the microbe-soil-plant system, i.e., stabilization in soil, plant uptake, or loss from the system due to respiration. While these general decomposition patterns based on C/N as a proxy for organic material quality are well established and microbial C use is extensively studied, the fate of C and N from organic material is rarely simultaneously tracked. In this contribution, we explore the fate of C and N from various organic sources with variable C/N (e.g., plant litter, microbial necromass, small organic molecules mimicking plant exudates) in different microbe-soil-plant systems. We do so by collecting data from publications that applied organic sources enriched in 13C and 15N, as these isotopes allow the detection of C and N fluxes much smaller than the total soil stocks. We aim to determine across studies how the recovery of C and N in the microbial biomass over time is impacted by the organic source C/N and system-specific (soil) properties.

Effect of Pollution on the Reproductive Biology of the Brown Macroalga Fucus vesiculosus

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Heavy metal (HM) pollution threatens biodiversity due to its high toxicity and persistence in natural ecosystems. Brown macroalgae, particularly Fucus vesiculosus, can accumulate and tolerate substantial concentrations of HMs. However, the impacts of chronic exposure on their fitness remains poorly understood. This study evaluates whether prolonged HM exposure adversely affects the sexual reproductive capacity of F. vesiculosus. We collected 20 reproductively mature individuals of this species from each of four populations from northwest Spain: one reference – unpolluted - (P1) and three with elevated levels of Pb (P2), Cr, Ni, Cu and Zn (P3), and As, Ag and Cd (P4). For each individual, we determined maximum thallus length, vegetative and reproductive biomass, number of receptacles (reproductive structures), and reproductive effort (proportion of total biomass allocated to reproduction). Thalli from P1 were larger and heavier, and had significantly more receptacles than the other three. The reproductive effort, however, was similar to that of two polluted populations (P2, P3). Notably, P4 showed the lowest reproductive allocation. While the proportion of biomass allocated to reproduction was not negatively affected across all polluted populations, our preliminary results show an overall reduction in absolute reproductive biomass and number of reproductive structures. This decline may negatively impact the long-term persistence of these populations.

Primary bark beetle damage in structurally variable spruce forests

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By increasing structural diversity and maintaining forest continuity, uneven-aged forestry has potential to mitigate the negative effects of even-aged forestry on biodiversity. In addition, higher structural diversity may contribute to decreased level of bark beetle damage. The heterogeneous stand structure in uneven-aged forests, with multiple age classes, irregular canopy openings due to partial harvesting and as such increased understory diversity may benefit overall biodiversity of bark beetle enemies. Further, lower density of older trees and reduced risk of wind-throw in uneven-aged stands may make the stands less vulnerable to bark beetle attack. This study focuses on three primary bark beetle species: the European spruce bark beetle (Ips typographus), the Six-toothed spruce bark beetle (Pityogenes chalcographus) and the Small spruce bark beetle (Polygraphus poligraphus), all of which are potentially harmful pest species. The aim is to determine if levels of bark beetle damage varies depending on forest management strategy, specifically comparing even-aged, uneven-aged and unmanaged forest systems. Preliminary results indicate no difference in bark beetle occurrence between management types for I. typographus and P. poligraphus, but an increased level of P. chalcographus in even-aged stands. These results provide insight into how management strategies may affect a forest’s susceptibility to bark beetle damage.

Diet composition investigation of harbour seals (*Phoca vitulina*) in Skagerrak

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The harbour seal is the most widespread coastal pinniped in the northern hemisphere. They are piscivorous and opportunistic predators. However, their diet is often dominated by some key species. Reconstructing of predators' diets, like seals, helps understand predator-prey interactions and assess harbour seals' ecological role in the marine ecosystem. Harbour seal diets were examined in the northern Skagerrak in fall 2020. Fish otoliths were recovered from seal scats and analysed. A total of 2671 otoliths from 73 seal scats were identified to species level and measured. The data indicated a diverse diet, including 28 different fish species, from 19 taxonomic fish families, enhancing the opportunistic hunting behavior of harbour seals. The species with the highest number of otoliths were sandeels (Ammodytes spp.) 39.6%, Norway pout (Trisopterus esmarkii) 21.8%, the pooled group haddock (Melanogrammus aeglefinus)/pollack (Pollachius pollachius)/saithe (Pollachius virens) 12.8% and blue whiting (Micromesistius poutassou) 7.9%. The most biomass-contributing species were haddock/pollack/saithe and ballan wrasse (Labrus bergylta), 18.7% and 13.5% respectively.

How many more? Linear transect sampling efficiency for characterization of boreal forest stands

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Forest Biodiversity Assessments (FBA) are crucial for identifying and preserving high conservation value forests. Various methods assess biodiversity and quantify forest structures, but guidelines for adjusting time settings based on forest type, size, or study aim are lacking. Sampling cost and efficiency may influence forest owners' willingness to invest in FBAs and pursue certification. Inefficient sampling can lead to insufficient size, uncovered spatial heterogeneity. The study aimed to evaluate how subsampling levels affect the accuracy of describing forest structural complexity and indicator species detectability in boreal forests. It examined the risk of missing features or species with a fixed linear transect survey protocol and examined when subsampling is advisable. Using a transect-based protocol for general and quantitative forest descriptions, the study tested different subsampling scenarios. Stand-level means for continuous variables were correctly estimated with minimal effort, i.e. maximum 5 sampled 10 m – segments. However, reliably estimating standard deviation required sampling at least 40 10 m - segments. The probability of detecting less species was higher the richer the stand. Only the most conservative subsampling scenario ensured high probability of detecting all species. These findings impact FBA cost-effectiveness. Subsampling scenarios save time and reduce costs, but detecting indicator species requires the full protocol or 40 segments.

Biomass distribution of sympatric mammals in the Cantabrian mountains, northern Spain

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The distribution of biomass, both among trophic levels and among different taxa, is an important characteristic of ecosystems. Such biomass distributions has seen large perturbations caused by human activities. Using long term camera trap data, an occupancy based abundance model and literature values of body mass we quantified the total biomass of 10 mammal species in a 1125 km2 large area in the Cantabrian Mountains in northern Spain. The distribution of body mass among mammals belonging to different trophic levels did not follow the rule of 10 % trophic biomass transfer, nor did predator biomass scale with a ¾ power exponent in relation to the biomass of potential prey. Instead, the distribution was bottom heavy with a disproportionately low predator biomass, in particular large carnivore biomass. In addition, herbivore to plant biomass, estimated from literature data, was substantially lower than theoretical expectations. The results in this study likely represent the upper end of the range of mammal biomass in southern European temperate forest, as the data were mostly derived from cameras placed inside protected areas. We suggest that the deviations between the observed biomass distributions and theoretical expectations provide a strong example of the radical effects human activities has had on the structure of terrestrial ecosystems.

Spatial components of plant and spider diversity on high Arctic peninsulas

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Climate change is shifting species distributions and transforming community composition worldwide. Such alterations to species communities may have particularly large ecological consequences for terrestrial Arctic environments. One such consequence is an increased fragmentation when species communities are being confined to high Arctic climate refugia. Therefore, quantifying the spatial distribution of biodiversity in high Arctic fragments may provide important insights into the ecological consequences of a warming Arctic. We quantified the spatial components of taxonomic, phylogenetic and functional diversity of vascular plants and spiders on geographically isolated peninsulas in the region surrounding the Nares Strait. The peninsulas were distributed both on Ellesmere Island (Judge Daly Promontory) and north Greenland (Washington Land, Hall Land, and Warming Land), and represent some of the northernmost land areas on Earth. We observed biodiversity differences among peninsulas, but that these differences where not uniform among organism groups, biodiversity dimensions, or spatial scales. We suggest that our results were caused by interacting effects of past evolutionary processes coupled with ongoing ecological ones, including environmental filtering of ecological communities and competitive interactions among community members. We argue that the results will have strong ramifications for the ability to predict ecological responses to climate change in northern ecosystems.

Electricity or eel? Migration behaviour and survival in a regulated river

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River ecosystems serve an important role for biodiversity, and they convey direct benefits for humans in terms of drinking water, recreation, fishing, and renewable energy. Hydropower plants, however, hinder river connectivity and cause severe ecological damage. The critically endangered European eel is one of many species that suffers greatly from hydropower. It is affected both by up- and downstream migration barriers, hydropower induced mortality, and habitat destruction and alteration. Our knowledge on the effects of hydropower on the European eel is currently insufficient to provide policymakers and stakeholders with tools to improve the conditions. In this study, we will quantify downstream migration survival, route choice, and behaviour year-around prior to and after the implementation of fish passage solutions. The study site, River Kävlingeån in Skåne county, is the Swedish index-river for eel monitoring within the EU monitoring program. The three hydropower plants in the river have already been through environmental retrials, prior to the commencement of the national retrial plan (NAP process). All three plants were granted to continue, but several legal terms must be met, one being the construction of fauna bypass solutions. This provides a unique opportunity to study downstream migration survival prior to and after the implementation of fish passage solutions. This project will provide highly important results to the hydropower retrials within the national plan.

Tools and services for metabarcoding data in the Swedish Biodiversity Data Infrastructure (SBDI)

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Daniel Lundin, Linnaeus University
Anna Rosling, Uppsala University
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The Swedish Biodiversity Data Infrastructure (SBDI) offers tools for publishing, harvesting, and analyzing species observation data, supporting interdisciplinary research on biodiversity and ecosystems. Recognizing the growing importance of molecular methods like metabarcoding of environmental DNA for documenting the diversity of life across all kingdoms and biomes, SBDI has created a suite of tools and services for genetic-based biodiversity data. These include: 1) a guide for simplified submission of raw sequence reads and metadata to the European Nucleotide Archive (ENA), 2) a flexible and user-friendly workflow (nf-core/ampliseq) for reproducible denoising and taxonomic annotation of metabarcoding data into classified Amplicon Sequence Variants (ASVs), and 3) a web interface to ASVs and associated species occurrence data in SBDI, providing features like sequence alignment (BLAST) search, and download of condensed Darwin Core archives that can be processed with our R package (asvoccur).

Understory plant diversity and carbon storage along an overstory density gradient in wooded pastures

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Silvopastoral systems are increasingly recognized as land-use systems with potential to sustain both biodiversity, climate mitigation and food production. Here we investigate the effects of overstory density on understory plant diversity and total carbon storage, measured as the sum of C in soil and overstory biomass. Soil samples and vegetation data were collected in 38 plots along an overstory density gradient in traditionally managed wooded pastures in southern Sweden. To enable upscaling, we related in-situ measurements to remote sensing proxies for predictors: wetness and overstory density. Results show that understory taxonomic diversity (species richness and Simpson diversity) had a slight negative relationship with overstory density, while the functional diversity response varied depending on community trait composition. Carbon storage in soil was unaffected by overstory density, but increased in overstory biomass, making total carbon storage positively related to overstory density. Our results strengthen the notion of a multifunctionality potential in wooded pastures and highlight the need to continue management of long-legacy systems.

Effect of tundra vegetation on extracellular enzyme activity in Arctic permafrost soil

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The Arctic is warming rapidly, causing permafrost thaw and vegetation shifts. Shrubs from lower latitudes are encroaching into the tundra, altering biomass distribution above and below ground. These changes impact greenhouse gas emissions by influencing litter input, root distribution, and microbial activity. A key mechanism is the rhizosphere priming effect, where labile carbon inputs stimulate microorganisms to produce enzymes that decompose both labile and recalcitrant soil organic matter (SOM). However, the effects of rhizosphere priming on SOM decomposition remain poorly understood. To address this, we simulated tundra conditions to study SOM decomposition via extracellular enzyme activity (EEA). Soil and plants from the Canadian tundra were sampled, root-picked, and homogenized before being placed into macrocosms with three characteristic Arctic plant species. After 12 weeks, macrocosms were opened, and soils were analyzed photometrically for hydrolytic and oxidative EEA. Macrocosm properties exhibited distinct variations with depth. Water content increased with depth, whereas dissolved organic carbon and microbial carbon decreased. Hydrolytic EEA declined with depth, while oxidative EEA increased. No significant differences were observed between planted macrocosms and the control; however, notable differences were detected between rhizosphere and bulk soils. This highlights that depth-dependent variations in soil properties and root influence are critical to EEA.

Share and publish data biodiversity research data with SBDI

LSBDI data mobilisation and support

Are you collecting data on where species occur in space and time? How many they are and additional measurements and information collected during your inventory? Do you want to show you data, make it findable and also easily available and understandable by others?
Are you wondering how to share and publish your data?
The Swedish Biodiversity Data Infrastructure SBDI is an aggregator and facilitator of biodiversity data. SBDI allows you to not only find data from national data providers but also publish your biodiversity research data.
We describe the steps for sharing your data in a common and standardised format. We compare data sharing through SBDI to other possible routes. We demonstrate three advantages for sharing your biodiversity data through SBDI: 1) Open science and FAIR: it will be easy to find, access, understand and reuse your data, 2) integration to the Global Biodiversity Information Facility GBIF: your data will be easily findable by and available to the international biodiversity community by, 3) link to the National Data Service SND: your data can also be found through SNDs national portal for research data researchdata.se.
Your data will be FAIR and can be found by either searching SBDI, GBIF or SND.

Store, find, explore and access Swedish Biologging data - a new SBDI tool

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Do you collect sensor data from moving animals? Do you want to store this data, manage it and make it easily findable?
Are you interested in finding data on moving animals to explore how they move, their activity patterns and how this interacts with physiology?
We showcase an example of how biologging data are collected and used to get insights to animal spatial behaviour. We present a new SBDI tool for Swedish biologging data for researchers to store and manage their data, and to be able to find, explore and access Swedish biologging data. SBDI Biologging can host data from any kind of sensor, including geographic positions, activity, heart rate and altitude. Our vision is of the Swedish Biologging Portal giving access to Swedish biologging data and making it easy to get an overview of animal movement and behaviour.
In the first version of the Swedish Biologging Portal you can find sensor data from animals, including movement trajectories and data characterising behaviour or physiology of animals. More datasets will become available continuously. New datasets are described by metadata and stored in a structured format according to biologging data standards. New functionality will improve ease of managing and sharing your data, data exchange with other repositions and data visualisation tools.
The portal is a joint venture between Lund University (CAnMove) and SLU (WRAM).
https://biodiversitydata.se/news/new-biologging-sensor-data-portal/

Long-term genetic consequences of admixture in a sand lizard population

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The sand lizard (*Lacerta agilis*) occurs in fragmented populations in southern Sweden, including small, isolated populations that are of conservation concern. These populations have low genetic diversity and show signs of inbreeding depression. The semi-natural population of Stora Keholmen was established approximately 20 years ago by interbreeding different Swedish sand lizard populations. Stora Keholmen appears to have recovered from the inbreeding depression of its main parental population and has comparatively high genetic diversity. Here, we use whole genome sequencing to compare genetic diversity of the main parental population, the inbred Asketunnan population, to the admixed Stora Keholmen population. We determine genomic diversity within and between both populations and identify regions of high diversity in the admixed population. Similarly, we determine if the inbred population has retained diversity in some genomic regions, which may indicate ongoing selection.

Epigenetic regulation of immune response in the Swedish sand lizard (*Lacerta agilis*)

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Sand lizards (*Lacerta agilis*) are found across Europe, even stretching as far north to extremely cold environments such as in Sweden. Being highly adapted to such extreme temperatures makes them highly susceptible to climate change, and the knock-on effects this could have on disease dynamics. Using an experimentally isolated, outbreed, island population in southern Sweden we are investigating immunogenetics and epigenetics in these highly adaptable populations. Using immune challenge experiments, we are characterising the sand lizard immune response using RNA and bisulfite sequencing, and assessing the role of DNA methylation in reptilian immunity. This study will greatly improve our understanding of epigenetic regulation of immunity in reptiles in general but also give us key insights into specific genes underlying the Swedish sand lizard immune response. Our results are also important for the conservation of the species in Sweden, which are expected to face novel changes in disease dynamics as a result of climate change.

Using suitability map for planning restoration of grasslands

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The recovery of habitats following restoration requires that environmental conditions, propagule sources and active management all co-occur on one spot. Identifying the extent to which these different factors can co-exist can support post-restoration actions and pin-point possible locations for colonization by plant species at a landscape scale. We studied a 400-ha landscape undergoing restoration to identify the suitable habitats for establishment of grassland communities. We combined environmental data with variables which are key for plant species occurrence and layers of connectivity to classify restored sites according to their potential to support establishment of grasslands. We tested the relationship between suitability values from models and aspects of plant community composition by using field inventories. Our map identified locations that are highly suitable for grassland species to occur in the area and by adding proximity to sources of target species and activity of grazing animals in the area increased the likelihood for grassland communities to colonize. This shows that using suitability maps in restoration plans can be useful tool for locating candidate site and planning post-restoration management actions. In addition, using suitability maps would allow prioritizing certain locations where restoration could be most effective, for instance by steering the grazing regime to enhance the colonization of target species.

Temporal variation of brominated algal toxins in the Baltic Sea - Field Study

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Climate change and eutrophication have led to an increase of cyanobacterial blooms and growth of filamentous algae in the Baltic Sea. As these algae and bacteria produce toxins, there are apprehensions that algal toxin are becoming increasingly abundant in Baltic Sea food webs.

Natural production of the group of compounds known as hydroxylated polybrominated diphenyl ethers (OH-PBDEs), occur in both algae and cyanobacteria. These substances are highly toxic as they, among other things, impede the cellular energy production, by disrupting the oxidative phosphorylation in mitochondria. The production of OH-PBDEs have been seen to fluctuate over time, with strong indications that the production is induced by environmental stress. Mussels, being filter-feeders, provide an excellent medium to track the seasonal changes of toxins.

Mussels are collected from two sites in the southern Baltic Sea, at two points, and two depths, on 36 occasions, throughout one year. Salinity, chlorophyll, phycocyanin, and other environmental variables are collected via sensors located at the site. The mussels will be analysed for OH-PBDEs, and toxin levels compared with collected data of environmental variables, aiming to correlate trends in, and identifying connections of OH-PBDE levels with environmental factors such as algal activity and temperature. This project will give high-resolution data on the seasonal fluctuations of OH-PBDEs, and deepen our insight in what triggers toxin production.

Exploring plant diversity changes over the last century

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Human activities in the Anthropocene have profoundly altered ecosystems, transforming around 80% of Earth's terrestrial surface, driving species declines, and acceleration extinction rates to levels suggesting a potential sixth mass extinction event. While global biodiversity loss is evident, local and regional scales often show inconsistent trends in species richness, which remains critical for maintaining ecosystem functions. Instead, a consistent and rapid turnover in species composition has been observed, often occurring without concurrent changes in overall species richness. This turnover has significant implications for ecosystem functionality, potentially rivaling or surpassing the impacts of species loss, yet it remains underexplored. To address this knowledge gap, we synthesized nearly a century of extensive vegetation time-series data from diverse habitats worldwide. Our findings reveal heterogeneous trends in plant species richness: some habitats show no change, while others exhibit rapid increases. Importantly, the data highlight widespread and substantial species turnover over time across most habitats. These results underscore the need to prioritize understanding compositional turnover to better predict and manage ecosystem dynamics in the face of ongoing changes.

Integrating Economy and Ecology in Aquaculture: A Novel Mechanistic Approach

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Aquaculture is vital for global food security and the economy, but its sustainability is challenged by ecological impacts and vulnerabilities to climate change and biodiversity loss. Understanding the interplay between ecological and economic sustainability is essential for developing effective resource management policies. This study presents an integrated ecological-economic modeling framework to optimize sustainability in aquaculture systems, using shrimp farming as a case study.

The ecological model captures shrimp population dynamics, nutrient cycling, and waste production, exploring how management strategies like nutrient input and harvesting rates affect environmental stability. The economic model evaluates profitability by integrating ecological outputs with cost-benefit analyses of feed, seeding, and market price dynamics. Together, these models identify scenarios that balance ecological and economic goals. For instance, strategies maximizing short-term profits may lead to resource depletion, whereas optimized management ensures long-term stability and profitability.

This framework demonstrates the value of combining ecological and economic modeling to inform sustainable resource management, offering insights that can guide policymakers and aquaculture practitioners toward resilient and sustainable practices.

Informing European eel conservation using a long-term data series from a Swedish river system

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The European eel (*Anguilla anguilla*) has for the past 50 years experienced a dramatic decline over its entire distribution area in Europe and North Africa. To conserve this species, accurate assessment models of the changing stock is necessary to track and predict stock development. However, the European eel's long life span (10 to >30 years) as well as its long migration between freshwater and the Sargasso Sea makes it challenging to track and acquire the life history data needed for such models. At the same time, few of the models in use today have been tested against real-world data on eel stock developments. Uncertainties in these models can lead to under- or overestimation of the current status of the European eel, as well as less informative prediction on the effect of conservation measures. Here, we present for the first time a unique long-term data series spanning over 20 years of migration and catch data for European eel in a Swedish river system: Kävlingeån. This system includes monitoring data of all upstream migrating young eels (elvers), the number and size of downstream migrating adult eel (silver eel), fisheries landings, and restocking efforts in this area. We demonstrate how this data can be used to test and update population models for species conservation, and how data from such high-information systems can be used to help inform management in low-information systems.

The genetic background of parallel seasonal adaptation in a range-expanding butterfly

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Climatic factors drive species to expand their ranges and adapt to new environments, providing evidence of adaptive evolution. Insects, for example, exhibit shifts in daylength sensitivity due to climate change and form adaptations in expanding populations demonstrating evolvability despite constraints like bottlenecks. Parallel evolution, where populations independently evolve similar phenotypes in similar environments, highlights natural selection's role but to what degree this is due to parallel genetic changes is often poorly understood. For instance, the critical daylength (CD) responses of the wall brown butterfly (Lasiommata megera), referred to as the daylength inducing diapause in 50% of a population, show parallel adaptation in two independently expanded Swedish populations, in the north-west (Strömstad) and the north-east (Rindö). Our study tests whether these populations evolved similar CD thresholds via different genetic changes. By crossing individuals from both populations and comparing hybrid responses under controlled conditions, we aim to determine if adaptations share genetic pathways or arise through distinct mechanisms. The results will deepen our understanding of parallel evolution and adaptive responses to environmental change.

Avian abundance in Arctic palsa mires

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The Arctic is recognized as being an important breeding area for migratory birds, but their preference for different habitat-types is poorly known. Palsa mires, Arctic wetland habitats characterised by mounds of peat with permanently frozen cores, are one such habitat. Due to climate change, palsa mire distribution is decreasing and the conservation status in Europe is recognized as unfavourable. Therefore, it is necessary to clearly document the use of palsa mires by Arctic breeding birds and take protective action if warranted. In the present study, bird communities in five sites in Torne Lappmark, Sweden, have been inventoried using line transect distance sampling methodology between 2021 and 2024, and habitats along these transects have been classified into nine habitat types. Densities for several bird species were calculated using the R package “Distance” and habitat importance was inferred with a partial least squares regression. The forthcoming results should help clarify how different habitats in the Arctic landscape, including palsa mires, affect the density and community composition of Arctic breeding birds, and therefore inform us about the consequences of a warming climate.

The Impacts of Feralization on the Horse Gut Microbiome

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Feralization is a process that occurs when a population of domestic animals returns to the wild and can be thought of as a reverse domestication event. Due to the sudden return of both natural and sexual selection, it can lead to large changes in the morphology, physiology, and behavior of animals. When animals become feral, their microbiomes need to adapt as well. However, despite intense focus on the microbial changes associated with domestication, we know extremely little about how feralization affects the microbiome of animals. Thus, feralization provides a unique opportunity to observe the microbiota responses to selection from a known (domesticated) standpoint. In this study, we investigate the impacts of feralization on the gut microbiomes of two populations of feral Pottoka horses in Spain by using 16S rRNA metabarcoding. Variation in gut microbiome composition and diversity was evaluated both across individuals and in comparison with domesticated horses. The results enable a better understanding of the process of feralization of the microbiota, as microbes are able to adapt more quickly than the host to new environmental challenges. Feralization of domestic species for which the ancestral wildtype is extinct, such as horses, facilitates opportunities to bring back equivalents of extinct fauna to restore ecosystem function in benefit of biological diversity.

Evaluating stress, migration and mortality during trap and transport in the European eel

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Many water systems suffer from reduced or completely disrupted connectivity due to human activities, causing negative effects for species and ecosystems. Artificial transport past migration barriers, called trap and transport, can be used as a management tool to mitigate connectivity loss. However, few studies have evaluated the effects of trap-and-transport, especially for catadromous fish such as the European eel. In this study, we analysed seven years of trap and transport data, encompassing >58 000 transported eels, to evaluate stress and mortality during trap-and-transport. We found that average mortality rate was generally low but could be as high as 10%. The factors affecting mortality differed across the trap and transport steps, with season (day of year), temperature, mortality in the previous step, and holding and transport time being the factors generally having an effect. We further evaluated stress during trap and transport by implanting eel with biologgers measuring heart rate, used as a proxy for stress. Similar to mortality, stress was affected by temperature, with higher temperatures causing higher stress. We conclude that although mortality was low and trap-and-transport can mitigate connectivity loss, it requires human interference and handling causing stress, wherefore removal of migration barriers should be the long-term goal.

Arctic plant phenology and climate change

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Phenology, or the timing of life events, can strongly influence reproductive success in an individual or population. Theory suggests that species whose phenology is sensitive to environmental cues will be better able to cope with environmental change. The aim of this research is to investigate if the temperature-sensitivity of a plant's phenology influences how well it copes with climate change. Phenological observations where conducted on Disko Island, Greenland in open top chambers (OTC) and in control sites. Previously recorded species abundance data from the same sites was used to estimate performance (abundance) change as a response to artificial warming. We found that temperature sensitivity and performance varies between species but for shrubs such as Betula nana it was clear that warming has a large impact, contributing to almost one week earlier flowering and a performance increase with more than 100% in the warmed plots. This indicates that species that change their phenology might also perform better as a response to warming. Phenological monitoring could be an important tool for future conservation priorities since it may predict which species will persist and which will decline.

Warm Pockets in cold places: Landscape heterogeneity and plant adaptation

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et al.

The Arctic, Earth's fastest-warming region, holds vast carbon reserves in its permafrost, making vegetation dynamics critical to either maintaining carbon storage or amplifying climate change. Despite the well-documented impacts of climate warming on species' survival and fitness, the role of landscape heterogeneity and microclimatic variation in mitigating these effects is not well understood. This project aims to fill this research gap by exploring whether warmer microclimates in the Arctic's diverse landscapes harbor warm-adapted genotypes of tundra plants, potentially enabling species adaptation to warming and acting as a natural buffer against drastic shifts in vegetation and community composition. Using reciprocal transplant and warming experiments at the Latnjajaure field station in Sweden, we will assess the adaptability of Arctic plant species to climate change. By transplanting seeds of key species from and into various microclimates and warming chambers, we aim to compare the resilience of warm-adapted plants with that of their cold-adapted counterparts. Following transplantation, we will assess phenology, reproductive success, and key functional traits related to plant size and resource economics to understand plant response mechanisms. This study aims to address a significant knowledge gap regarding the contribution of microclimatic variation to biodiversity and ecosystem resilience, improving predictions on Arctic plant dynamics and carbon cycling globally.

Shedding light on the Arctic tundra carbon uptake potential under climate warming

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The Arctic tundra is undergoing rapid changes due to climate warming, with critical consequences for the carbon cycle. A circumpolar experimental warming set-up (the International Tundra Experiment; ITEX) has shown that 25 years of enhanced warming by an average of 1.4 °C increased ecosystem respiration by 30 %. At the same time, plant communities are getting taller due to a) shifts in community composition and b) warmer temperatures allowing for more growth. The Arctic tundra is therefore expected to take up more and more carbon via photosynthesis at the same time as it is expected to release more via ecosystem respiration. To what extent tundra plant communities will be able to increase carbon uptake still remains unclear. Furthermore, most studies are conducted during day-time, whereas brightness persists through the Arctic night, allowing plants to photosynthesize around the clock. Therefore, we aim to study how night-time carbon fluxes respond to experimental warming.

Besides shifts in plant community composition and increased growth, warmer temperatures are also expected to impact potential photosynthetic activity. We aim at measuring leaf-level carbon exchanges to gain insights into the smaller scale mechanisms impacting ecosystem fluxes.

Our study will shed day- and night-light on the summer carbon uptake behavior of plant communities from the physiology level to the ecosystem level.

Tundra vegetation change does not alter community litter decomposability

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ITEX consortium et al.

The Arctic biome is a globally important store of organic soil carbon and the impact of warming on the carbon balance of this region is a critical unknown for predicting global climate change feedbacks. Plant litter represents the primary carbon input to Arctic soils, yet it is unclear whether warming-induced changes in plant species composition are altering litter decomposability. Here, we conduct a biome-scale synthesis of in situ plant survey data from 1,967 unique plots across the Arctic to quantify changes in plant community decomposability and address the knowledge gap on how ongoing vegetation changes will influence decomposition. We collated three separate datasets; 1) a multi-site litter bed decomposition experiment, 2) a database of more than 90,000 plant functional trait measurements, and 3) long-term plant composition monitoring in the Arctic to predict community-level decomposability of plant communities over time (three decades), over space (biogeographic gradients) and with experimental warming. We find that litter decomposability increases with higher temperature over biogeographic gradients but find no significant change in community-level decomposability over three decades of vegetation monitoring. Our results suggest that tundra vegetation change has so far had no net impact on litter decomposability, but that in the long-term, if responses follow space for time predictions, vegetation change could produce a positive-feedback to climate change. Besides shifts in plant community composition and increased growth, warmer temperatures are also expected to impact potential photosynthetic activity. We aim at measuring leaf-level carbon exchanges to gain insights into the smaller scale mechanisms impacting ecosystem fluxes.

Our study will shed day- and night-light on the summer carbon uptake behavior of plant communities from the physiology level to the ecosystem level.

Long-term genetic monitoring with ARMS-MBON reveals marine non-indigenous species along European coasts

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The rise of non-indigenous species (NIS) in marine ecosystems poses significant challenges to biodiversity and ecosystem management. Advances in molecular techniques now enable early detection and long-term monitoring of these taxa, particularly through wide spatio-temporal sampling by networks like the European ARMS Marine Biodiversity Observation Network (ARMS-MBON). ARMS-MBON conducts standardized sampling campaigns using Autonomous Reef Monitoring Structures (ARMS) along European coasts and adjacent regions, generating open-access DNA metabarcoding datasets. We evaluated the potential of genetic observatory networks for detecting and monitoring marine NIS using publicly available ARMS-MBON cytochrome c oxidase subunit I (COI) and 18S rRNA amplicon data as of February 2024. Applying a custom bioinformatics pipeline, we screened the data against the World Register of Introduced Marine Species (WRiMS) and performed manual curation, identifying 63 NIS across multiple locations, including potential new introductions such as Eucheilota menoni in the Adriatic Sea. Contrary to expectations, we found no significantly higher NIS numbers in areas with heavy maritime traffic. Our findings highlight the effectiveness of genetic observatory networks for NIS detection while emphasizing the need for manual curation to ensure reliable results. We recommend expanding sampling to diverse habitats and improving NIS reference databases to strengthen future monitoring efforts across Europe. Our study will shed day- and night-light on the summer carbon uptake behavior of plant communities from the physiology level to the ecosystem level.

CRISPRs reveal the temporal dynamics of microbe-virus interactions in the Baltic Sea

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Bacteria and archaea are drivers of biogeochemical cycles and play a crucial ecological role in aquatic ecosystems. Viruses that infect bacteria and archaea also influence ecosystem dynamics by altering community metabolic profiles via host-specific lysis or the expression of auxiliary metabolic genes. We used a time-resolved meta-omic dataset to explore microbe-virus interactions in the Baltic Sea. This approach enables the recovery of thousands of microbial and viral genomes, but a major challenge remains in linking viruses to their microbial hosts. We applied short- and long-read sequencing to construct a database of thousands of complete and high-quality viral genomes from the Baltic Sea virome. Comparative analyses revealed that most viral genomes were novel and could not be linked to a host based on sequence similarity alone. To overcome this, we leveraged the CRISPR-Cas system (clustered regularly interspaced short palindromic repeats) in microbial genomes to connect viruses to their hosts through DNA spacer-protospacer matching. By identifying CRISPR arrays in microbial metagenome-assembled genomes (MAGs) and augmenting them with spacers from metagenomic reads, we established connections between multiple viruses and key microbial players in the Baltic Sea ecosystem. Our findings underscore the importance of resolving virus-host interactions to better understand ecosystem processes and microbial dynamics in aquatic ecosystems.

Whole-ecosystem warming and size-dependent diet drive radioactivity in a piscivorous but not a benthivorous fish

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Fish living in the same area can exhibit varying contaminant concentrations due to differences in diet and trophic position. While interspecific differences are well studied, less is known about how contaminant concentrations vary within species, particularly under stressors like warming, which can alter food web structure, metabolic rates, and bioaccumulation pathways. We studied how warming influences intraspecific variation in radiocesium (137Cs) bioaccumulation in the piscivorous perch (Perca fluviatilis) and benthivorous roach (Rutilus rutilus). By comparing 137Cs activity concentrations in fish and their prey from a heated vs. a non-heated coastal area, we estimated the dietary contributions to 137Cs exposure and assessed warming effects. We found that while both species exhibited ontogenetic dietary shifts towards 137Cs-rich prey, only perch accumulated higher 137Cs concentrations with increasing body size, while roach 137Cs concentrations were fairly constant and independent of body size. Under warming, perch had lower 137Cs concentrations and trophic positions than in the unheated area, while roach showed no significant differences between the two areas. Our findings suggest that diet is a key driver of 137Cs bioaccumulation in the piscivorous perch, but that other factors determine bioaccumulation in the benthivorous roach, and that warming affects bioaccumulation in some but not all fish species.

Evolutionary History of Transposable Elements in the Sand Lizard, *Lacerta agilis*

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Transposable Elements (TE's) or transposons are DNA sequences that are able to move independently inside eukaryotic genomes using self-coded enzymes. Transposable Elements can be divided into two Classes, Class I, which replicate themselves using an RNA intermediate, and Class II, which do not use an RNA intermediate. The aim of this project is to understand the evolutionary history of Transposable Elements in the Sand Lizard, Lacerta agilis.The first step is to characterise the TE content of the sand lizard genome. For this, we are using the genome assembly generated by the Vertebrate Genome Project (VGP; Genbank accession: WNMS00000000.1). We are currently using the protocol by Goubert, et. al. to manually curate the TE families in the genome. Once we have the manually curated set of TE families, we can use this to characterise the TE content of the sand lizard genome. Here, we will find the age of the various TE families, how many members of each family there are in the genome and their genomic locations, and construct phylogenies for every TE family. From this, we will know which classes, orders, and superfamilies of TE's are present in sand lizards, and which families, if any, have undergone large expansions. After this, we will study TE polymorphism across natural sand lizard populations. Here, I will be presenting preliminary results on the TE content of the sand lizard genome, and outline future plans for this project.

Quantitative digital spatial tools used in green infrastructure planning: insights from a systematic literature review

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Green infrastructure (GI) integrates natural and semi-natural spaces into landscapes to promote biodiversity. GI planning often relies on digital tools to identify and delineate habitat networks. The quality of ecological data used to parameterize these tools can significantly affect their effectiveness. To evaluate the integration of ecological information in GI planning, we conducted a systematic review of 96 papers. Most were located using keyword searches with “diversity,” “planning,” “conservation,” and “green infrastructure” in Web of Science. Extracted data included geographic location, spatial extent, methods, data sources, and software used. The studies covered diverse spatial scales and approaches. Habitat quality was usually assigned to landcover map classes. Resistance maps, central to connectivity modeling, were often derived from expert opinions rather than empirical movement or habitat quality data. A case study on oak-associated arthropods in Fennoscandia showed dispersal data were available for only five species. The lack of empirical data limits the ecological robustness of GI plans. Enhancing the availability of habitat quality and movement data is critical for refining GI planning. Strengthening scientific knowledge of species’ landscape needs and monitoring GI performance can improve biodiversity outcomes and ensure planned networks effectively support ecological functions.

Wide-spread diel vertical migration in phytoplankton revealed by high-throughput imaging and deep-learning

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Some phytoplankton are known to migrate between shallower and deeper water layers on a daily basis, a behavior known as diel vertical migration (DVM). At coastal Skagerrak and central Baltic Sea sites, we used imaging flow cytometry for high-throughput, high-resolution community analysis with images classified via neural networks. In one location, an Imaging FlowCytobot (IFCB) sampled depth profiles continuously over the entire water column. The obtained vertical biomass distributions reveal that the median depth abundance of some taxa fluctuates more than 10 meters in diel cycles while others maintain a stable distribution. Significant diel migration was observed in many of the surveyed taxa, including many in the groups of cyanobacteria, ciliates, dinoflagellates, and diatoms. Most migrators peaked in surface water during mid-day, and species observed in both locations exhibit consistent patterns across them. Seasonal variations were evident, with the strongest vertical migration observed in the Baltic Sea in July, diminishing to non-significant levels by October.

This study indicates that the bulk phytoplankton community exhibits vertical migration at both locations, enabling unprecedented species-level comparisons. The results show how widespread diel vertical migration is among phytoplankton taxa and the utility of the IFCB for studying it. Unraveling the drivers and ecological consequences of the observed patterns remains an exciting challenge for future research.

Advancing Plankton Monitoring: Insights from Automated Imaging in the Skagerrak, Kattegat, and Baltic Sea

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Understanding marine ecosystems is partly driven by continuous and long-term monitoring efforts. Since 2021, the integration of the Imaging FlowCytobot (IFCB) with the FerryBox system aboard the R/V Svea has significantly enhanced observational capabilities of plankton in the Skagerrak, Kattegat, and Baltic Sea. This state-of-the-art in-flow imaging technology enables automated, high-frequency monitoring of phyto- and microzooplankton. Using AI-assisted image analysis, the system processes plankton images (organisms ≥5 µm), achieving rapid species- and genus-level identification. Operating autonomously with minimal crew intervention, the IFCB samples seawater every 25 minutes, corresponding to approximately every 5 km depending on ship speed, providing unprecedented temporal and spatial resolution in plankton monitoring. The images are classified using a random forest algorithm and a data pipeline has been developed to channel the data to the Swedish National Oceanographic Data Centre (NODC), ensuring seamless integration with broader platforms like the Swedish Biodiversity Data Infrastructure (SBDI) and the European Marine Observation and Data Network (EMODnet). This study highlights findings from these cruises, demonstrating the utility of automated imaging for monitoring cyanobacterial blooms in the Baltic Sea area and comparing its effectiveness to traditional microscopy-based techniques, which have been a cornerstone of phytoplankton monitoring since the 1980s.

Mapping the impacts of legacy oil wells and permafrost thaw on vegetation in the Northwest Territories, Canada

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Thawing permafrost threatens the integrity of legacy sites from resource exploration and extractive industries. In the Northwest Territories of Canada, over 200 sumps containing drilling wastes within permafrost pose considerable environmental and health risks to local ecosystems and Indigenous populations relying on the land for subsistence. Exploratory drilling activities have resulted in long-term disturbances of permafrost terrains and tundra vegetation, calling for continuous monitoring and research.

This study investigates the complex relationships between sump-induced disturbances, permafrost thaw, and vegetation changes. Using a combination of field-based and remote sensing techniques, we mapped and assessed the impacts of four sumps located along the Inuvik-Tuktoyaktuk Highway (Northwest Territories, Canada). Multispectral drone surveys were conducted at the sites to obtain high-resolution orthophotos, digital elevation models, landcover and normalized difference vegetation index maps. Additionally, we measured the active layer thickness, percent cover of plant functional types, and canopy height along transects that covered both undisturbed and disturbed terrains.

Here, we present preliminary results from these investigations, including statistical and spatial analyses of the collected data. Decades after decommissioning, the effects of legacy sumps and ongoing permafrost degradation on plant communities, shrub growth and vegetation productivity remain evident.

A common biodiversity organization in biogeographical regions of vertebrates, invertebrates, and plants

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Are the primary forces shaping life on Earth context-dependent or universal? Life is compartmentalized into distinct biogeographical regions, each harboring unique species pools influenced by specific historical and eco-evolutionary factors. This suggests that biodiversity organization within bioregions might be context-dependent. However, our analysis of over 30,000 species, including terrestrial and marine vertebrates, invertebrates, and plants, reveals a universal regional biodiversity organization. By examining the spatial covariance of four biodiversity aspects—species richness, distribution range, endemism, and biota overlap—we identified a ubiquitous pattern across all bioregions and taxa, termed core-to-transition. This general pattern across bioregions is consistently associated with environmental variables, supporting the idea that regional biodiversity is largely shaped by species sorting driven by environmental filters from two primary sources: dispersion from the most representative or suitable areas within the biogeographical region and colonization by species from other regions. Additional analyses demonstrate that these regional patterns are crucial for understanding global biodiversity trends in species richness. Our findings highlight the presence of universal environmental mechanisms in spatially organizing taxonomic biodiversity.

Searching to control Japanese knotweed – evaluation of in-situ heat methods

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After decades of being considered to have low impacts on the biodiversity of northern regions, invasive alien species cause increasingly adverse effects on northern biodiversity. To control invasive alien species, information, prevention and early discovery are considered the most effective methods. In the comparatively few cases where alien species become invasive, effective control methods nevertheless need to be in place. To control the invasive alien plant Japanese knotweed, glyphosate is most effective but is prohibited for use in areas near water and many urban areas where the plant is commonly found. The belowground rhizome systems have proven difficult to kill and the results of mowing or pulling have often been found unsatisfactory. As steam has proven effective to kill excavated rhizomes, the potential of conductive heating or steam as a means of eradicating Japanese knotweed in-situ was tested in field trials. Growth trials showed that high temperatures resulted in no regrowth from rhizomes, but that the duration of the heat treatment was crucial. The potential of on-site control treatments are discussed in comparison to the common practice of large scale excavation and land fill of top soil contaminated with Japanese knotweed.

Indicator Species as Tools for Identifying Conservation Areas: A Quantitative GIS-Based Approach

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Indicator species are essential for biodiversity assessments and conservation planning. While forest habitats have established frameworks (e.g., Nitare, 2023), grassland ecosystems lack comparable methods. This study develops a GIS-based approach to identify indicator species for conservation in grass-dominated landscapes.

A pilot analysis of 100 grassland indicators utilized 25 years of occurrence data from the Swedish Species Observation System. For each target species, 350 random locations were analyzed, identifying associated species within a 50-meter radius. Rare species were excluded to reduce noise. Species diversity and richness were quantified using Margalef's and Shannon's indices, alongside a project-specific metric estimating the likelihood of encountering red-listed species.

Results show that the number of associated and red-listed species increases with overall species associations but is independent of target species abundance. Classification into four association and red-listing categories revealed robust distributions. Signal values were calculated based on red-list status and ecological dependencies, with adjustments following Swedish biodiversity standards.

Preliminary findings demonstrate the method's effectiveness in identifying indicator species, providing a foundation for improved conservation planning in grassland habitats.

Mapping areas for climate refugia and assisted migration using plant community temperature preferences

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Climate change is driving species redistributions as species shift their ranges due to warming temperatures.This process is heavily influenced by the microclimate—the local climate that organisms experience, shaped by factors such as topography, soil moisture, and vegetation structure. Relatively cold, buffered microclimates can act as climate refugia, helping species persist in a warming climate. In contrast, warming microclimates risk losing ecosystem functions if displaced species are not replaced by warm-adapted species, potentially necessitating assisted migration. Landscape managers require tools to identify these critical areas for targeted climate adaptation. In this study, we developed one such tool: a map of potential areas for climate refugia and assisted migration within forests across Sweden. Using vegetation plot data from the Swedish National Forest Inventory, we derived a relative Community Temperature Index (CTI) for each plot. We then modelled relative CTI using relevant climate forcing factors that were neutral to macroclimate gradients. Using this model we produced a map of relative CTI across Swedish forests, highlighting areas of cooler and warmer microclimates. This map identifies regions that may serve as climate refugia or may require assisted migration, providing a valuable tool for climate adaptation and conservation planning.

Combining opportunistic and systematic data to track Swedish biodiversity trends

Hedvig Nenzen, SLU

To improve ecological understanding and improve conservation planning, it is essential to know if species are changing their distributions. The first goal of this project is to provide species trends from both opportunistic citizen science data and systematic monitoring data. Integrated Species Distribution Models (ISDMs) make it possible to extract the information contained in different data types while avoiding biased conclusions. I will present preliminary spatio-temporal trends of some species, and the full project will focus on plants, insects and birds. To correctly anticipate and mitigate biodiversity changes, we need to understand what causes the observed biodiversity changes. Models usually attribute species trends to environmental drivers, but I aim to include species interactions as a potential driver. I will infer species interactions from extinction cascades in the data. Estimated interactions will be validated with a database of interactions among 4125 Swedish species.

Effect of cyanobacterial blooms on fish: an experimental study focused on enzymatic activities and swimming performance

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Cyanobacterial blooms in the Baltic Sea are intensifying due to eutrophication and climate change, leading to increased exposure of marine organisms to cyanotoxins. This study aims to assess the physiological, biochemical, and behavioural impacts of cyanobacterial blooms on sticklebacks. Adult sticklebacks were exposed to bloom material dominated by either the toxic Nodularia spumigena or the non-toxic Aphanizomenon sp., alongside mixed bloom, under controlled laboratory conditions for two weeks. Toxin accumulation, enzymatic activities (i.e.; EROD, GSTs, GR and Catalase) and swimming performance (angular velocity, COM velocity, distance and duration of escape response) were evaluated. We hypothesized that toxic bloom material would elevate toxin accumulation, enzymatic activities and impair swimming performance. Results indicated that toxic-dominated treatments led to significant increases in hepatic detoxification enzyme activities and reduced efficiency in fish escape responses, suggesting a trade-off between detoxification and energy allocation for locomotion. Moreover, our findings proved that EROD can serve as effective biomarker of cyanobacterial toxicity, as already demonstrated for others algae produced toxic compounds. Overall, our study demonstrates that integrating enzymatic activities with swimming performance provides a more comprehensive understanding on how physiological processes interact under climate-driven toxicity in the Baltic Sea.

The use of 16S amplicon data to investigate spatial relations between mosquito breeding sites and microbiota

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Mosquitoes have long been vectors of diseases around the world, with yet not so many strategies to prevent the spread of diseases such as Malaria, Dengue virus, West Nile virus and others. Hindering transmission in rural areas revolves around the use of methods like insecticide traps or mosquito nets. Independent of their different flying and behavioral patterns, all genera of mosquitoes have a very strong connection with their own breeding sites. The mosquito microbiota is influenced by the microbial communities of the aquatic environment they inhabit, making it possible to distinguish between individuals coming from two different locations even on a very small scale. We developed a bioinformatic pipeline for 16S amplicon microbial analysis leveraging the use of the workflow manager Snakemake and package manager Conda to facilitate its use, distribution and scalability to different systems and resources. Using the pipeline, we successfully proved that the microbial community of Anopheles larvae can be used to distinguish between location sites or types of location. Furthermore, random forest-based classification of mosquito larvae resolves the separation between different spatial locations better than water. This proves that the use of microbiota as an indicator of vector location can be used in the development of more efficient control strategies.

Effect of benthic macrofauna bioturbation on methane diffusive flux from marine sediments

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Coastal ecosystems contribute over half of marine methane (CH_4) emissions despite covering only a small fraction of ocean area. In anoxic marine sediments, CH_4 is produced by methanogens and transitions to the water column via diffusive fluxes or ebullition. Ebullition dominates emissions in stratified coastal environments, but remains poorly quantified. Bioturbation by benthic macrofauna, which alters sediment structure and geochemistry, may influence CH_4 production by enhancing diffusion and suppressing ebullition. By increasing sediment porosity and oxygen penetration, CH_4 porewater saturation may be decreased, leading to an increased diffusive flux. To test this, we collected sediment cores from Tvären, a hypoxic area of the Baltic Sea and manipulated its faunal composition to include different types of bioturbation. The macrofauna species Macoma balthica, Monoporeia affinis, and Marenzelleria spp. were added to our cores with the same abundance. Organic matter was added to stimulate CH_4 production, and ebullition and diffusive flux measurements were measured at regular intervals to determine how each species' burrowing and reworking behaviors altered emission pathways. Our findings indicate that the bioirrigator Marenzelleria spp. had a significant decrease in the overall ebullitive flux. These results provide insight into the effects of bioturbation mode on CH_4 cycling and help to better predict future coastal CH_4 emission scenarios.

Microbial hydrocarbon degradation potential of the Baltic Sea

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The Baltic Sea is loaded with petroleum-based substances, e.g., hydrocarbons and plastic waste, from various sources. Microbial communities drive organic matter degradation and can naturally degrade environmental pollutants. The information on the degradation potential of contaminant-exposed microbial communities can be used to estimate persistence or to predict the fate or accumulation of petroleum-based pollutants in the environment. This would be useful in managing and mitigating the crisis in crude oil and plastic pollution in the Baltic region. However, there is still limited information on the degradation potential of microbial communities in the Baltic Sea, alongside the lack of environmental monitoring information on these contaminants. This prompts the need for a comprehensive profile of the region's microbial degradation capacity. In this study, we compiled metagenomic datasets, profiled the microbial community structure, and identified hydrocarbon degradation genes from benthic sediment and water column samples collected from the Baltic Sea. We report the taxonomic and functional information on the potential of Baltic Sea microbes to degrade various types of hydrocarbon contaminants. Our report aims to deepen our understanding of microbial degradation of contaminants that would be useful for improving mitigation strategies for crude oil spills and plastic pollution in the Baltic Sea while addressing critical environmental concerns.

The Swedish Reference Genome Portal: A new service facilitating access and discovery of genome data studied in Sweden

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The Swedish Reference Genome Portal (https://genomes.scilifelab.se/) is a new service aiming to facilitate access and discovery of genome data of non-model eukaryotic species studied in Sweden. For each species, the portal aggregates taxonomic data, genome assemblies and annotation tracks, metadata, and links to external resources in a single place. The genome data is displayed in an embedded JBrowse 2 genome browser, allowing for visual representation of a variety of data types, and sharing of sessions between users. With this service, we aim to make genomics data more accessible for all users regardless of their prior level of bioinformatics knowledge, and promote FAIR data sharing. The poster will introduce key features of the Genome Portal and illustrate how researchers affiliated to Swedish institutions can submit their data. We are always interested in new additions to the portal! If you are interested, please contact us at dsn-eb@scilifelab.se.

Fishing in the dark – Hydroacoustic estimates of jellyfish

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Anthropogenic stressors are predicted to benefit mass occurrences of jellyfish, which could have a versatile impact on fish: On one hand, jellyfish can compete for food, act as vectors of parasites, or predate on fish eggs and larvae. On the other hand, jellyfish provide shelter and food for some fish species. Since the Baltic Sea is experiencing a combination of stressors, environmental monitoring programs should aim to include jellyfish estimates. However, due to their fragility, sampling jellyfish with trawling has been proven difficult. Hydroacoustics offers a non-invasive option to assess fragile organisms on a large spatiotemporal scale. One of the major challenges in this field is the acoustic categorization of weak scatterers such as jellyfish. If mastered, echo sounding offers a promising opportunity better to understand the causes and consequences of jellyfish blooms. Our study assesses the distribution and biomass of the moon jellyfish Aurelia aurita at two stations in the Stockholm Archipelago: the open sea area Askö and the sheltered bay Himmerfjärden. Between 2022 and 2023, we conducted pelagic midwater trawls and hydroacoustic surveys with the echo sounder EK80. This study can contribute to (1) a better understanding of jellyfish occurrences and mediated impacts on other biota, (2) advancing the implementation of non-invasive methodology such as hydroacoustic surveys in fisheries science, and (3) developing the acoustic classification of weak scatterers.

Exploring the effect of the invasive mussel Mytilopsis leucophaeata on the native Mytilus edulis in the Baltic Sea

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Invasive species can pose serious danger to any ecosystem by outcompeting and displacing keystone native organisms. However, in species-poor areas like the Baltic Sea, invasive species can occupy vacant niches without disrupting native populations. This study investigates the ecological interactions between two mussel species in the Baltic Sea- the invasive Mytilopsis leucophaeata and the native blue mussel Mytilus edulis and their physiological adaptations to the brackish water environment. Environmental and observational data showed that salinity is key to their distribution. Both species coexist at salinities of 5.61–5.75, but M. edulis dominates at higher salinities and open waters, while M. leucophaeata thrives in lower salinities and inland waters. A scope-for-growth experiment revealed that M. edulis had higher assimilation efficiency and oxygen consumption, suggesting superior energy utilization. In contrast, M. leucophaeata showed energy-conserving traits, supporting its brackish water specialization. Niche overlap regarding resource utilization will be explored using stable isotope niche analyses at sites where the species occur in isolation or together. These findings will be crucial in understanding more about the potential effects of the newly found M. leucophaeata on the Baltic Sea ecosystem and on one of its keystone native species. Future research is needed to explore seasonal variations to predict long-term ecosystem impacts of its invasion.

Eutrophication and Mercury Biomagnification: How are They Linked in the Baltic Sea Food Web?

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The Baltic Sea faces significant nutrient and contaminant pollution, raising questions about how food web changes and eutrophication will affect future contaminant levels. This study analyzed mercury biomagnification in pelagic and benthopelagic species across varying trophic levels and eutrophication conditions. Eutrophication, particularly algal blooms, could dilute mercury through sorption to phytoplankton. Mercury levels were measured in fish muscle tissues of different diets and sizes, as well as in plankton. Stable nitrogen isotope analysis in amino acids (δ15N-AA) determined species' trophic positions and their correlation with mercury levels.

Results showed that mercury concentration increased with the size of juvenile herring (Clupea harengus) at both stations, though size increases were not matched by higher trophic positions. In contrast, sticklebacks exhibited the expected link between trophic position, size, and mercury levels. The lack of biomagnification in herring may reflect limitations in the δ15N-AA method, with fast-growing herring showing metabolic effects that skew amino acid isotope interpretations. Contrary to expectations, no evidence of mercury bio-dilution due to blooms was found, as mercury concentrations were higher at the eutrophicated site. This may be explained by oxygen conditions affecting mercury bioavailability or increased mercury runoff at eutrophicated locations.

Deterministic vs. Stochastic Processes in Shaping Benthic Communities of the Baltic Sea

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Understanding the drivers of biodiversity in aquatic ecosystems is essential for maintaining ecosystem services. The Baltic Sea, facing eutrophication, overfishing, pollution, and climate change, provides an ideal system to investigate the roles of deterministic and stochastic processes in community assembly. Deterministic factors, such as environmental filtering, and stochastic factors, such as random dispersal and ecological drift, can influence the diversity and structure of benthic communities differently across taxonomic size classes—macrofauna (bigger than 0.5 mm) and meiofauna (smaller than 0.5 mm).

This study tests the hypothesis that deterministic processes dominate benthic community assembly in the Baltic Sea, but its relative importance in community assembly is variable across communities of different sizes. Using existing datasets, we compare observed community compositions against null models simulating stochastic processes. Preliminary results suggest that while both macrofauna and meiofauna communities are mainly shaped by stochastic processes, primarily ecological drift, meiofaunal community assemblies appear to be slightly more influenced by these processes than macrofaunal communities.

This work advances our understanding of the community assembly processes that drive the Baltic benthic ecosystem and how they might change in response to environmental disturbances.

Researchdata.se – a new national portal for research data

Ylva Toljander, Swedish University of Agricultural Sciences (SLU) & Swedish National Data Service (SND)

In 2025, a new national portal for research data from Swedish universities and governmental authorities will be launched. In Researchdata.se it will be possible to find scientific data from a number of collaborating research infrastructures including SITES (Swedish Infrastructure for Ecosystem Science), SciLifeLab, SBDI (Swedish Biodiversity Data Infrastructure), NBIS (National Bioinformatics Infrastructure Sweden), Bolin Centre for Climate Research and SND (Swedish National Data Service).
Researchdata.se will also provide a platform to help researchers describe and publish data free of charge. Data described in Researchdata.se are made available "as open as possible, as closed as necessary". Many funders and journals require that data underlying scientific results are published openly, in accordance with the FAIR principles (published data should be Findable, Accessible, Interoperable and Re-useable). On Researchdata.se researchers will find support to meet these requirements, and gain more visibility for their research.

Impact of livestock trampling and soil water levels on emerging insects in riparian wet grasslands

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Wetlands are important ecosystems, hosting a rich array of species and offering diverse ecosystem services. However, they are often threatened by anthropogenic pressures including climate change and agricultural practices. Land management, primarily through livestock grazing, is critical to maintain shorelines and wet ecosystems open, yet it can have direct and indirect negative effects on arthropods through processes like defoliation, trampling and modification of soil and plants properties.

While impacts of grazing on some life-stages are well studied in many grassland types, effects on belowground stages remain understudied. However, trampling by livestock is expected to affect soil and plant properties as well as causing direct mortality of belowground early life stages of insects.

By using arthropod emergence traps in study sites with varying trampling and moisture levels within the same wetland, this microhabitat-level study aims to investigate the local-scale effects of the interaction between moisture and livestock trampling on emerging stages of insects in riparian wet grasslands in Sweden. We hypothesize that soil moisture and trampling interact to influence insect communities, following patterns predicted by the intermediate disturbance hypothesis. The results will help improve our understanding of the effects of different management practices through their impact on arthropod diversity to better balance livestock management and ecosystem function protection.

Can we manage a forest while retaining the methane in the soil?

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Forests are of great importance for the global carbon cycle. How we manage our forests affects the sequestration rate and allocation of carbon within the forest, both above and below ground. The common management method in Sweden is clear-cutting, a method that has a long-term negative impact on both biodiversity and carbon fluxes. There is a need for more knowledge about alternative management strategies to limit those negative impacts. Forestry also has a large impact on soil parameters where for example greater soil moisture might turn a forest from a former sink for methane into a source, impacting the role of forests in mitigating climate change. In our study, we examine how different forest management methods affect methane fluxes from the forest floor: clear-cut, continuous cover forestry and an unharvest control, of a mature spruce forest on mineral soil. Flux measurements started the year before harvest and continued 2 years after. Preliminary results show that the clear-cut has become a source of methane, while both the control forest and the continuous-cover forest remain a sink of methane.

Not all diversification is equal: role of crop diversity on yields and vulnerability to adverse climatic conditions

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Long-term permanent grassland experiments, like those in Jena and Cedar Creek, have shown that biomass output increases and vulnerability to adverse climatic conditions decreases as the number of species increases. Based on 32 long-term field experiments in Europe and North America, we explored how these relationships are for the case of annual cereals, grown in monoculture or sown in rotation with other crops. Simply increasing the number of species rotated improved cereal yields and reduced their vulnerability to detrimental climatic conditions to a point, beyond which benefits began to fell. Conversely, adding functionally different species, such as legumes, ley and broadleaves increased yields and reduced vulnerability. This shows the importance of how diversity is defined and the need to consider the specificities of the ecosystem at hand when assessing the effects of diversity.

Microbial responses to a plant hormone across the continent

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The plant microbiome can affect plant nutrient uptake, immune response and phenology. It is therefore valuable for the plant to acquire and retain beneficial microbiomes. Could a plant alter its microbiome through hormonal pathways? Although some studies provide support for this hypothesis, most research has been confined to crops and to root microbiome interactions. In this project we broaden the scope by investigating the impact of the application of jasmonic acid, a plant hormone involved in plant development and induced defence pathways, on the foliar fungal microbiome of oak trees. In addition, we also look specifically at the treatment effects on a major oak pathogen (powdery mildew). Because the inducibility of defence pathways in plants is hypothesized to vary along the primary productivity gradient, we place all the findings in a spatial context. To find answers to the questions in this study, we make use of samples collected by 30 collaborators in a pan-European project.

Using museum collections to study the evolution of seasonal camouflage

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Seasonal alternation between white and brown color allows several species of mammals and birds to camouflage in high latitude habitats seasonally covered with snow. Climate change is driving declines in the period of snow cover, creating periods of mismatch where winter white animals are exposed in dark snowless habitats. This mismatch has a documented fitness cost in different species, but adaptation to shifts in snow cover could occur via natural variation in molt. There is thus the need to characterize natural variation in seasonal camouflage to determine the adaptive potential of species to declines in snow cover. Museum collections are invaluable resources that allow large scale quantification of phenotypic data from natural populations. Here we demonstrate how we have used photography and spectrophotometry of museum specimens from white-tailed jackrabbits (Lepus townsendii) and willow grouse (Lagopus lagopus) to study variation in seasonal camouflage. We further show how we can use genomics to link phenotypic variation to the genetic basis of adaptation and study the evolution of seasonal camouflage in response to future climates.

Assessing the Ecological Impact of Seabed Mining: Recovery of Macrofauna, Meiofauna, and Bacterial communities

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The increasing demand for rare earth elements (REEs), driven by the green transition, has sparked interest in marine polymetallic nodules. These nodules, rich in REEs, are found in both shallow coastal areas and deep-sea plains. In the Baltic Sea, relatively accessible nodules have attracted attention for their easier retrieval compared to deep-sea deposits. However, harvesting these nodules can pose significant ecological risks, which remain unquantified.

Seabed mining threatens benthic ecosystems by reducing biodiversity, disrupting habitats, and impairing ecosystem processes. Recovery after such disturbances is poorly understood but expected to be slow. To evaluate impact and recovery trajectories of benthic fauna after mining disturbance, we conducted an experiment with 63 sediment cores divided into disturbed, settled, and control treatments. Disturbed cores had their upper 10 cm removed, and redistributed into settled cores to mimic seabed mining and bottom blanketing. Controls were left unmanipulated. Samples from each core were taken 48 hours, 30 days, and 120 days after disturbance to assess macro- and meiofauna and bacteria abundance, diversity and community structure. We anticipate that bacterial communities would show the earliest signs of recovery due to their typically rapid response times. Our research will quantify impacts of seabed mining on benthic communities and assess their recovery trajectories, providing important data to regulate this activity.

Studies on thiamine deficiency in the Baltic Sea from primary producer to top consumer

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Thiamine, also known as vitamin B1 is essential in organism's conversion of food into energy and early development of the central nervous system as well as internal organs. In the Baltic Sea region, Atlantic Salmon (Salmo salar) suffer from thiamine deficiency and are susceptible for high mortality rates during their yolk-sac fry phase. Both wild and hatchery reared salmon yolk-sac fry has occurring thiamine deficiency but to what exact extent and significance is currently not known.

The purpose with this study is to understand how this deficiency is expressed in wild versus reared salmon. Our approach has been focused on an experiment comparing the thiamine content of wild versus hatchery reared Baltic salmon (Salmo salar) roe from Swedish rivers: Hartijokki, Kalixälven, Testeboån, Vindelälven (wild), Dalälven, Skellefteälven, Umeälven, Luleälven (hatchery reared).

Fertilized salmon roe from was collected during October/November 2024 from compensatory hatcheries and from unregulated river beds. Concentrations of total thiamine status in the eggs was measured using a spectrophotometric method.

Knowledge in how thiamine concentrations varies between wild and reared salmon are important because they help us understand how thiamine deficiency affects the various salmon populations, which can assist in conducting reliable stock assessment for sustainable fishery strategies in the Baltic Sea.

Why do oaks have lobed leaves? The origin and climatic relationships of lobed leaves in *Quercus* spp.

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Oaks (*Quercus* L., Fagaceae) are among the most successful tree genera across the northern hemisphere in terms of diversity and distribution. Lobed leaves are a characteristic feature of oaks, although only a subset of the more than 400 species do possess such leaves. We aimed to 1) trace the origin of lobed oak leaves in the fossil record, 2) assess how leaf lobedness is distributed across the global oak phylogeny, and 3) explore how the distribution of lobedness in extant species is constrained by climate. We found that oaks became abundant in the northern hemisphere during the early Eocene (ca. 50 million years, myrs, ago) but the first records of deeply lobed leaves are only known from Oligocene deposits, at least 15 myrs later. Lobed leaves started to radiate during the Eocene-Oligocene transition (EOT, ca. 34 myrs ago), which denotes the most dramatic global drop in temperature during the past 65 million years. We still find the legacy of this in the species that exist today, as lobedness is linked to colder and more seasonal climates. At the same time, there is also a strong phylogenetic signal, with lobedness appearing in some clades but not in others. Our results shed light on how a key leaf architectural trait has contributed to the evolutionary success of oaks in temperature ecosystems.

Sustaining marine biodiversity under climate change in the Swedish Baltic Sea marine protected area network

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Many aquatic species are exhibiting distributional changes in response to climate change, and substantial geographic shifts are predicted to continue at rates even faster than that of terrestrial species. Projections of global temperatures under a variety of emissions scenarios are now widely available, however projections of species distributions and suitable habitat under these scenarios are lacking. Including these distributional changes in conservation planning is essential to enhance the resilience of ecosystems to climate change and ensure their persistence. This project aims to develop species distributions and connectivity models under a variety of climate scenarios in the Swedish Baltic Sea. These projections will then be used to optimise the marine protected area (MPA) network to maximise the protection of climate refugia, sensitive habitats, and to maximise connectivity between habitats under future climate change scenarios. Doing so will provide managers and policy-makers with important, spatially-explicit, information to support evidence-based conservation measures to improve the resilience and ensure the persistence of habitats within the MPA network.

Enabling effective spatial conservation of marine biodiversity

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Developing ecologically coherent and representative networks of protected areas (PAs) and marine protected areas (MPAs) has been mentioned in target 3 of the Kunming-Montreal Global Biodiversity Framework. Despite its importance globally, there are no generally accepted scientific definitions of the concept and no agreed practices to assess the ecological coherence of MPA networks. A common method consists in defining four criteria: representation, replication, connectivity and adequacy. Along those criteria, specific features and targets linked to the geographical area where the assessment is made can be defined. My poster will aim to give an overview of the concept of ecological coherence assessment within terrestrial and marine protected areas networks and discuss how a common method could be established for future coherence assessments. This is based on the first chapter of my PhD where I will review methods used to evaluate PA and MPA networks, which will then be used in my third chapter to evaluate the ecological coherence of the Baltic Sea.

Unravelling the Cost of Pigmentation: Gene Knockouts and Their Effects in Pieris brassicae

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Butterflies are known for their vibrant colouration, but the costs of producing these colours is not well understood. Pieris brassicae use pteridine for their white pigments, which are stored in specialized pigment granules known as pterinosomes. Transport of pteridine precursors to these granules is mediated by an ABC transporter complex, formed through the heterodimerization of the proteins White and Brown. In lepidoptera, the ok gene, which is a paralog for brown, also heterodimerize with White. Disruption of these complexes is hypothesized to impair pteridine transport, potentially leading to an alteration of the pigmentation. To explore the functional role of these genes in pigmentation, we used CRISPR/Cas9 to knockout white, brown, and ok in the embryos of Pieris brassicae. The resulting mutant phenotype exhibited various developmental and pigmentation defects, including translucent larval epidermis and pupal colour disruption. Adult butterflies displayed suppressed wing development, and absence of wing pigmentation, along with distinct alteration in eye coloration. These findings reveal the relative roles of the genetic mechanisms behind butterfly pigmentation and ultimate shed light on the cost of producing colour.

Holistic ecosystem effects of herbicide pollution in crop production and protection

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Glyphosate is the active ingredient in most widely used herbicides causing a persistent agrochemical pollution in agricultural habitats across the globe. Glyphosate disrupts the shikimate pathway, which is the biosynthetic basis for several metabolite groups produced by plants and a majority of microbes but the effects of glyphosate residues in soil on crop metabolism and species interactions is largely unexplored.

We studied how soil pollution from field realistic application of glyphosate-based herbicide affects plant biochemistry and plant defense and cascading effects on plant-insect interactions in various important crop plants.

Plants responded on phytohormone level and altered levels of antioxidant biosynthesis. Particularly, strawberry plant and fruit antioxidant levels were affected by soil herbicide pollution.

We conclude that herbicide residues in soil have multifaceted consequences on crop plants by modulating plant metabolite concentrations with cascading effects on plant protection and plant-insect interactions. Our results indicate that the exaggerated use of pesticides in recent decades created a soil legacy which reduces the effectivity of plant traits essential for sustainable crop protection and ecosystem functionality.

Effects of oil spill from Marco Polo on fish communities in eelgrass meadows in Blekinge

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After the Marco Polo accident in Hanö Bay in October 2023, approximately 150 tons of bunker oil floated ashore along the beaches of Blekinge. This study follows up on how individual fish health and fish populations have been affected by this oil spill. We have studied individual health status of eelpout from locations with varying degrees of oil impact, and we have monitored changes in population densities of fish species in eelgrass meadows between 2022 (before the spill) and 2024 (after the spill) in locations that were affected by the oil spill to varying degrees. The results show that all eel pout, including those in the reference area, showed minor damage to their gills and liver, but as visible also in the reference area it cannot support these were due to oil spill. We observed changes in the density of different fish species, with a decrease in eelpout in affected areas relative reference areas. Instead, there was more threespined sticklebacks in the affected areas. In general, the difference between years was greater than the difference between locations, indicating a relatively low impact of oil spills on the occurrence of fish species. Large amounts of oil were cleaned up in the area during the winter of 2023–2024, which probably reduced the impact of the spill on fish. To conclude, the differences we could see between areas with different oil impacts were relatively small and other more regional factors seem to affect the health and density of fish.