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Contents

Plenary 1

Oral Presentations 7
T01: Bio sciences, including food, soil, textile, wood 7
T02: Patterns of species richness and diversity 19
T03: Ecological networks and food webs 35
T04: Effects of global change 45
T05: Conservation biology 54
T07: Statistical ecology 61
T08: Resilience, stability and health of ecological communities 67
T09: Ecosystem services 73

Poster Presentations 76
T01 Biodiversity and ecosystem functioning 76
T02: Patterns of species richness and diversity 80
T04: Effects of global change 82
T05: Conservation biology 84

Plenary

The dialectic of sustainability: the case of the post-conflict Colombia

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The long-lasting internal conflict in Colombia has formally ended in 2016 when the central government and the FARC guerilla groups signed a peace agreement. This agreement indicates environmental and biodiversity protection as well as sustainable development as major goals for the new Colombian society. One question of interest is whether the dynamics imposed by the conflict and that still persist can affect policies or interventions conceived to pursue these goals. I explore this issue representing the socio-ecological system as a parsimonious set of characteristic variables whose interactions I visualize as signed digraphs. Applying the qualitative technique of loop analysis combined with numerical simulations, I can predict the response of the system to policies, such as subsidised credit to capital intensive activities or that increase small farming competitiveness and access to market. The analysis of the socio-ecological network reveals hidden causal linkages due to the persistence of conflict factors and that determine unexpected interdependencies between licit and illicit activities. The persistence of these mechanisms seldom allows synergies between desirable goals.

The importance of habitat connectivity for biodiversity in pond networks

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Keywords: metacommunities, connectivity, habitat networks, biodiversity loss, dispersal

Connectivity within habitat networks is essential for sustaining biodiversity. Ponds and pond networks have long served as model systems in metacommunity ecology due to their insular nature within the terrestrial matrix. In this talk, I draw on empirical and experimental work using pond "archipelagos" to illuminate how connectivity shapes biodiversity patterns and processes. I highlight long-term trends in habitat loss and fragmentation in a network of temporary soda pans in Austria, explore how connectivity structures biodiversity within a smaller pondscape of sodic bomb crater ponds in Hungary, and share findings from a mesocosm experiment that tested the ecological consequences of fragmentation on microbial metacommunities. Together, these studies demonstrate the critical role of spatial structure in maintaining biodiversity in dynamic pondscapes.

Acknowledgments
This work was supported by the National Multidisciplinary Laboratory for Climate Change (RRF-2.3.1-21-2022-00014) project within the framework of Hungary's National Recovery and Resilience Plan supported by the Recovery and Resilience Facility of the European Union,with further support from OTKA FK146095 and FK132095 (NKFIH), and the Sustainable Development and Technologies National Programme (FFT NP FTA) and the János Bolyai Research Scholarship (grant no. BO/00418/24/8) of the Hungarian Academy of Sciences.

Status of community ecology in Africa: a systematic review

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Keywords: Africa, community ecology, progress, systematic review

Community ecology as a science is about 100 years old, we discuss in this work what approaches have progressed well and possible future directions in Africa. Our major objective is to evaluate the status of African community ecology, to understand what factors determine the progress of scientific production in Africa and to evaluate the progress of scientific papers in Africa regarding the whole world. We will present in this work a review of community ecology and we will also evaluate the achievement and the progress in Africa. We will also determine what are the most studied disciplines of the community ecology in Africa and to determine the future directions. It is in this spirit that we will offer this critical review of the current state of this area of the world and in this field, we hope that it will stimulate discussion since we have no pretence of complete knowledge. We focus on understanding the reasons behind the scientific production on community ecology in Africa, why they change over time and discipline, and how they interface with the whole production and directions in the world. The most recent development in community ecology in Africa has revolved around conservation, biodiversity, resilience, and stability. Not all community ecology problems can be investigated in Africa, but evidence from general studies using simple comparison can greatly increase our ecological knowledge in Africa. We will make recommendations on how to advance the field with advice for the present and future generations of community ecologists in Africa. According to the difficulty and the big need of fund to make a complex work on community ecology in Africa, we offer some recommendations with this caveat in mind. In summary, we will decide for the most important area of interest for the big questions we can ask, the types and diversity of outcomes and contexts underpinning the most studied disciplines, highlight important gaps in the existing research, and offer guidelines for research and evaluation moving forward.

Interplay between climate forcing and evolutionary rescue may explain mass extinctions in the earth history

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Keywords: climate change, adaptive evolution, evolutionary rescue, mass extinction

Species get extinct all the time with a certain background extinction rate; this is a normal course of macroevolution. However, several times through the 540 Ma of the recorded history of life on Earth, the extinction rates exceeded the average background rate by more than an order of magnitude, resulting in 50-90% loss in the global biodiversity. Apart from the "Big Five", there were many smaller mass extinctions with the global biodiversity loss ranging between 10-50%. Mass extinctions came into the focus of scientific community in early 1980s and significant progress has been made over the last few decades. However, given the inherent deficiency of the fossil data, statistical analysis alone (which is the main research tool used in paleontology) does not always allow to distinguish between the effect of different processes, which hampers further progress. Process-based mathematical models are needed. In my talk, I introduce a novel model that combines (i) the effect of a fast climate change on the population dynamics with (ii) species' active feedback on the global energy balance and (iii) with species evolutionary response. The model also takes into account the dependence of population growth rate on the ambient temperature, which is a generic property of many plant and animal species. The model shows that species extinction or survival following a climate change depends on a subtle interplay between the magnitude of the climate change and the rate of species's adaptive evolution. The model predicts a distribution of extinction frequencies which is generally consistent with the fossil data.

Managing the seas: how marine sciences impact national policies

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Keywords: marine science, science-policy interface, ocean governance, IEO-CSIC, scientific advice

The Spanish Institute of Oceanography (IEO) is a century-old institution whose mission has remained constant: to provide scientific advice to the Spanish State on matters related to the ocean and its resources. Its history clearly illustrates the essential role of science in public decision-making. After the Spanish Civil War, the institute was dismantled due to the political alignment of its scientists with the defeated side. However, the Franco regime soon recognized the strategic necessity of oceanographic research and reactivated the IEO. In 2020, the institute faced another major crisis due to administrative paralysis, which led the Spanish government to once again reaffirm its value by initiating a process of revitalization.

Today, the IEO employs close to 1,000 people, with an annual budget of approximately €100 million. Although its headquarters are in Madrid—far from the sea but close to the seats of government—it maintains a network of coastal research centers along the Spanish coastline, including both the Canary and Balearic islands. These centers host an extensive infrastructure, including a scientific research fleet and state-of-the-art instrumentation, designed to generate knowledge for evidence-based policymaking.

The IEO provides expert advice in areas such as fisheries management (e.g., scientific input for fishing quotas), the impacts of climate change on marine resources, the design of marine protected areas under Spain's international commitments, and responses to environmental crises such as the Mar Menor collapse or the La Palma volcanic emergency. The institute also supports the expansion of Spain's Exclusive Economic Zone and the protection of underwater cultural heritage, leveraging its scientific infrastructure. Additionally, the IEO is entrusted by the government to represent Spain in international marine science organizations.

Currently, the IEO is integrating its efforts with other marine research institutes within the Spanish National Research Council (CSIC), creating synergies that further reinforce the role of marine science in promoting Spain's national and international maritime interests. This trajectory demonstrates that scientific institutions, even in times of crisis, are indispensable for informed and sovereign governance.

The hidden community traits ruling aquatic ecosystems

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Keywords: trait-based models, behavior, food-web structure, phytoplankton, migration, stoichiometry

Trait-based ecology holds the promise of providing mechanistic and quantifiable descriptions of how communities function within their environments. However, the approach has traditionally been biased toward easily measurable traits, such as body size or morphology. Here, I highlight three less obvious—but ecologically critical—traits related to behavior and resource use strategies. Each profoundly shapes ecosystem interactions in aquatic communities on a global scale.

(1) First, over 90% of observed trophic linkages across 20 investigated marine and freshwater ecosystems worldwide follow a simple pattern when specialization is considered a fundamental ecological trait (Garcia & Wirtz 2025). Specialization universally quantifies prey selection behavior, from the smallest to the largest predators on the planet. Recognizing this trait enables the construction of highly accurate yet simple food-web models.

(2) A second, poorly studied behavioral trait is the ability of small unicellular autotrophs to move or adjust buoyancy to bridge the depth zones of light and nutrient availability. Phytoplankton vertical migration and associated nutrient uptake can account for up to 40% of total oceanic new production (Wirtz et al 2022). Variation in mobility among species and phyla further helps explain the high diversity of phytoplankton in lakes and oceans (Wirtz & Smith 2020).

(3) A prerequisite for such resource acquisition via vertical migration is flexible intracellular carbon:nitrogen:phosphorus (C:N:P) stoichiometry. Variable C:N:P ratios also reflect divergent resource uptake strategies among phytoplankton functional groups, which can be inferred using inverse modeling techniques. The resulting shifts in elemental stoichiometry can shape global biogeochemical cycles.

To sum up, traits that are not easily measurable are essential to the functioning of aquatic ecosystems. This insight should motivate not only the development of advanced trait-based models, but also the creation of innovative observation technologies to reveal what has remained hidden until now.

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Oral Presentations

T01: Bio sciences, including food, soil, textile, wood

On the role of diversity and dominance in natural phytoplankton communities

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Keywords: biodiversity, ecosystem functioning, species pool, species sorting

The BEF theorem states that higher species richness enhances functioning, e.g. resource use efficiency. Recent studies, however, also indicate community dominance may be a stronger predictor of community functioning than species richness. Since dominance can reflect disturbance or proceeding competitive exclusion, high dominance could come with species loss, thus challenging the generality of a positive BEF relationship. In this talk, we will present experimental evidence showing how community dominance may generally arise from the available species pool (starting communities) and how neither initial nor realised species richness (end communities) necessarily enhances resource use efficiency. We will also present large river phytoplankton data, further supporting the crucial role of community dominance over realised species richness in predicting resource use efficiency. In conclusion, while the BEF relationship may depend on system type, community assembly processes, or the ecosystem functioning measure used, community dominance appears to be a more consistent predictor of resource use efficiency in natural phytoplankton.

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A meta-ecosystem perspective on phytoplankton response patterns to localized impacts in river-connected lakes

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Keywords: connectivity, water retention time, phytoplankton, mesocosm, lakes

Worldwide, freshwater ecosystems are under increasing anthropogenic pressure by land use as well as global warming-induced changes in hydrological regimes. This has far-reaching consequences for connected river-lake systems as nutrients and organic matter received from the terrestrial surrounding at upstream locations may unfold short and long-term effects throughout the entire aquatic network. In particular, eutrophication effects following extreme weather events may differ in river-connected vs. more isolated lakes. Conceptually, a local pressure creates an impact propagating along a chain of lakes, with discharge in lotic sections and residence time in lentic basins acting as hydrological controls. Indeed, this lake-to-lake connectivity must be recognized as a vital regional landscape feature when using a meta-ecosystem perspective. By linking theoretical models with field studies and mesocosm experiments we investigated how local nutrient loading impacts phytoplankton growth and the propagation of eutrophication along connected lake systems differing in flow rate, lake depth/volume and water residence time. In a large-scale experiment conducted in the IGB-LakeLab in Lake Stechlin, Germany, we manipulated water residence times in connected enclosures to follow the propagation of a nutrient pulse and subsequent phytoplankton development. In the field, we investigated effects of local nutrient loading on regional-scale plankton development in a river-lake system lake. Our field study encompassed 19 lakes in NE-Germany, contrasting in connectivity and morphology. Here, data collection at high temporal and spatial resolution was achieved by combining periodic water sampling, in-situ measurements and a distributed sensor network with space- and airborne remote sensing products. Connectivity facilitated the spatial impact propagation of phytoplankton biomass in the experiment, causing homogenised phytoplankton biomass at strongly connected experimental lakes, but dominant local biomass peaks at low connectivity. In the field, upstream nutrient input drove phytoplankton development along the entire lake chain due to tight lake-to-lake connectivity. Our results suggest that similar point sources can result in profoundly different maximum magnitude and spatial range of eutrophication impacts at the regional scale of entire lake chains.

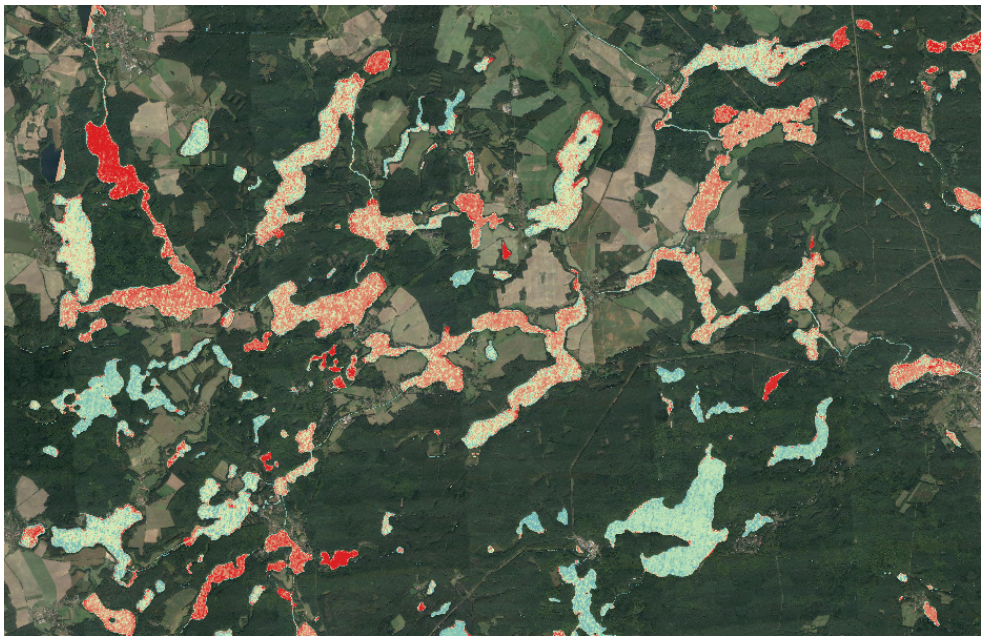

Figure: Remotes sensing derived chlorophyll-a content in a river-corrected lake system in NE-Germany.

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This work was further supported by the the EU H2020-INFRAIA project (No. 871081) AQUACOSM-plus: Network of Leading Ecosystem Scale Experimental AQUAtic MesoCOSM Facilities Connecting Rivers, Lakes, Estuaries and Oceans in Europe and beyond - funded by the European Commission.

Study of the floristic diversity of an ecosystem in south-west Morocco: focus on *Thymus broussonnetii*, a threatened endemic species

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Keywords: red list, diversity, endemic, rare, threatened, Essaouira's Thuja Forest, therophytes

South-west Morocco is an area of refuge for a variety of phytogeographical elements, with exceptional plant diversity. This geographical area is undergoing multiple degradations, with its flora threatened by recurrent droughts, the destruction of natural habitats and overgrazing. This is particularly the case of the emblematic subspecies *Thymus broussonnetii* subsp. Broussonnetii, endemic to Morocco and presently threatened with extinction. The context of our study is the floristic diversity of an ecosystem in south-west Morocco, "Essaouira's Thuja Forest".

A systematic and biological synthesis have been presented using flora determination keys. The most recent basic reference was exploited, adopting the updated provisions of the IUCN Red List categories and criteria. The 157 floristic samples carried out inventoried 187 species belonging to 44 different botanical families, around 92% of which are dicotyledons. The six most dominant botanical families were: *Asteraceae* (37 species), *Brassicaceae* (15 species), *Fabaceae* (14 species), *Lamiaceae* (9 species), *Geraniaceae* (8 species) and *Plantaginaceae* (7 species). The life-form categories were distinguished. Therophytes were the dominated life-form with 47%. Endemic, rare and threatened flora in the Essaouira's Thuja Forest accounts for a significant proportion of all Moroccan endemic, rare and threatened flora. The number of endemics (species and subspecies) represents 1.49% of all Moroccan endemics. The rare and threatened flora is represented by 1.82% of Morocco's total rare and threatened flora. It is important to note that it is the first study to draw up a Red List of the endemic, rare and threatened vascular flora in the Essaouira's Thuja Forest coastline.

The effect of gap size and shape on understory and regeneration in an oak-hornbeam forests managed by continuous cover forestry

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Keywords: forest management, continuous cover forestry, forest herbs, regeneration, forest gaps

Forest biodiversity is primarily threatened by the conventional rotation forestry system. The fine-scale interventions of continuous cover forestry, such as gap-cutting, could serve as a valuable tool to protect forest habitats and enhance structural heterogeneity of the stand. However, it is unclear which gap sizes and shapes can trigger the natural regeneration while simultaneously maintaining or improving the near-natural character of the forest understory. This issue is particularly relevant for light-demanding tree species such as sessile oak (*Quercus petraea*). In this case, optimal abiotic conditions may also have an indirect negative effect by enhancing the competitive pressure.

In the Pilis Gap Experiment, we examined the five-year effects of four gap types, comparing two gap sizes (150 and 300 m^2) and shapes (circular and elongated), on light conditions, understory vegetation and oak regeneration in an oak–hornbeam forest. The investigated understory variables included species richness, total cover, cover of different functional groups and species composition, while for the regeneration the survival, growth and abundance of sessile oak and the abundance of the main competing woody species were studied.

Our results indicate an increase in light in all gap types. However, light decreased over the years in large circular gaps, while remaining more stable in other gap types. Species richness experienced a temporary increase in large circular gaps, whereas total cover increased in all gap types. Understory height and shrub cover also increased in large circular gaps. Annual and perennial forb cover remained unchanged in all studied gap types, although graminoid cover showed a transient growth in large elongated gaps. Small gaps had the highest cover of woody regeneration, whereas bramble (*Rubus fruticosus* agg.) cover increased in large circular gaps. Species composition changed most in large circular gaps, and least in small elongated ones. Tended oak saplings showed the greatest height increment in large circular gaps, but without tending they were outcompeted in this gap type by hornbeam (*Carpinus betulus*) and bramble. When competition was also considered, small gaps proved to be the most favourable treatments for oak regeneration.

Vegetation changes have been most prominent in large circular gaps. While these gaps are favourable from a conservation aspect as they enhance the structural diversity of the stand, the dense cover of bramble and woody competitors hinders the effective sessile oak regeneration. Smaller gaps slightly increase the understory heterogeneity. These gap types also ensure ample light to initiate regeneration while prevent the expansion of competitors. However, in a later phase of the regeneration process, the extension of these gaps is necessary. If oak is

regenerated in larger gaps, competition could be mitigated by using an elongated shape. In all cases, control of hornbeam is necessary, but its extent is lower in small and elongated gaps. The experiment proves that the regeneration of the light-demanding oak species can be successfully initiated by closer-to-nature continuous cover forestry system.

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Mycorrhizal status of two vulnerable endemic subspecies of *Thymus* in two different natural ecosystems in South-West Morocco

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Keywords: Essaouira's Thuja Forest, Agadir Ida Outanane, endemic, thymus

The aim of the present work is to compare the mycorrhizal potential of two *Thymus* subspecies endemic to southwestern Morocco, by studying their contribution to the mycorrhizogenic potential of the soil and their impact on the richness and diversity of the arbuscular mycorrhizal fungi community in the soil. This study was carried out in two different natural ecosystems, the Essaouira's Thuja Forest and the Agadir Ida Outanane region. After extracting and counting isolated spores, we were able to differentiate 13 and 14 morphotypes respectively of arbuscular mycorrhizal fungi with different colors (light brown, dark brown, black, white...) in the two ecosystems. The rhizospheric soils of both subspecies are rich in mycorrhizal fungi spores, with total spore counts of around 1,700 and 2,000 spores per 100 grams of soil. Roots examination revealed significant colonization of over 60% of the root system of both subspecies. Statistical analysis of the data showed that the rhizospheric soils of these plants contained around 1230 infectious propagules per100 grams of soil. The most probable number method showed that both subspecies are capable of enriching the soil with fungal propagules and highly significantly increasing the mycorrhizogenic potential of both ecosystems.

Functional diversity in Hungarian forest grassland-mosaics

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Keywords: functional diversity, plant traits, ecosystem functioning, forest grassland

Functional diversity has a fundamental impact on ecosystem processes, dynamics, and stability. This study investigated functional diversity across eight habitats within Hungarian forest-grassland mosaics, including differently sized forest patches, differently exposed forest edges, and various types of grasslands. We assessed three functional diversity indices: functional evenness, functional richness, and functional divergence. Vegetation was studied using phytocoenological relevés, and functional diversity indices were calculated based on nine plant functional traits. Results revealed significant functional diversity variations among habitats for all three diversity indices. The highest functional richness was observed at habitat edges, grasslands showed the lowest functional richness, while forest interiors were intermediate in this respect. Functional divergence was highest in small forest and at habitat edges, whereas closed grasslands exhibited the lowest values and differed significantly among the other habitats. Large and medium forest also open perennial and open annual grassland showed intermediate functional divergence. Functional evenness was highest in the north-facing edge, open perennial, and open annual grassland, while the lowest values were recorded in large forest. The pattern of the three indices exhibits remarkable differences, which means that ecological studies should not focus on a single index but should instead consider all three aspects of functional diversity.

Impact of run-off variability on phytoplankton community structure and function

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Keywords: run-off, phytoplankton, variability, nutrients, browning

Extreme rainfall can cause high loadings of coloured dissolved organic matter (cDOM) and nutrients from the catchment into lakes. While phytoplankton and bacteria compete for nutrients, the outcome depends on whether the phytoplankton is limited by light reduction caused by cDOM, and how much the bacteria are able to utilise DOM-carbon. In addition, we propose that the temporal variability in loading may strongly impact the plankton community, specifically phytoplankton community composition, biomass and function. We tested the run-off variability in a mesocosm experiment at SITES AquaNet in Lakes Erken and Bolmen, Sweden, in summer 2022. The same amount of cDOM and nutrients were added, but at different frequency and intensity: Daily, Intermittent, Extreme, no addition (Control) over 20 days, followed by a 16-day recovery phase of no additions. Phytoplankton community composition was analysed using microscopy and FlowCam with a semi-automated machine-learning approach for classification. We show that the Daily and Intermittent cDOM and nutrient additions promoted opportunistic taxa such as cyanobacteria and small green algae, while light limitation resulted in lower phytoplankton growth and biomass, but appeared to promote competition with bacteria in the Extreme additions. Phytoplankton functional groups showed pronounced differences between treatments in terms of size, coloniality and trophic strategy and between the two lakes. We conclude that run-off variability impacts the taxonomic and functional composition of the phytoplankton community, thus affecting energy transfer and food web processes in lakes.

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Resource use efficiency positively scales with biodiversity in large river zooplankton (Danube River, Hungary)

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Keywords: biodiversity–ecosystem functioning, resource use efficiency, nutrient cycling

The Danube River, as a complex ecosystem, supports diverse life forms and intricate biological interactions. Plankton communities, vital for river ecosystems, contribute significantly to ecological processes and nutrient cycling. However, the biodiversity–ecosystem functioning (BEF) relationship in riverine communities, particularly at the phytoplankton–zooplankton trophic interface, remains underexplored. Trophic interactions and efficient resource use are key factors influencing ecosystem functioning, affecting nutrient dynamics and energy transfer to higher trophic levels.

This study examines zooplankton resource use efficiency, measured as the zooplankton-to-phytoplankton biomass ratio, and its relationship with zooplankton taxonomic and functional diversity and community evenness. The dataset comprises weekly zooplankton samples collected over three years from the middle Danube section, along with spring and summer sampling campaigns covering the Hungarian stretch of the river.

The BEF relationships of zooplankton communities varied. Rotifera biodiversity and community composition primarily influenced ecosystem functioning, despite small crustaceans contributing the most to total biomass. Significant positive relationships were observed for both BEF and dominance patterns. Notably, high community dominance did not necessarily correspond with lower species richness or heightened competition. Instead, community organization appeared to differ among zooplankton functional groups, likely shaped by local environmental conditions linked to hydrology. These findings highlight that BEF relationships in large river zooplankton are predictable, with biodiversity playing a crucial role in ecosystem functioning.

The role of lake connectivity in shaping plankton diversity and trait distribution: a large-scale enclosure experiment

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Keywords: connectivity, water retention time, plankton, functional traits, harmful algal blooms

Lake ecosystems are increasingly impacted by anthropogenic pressures, including climate and land use changes, which disrupt water quality and ultimately putting ecosystem services at risk. In river-connected lakes, the connectivity between lakes plays a crucial role in regulating eutrophication processes, influencing the transport, supply and dilution of nutrients, and the potential formation and transport of algal blooms. In a large-scale enclosure experiment in the IGB LakeLab, we simulated a nutrient run-off event (nutrient input and deep mixing) in one enclosure of an experimental lake-chain and monitored its propagation through the entire chain. We installed experimental circular lake chains of two connectivity levels, each replicated in three chains of four enclosures (3 chains of 4 mesocosms × 2 connectivity). Hydrological connectivity - defined as high or low water residence time – was achieved through different amounts of water exchange among enclosures of each chain.

Our objective was to assess the degree of independent development of plankton diversity and dynamics and diversity patterns of each enclosure, in light of connectivity as an effect-propagating but also homogenizing force, following local exogenous shocks. Using imaging flow microscopy (FlowCam) and AI-based classification, we analyzed the phytoplankton and microzooplankton communities with a focus on taxonomic, morphological and functional diversity. Initial results indicate that strong connectivity enhances coherence in physicochemical responses to nutrient pulses and biological parameters. Further analysis will look into the conditions promoting harmful algal blooms important to develop strategies for mitigating eutrophication impacts in connected freshwater systems.

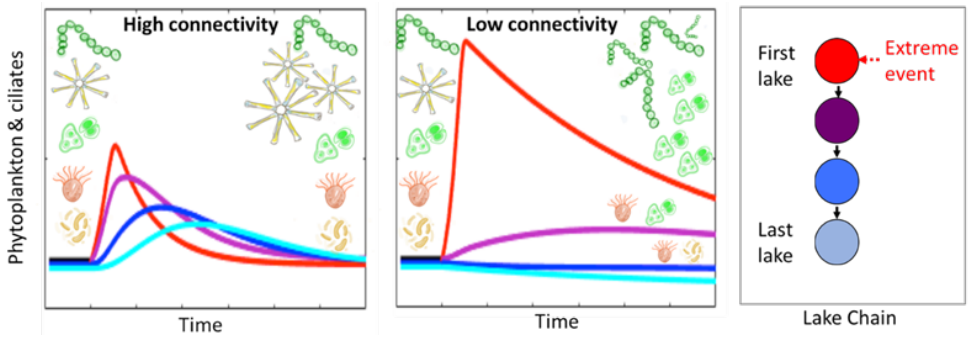

Figure: Graphical abstract of the objectives. Shown are expected phytoplankton biomasses (lines). Colors represent the order of the lakes in a lake chain (right panel) in high and low connected lake systems.

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T02: Patterns of species richness and diversity

Italian fish diversity in protected areas

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Keywords: invasive fish species, river connectivity, eutrophication, anthropogenic pressures, biodiversity

Protected areas are fundamental to global biodiversity conservation. However, their effectiveness in the conservation of specific taxa, such as freshwater fish, is still being investigated. Freshwater fish are among the most vulnerable species, facing numerous anthropogenic disturbances. This study investigated the effectiveness of the protected areas of the European network of protected areas, the Natura 2000 network, in Italy, hypothesising that the protected areas would show reduced anthropogenic pressure, higher native fish species richness and lower non-native species richness compared to areas outside the network. Analysing 3777 sampling sites across Italy, the research found that Natura 2000 sites did not consistently show lower anthropogenic impacts or higher fish species richness. These findings suggest that protected areas alone are not sufficient to mitigate anthropogenic pressures and ensure the conservation of fish diversity. The study highlights the limitations of protecting isolated river reaches within larger ecosystems. Effective conservation requires a holistic, catchment-wide approach, particularly about invasive species management, which is challenging at such scales.

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Does clonal plant growth rate vary during succession?

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Keywords: clonality, clonal plant growth, *Fragaria viridis*, long-term monitoring, old-field, spontaneous succession

Clonality is a widespread reproductive strategy among plants in diverse open terrestrial communities. Old-growth grasslands are particularly characterized by high proportion of slow-growing, long-lived clonal forbs with substantial belowground storage organs. These traits enable them to resprout after natural disturbances, playing a crucial role in the dynamics of grassy habitats. Therefore, the establishment of these species is vital for successful regeneration. Moreover, clonal plants have a profound impact on community assembly during spontaneous succession by shaping abundance relations and spatial vegetation structure.

In our study, we aimed to examine the colonization and expansion of a clonal perennial forb, *Fragaria viridis* (Rosaceae), during old-field succession. This species reproduces vegetatively through horizontal stolons (runners) and is typically associated with natural dry grasslands (e.g. meadow steppes). The annual clonal growth of colonizing genets was measured, and their cover was estimated each year for 14 years in a spontaneously recovering former cropland abandoned in 2009 in southeastern Hungary. The old-field was located directly adjacent to one of the largest ancient loess meadow steppe remnants of Hungary ('Tompapusztai-löszgyep' loess meadow steppe near Battonya, Körös–Maros National Park), which served as a natural propagule source for the study. We recorded the maximum diameter (the distance in cm between the furthest rooting daughter plants) of colonies from 2011 to 2024 in three permanent plots of 1,000 m^2, along with the estimated cover in m^2. To analyse yearly changes in maximum diameters and covers, we calculated yearly clonal growth rates and cover changes by computing the difference between consecutive years. Colonies were individually identified using GPS coordinates. Recorded genets were divided into early and late colonizers based on their germination dates: those found before year 6 after abandonment were classified as early colonizers.

In the group of early colonizers, both the maximum diameter and estimated cover followed a sigmoid curve, with a changepoint occurring at year 8 after abandonment. Beyond this point, the expansion of colonies slowed considerably, and in some cases, even declined. The average yearly clonal growth before year 8 was 181.4 cm, but afterward, it decreased to 59.9 cm. The yearly change in cover of early colonizers up until the changepoint was on average 2.4 m², and afterward, it decreased to 2.1 m². In contrast, late colonizers after year 8 had an average yearly growth of only 29.1 cm, with a mean increase in cover of just 0.03 m². To further explore these patterns, we fitted generalized additive mixed models to the maximum

diameter and cover of colonies, which also revealed significant differences between early and late colonizers, as well as their interaction with successional stage in both models.

Our findings indicate that the annual growth rate and increase in cover slow down during spontaneous succession in our model species, *Fragaria viridis*, especially for early colonizers. Additionally, there was a substantial difference in the growth potential between early- and late-germinating colonies. The presented results suggest that successional stage can determine the success of expansion in case of this target clonal forb species.

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Local and landscape drivers of amphibian metacommunities along a broad urban-rural gradient

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Keywords: occupancy, ponds, species richness, urbanisation

Urbanisation modifies and fragments natural ecosystems, shaping local species assemblages that often have non-linear responses to multiple stressors (Alberti and Wang 2022). There can be divergent responses within metacommunities along urban-rural gradients due to different habitat requirements, which filters communities into urban sensitive and urban tolerant species (McKinney 2002). Moreover, there is selection within amphibian communities along the pond-permanence gradient (Wellborn et al. 1996). However, few studies have explored non-linear and interactive relationships between amphibians and urban-associated parameters. Here, we examined relationships between amphibian species richness and occupancy and environmental covariates at ponds distributed along an extensive urban-rural gradient in Hungary.

We conducted three surveys for amphibians at 100 ponds around Budapest during the breeding season in 2023, using multiple methods to detect all developmental stages. Multi-species occupancy models were used to assess relationships between the probability of occupancy and 10 covariates (connectivity, two landscape-level and seven pond-scale) in four models, while accounting for imperfect detection. We used estimates of number of species at each pond derived from the four models in generalised linear models to examine the influence of each covariate on species richness.

We detected nine species. Species richness showed negative linear relationships with urban land cover within a 1000-m radius, fish presence and canopy cover, with pond area peaking at 700 − 800 m^2. We found positive linear relationships between species richness and connectivity, water level fluctuation, aquatic vegetation cover and the proportion of total habitat cover within a 1000-m radius. There were divergent patterns in occupancy among individual species. One species was positively associated with urban land cover (urban adapter), whereas seven species responded negatively.

Our results showed that the amphibian communities were filtered along the urban-rural gradient according to habitat requirements, highlighting the species-sorting perspective of metacommunity theory. We hypothesise that the increase in species richness with decreased connectivity was due to turnover occurring within dense pond clusters on the rural end of the urban gradient. We will explore this relationship further using data collected in subsequent years to model relationships between connectivity and pond colonisation.

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Distribution of macroinvertebrate communities in high-mountain tropical lakes of Ecuador

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Keywords: tropical mountain lakes, macroinvertebrates, spatial-temporal distribution, response curves

The glaciation process in many mountain regions across the world formed alpine lakes, which are important features of these landscapes. Worldwide, approximately 10% of lakes are located at higher elevations than 2100 m above sea level (a.s.l.). These lakes are often remote and could differ greatly from lower-elevation lentic ecosystems in their physical and biological characteristics. Tropical high-mountain lakes are low-temperature oligotrophic ecosystems with biological communities adapted to extreme conditions. Ecological information of these communities constitutes an important baseline, especially, facing climate change and anthropogenic activity.

Hence, the objective of this study was identifying environmental variables that control the spatial/temporal distribution of littoral macroinvertebrate communities in quasi-pristine high mountain lakes of Ecuador. Hydro-morphological, water quality and micro-habitat variables were monitored and macroinvertebrates sampled in 202 lakes. Further, 24 environmental variables were measured and macroinvertebrates sampled monthly in 10 lakes. Relative abundance of taxa and 22 community metrics per lake were calculated. These study lentic systems were characterized by low richness with Hydracarina, and Chironomidae as the dominant groups. Partial Redundancy Analysis and Generalized Linear Model analyses revealed that the ecosystem response of macroinvertebrate communities to environmental variables is complex, spatially and temporally.

Altitude was associated, negatively, with some richness community metrics (Total, Non-insect, Insect, Trichoptera, Odonata-Coleoptera-Heteroptera) and, positively, with the relative abundance (RA) of some taxa (*Andesiops, Anomalocosmoecus, Limnophora*). The RA of several taxa (Ostracoda, *Metrichia, Palpomyia, Aeshna* and *Dixa*) increased in larger lakes having alkaline pH. Smaller lakes had lower biodiversity and number of Trichoptera taxa. Further, in smaller lakes the increase of RA of *Liodessus, Dixella, Rhinaeshna* was related to the higher ammonium concentrations and *Allopetalia* and *Rhinoaeshna* was abundant in these smaller lakes due to their soil micro-habitats. Monthly macroinvertebrate community variation was not detected. However, Ephemeroptera, Plecoptera and Trichoptera RA varied significantly between three climatic phases, which could be influenced by a combination of several aspects/variables (i.e., hatching of Oxyethira (Trichoptera), temperature, dissolved oxygen, sulphate concentration or the more stable conditions of strongly stratified lakes). Time variability of turbidity and apparent color influenced the sample relative abundance and the RA of *Hellobdela*.

Zooplankton communities in garden and public urban ponds: a case study in Hungary

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Keywords: garden pond, public pond, zooplankton, fish, urbanization, urban landscape

Cities globally are rapidly expanding, posing significant threats to natural habitats, particularly freshwater ecosystems. As a result, public and garden ponds are emerging as novel habitats within these urban landscapes and play a pivotal role in contributing to freshwater conservation efforts. In 2021, we launched the MyPond project (www.mypond.hu) at the Institute of Aquatic Ecology, Centre for Ecological Research, Hungary. As part of this project, during the spring and summer of 2022, we conducted sampling campaigns to collect zooplankton samples from 52 public ponds located in parks, recreational areas, and private company premises, as well as 38 garden ponds located in private areas in Budapest, Hungary. Our study aims to investigate the role of artificially created public and garden pond environments in zooplankton biodiversity, which has not been previously explored in Hungary. We identified 95 zooplankton species in total, with 55 Rotifera species, followed by 24 Cladocera species and 16 Copepoda species. Out of 95 zooplankton species, we recorded three non-native species: *Eurytemora velox*, *Daphnia ambigua*, and *Pleuroxus denticulatus*, as well as two Rotifera species that are reported for the first time in Hungary: *Lecane tudicola* and *Monommata arndti*. Our results revealed a significantly higher local richness (α diversity) and regional richness (γ diversity) of zooplankton in the public ponds compared to the garden ponds. Together with that, we found a significant effect of urbanization on the zooplankton community in the public ponds, whereas no such effect was recorded in the garden pond. In line with that, we found that local environmental variables play a crucial role in structuring pond communities and affect zooplankton biodiversity. Our findings suggest that fish play an important role in shaping the zooplankton community in both the public and garden ponds. This study highlights the important implications for maintaining aquatic biodiversity conservation within urban landscapes, particularly in garden ponds.

Organisation of terricolous lichen assemblages in an East Hungarian sandy grassland: abiotic and biotic factors

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Keywords: lichen diversity, topography, vascular biomass, vascular diversity

Environmental factors affecting spatial distribution of terricolous lichens are among the less studied problems in spite these lichens can comprise a significant part of diversity in dry grassland ecosystems. The reasons can be the low number of lichenologists (mostly occupied by taxonomic and floristic studies) as well as the time consuming sampling of biomass and challenging identification and separation from dried samples of vascular plants.

We sampled spatial distribution of terricolous lichens and specific biomass of vascular plants at a *ca* 0.48 ha sized area in an undulating terrain in Nyírség region of East Hungary. Functional groups the role of which we compared included growth forms foliose (*Xanthoparmelia pokornyi*, *X. pulvinaris*) and fruticose (*Cladonia foliacea*, *C. rangiformis*, *C. furcata* subsp. *subrangiformis*) in lichens while in vascular plants life-form groups (perennial dicots, perennial monocots and annuals) were distinguished, respectively. The elevation difference within the study area was 3.5 m and it included dry dune tops and temporarily wet dune slacks, as well as slopes between them. Spread all over the study area, in a rectangular network we collected a total of 480 samples, each of 0.04 m^2 in size. In each sample we compiled list of lichen species and harvested aboveground standing crop of vascular plants in midsummer of 2018. We measured the topographic elevation of sample spots and samples of topsoil (0 –2.5 cm) have also been collected. Soil organic matter (SOM), soil reaction (pH_{KCl}), as well as concentrations of P_2O_5 and K_2O, have been analyzed, respectively.

As expected, values of SOM, pH as well as K and P content were lower in the higher elevations of the area. Lichens were most abundant at dune top and upper slope sampling sites with low SOM content (1-2%) with vegetation dominated by *Corynephorus canescens*, *Cynodon dactylon* and *Digitaria* spp. Some of the *Cladonia* spp. as well as *X. pulvinaris* also occurred in lower-lying sites dominated by *Cynodon dactylon*, *Eragrostis minor* or *Festuca pseudovina*. Absorbable P_2O_5 concentrations were 45–70 ppm on dunetop and 70–90 ppm in lower sites. Among the two protected *Xanthoparmelia* species, both SOM and pH were significantly higher at the sites where only *X. pulvinaris* was present than where *X. pokornyi* was also present.

In the biomass, a total of 46 vascular taxa have been detected and their summed aboveground standing crop varied between 25 and 380 g/m^2, with an average of about 90 g/m^2. About 58% of harvested biomass consisted of perennial monocots, about 29% belonged to perennial dicots while only 13% to annuals (monocots as well as dicots).

Total vascular biomass and summed lichen frequency had a weak but significant negative correlation (Spearman rank order, -0.294, $p<0.05$). Biomass of annuals has been highly positively correlated with lichen frequencies (summed: 0.511, fruticose: 0.486, foliose: 0.515 all: $p<0.001$). Surprisingly, lichen frequencies have shown negative and highly significant correlations with perennial dicots (summed: -0.676, fruticose: -0.659, foliose: -0.674, all: $p<0.001$). No significant correlation has been detected, however, between the perennial monocot biomass, the largest biomass fraction, and lichen frequencies. Lichen frequencies have been significantly positively correlated with the biomass of some dominant grass species (*Corynephorus canescens*) while more or less significantly negatively correlated with that of other grasses (*Cynodon dactylon*, *Festuca pseudovina* and *Calamagrostis epigeios*).

Silvicultural practices shape ectomycorrhizal fungal diversity and community composition in an oak-hornbeam forest in northern Hungary

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Keywords: alpha diversity, beta diversity, forest ecology, ITS2 metabarcoding, microclimate

The purpose of this study was to better understand the effects of forestry treatments (clear-cutting, gap-cutting, preparation-cutting, tree retention in clear-cut areas, and control) on the diversity and community compositional of ectomycorrhizal fungi an oak-hornbeam forest in northern Hungary. We sampled soil in all 30 plots of the Pilis Forestry Systems Experiment, operated by the Centre for Ecological Research and the Pilis Park Forestry Company, in the autumn of 2020 and 2021, 6 and 7 years after the treatments were implemented. We performed ITS2 rDNA metabarcoding of the soil-borne fungal communities, completed bioinformatic analyses, and assigned the resulting high-quality fungal sequences to taxonomic and functional groups. For this presentation, we compared the richness and community composition of ectomycorrhizal (ECM) fungi among forest treatment types and between years using analysis of variance for alpha diversity and nonmetrical multidimensional scaling and permutational analysis of variance for beta diversity analyses. Out of the 1035 detected fungal genotypes, 267 represented ECM fungi, of which the five most diverse phylogenetic clades were /tomentella-thelephora (47), /inocybe (40 genotypes), /russula-lactarius (52), /sebacina (27), and /cortinarius (20). ECM fungal richness decreased with increasing disturbance in both years, with the greatest found in the clear-cutting plots. We did not find significant differences in richness between the years. Conversely, there was a significant compositional difference between the two years, in addition to the strong treatment effect. Treatment was partly explained by altered environmental variables, such as soil water content, microclimate (predominantly relative humidity and upper soil temperature), understory vegetation, and distance from the plot to surrounding ECM host trees, while interannual variation may partly be caused by differing weather conditions during growing season, as the year 2021 was noticeably drier than 2020. In conclusion, forestry practices exert significant influences on ECM fungal communities in the studied forest, impacting both richness and composition. Understanding these effects is crucial for sustainable forest management and ecosystem conservation.

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Environmental filtering and dispersal limitation in stormwater ponds mimics natural systems for benthic macroinvertebrate communities around Canada's largest city

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Keywords: community assembly, urban, macroinvertebrate, aquatic, dispersal

Stormwater management ponds (SMPs) have emerged as a novel habitat for macroinvertebrates and other aquatic organisms in urban environments. Designed as infrastructure to ameliorate water quality and prevent flooding, these highly degraded systems have received growing attention for their un-intended habitat function over the past decade. However, existing research on the value of SMPs as aquatic habitats and the drivers of diversity in these systems is sparce and often contradictory, making a more general understanding of how invertebrate communities assemble and function in SMPs difficult to ascertain. To glean a broader understanding, we examined the relative importance of environmental filtering and dispersal limitation in structuring SMP communities and explored how the importance of these processes depended on functional traits of organisms. We used macroinvertebrate data from 30 SMPs around Canada's largest city, Toronto, Ontario to ask: i) What local and landscape factors determine diversity and community structure of invertebrate communities in SMPs?; ii) Is there evidence of dispersal limitation and environmental filtering in structuring invertebrate communities?; and iii) Do the importance of spatial structure and environmental conditions depend on dispersal traits? We find that SMPs show trends predicted by classic ecological theory in natural environments, with strong environmental filtering structuring flying invertebrate communities and dispersal limitation structuring flightless community composition across the landscape. Contrary to our expectation, despite highly degraded environmental conditions, environmental filtering does not appear to be the dominant driver of community composition for all memebers of the macroinvertebrate community. We find important roles for a variety of water chemistry and pond morphometry parameters in structuring both diversity and community composition, including chloride from road salts, and total suspended solids from runoff. We also demonstrate negative impacts of fish on invertebrate diversity, mediated through changing water chemistry conditions, highlighting the ecological complexity of these ponds and the need for further research. Our work helps to better understand the habitat role that stormwater ponds are performing in urban environments and provides a compelling case for the management of these systems as both habitat and infrastructure.

Public and garden ponds as amphibian habitats in a European city (Budapest, Hungary)

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Keywords: amphibians, urban ponds, habitat connectivity, biodiversity, metapopulation

Amphibians are among the most threatened vertebrates, facing risks of urbanization, habitat loss, fragmentation, and the spread of invasive species. Urban freshwater habitats, such as public and garden ponds, can serve as important refuges for amphibian populations, while public ponds support freshwater biodiversity, garden ponds may enhance habitat connectivity and stabilize urban metapopulations, yet their ecological role remains understudied.

We assess differences in amphibian community composition between public and garden ponds and identify key environmental, spatial, and landscape-scale drivers influencing habitat use.

Our results show significant differences in environmental conditions between public and garden ponds, which in turn shape patterns of amphibian community structure. While overall variation in amphibian communities is complex, analyzing public and garden ponds separately reveals clearer patterns: species composition in garden ponds is primarily driven by local environmental factors, whereas in public ponds, spatial autocorrelations and connectivity indices play a greater role in shaping community structure. Species-level analyses support this pattern, with garden ponds being strongly influenced by local management practices, whereas public ponds reflect broader spatial and connectivity dynamics. Our analysis based on the relative role of habitat characteristics and spatial connectivity revealed contrasting patterns between the two pond types: in garden ponds, spatial structuring (outskirts vs. city centre) was the dominant factor, whereas in public ponds, fringing vegetation and canopy cover were the strongest predictors of amphibian presence.

Both pond types support urban amphibian conservation, but their communities are shaped by different ecological mechanisms—garden ponds by local management and public ponds by urban connectivity. Recognizing these differences can help refine conservation strategies to strengthen urban biodiversity and counteract habitat fragmentation.

Interactive effects of wild boar rooting and shrub encroachment on the vegetation and seed bank of abandoned dry grasslands

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Keywords: ecosystem engineering, microsite, recruitment by seed, shrub encroachment, soil seed bank, spatial heterogeneity, vegetation dynamics

Wild boar (*Sus scrofa* L.) is one of the most widespread mammal species on Earth, occurring on all continents except Antarctica. While foraging, wild boars cause extensive biopedturbation by rooting, which alters soil properties and vegetation. They are considered ecosystem engineers, and their ubiquity, high abundance, and increasing populations necessitate evaluating their impacts on plant regeneration in affected natural communities. We examined the effects of wild boar rooting on vegetation and seed bank dynamics in shrub-encroached grasslands, assessing both positive and negative conservation implications.

Our research was conducted in a shrub-encroached, abandoned dry grassland near Budapest, Hungary (Central Europe). We selected 40 sites and established four plots per site representing four microhabitats: (i) the central part of wild boar roots, (ii) the edge of the roots consisting heaped soil, (iii) shrub-encroached unrooted grassland, and (iv) control grassland. In total, 160 plots were surveyed for vegetation, and additionally we measured soil moisture, microclimate, and collected soil samples for seed bank analysis.

Multivariate ordination analyses revealed that vegetation composition differed markedly among the four microhabitats, although seed bank composition remained similar. Indicator species analysis identified several grassland specialists characteristic of either the rooting zones or shrubby patches, enhancing beta-diversity compared to undisturbed grassland. The central root zone exhibited the highest soil moisture and poorest vegetation, dominated by weedy and invasive species with few grassland specialists. However, it provided the only suitable habitat for some rare red-listed weed species. In contrast, the root edge was the driest microhabitat, harbouring more grassland specialists and fewer weeds. Shrub patches maintained dry conditions, but their shading promoted forest-edge specialists and minimized weed abundance. The lowest seed bank density was observed in the central root zone, while the root edge showed a seed bank inversion with higher seed density in lower soil layers. Shrub canopies appeared to trap seeds, contributing to a higher overall seed bank density.

Our results indicate that in abandoned grasslands with substantial biomass accumulation, wild boar rooting creates unique microsites that support both specialist and weed species (including rare weeds), while shrubs offer cooler microhabitats with distinct species compo-

sitions. Our findings suggest that despite in general wild boar rooting is considered a threat to species rich grassland communities, it might support conservation purposes in abandoned grasslands by providing establishment gaps for species of conservation interest.

Acknowledgments
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Local gamma: the missing piece in Whittaker's diversity puzzle

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Entropy's special cases, like Shannon or Simpson's index, are frequently used in ecology to assess alpha diversity. The associated notion of divergence could be used to measure beta diversity, but it is rarely applied in ecology. Expanding on these concepts, we introduce a third informational metric that bridges alpha, beta, and gamma diversity. We demonstrate that when alpha corresponds to Shannon entropy and beta is the Kullback-Leibler divergence, our proposed index—local gamma—precisely decompose Whittaker's gamma diversity, which is also directly computable via cross-entropy. To illustrate the ecological utility of this novel index and its broader applicability, we calculate local gamma across multiple orders using a large biological dataset. This index establishes a diversity gradient, ranging from communities dominated by a few common species to those where rarer species are evenly distributed. Our results advocate for divergence as the optimal measure for estimating beta diversity. Additionally, our entropy-based framework, incorporating divergences and cross-entropies, facilitates the computation of classical gamma diversity while offering components that are distinct, comparable, self-contained, and pointwise distributed.

T03: Ecological networks and food webs

Seasonal shifts in trophic interaction strength drive stability of natural food webs

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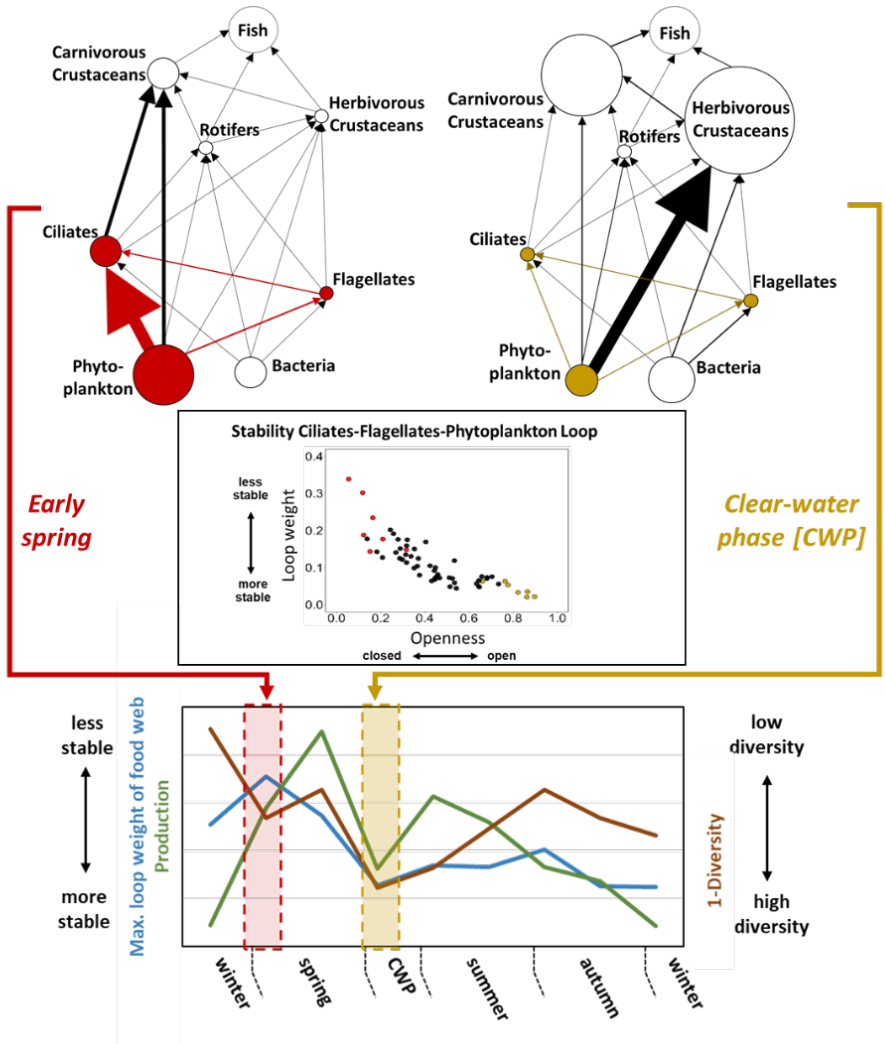
Keywords: trophic interaction loops, maximum loop weight, asymptotic stability, diversity- stability, mass-balanced network, long-term data, pelagic food web, seasonal and interannual dynamics

It remains challenging to understand why natural food webs are remarkably stable despite highly variable environmental factors and population densities. We investigated the dynamics in the structure and stability of Lake Constance´s pelagic food web using seven years of high-frequency observations of biomasses and production, leading to 59 seasonally resolved quantitative food web descriptions. We assessed the dynamics in asymptotic food web stability through maximum loop weight, which revealed underlying stability mechanisms. Maximum loop weight showed a recurrent seasonal pattern with a consistently high stability despite pronounced dynamics in biomasses, fluxes and productivity. This stability resulted from seasonal rewiring of the food web, driven by energetic constraints within loops and their embedding into food web structure. The stabilizing restructuring emerged from counteracting effects of metabolic activity and competitiveness/susceptibility to predation within a diverse grazer community on loop weight. This underscores the role of functional diversity in promoting food web stability (cf. Gaedke et al. 2025, Ecol. Lett.).


Fish
Carnivorous Crustaceans
Herbivorous Crustaceans
Rotifers
Ciliates
Flagellates
Phyto-plankton
Bacteria
Fish
Carnivorous Crustaceans
Herbivorous Crustaceans
Rotifers
Ciliates
Flagellates
Phyto-plankton
Bacteria
Stability Ciliates-Flagellates-Phytoplankton Loop
less stable
more stable
Loop weight
0.4
0.3
0.2
0.1
0.0
0.0 0.2 0.4 0.6 0.8 1.0
Openness
closed
open
Early spring
Clear-water phase [CWP]
less stable
more stable
Max. loop weight of food web
Production
low diversity
high diversity
1-Diversity
winter
spring
CWP
summer
autumn
winter

Diversity and adaptability in marine microbial co-occurrence networks: responses to environmental change

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Keywords microbial community, co-occurrence network, spatial gradient, macroscopic properties

Climate change and pollution significantly drive global environmental transformations. While responses of many organisms to these factors are well documented, our understanding of the effects and vulnerability of microbial communities remains limited. Environmental conditions can influence microbial interactions, detectable through alterations in their co-occurrence network structures. Studying microbial communities at the ecosystem level provides insights into their variability, vulnerability, and resilience.

In this study, marine microbial communities were examined at multiple locations along an approximately 2800 km transect of the Southern Ocean and throughout the water column. Amplicon sequence variants (ASV) obtained from 16S rRNA gene sequencing were analyzed to construct co-occurrence networks, exploring variations across latitudinal and depth gradients. The resulting networks featured weighted, signed, yet undirected links. We developed multiple network models: one inclusive of all associations regardless of interaction sign, and others focusing separately on positive and negative interactions.

To quantify system-level characteristics, we utilized macroscopic network indicators historically employed in food-web research alongside novel topological metrics (e.g., clustering coefficient, compactness). Network topology measures were correlated with environmental variables measured at each location and depth. Some metrics appeared particularly sensitive to environmental changes.

Topological properties demonstrated considerable variability, with certain indices occasionally exhibiting linear trends along environmental gradients. Given the increasing recognition of microbial community structure as critically important to marine ecosystem health—where disturbances may generate bottom-up effects comparable to top-down impacts such as overfishing—it is crucial to enhance monitoring efforts and deepen our understanding of microbial ecosystem variability.

Interaction profiling species and functional redundancy in ecological networks

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Keywords: food web, trophic field, redundancy, functional groups

Key species in ecological networks may be in either central or unique positions. There is a rich literature on centrality with a number of network indices routinely used. The uniqueness versus redundancy of network positions is less studied but it is at least as important as centrality from a functional ecological point of view.

We overview a few approaches proposed in the past decades and discuss their ecological relevance. These include the topological overlap index (TO), species trophic overlap (STO) and interaction profile diversity (IPD). We also present a new index based on both of the input and output interaction system. This is paralleled with the classical concepts of input and output environ in systems ecology. Our work is demonstrated on field databases describing a few case studies and we discuss applicability in management and systems-based conservation.

Acknowledgments
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Establishing an *in vitro* gut microcosm for measuring the effects of prey chemical defences on great tit microbiota

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Keywords: microcosm, great tit, predatory behaviour

Gut microbiota plays a major role in organism health and behaviour. In great tits (*Parus major*), microbiota composition can be altered by the birds' foraging decisions, particularly the consumption of aposematic insects that advertise their chemical defences through warning signals. These toxin-microbiome interactions may influence great tit physiology and foraging behaviour, yet are challenging to study in wild populations.

This project aimed to develop a standardized *in vitro* cultivation method for great tit gut microbiota to test the effects of prey toxins on microbial diversity and abundance under controlled conditions. Various media formulations were evaluated, incorporating specific carbon and nitrogen sources selected to closely mimic the avian gut environment. Faecal samples from wild great tits were inoculated at different concentrations, with pH monitoring to track microbial growth dynamics. The resulting bacterial microcosms were analysed using 16S rRNA gene sequencing and compared with the original faecal samples to assess community composition and representativeness.

Our results identified an optimal media formulation that maintained key taxonomic groups and functional diversity comparable to those observed in wild great tit gut microbiota.

This validated *in vitro* model provides a valuable tool for analysing prey toxin effects on avian gut microbiota by eliminating confounding environmental variables and enabling higher-dose toxin experiments without ethical concerns related to animal welfare. The system will facilitate mechanistic studies advancing our understanding of predator-prey coevolution and the microbiome's role in ecological interactions. Beyond predator-prey dynamics, this methodology can be applied to investigate numerous ecological contexts, including gut microbiome disturbances in response to anthropogenic stressors such as pollution, habitat fragmentation, and climate change, opening avenues for diverse research applications across ecological and environmental sciences.

Climate change, an invasive omnivor, and planktonic food web dynamics – insights from a process-based model

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Keywords: planktonic food web, invasive omnivor, community dynamics, climate change, nutrient cycling, process-based model

Despite the growing amount of data available on surface waters, our understanding of the long-term effects of climate change, invasive species spread, and altered nutrient loads on aquatic communities is still limited. Process-based models have become powerful tools for disentangling the mechanistic links between environmental impacts and shifts in community structure and functioning. The aim of this study was to develop a multitrophic model that complements experimental efforts in elucidating the combined impact of invasive, omnivore mysids and changing temperature patterns on plankonic food web dynamics. The model is the extended version of an existing multispecies, multi-nutrient numerical model for phytoplankton, and has been designed to simulate tri-trophic food web dynamics in a mesocosm-scale setting. We conducted simulations to examine the stability of a community consisting of algae, ciliates, rotifers and daphnids under varying nutrient loads and in response to the presence of the mysid *Limnomysis benedeni* across different temperature scenarios (e.g., gradual long-term warming, increased heatwave frequency). The presentation will discuss key findings from these simulations, highlighting the implications for aquatic ecosystem resilience. Additionally, we will explore the model's advantages, potential applications and extension possibilities.

Acknowledgments
This work has been implemented by the National Multidisciplinary Laboratory for Climate Change (RRF-2.3.1-21-2022-00014) project within the framework of Hungary's National Recovery and Resilience Plan supported by the Recovery and Resilience Facility of the European Union.

Food density drives diet shift of the invasive mysid shrimp, *Limnomysis benedeni*

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Keywords: invasive species, *Limnomysis benedeni,* diet shift, food selectivity, trophic interactions

Understanding the diet preferences and food selection of invasive species is crucial to better predict their impact on community structure and ecosystem functioning. *Limnomysis benedeni*, a Ponto-Caspian invasive mysid shrimp, is one of the most successful invaders in numerous European river and lake ecosystems. While existing studies suggest potentially strong trophic impact due to high predation pressure on native plankton communities, little is known of its food selectivity between phyto- and zooplankton, under different food concentrations. Here, we, therefore, investigated the feeding selectivity of *L. benedeni* on two commonly occurring prey organisms in freshwaters, the small rotifer zooplankton *Brachionus calyciflorus* together with the microphytoplankton *Cryptomonas* sp. present in increasing densities. Our results demonstrated a clear shift in food selection, with *L. benedeni* switching from *B. calyciflorus* to *Cryptomonas* sp. already when the two prey species were provided in equal biomasses. Different functional responses were observed for the two food types, indicating somewhat different foraging mechanisms for each food type. These findings provide experimental evidence on the feeding flexibility of invasive mysid shrimps and potential implications for trophic interactions in invaded ecosystems.

Feeding selectivity and trophic links of a dominant cyclopoid copepod

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Keywords: aquatic food webs, zooplankton diet, feeding preferences

As a key link between producers and fish, zooplankton grazing regulates the transfer of energy and nutrients. Cyclopoid copepods often dominate the zooplankton of freshwater ecosystems and are considered omnivores. Yet, we know little about their diets or prey selection, and even less so for different life stages. Most work focuses on large bodied Cladocera, while large bodied copepods – often equally or more abundant – remain less understood. *Macrocyclps* is a common and abundant genera of large bodied cyclopoid copepod in Northern temperate freshwater lakes and often dominates zooplankton biomass in colder months. We aimed to quantify prey specific clearance rates and selectivity of *Macrocyclops albidus* adults and nauplii via short term grazing micro assays with unicellular alga including cyanobacteria and chlorophytes, and heterotrophic ciliates (*Paramecium*). We evaluated grazing rates on single prey and paired mixed prey diets using 5 mL well plates by comparing prey abundance in no-grazer controls and grazer present treatments over a period of 3 hours. Algal abundance was measured via pigment specific chlorophyll concentrations (PHYTO-PAM) and ciliate abundance was counted with microscopy. Prey abundance was standardized to 0.5 mgC/L equivalent biomass, which is the optimal density for most zooplankton. Initial results suggest that adult copepods strongly select for ciliates while nauplii graze more on phytoplankton. The ontogenic diet shift has implications for trophic dynamics and subsequent ecosystem functions.

Trophic modeling and ecosystem insights for the Sylt Outer Reef (Eastern German Bight): a pathway to policy-oriented management

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Keywords: marine protected area, Sylt Outer Reef, ecopath, food web modelling, ecosystem structure and functioning, keystone species

The marine protected area Sylt Outer Reef (SOR), located in the Eastern German Bight of the North Sea, has garnered attention for the exclusion of bottom trawling that has been implemented in 2023.The area is characterized by a high diversity of species and habitat structures.To assess ecosystem responses to trawling exclusion, we first developed a mass balanced trophic model using the Ecopath with Ecosim software, incorporating 44 functional groups, mainly based on recent field data from the period 2010-2020. Ecological indicators were applied to describe the trophic structure, quantify energy flow, and identify the keystone species, and additionally applied to compare the Sylt Outer Reef model with previously published models covering adjacent or overlapping regions of the North Sea. The estimated trophic levels (TL) ranged from 1.0 to 4.17. Results showed that the SOR ecosystem is primarly detritus-driven,with detritus recycling largely supported by benthic organisms. The overall mean transfer efficiency was 14%, with 14.52% from detritus and 9% from primary producers. Key species structuring the food web include *Ammodytes spp*., *Eutrigla gurnardus*, *Limanda limanda,* carnivorous polychaetes, and *Phocoena phocoena.* A comparaion of our SOR model with other North Sea models suggests that the SOR ecosystem is complex, resilient, and mature. The developed model provides a valuable tool for simulating the ecological impacts of fisheries management and conservation scenarios.

Comparing co-occurrence network methods for assessing invertebrate associations in a tropical high mountain river ecosystem

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Keywords: co-occurrence networks, network analysis, comparative analysis, freshwater invertebrates

Understanding species coexistence and ecological associations is a major challenge in ecology. Co-occurrence networks are increasingly used to infer potential interactions from large-scale omics datasets (Freilich et al., 2018), but their ability to predict real ecological interactions remains uncertain. While most studies focus on prokaryotic communities, we apply co-occurrence network analysis to eukaryotic communities, namely freshwater macroinvertebrates, in a tropical high mountain river system, Ecuador. Our key objective is to assess the sign (positive and negative) and consistency (temporal and spatial) of species associations across different network inference methods. We will present and discuss the variability in co-occurrence patterns and compare different methodology approaches to evaluate their reliability. Our findings will contribute to improving the interpretation of co-occurrence networks for ecological inference.

Acknowledgments
This work was supported by the Romanian Ministry of Education and Research, within the National Recovery and Resilience Plan PNRR/2022/C9/MCID/I8, CF 72/14.11.2021, Contract Nr. 760102/23.05.2023 (PredAqua).

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T04: Effects of global change

Climate change impacts Mediterranean seagrass' seascape structure: what are the cascading effects on the associated communities?

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Keywords: Posidonia oceanica, Cymodocea nodosa, landscape fragmentation, alpha diversity, beta diversity, neutral metacommunity model

Seagrass meadows are a key element of coastal ecosystems in the Mediterranean Sea due to the high biodiversity they host. Climate change poses a threat to the persistence of *Posidonia oceanica* and *Cymodocea nodosa* meadows in large extents of the Mediterranean Sea, with major range shifts projected under climate change scenarios (Chefaoui et al., 2018), and cascading effects on the structure of the landscapes they form. The biotic populations and communities associated to seagrass meadows might experience significant changes in connectivity, with cascading effects on their persistence. However, frameworks to assess the impacts of climate change on biotic communities inhabiting biogenic habitats are largely missing. In this contribution, we aim at assessing the cascading effects of climate change on Mediterranean seagrass habitats and the associated biodiversity. We employed high resolution physical and biogeochemical data for the Mediterranean Sea to model the seagrass distribution in the present climate using an ensemble approach (Baldan et al., 2024). Based on the identified habitats configuration, we employ a neutral coalescent model (Cunillera-Montcusì et al., 2021) to simulate virtual metacommunities structured by stochastic demographic processes and dispersal. Our results at the Mediterranean scale show a strong range contraction for both seagrass species, a decrease in alpha diversity of associated communities, and an increase in beta diversity. At the local scale, we show that patterns of alpha diversity under realistic species dispersal are strongly correlated with habitat availability, while beta diversity is also influenced by the changes in the spatial configuration of seagrass habitats. By highlighting hotspots of metacommunity change linked to habitat fragmentation, our method can be useful for planning conservation and restoration measures at local and regional scales.

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The adaptive responses of *Skeletonema marinoi* under long-term global change scenarios

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Climate change is altering marine environments in ways that challenge the resilience of phytoplankton - the base of the oceanic food web. Yet, our understanding of how evolutionary history and regional origin influence phytoplankton responses to global change remains limited. In this study, we examined whether long-term acclimation to elevated temperature and CO_2 levels influences the ecological performance of the coastal diatom *Skeletonema marinoi* under simulated future ocean conditions.

We used two genetically distinct strains of *S. marinoi* - one from northern Norway (S8) and one from southern Norway (S16), spanning over 2500 km in latitude - that had been maintained for three years under four combinations of temperature (13°C and 19°C) and CO_2 (400 ppm and 1000 ppm). These pre-adapted populations were then used in a mesocosm experiment conducted at the Scottish Association for Marine Science (SAMS, Oban, UK), where both temperature and pCO_2 were controlled to mimic present-day and projected end-of-century ocean conditions. Over the course of two weeks, chlorophyll concentration was tracked every second day, and microbial community composition was assessed via DNA metabarcoding at the end of the experiment.

This design allowed us to test whether prior acclimation to warming and acidification confers a competitive advantage in complex communities, and whether geographic origin influences adaptive potential. By comparing the ecological responses of S8 and S16 under matched and mismatched conditions, we aimed to shed light on the predictability of adaptation and its consequences for community interactions in future oceans.

Our findings underscore the importance of strain identity and evolutionary history in shaping phytoplankton responses to environmental change - critical factors that should be incorporated into ecosystem models and climate projections.

Fate and effects of microplastics on a freshwater plankton food web in a whole-lake addition experiment

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Keywords: microplastics, zooplankton, phytoplankton, ecotoxicology, plastic

Despite the ubiquity of microplastics in the environment, their fate and effects on freshwater aquatic ecosystems are largely unknown. At the International Institute for Sustainable Development - Experimental Lakes Area (IISD-ELA) in northwestern Ontario, Canada, a long-term study is being conducted involving microplastic additions to an entire lake. Data collected post-microplastic additions are being compared to four years of baseline data from the same lake, as well as to a nearby unmanipulated lake using a before-after-control-impact (BACI) design. The planktonic food web, including phytoplankton, zooplankton, and their invertebrate predator, *Chaoborus*, is an important part of the overall ecosystem and affects overall water quality of the lake. Various zooplankton were analyzed for ingestion of microplastics at multiple timepoints to better understand the movement of microplastics through the food web. These organisms were also monitored for changes in community structure (abundance, biomass, and species composition) resulting from the microplastic additions. Ingestion differed across taxa and there was a clear relationship between concentrations of ingested microplastics and concentrations in the water column. No evidence was observed for biomagnification or trophic transfer of microplastics from zooplankton to *Chaoborus*. Preliminary results for the effects on these communities show a decrease in phytoplankton abundances in the first year of the experiment followed by a decrease in zooplankton abundances in the second year. Understanding impacts to these planktonic organisms which make up the base of the food web will contextualize effects seen across other organisms in the lake, helping to develop the full picture of the impacts microplastics have on a freshwater ecosystem. Broadly, this whole-lake manipulation experiment is the first of its kind and will inform industry and government level policies to mitigate plastic pollution.

Microclimate-driven functional mismatches in Mediterranean soil nematofauna

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Many parts of the Mediterranean, like Sicily, Morocco, Greece and Israel, are severely threated by coastal erosion, drought and aridity, although they are known for an exceptionally high biodiversity, not inflated during the Pleistocene Ice Ages as happened in the central and northern part of Europe. Our aim at SOB4ES is to focus on patterns according to environmental trends as detected by remote sensing (e.g., COPERNICUS) and wish to see the extent to which the strongly increased aeolian dust deposition and the temperature offsets between air and soil (e.g., SoilTemp) affect the soil biota. Understanding the environmental consequences of these changes requires strong and reliable climate models and strict lab protocols. Being able to forecast future scenarios is mandatory to conservation and restoration efforts aimed at managing, restoring, or preserving the constant delivery of ecosystem functions and services. Whilst more and more is known about the drivers of microclimate heterogeneity, we don't know how microclimate heterogeneity and aeolian dust deposition relate to supporting ecosystem services in the Mediterranean Sea with either the same or a different soil type.

Earth Observation data have a pivotal role in DIEB and are the prior of boosting Big Data technologies, from genes up to satellites. For the latter, COPERNICUS and LANDSAT produce over 15 TB of open data daily that need processing and storage. Pursuing exploitation of data as part of the Earth Observation downstream sector requires innovative application of mature solutions; they are essential to address the related issues pertaining to data processing, characterized by the four Big Data Vs: Volume, Velocity, Variety, Veracity. Volume and Velocity of aeolian dust deposition of Saharian particles will be addressed by remote sensing, whilst Variety and Veracity of habitat responses of free-living nematodes to elemental and thermal mismatches in the soil will be addressed.

In this way we merge two observational layers together, one by investigating the linkages between the complex structure of microecosystems, and the other by gathering and mining of satellite data and direct observational/experimental evidence from the functional response of the most peculiar component of the soil fauna, the nematodes. The predictions of these two layers will then be tested in Sicily, Morocco, Greece and Israel using the climatological data and the direct observational data.

The project will start with the integration of data obtained from remote sensing, and existing data will allow us to formulate hypotheses on the role of biodiversity for sustaining ecosystem functions and ecosystem services. Then, according to demonstrative models obtained, Earth Observations applied systems will inform which areas are most at risk from microecological and geological perspectives. Priority ranking of protected areas, multicriteria analysis and a weighted comparison of the results will be undertaken, discussed in the SOIL EU Mission and communicated to stakeholders and policy.

Trophic state dynamics in rivers: a global perspective on trends, indicators, and implications

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Keywords: eutrophication, oligotrophication, long-term trends, systematic review, trophic status, river

Trophic status indicates water quality which in turn affects biodiversity and ecosystem functioning in aquatic ecosystems. Recent research suggests that re-oligotrophication, the return of trophic status from eutrophic to oligotrophic, is widespread. However, its spatial extent remains understudied, as well as the heterogeneity of definitions for trophic change and their indicator parameters.

Here, we systematically review 1182 publications (Scopus, 955; Web of Science, 526) to address: 1) How are oligotrophication and eutrophication defined, and what variables are most commonly associated with the processes?; 2) What is the global distribution of oligotrophication and eutrophication in river systems? To this end, we 1) identified the most common variables used to assess eutrophication and oligotrophication; and 2) selected long-term studies (> 10 years) reporting significant trends in trophic status changes.

Our study reveals heterogeneity in the definitions and indicator variables for eutrophication and oligotrophication, with the latter being influenced by diverse anthropogenic, climatic, and hydrological factors. Significant temporal trends indicating eutrophication are mainly linked to high nutrient loading and prolonged hydraulic residence times caused by agriculture, dams and dikes, while oligotrophication are linked to improved wastewater management but also agricultural practices. The ecological effects are profound, often leading to ecosystem-level shifts, such as transitions between planktic and benthic primary production dominance. Understanding the mechanisms behind ecosystem-level changes will require sustained monitoring programs, that will also help predict future trajectories.

Acknowledgments
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Warming and acidification alter essential fatty acid profiles in marine diatom *Skeletonema marinoi*

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Keywords: *Skeletonema marinoi*, climate change, diatom, fatty acids, adaptive evolution

Climate change conditions, such as warming and ocean acidification, could negatively impact marine ecosystems by altering the biogeochemical cycles, promoting harmful algal blooms and affecting the nutritional quality of phytoplankton. Shifts in the lipidic profile in primary producers could propagate to higher trophic levels and influence the entire aquatic community, with potential implications in human diets as well.

This study aimed to investigate how one of the most common and abundant marine diatoms, *Skeletonema marinoi*, adapts to warming and acidification conditions after one year of exposure to higher temperatures (19°C) and elevated CO2 (1000 ppm). We examined the individual and combined action of these factors on the lipidic profile of three strains of *S. marinoi*. Our aim was to determine whether the long-term exposure to warming and/or acidification led to adaptive changes that would translate in modifying the fatty acid composition of the three strains. The focus was mainly on the essential omega-3 (n-3), omega-6 (n-6) fatty acids and their ratio, due to their vital importance in animal and human diets.

Our results indicated the long-term exposure to warming and/or acidification altered the fatty acid profiles of *S. marinoi* in a strain-specific manner, highlighting the strain plasticity under climate change conditions. Notably, acidification seems to have a high influence on the essential fatty acid production of the marine diatom, when acting alone or combined with warming. These findings underline the nutritional value of marine diatoms in the context of global change and bring valuable insights regarding the quality and possible impact of primary producers within trophic networks.

Ecotone shifts in a changing climate

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Keywords: climate change, habitat tracking, connectivity, percolation, critical transition, treeline

Several types of ecotones are undergoing spatial shifts in response to climate change. Monitoring these shifts is often challenged by the inherently complex geometry of ecotones. A key difficulty lies in disentangling random fluctuations from systematic, trend-like changes within these intricate patterns. We propose a novel approach to detecting ecotone shifts, grounded in percolation theory. The method is illustrated through case studies of alpine treelines. Its effectiveness is evaluated through computer simulations modeling colonization-extinction dynamics across environmental gradients. Percolation theory reveals a general scaling law in ecotone geometry, enabling consistent comparisons across time and space. This, in turn, facilitates the early detection and monitoring of ecotone shifts across broad geographic scales.

Acknowledgments
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Fish invasions alter size-density relationships through temperature-mediated ecological mechanisms across the globe

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Keywords: body size distribution, community assembly, non-native, trophic guilds, lake

In ecology, analyzing size spectrum (or individual size distribution) is a simple approach widely recognized as linking individual and population traits with the structure of ecological communities. Conversely, the assessment of size spectra in the context of biological invasions remains poorly investigated. We aimed to assess the impact of non-native (NN) fish on the size structure of freshwater communities. Additionally, we sought to explore the ecological mechanisms behind the potential effects of invasions and assess whether water temperature interacts with these processes. We hypothesized that flatter size spectra in fish communities are associated with higher pressure from NN fish (in terms of abundance, richness, and biomass), which is more pronounced in warmer lakes (H1). We also hypothesized that NN piscivorous and those from other trophic groups could disrupt native fish size spectra decline, excluding smaller fishes via direct biotic interactions, i.e., predation and competition, respectively (H2). To test these hypotheses, we assessed size spectrum parameters (total biomass and slope) estimated in 420 lakes (both natural and artificial) across temperate and tropical regions using linear mixed models (LMMs). We found that NN fish's pressure turns flatter the size spectra of communities, especially in warmer lakes in the tropics. This is because NN fish tend to be larger than natives and thrive in warmer lakes where metabolic rates and resources are greater than in colder environments, fostering their population growth. When assessing only the size spectrum patterns for the native community and the effect of the proportion of NN from different trophic groups, we found that native total biomass decreases more in lakes predominantly dominated by NN species from more basal trophic groups, although NN piscivores were also important. Also, regarding slope patterns, NN piscivores are only important in warmer lakes, making them flatter. This is because, in colder lakes, these species likely reduce their predation activities and prey-on efficiency (of smaller native individuals). Therefore, competition exerted by NN species from more basal trophic groups seems to be the primary direct mechanism of reducing total biomass and flattening slopes of native communities invaded. These results show a direct NN's impact by biotic interactions with natives, which was greater in warmer lakes in the tropical zone. The proposed study will help to fill significant gaps in literature and provide a comprehensive understanding of how the size spectra of freshwater communities in different environmental contexts respond to fish invasion disturbance interacting with temperature.

Soil fungal communities along an aridity climate gradient

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Keywords: soil fungal communities, soil microorganisms, facing slopes, climatic gradien

In drylands, the distribution of vegetation is comprised of shrubby patches, livestock trampling routes, and the remaining interpatch spaces, forming a distinct three-phase mosaic ecosystem. These microhabitats are essential for regulating the redistribution of surface and soil water, which directly influences critical ecosystem functions. Soil fungal communities are integral to these processes, yet their abundance, diversity, and composition in such patchy environments have been insufficiently studied. This study definitively assesses the impact of microhabitats on soil fungal communities along an aridity gradient in southern Israel, spanning semi-arid, arid, and hyper-arid sites across two contrasting hillslope aspects (north and south) and within three microhabitats. The findings clearly demonstrate that both location along the aridity gradient and hillslope aspect significantly shape fungal taxonomic richness. However, these factors do not influence the composition of functional guilds. Furthermore, the effect of microhabitat is notably minimal. This research emphasizes the critical role of site location and hillslope aspect in determining the composition, distribution, and functional groups of soil fungal communities, with dispersal diminishing as aridity increases. Importantly, network analysis reveals that increased aridity leads to a marked reduction in microbial community diversity, primarily due to declining soil moisture levels.

T05: Conservation biology

Out-of-production sites provide safe-havens for rare weeds in intensively used agricultural landscapes

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Rare weed (RW) species are disturbance-adapted plants that can considerably contribute to agrobiodiversity and related ecosystem services without negatively affecting agricultural production. However, agricultural intensification of the past decades led to an enormous decline of RWs globally, making their conservation dependent on targeted measures addressing their special ecological needs. Our study aimed to assess the potential of out-of-production sites (i.e., former arable lands where management was ceased allowing spontaneous grassland regeneration) to sustain RW populations characteristic of arable lands, old-fields, and grasslands. In an extensive field survey covering approximately 21,500 km², we collected data from 216 sites in Hungary (Central Europe), including areas with spontaneously recovering grassland vegetation and reference grasslands. Of the 216 sites, 192 supported successional vegetation ranging in age from one to 144 years, while 24 were covered with ancient semi-natural grasslands. The sites were embedded in lowland agricultural landscapes, representing a gradient from less transformed, complex landscapes to intensively used, cleared landscapes. We used zero-inflated generalized linear mixed models to identify site- and landscape-specific factors (such as geographic location, landscape transformation, habitat size, environmental heterogeneity, soil properties, vegetation age, and other vegetation attributes) that can influence the occurrence and species richness of RWs. In total we recorded 38 RW species, including 15 red-listed and two protected ones. RWs were present in 51% of the study sites, demonstrating that out-of-production sites can serve as refuge for RWs associated with croplands, old-fields, and grasslands. Zero inflated models showed that environmental heterogeneity emerge as a key factor supporting RW occurrence, particularly for species linked to grasslands. Poisson models revealed that overall RW species richness declined in northern sites. The number of arable RWs was higher in sites with high soil CaCO3 content, whereas high soil phosphorus content supported fewer grassland RW species. Sites with diverse vegetation supported more old-field and grassland RWs. Our results suggest that land

sparing measures targeting the maintenance of out-of-production sites and supporting environmental heterogeneity and establishment gaps can considerably contribute to the conservation of RWs in agricultural landscapes.

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Poor fen degradation increased the density and diversity of soil microarthropods and altered their community structure

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Keywords: Oribatida, Collembola, poor fen, mesofauna, springtail

Poor fens act as important refugia for endangered plant and animal species, play a role in water balance and also serve as important carbon sinks. In the last century, they experienced a remarkable loss of habitat specialists, decline in area, and the last remnants of well-developed poor fens are critically endangered in Central Europe. Their degradation is usually indicated by an expansion of competitive tall herb species and later by woody species at the expense of mosses and low-growth, competitively weak herbs.

The goal of our study was to identify the response of soil microarthropods community to this degradation and the mechanisms responsible for the changes. Springtails (Collembola) and oribatid mites (Acari: Oribatida) play an important role in the decomposition of plant litter and are considered efficient bioindicators due to their high diversity and sensitivity to environmental factors.

We compared the microarthropod communities of well-preserved and degraded parts in 30 poor fens across the Czech Republic, along with physical and chemical properties of their environment. Density and species richness of oribatids and collembolans were higher in degraded parts, indicating a higher input of decomposing plant material. The degradation expressed as an expansion of tall, competitive graminoids facilitated the occurrence of ubiquitous, non-specialized microarthropod species, but concurrently it increased the numbers of some tyrphofilous species as well.

The presence of specialised tyrphobionts in both well-preserved and degraded parts indicated a potential for the restoration of this endangered habitat.

Seeding year is more important than short-term seed storage in seed-based restoration of Pannonian sandy grasslands

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Keywords: grassland restoration, invasive alien species, long-term restoration success, seed bank, seed introduction, short-term seed storage, target species

The restoration of native grasslands can be an important contribution to the global and EU targets. To achieve effective restoration, ensuring a sufficient and high-quality supply of native seeds is essential. Ex situ seed banks can play a crucial role in supporting grassland restoration by providing seeds and mitigating the negative impacts of climate change on seed availability and quality. Seeding of native species has been shown not only to accelerate grassland recovery but also be of paramount importance in enhancing resistance to invasion. We studied the effects of short-term seed storage (one-, two- and three-year stored seeds) and seeding year (2011–2014) on the restoration of open sandy grassland using seed accessions from the Pannon Seed Bank in Hungary. We investigated two key questions: (1) Does the initial seeding of sandy grassland species from the Pannon Seed Bank accelerate vegetation development toward the reference grassland? (2) How do short-term seed storage and the year of seeding influence vegetation development over time? Our study was conducted at a sandy old field site with five blocks, each containing ten parcels subjected to nine different restoration treatments (storage duration x seeding year), along with an unseeded control. We sowed seed mix of ten native sandy grassland species each year between 2011–2014, arranged in ten lines of 25 meters, and monitored species cover twice annually until 2017, plus in 2020. We applied multivariate analyses to assess vegetation development trajectories and applied generalized linear mixed models to evaluate the effects of seed storage, seeding year, and elapsed time after sowing on vegetation dynamics. To indicate restoration progress, we studied two groups of species: sandy grassland species as target for restoration and neophyte species that threaten the success of restoration by invasion. Seeding of short-term stored seeds of native species resulted in a vegetation change towards the reference grassland from the fifth year on. The relative cover of target species reached 90%, mainly due to the sown species, while non-target and neophyte species decreased in seeded plots. Most differences between seed storage treatments disappeared over time for both target and neophyte species. Seeding years with favorable weather conditions had a positive long-term effect on target species, and year-specific conditions influenced the invasion dynamics. Our results suggest that seeding with

fresh seeds is more efficient in enhancing species richness in the short-term, but that both fresh and stored seeds are equally effective in the long term. Restoration progress was more influenced by the year of seeding than by seed storage for both target and neophyte species, which highlights the need for continued monitoring and adaptive management to meet year-specific challenges. We conclude that the use of short-term stored seeds can mitigate weak seed yields or weak establishment due to climatic effects. Multi-year, scheduled seeding is recommended to minimize the risk of negative weather impacts on grassland restoration and seeds can be stored for this purpose in the short term.

Modelling habitat suitability and connectivity for grey wolves, wild goats and goitered gazelles in the central Iranian plateau

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Keywords: habitat suitability, landscape connectivity, ungulates, grey wolf, resistance kernel

Habitat fragmentation is a critical threat to biodiversity, particularly for wide-ranging species. This study models habitat suitability and connectivity for the goitered gazelle (*Gazella subgutturosa*), wild goat (*Capra aegagrus),* and grey wolf (*Canis lupus*) in Kolah Ghazi National Park, Iran, within the framework of an Environmental Impact Assessment (EIA) for the proposed eastern bypass road. Using species occurrence data, landscape variables, and a resistance-kernel approach (Landguth et al., 2012), we identified core habitats and potential movement corridors. Habitat suitability was predicted using the maximum entropy model (MaxEnt) (Phillips, 2005) in R v.4.1.0, and resistance surfaces were derived through a negative exponential function (Wan et al., 2019). Connectivity was assessed using cumulative resistant kernels.

Results highlight key habitat patches (Figure 1) and connectivity pathways (Figure 2), revealing critical areas for conservation. Wolves showed the highest dispersal potential, while gazelles exhibited more fragmented habitat use. Identified corridors align with ecological processes but face threats from degradation and road expansion. Similar studies have shown the significant impact of infrastructure on wildlife connectivity, emphasizing the importance of preserving ecological corridors. These findings highlight the importance of maintaining ecological corridors and mitigating the impact of infrastructure development on wildlife habitats. Future conservation efforts should focus on protecting these critical areas to ensure the long-term viability of these species in the region.

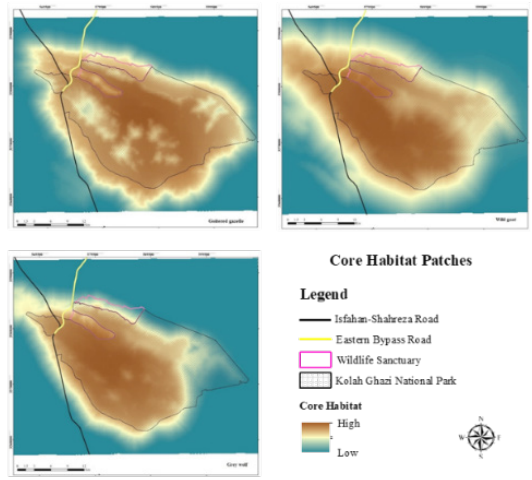

Figure 1 Core habitat patches for wild goat, goitered gazelle, and grey wolf at two levels of dispersal ability (70 and 100 km), along with CAs and roads.

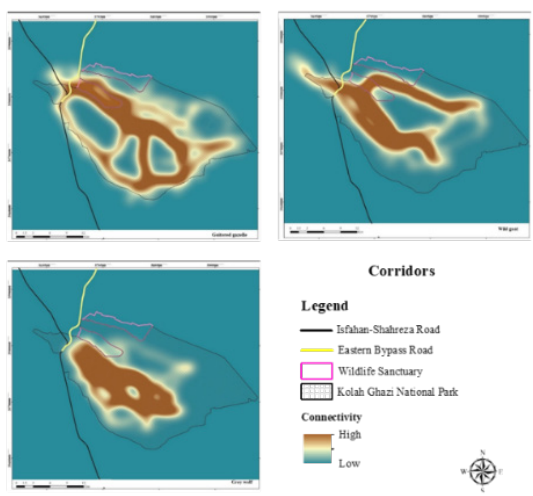

Figure 2 Corridors for goitered gazelle, wild goat, and grey wolf in the central Iranian plateau, estimated with a dispersal ability of 70 and 50 km. The connectivity strength of the corridors is visually depicted, ranging from weak (yellow) to strong (brown).

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T07: Statistical ecology

A probabilistic sampling strategy for estimating plant density in *Posidonia Oceanica* meadows

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Keywords: design-based inference, spatial maps, pseudo-population bootstrap, simulation study

Marine and coastal ecosystems, such as seagrasses, mangroves, and coral reefs, provide essential provisioning, regulating and cultural ecosystem services. Recent United Nations guidelines on ecosystem accounting emphasise the importance of biophysical data in developing effective policies and interventions. However, compared to terrestrial ecosystems, data on marine ecosystems are limited.

In this context, the paper proposes a methodology for collecting and analysing biophysical data on the habitat of *Posidonia oceanica* (L.) Delile, an endemic seagrass of the Mediterranean Sea often used as an indicator of the overall ecological status of the marine ecosystem (Bellissimo et al. 2020). We propose the application of design-based inference for estimating, mapping, and monitoring key ecological attributes of *P. oceanica* habitat. The main advantage of design-based inference is its objectivity, as the precision of the estimators stems from the adopted sampling scheme, rather than relying on model assumptions (Särndal et al. 1992). Specifically, this methodology aims to: (i) be statistically robust, ensuring reliable estimates as well as associated measures of uncertainty and (ii) be readily scalable and adaptable to different ecosystems and habitats. This strategy allows for the collection and analysis of biophysical data which are compliant with the new United Nations guidelines and current monitoring directives.

The methodology is empirically evaluated through an extensive simulation study in which two different sampling schemes (uniform random sampling and tessellation stratified sampling) and two interpolation methods (nearest neighbour and inverse distance weighting) are exploited for estimating, mapping and monitoring *P. oceanica* density in four artificially generated populations. The populations have different spatial patterns, but a fixed density of $D = 250$ shoots/m^2 derived from the ISPRA monitoring protocol (www.isprambiente.gov.it). Simulation results show that reliable estimates of density as well as their precision can be obtained even with low sample sizes.

Finally, our proposal is applied to a meadow located in an Italian Marine Protected Area in Apulia (Southern Italy).

Acknowledgments
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A Monte Carlo procedure for the estimation of species coverage in dunes

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Keywords: strip sampling, spatially balanced sampling, design-based inference

Coastal sand dunes are among the most fragile ecosystems in the Mediterranean basin. These habitats naturally face several limiting factors, including sand burial, marine aerosols, and low soil fertility (Tordoni et al. 2018). Additionally, they have experienced significant biodiversity loss (Dolan and Walker 2006), primarily due to increasing human pressure over recent decades. Despite these challenges, coastal dunes often support species of high conservation value. Monitoring their health requires accurate species coverage assessments, making reliable statistical estimation methods essential.

For this purpose, aiming to avoid potentially unrealistic assumptions about the community under study, a design-based inferential approach is considered. In this framework, the study area is viewed as a continuum of locations, with the value of a survey variable indicating species presence or absence considered fixed at each location. Uncertainty arises solely from the selection of sampling locations where the variable is observed and therefore the choice of the sampling scheme for placing sample sites plays a crucial role in ensuring reliable inference.

Sampling sites can be selected by randomly choosing "strips", which are then divided into plots where species occurrence and percentage cover are quantified. Due to the presence of spatial autocorrelation and heterogeneity, it is crucial to employ sampling schemes that ensure sample strips are evenly distributed across the study area. Moreover, since species coverage can be effectively represented as an integral, it can be unbiasedly estimated using a Monte Carlo estimator (Gregoire and Valentine 2007).

The results of a simulation study comparing various spatially balanced sampling schemes for strip placement and a case study are presented.

Acknowledgments
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Visualizing earth's pulse: ridgeline plots for satellite data analysis

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Keywords: ecological informatics, remote sensing, spatial data visualization

Ridgeline plots, also known as joy plots, are an effective and visually compelling method for comparing the distributions of a continuous variable across multiple categories. Traditionally implemented using vector-based data in structured formats such as dataframes, these plots have gained popularity in data science and statistics for their ability to reveal patterns, trends, and overlaps in complex datasets. However, the application of ridgeline plots to raster data - commonly used in spatial analysis and ecology - has remained limited due to the lack of suitable tools. In this study, we introduce a novel function within the imageRy R package that extends the utility of ridgeline plots to raster data (Figure 1). This function enables users to generate ridgeline plots from multiple raster layers, facilitating intuitive comparison of spatial distributions in grid-based datasets. By adapting kernel density estimation techniques to work with raster matrices, our approach bridges a methodological gap in geospatial data visualization. This advancement provides researchers and analysts with a new, accessible tool for exploring and interpreting spatial variation in fields such as remote sensing, environmental monitoring, and geospatial studies.

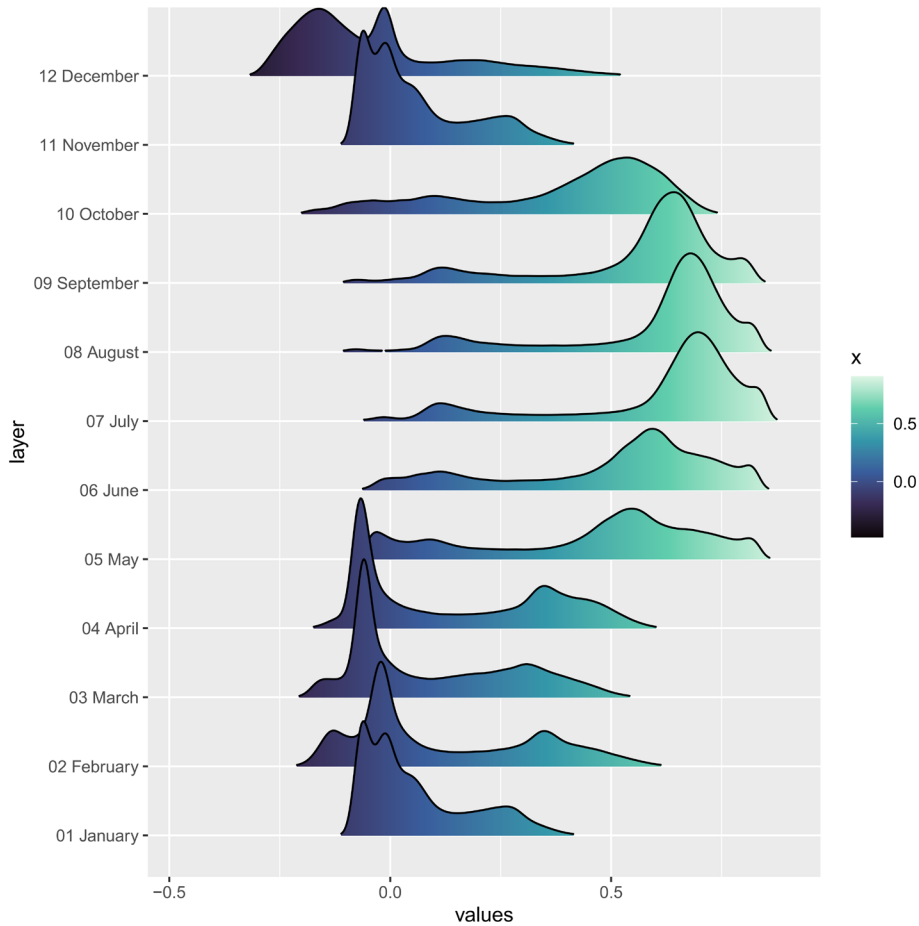

Figure 1: An example of a ridgeline plot showing the variability of biomass (NDVI values in the x axis) in the Brenta Mountain (Northern Italy) over different months.

Modeling freshwater phytoplankton phenology: a Bayesian approach linking long-term dynamics and the PEG model

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Keywords: algae, seasonality, Lorentz-Cauchy, climate change, trophic state

Phenology, the study of periodic biological events and their relationship to the environment, is crucial for understanding changes in complex living systems, such as planktonic communities. The Plankton Ecology Group (PEG) model qualitatively describes seasonal phytoplankton dynamics, but a quantitative representation of its ecological statements remains challenging due to the nonlinear nature of phenological patterns. In this study, we developed a non-linear model to describe the phenology of phytoplankton in Lake Constance, Germany. Lake Constance is a large, deep peri-alpine lake that has undergone warming and oligotrophication during the last decades and also faced biological invasions in recent years. By using a comprehensive time series of biweekly data on phytoplankton biovolumes from 1966 to 2020, we applied a Bayesian approach to fit our model parameters. The model effectively captures up to three phenological peaks during the year, corresponding mostly to spring, summer and autumn blooms, respectively. We linked model parameters to temporal trends and environmental variables such as phosphorus concentration and temperature, allowing us to identify significant phenological changes aligned with the PEG model predictions. Moreover, by using the posterior distributions of model parameters, we identified clusters of years with similar phenological shapes. Our findings offer a robust quantitative validation and refinement of the PEG model, enhancing its value for predicting phytoplankton responses to environmental change.

T08: Resilience, stability and health of ecological communities

Disentangling landscape degradation impacts on metacommunity diversity patterns by coupling 60-year pond network communities with an in-silico modelling approach

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Habitat fragmentation is one of the major drivers of current diversity crisis, its consequences involve the loss of the number of habitats as well as the change in regional connectivity patterns. The consequences of this major threat have been studied both theoretically (i.e., in silico models) and empirically (i.e., observational studies). As fragmentation progresses, local and regional conditions are altered reshaping main metacommunity drivers such as dispersal but also abiotic features linked to the decrease in habitat size or environmental changes (e.g. conductivity). Overall, landscapes fragmentation through time generates a progressive rearrangement in metacommunity assembly. While these dynamics have been reported, we are still far from fully comprehending the way in which landscape degradation drives metacommunity re-assembly through time. On one hand, the lack of observational datasets spanning periods long enough to capture both fragmentation and metacommunity changes prevents a deeper understanding of empirical trends. On the other hand, in-silico approaches often require specific information that is not available for most groups of species (e.g. survival, extinction, reproduction rates). In this work we aim to bridge these two perspectives. First, analysing a dataset spanning a 60-year period and reporting the degradation of a pond network and its associated zooplankton metacommunity. Second, comparing the observed trends with the outputs from a coalescent and neutral in-silico metacommunity model. We used this model to simulate expected diversity in response to some or all the reported changes at local (i.e. habitat reduction and conductivity increase) and/or regional (i.e. habitat loss and network fragmentation) scales. For each of these simulation scenarios we obtained diversity patterns that we compared against observed alpha, beta and gamma diversities. This exercise indicated that alpha, beta and gamma diversities did not fit equally to the same scenarios. For example, alpha diversity was better predicted when considering both changes in fragmentation and in habitat size while gamma diversity was better predicted when considering only change in habitat size. This mismatch highlights the differential role that landscape fragmentation and habitat loss play in defining diversity at local and regional scales. However, it also shows that the combination of observational and simulation approaches can provide key insights to disentangle these patterns. The current work paves the way to couple these different perspectives by benefiting from a unique dataset and combining it with digital tools. Such approaches may hold the key to overcome current halts in aquatic systems conservation.

Compositional dynamics of fungal communities along environmental and disturbance gradients

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Keywords: biodiversity, DNA metabarcoding, forest ecology, forestry, fungal ecology

Soil microbial communities represent the greatest reservoir of biological diversity, with thousands of microbial species found a single gram of soil. Soil and plant-associated fungi (e.g., root symbionts, decomposers, mutualistic endophytes, and pathogens) have key roles in nutrient cycling and water and nutrient acquisition by plants, and they shape plant resistance and resilience to biotic and abiotic stresses.

We carried out ITS rDNA metabarcoding of forest fungi to characterize fungal community composition in different forest types along environmental gradients and along disturbance gradient represented by various silvicultural practices. For the first projeck, we sampled soil at 62 sites in the Bükk Mountains in northern Hungary. The selected sampling sites represent the characteristic Pannonian forest types distributed along elevation (i.e., temperature), soil pH and slope aspect gradients. We compared richness and community composition of various functional and taxonomic groups of fungi among forest types and explored relationships among environmental variables and fungal alpha and beta diversity. The data generated in this study indicated strong correlations between fungal community composition and environmental variables in all studied functional groups, particularly with pH, soil moisture, and temperature, influenced by both elevation and slope aspect. Many fungi showed preference for specific zonal, topographic or edaphic forest types. Species richness in several fungal genera showed significant correlations with climatic and edaphic factors, often highlighting contrasting trends among genera.

In the second project, we sampled soil in all 30 plots of the Pilis Forestry Systems Experiment, operated by the Centre for Ecological Research and the Pilis Park Forestry Company. Treatments, established in the winter of 2015–2016, included clear-cutting, gap-cutting (20 m in diameter), preparation-cutting (30% thinning), tree retention group (20 m in diameter) in clear-cut areas, and control. Fungal communities in all functional groups exhibited moderate to strong compositional turnover among silvicultural treatments. In most cases, compositional changes were proportional to the severity of disturbance, e.g., clear-cutting, and to a lesser extent gap-cutting, resulted in the highest species turnover compared to the control, while preparation-cutting and retention tree group only differed slightly from the control. We observed relationships with fungal community turnover and changes in abiotic variables, such as air temperature relative humidity, and soil moisture, suggesting that some effects of the silvicultural practices on fungal communities are mediated through microclimate.

Overall, compositional turnover in fungal communities is driven by niche-based environmental filtering due to contrasting habitat preferences among fungal species in all functional and taxonomic groups. The compositional and functional turnover along environmental and disturbance gradients implies that many soil fungi are sensitive to environmental changes, including climate change and disturbance, and are well-suited for monitoring purposes as indicators of environmental conditions.

Acknowledgments
The forest microbiome project is funded by Hungarian National Research, Development and Innovation Office (OTKA K 139387, PI J Geml). The Pilis Forestry Systems Experiment was funded by Interreg VI-A Hungary-Slovakia Programme (HUSK/2302/1.2/168) and the Hungarian Academy of Sciences, Sustainable Development and Technologies National Programme. The authors thank the Bükk National Park Directorate and the Pilis Park Forestry Company for their continued logistical support and collaboration.

Assessment of bioaccumulation processes in ichthyofauna of industrially polluted waters of small rivers of East Kazakhstan on the example of Ridder c.

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Keywords: small rivers, ichthyfauna (fish), bioaccumulation, heavy metals, industrial water pollution, ICP-MS, ICP-AES

Small rivers represent the most vulnerable components of the hydrographic network. They remain among the least studied in hydrological and hydrobiological contexts. These rivers serve as the uppermost elements of extensive landscape systems and are predominantly influenced by the detrimental effects of anthropogenic activities.

In the city of Ridder, located in East Kazakhstan, industrial sites associated with mining enterprises are present, along with tailings, sludge, and ore and overburden dumps. The proximity of these pollution sources to rivers results in the accumulation and deposition of contaminants, particularly heavy metals, which contribute to the poisoning and eventual death of aquatic ecosystems [1,2]. There have been documented instances of emergency discharges of industrial effluent into the small rivers of Ridder from major mining companies operating in the region.

Heavy metals are redistributed across the various components of the aquatic ecosystem, accumulating in hydrobionts at different trophic levels, including fish [3]. The capacity of toxic substances to circulate through trophic chains presents a significant risk to humans who consume hydrobionts from contaminated water bodies [4].

This study presents an evaluation of the bioaccumulation processes of heavy metals and toxic elements in the dominant fish species (*Carassius carassius, Phoxinus phoxinus, Perca fluviatilis*) within the hydrographic network (rivers Filippovka, Tihaya, Zhyravliha, Ulba) of the industrial city of Ridder during the period of 2023-2024. Laboratory analyses were conducted using ICP-MS and ICP-AES techniques. A comparative assessment was made with state regulations and international standards for food products. The findings revealed elevated concentrations of Cd, Pb, and Mn in the raw weight of the fish, with Mn levels exceeding WHO standards by up to 20 times. Accumulation coefficients for pollutants in the "water-bottom sediments-fish" system were also calculated.

The results of this research provide valuable insights into the efficiency of bioaccumulation processes in the ichthyofauna of small rivers affected by industrial pollution. This assessment is crucial for the ongoing monitoring of these processes and their potential impact on the health of the local population.

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Eco-evolutionary hotspots in a heterogeneous landscape – an experimental test in saline ponds

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Keywords: eco-evolutionary dynamics, local adaptation, zooplankton, salinity, ponds

There is rapidly increasing evidence that evolution can act at small temporal and spatial scales with important implications for ecological dynamics. Yet, most studies on eco-evolutionary dynamics use simplified experimental settings and our understanding on its relevance in natural ecosystems remains limited. Here we tested whether local adaptation of the cladoceran *Daphnia magna* to a salinity gradient influences population dynamics, top-down control of algae, and resistance to species immigration in a dense network of sodic bomb crater ponds. We carried out a full-factorial *in situ* transplant experiment involving common-garden grown clones isolated from five ponds exhibiting a salinity gradient. We show that local genetic adaptation in the high-salinity pond increased *D. magna* population densities, top-down control of phytoplankton, and resistance to the establishment of other cladoceran species. At the same time, it does not influence these endpoints in low-salinity ponds. Our study shows that eco-evolutionary feedback can differentially affect dynamics across habitats along environmental gradients, being more important in habitats that offer extreme conditions.

T09: Ecosystem services

Predation pressure does not necessarily diminish with advancing urbanisation

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Keywords: artificial caterpillars, predation, sentinel prey, urban forests

We studied predation pressure over a full season (from April to November) in rural vs. urban forests using the sentinel approach in and near the city of Debrecen, eastern HungaryModel caterpillars made of non-drying green plasticine were readily attacked by arthropods, birds and mammals. From attack marks left by potential predators, a high predation pressure was documented: up to 40% of the caterpillars exposed for 24 h showed attack marks. Seasonal differences were also obvious, with predation pressure during summer being significantly higher than in spring or autumn (Table 1). This trend held for overall attack rates, also for attacks by arthropods and mammals but not birds. Surprisingly, attack rates were higher in urban than rural habitats in nearly all situations, contradicting previous results. As attack rates depend on both predator abundance and activity, and general data indicate lower predator abundances in urban habitats, this phenomenon may have been caused by hungrier predators in urban forest fragments or by the predator relaxation/safe habitat hypothesis that argues that a reduced need for vigilance allows more time to search for prey.

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Table 1. Seasonal attack rates on artificial caterpillars in rural and urban forests by the main types of predators near the city of Debrecen, Hungary. Numbers are means, s.d. values are in parentheses.

Season	Habitat	Attack rates (% d^{-1}) by				Sample size[§]
		All predators	Arthropods	Birds	Mammals	
Spring	rural	8.75 (5.8)	5.63 (4.2)	2.50 (3.8)	0.63 (1.8)	8
	urban	10.76 (8.8.)	8.82 (5.8)	0.63 (1.8)	3.82 (5.9)	8
Summer	rural	24.76 (11.2)	13.46 (8.6)	2.94 (3.4)	9.19 (12.6)	12
	urban	36.44 (21.8)	25.31 (21.9)	2.54 (3.4)	11.13 (11.0)	12
Autumn	rural	7.76 (7.9)	3.26 (5.6)	2.60 (4.0)	1.91 (3.8)	8
	urban	20.03 (11.3)	13.13 (11.6)	1.25 (2.3)	5.66 (6.2)	8

[§]sample size equals the number of monthly sessions x habitat patches

Seagrass meadows and methane fluxes: assessing their role in coastal climate regulation and ecosystem services

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Keywords: methane emissions, seagrass meadows, greenhouse gas emissions, targeted metagenomics, microbial functional groups, coastal restoration, climate regulation service

Coastal sediments are dynamic interfaces where abiotic and biotic factors jointly regulate greenhouse gas fluxes, particularly methane (CH_4). This study, conducted in Arcachon Bay, France, the largest Zostera noltei seagrass meadow in Europe, aims to investigate how sediment physicochemical properties and microbial community composition influence CH_4 dynamics. Specifically, we applied a targeted metagenomic approach focusing on methane-cycling functional genes to compare microbial communities between Zostera noltei meadows and adjacent unvegetated areas. Our objective is to gain a deeper understanding of the role of seagrass meadows in CH_4 emissions and their potential implications for coastal restoration strategies. Key sediment parameters, such as texture, organic matter content, were quantified as well as the diversity and abundance of microorganisms involved in methanogenesis and methanotrophy, using specific genetic markers. Our preliminary results indicate that sediments with Zostera meadows have higher CH_4 fluxes compared to unvegetated areas. These findings suggest that the presence of seagrasses may influence CH_4 emissions and highlight the need for further investigation into the underlying mechanisms, while also for assessing the actual benefits of these seagrass meadows. Understanding the complex interplay between sediment abiotic properties and microbial processes is crucial for developing effective coastal restoration practices. Our study provides a valuable framework for optimizing ecosystem services in coastal environments, balancing biodiversity conservation with climate regulation objectives.

Valuing ecosystem services by system dynamics simulation analysis in Essaouira, Moroccan Atlantic Coast

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Keywords: ecosystem services, system dynamics, payments for ecosystem services, sustainable development, Moroccan Atlantic Coast

Coastal and marine ecosystem services are critical for the socio-economic resilience and ecological integrity of coastal communities [1] like Essaouira, Morocco. But climate change, and unsustainable exploitation are putting these ecosystems at greater risk.

The potential of simulating the complex feedback mechanisms affecting ecological health, economic development, and policy responses using a system dynamics (SD) modeling approach [2] is investigated in this work. We evaluate the long-term sustainability effects of various policy scenarios by using a dynamic simulation model that incorporates a Payments for Ecosystem Services (PES) framework [4]. The model illustrates essential interconnections between tourism, fisheries, marine biodiversity, local livelihoods, and conservation incentives. However, case studies in many developing countries demonstrate that well-designed PES schemes embedded in adaptive governance systems can reverse ecosystem degradation, provide income stability, and contribute to sustainable development [3]. This study contributes a novel methodology for the management of data-poor environments [5] in addition to facilitating evidence-based policy formulation for coastal zones in Morocco.

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Poster Presentations

T01 Biodiversity and ecosystem functioning

Community composition of pathogenic fungi associated with forest plants differ among hosts and are influenced by silvicultural practices

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Keywords: biodiversity, DNA metabarcoding, forest ecology, forestry, fungal ecology

The effects of different forest management approaches on vegetation have been extensively studied. However, little is known about how environmental variables influenced by forest management affect plant-associated fungal communities. As part of the long-term Pilis Forestry Systems Experiment in northern Hungary, we generated and analyzed DNA metabarcoding data from leaves of three plant species that are common throughout the study area and represent different growth forms as well as three major phylogenetic clades of plants: a bark-dwelling bryophyte (*Hypnum cupressiforme*), an understory monocot sedge (*Carex pilosa*), and a woody dicot (*Quercus petraea*). Our goal was to characterize plant pathogenic fungal communities found in the leaves the above-mentioned plant species and to compare their responses to forestry treatments. We sampled six replicate plots of clear-cutting (CC), gap-cutting (G), preparation cutting (P), retention tree group (R), and control (C). DNA sequences were identified and assigned to functional categories using the UNITE and FungalTraits databases, respectively. We found 810 plant pathogenic fungal genotypes, of which 261 occurred in mosses, 551 in sedges, and 410 in oak leaves. We observed compositional differences of plant pathogenic fungi among the plant species, particularly between the moss and the vascular plants. Several fungal genera preferred a specific host and we identified several indicator species for each host. Treatments accounted for 21.55% of fungal compositional variance in mosses, 42.98% in sedges and 34.75% in oak leaves. Compositional changes appeared to be proportional to the disturbance severity, with clear-cutting resulting in the greatest turnover of fungal species. Changes in plant pathogenic fungal communities correlated significantly with relative humidity, temperature measured at soil surface and at heights of 15 cm and 130 cm, and with vapor pressure decifit, indicating that a substantial effect of treatments on leaf

fungal communities are mediated through changes in microclimate. The observed compositional dynamics in leaf-associated fungal communities provide valuable insights into how different forest management activities shape plant pathogenic fungal communities in forests, with possible implications for forest health.

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The diversity of soil hydrobionts (Nematoda) in the riparian forests invaded by ash-leaved maple (*Acer negundo*)

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Keywords: diversity, nematoda, indicators, riparian forests, ash-leaved maple, alder, ash

Invasive plants can significantly alter the composition and functioning of soil ecosystems, which in turn affects soil fauna such as microorganisms, mesofauna, insects, and other invertebrates. We used clusters of three different tree species to investigate how affect the composition of belowground soil nematode communities. The clusters of tree species included *Acer negundo* (invasive, no-native taxa), *Fraxinus excelsior* and *Alnus glutinosa* (as native representatives) in Morava River floodplain forest habitats. We investigated the families, genera, trophic groups and functional guilds of soil nematodes in each tree cluster to assess nematode usefulness as indicators of impact of alien tree species on native communities. The study was complemented by measuring basic soil physico-chemical properties. The data have shown, that nematode communities were not sensitive to *A. negundo* invasion, when the clusters of ash-leaved maple having similar nematode abundance, generic richness, generic diversity, family and genera composition as well as trophic structure as species specific clusters of two native trees. A cumulative total of 96 nematode genera, belonging to 52 nematode families were recorded in the investigated floodplain forest sites. The most abundant families were Alaimidae, Cephalobidae, Hoplolaimidae and Rhabditidae for all tree clusters. Among genera, *Helicotylenchus, Pratylenchus, Paratylenchus, Filenchus* and *Malenchus* (as plant parasites), and *Acrobeloides, Eucephalobus, Plectus* and *Rhabditis* (as bacterivores) were most abundant taxa. The measured soil properties did not differ significantly among the tree species ($p < 0.05$). Nevertheless, redundancy analysis identified a significant negative correlation between soil moisture content and abundance of several nematode genera, nematode trophic groups and functional guilds. The results indicated, that presence of invasive ash-leaved maple trees in the studied floodplain forests has not negative influence on the diversity and functional structure of soil nematode. Due the absence of nematological studies from *A. negundo* invaded habitats, however, definite close our finding is impossible, but further studies may answer this.

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The role of traditional cattle crazing in the maintenance of diversely restored Grasslands

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Keywords: biogeographic, pannonian, pasture, phytosociologic, treatments

In our study, we analyzed the impact of grazing by the Hungarian Grey cattle, a traditional local breed, on the vegetation composition of grasslands restored and established through different methods. The primary objective of our research was to assess the botanical composition and pasture management value of the examined sites. The study was conducted in a 260-hectare sample area located in the Pannonian biogeographical region, which was subdivided into smaller experimental plots. Grassland establishment and various restoration treatments were implemented in 2009. Five different restoration treatments were applied: spontaneous succession on abandoned land, hay-transfer-based grassland establishment, seed mixture sowing after soil preparation, grazing of an abandoned alfalfa field, and a site overseeded in 1989 and subsequently left fallow. The sample sites were uniformly mown until 2011, after which they were subjected to free-range grazing by Hungarian Grey cattle from 2012 onward. The objective of this grazing system was to restore the original land-use practice of grazing on dry grasslands. Phytosociological surveys were conducted in the first year after grazing was introduced (2011) and again after eight years (2020) to investigate the long-term effects of different grassland restoration techniques on botanical composition and pasture management value, as well as to identify the most effective restoration methods. Our results indicate that the most successful restoration methods, based on the 2020 sampling data, were hay transfer and the treatment of the site that had been overseeded in 1989 and subsequently left fallow. In contrast, the directly sown and overseeded fallow grasslands exhibited the most pronounced differences compared to the other grassland types. After eight years of cattle grazing, all treated areas showed an increase in species richness and total cover, while changes in species composition reflected an improvement in naturalness. Overall, the reintroduction of the traditional land-use practice had a beneficial effect on grassland conditions. The grazing regime, following an initial two-year mowing period, optimized the restoration process. Grazing by Hungarian Grey cattle, a local breed known for its gentle foraging behavior, proved to be an effective tool for grassland restoration, contributing significantly to favorable ecological outcomes. This research was funded by OTKA K-147342 and the Strategic Research Fund of the University of Veterinary Medicine Budapest (Grant No. SRF-002).

T02: Patterns of species richness and diversity

Spatio-temporal phytoplankton biodiversity along the Italian peninsula

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Keywords: phytoplankton, biodiversity, spatial patterns

Phytoplankton are fundamental to marine ecosystem dynamics, as they respond directly to abiotic factors and serve as key indicators of environmental changes. Their populations exhibit cyclic inter-annual variability and are subject to dispersal, potentially fostering metacommunity formation. We explored, for the first time, the spatial and seasonal biodiversity of phytoplankton communities along the Italian coast. Using microscopy-based count data from monthly samples collected at 162 sites between 2015 and 2017, We applied univariate and multivariate statistical methods from numerical ecology to examine community composition and its relationship with environmental factors. The first important result is that phytoplankton abundances varied across the peninsula by several orders of magnitude, likely driven by river runoff and differing responses to nutrient availability. Diatoms and dinoflagellates dominated nearly all regions and seasons, and clustering analyses identified nine distinct zones, each characterized by unique seasonal dynamics and dominant species. Multivariate regression analyses highlighted the role of nutrient availability in shaping communities, though much of the variability remains unexplained, suggesting the influence of additional drivers. This large-scale study provides novel insights into biodiversity patterns and their environmental determinants in Italian coastal waters.

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Buzzing around town: exploring insect pollinator diversity across urban habitat types

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Keywords: transect survey, wild bees, hoverflies, pollinator diversity, urban habitats

The conversion of natural habitats into urban landscapes has a significant effect on pollinator populations, underscoring the importance of understanding how urban areas and habitats can support pollinator diversity in the face of challenges like habitat fragmentation and environmental stressors. This study examines species diversity within two insect pollinator groups (wild bees and hoverflies) across various urban habitat types. Field investigations were conducted in the spring and summer of 2024 in Novi Sad, Serbia. A total of 80 sites were surveyed across 10 landscapes, each with a 750-meter buffer for comprehensive city coverage, representing the primary green habitat types in the city: abandoned areas, parks, gardens, road margins, and field margins. Each site was sampled four times during the study, using 20-meter transect walks. Pollinator abundance and species richness were assessed using standardized sampling methods, and diversity indices were calculated to compare habitat types. In total, we recorded 844 individual wild bees representing 103 species, as well as 929 hoverflies across 25 species. A Kruskal-Wallis test revealed no statistically significant differences in species diversity between habitat types ($p = 0.406$), suggesting that urban habitats may provide variable but complementary resources for different pollinators. Despite the lack of statistically significant differences, variations in species richness suggest that parks and gardens support fewer pollinator species, likely due to management practices that simplify habitat structure and limit resource availability. In contrast, abandoned areas within urban landscapes have emerged as important refuges for pollinators, providing diverse floral resources and nesting sites that promote higher visitation rates.

Variations in species composition highlight the need for targeted conservation efforts to enhance pollinator-friendly urban planning. Our findings underscore the importance of maintaining diverse habitat types within urban landscapes to support pollinator biodiversity.

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T04: Effects of global change

Urban edge effect on reptile assemblages and diversity along the Mediterranean coastal dunes in Israel

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Keywords: coastal dunes, urban edge, reptiles, Mediterranean

Coastal areas are considered to be the places that have the most significant impact when it comes to changes in the physical environment and the living environment of plants and animals (Kutiel 2001).

The study examines the effect of the cities' edges on reptile assemblages and diversity along the Mediterranean coastal dunes in Israel, from the dunes of Caesarea in the north to the dunes of Zikim in the south.

There are currently 97 species of reptiles known in Israel, of which 37 are terrestrial reptiles that live along the coastal dunes.

A limited number of studies have been done on the subject, and not a single one on coastal dunes. These studies showed that reptiles are adversely affected by recreation impacts, direct vehicular mortality along roads and trails, predation, competition with generalist species and domestic animals, artificial light at night, and being targets of unsustainable collection (Larson et al. 2024).

Four sites were selected along the coastal dunes in Israel. At each site, nine fixed plots (50×50 m each) categorized into three habitat or "location types" according to dune type and proximity to settlements (Shifting Far, Semi-Fixed Far, and Semi-Fixed Near) were sampled during summers (August-September) of the years 2015, 2017, 2019, 2021, and 2023. Since different reptile species differ in size, behavior, and detectability using any single method, we used three sampling methods at all the study sites and plots: pitfall trapping, track trail, and visual scan. The individuals, tracks, and sighting counts were combined into an "activity rank" ranging between 0 and 5.

The results indicate that the proximity of the coastal dunes to the cities affects the reptile assemblages (Fig. 1), followed by an overall species abundance decrease, especially the psammophilic species, apparently due to the lack of shifting dunes near the settlements, i.e., habitat loss and habitat degradation.

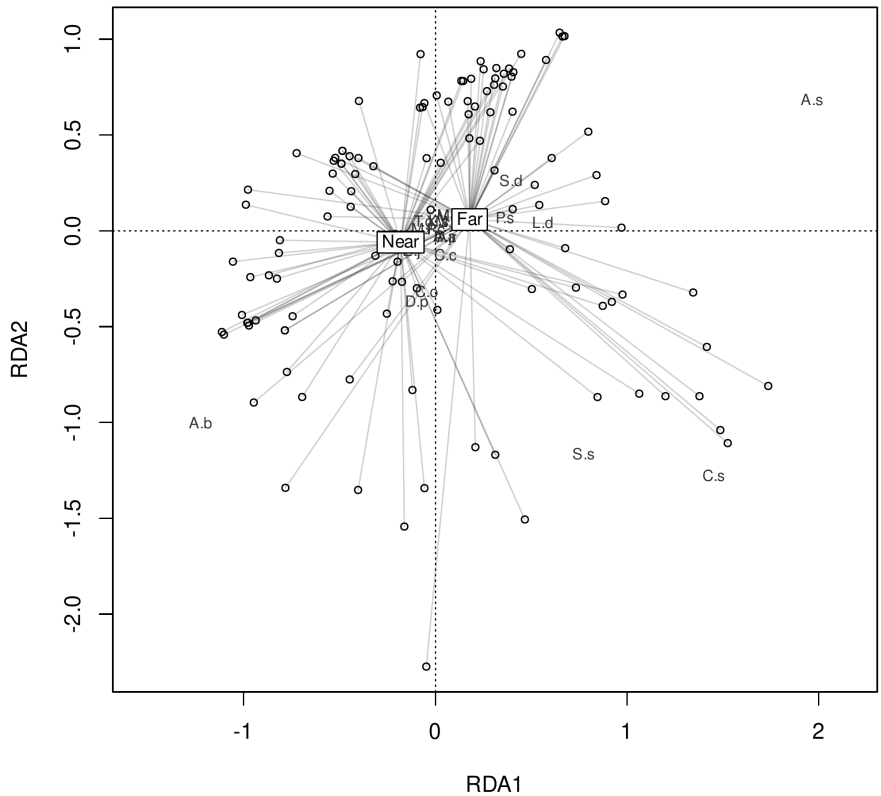

Figure 1 – Site scores on axes 1 and 2, using Redundancy Analysis (RDA) constrained by year, site (Zikim, Ashkelon, Ashdod, and Caesarea), and type of proximity to settlements (Near and Far), for samples taken in Semi-Fixed dunes only. Text labels mark the centroid of samples belonging to each type of proximity to settlements.

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T05: Conservation biology

Long-term effect of forestry skid trails on the abiotic conditions and understory vegetation of a beech forest

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Keywords: skid trail, light, soil moisture, understory species richness, cover, composition

There is a growing demand for multifunctional forests that, besides timber production, provide a variety of ecosystem services (preserving biodiversity, buffering of climate extremes, meeting recreational needs). Continuous cover forestry (CCF) is a good alternative to conventional rotation forestry systems to achieve these goals. It uses small-scale gap-cuttings instead of clearcutting, keeping the continuity of forest habitat. A major criticism of CCF, however, is that it requires a dense network of skid trails (small, unpaved forestry roads) to reach each trees in the stand marked for felling and to protect the soil and regeneration layer during harvesting. The return period of the interventions is 5–8 years, so the trails are only used with this frequency. Yet, it is unclear whether the trails have harmful effects on the understory via mechanical disturbance, soil compaction, introduction of (potentially invasive) weeds, and increased light. We aimed to explore the long-term effect of skid trails on light conditions, soil moisture and understory vegetation through a chronosequential study.

The research was carried out in the framework of the Skid Trail Project (STRIPE), and was located at Pilis-tető (Pilis Mountains, Hungary), in 81–141 year old beech stands managed by CCF for different (5–27) years. Five skid trails were selected from each of four age classes (A1-A4): 5, 10–12, 15–22 and 27 years, they were used over 1, 2, 3 or 4 return periods, respectively. As a dense regeneration layer forms on the trails over the years, the saplings were cut after the third return period, reopening the trails of the fourth age class. On each trail, 12 quadrats were sampled in three positions (centreline, rut, edge) and 4 control quadrats were sampled in the forest interior besides each trail.

In the first age class, light on the centreline and ruts of the trails increased compared to the control, resulting in an increase in understory cover and species richness. Later (age classes A2, A3) a dense regeneration layer formed on the trails, and in parallel, light, cover and species richness decreased. After the harvesting of this shrub layer (A4), light, cover and species richness increased again. Soil moisture initially increased, and it remained elevated at the ruts, but decreased to control levels in the centrelines, even after the re-opening of the trails. According to the ordination analysis, species composition of the positions showed a nested arrangement: the control was nested with the edges and both with the rut and centreline quadrats. Composition of closed age classes (A2, A3) was nested to those of the open age classes (A1, A4). Vegetation was mainly composed of non-disturbance-tolerant forest species, even

on the trails, in all age classes. Besides, on the A1 trails, disturbance-tolerant forest and non-forest species occurred temporarily, while on 27-year-old trails, mainly disturbance-tolerant forest species increased. Freshly cut age classes (A1, A4) consisted a large amount of graminoids. Invasive species occurred only sporadically. The edges were transitional between the trail and control positions for most variables, showing significant differences from the control mainly after 27 years. We can conclude that in old beech stands, in the case of careful management, 4 m wide unpaved skid trails slightly increase the diversity of the vegetation, but do not alter drastically its forest character in the long term. Even the most altered conditions that have been experienced (in centrelines of old trails) are similar to those found in natural forests after small-scale disturbances.

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